The *ivory* lncRNA regulates seasonal color patterns in buckeye butterflies

Richard A. Fandino[a1], Noah K. Brady[a], Martik Chatterjee[a], Jeanne M. C. McDonald[a], Luca Livraghi[b], Karin R. L. van der Burg[a,c], Anyi Mazo-Vargas[a,b], Eirene Markenscoff-Papadimitriou[d], and Robert D. Reed[a1]

[a]Department of Ecology and Evolutionary Biology, Cornell University; Ithaca, New York, United States of America.
[b]Department of Biological Sciences, The George Washington University; Washington D.C., United States of America.
[c]Department of Biological Sciences, Clemson University; Clemson, South Carolina, United States of America.
[d]Department of Molecular Biology and Genetics, Cornell University; Ithaca, New York, United States of America.

[1]To whom correspondence may be addressed: Richard A. Fandino, Robert D. Reed

Email: raf272@cornell.edu, robertreed@cornell.edu

Author Contributions: R.A.F. and R.D.R. designed research. R.A.F., N.K.B., M.C., J.M.C.M., L.L., K.R.L.vdB., and A.M.-Z collected and/or analyzed data. R.A.F. and R.D.R. wrote the manuscript. E.M.-P. and R.D.R. provided facilities, resources, and funding.

Competing Interest Statement: The authors declare no competing interest.

Classification: Biological Sciences: Evolution; Genetics; Developmental Biology

Keywords: Butterfly wing patterns, evo-devo, long non-coding RNA, cortex, plasticity

This PDF file includes:

Main Text
Figures 1 to 5
Supplemental Figure S1-S6
Supplemental Tables S1-S12

Abstract

Long non-coding RNAs (lncRNAs) are transcribed elements increasingly recognized for their roles in regulating gene expression. Thus far, however, we have little understanding of how lncRNAs contribute to evolution and adaptation. Here we show that a conserved lncRNA, *ivory*, is an important color patterning gene in the buckeye butterfly *Junonia coenia*. *ivory* overlaps with *cortex*, a locus linked to multiple cases of crypsis and mimicry in Lepidoptera. Along with a companion paper by Livraghi et. al, we argue that *ivory*, not *cortex*, is the color pattern gene of interest at this locus. In *J. coenia* a cluster of *cis*-regulatory elements (CREs) in the first intron of *ivory* are genetically associated with natural variation in seasonal color pattern plasticity, and targeted deletions of these CREs phenocopy seasonal phenotypes. Deletions of different *ivory* CREs produce other distinct phenotypes as well, including loss of melanic eyespot rings, and positive and negative changes in overall wing pigmentation. We show that the color pattern transcription factors Spineless, Bric-a-brac, and Ftz-f1 bind to the *ivory* promoter during wing pattern development, suggesting that they directly regulate *ivory*. This case study demonstrates how *cis*-regulation of a single non-coding RNA can exert diverse and nuanced effects on the evolution and development of color patterns, including modulating seasonally plastic color patterns.

Significance

The genomic locus hosting the *cortex* gene has been linked to numerous cases of color pattern adaptation in moths and butterflies, including crypsis, mimicry, and seasonal polyphenism. Here we show in buckeye butterflies that the actual color pattern gene at the *cortex* locus is an evolutionarily conserved long non-coding RNA (lncRNA), dubbed *ivory*, that overlaps with *cortex*. Compared with other wing pattern genes, *ivory* stands out because of the highly nuanced, quantitative changes in pigmentation that can be achieved by manipulating adjacent *cis*-regulatory sequences. This study highlights how lncRNAs can be important factors underlying morphological evolution, and emphasizes the importance of considering non-coding transcripts in comparative genomics.

Main Text

Introduction

Seasonal cycles are deeply ingrained in the genomes of many animals. Evolutionary adaptation to annual fluctuations in conditions such as daylength, temperature, and precipitation is often realized in the form of phenotypic plasticity, where trait expression is determined in response to external cues. While the physiological and endocrine mechanisms underlying plasticity have been well characterized in many systems, there are still relatively few case studies that highlight the genetic basis of plasticity in natural populations. Buckeye butterflies, *Junonia coenia*, have been a useful model in this regard. Across much of their range, these butterflies are polyphenic, and show distinct seasonal color patterns – in the summer they are a light tan color, while in the autumn they are dark red and thus absorb heat more efficiently (1). This polyphenism is mediated by seasonal changes in daylength and temperature, and natural genetic variation in this response has been mapped to three loci: *herfst*, *trehalase*, and *cortex* (2). Of these, the *cortex* locus is of particular interest because it has also been implicated in adaptive melanism in moths (3), leaf mimicry in *Kallima* (4), and color pattern mimicry in *Heliconius* (5, 6). It remains a question of fundamental interest how a single locus like this can control such a wide variety of adaptive variation between species, populations, and even seasons. Such multifunctionality is presumably driven by *cis*-regulatory innovation, but we still have a poor understanding of how adaptive changes, including plasticity, are distributed across *cis*-regulatory regions of individual genes. Genetic association mapping coupled with chromatin accessibility comparisons in *J. coenia* have linked several *cis*-regulatory elements (CREs) at the *cortex* locus to plasticity, which now motivates us to functionally characterize how adaptive color pattern variation is encoded at this locus (2).

While there has been significant interest in the *cortex* locus for the reasons described above, functional studies have, in fact, proven vexing. First, expression work looking at *cortex* mRNA and protein localization in developing butterfly wings has largely failed to show obvious associations with color patterns (5, 6). Second, mosaic deletion phenotypes occur at such low frequencies they could possibly be explained by spurious long deletions affecting adjacent genes or enhancers (7). And last, and most importantly, Cas9-induced germ line deletions in *cortex* show no phenotypes in F1 individuals (8). Remarkably, as we show below, and is also shown in a companion paper by Livraghi et al. (8), this all seems to be explained by the fact that *cortex* is not the color pattern gene we once thought it was – rather, the actual gene of interest is a long non-coding RNA (lncRNA), dubbed *ivory*, that partially overlaps with the *cortex* gene on the antisense strand. This is interesting because few lncRNAs have thus far been implicated in adaptation, even though lncRNAs are of major emerging interest in developmental biology due to their roles as chromatin and spatially restricted transcription regulators (9, 10).

The goals of this study, then, were threefold. First, we sought to provide functional validation of the *ivory* lncRNA as a color patterning gene in the buckeye butterfly *J. coenia*, with a focus on seasonally plastic wing pattern phenotypes (11, 12). Second, we aimed to characterize some of the *cis*-regulatory architecture of the *ivory* locus using both comparative and functional approaches. Last, using a deletion

line, we aimed to assess the effects of *ivory* on gene expression during wing development. We show that the *ivory* lncRNA is a fundamental regulator of wing pigmentation with a deeply conserved *cis*-regulatory region. Deletions at different regulatory regions of the *ivory* locus not only phenocopy seasonal color pattern phenotypes but can have broader positive and negative quantitative effects on pigmentation. This work, accompanied by Livraghi et al.'s comparative study (8), calls for a major revision of our models of butterfly wing pattern development, and more generally demands that researchers working on similar biological questions must be vigilant for non-coding RNA molecules that may not be properly annotated in current genome assemblies.

Results

The *ivory* lncRNA promoter is conserved in butterflies and is bound by color pattern factors

As described above, efforts to characterize the function of the *cortex* gene in wing pattern development have proven inconsistent. We thus sought to identify previously unrecognized features of the locus through a more careful annotation of transcribed elements and chromatin marks within the *cortex* topologically associated domain (TAD) (Fig. 1A). We generated long-read PacBio transcript sequences from a collection of tissues that included wings at different stages of development (Table S1). These data identified a lncRNA that partially overlaps with the 5' end of the *cortex* gene. The 3' region of this predicted lncRNA also overlaps with the previously described 78kb *ivory* mutation – a spontaneous deletion identified in *Heliconius melpomene* that produced largely unpigmented butterflies (13) – thus, this novel lncRNA is dubbed *ivory* after the original *Heliconius* mutation.

We next annotated the *ivory* region with RNA Polymerase II (Pol II) ChIP-seq data to identify potential transcription start sites (promoters) within the TAD (Fig. 1A). We identified a major Pol II binding site during pupal development, which occurred at the 5' end of the first exon of *ivory*. To identify CREs of potential interest, we generated and/or compiled pupal wing ChIP-seq data from several transcription factors implicated in pigment regulation (Table S3). We looked at previous ChIP-seq data for the wing pattern transcription factor Spineless (14), which produces similar wing depigmentation mutant phenotypes as *ivory* (15), and generated new ChIP-seq data for Fushi tarazu-F1 (Ftz-F1) and Bric-a-brac (Bab) (Fig. 1B), for which mutants have globally reduced or enhanced pigmentation, respectively (Fig. S1). All three transcription factors showed strong binding signals at the presumptive *ivory* promoter, as well at a handful of other apparent CREs within the TAD, as inferred from ATAC-seq data (Table S4) (Fig. 1). Spineless, in particular, showed a strong cluster of binding sites in the first intron of *ivory*, in an interval previously identified as showing nucleotide polymorphism associations with seasonal polyphenism in *J. coenia* (2). A broad comparison with ATAC-seq-annotated genomes of multiple nymphalid butterflies showed that the first exon of *ivory* is conserved across the family, along with many conserved CREs, as inferred from the chromatin accessibility profiles (Fig. 1B, Table S5). Together, these data demonstrate activity of the conserved *ivory* lncRNA promoter and transcript during pupal wing development, and that

ivory is directly bound by broad color pattern transcription factors Spineless, Ftz-F1, and Bric-a-brac, including Spineless binding at CREs associated with seasonal polyphenism.

ivory is expressed in color patterns

The above data, in the context of previous mapping studies from many different butterfly and moth species, identify *ivory* lncRNA as a strong candidate gene for wing pattern adaptation. This lncRNA was overlooked in previous mRNA-seq studies, however, and therefore escaped annotation. Our Iso-Seq data allowed us to identify a long *ivory* transcript, for which our Pol II data imply transcription is occurring in developing pupal wings. To characterize spatial expression of *ivory* we performed hybridization chain reaction *in situ* hybridizations in early pupal wings. We observed high expression levels of *ivory* lncRNAs in specific color pattern elements, especially the outer boundaries of the discal bands (Fig. 2A) the eyespot central and outer rings (Fig. 2B-D). This strong association with melanic color pattern elements was consistent with chromogenic ivory *in situs* in other butterflies, as shown in Livraghi et al. (8), and suggests a positive role for *ivory* in regulating these patterns.

ivory plays roles in wing pigmentation and eyespot development

To assess the role of *ivory* in color pattern development we generated two mutant deletion lines using CRISPR/Cas9. We targeted the promoter and first exon of ivory with three single guide RNAs (sgRNAs) (Fig. 3A, Table S6, S7). After inter-crossing mosaic knockout (mKO) parents, progeny with strong ventral wing pigmentation phenotypes were selected and crossed. We generated two lines: one with an 18bp deletion ($ivory^{\Delta 18bp}$) of the core promoter that does not affect the first exon of ivory (Fig. 3A), and one with a 17kb deletion ($ivory^{\Delta 17kb}$) that spans the promoter and first exon, but that does not affect any *cortex* coding regions (Fig. 3B). The $ivory^{\Delta 18bp}$ lines presented an overall faded phenotype, but still appeared to have most pigment types represented (Fig. 3C). This mutation shows that even minor modifications to the *ivory* promoter are sufficient to produce global quantitative effects on pigmentation.

The $ivory^{\Delta 17kb}$ line, which was confirmed through whole genome sequencing, produced nearly pigmentless butterflies (Fig. 3C). This phenotype resembled the original *H. melpomene ivory* spontaneous mutants (13), where almost all melanins appeared to be lost, and only weak traces of presumptive ommochrome pigmentation remained. $ivory^{\Delta 17kb}$ did not prove to be embryonic lethal, although homozygous butterflies were flightless and not as active as heterozygotes or wildtypes. Heterozygous $ivory^{\Delta 17kb}$ mutants showed an intermediate phenotype of partially faded pigmentation. We were able to maintain this line for several generations by occasional backcrossing to the wildtype line and genotyping.

Transcription of *ivory* in melanic eyespot rings during early pupal development suggests that this gene has a regulatory program to specifically activate expression in these pattern elements. We were thus intrigued to note that while the $ivory^{\Delta 18bp}$ line showed the faded pigmentation phenotype typical of various *ivory* knockouts, it nonetheless retained fully pigmented melanic center rings in the major

eyespots that did not appear to show similar fading (Fig. 3C). This contrasts with the *ivory*$^{\Delta 17kb}$ homozygotes which show a complete loss of melanic inner eyespot rings (Fig. 3C). These results do not identify a specific eyespot regulatory element, but they do suggest that the pigment fading effect can be decoupled from *ivory*'s role in determining internal melanic eyespot rings.

Importantly, none of the mutants we observed appeared to show any change in the size or location of identifiable color pattern elements themselves, leading us to infer that the main function of *ivory* lies in regulating pigmentation, and not pattern formation *per se*.

cis-Regulatory deletions replicate alternate seasonal phenotypes

J. coenia presents different ventral hindwing phenotypes depending on seasonal conditions (Fig. 4A). As described above, a region of open chromatin and Spineless binding in the first intron of *ivory* has been genetically linked to natural variation in this polyphenic response (Fig. 1A, Fig. 4B) (2). To determine how this and other *ivory cis*-regulatory regions may be involved in color pattern regulation, we used CRISPR/Cas9 to generate "shotgun deletion" somatic mosaic knockouts (mKO) at five presumptive *ivory* regulatory regions: the promoter, one upstream element (E149), and three CREs in the polyphenism-associated interval (E205, E209, and E230) (Fig. 4A, Table S7). As previously described, this CRISPR/Cas9 approach targets a CRE with multiple sgRNAs to induce a spectrum of mutations of differing lengths, thus generating G^0 somatic mosaics that represent a diversity of mutant alleles that allow us to survey the breadth of effects that regulatory mutations can produce (7).

This exercise produced three distinct phenotypes (Fig. 4C, D). The first, and most compelling, class of phenotypes is the replication of seasonally plastic color patterns that originally led to the mapping of this locus in *J. coenia*. Specifically, deletions at all elements generate mosaic clones with partially hypomorphic reduction of dark red pigmentation on the ventral hindwing in a fashion that phenocopies summer phenotypes of *J. coenia* (Fig. 4C, D). In these mutants the "background" beige and brown coloration was minimally affected, while red interspersed through an otherwise beige background field was reduced. Many of these mutants showed reduced or undetectable effects on the dark red umbral band as well (e.g., Fig. 4C), in a manner highly reminiscent of natural seasonal variation (Fig. 4A). Thus, mutant butterflies that would otherwise show an autumn phenotype display mutant clones that resemble the summer phenotype. This contrasts with *ivory* exonic knockouts (e.g. *ivory*$^{\Delta 17kb}$), or strong CRE hypomorphs, as described below, which show a uniform loss of almost all pigmentation across the ventral hindwing, including the umbral band (Fig. 4D).

Second, deletions at all elements were all capable of producing strongly hypomorphic mutant clones that resembled the *ivory*$^{\Delta 17kb}$ line, and as evidenced in other species (6, 13) – an almost complete loss of most pigmentation on both dorsal and ventral wing surfaces (Fig. 4D). We infer that these elements function as enhancers, or positive regulators, of *ivory* transcription, and that the fading phenotypes are likely a result of decrease in *ivory* transcription or dosage. The final class of phenotypes, seen in a subset of E209 and E230 mutants, were pigmentation hypermorphs that showed darkening of

both dorsal and ventral pattern elements (Fig. 4D). We infer that these CREs possess some silencer-like functionality, and that their deletion likely results in increased *ivory* dosage.

Together, these results demonstrate that *ivory* can be regulated by non-coding sequences in a relatively refined fashion, likely through dosage-like effects on global pigment intensity, but also showing evidence of potentially pattern-specific strength-of-effect (e.g., umbral band and eyespot center rings). Importantly, the replication of nuanced seasonal phenotypes serves to validate previous genetic mapping work linking this locus to color pattern plasticity.

ivory regulates a large and dynamic cadre of transcripts during wing development

The diverse effects of *ivory* on wing coloration, including regulation of multiple pigment types, implies that this lncRNA directly or indirectly regulates multiple biological processes. To assess the transcriptional impact of *ivory* loss of function, we characterized the wing transcriptome at three stages of development in the $ivory^{\Delta 17kb}$ line: (1) last (5th) instar wing imaginal discs, when pattern formation begins; (2) pupal wings two days after pupation when patterns are finalized, but before scales mature, and when our *in situ* hybridizations in Fig. 2 were performed; and (3) late pupal wings, 6-7 days after pupation, when scales are nearly matured and pigments are being synthesized. We compared wild type and mutant transcriptomes and identified the most differentially expressed genes at each timepoint (Tables S9-S12). There was an overall large effect of the *ivory* knockout on gene expression during wing development with thousands of significantly differentially expressed transcripts (5th: 518; Day 2: 3629; Day 6: 469) at FDR of p^{adj} =0.01 (Fig. 5).

We looked specifically at differentially expressed genes with known or suspected roles in wing pigmentation and/or patterning (Table S9) to ask if the *ivory* knockout phenotype is consistent with functions of these genes. In this respect, there were a number of pigmentation genes that were downregulated in knockouts, including the ommochrome gene *kynurenine formamidase*, and melanin genes including *laccase2*, *dopa decarboxylase*, *black*, and *yellow* gene family members *yellow-d2* and *yellow-c* (16). *kynurenine formamidase* was of particular interest because of its high normalized read counts in late pupal wild type wings (> 2k), implying very high expression, perhaps consistent with the whole-wing effects of the ivory loss of function phenotype. Interestingly, there were also a few pigment-related genes upregulated in mutants, including the melanin-related genes *dopamine N-acetyltransfrease* (*Dat*), *mamo*, *tan*, and multiple *prophenoloxidase*- and *yellow*-family genes. *trehalase* and several homologs of *tret 1-2*, a predicted trehalose transporter, were also highly upregulated in early pupal wings, which is notable because *trehalase* knockouts present a summer-morph phenotype similar to *ivory* CRE knockouts (2). A >10-fold change increase in *trehalase* and *tret 1-2* expression in early pupal wings of $ivory^{\Delta 17kb}$ thus provides extra support for a functional connection between these loci in the context of wing pigmentation, yet the inverse correlation between their expression suggests a more nuanced relationship than previously surmised.

In terms of known color pattern genes that were differentially expressed, the best supported candidates included *spineless*, *engrailed*, *washout/domeless*, *herfst/crooked legs*, *bar-H1*, and *ecdysone receptor* (2, 15, 17, 18). While it is perhaps premature to speculate about the functional connection between *ivory* and most of these genes, *spineless* stands out for three reasons: [1] knocking it out produces global, wing-wide effects on pigmentation just as *ivory* does; [2] it binds to the *ivory* promoter (Fig. 1B), suggesting reciprocal regulation; and [3] it has surprisingly high expression levels in mutant wings during early pupal development, with normalized read counts exceeding 10k in *ivory*$^{\Delta 17kb}$ wings (Tables S3, S9). *ecdysone receptor* is also an attractive candidate because titers of the steroid hormone ecdysone determine seasonal wing pattern phenotypes (2), thus providing a possible mechanism for *ivory*'s role in color pattern polyphenism.

A final notable pattern that emerged from the RNA-seq analysis was the strong upregulation of multiple *Osiris*-family genes in in *ivory*$^{\Delta 17kb}$ wings during early pupal development, in terms of fold change, significance, overall read count magnitude, and overall number of *Osiris* genes (Table S11). This gene family is thought to encode transmembrane transporters, although *Osiris* genes have not been well characterized outside of tracheal function in *Drosophila* (19), and they have not previously been linked to butterfly wing pigmentation. This gene family may provide candidates for future functional assessment.

Discussion

In this study we show that the lncRNA *ivory* regulates *J. coenia* color patterns, and that perturbation of *ivory* CREs can produce nuanced color pattern variations, including replicating seasonal phenotypes (2, 20). In terms of color pattern evolution, these results are of broad interest because they prompt a rewrite of our understanding of the *cortex* locus, which has received significant attention for its association with wing pattern adaptation across numerous species of moths and butterflies. Our findings, particularly in the context of recent *cortex* deletion lines lacking color pattern phenotypes (8), show that *ivory*, not *cortex*, is the color pattern gene of interest. Therefore, important molecular case studies of industrial melanism (3), Müllerian mimicry (6), and crypsis (4) should perhaps be revisited. Our work provides a cautionary example for anyone working to identify genes underlying variation that we need to look more carefully for evidence of causative non-coding transcripts.

More broadly, *ivory* represents a potentially novel case study of deeply conserved non-coding RNA underlying repeated instances of adaptation. Non-coding RNAs are now known to be abundant in genomes, and are being increasingly recognized as important regulators of gene expression (9). lncRNAs like *ivory* are generally thought to act as *trans*-regulators of gene expression through interactions with various protein, RNA, and DNA targets. This process may include intermediate posttranscriptional processing of lncRNAs into smaller effector RNAs with specific functions (21, 22). Indeed, a preprint posted in parallel with our study presents evidence that a micro-RNA (*miR-193*) immediately 3' of *ivory* may be derived from the nascent *ivory* transcript to play a role in pigment regulation (23). Deletion lines of

miR-193 in *Bicyclus anynana* produced melanin-deficient fading phenotypes similar to many *ivory* knockouts. These deletions, however, did not produce strongly hypomorphic pigmentless phenotypes as seen in *ivory*$^{\Delta 17kb}$ or various *ivory* mutants in other species (8), and they showed a relatively limited effect on downstream gene expression. Thus, it is interesting to speculate whether *miR-193* might be the effector for some subset of *ivory* functions, perhaps as a *trans*-regulator specifically of melanin genes. In any case, the specific molecular mode of *ivory* action remains an open question.

While lncRNAs have been linked to various human health conditions, including morphological and neurodevelopmental disorders (24, 25), little is known about how they may function in contexts such as adaptation or phenotypic plasticity. One of the few case studies that directly implicates any kind of non-coding RNA in trait adaptation concerns the role of small RNAs at the *YUP* locus in monkeyflowers, which affect carotenoid flower pigmentation (26). It is interesting that the *YUP* case study involves pigmentation, as does our *ivory* study. The similarities end there, however, as the *YUP* locus encodes multiple small RNAs that are evolutionarily labile, and individual RNAs can be specific to individual species. The *ivory* gene appears to behave in an evolutionary mode more consistent with other wing pattern adaptation loci like *optix* (a transcription factor) or *WntA* (a ligand), where a deeply conserved gene with a core developmental role diversifies phenotypes via *cis*-regulatory innovation (7, 27).

Our study was prompted by *J. coenia* DNA sequence associations that link a cluster of intronic CREs to variation in seasonal color pattern plasticity (2). Targeted deletions in this regulatory region caused a switch from autumnal color pattern to a summer color pattern, and thus appear to confirm a role for these CREs in modulating seasonal color patterns. What is interesting beyond simply being a validation of previous association work, however, is that these phenotypes also demonstrate that CREs of *ivory* can exercise nuanced, quantitative control over the color identity of large fields of cells. Clearly, natural butterfly color pattern diversity consists of much more than binary cell fate decisions across a fixed palette of colors - there is also natural quantitative variation in hue, intensity, and semi-stochastic expression of local color schemes across specific wing fields. Thus far, however, we know very little about the developmental genetic basis of variation in these kinds of quantitative color qualities (28). *ivory* stands out for playing this kind of role, and we wonder whether its identity as a lncRNA may be tied to this nuanced functionality in color regulation.

lncRNAs are known for their gene regulatory functions (24), but they can also play other functional roles within cells, including in protein interactions, organelle regulation, etc. (9). We were thus curious to determine to what extent differential expression of *ivory* affected gene expression. Does it regulate many genes, or only a handful of key pigmentation genes? Or perhaps it has no effect on gene regulation, and plays a direct role in pigment synthesis, precursor transport, or other aspects of scale cell biology. Our developmental RNA-seq data from wings of *ivory*$^{\Delta 17kb}$ individuals, with nearly pigmentless *ivory* loss-of-function phenotypes, show clearly that *ivory* has strong effects on transcript abundance during wing development, and that many genes show evidence of both upregulation and downregulation in mutant wings (Fig. 4). The transcripts include a number of candidate pigmentation and wing patterning

genes that are suggestive for explaining the pigment-related phenotypes (Table S8). Downregulation of various melanin and ommochrome genes (e.g. *dopa decarboxylase*, *black*, *kynurenine formamidase*) in *ivory* mutants makes immediate sense because of the pigment loss phenotypes, but also compelling is the upregulation of other pigmentation genes, such as *mamo*, a recently characterized melanin repressor in the silkmoth (29). Of course, however, we do not know which genes or transcripts are direct targets of *ivory* activity versus indirect downstream effectors. Livraghi et al. (8) speculate that a primary function of *ivory* function lies in regulating melanin synthesis genes, which we think is likely to be true. But our RNA-seq data also make it clear that *ivory* has a strong and broad influence over expression of many genes, even in larval imaginal discs, which may help explain its apparent effects on other non-melanic pigment types as well. Future work on this lncRNA would benefit from characterizing its molecular mode of action and identifying its direct targets during wing development. Through more functional work we will be able to understand how lncRNAs like *ivory* facilitate adaptive variation and plasticity in rapidly evolving gene regulatory networks.

Materials and Methods

Butterfly husbandry

Our primary *J. coenia* stock originated from Durham, North Carolina, and was reared in the lab at 27°C, 16 : 8 hrs light : dark on an artificial wheat germ diet supplemented with dried *Plantago lanceolata*, as previously described (30). We used a genetic assimilation “red line” of this stock with constitutive autumn red ventral hindwing coloration (2) to enhance detection of CRISPR/Cas9 mutation effects on red pigment patterns. Genetic mutant lines were visually assessed by pigment fading in the ventral wing (Fig. 4C).

Iso-Seq long read transcriptome annotation

For whole organism long read RNA annotations we sampled an array of tissues at different developmental stages (Table S1). Tissues were dissected into Trizol and stored at -80 °C. RNA was extracted using RNeasy Mini Kit (Qiagen) with on column DNase treatment and quantified with a Qubit RNA BR Assay kit (Molecular Probes). RNA samples were sent to Maryland Genomics (University of Maryland School of Medicine) for quality control (RIN = 9.9), full length cDNA synthesis and Iso-Seq library preparation. Libraries were sequenced on a PacBio Sequel II 8M SMRT Cells on a 30 hr movie run. The sequencing run provided 1.1 TB of data that was concatenated using the PacBio SMRT Iso-Seq pipeline (https://www.pacb.com/support/ software-downloads/) to generate a circular consensus sequence file (.ccs) along with high quality (hq) and low quality (lq) full length transcript files. A SMRT PacBio wrapper (PBMM2) based on pairwise alignment (MINIMAP2) script was applied using the .css file against the jcgenv2.fa genome (Lepbase). The generated alignment file (.bam) was used for downstream transcriptome re-annotation using the BRAKER3 pipeline (31). Briefly, BRAKER 3 incorporates transcript selector algorithm TSEBRA with AUGUSTUS predictions through BRAKER1 and BRAKER2 pipelines. This allowed us to combine long read sequences (this manuscript) with previous short read data (2) to

produce an updated version 3 *J. coenia* transcriptome annotation (Jcv2_OGSv3.gff). Assessment of completeness was performed with BUSCO v5.4.7 with complete BUSCO score of 97.9 % (Table S1). The v3 *J. coenia* gene predictions are available on the Dryad repository (DOI: 10.5061/dryad.qz612jmpb).

Chromatin immunoprecipitation and sequencing

Pupal wing tissue for chromatin immunoprecipitation of Bric-a-brac, Ftz-F1, and Pol II bindings sites was collected and processed as previously described (2, 17). Further information on antibodies, pipelines, and dataset sources used for this study are found in Table S3. ChIP-seq and input libraries were prepared using an NEBNext DNA Ultra II kit without size selection. Libraries were sequenced using the Cornell Biotechnology Resource Center Genomics Facility on an Illumina NextSeq 500/550 at 20 million bp reads for treatment (ChIP) and 30 million for control (Input).

ATAC-seq, ChIP-seq, and Hi-C dataset analysis

Chromatin profiled TAD boundaries and comparative ATAC-seq alignments within the *cortex* locus (Fig. 1) were accessed and adapted from Mazo-Vargas et al. (7). Comparative noncoding genome alignments for Scaffold 15 were performed using CACTUS/HALPER on *J. coenia* wing tissue ATAC-seq peak calls (MACS2) (7). Peak calls representing sites of open chromatin were given a score from (0.001 – 1.000), with the lowest score representing regions of least conservation and a score of 1.0 representing conservation in at least eight of twelve species used in the Mazo-Vargas et al. (7) alignment. Pupal wing ATAC-seq datasets of representative nymphalid clade butterfly species were gathered from previous studies: *J. coenia, Vanessa cardui*, *Heliconius erato demophoon*, and *Danaus plexippus* (Table S4). Peak calls for regions of high ATAC-peak conservation were imported into Geneious Prime (v2023.1.1) and manually annotated for position and chromatin accessibility (i.e. ATAC-seq signal) Table S5. ATAC-seq peaks below (RPKM normalized count values < 10) were characterized as not accessible and marked with a gray line in Fig 1.

ChIP-Seq alignment data for the transcription factor Spineless was taken from van der Burg et al, (12), and we generated new Bric-a-brac (three replicates), Ftz-F1 (two replicates), and Pol II (three replicates) ChIP-seq data as described above. ChIP libraries were aligned to the lepbase.org *J. coenia* genome version 2 (jcv2). Alignment, duplicate removal, and peak calling was done as previously described (17).

Hybridization chain reaction *in situ* hybridization

The first exon of *ivory* was used to design hybridization chain reaction probe pairs with sequences unique to the *ivory* transcript. Wings were removed from 2-day old pupae and *in situs* were performed following the protocol of Chatterjee et al. (32). B1 hairpin amplifiers were tagged with AlexaFlour 647 fluorophores, and wings were imaged on a Leica Stellaris 5 confocal microscope.

CRISPR/Cas9 targeted mutagenesis and genotyping

To generate *ivory* loss-of-function lines we designed two sgRNAs targeting the 5' promoter where Pol II binds (Table S10). We carried out sgRNA-Cas9 embryo injections in *J. coenia* as previously described (33), with modification to microinjection needle shape pull on Sutter-P97 (Sutter Instruments). We selected G^0 adults with large clonal mosaics for sib mating, the resulting G^1s were purified to two lines: one with a nearly complete loss of pigmentation, and one with highly faded pigmentation. Whole genome Illumina sequencing of three individuals from each line confirmed that the former had an 17kb deletion (*ivory*$^{\Delta 17kb}$) and the latter an 18bp promoter deletion (*ivory*$^{\Delta 18bp}$) (Fig. 3A, B, Table S8).

To test the function of *ivory* CREs in red line *J. coenia* we generated somatic mKO mutants using sgRNA pairs targeting selected ATAC-seq peaks, as previously described (7). This approach generates mosaic G^0 individuals, where bilateral asymmetry of mKO clones provides a useful assay for ruling out natural variation or other non-CRISPR effects that would otherwise produce symmetrical phenotypes (16). Cas9 targeting was confirmed by PCR and sequencing of selected mutants for each locus (Table S6, S7).

***ivory*$^{\Delta 17kb}$ mRNA sequencing and expression analysis**

We dissected wings from late 5th instar larvae, day 2 pupae, and day 6 pupae of red line and *ivory*$^{\Delta 17kb}$ *J. coenia.* Each of the three experimental replicates for each stage represented all forewings and hindwings pooled from three individuals. PolyA-enriched transcripts were isolated and bidirectionally sequenced as previously described (TableS1, S8). *ivory*$^{\Delta 17kb}$ mutants were genotyped with TaqPhire Pol Direct-Tissue PCR (Invitrogen), DNA was extracted from a third to fourth instar caterpillar spine and added to a reduced 20 µl lysis reaction mix, 1µl of this lysis reaction was used as template for PCR. RNA-Seq datasets (Novogene) were aligned using HiSAT2 on jcgenv2.fa genome followed by Featurecounts using the Iso-Seq informed v3 annotations (Table S1) Refer to Dryad for predicted amino acid sequences corresponding to Jcv2_OGSv3.gff (DOI: 10.5061/dryad.qz612jmpb). Differential gene expression analysis was performed using default settings for DESeq2 on the Galaxy Server webtools (34).

Acknowledgments

We thank Samantha Pires and Julia Marie Forte for help with butterfly rearing, and Arnaud Martin and Joseph J. Hanly for helpful comments on the manuscript. This work was funded by U.S. National Science Foundation Grants IOS-2128164 and DEB-2242865 to R.D.R.

References

1. V. V. Järvi, K. R. L. van der Burg, R. D. Reed, Seasonal Plasticity in *Junonia coenia* (Nymphalidae): Linking wing color, temperature dynamics, and behavior. *The Journal of the Lepidopterists' Society* **73** (2019).
2. K. R. L. van der Burg *et al.*, Genomic architecture of a genetically assimilated seasonal color pattern. *Science* **370**, 721-725 (2020).
3. A. E. van't Hof *et al.*, The industrial melanism mutation in British peppered moths is a transposable element. *Nature* **534**, 102-105 (2016).
4. S. Wang *et al.*, The evolution and diversification of oakleaf butterflies. *Cell* **185**, 3138-3152 e3120 (2022).
5. N. J. Nadeau *et al.*, The gene *cortex* controls mimicry and crypsis in butterflies and moths. *Nature* **534**, 106-110 (2016).
6. L. Livraghi *et al.*, *Cortex cis*-regulatory switches establish scale colour identity and pattern diversity in *Heliconius*. *eLife* **10** (2021).
7. A. L. Mazo-Vargas, A. M.; Wilder, A.; van der Burg, K. R.; Lewis, J.J.; Messer, P. W.; Zhang, L.; Martin, A.; Reed, R. D. , Deep *cis*-regulatory homology of the butterfly wing pattern ground plan. *Science*, 304-308 (2022).
8. L. Livraghi *et al.*, A long non-coding RNA at the *cortex* locus controls adaptive colouration in butterflies. *bioRxiv* https://doi.org/10.1101/2024.02.09.579710 (2024).
9. L. Statello, C. J. Guo, L. L. Chen, M. Huarte, Gene regulation by long non-coding RNAs and its biological functions. *Nat Rev Mol Cell Biol* **22**, 96-118 (2021).
10. L. A. Goff *et al.*, Spatiotemporal expression and transcriptional perturbations by long noncoding RNAs in the mouse brain. *Proc Natl Acad Sci U S A* **112**, 6855-6862 (2015).
11. K. R. L. van der Burg, R. D. Reed, Seasonal plasticity: how do butterfly wing pattern traits evolve environmental responsiveness? *Curr Opin Genet Dev* **69**, 82-87 (2021).
12. E. V. Daniels, K. A. Mooney, R. D. Reed, Seasonal wing colour plasticity varies dramatically between buckeye butterfly populations in different climatic zones. *Ecological Entomology* **37**, 155-159 (2012).
13. J. J. Hanly *et al.*, A large deletion at the *cortex* locus eliminates butterfly wing patterning. *G3 (Bethesda)* **12** (2022).
14. K. R. L. van der Burg *et al.*, Contrasting roles of transcription factors Spineless and EcR in the highly dynamic chromatin landscape of butterfly wing metamorphosis. *Cell Rep* **27**, 1027-1038 e1023 (2019).
15. M. Perry *et al.*, Molecular logic behind the three-way stochastic choices that expand butterfly colour vision. *Nature* **535**, 280-284 (2016).
16. L. Zhang *et al.*, Genetic basis of melanin pigmentation in butterfly wings. *Genetics* **205**, 1537-1550 (2017).
17. J. J. Lewis, K. R. L. van der Burg, A. Mazo-Vargas, R. D. Reed, ChIP-seq-annotated *Heliconius erato* genome highlights patterns of *cis*-regulatory evolution in Lepidoptera. *Cell Rep* **16**, 2855-2863 (2016).
18. K. Tunström *et al.*, Evidence for a single, ancient origin of a genus-wide alternative life history strategy. *Science Advances* **9** (2023).
19. A. Scholl *et al.*, The *Osiris* family genes function as novel regulators of the tube maturation process in the *Drosophila* trachea. *PLoS Genet* **19**, e1010571 (2023).
20. E. V. Daniels, R. Murad, A. Mortazavi, R. D. Reed, Extensive transcriptional response associated with seasonal plasticity of butterfly wing patterns. *Mol Ecol* **23**, 6123-6134 (2014).
21. A. Dhir, S. Dhir, N. J. Proudfoot, C. L. Jopling, Microprocessor mediates transcriptional termination of long noncoding RNA transcripts hosting microRNAs. *Nat Struct Mol Biol* **22**, 319-327 (2015).
22. D. He *et al.*, miRNA-independent function of long noncoding pri-miRNA loci. *Proc Natl Acad Sci U S A* **118** (2021).
23. S. Tian *et al.*, A micro-RNA drives a 100-million-year adaptive evolution of melanic patterns in butterflies and moths. *bioRxiv* https://doi.org/10.1101/2024.02.09.579741; (2024).

24. L. Allou *et al.*, Non-coding deletions identify Maenli lncRNA as a limb-specific *En1* regulator. *Nature* **592**, 93-98 (2021).
25. T. C. Roberts, K. V. Morris, M. J. A. Wood, The role of long non-coding RNAs in neurodevelopment, brain function and neurological disease. *Philosophical Transactions of the Royal Society B: Biological Sciences* **369**, 20130507 (2014).
26. W. C. Mei Liang, Amy M. LaFountain, Yuanlong Liu, Foen Peng, Rui Xia, H. D. Bradshaw, and Yao-Wu Yuan, Taxon-specific, phased siRNAs underlie a speciation locus in monkeyflowers. *Science* DOI: 10.1126/science.adf1323, 576-582 (2023).
27. J. J. Lewis *et al.*, Parallel evolution of ancient, pleiotropic enhancers underlies butterfly wing pattern mimicry. *Proc Natl Acad Sci U S A* **116**, 24174-24183 (2019).
28. K. Bachem *et al.*, Regulatory evolution tuning pigmentation intensity quantitatively in *Drosophila*. *Science Advances* **10** (2024).
29. S. Wu *et al.*, The BTB-ZF gene *Bm-mamo* regulate pigmentation in caterpillars. *eLife* 10.7554/eLife.90795.1 (2023).
30. H. F. Nijhout, Pattern formation on lepidopteran wings: Determination of an eyespot. *Developmental Biology* **80**, 267-274 (1980).
31. L. Gabriel *et al.*, BRAKER3: Fully automated genome annotation using RNA-Seq and protein evidence with GeneMark-ETP, AUGUSTUS and TSEBRA. *bioRxiv* https://doi.org/10.1101/2023.06.10.544449 (2023).
32. M. Chatterjee, K. J. Siegel, L. S. Loh, J. M. C. McDonald, R. D. Reed, Butterfly wing iridescence is regulated by *araucan*, a direct target of optix and spalt. *bioRxiv* https://doi.org/10.1101/2023.11.21.568172 (2023).
33. L. Zhang, A. Mazo-Vargas, R. D. Reed, Single master regulatory gene coordinates the evolution and development of butterfly color and iridescence. *Proc Natl Acad Sci U S A* **114**, 10707-10712 (2017).
34. D. Blankenberg *et al.*, Integrating diverse databases into an unified analysis framework: a Galaxy approach. *Database (Oxford)* **2011**, bar011 (2011).

Figures and Tables

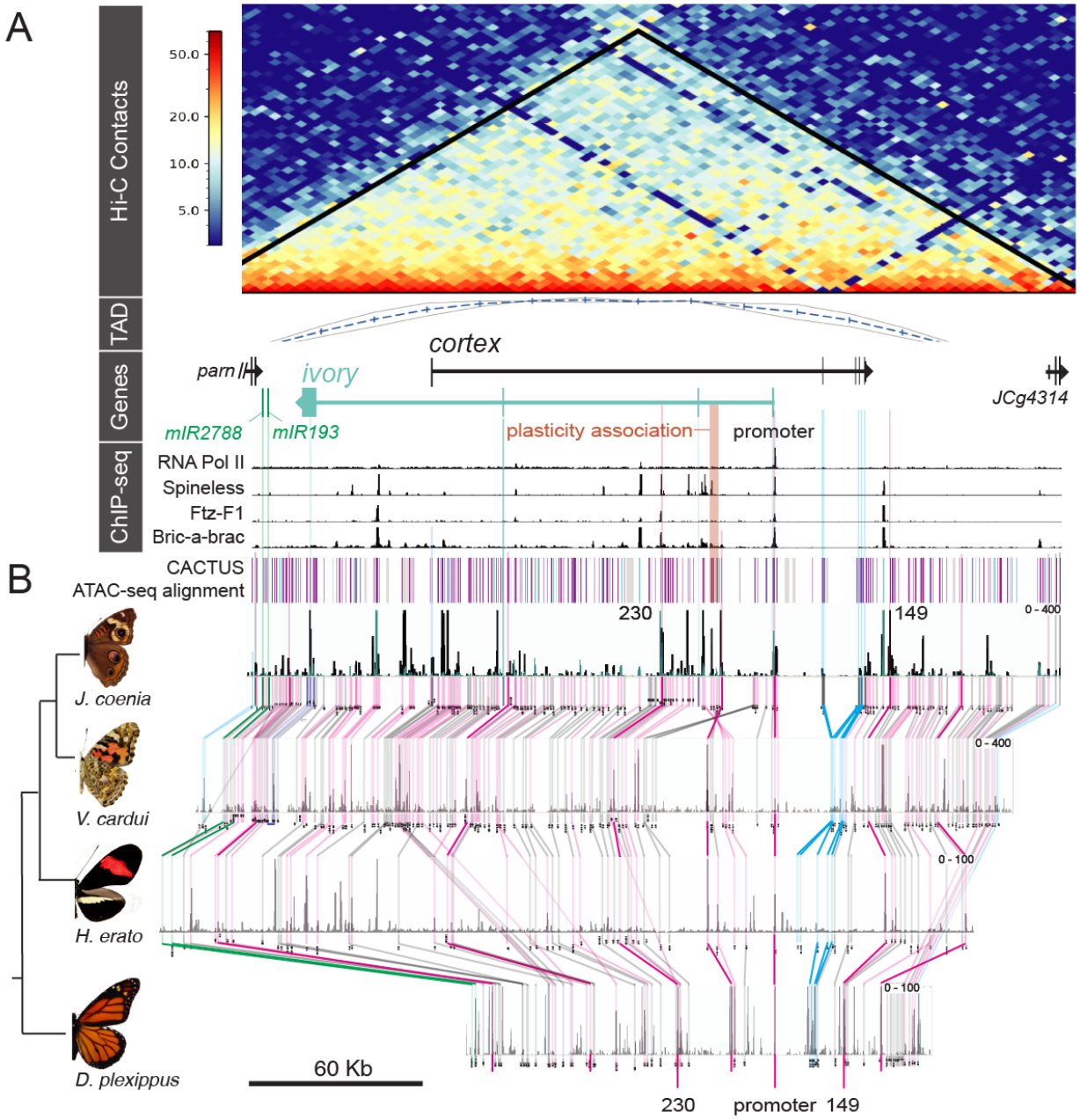

Figure 1. The *ivory* / *cortex* locus is deeply conserved in butterflies. (A) Hi-C chromatin conformation capture reveals a topologically associating domain (TAD) that centers on the overlapping *ivory* and *cortex* genes. The heat map displays chromatin interaction strength. ChIP-Seq annotates binding of Pol II and three transcription factors during early pupal wing development. The orange column highlights a region of nucleotide variant associations linked with natural variation in seasonal polyphenism of *J. coenia* wing coloration (2). (B) Wing ATAC-seq data from four nymphalids highlights deep conservation of genes and CREs across species. Orthology of specific sequences is indicated by color coded lines (green: micro RNAs; magenta to gray: ATAC-seq peaks; turquoise: *ivory* exons; light blue: *cortex* exons).

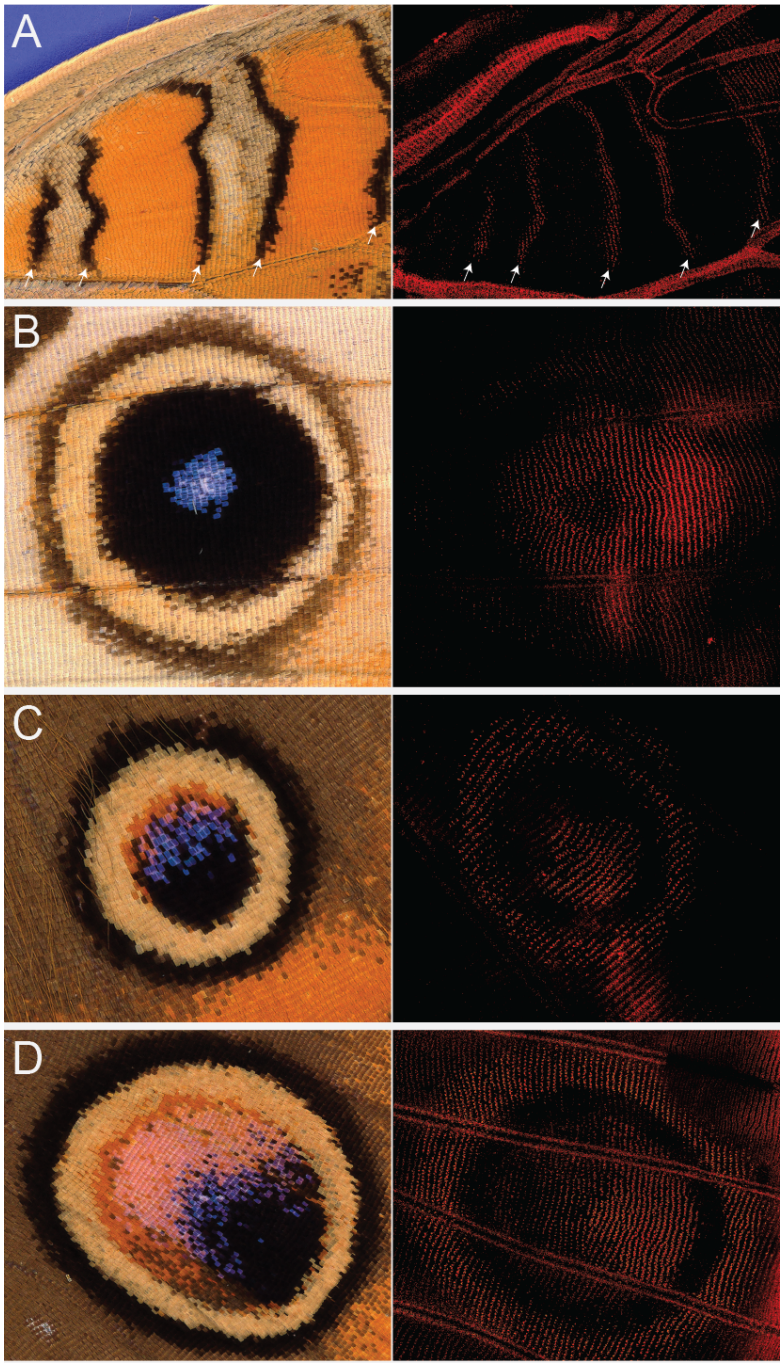

Figure 2. *ivory* is expressed in color pattern elements. Pictured are HCR *in situ* hybridizations of early pupal wings revealing *ivory* transcripts in (A) black borders of ventral discal bands (white arrows), (B) center ring of ventral forewing eyespot, and center and rings of dorsal hindwing (C) anterior and (D) posterior eyespots.

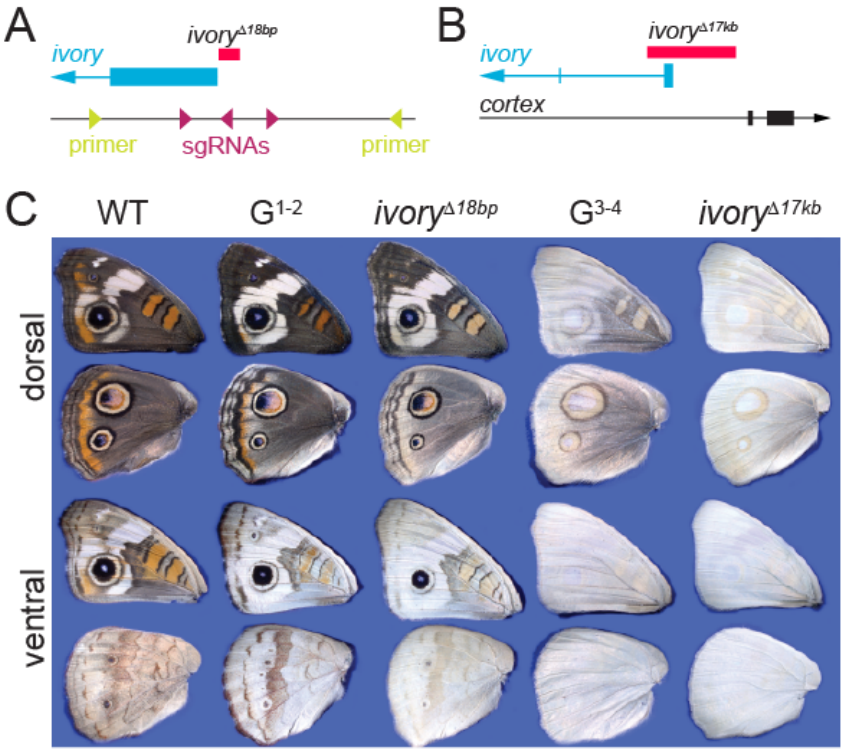

Figure 3. *ivory* promoter deletion lines show reduction and loss of pigmentation. (A) The *ivory*$^{\Delta p18bp}$ deletion (red) is adjacent to the *ivory* 5' exon, in the promoter. Location of PCR genotyping primers (green) and sgRNAs (magenta) is shown. (B) Expanded view of the *ivory* 5' region illustrating the location of the *ivory*$^{\Delta 17kb}$ deletion. (C) Phenotypes from promoter deletion line purification process. Pictured are representative intermediate individuals (likely heterozygotes), along with pure *ivory*$^{\Delta p18bp}$ and *ivory*$^{\Delta 17kb}$ individuals. Notable is the quantitative variation in overall pigmentation, but consistent presentation of the melanic center rings of the large eyespots.

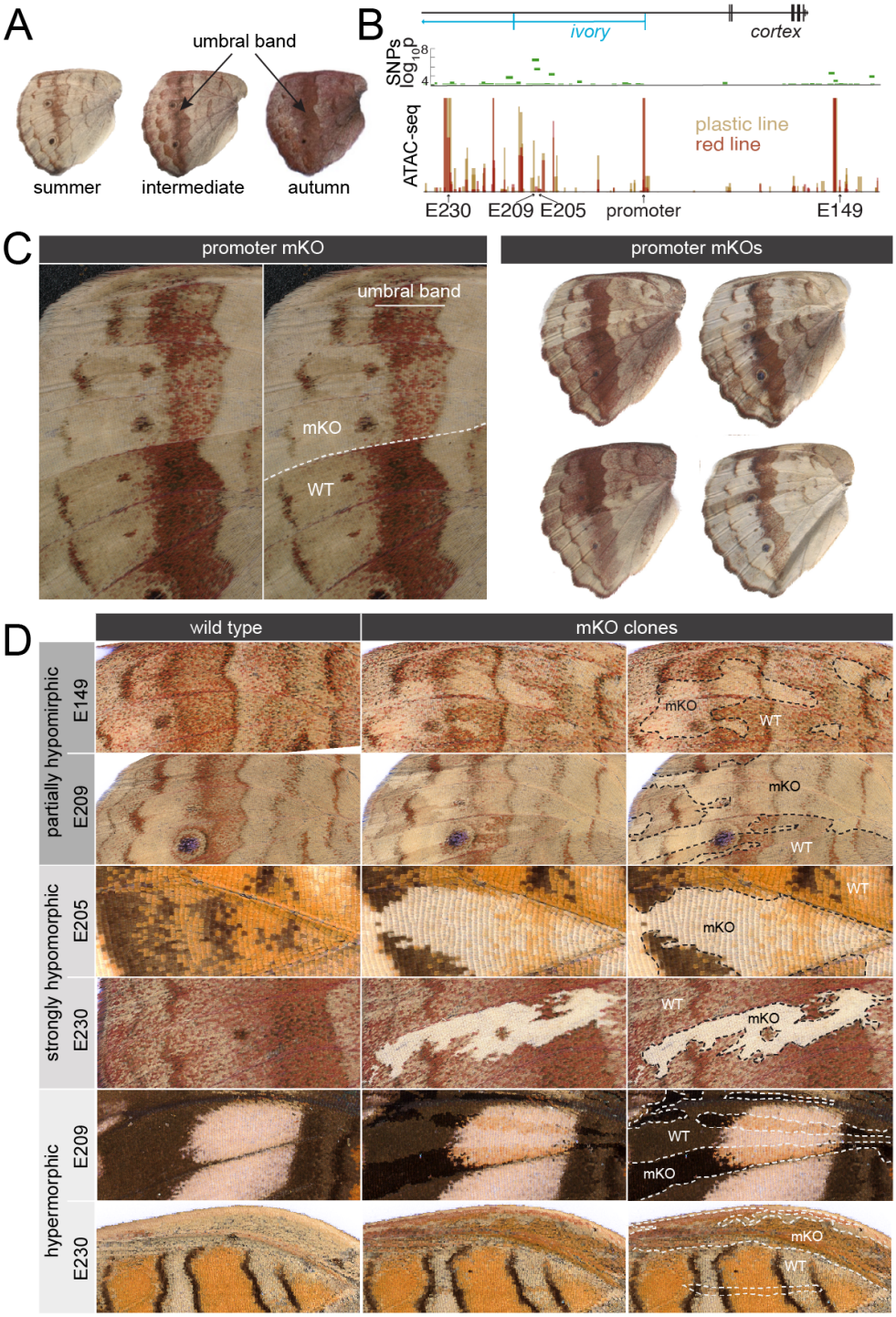

Figure 4. CRISPR mKOs of *cis*-regulatory regions result in several distinct phenotypes. (A) Examples of natural seasonal ventral hindwing phenotypes, including an intermediate form. (B) Locations of single nucleotide polymorphisms (SNPs) linked to variation in seasonal plasticity, along with ATAC-seq peaks from previously published "plastic" and "red" selection lines (2). Targets of CRISPR-Cas9 mKOs are annotated relative to SNPs and ATAC-seq. (C) Examples of promoter mKOs showing partially hypomorphic phenotypes resembling seasonal variation. (D) Examples of the different classes of mKO phenotypes from deletions in the targeted CRE regions.

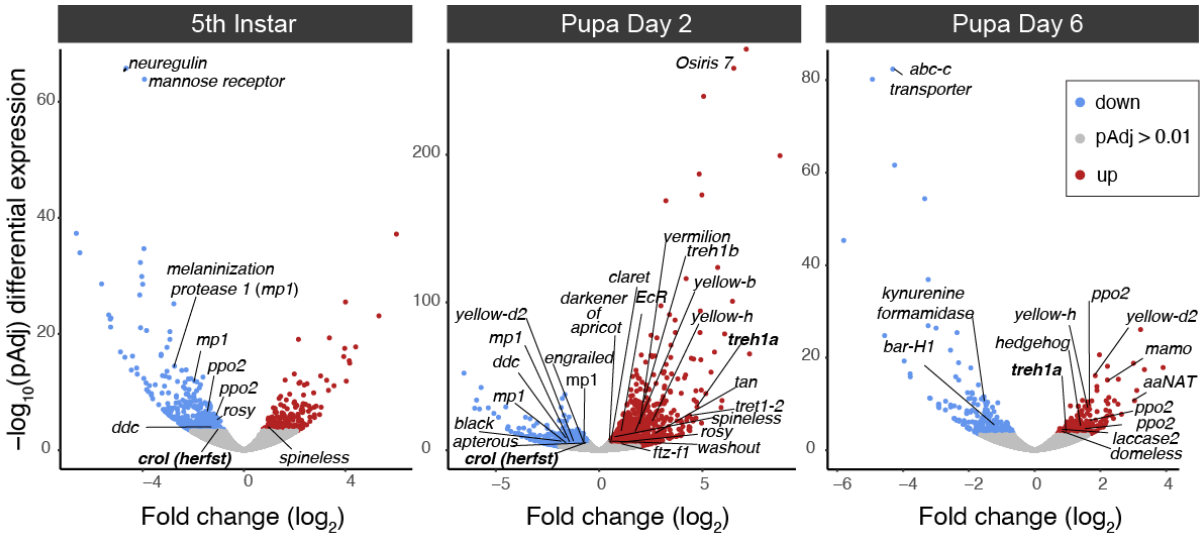

Figure 5. *ivory* loss-of-function causes major changes in gene expression during wing development. Volcano plots illustrate differences in transcript abundance in wild type versus pigmentless *ivory*$^{\Delta 17kb}$ wings at three stages of development. Blue dots mark genes downregulated in mutants and red dots mark genes upregulated in mutants. Genes potentially implicated in pigmentation or wing pattern development are highlighted. Genes previously identified in seasonal plasticity are in bold. *ddc*: *dopa-decarboxylase*; *EcR*: *ecdysone receptor*; *ppo*: *prophenoloxidase*.

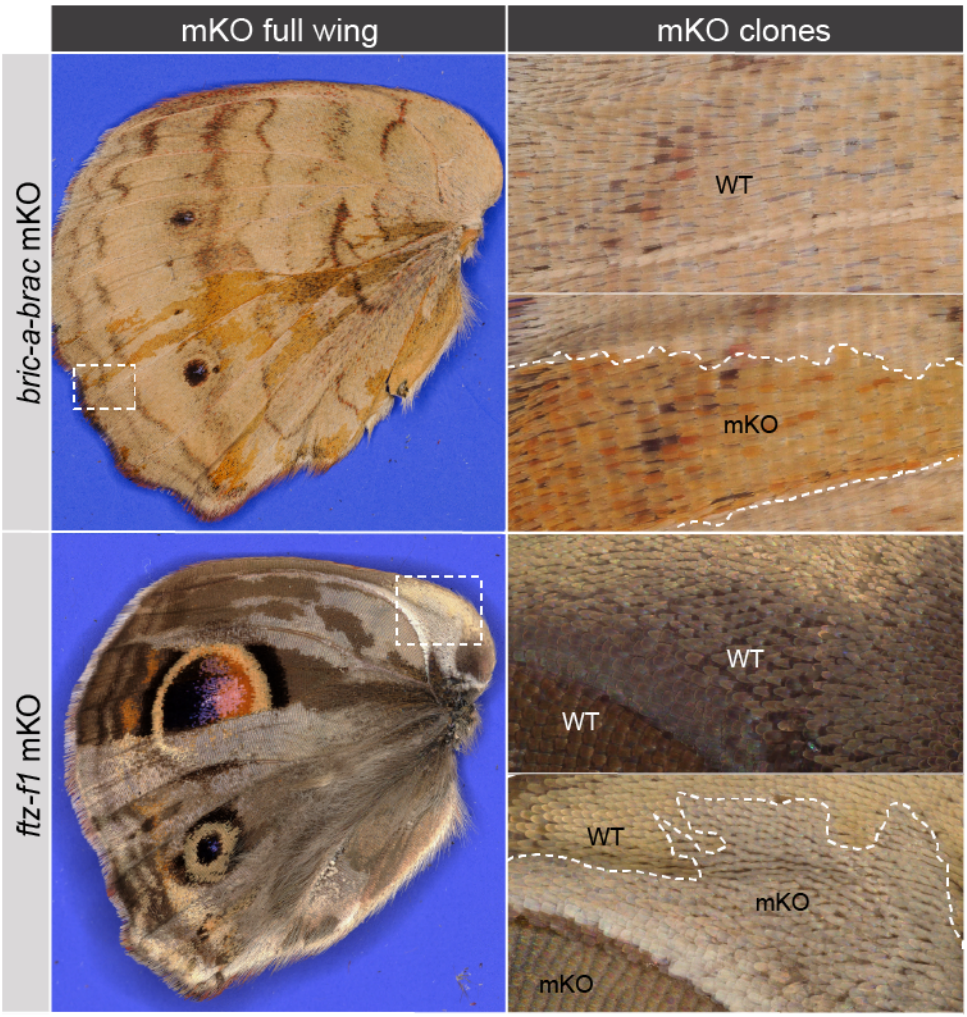

Figure S1. CRISPR deletions of transcription factor genes *bric-a-brac* and *ftz-f1* produce positive and negative global effects on pigmentation, respectively. mKO of *bric-a-bac* shows hyperpigmentation of ommochrome scales in ventral hindwings. mKO of *ftz-f1* results in strong reduction or loss of pigmentation and possible structural effects as well.

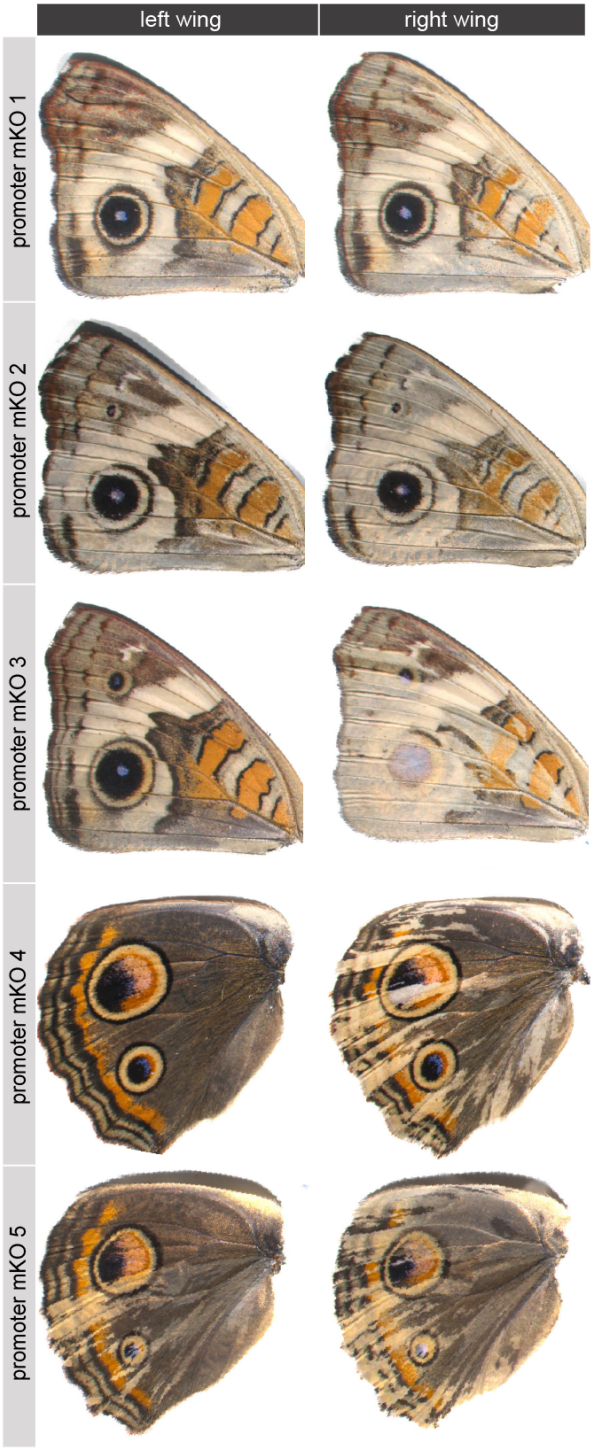

Figure S2. mKOs from sgRNAs targeting the *ivory* promoter (see Fig. 3A). Shown are contralateral pairs of wings from single individuals, emphasizing the asymmetrical mosaicism if G^0 mKOs.

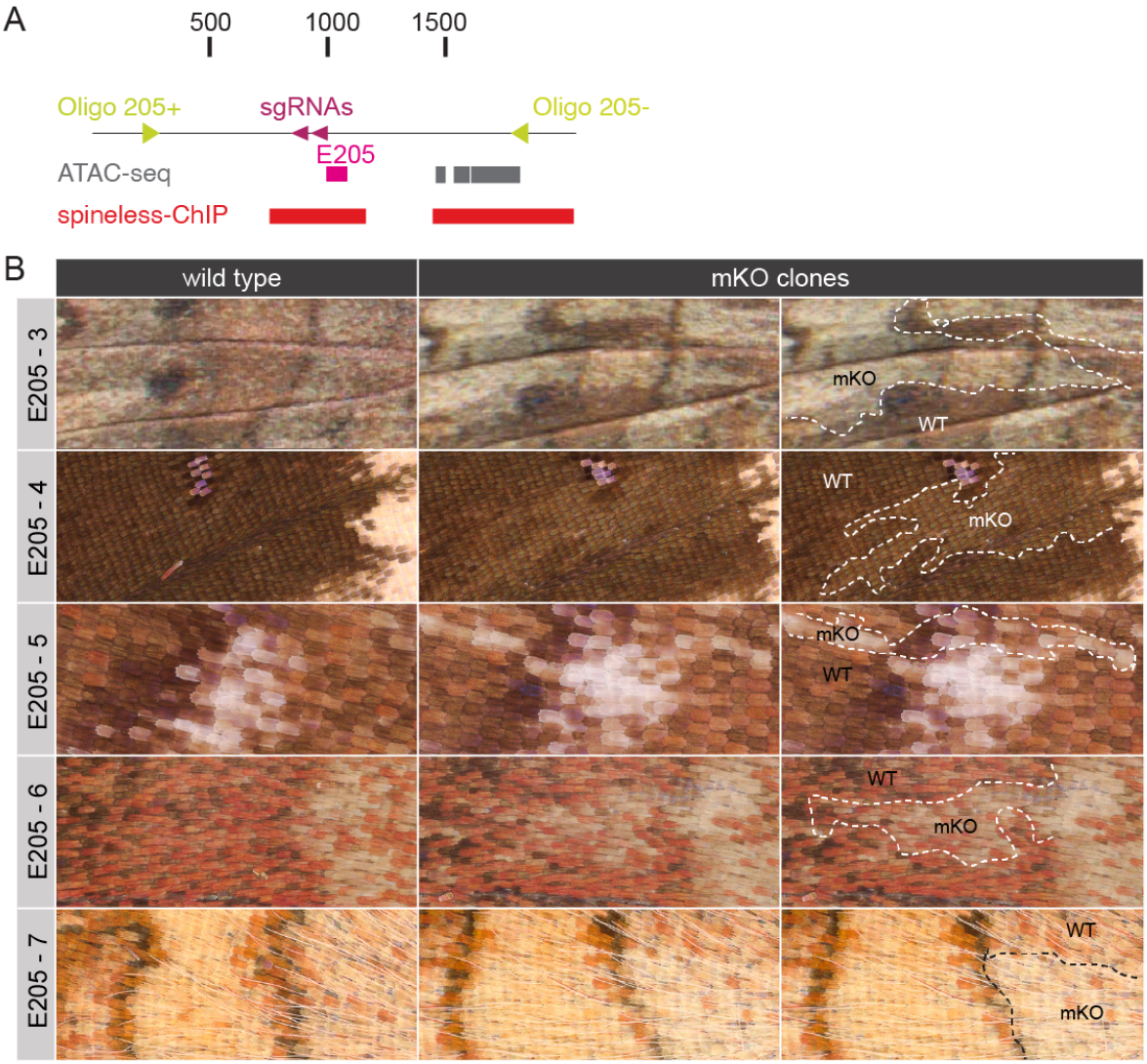

Figure S3. mKO phenotypes from CRISPR deletions of CRE 205. (A) A map of sgRNAs, including ATAC-seq and Spineless ChIP-seq peak calls. (B) mKO individuals showing pigmentation phenotypes.

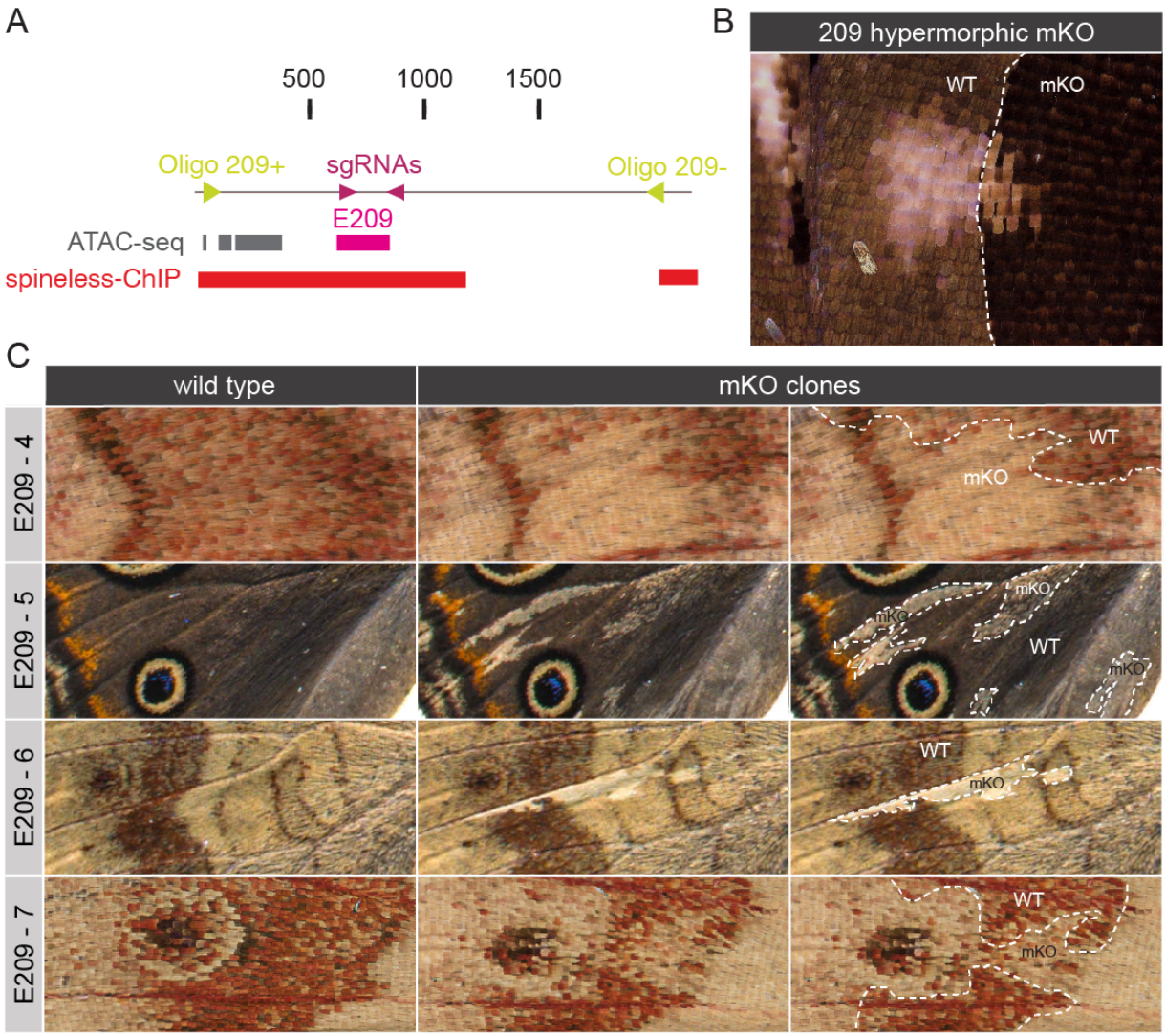

Figure S4. mKO phenotypes from CRISPR deletions of CRE 209. (A) A map of sgRNAs, including ATAC-seq and Spineless ChIP-seq peak calls. (B) A high magnification image of a hypermorphic clone boundary. (C) mKO individuals showing various pigmentation phenotypes.

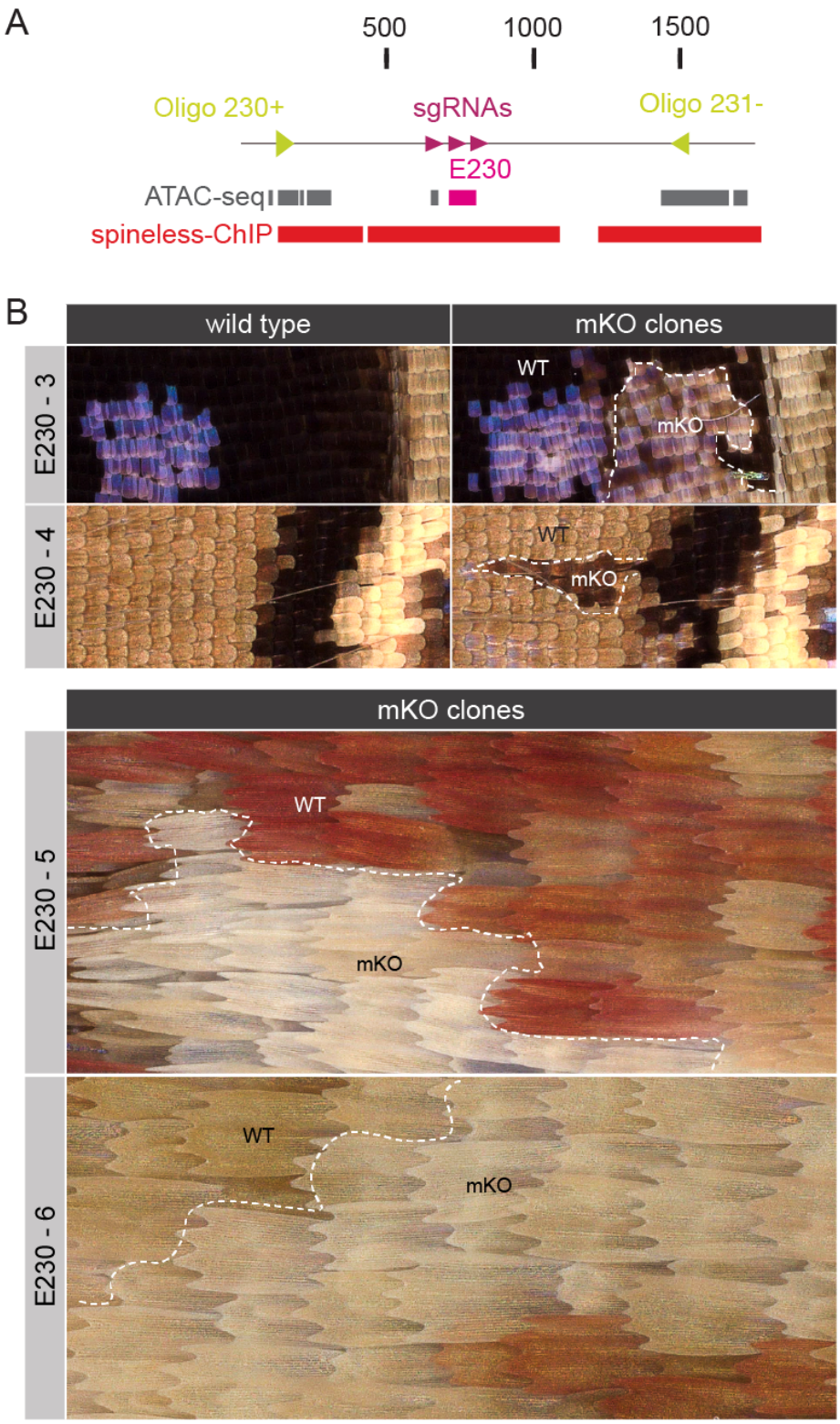

Figure S5. mKO phenotypes from CRISPR deletions of CRE 230. (A) A map of sgRNAs, including ATAC-seq and Spineless ChIP-seq peak calls. (B) mKO individuals showing pigmentation phenotypes.

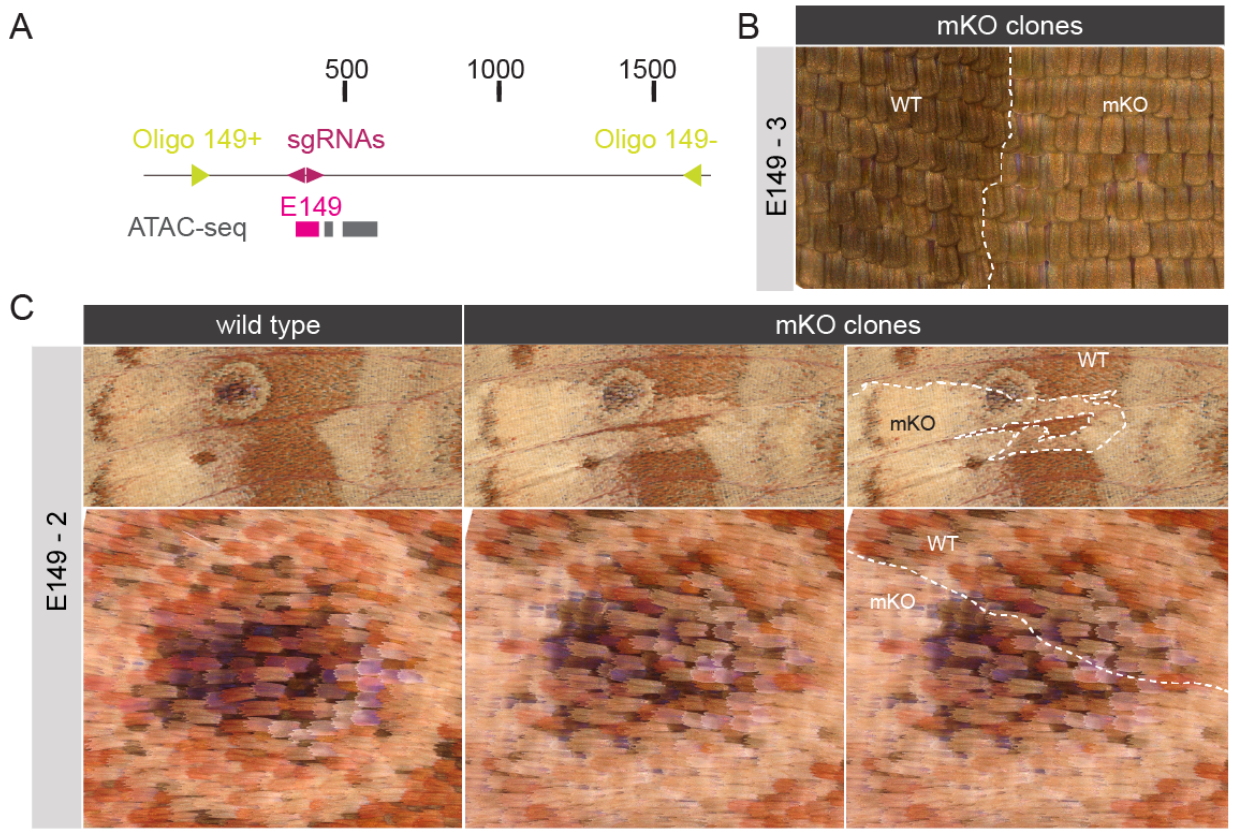

Figure S6. mKOs phenotypes from CRISPR deletions targeting of CRE E149. (A) A map of sgRNAs, including ATAC-seq peak calls. (B) An example mKO individual showing a partially hypomorphic pigmentation phenotype. (C) Another mKO example showing partially hypomorphic clones.

Table S1. *J. coenia* multi-tissue PacBio Iso-Seq

Species	Tissue, Developmental Stage (Days)	Sequencing	Pipeline	Files	DRYAD	Author
J. coenia	Multi-tissue/stage	Iso-Seq (U of Maryland)	SMRT.IsoSeq pdmm2	.css	DOI: 10.5061/dryad.qz612jmpb	This paper
J. coenia	Multi-tissue/stage	Iso-Seq (U of Maryland)	SMRT.IsoSeq pdmm2	hq/lq.fasta	DOI: 10.5061/dryad.qz612jmpb	This paper
J. coenia	Multi-tissue/stage	Iso-Seq (U of Maryland)	BRAKER3	jcv2_Isoseqv3.gff	DOI: 10.5061/dryad.qz612jmpb	This paper
J. coenia	Hindwing, 5th instar ; pre-pupae ; pupae day 3 ; pupae day 6	RNAseq (Cornell Genomics Core)	stringtie; DESeq2	.fasta.gz, .bam	DOI: 10.5061/dryad.rjdfn2z89	van der Burg etal., 2020

Table S2. Genome annotation ogs3 BUSCO measure of completeness

Title	n	Percent
Complete BUSCOs	**5173**	**97.9**
Complete and single-copy BUSCOs	4814	91.1
Complete and duplicated BUSCOs	359	6.8
Fragmented BUSCOs	50	0.9
Missing BUSCOs	63	1.2
Total BUSCO groups searched	5286	100

Note: Genome annnotations were assessed using dataset lepidoptera_odb10 https://busco.ezlab.org, gene feature files DOI: 10.5061/dryad.qz612jmpb

Table S3. ChIP-Seq data sources

Species	Tissue, Developmental Stage (Days)	Sequencing	Antibody	Pipeline	Files	Author
J. coenia	Forewing and hindwing, pupae day 3	ChIP-Seq	anti-RNA-polymerase II (ab5408)	Lewis et al, 2016	.bw	This paper
J. coenia	Hindwing, pupae day 3	ChIP-Seq	anti-spineless (Gift Matthew Perry) (Perry et al, 2016)	Galaxy	.bw	van der Burg et al, 2017
J. coenia	Hindwing, pupae day 3	ChIP-Seq	Developmental Studies Hybridoma Bank, RRID:AB_528212	Lewis et al, 2016	.bw	van der Burg et al, 2017
J. coenia	Forewing and hindwing, pupae day 3	ChIP-Seq	anti-beta Ftz-F1 (Gift: Chris Doe)	Galaxy	.bw	This paper
J. coenia	Forewing and hindwing, pupae day 3	ChIP-Seq	anti-bab (Gift: Arnaud Martin)	Lewis et al, 2016	.bw	Chatterjee et al, In Prep

Table S4. Hi-C, ATAC-seq, and alignment data sources for Figure 1

Species	Tissue, Developmental Stage (Days)	Sequencing	Pipeline	Files	Author
J. coenia	Forewing and hindwing, early 5th instar	HI-C	Mazo-Vargas et al, 2022	DOI: 10.5061/dryad.8cz8w9gpr	Mazo-Vargas et al, 2022
J. coenia	Forewing and hindwing, 5th instar, pupae day 3	ATAC-Seq (Cornell Genomics Core)	Mazo-Vargas et al, 2022	DOI: 10.5061/dryad.8cz8w9gpr	Mazo-Vargas et al, 2022
V. cardui	Hindwing, pupae day 3	ATAC-Seq	Mazo-Vargas et al, 2022	DOI: 10.5061/dryad.8cz8w9gpr	Mazo-Vargas et al, 2022
Heliconius erato demophoon	Forewing and hindwing, pupae day 2	ATAC-Seq	Lewis et al, 2019	SRA: PRJEB43672	Livraghi et al, 2021
Danaus plexippus	Hindwing, pupae day 3	ATAC-Seq	Mazo-Vargas et al, 2022	DOI: 10.5061/dryad.8cz8w9gpr	Mazo-Vargas et al, 2022
J. coenia	Forewing and hindwing, 5th instar; pupae day 3	Analysis: Comaprative alignment of ATAC peaks calls	CACTUS/HALPER	strong-cons.bed; scores.bed (this paper)	Mazo-Vargas et al, 2022

Table S5. Candidate targets highly conserved and putatively functional (ATAC-seq) in nymphalids

***Junonia coenia* Jcgenv2.fa Scaffold15. 3358377 - 3005902**				
Name	**Type**	**Sequence**	**Min**	**Max**
404 (miR-2788)	miRNA	GCCGTATTGCTGGGGTTTCCTAGCGGCATGTGCCTTCTATCATGCAATGCCCTTGGAAAT	3312783	3312868
398-399 (miR-193)	miRNA	TGAAGAGGTCCCAGCCTTAGCGAGGGTCTTGGTGGTCTAGTGGGTTTTCCGTTTCTTACT	3309914	3310015
387	Conservation	ACGGTACCATTGTAGGAAATTAAGCTAAATTTCCTACGTTGTCGACGCTACATTTATGAAA	3302520	3302687
295-296	Conservation	AAGCGACCTCCAACGGACTTTAATGTAGCTATTTCATTCATGAAATAAATATGAACCTATT	3219796	3220009
230	CRISPR	ATCGCATCGGAAATTACATCTCAGCATAAATGGCGTCGCTTAAGAACAGTCATGTTCTCA	3161412	3161471
209	CRISPR	GCAAAAAACGTGATGCTGCGTCACGCACGAGCTCTCCGAGTCGAATCTCGATGTCAAAG	3143206	3143279
205	CRISPR	GCAAAGTCATTGAAGAATCTCGACCAATCAGAATCGTGTTGTTCATTTTTTGATCGCACG	3142046	3142105
ivory Exon1	PacBio string 12488139.ccs	CGCGCGTTCAACACGAATTCAAACACATTTACGGTCCGCCTGTTTCGAGTGCAACGACCT	3119250	3119564
ivory$^{\Delta 18bp}$	KO allele	CGTCGCGTAGATCGCGAGC	3119225	3119243
187	Promoter	GATTAGAGAAAAGATGTTTGAAATAGTTCTAAGACTCCTCATTCGTCGCGTAGATCGCGA	3119182	3119258
ivory$^{\Delta 17kb}$	KO allele	GATACTTCACTGAATTTCCAATATTTAACAAATATTAAAATTTACGACGGCCCGGCGTGCA	3110453	3127042
149	CRISPR	CCGCGCTGGGTGGCTAACGTCAATTATGAGAGTTATTGCTGGGACAGATCGTGCTCGGT	3075203	3075262
122	Conservation	AACGGTTCCTAAGTAGCGGTTAATTTGCGTTGACACGCACTTTGCGCGGGCGTGTACGTT	3048083	3048173

***Vanessa Cardui* Scaffold13 2319780 - 1926386**				
Name	**Type**	**Sequence**	**Min**	**Max**
404 (mir2788)	miRNA	TATTGCTGGGGTTTCCTAG	2238906	2238924
398-399 (miR193)	miRNA	GTCCCAACCTTAGCGAGGGTCTTGGTGGTCTAGTGGGTGTGTTCGTTTCTTACTGGCCTG	2235661	2235720
387	Conservation	CAGTGTATTCGGCCCTATCCCTAACAAGCGACCTGAATATACAGATAAGGCTATAAAGAT	2226560	2226619
295-296	Conservation	AAGCGACCTCTAACGGACATTAATGTGGCTATTTCATTCATGAAATAAATATGAACCTATT	2146720	2146934
230	CRISPR	ATGTTTAATAAATGTTTATTATACGACAAAACACGTGCGCGGTCAATCTGAATGCATTTGT	2091193	2091377
199	Conservation	TCGTCGGTATGCCAGCACCTAAGTAATGGGCGGGAACGCGGTCACCGCGTCCGCGTCG	2055953	2056162
205	CRISPR	GCAAAGTCATTGAAGAATCTCGACCAATCAGAATCGTGTTGTTCATTTTTTGATCGCACG	2050345	2050414
209	CRISPR	TGCCATGAATCAGTTATCGATGTCAAAGACTTCGAGATTCGACTCGGAGAGCTCGTGCG	2048679	2048746
187	Promoter	GATTAGAGAAAAGATGTTTGAAATAGTTCTAAGACTCCTCATTCGTCGCGTAGATCGCG	2030384	2030471
149	CRISPR	CCATATTCTCCGCACTGGGTGGCTAACGTCAATTATGAGAGTTATTGCTGGGACAGATC	1995086	1995146
122	Conservation	AATGGTTCCTAAGTAGCGGTTAATTTGCGTTGACACGCACTTTGCGCGGGCGTGTCCGTT	1969028	1969119

***Heliconius erato demophoon* Herato1505.2355092 - 1969424**				
Name	**Type**	**Sequence**	**Min**	**Max**
404 (mir2788)	miRNA	GTCGCTGTATTGCTGGGGTTTCCTAGCGGCATGTGCCTTCTTCTATGCAATGCCCTTGGA	2305095	2305181
398-399 (miR193)	miRNA	TCCCAGCCTTGGTGAGGGTCTTGGCGGTCTAGTGGGTGTGCTCTGTTCTTACTGGCCTG	2301756	2301847
387	Conservation	AATTAAGCTAAATTTTCGAGCGATGTCGCCGCTTCGTTTATGAAATGCGGTGTTAACAC	2285807	2285900
295-296	Conservation	TTAATGTAGCTTTTTCATTCACAATATAAATAATCACCCATTCCGTGTTTGCCCGCGCTTT	2206869	2207069
230	CRISPR	AATTTATTCAAAGATCAAGCCAACCGTAAAACACCGTGACGTTGTAAGATCGTTTTAATT	2149256	2149434
199	Conservation	ACAATGTTAAAGGCGACACTCTTTAACCATTTTTTAATCAAGATTTTATTGCATCCTCCGA	2117247	2117345
205	CRISPR	GCAAAGTCATTGGGGAATCTCAACCAATCAAAAACGTGTTGTTCATTTTTTAAGCGCACG	2108054	2108113
209	CRISPR	TGACATTCCAATTACAAAAGAAGTTGTCAAGATATTTCCCCGCTATGAATCAGTTATCGA	2103985	2104098
187	Promoter	GATTAGAGAAAAGATGTTTGAAATAGTTCTAAGTCTCCTCATTCGTCGCGTAGATCGCGA	2094029	2094103
149	CRISPR	CCGCACTGGGTGGCTGACGTCAATTATTAGAGTTATTGCTGGGACAGATCGTGC	2056032	2056085
122	Conservation	AAGTAGCGGTTAATTTGCGTTGACACGCACTTTACGCGGGCGTGTCCGTTCGATCAATCA	2028413	2028494

***Danaus plexippus* NC_045809.1 9810282 - 9633350**				
Name	**Type**	**Sequence**	**Min**	**Max**
404 (mIR2788)	miRNA	GTCGCTGTATTACTGGGGTTTCCTAGCGGCATGTGCTTACCCTCATCACCCACGCAATGC(	9791129	9791214
398-399 (miR193)	miRNA	CAAGTCCCAACCTTGGCAAGGGCCTTCGCGGTCCAGTGGGTTTGATTTTCGTACTGGCCT	9789985	9790069
387	Conservation	CGGTACTTTTTAAGGAAATTAAGGTAAATTTGAGTGCGATGTCGGCGCGTGGCTTCAT	9784155	9784298
295-296	Conservation	AAGCGACCTCTGGGAGACATTAATGTAGCTATTTCATTTATATAATAAATAACACCCCAT	9750130	9750315
230	CRISPR	ATCGCGTCGGAAATTACATCTCCGCATAAATAGCATCGCTTAAGAAATCATGTACTCATTA	9719848	9719910
199	Conservation	TCGCGGAAATTGAATTGGTTGCCTTAGTTATGGGAGGTATGATTCAATGTTAAGGACA	9701097	9701203
209	CRISPR	ATCAGTAACAGAAGTCAAAGACATCGAAATTCGGCTCGAGCAGTCCGTGCGTGACGCAG	9696570	9696643
187	Promoter	AAAGGATTAGAGGAAAGATCTTTGAAATAGTTCTAAGACTCCTCATTCGTCGCGGAGATC	9686031	9686114
149	CRISPR	TTCTCGCCGCCCCCCACACTGGGTGGCTAACGTCAATTATGAGAGTTATAGCAGATCGT	9662143	9662223
122	Conservation	AACAGGTCCCATATAACAGTTAATTTGCGTGGACACGCACTTTAAACAGGCGTCTTCGTT	9649164	9649256

Note: Nomenclature for putative CREs are based on the last three digits of labeled alignments from multiple alignment files (.maf) labeled strong_cons.bed, scores.bed.
Access DOI: 10.5061/dryad.qz612jmpb

Table S6. CRISPR-Cas9 sgRNAs used in this study

Scaffold 15 (non-coding)					
Name IDT	**Enhancer Locus**	**Type**	**Sequence**	**Min (Scaffold15)**	**Max (Scaffold15)**
Cort.P2a.F1.700bp	187	genotyping	GCTTTTTCCATGAAGGGCAAATTTT	3118852	3118876
Cort.P2a.R1.700bp	187	genotyping	CCACAATCACAGTACCACATCAAAA	3119520	3119544
Jc.Cort.Pol2a	187	sgRNA	**CCG**CCATTTTTTTTTCAACGAAC	3119315	3119334
Jc.Cort.Pol2b	187	sgRNA	TTCGTCGCGTAGATCGCGAG**CGG**	3119223	3119242
Jc.Cort.Pol2c	187	sgRNA	**CCG**TGTCGAACCGATAGCCCCAC	3119108	3119127
150,710 F	230	genotyping	TAGACCTGACACCTACAGAACTATTGT	3160796	3160822
152,107 R	230	genotyping	TGGGATCTACCGTGTATTTAATAAGTAGG	3162165	3162193
Plas4a	230	sgRNA	TATACGACAAAACACGTGCG	3161349	3161368
Plas4.b	230	sgRNA	TTTCACGAGATGCATCGCAT	3161399	3161418
Plas4.c	230	sgRNA	CAGTCATGTTCTCATTAAGG	3161458	3161477
132,438 F	209	genotyping	TTACAACCGCATCGTGTATCAGA	3142524	3142546
134,432 R	209	genotyping	ATATGAGAAACATGAAACGAAATGATG	3144492	3144518
JC.Plas3.CP1a	209	sgRNA	AAACCTCAACTGCATAATAT	3143116	3143135
JC_Plas3.CP1b	209	sgRNA	GAATGTAAACTATCAGATAA	3143374	3143393
131,190 F	205	genotyping	TATATTTCGTTTAATACTTTTCAACCCTCG	3141276	3141305
132,811 R	205	genotyping	AGAATCTGAACAGAGAGCCTCAC	3142875	3142897
JC.CP2.1a	205	sgRNA	ACGCGCAACGTTTCTAAAGA	3142029	3142048
JC.CP2.1c	205	sgRNA	TTGGAATTGAGAAGCGCTT	3141947	3141965
64,780 F	149	genotyping	GCTGAACCGATTAGGCTAAAAGTTG	3074866	3074890
66,421 R	149	genotyping	AAGCGTTTAAAAGTTTACATGCTAT	3076483	3076507
Yb2.sgA	149	sgRNA	TTGCTGGGACAGATCGTGCT**CGG**	3075238	3075260
Yb2.b	149	sgRNA	TTGACGTTAGCCACCCAGCG	3075206	3075225

Scaffold 22 (JC_g12129.t1)					
Name IDT	**Date Injected**	**Type**	**Sequence**	**Min**	**Max**
Jc.FtzF1.Ex2.1F	8/2/21	genotyping	CCCGCAAATTACAAATGATGAGACA	14,694,013	14,694,037
Jc.FtzF1.Ex2.1R	8/2/21	genotyping	CAAATTTTGGTCCAGCACTTTGC	14,694,512	14,694,490
Jc.FtzF1.Ex2a	8/2/21	sgRNA	GTCATCGCCGGAGTCCTCGC	14,694,167	14,694,189
Jc.FtzF1.Ex2b	8/2/21	sgRNA	GCTCTGCAAGAGTCCGAACA	14,694,284	14,694,262

Note: Max and Min coordinates provide nucleotide location on Scaffold 15 from *Junonia coenia* genome (jcgenv2.fa)

Table S7. CRISPR-Cas9 microinjection

Targets	Injected Embryos	Pupae	Adults (mKOs)	mKO efficiency (%)	# of guides	RNP (Cas9:sgRNA)	Working sgRNA (ng/ul)	Genotyping
Promoter (P187)	282	89	75	27	3	1:2	250	Nanopore
E205	481	93	19	4	2	1:2	250	Nanopore
E209	282	79	14	5	2	1:2	250	Nanopore
E230	87	20	12	14	3	1:2	250	Nanopore
E149	123	27	9	7	2	1:2	250	Nanopore
Ftz-F1 exon2	394	20	12	3	2	1:5	100	PCR

Note: All injections were done in *J. coenia* 1-2 hours post oviposition

Table S8. Confirmation of *ivory* knockouts and sequencing sources

Species	Tissue, Developmental Stage (Days)	Sequencing	Pipeline	Files	Author
J. coenia (Red Colony)	Forewing and hindwing, 5th instar; pupae day 2; pupae day 6	RNAseq (Novogene) 3 Replicates	Galaxy: HiSAT2; DESEQ2	.fa	This Paper
ivory$^{\Delta 17kb}$	Forewing and hindwing, 5th instar; pupae day 2; pupae day 6	RNAseq (Novogene) 3 Replicates	Galaxy: HiSAT2; DESEQ2	.fa	This Paper
ivory$^{\Delta 17kb}$	Forwing and hindwing, pupae day 2	Full Genome Sequence - Genotyping (Novogene)	Galaxy	.fa	This Paper
ivory$^{\Delta 18bp}$	Forwing and hinwing, pupae day 2 (Heteroallelic)	Full Genome Sequence - Genotyping (Novogene)	Galaxy	.fa	This Paper
J. coenia ; CRE mKO ; ivory$^{\Delta 18bp}$	Thorax muscle, adult butterfly	Nanopore PCRGenotyping 96-well (Cornell Genomics Core)	Mazo-Vargas et al, 2023	.bam	This Paper
J. coenia ; ivory$^{\Delta 18bp}$	Forwing and hinwing, pupae day 2 (Homoallelic)	RNAseq (Novogene) High coverage 1 Replicate	Stringtie	.bam	This Paper

Note: Whole genome sequencing and nanopore were used to confirm homoallelic ivory$^{\Delta 18bp}$

Table S9. Differential expression of known and suspected pigmentation and wing patterning genes

5th instar imaginal discs

ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	Normalized read counts					
					WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g8907.t1	ss: Spineless, isoform C	0.8816	8.18E-04	1.60E-02	155.61	121.04	136.83	266.01	260.97	260.97
JC_g4349.t1	crol: Crooked legs, isoform G (Herfst)	-0.9072	6.58E-04	1.36E-02	881.80	1210.41	809.23	507.22	493.73	493.73
JC_g5107.t1	PPO2: Phenoloxidase 2	-1.1169	1.32E-06	7.61E-05	1500.73	1335.09	1322.97	546.31	656.96	656.96
JC_g24987.t1	ry: Xanthine dehydrogenase	-1.1248	7.17E-06	3.19E-04	796.52	860.60	1013.21	342.28	419.17	419.17
JC_g16569.t1	Ddc-RC: LP11638p	-1.3453	3.37E-04	8.07E-03	560.03	619.73	244.28	151.60	174.32	174.32
JC_g5233.t1	PPO2: Phenoloxidase 2	-1.4293	2.11E-07	1.54E-05	440.46	451.48	379.43	119.18	163.23	163.23
JC_g13285.t1	MP1: Melanization protease 1	-1.9499	1.23E-12	2.62E-10	1419.85	1339.93	951.09	329.89	279.11	279.11
JC_g13281.t1	MP1: Melanization protease 1	-2.7415	3.45E-15	1.12E-12	2075.71	1733.31	902.41	174.48	203.54	203.54
JC_g4218.t1	Protein of unknown function (Mannose Receptor-like)	-3.9273	1.41E-64	8.24E-61	4167.24	3821.28	3478.67	204.99	235.78	235.78
JC_g15695.t1	Nrg-RC: RT01988p (Fragment)	-4.6473	1.78E-66	2.08E-62	6987.60	4592.31	5682.22	210.71	182.38	182.38

Pupal wings, 2 days after pupation

ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	Normalized read counts					
					WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g22472.t1	Osi7: FI03362p	6.52	3.5E-259	2.02E-255	374.13	366.07	549.42	39475.30	51663.33	41048.42
JC_g4287.t1	Treh1a: Trehalase (Fragment)	4.74	6.5E-30	6.86E-28	2.18	1.97	6.95	193.34	167.06	139.70
JC_g7439.t1	Tret1-2: Facilitated trehalose transporter	4.38	5.2E-24	4.01E-22	1.45	3.95	5.96	145.85	148.12	102.66
JC_g12075.t1	t: Mutant tan	2.69	1.6E-11	4.19E-10	29.06	40.46	38.75	442.08	112.49	335.50
JC_g4577.t1	yellow-h: Yellow-h	2.56	2.9E-20	1.59E-18	451.86	470.66	736.20	5129.73	3404.65	2246.89
JC_g4286.t1	Treh1b: Trehalase	2.01	7.2E-33	9.41E-31	403.91	408.50	323.89	1637.17	1721.81	1357.87
JC_g21003.t1	v: Tryptophan 2,3-dioxygenase	1.98	3.7E-18	1.73E-16	254.26	240.76	329.85	1329.64	1280.78	807.53
JC_g4745.t1	yellow-b: LD43175p	1.76	7.4E-13	2.22E-11	302.93	347.32	567.30	1673.35	1477.91	1165.25
JC_g18351.t1	EcR: Ecdysone receptor, isoform E	1.10	1.8E-13	5.60E-12	704.66	700.56	663.68	1616.82	1589.28	1281.67
JC_g24988.t1	ry: Xanthine dehydrogenase	1.00	2.0E-05	1.81E-04	176.53	190.43	161.94	470.35	297.36	319.62
JC_g8907.t1	ss: Spineless, isoform C	0.63	1.9E-05	1.74E-04	6535.93	6862.55	8397.28	12594.24	10668.34	10668.25
JC_g7735.t1	ca: Claret, isoform A	0.54	8.2E-04	4.50E-03	459.85	565.38	558.36	840.07	718.35	757.78
JC_g1969.t1	Doa: Darkener of apricot, isoform P	0.52	5.3E-06	5.48E-05	2991.55	3287.71	3450.51	4764.53	4627.51	4628.20
JC_g4327.t1	wash: Washout	0.50	5.7E-04	3.31E-03	1919.30	2450.00	2282.13	2854.88	3265.43	3352.88
JC_g20885.t1	Sox102F: LD16247p	-0.39	5.6E-04	3.22E-03	4867.26	4638.51	5092.81	3640.67	3592.87	3916.98
JC_g13285.t1	MP1: Melanization protease 1	-0.52	1.3E-04	9.50E-04	11371.96	10951.47	10440.96	6591.65	7656.84	8542.01
JC_g4349.t1	crol: Crooked legs, isoform G (Herfst)	-0.54	7.3E-04	4.09E-03	750.43	905.80	932.92	633.16	592.50	545.05
JC_g11934.t1	ap: Apterous, isoform C	-0.61	1.8E-04	1.21E-03	996.70	1022.23	877.28	539.32	642.62	702.75
JC_g917.t1	en: Segmentation polarity homeobox protein engrailed	-0.68	6.9E-05	5.32E-04	1166.69	1065.64	1025.32	576.63	639.28	802.24
JC_g4583.t1	yellow-d2: RH49821p	-1.21	6.8E-07	8.56E-06	986.53	976.84	786.87	264.57	357.50	526.00
JC_g13284.t1	MP1: Melanization protease 1	-1.38	2.1E-03	9.83E-03	82.09	54.27	31.79	15.83	21.16	17.99
JC_g14431.t1	MP1: Melanization protease 1	-1.40	4.1E-06	4.42E-05	1133.27	993.61	727.26	167.34	422.10	420.17
JC_g16569.t1	Ddc-RC: LP11638p	-1.59	7.9E-09	1.37E-07	183.07	305.88	272.23	72.36	92.44	74.09
JC_g17832.t1	b: Black, isoform A	-1.67	9.5E-04	5.11E-03	26.88	94.72	34.77	11.31	12.25	12.70

Pupal wings, 6 days after pupation

ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	Normalized read counts					
					WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g9980.t1	Dat: Dopamine N-acetyltransferase (aaNAT)	2.4289	2.0E-11	4.29E-09	30.96	16.82	22.33	244.45	108.91	199.75
JC_g9478.t1	mamo-RC: FI17807p1	2.2136	6.6E-16	2.57E-13	94.76	64.14	107.41	588.81	431.01	427.47
JC_g4583.t1	yellow-d2: RH49821p	1.8447	7.6E-17	3.52E-14	12575.71	15049.81	9409.28	39805.96	51175.02	53002.17
JC_g5106.t1	PPO2: Phenoloxidase 2	1.6911	5.2E-07	3.95E-05	116.34	91.47	57.43	213.41	310.11	532.34
JC_g5232.t1	PPO2: Phenoloxidase 2	1.6478	2.0E-10	3.21E-08	193.27	216.59	144.63	496.65	642.36	786.02
JC_g4577.t1	yellow-h: Yellow-h	1.628	8.8E-10	1.19E-07	109.77	177.69	165.90	495.68	624.83	437.46
JC_g5107.t1	PPO2: Phenoloxidase 2	1.5206	1.6E-05	6.80E-04	153.87	252.34	73.38	676.11	708.82	315.61
JC_g5107.t1	PPO2: Phenoloxidase 2	1.5206	1.6E-05	6.80E-04	153.87	252.34	73.38	676.11	708.82	315.61
JC_g9337.t1	hh: Protein hedgehog	1.4121	5.9E-06	3.05E-04	104.14	49.42	97.84	236.69	303.65	229.71
JC_g13281.t1	MP1: Melanization protease 1	1.0726	3.5E-04	8.12E-03	344.32	405.84	215.88	940.92	438.40	856.94
JC_g13285.t1	MP1: Melanization protease 1	1.0135	3.5E-05	1.28E-03	1414.81	1395.21	880.53	1980.79	3003.24	2888.41
JC_g4287.t1	Treh1a: Trehalase (Fragment)	0.9805	7.7E-05	2.44E-03	691.46	827.46	1278.25	2115.63	1642.83	2070.43
JC_g4328.t1	dome: Cytokine receptor	0.8521	1.2E-04	3.64E-03	547.91	619.28	414.74	904.06	1026.31	1032.72
JC_g18266.t1	laccase2: Laccase 2, isoform D	0.7504	2.8E-04	6.78E-03	612.65	506.78	533.85	1056.36	941.40	861.93
JC_g23411.t1	B-H1: Homeobox protein B-H1	-1.2113	2.2E-06	1.31E-04	474.73	522.55	440.26	239.60	195.66	141.82
JC_g23380.t1	KFase: Kynurenine formamidase	-1.5129	2.6E-11	5.27E-09	3722.80	4597.79	5602.18	1668.44	1183.21	1702.89

Note: DESeq2 Benjamini-Hochburg normalized read count FDR 0.01; exclude below 0.01

Table S10. Differentially expressed transcripts from 5th instar imaginal discs

5th instar imaginal discs					Normalized read counts					
ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g25003.t1	CG17109: Aminoacylase (Drosoph	6.01	6.34E-38	1.85E-34	2.64	0.00	0.00	288.89	258.96	258.96
JC_g21190.t1	Protein of unknown function	5.32	7.56E-24	5.89E-21	0.00	0.00	0.00	139.20	102.78	102.78
JC_g9203.t1	RTase: ORF2 for putative reverse	4.41	1.66E-18	7.75E-16	1.76	0.00	1.68	102.97	79.60	79.60
JC_g3273.t1	pol: Pol protein (Drosophila melan	4.17	1.05E-15	3.52E-13	1.76	0.00	0.84	69.60	63.48	63.48
JC_g4747.t1	Protein of unknown function	4.15	4.03E-16	1.39E-13	0.00	2.42	1.68	85.81	69.53	69.53
JC_g12413.t1	pol: RNA-directed DNA polymeras	4.03	1.30E-12	2.72E-10	0.00	0.00	0.00	46.72	41.31	41.31
JC_g24001.t1	PIF1: ATP-dependent DNA helica	4.00	3.12E-26	3.04E-23	20.22	55.68	53.72	831.39	1049.93	1049.93
JC_g24819.t1	Cyp28d1: Probable cytochrome P	3.97	3.00E-18	1.30E-15	7.03	21.79	10.07	582.54	258.96	258.96
JC_g25241.t1	Cyp4c3: Cytochrome P450 4c3 (D	3.93	7.77E-17	2.84E-14	1.76	2.42	4.20	109.64	81.62	81.62
JC_g8266.t1	hng2: Hinge2 (Drosophila melano	3.55	8.11E-12	1.39E-09	11.43	48.42	11.75	222.15	863.52	863.52
JC_g4245.t1	"CG42331: Uncharacterized prote	3.37	4.71E-20	2.50E-17	461.56	209.40	537.25	6601.54	4876.84	4876.84
JC_g10017.t1	"rad: Radish, isoform M (Drosophil	3.33	5.05E-11	7.88E-09	1.76	8.47	3.36	51.49	115.88	115.88
JC_g1370.t1	Protein of unknown function	3.26	9.29E-13	2.01E-10	29.01	31.47	20.15	149.69	552.17	552.17
JC_g9202.t1	CHKov1: GH03753p (Drosophila r	3.04	4.06E-08	3.57E-06	1.76	0.00	1.68	26.70	35.27	35.27
JC_g25005.t1	ORF: Orf protein (Drosophila mela	3.02	1.66E-13	4.32E-11	297.16	77.47	204.83	2157.61	2180.47	2180.47
JC_g24031.t1	Protein of unknown function	2.98	7.62E-07	4.66E-05	0.00	0.00	0.00	5.72	74.56	74.56
JC_g10443.t1	AOX4: Aldehyde oxidase 4 (Drosc	2.85	2.58E-08	2.35E-06	58.02	8.47	12.59	478.62	294.22	294.22
JC_g21191.t1	pol: Pol protein (Drosophila melan	2.78	2.36E-06	1.26E-04	1.76	0.00	0.00	39.09	19.14	19.14
JC_g3279.t1	Protein of unknown function	2.78	7.79E-07	4.74E-05	6.15	0.00	0.84	61.02	40.30	40.30
JC_g1714.t1	Protein of unknown function	2.76	4.20E-08	3.61E-06	1.76	3.63	7.56	41.95	60.46	60.46
JC_g23254.t1	CG13516-RA: FI16615p1 (Drosop	2.75	1.37E-10	2.03E-08	165.28	67.78	47.85	653.10	989.48	989.48
JC_g23640.t1	CG32645-RB: FI21449p1 (Drosop	2.63	7.26E-08	5.78E-06	16.70	9.68	3.36	138.25	80.61	80.61
JC_g23229.t1	Protein of unknown function	2.60	1.07E-05	4.51E-04	1.76	0.00	0.00	17.16	22.17	22.17
JC_g3922.t1	"CG42700: Uncharacterized prote	2.60	1.97E-06	1.07E-04	3.52	0.00	11.75	58.16	76.58	76.58
JC_g23371.t1	obst-E: Protein obstructor-E (Dros	2.56	2.38E-08	2.23E-06	106.38	30.26	36.10	303.19	593.48	593.48
JC_g25057.t1	"VGlut: Vesicular glutamate transp	2.54	2.01E-07	1.48E-05	8.79	4.84	2.52	57.21	48.37	48.37
JC_g13200.t2	Polyprotein (Drosophila melanoga	2.49	3.70E-12	6.87E-10	209.24	223.93	226.65	2303.48	1072.10	1072.10
JC_g16459.t1	Protein of unknown function	2.47	4.28E-05	1.53E-03	0.00	0.00	0.00	23.84	12.09	12.09
JC_g5280.t1	CG4830: CG4830 (Drosophila me	2.43	1.34E-08	1.35E-06	15.82	53.26	27.70	169.71	261.98	261.98
JC_g6189.t1	Protein of unknown function	2.39	1.18E-08	1.24E-06	54.51	16.95	26.86	281.26	201.52	201.52
JC_g9424.t1	"cep290: Cep290, isoform A (Dros	2.38	6.08E-12	1.08E-09	45.72	37.52	28.54	286.03	198.50	198.50
JC_g5408.t1	"CG42339: Uncharacterized prote	2.35	2.63E-05	1.00E-03	19.34	0.00	15.95	71.51	164.24	164.24
JC_g7485.t1	Dmel\CG10585: GH23839p (Dros	2.35	3.18E-10	4.33E-08	381.56	426.07	181.32	2708.69	1703.87	1703.87
JC_g21318.t1	Snmp2: FI17830p1 (Drosophila m	2.33	9.86E-09	1.04E-06	54.51	38.73	20.15	322.26	203.54	203.54
JC_g20875.t1	zye: Zye (Drosophila melanogaste	2.33	1.70E-07	1.26E-05	31.65	31.47	12.59	96.30	212.61	212.61
JC_g7306.t1	Protein of unknown function	2.32	1.25E-04	3.68E-03	0.00	0.00	0.00	11.44	14.11	14.11
JC_g23338.t1	Protein of unknown function	2.31	3.20E-07	2.24E-05	19.34	6.05	9.23	67.69	87.66	87.66
JC_g9703.t1	"Dmel\CG7365: CG7365, isoform	2.30	9.96E-08	7.74E-06	20.22	14.52	6.72	84.86	93.71	93.71
JC_g4201.t1	"CG9518-RA: CG9518, isoform A	2.30	3.21E-08	2.86E-06	8.79	9.68	15.95	73.41	73.56	73.56
JC_g9355.t1	Protein of unknown function	2.28	1.17E-05	4.90E-04	10.55	14.52	8.39	25.74	123.94	123.94
JC_g13216.t1	Protein of unknown function	2.27	7.35E-06	3.26E-04	4.40	12.10	3.36	66.74	42.32	42.32
JC_g11684.t1	CG17443: RE19569p (Drosophila	2.26	1.27E-07	9.58E-06	307.71	203.35	78.91	1604.62	1061.02	1061.02
JC_g23450.t1	Atac1: Ada2a-containing complex	2.26	1.16E-07	8.84E-06	94.95	33.89	86.46	261.24	544.11	544.11
JC_g5101.t1	ORF: E239.9-1 (Fragment) (Droso	2.25	1.92E-04	5.14E-03	0.88	0.00	0.00	25.74	10.08	10.08
JC_g2025.t1	"CG11836: Uncharacterized prote	2.21	2.05E-12	4.05E-10	34.29	31.47	31.90	190.69	160.21	160.21
JC_g14049.t1	CG5255: CG5255 (Drosophila me	2.20	5.72E-05	1.94E-03	4.40	1.21	2.52	20.98	27.21	27.21
JC_g6442.t1	Protein of unknown function	2.20	1.24E-04	3.66E-03	1.76	1.21	1.68	14.30	20.15	20.15
JC_g11536.t1	Protein of unknown function	2.17	2.97E-12	5.60E-10	59.78	65.36	44.49	332.75	258.96	258.96
JC_g10464.t1	Protein of unknown function	2.16	7.42E-05	2.42E-03	4.40	2.42	1.68	29.56	22.17	22.17
JC_g18207.t1	lectin-33A: Lectin-33A (Drosophila	2.15	2.54E-06	1.33E-04	8.79	15.74	11.75	41.95	88.67	88.67
JC_g11395.t1	"nAChRalpha6: Nicotinic acetylcho	2.15	8.44E-20	4.11E-17	545.96	643.94	530.53	2383.57	2856.58	2856.58
JC_g7825.t1	"Blimp-1: Blimp-1, isoform A (Dros	2.15	9.14E-06	3.91E-04	11.43	2.42	11.75	63.88	53.40	53.40
JC_g24994.t1	bchs: Blue cheese (Drosophila me	2.14	1.05E-04	3.22E-03	7.91	0.00	4.20	32.42	38.29	38.29
JC_g1799.t1	CG31274: LP05795p (Drosophila	2.13	6.41E-07	4.11E-05	50.11	14.52	57.92	244.08	228.73	228.73
JC_g24954.t1	jhamt: Juvenile hormone acid O-m	2.13	7.21E-07	4.48E-05	361.34	697.20	161.17	2368.32	2265.11	2265.11
JC_g24211.t1	Protein of unknown function	2.13	4.16E-04	9.52E-03	0.00	0.00	0.00	3.81	22.17	22.17
JC_g1778.t1	"CG5961: CG5961, isoform A (Dro	2.11	1.14E-04	3.43E-03	99.35	4.84	88.14	378.51	567.29	567.29
JC_g664.t1	CG30503: RH50933p (Drosophila	2.09	1.84E-06	1.02E-04	29.01	14.52	16.79	64.83	138.04	138.04
JC_g4502.t1	"CG9395: CG9395, isoform C (Dro	2.08	2.00E-08	1.90E-06	26.37	15.74	32.74	137.29	121.92	121.92
JC_g4263.t1	"mwh: Multiple wing hairs, isoform	2.07	1.87E-08	1.82E-06	18.46	25.42	31.90	148.73	113.86	113.86
JC_g1774.t1	Protein of unknown function	2.06	4.84E-05	1.67E-03	144.18	15.74	137.67	579.68	658.98	658.98
JC_g13902.t1	CG11151: GEO07753p1 (Drosopl	2.04	4.14E-04	9.50E-03	9.67	66.57	1.68	228.82	252.91	252.91
JC_g2169.t1	TkR86C: Tachykinin-like peptides	2.03	4.13E-08	3.58E-06	65.94	38.73	46.17	335.61	196.48	196.48
JC_g8417.t1	Oatp33Eb: Organic anion transpo	2.02	4.75E-05	1.66E-03	15.82	3.63	29.38	89.62	103.78	103.78
JC_g711.t1	R1A1-element\ORF1: Uncharacter	2.01	1.50E-04	4.23E-03	4.40	8.47	1.68	32.42	31.24	31.24
JC_g18618.t1	tnc: Tenectin isoform 1 (Drosophil	1.99	4.61E-09	5.34E-07	4077.57	6526.55	5120.63	34148.95	18593.47	18593.47
JC_g2968.t1	"futsch: Futsch, isoform F (Drosop	1.98	7.69E-14	2.14E-11	89.67	89.57	82.27	327.03	392.97	392.97
JC_g11166.t1	CG6295: CG6295 (Drosophila me	1.97	5.94E-05	2.00E-03	9.67	67.78	26.86	194.50	196.48	196.48
JC_g19635.t1	"Duox: Dual oxidase, isoform C (D	1.97	7.68E-09	8.39E-07	110.77	72.62	84.78	545.36	327.47	327.47
JC_g7919.t1	niki: NimA-like kinase (Drosophila r	1.94	2.67E-04	6.75E-03	14.95	2.42	4.20	37.18	50.38	50.38
JC_g21266.t1	CG16723-RB: FI22618p1 (Drosop	1.94	6.72E-06	3.01E-04	40.44	36.31	33.58	301.28	116.88	116.88

JC_g20407.t1	Protein of unknown function	1.94	2.27E-06	1.22E-04	19.34	9.68	24.34	83.90	85.65	85.65
JC_g3879.t1	"Dmel\CG7470: CG7470, isoform	1.94	1.93E-06	1.05E-04	14.07	25.42	36.94	102.97	127.97	127.97
JC_g3091.t1	Acp65Aa: Adult cuticle protein 65	1.93	1.37E-04	3.97E-03	33.41	32.68	5.04	183.06	109.83	109.83
JC_g5272.t1	CG17999: GH16244p (Drosophila	1.92	3.26E-04	7.86E-03	7.03	110.15	62.96	307.00	405.06	405.06
JC_g24242.t1	hop: Tyrosine-protein kinase hops	1.92	1.44E-04	4.12E-03	23.74	3.63	35.26	127.76	112.85	112.85
JC_g10040.t1	AT12189p (Drosophila melanogas	1.91	7.29E-07	4.51E-05	36.05	15.74	23.50	116.32	111.84	111.84
JC_g22144.t1	SP1029: SP1029 protein (Drosop	1.89	3.18E-06	1.58E-04	44.84	18.16	28.54	176.38	118.90	118.90
JC_g1066.t2	Sin3A: SD07795p (Drosophila me	1.88	4.65E-06	2.19E-04	59.78	59.31	27.70	134.43	261.98	261.98
JC_g4087.t1	Dmel\CG7458: CG7458 (Drosophi	1.85	5.35E-05	1.84E-03	18.46	14.52	5.88	69.60	57.43	57.43
JC_g18453.t1	Polyprotein (Drosophila melanoga	1.85	5.99E-07	3.89E-05	33.41	31.47	19.31	97.25	126.96	126.96
JC_g27.t1	"CG45002: Uncharacterized prote	1.84	6.51E-05	2.16E-03	34.29	9.68	13.43	107.74	83.63	83.63
JC_g5457.t1	"Mer: Merlin, isoform B (Drosophila	1.84	1.80E-06	1.00E-04	232.98	124.67	344.17	732.23	1122.48	1122.48
JC_g24798.t1	BEST:GH06505: UDP-glucuronos	1.83	1.90E-04	5.12E-03	75.61	20.58	85.62	511.99	195.48	195.48
JC_g25417.t1	"Ets21C: Ets at 21C, isoform C (D	1.81	1.16E-06	6.86E-05	133.63	255.40	99.89	579.68	699.28	699.28
JC_g8231.t1	Protein of unknown function	1.80	2.29E-10	3.17E-08	104.62	70.20	97.38	338.47	345.61	345.61
JC_g18995.t1	Protein of unknown function	1.80	3.53E-05	1.29E-03	15.82	7.26	16.79	66.74	55.42	55.42
JC_g17834.t1	Cyp6a2: Cytochrome P450 (Drosc	1.80	1.06E-04	3.24E-03	31.65	20.58	62.96	89.62	220.67	220.67
JC_g15822.t1	CG6178: CG6178 (Drosophila me	1.77	1.35E-04	3.94E-03	14.07	24.21	6.72	74.37	61.46	61.46
JC_g3542.t1	Desat1: Fatty acid desaturase (Dr	1.75	6.38E-06	2.89E-04	21.98	15.74	31.06	102.97	85.65	85.65
JC_g10038.t1	Dmel\CG15020: Uncharacterized	1.75	2.35E-05	9.09E-04	29.01	58.10	37.78	97.25	203.54	203.54
JC_g15749.t1	Scgbeta: Beta-sarcoglycan-like pr	1.73	3.55E-04	8.37E-03	9.67	21.79	6.72	39.09	65.49	65.49
JC_g8425.t1	"c-SP18: CG1299, isoform B (Dros	1.72	2.60E-04	6.60E-03	32.53	7.26	15.95	90.58	76.58	76.58
JC_g2905.t1	"dpy: Dumpy, isoform S (Drosophil	1.70	7.49E-08	5.91E-06	253.20	163.41	152.78	540.59	748.66	748.66
JC_g21426.t1	"CG3106: CG3106, isoform A (Dro	1.69	1.72E-04	4.73E-03	24.62	56.89	46.17	285.08	116.88	116.88
JC_g9246.t1	CG15537-RB: IP18706p (Drosoph	1.68	1.69E-04	4.66E-03	19.34	13.31	10.91	81.99	47.36	47.36
JC_g1702.t1	BcDNA.GH08773: BcDNA.GH087	1.67	3.80E-05	1.38E-03	96.71	38.73	89.82	398.53	229.74	229.74
JC_g19811.t1	"Dmel\CG5150: CG5150, isoform	1.67	2.19E-09	2.70E-07	292.76	427.28	353.41	1455.89	1098.30	1098.30
JC_g22913.t1	"CG2016-RB: CG2016, isoform B	1.64	8.51E-05	2.72E-03	1980.76	4604.41	2112.05	17026.32	7805.97	7805.97
JC_g9208.t1	CG17319-RA: RT09926p (Fragme	1.64	1.21E-04	3.57E-03	25.50	15.74	47.01	90.58	123.94	123.94
JC_g23370.t1	obst-E: Protein obstructor-E (Dros	1.64	2.28E-06	1.22E-04	841.36	458.75	407.97	1576.97	2180.47	2180.47
JC_g17726.t1	Pdk1: FI19402p1 (Drosophila mel	1.63	2.36E-05	9.10E-04	1532.38	2160.59	1717.51	10740.37	4372.03	4372.03
JC_g5279.t1	CG17999: GH16244p (Drosophila	1.63	4.11E-04	9.49E-03	53.63	21.79	32.74	237.40	95.72	95.72
JC_g22498.t1	Osi24: Osiris 24 (Drosophila melar	1.63	6.12E-06	2.78E-04	105.50	202.14	109.97	632.12	412.11	412.11
JC_g23404.t1	GIP: Copia protein (Drosophila me	1.62	1.15E-04	3.45E-03	203.09	55.68	192.23	567.29	553.18	553.18
JC_g4242.t1	CG10184: LD34157p (Drosophila	1.62	8.63E-13	1.90E-10	1146.43	974.38	1263.37	3644.96	3611.28	3611.28
JC_g19708.t1	"mthl10: Methuselah-like 10, isofo	1.61	3.43E-04	8.15E-03	14.07	12.10	35.26	75.32	80.61	80.61
JC_g15583.t1	CG12746: RE23632p (Drosophila	1.61	8.04E-05	2.58E-03	70.33	32.68	45.33	109.64	213.61	213.61
JC_g6110.t1	Protein of unknown function	1.60	2.05E-04	5.41E-03	97.59	50.84	37.78	133.48	275.08	275.08
JC_g21684.t1	CG9683: GH26663p (Drosophila	1.59	3.75E-04	8.74E-03	25.50	72.62	29.38	225.01	124.94	124.94
JC_g2517.t1	Protein of unknown function	1.59	1.17E-06	6.86E-05	58.90	36.31	44.49	162.08	151.14	151.14
JC_g21319.t1	"Snmp1: Sensory neuron membra	1.57	3.43E-04	8.15E-03	174.95	227.56	58.76	759.88	460.48	460.48
JC_g5284.t1	"Pgam5: Serine/threonine-protein	1.57	2.73E-08	2.45E-06	450.13	662.10	744.59	1779.10	2064.60	2064.60
JC_g3227.t1	Bteb2-RA: RT01142p (Fragment)	1.57	6.56E-05	2.17E-03	21.98	16.95	15.11	62.93	61.46	61.46
JC_g9608.t1	Protein of unknown function	1.56	6.44E-07	4.11E-05	2292.86	3446.05	2379.83	11582.25	7259.85	7259.85
JC_g8219.t1	Protein of unknown function	1.55	5.33E-07	3.54E-05	121.32	91.99	69.67	301.28	299.26	299.26
JC_g338.t1	Protein of unknown function	1.53	4.79E-05	1.67E-03	210.12	79.89	199.79	599.71	509.85	509.85
JC_g13580.t2	Protein of unknown function	1.53	1.76E-04	4.81E-03	64.18	169.46	82.27	480.53	293.22	293.22
JC_g25301.t1	ninaB: Carotenoid isomerooxygen	1.51	3.72E-04	8.72E-03	14.07	29.05	42.81	90.58	101.77	101.77
JC_g13014.t1	Polyprotein (Drosophila melanoga	1.51	2.10E-05	8.28E-04	460.68	186.40	402.93	1156.51	1095.27	1095.27
JC_g69.t1	"CT30701: Uncharacterized protei	1.50	3.19E-04	7.72E-03	19.34	20.58	32.74	54.35	94.72	94.72
JC_g9584.t1	CG14073: SD21394p (Drosophila	1.50	3.63E-07	2.53E-05	181.99	159.77	202.31	703.63	472.57	472.57
JC_g17332.t1	LPCAT: Lysophosphatidylcholine	1.49	2.38E-04	6.17E-03	156.49	46.00	111.65	370.88	331.50	331.50
JC_g23236.t1	"CG4374: CG4374, isoform B (Dro	1.49	2.27E-04	5.93E-03	443.10	365.55	344.17	2157.61	803.07	803.07
JC_g23271.t1	"Dmel\CG32448: Uncharacterized	1.48	1.49E-06	8.45E-05	479.14	538.63	301.36	1117.42	1419.73	1419.73
JC_g19688.t1	CG15117: Beta-glucuronidase (Dr	1.47	3.94E-05	1.43E-03	47.47	56.89	38.61	193.55	122.93	122.93
JC_g17252.t1	Cc2d2a: SD16006p (Drosophila m	1.46	4.20E-05	1.50E-03	59.78	128.30	131.79	305.10	336.54	336.54
JC_g1783.t1	Protein of unknown function	1.46	2.86E-06	1.46E-04	181.99	121.04	139.35	332.75	490.71	490.71
JC_g8771.t1	"CG31100: Uncharacterized prote	1.45	5.48E-10	7.19E-08	548.60	641.52	629.59	1935.46	1614.20	1614.20
JC_g23156.t1	"Prip: CG7777, isoform A (Drosopl	1.45	1.48E-08	1.47E-06	772.79	607.63	527.17	1734.29	1864.08	1864.08
JC_g8627.t1	Cht5: Cht5 (Drosophila melanogas	1.44	5.38E-05	1.84E-03	1162.26	2546.71	1202.93	5790.17	4547.35	4547.35
JC_g9544.t1	Ppn-RC: GH25513p (Fragment) (D	1.44	9.15E-05	2.91E-03	1906.03	1838.62	863.79	6287.86	3889.38	3889.38
JC_g12446.t1	"f: Forked, isoform I (Drosophila m	1.43	1.76E-04	4.81E-03	53.63	37.52	24.34	131.57	110.84	110.84
JC_g11694.t1	"EG:125H10.1: CG3777, isoform	1.40	1.23E-05	5.14E-04	2729.81	2909.84	1590.75	8566.55	6087.99	6087.99
JC_g11172.t1	"nAChRalpha5: Nicotinic acetylcho	1.40	4.41E-04	9.96E-03	41.32	16.95	30.22	90.58	89.68	89.68
JC_g17830.t1	Dmel\CG32091: FI02074p (Droso	1.39	4.19E-06	2.00E-04	147.70	87.15	133.47	370.88	335.53	335.53
JC_g597.t1	"Neto: Neuropilin and tolloid-like, i	1.39	3.02E-04	7.43E-03	31.65	19.37	25.18	90.58	68.52	68.52
JC_g15996.t1	ATPCL: ATP-citrate synthase (Dro	1.38	1.27E-09	1.60E-07	3302.14	2569.71	3080.77	8598.97	7811.01	7811.01
JC_g22754.t1	Protein of unknown function	1.38	1.90E-04	5.12E-03	66.82	82.31	97.38	351.82	183.39	183.39
JC_g23247.t1	"mTerf5: Transcription termination	1.37	1.41E-04	4.04E-03	144.18	108.94	78.07	215.47	365.76	365.76
JC_g19222.t1	Protein of unknown function	1.36	3.07E-06	1.54E-04	552.99	457.54	359.28	1519.76	1107.37	1107.37
JC_g23237.t1	Spn88Ea: Serine protease inhibito	1.36	5.68E-05	1.93E-03	1289.73	714.14	699.26	1930.69	2807.21	2807.21
JC_g24002.t1	"CG8726-RB: CG8726, isoform B	1.33	4.58E-05	1.62E-03	279.57	154.93	148.58	522.48	536.05	536.05
JC_g22554.t1	T: Transposable element P transp	1.33	1.42E-04	4.08E-03	35.17	36.31	43.65	81.99	118.90	118.90
JC_g24298.t1	"Pde8: Phosphodiesterase 8, isof	1.32	1.97E-04	5.24E-03	72.09	38.73	42.81	135.39	144.09	144.09
JC_g23384.t1	Cg25C-RC: RE33133p (Drosophila	1.32	1.28E-04	3.75E-03	341.12	169.46	180.48	542.50	672.08	672.08

JC_g862.t1	CG5493: RH34904p (Drosophila r	1.31	1.60E-06	9.06E-05	129.24	156.14	117.52	390.91	328.48	328.48
JC_g15689.t1	"Hsc70-5: Heat shock protein cog	1.30	2.50E-05	9.51E-04	1869.98	998.59	1830.83	4374.33	4026.42	4026.42
JC_g19457.t1	pdm3: AT16994p (Drosophila mel	1.28	1.95E-04	5.21E-03	80.88	44.79	84.78	167.80	195.48	195.48
JC_g9545.t1	"AdamTS-A: ADAM metallopeptida	1.27	2.86E-07	2.03E-05	577.61	432.12	465.89	1356.73	1179.91	1179.91
JC_g5379.t1	CG12123: GH02722p (Drosophila	1.25	2.45E-05	9.34E-04	275.18	458.75	474.29	1009.68	1014.67	1014.67
JC_g10271.t1	PCB: Pyruvate carboxylase (Drosc	1.23	2.72E-04	6.86E-03	2356.16	4171.09	2218.66	9437.99	6400.35	6400.35
JC_g4852.t1	Mipp1: Multiple inositol polyphospl	1.23	1.73E-04	4.74E-03	618.05	491.43	303.88	1399.63	1086.21	1086.21
JC_g23241.t1	"nct: Nicastrin, isoform D (Drosoph	1.23	6.53E-08	5.30E-06	1304.68	1270.93	1097.16	2655.30	3114.53	3114.53
JC_g16575.t1	"Hr38: Hormone receptor-like in 38	1.22	1.29E-05	5.36E-04	211.88	205.77	159.49	387.09	515.90	515.90
JC_g7651.t1	"GV1: GV1, isoform B (Drosophila	1.22	2.89E-07	2.03E-05	655.86	515.64	522.98	1447.30	1321.99	1321.99
JC_g2651.t1	mRpL2: RE45450p (Drosophila m	1.20	1.68E-04	4.65E-03	680.47	600.37	346.69	1475.91	1255.49	1255.49
JC_g11421.t1	Fic: Adenosine monophosphate-p	1.19	2.93E-04	7.28E-03	202.21	113.78	234.21	475.76	440.33	440.33
JC_g15943.t1	CG6659: C-mannosyltransferase c	1.19	4.24E-04	9.67E-03	240.89	131.94	289.61	536.78	546.13	546.13
JC_g13966.t1	Nup133: Nup133 (Drosophila mela	1.17	1.60E-05	6.46E-04	271.66	344.97	385.31	918.15	724.47	724.47
JC_g83.t1	"CG3394: CG3394, isoform A (Dro	1.17	9.46E-05	2.99E-03	312.10	561.63	465.05	947.71	1123.49	1123.49
JC_g19243.t1	"Ubr3: Ubr3 ubiquitin ligase, isofor	1.17	4.40E-05	1.56E-03	683.11	462.38	768.93	1692.34	1423.76	1423.76
JC_g19731.t1	R1A1-element\ORF2: Putative 115	1.17	5.51E-06	2.55E-04	360.46	266.29	359.28	834.25	737.57	737.57
JC_g14578.t1	"stum: Stumble, isoform D (Drosop	1.16	6.88E-05	2.26E-03	94.95	112.57	108.29	302.24	221.67	221.67
JC_g22891.t1	MBD-R2: SD10773p (Drosophila n	1.16	5.15E-08	4.30E-06	1731.95	1896.72	1633.56	3798.46	4125.17	4125.17
JC_g23179.t1	pck-RC: LD14222p (Fragment) (Dr	1.15	3.77E-04	8.79E-03	4062.62	2004.45	3390.53	6280.23	8063.92	8063.92
JC_g21285.t1	Prosap: LD13733p (Drosophila me	1.11	1.87E-06	1.03E-04	455.41	525.32	412.17	993.47	1057.99	1057.99
JC_g1785.t1	CG13827: RE30473p (Drosophila	1.11	2.87E-04	7.16E-03	398.26	217.87	379.43	755.12	764.78	764.78
JC_g19581.t1	sog: Dorsal-ventral patterning prot	1.10	5.10E-06	2.37E-04	682.23	611.26	501.99	1312.87	1327.03	1327.03
JC_g5474.t1	"CG2663: CG2663, isoform A (Dro	1.10	6.66E-06	2.99E-04	267.27	240.87	211.54	546.31	521.94	521.94
JC_g4280.t1	Protein of unknown function	1.08	3.39E-04	8.08E-03	960.93	513.22	827.69	1637.99	1752.24	1752.24
JC_g14428.t1	CG9737: CG9737 (Drosophila me	1.08	1.72E-04	4.74E-03	2844.98	2273.16	1677.22	5745.36	4663.23	4663.23
JC_g19241.t1	"Ubr3: Ubr3 ubiquitin ligase, isofor	1.07	5.89E-05	1.99E-03	161.77	125.88	169.57	319.40	340.57	340.57
JC_g19507.t1	CG17636-RA: MIP19773p (Drosop	1.06	1.14E-04	3.44E-03	187.26	199.72	228.33	358.49	489.70	489.70
JC_g22897.t1	CG14694: IP11787p (Drosophila	1.06	2.64E-06	1.38E-04	1345.12	1273.36	1202.93	3075.76	2548.25	2548.25
JC_g18715.t1	Protein of unknown function	1.05	4.09E-04	9.46E-03	1047.96	593.10	1001.46	1942.13	1895.32	1895.32
JC_g3549.t1	CG32603: RE22786p (Drosophila	1.04	4.13E-04	9.49E-03	247.92	284.45	274.50	414.74	664.02	664.02
JC_g7641.t1	Protein of unknown function	1.04	5.14E-05	1.77E-03	627.72	601.58	857.08	1424.42	1505.37	1505.37
JC_g23745.t1	Protein of unknown function	1.01	1.47E-04	4.19E-03	348.15	265.08	385.31	630.22	730.52	730.52
JC_g10528.t1	CG1371-RA: FI04003p (Fragment	1.00	8.88E-06	3.82E-04	1724.04	1474.28	1853.50	3706.93	3350.31	3350.31
JC_g3129.t1	Syt4: FI18813p1 (Drosophila mela	1.00	2.02E-04	5.36E-03	398.26	623.36	471.77	1031.61	1033.81	1033.81
JC_g7465.t1	Pmp70: LD11581p (Drosophila me	0.98	4.24E-04	9.67E-03	781.58	726.25	1030.84	2108.03	1555.75	1555.75
JC_g13373.t1	Fmo-1: Flavin-containing monooxy	0.97	3.51E-04	8.31E-03	1935.92	1538.44	1186.98	3184.45	3131.66	3131.66
JC_g23197.t1	Golgin245: Golgin-245 ortholog (D	0.96	1.63E-04	4.53E-03	648.82	752.88	959.49	1581.74	1586.99	1586.99
JC_g23278.t1	"CG6769: CG6769, isoform A (Dro	0.96	2.89E-06	1.47E-04	1108.63	1016.75	1040.07	2110.89	2091.80	2091.80
JC_g5294.t1	"Mhcl: Myosin heavy chain-like, iso	0.95	3.45E-05	1.27E-03	2048.45	2124.28	2008.80	3454.27	4414.35	4414.35
JC_g23996.t1	"Cpr62Bb: Cuticular protein 62Bb,	0.95	5.76E-06	2.64E-04	1143.79	1191.05	1047.63	2176.68	2250.00	2250.00
JC_g1591.t1	"Sec24CD: Sec24CD ortholog, iso	0.92	3.37E-04	8.07E-03	1481.39	1053.06	1478.27	2829.78	2492.83	2492.83
JC_g13098.t1	"Sec31: Sec31 ortholog, isoform D	0.90	9.51E-05	2.99E-03	2570.68	2940.10	2591.37	5890.28	4782.13	4782.13
JC_g13963.t1	Nup133: Nup133 (Drosophila mela	0.86	4.39E-04	9.95E-03	333.20	331.65	415.53	709.35	648.90	648.90
JC_g1391.t1	PMCA: Calcium-transporting ATPa	0.85	2.54E-04	6.50E-03	4038.00	2970.36	3436.70	6604.40	6370.13	6370.13
JC_g7973.t1	"heph: Hephaestus, isoform Y (Dr	0.83	2.41E-04	6.22E-03	7803.47	9400.07	8933.40	17822.44	14914.68	14914.68
JC_g17389.t1	CG12339: GH08706p (Drosophila	0.83	3.90E-04	9.05E-03	1856.80	1364.14	1613.42	2894.61	2967.42	2967.42
JC_g25336.t1	Ndg-RA: RE69505p (Drosophila m	0.82	1.38E-04	3.98E-03	1044.45	886.02	926.75	1707.59	1722.01	1722.01
JC_g9535.t1	kuz: FI21209p1 (Drosophila melan	0.82	2.08E-04	5.49E-03	1500.73	1445.23	1516.88	3032.86	2508.95	2508.95
JC_g13080.t1	"Dlg5: CG6509, isoform D (Drosop	0.79	1.89E-04	5.11E-03	875.65	785.56	841.97	1510.23	1444.92	1444.92
JC_g4235.t1	"FoxK: Forkhead box K, isoform N	0.75	2.34E-04	6.10E-03	3155.32	3108.34	3380.45	5211.44	5646.66	5646.66
JC_g3258.t1	"CG4096: CG4096, isoform B (Dro	-0.81	2.53E-04	6.48E-03	8425.91	10583.86	9858.47	5601.39	5288.96	5288.96
JC_g18983.t1	"CG14442: Uncharacterized prote	-0.81	2.85E-04	7.13E-03	581.13	648.78	618.67	342.28	344.60	344.60
JC_g5054.t1	"Esp: Epidermal stripes and patch	-0.85	2.49E-04	6.39E-03	1186.87	1321.77	1061.90	693.14	621.70	621.70
JC_g8176.t1	Cpr67B: Cuticular protein 67B (Dro	-0.90	3.21E-04	7.75E-03	4172.52	3247.54	3264.61	1575.06	1986.00	1986.00
JC_g24898.t1	Sp7: Serine protease 7 (Drosophil	-0.93	9.85E-06	4.17E-04	14941.40	15891.52	13305.24	7321.38	7661.88	7661.88
JC_g5941.t1	"Cpr57A: Cuticular protein 57A, is	-0.94	4.12E-04	9.49E-03	1257.21	1684.90	1127.38	635.94	709.36	709.36
JC_g21599.t1	ZnT77C: RE32485p (Drosophila m	-0.94	1.03E-04	3.18E-03	523.10	512.01	584.26	304.14	258.96	258.96
JC_g16638.t1	slmo: RH14110p (Drosophila mela	-0.98	2.27E-04	5.93E-03	10558.77	15197.96	9810.62	5999.93	5658.75	5658.75
JC_g15991.t1	CG5390: SD23103p (Drosophila r	-1.00	1.56E-04	4.38E-03	4775.62	6700.85	4639.62	2890.79	2451.52	2451.52
JC_g9636.t1	Protein of unknown function	-1.00	4.36E-04	9.90E-03	207.48	283.24	266.94	108.69	126.96	126.96
JC_g2834.t1	CG10026: AT17811p (Drosophila	-1.01	5.45E-05	1.86E-03	291.00	282.03	274.50	142.06	133.00	133.00
JC_g13035.t1	"GstS1: Glutathione S transferase	-1.01	6.25E-05	2.09E-03	6664.95	6896.94	5281.80	2513.24	3252.57	3252.57
JC_g22109.t1	"Mob2: Mob2, isoform E (Drosoph	-1.02	1.90E-04	5.12E-03	610.14	768.61	501.15	309.86	290.19	290.19
JC_g340.t1	Nf-YC: Nuclear factor Y-box C (Dro	-1.03	1.93E-05	7.69E-04	702.45	570.10	657.29	284.12	317.40	317.40
JC_g2622.t1	CG3823: CG3823 (Drosophila me	-1.03	3.11E-06	1.55E-04	1022.47	1181.36	1023.29	501.50	516.91	516.91
JC_g5872.t1	CG5255: CG5255 (Drosophila me	-1.04	8.44E-06	3.64E-04	4947.06	5018.38	4614.44	2694.39	2105.91	2105.91
JC_g3508.t1	Protein of unknown function	-1.04	3.79E-04	8.80E-03	716.52	630.63	918.36	270.77	388.94	388.94
JC_g17344.t1	CG10802: LD13611p (Drosophila	-1.06	1.12E-05	4.70E-04	676.08	763.77	879.74	361.35	359.72	359.72
JC_g486.t1	Protein of unknown function	-1.08	4.36E-04	9.90E-03	9934.56	10529.39	16684.85	4480.16	6098.07	6098.07
JC_g12683.t1	"CG9864: CG9864, isoform A (Dro	-1.08	2.82E-04	7.08E-03	764.87	525.32	881.42	282.21	347.63	347.63
JC_g8320.t1	anon-EST:fe1A11: CG7492 (Dros	-1.08	3.11E-05	1.15E-03	969.72	792.82	1016.57	494.83	385.92	385.92
JC_g11429.t1	"l(2)efl: Lethal (2) essential for life,	-1.09	3.54E-05	1.29E-03	4413.41	6300.20	4694.19	2654.34	2158.31	2158.31
JC_g25091.t1	Protein of unknown function	-1.11	3.44E-04	8.15E-03	310.35	367.97	219.94	116.32	138.04	138.04
JC_g5107.t1	PPO2: Phenoloxidase 2 (Drosoph	-1.12	1.32E-06	7.61E-05	1500.73	1335.09	1322.97	546.31	656.96	656.96

JC_g24987.t1	ry: Xanthine dehydrogenase (Dros	-1.12	7.17E-06	3.19E-04	796.52	860.60	1013.21	342.28	419.17	419.17
JC_g20743.t1	Dmel\CG14985: FI11682p (Drosop	-1.13	1.48E-05	6.04E-04	650.58	950.17	755.50	350.86	340.57	340.57
JC_g9243.t1	CG8483: CG8483 (Drosophila me	-1.13	4.15E-04	9.51E-03	2273.52	3712.34	2876.79	877.15	1453.98	1453.98
JC_g1435.t1	"l(2)efl: Lethal (2) essential for life,	-1.16	3.64E-05	1.32E-03	4394.07	7040.98	4999.75	2053.68	2487.80	2487.80
JC_g22806.t1	Protein of unknown function	-1.19	2.03E-04	5.38E-03	803.56	1584.43	965.36	446.20	463.50	463.50
JC_g20053.t1	Ccs: Superoxide dismutase [Cu-Zr	-1.20	5.50E-07	3.63E-05	1684.48	2276.79	1918.98	859.99	808.11	808.11
JC_g8761.t1	CG18643: D-tyrosyl-tRNA(Tyr) dea	-1.20	1.01E-04	3.13E-03	345.51	581.00	399.58	205.94	167.26	167.26
JC_g20319.t1	"Coq2: 4-hydroxybenzoate polypr	-1.20	1.03E-04	3.18E-03	375.40	226.35	258.55	115.36	117.89	117.89
JC_g3167.t1	"disco-r: Disco-related, isoform A (I	-1.21	1.08E-04	3.29E-03	401.78	590.68	469.25	144.92	224.70	224.70
JC_g10770.t1	Protein of unknown function	-1.21	1.37E-04	3.97E-03	312.98	274.76	302.20	163.04	98.75	98.75
JC_g24920.t1	GH20910p (Fragment) (Drosophila	-1.21	2.67E-04	6.75E-03	3383.03	5771.25	2897.77	1326.22	1758.28	1758.28
JC_g8434.t1	Klp61F: Kinesin-like protein Klp61	-1.21	3.39E-06	1.67E-04	4308.79	5251.99	6539.29	2008.87	2315.49	2315.49
JC_g19254.t1	"Mhc: Myosin heavy chain, isoform	-1.22	1.39E-04	4.00E-03	1106.87	870.29	1537.87	358.49	525.97	525.97
JC_g15432.t1	"Meics: Meiotic central spindle, iso	-1.22	3.71E-04	8.72E-03	422.00	694.78	388.66	254.57	170.29	170.29
JC_g8058.t1	GEO10175p1 (Fragment) (Drosop	-1.22	1.47E-04	4.18E-03	1146.43	1998.39	1034.20	535.83	568.29	568.29
JC_g1961.t1	CG34458: Uncharacterized protei	-1.23	1.03E-04	3.19E-03	771.91	587.05	643.02	177.34	310.34	310.34
JC_g25420.t1	nAChRalpha6: Nicotinic acetylcho	-1.24	7.41E-06	3.27E-04	569.70	819.45	563.27	243.12	271.05	271.05
JC_g7879.t1	"bves: Bves, isoform D (Drosophila	-1.24	2.87E-04	7.16E-03	178.47	133.15	104.93	51.49	55.42	55.42
JC_g25100.t1	CG3769: CG3769 (Drosophila me	-1.25	3.07E-04	7.50E-03	216.27	160.99	122.56	54.35	69.53	69.53
JC_g23925.t1	Spn42Da: RE31022p (Drosophila	-1.25	2.97E-04	7.35E-03	1776.79	4249.76	2774.37	1012.54	1187.98	1187.98
JC_g5848.t1	CG11005: LD44221p (Drosophila	-1.26	2.74E-06	1.42E-04	1149.95	988.91	904.08	492.92	359.72	359.72
JC_g12148.t1	"Idgf4: Imaginal disc growth factor	-1.26	3.22E-06	1.60E-04	9436.08	15248.79	12044.39	4488.74	5062.24	5062.24
JC_g25437.t1	Protein of unknown function	-1.27	6.54E-06	2.95E-04	548.60	785.56	718.57	223.10	293.22	293.22
JC_g13038.t1	"GstS1: Glutathione S transferase	-1.27	2.85E-06	1.46E-04	10514.81	17233.87	15375.31	5589.95	5689.99	5689.99
JC_g12540.t1	"drm: Drumstick, isoform C (Drosop	-1.28	4.59E-05	1.62E-03	412.33	340.13	559.07	135.39	185.40	185.40
JC_g16170.t1	sev: Protein sevenless (Drosophila	-1.28	4.61E-05	1.62E-03	402.66	360.70	297.16	96.30	155.17	155.17
JC_g20112.t1	Protein of unknown function	-1.28	2.67E-05	1.01E-03	1028.62	594.31	995.58	299.38	354.68	354.68
JC_g4309.t1	CG10581: IP06602p (Drosophila	-1.29	2.12E-04	5.57E-03	351.67	739.56	400.42	182.10	188.42	188.42
JC_g15601.t1	"CG11843: Uncharacterized prote	-1.29	2.48E-04	6.37E-03	122.20	99.25	130.95	57.21	37.28	37.28
JC_g18891.t1	Protein of unknown function	-1.29	4.40E-04	9.95E-03	79.12	93.20	62.12	27.65	29.22	29.22
JC_g24185.t1	"EbpIII: Ejaculatory bulb protein III	-1.30	3.30E-04	7.93E-03	125.72	245.71	200.63	54.35	77.59	77.59
JC_g14756.t1	Protein of unknown function	-1.31	2.12E-05	8.32E-04	373.65	406.70	369.36	99.16	167.26	167.26
JC_g13323.t1	RE04396p (Drosophila melanogas	-1.32	2.50E-08	2.30E-06	1222.04	1615.90	1423.70	559.66	542.10	542.10
JC_g20090.t1	CG5245: CG5245 (Drosophila me	-1.32	1.37E-05	5.63E-04	221.55	198.51	162.01	62.93	77.59	77.59
JC_g14532.t1	Dmel\CG12016: SD05789p2 (Dros	-1.32	3.05E-05	1.14E-03	698.94	1122.05	630.42	351.82	279.11	279.11
JC_g823.t1	BcDNA:GH10614: IP10737p (Frag	-1.32	1.95E-06	1.06E-04	2888.94	2310.68	2763.46	745.58	1132.56	1132.56
JC_g3049.t1	"crol: Crooked legs, isoform G (Dro	-1.33	6.62E-08	5.34E-06	1384.68	1212.83	1648.67	497.69	560.23	560.23
JC_g23023.t1	Protein of unknown function	-1.34	5.19E-07	3.47E-05	25219.72	34918.02	37540.91	10630.73	13098.96	13098.96
JC_g20602.t1	Dim1: Dim1 (Drosophila melanoga	-1.34	4.12E-05	1.48E-03	669.92	1335.09	823.50	307.00	361.73	361.73
JC_g24781.t1	"fusl: Fuseless, isoform A (Drosopl	-1.34	3.00E-04	7.41E-03	238.25	124.67	289.61	71.51	79.60	79.60
JC_g16569.t1	Ddc-RC: LP11638p (Drosophila m	-1.35	3.37E-04	8.07E-03	560.03	619.73	244.28	151.60	174.32	174.32
JC_g18961.t1	Sod3: Extracellular superoxide dis	-1.35	3.08E-06	1.54E-04	3344.34	3269.33	2132.20	1269.97	977.38	977.38
JC_g4186.t1	CG8778: CG8778 (Drosophila me	-1.36	1.35E-04	3.94E-03	288.37	577.37	294.65	122.04	144.09	144.09
JC_g24176.t1	modSP: Modular serine protease	-1.36	9.70E-05	3.05E-03	251.44	209.40	144.38	89.62	62.47	62.47
JC_g23928.t1	Spn42Da: Serpin 4 (Drosophila m	-1.36	1.49E-04	4.23E-03	382.44	436.96	220.77	88.67	138.04	138.04
JC_g18206.t1	ItgaPS4: Integrin alpha-PS4 (Dros	-1.37	4.76E-05	1.66E-03	1047.09	602.79	1260.85	290.80	372.82	372.82
JC_g8285.t1	"Meics: Meiotic central spindle, iso	-1.37	8.57E-09	9.27E-07	560.91	543.48	612.80	196.41	221.67	221.67
JC_g4571.t1	CG7322: RH08058p (Drosophila r	-1.38	6.68E-05	2.20E-03	147.70	239.66	141.87	53.39	65.49	65.49
JC_g3304.t1	CG13001: RE69682p (Drosophila	-1.40	1.12E-04	3.38E-03	277.82	169.46	162.01	89.62	58.44	58.44
JC_g15871.t1	His2B: Histone H2B (Drosophila m	-1.41	5.40E-05	1.84E-03	182.87	250.56	218.26	47.67	87.66	87.66
JC_g19778.t1	"mthl15: Methuselah-like 15, isofo	-1.41	2.49E-06	1.31E-04	204.85	159.77	169.57	57.21	65.49	65.49
JC_g17691.t1	Protein of unknown function	-1.43	1.08E-04	3.29E-03	2924.98	5110.37	2909.52	721.75	1452.98	1452.98
JC_g4348.t1	dwg: Deformed wings (Drosophila	-1.43	2.59E-08	2.35E-06	845.76	625.78	644.70	250.75	248.88	248.88
JC_g5233.t1	PPO2: Phenoloxidase 2 (Drosoph	-1.43	2.11E-07	1.54E-05	440.46	451.48	379.43	119.18	163.23	163.23
JC_g14956.t1	ORF: ORF (Drosophila melanogas	-1.44	3.55E-04	8.37E-03	104.62	93.20	55.40	32.42	24.18	24.18
JC_g22075.t1	CG11005: LD44221p (Drosophila	-1.44	2.17E-05	8.50E-04	210.12	348.60	353.41	77.23	113.86	113.86
JC_g595.t1	"Dmel\CG5665: CG5665, isoform	-1.45	1.84E-08	1.81E-06	413.21	347.39	428.12	147.78	133.00	133.00
JC_g21352.t1	up: MIP03205p (Drosophila melan	-1.46	2.55E-04	6.51E-03	271.66	271.13	620.35	88.67	139.05	139.05
JC_g15575.t1	CG5390: SD23103p (Drosophila r	-1.47	2.67E-05	1.01E-03	1120.06	658.47	790.76	393.77	221.67	221.67
JC_g12183.t1	PGRP-SA: Peptidoglycan-recognit	-1.47	1.06E-06	6.33E-05	198.69	242.08	180.48	79.13	64.49	64.49
JC_g20851.t1	"Dmel\CG7974: CG7974, isoform	-1.48	6.62E-07	4.18E-05	296.28	334.07	466.73	122.04	122.93	122.93
JC_g16474.t1	Tsp47F: Tetraspanin (Drosophila r	-1.49	3.74E-04	8.74E-03	53.63	52.05	39.45	15.25	14.11	14.11
JC_g821.t1	CG9436: CG9436 (Drosophila me	-1.50	9.95E-07	6.00E-05	237.37	319.55	212.38	74.37	88.67	88.67
JC_g13541.t1	CG31142: GEO07715p1 (Drosopl	-1.50	5.14E-06	2.39E-04	264.63	450.27	259.39	110.60	101.77	101.77
JC_g16921.t1	mys: Integrin beta (Drosophila mel	-1.51	1.98E-07	1.47E-05	444.86	374.02	465.05	106.78	157.19	157.19
JC_g5954.t1	sand: CG8713 (Drosophila melanc	-1.51	7.89E-07	4.78E-05	245.29	260.24	339.98	73.41	100.76	100.76
JC_g13613.t1	alpha-Est7: Carboxylic ester hydro	-1.52	7.98E-05	2.57E-03	88.80	156.14	202.31	45.76	45.34	45.34
JC_g2884.t1	Zip88E: FI24038p1 (Drosophila m	-1.52	1.04E-04	3.21E-03	126.60	93.20	136.83	20.98	43.33	43.33
JC_g24151.t1	pol: Reverse transcriptase (Drosop	-1.52	1.16E-04	3.45E-03	131.00	73.84	115.84	21.93	37.28	37.28
JC_g8429.t1	"c-SP18: CG1299, isoform B (Dros	-1.53	7.68E-05	2.49E-03	813.23	1635.27	599.37	247.89	333.52	333.52
JC_g4519.t1	CG9645: RH19136p (Drosophila r	-1.54	3.71E-04	8.72E-03	105.50	60.52	63.80	13.35	26.20	26.20
JC_g24128.t1	"Dmel\CG7201: CG7201, isoform	-1.54	1.77E-04	4.83E-03	912.57	421.22	302.20	127.76	175.32	175.32
JC_g7403.t1	Dmel\CG6638: CG6638 (Drosophi	-1.54	6.52E-09	7.26E-07	266.39	288.08	266.10	80.09	92.70	92.70
JC_g23052.t1	BEST:GH25183: MIP21654p (Dro	-1.56	3.12E-04	7.58E-03	63.30	52.05	46.17	20.98	12.09	12.09
JC_g2986.t1	Protein of unknown function	-1.56	1.85E-04	5.03E-03	3430.50	8654.46	3835.43	2275.83	1125.50	1125.50

JC_g2221.t1	CG15890-RA: FI18259p1 (Drosop	-1.57	8.29E-06	3.59E-04	1520.08	1091.79	2454.54	397.58	562.25	562.25
JC_g14445.t1	CG9645: RH19136p (Drosophila r	-1.58	4.28E-05	1.53E-03	68.57	117.41	89.82	20.98	29.22	29.22
JC_g196.t1	betaCOP: Coatomer subunit beta	-1.59	2.88E-05	1.08E-03	99.35	157.35	84.78	36.23	31.24	31.24
JC_g6.t1	Dmel\CG9701: CG9701 (Drosophi	-1.60	1.72E-05	6.92E-04	132.75	199.72	155.30	66.74	37.28	37.28
JC_g12511.t1	CG6426: CG6426 (Drosophila me	-1.60	1.78E-06	9.95E-05	960.05	837.61	567.47	162.08	271.05	271.05
JC_g14325.t1	AttA: Attacin A (Fragment) (Drosop	-1.62	6.48E-07	4.11E-05	444.86	623.36	368.52	177.34	123.94	123.94
JC_g13906.t1	CG9413: RH65810p (Drosophila r	-1.62	2.64E-13	6.57E-11	1052.36	1195.89	1155.92	368.02	348.63	348.63
JC_g24291.t1	"l(2)efl: Lethal (2) essential for life,	-1.63	2.43E-05	9.31E-04	73.85	121.04	125.92	37.18	26.20	26.20
JC_g4351.t1	CG2202: CG2202 (Drosophila me	-1.64	4.19E-06	2.00E-04	1917.46	780.72	1192.85	327.03	389.95	389.95
JC_g20165.t1	zf30C: LD23102p (Drosophila mel	-1.64	3.04E-04	7.47E-03	106.38	348.60	119.20	56.25	44.33	44.33
JC_g13908.t1	CG9413-RB: RE43767p (Drosoph	-1.65	4.03E-07	2.76E-05	1456.78	2627.81	1566.41	665.49	485.67	485.67
JC_g8083.t1	CG6765: RH15369p (Drosophila r	-1.65	1.61E-04	4.48E-03	763.99	1728.47	672.40	136.34	340.57	340.57
JC_g2967.t1	CG3141: RH30917p (Drosophila r	-1.66	9.61E-06	4.10E-04	202.21	100.46	153.62	49.58	38.29	38.29
JC_g2148.t1	"Mlc1: Myosin alkali light chain 1, i	-1.66	3.18E-04	7.70E-03	139.79	111.36	289.61	20.98	56.43	56.43
JC_g14473.t1	Protein of unknown function	-1.66	4.13E-06	1.99E-04	116.05	114.99	78.07	27.65	29.22	29.22
JC_g23929.t1	Spn42Da: Serpin 4 (Drosophila m	-1.67	1.24E-08	1.28E-06	2555.73	2245.32	1468.19	662.63	583.41	583.41
JC_g17644.t1	UK114: RutC family protein UK114	-1.67	1.08E-04	3.29E-03	52.75	116.20	84.78	28.60	18.14	18.14
JC_g23399.t1	Protein of unknown function	-1.67	2.97E-04	7.35E-03	123.96	438.17	200.63	92.48	46.35	46.35
JC_g2044.t1	"CREG: Cellular repressor of E1A-	-1.70	2.39E-05	9.20E-04	970.60	2626.60	950.25	388.05	395.99	395.99
JC_g16028.t1	O-fut2: GDP-fucose protein O-fuc	-1.70	7.66E-06	3.34E-04	534.53	507.16	517.94	225.01	94.72	94.72
JC_g2825.t1	"snk: Snake, isoform B (Drosophila	-1.71	2.35E-04	6.10E-03	45.72	90.78	100.73	9.53	23.18	23.18
JC_g21914.t1	wupA: GH08696p (Drosophila mel	-1.71	2.77E-06	1.43E-04	190.78	301.39	444.91	85.81	82.62	82.62
JC_g22514.t1	Protein of unknown function	-1.71	5.22E-08	4.32E-06	258.47	332.86	201.47	70.55	74.56	74.56
JC_g17376.t1	GNBP3: SD21560p (Fragment) (D	-1.71	5.46E-12	9.94E-10	740.26	988.91	870.51	237.40	255.93	255.93
JC_g2411.t1	CG31097: Uncharacterized protei	-1.73	5.00E-06	2.34E-04	76.49	95.62	65.48	20.98	20.15	20.15
JC_g1704.t1	CG6279: AT19107p (Drosophila n	-1.74	3.07E-05	1.14E-03	151.22	167.04	77.23	44.81	26.20	26.20
JC_g21280.t1	dpld: Cyt-b5-PB (Drosophila melar	-1.74	2.57E-09	3.10E-07	267.27	395.81	319.83	83.90	93.71	93.71
JC_g3047.t1	CG8132: CG8132 (Drosophila me	-1.76	1.88E-08	1.82E-06	304.19	487.80	422.24	130.62	97.74	97.74
JC_g16922.t1	mys: Integrin beta (Drosophila mel	-1.76	1.89E-11	3.11E-09	1041.81	784.35	1124.02	255.52	281.12	281.12
JC_g18204.t1	ItgaPS5: Integrin alpha-PS5 (Dros	-1.78	5.95E-07	3.89E-05	233.86	156.14	239.24	72.46	44.33	44.33
JC_g8152.t1	Cyp4d2: Cytochrome P450 4d2 (D	-1.78	3.05E-05	1.14E-03	74.73	153.72	67.16	22.88	23.18	23.18
JC_g7189.t1	ORF1: Nucleic-acid-binding protei	-1.78	5.90E-06	2.69E-04	127.48	85.94	69.67	20.98	24.18	24.18
JC_g5285.t1	EG:BACR7A4.12: RE52086p (Dro	-1.79	1.15E-04	3.45E-03	63.30	82.31	31.90	14.30	12.09	12.09
JC_g24023.t1	Protein of unknown function	-1.80	9.43E-05	2.99E-03	100.22	449.06	271.98	76.27	51.39	51.39
JC_g11264.t1	Protein of unknown function	-1.81	7.57E-06	3.33E-04	3475.34	2031.07	1495.89	304.14	680.14	680.14
JC_g8390.t1	CG1234: Nucleolar complex prote	-1.81	1.01E-07	7.74E-06	2172.42	4802.92	2639.22	828.53	802.06	802.06
JC_g4489.t1	"34F4T: CG6084, isoform A (Dros	-1.83	4.20E-06	2.00E-04	72.97	118.62	69.67	20.98	20.15	20.15
JC_g8994.t1	modSP: Modular serine protease	-1.83	2.20E-05	8.58E-04	73.85	41.15	74.71	12.39	15.11	15.11
JC_g18205.t1	scb: Integrin alpha-PS3 (Drosophi	-1.84	1.12E-06	6.63E-05	109.90	93.20	173.77	29.56	30.23	30.23
JC_g11284.t1	Protein of unknown function	-1.84	2.83E-04	7.10E-03	458.04	206.98	134.31	15.25	68.52	68.52
JC_g22233.t1	"CG1208: CG1208, isoform B (Dro	-1.84	3.58E-06	1.74E-04	65.94	107.73	91.50	15.25	23.18	23.18
JC_g22863.t1	CG4210: CG4210 (Drosophila me	-1.85	1.40E-04	4.02E-03	61.54	359.49	248.48	46.72	43.33	43.33
JC_g115.t1	ORF: Orf protein (Drosophila mela	-1.85	1.44E-05	5.90E-04	46.60	47.21	62.12	12.39	11.08	11.08
JC_g11008.t1	Protein of unknown function	-1.86	1.76E-12	3.54E-10	28216.79	33933.95	39501.86	7177.41	9527.98	9527.98
JC_g14514.t1	Protein of unknown function	-1.86	2.23E-05	8.64E-04	588.16	226.35	690.86	61.02	133.00	133.00
JC_g8014.t1	Protein of unknown function	-1.87	1.45E-06	8.26E-05	518.71	393.38	306.40	49.58	115.88	115.88
JC_g21460.t1	Protein of unknown function	-1.87	5.87E-11	9.03E-09	421.12	610.05	614.48	124.90	145.10	145.10
JC_g5242.t1	Rpb7: GH11867p (Drosophila mel	-1.87	3.06E-04	7.49E-03	19.34	68.99	72.19	12.39	8.06	8.06
JC_g3110.t1	Protein of unknown function	-1.88	9.89E-05	3.09E-03	210.12	1171.68	355.93	115.36	111.84	111.84
JC_g3134.t1	Tm2-RC: FI17819p1 (Drosophila n	-1.89	1.51E-04	4.25E-03	49.23	50.84	175.44	17.16	17.13	17.13
JC_g18684.t1	"CG6106: CG6106, isoform A (Dro	-1.89	5.98E-08	4.89E-06	137.15	217.87	234.21	54.35	42.32	42.32
JC_g11364.t1	Protein of unknown function	-1.89	3.20E-09	3.81E-07	181.11	216.66	151.10	40.04	46.35	46.35
JC_g22845.t1	CG11158: RH22417p (Drosophila	-1.89	2.97E-05	1.11E-03	61.54	199.72	118.36	33.37	22.17	22.17
JC_g10558.t1	CG7154: CG7154 (Drosophila me	-1.90	9.86E-06	4.17E-04	1059.39	2591.50	679.11	283.17	320.42	320.42
JC_g7180.t1	SD27140p (Drosophila melanogas	-1.90	1.95E-04	5.22E-03	43.96	47.21	26.86	2.86	9.07	9.07
JC_g17458.t1	Dmel\CG8281: CG8281 (Drosophi	-1.92	1.51E-04	4.25E-03	48.35	300.18	326.54	32.42	43.33	43.33
JC_g18513.t1	CG5390: SD23103p (Drosophila r	-1.94	2.36E-08	2.22E-06	135.39	129.51	97.38	29.56	26.20	26.20
JC_g13285.t1	MP1: Melanization protease 1 (Dro	-1.95	1.23E-12	2.62E-10	1419.85	1339.93	951.09	329.89	279.11	279.11
JC_g20741.t1	insc: Inscuteable (Drosophila mela	-1.97	8.14E-10	1.03E-07	1275.67	858.18	660.64	235.50	201.52	201.52
JC_g9634.t1	slo: Calcium-activated potassium c	-1.98	2.31E-10	3.17E-08	706.85	426.07	512.06	148.73	113.86	113.86
JC_g17552.t1	Protein of unknown function	-1.99	2.59E-04	6.60E-03	30.77	67.78	19.31	8.58	4.03	4.03
JC_g17689.t1	Protein of unknown function	-1.99	3.54E-08	3.13E-06	1234.35	2524.92	1336.40	266.01	418.16	418.16
JC_g14547.t1	BcDNA.GH05741: Carboxylic este	-1.99	1.59E-04	4.45E-03	137.15	131.94	29.38	25.74	10.08	10.08
JC_g8333.t1	Protein of unknown function	-2.00	3.10E-04	7.56E-03	19.34	71.41	21.83	6.67	4.03	4.03
JC_g16486.t1	"Tg: Transglutaminase, isoform B	-2.00	1.88E-04	5.10E-03	473.87	88.36	162.85	10.49	48.37	48.37
JC_g24134.t1	"loh: Lonely heart, isoform C (Dros	-2.01	8.31E-05	2.66E-03	21.10	44.79	45.33	7.63	5.04	5.04
JC_g24205.t1	Phk-3: GEO07322p1 (Drosophila	-2.01	1.27E-06	7.32E-05	1628.21	3856.38	1995.37	260.29	612.63	612.63
JC_g23926.t1	Spn42Da: Serpin 4 (Drosophila m	-2.01	3.42E-09	4.04E-07	676.08	1486.39	1078.69	266.96	217.64	217.64
JC_g14254.t1	Protein of unknown function	-2.02	1.67E-05	6.74E-04	213.64	183.98	149.42	62.93	17.13	17.13
JC_g7573.t1	CG10175: Carboxylic ester hydrola	-2.02	4.82E-05	1.67E-03	107.26	67.78	28.54	13.35	10.08	10.08
JC_g8619.t1	Protein of unknown function	-2.03	6.05E-05	2.03E-03	27.25	96.83	135.15	13.35	14.11	14.11
JC_g13234.t1	NLaz: Neural Lazarillo (Drosophila	-2.05	2.62E-04	6.65E-03	13.19	191.25	214.90	16.21	17.13	17.13
JC_g1055.t1	CG13675: CG13675 protein (Frag	-2.05	1.18E-04	3.50E-03	41.32	52.05	58.76	15.25	3.02	3.02
JC_g4288.t1	B9d1: B9d1 (Drosophila melanoga	-2.09	2.06E-05	8.13E-04	26.37	68.99	66.32	9.53	8.06	8.06
JC_g17351.t1	Protein of unknown function	-2.09	4.80E-13	1.12E-10	344.63	411.54	377.75	62.93	89.68	89.68

JC_g14480.t1	Protein of unknown function	-2.10	2.00E-04	5.31E-03	28.13	19.37	16.79	0.95	3.02	3.02
JC_g18652.t1	Protein of unknown function	-2.11	7.17E-05	2.34E-03	20.22	105.31	64.64	11.44	7.05	7.05
JC_g16426.t1	"CG5973: CG5973, isoform A (Dro	-2.11	9.81E-05	3.07E-03	162.65	715.35	68.83	51.49	35.27	35.27
JC_g16009.t1	modSP: Modular serine protease	-2.12	3.37E-04	8.07E-03	7.03	23.00	36.10	0.95	2.02	2.02
JC_g8588.t1	Protein of unknown function	-2.12	5.50E-09	6.24E-07	358.70	372.81	255.19	38.14	77.59	77.59
JC_g20010.t1	shu: Inactive peptidyl-prolyl cis-tra	-2.12	7.76E-06	3.37E-04	113.41	78.68	193.91	8.58	27.21	27.21
JC_g24142.t1	CG15890-RA: FI18259p1 (Drosop	-2.13	1.29E-08	1.31E-06	176.71	95.62	136.83	23.84	27.21	27.21
JC_g8334.t1	pol: Reverse transcriptase (Fragm	-2.13	3.00E-04	7.41E-03	11.43	19.37	25.18	0.00	2.02	2.02
JC_g13940.t1	"CG14372: Uncharacterized prote	-2.14	6.88E-10	8.93E-08	216.27	193.67	129.27	32.42	36.27	36.27
JC_g3046.t1	CG11236: GH12548p (Drosophila	-2.16	5.48E-09	6.24E-07	94.95	136.78	128.44	17.16	25.19	25.19
JC_g9838.t1	ORF: Uncharacterized protein (Dro	-2.16	2.09E-04	5.50E-03	13.19	47.21	13.43	1.91	2.02	2.02
JC_g2.t1	sut4: GH07001p (Drosophila mela	-2.17	3.58E-11	5.74E-09	3933.38	4898.55	2355.49	843.78	669.05	669.05
JC_g14150.t1	"CG6330-RB: CG6330, isoform B	-2.17	1.19E-04	3.52E-03	105.50	48.42	52.89	17.16	2.02	2.02
JC_g23614.t1	Protein of unknown function	-2.18	1.56E-05	6.34E-04	35.17	123.46	82.27	5.72	14.11	14.11
JC_g3054.t1	ORF: Uncharacterized protein (Dro	-2.18	3.11E-04	7.58E-03	17.58	7.26	14.27	0.00	0.00	0.00
JC_g11099.t1	"CG2145: CG2145, isoform B (Dro	-2.18	5.41E-13	1.22E-10	2626.94	4802.92	3120.22	747.49	666.03	666.03
JC_g9626.t1	"spz: Spatzle, isoform J (Drosophil	-2.19	5.43E-13	1.22E-10	390.35	658.47	494.43	100.11	101.77	101.77
JC_g6811.t1	gag-pol: Putative uncharacterized	-2.19	2.40E-04	6.20E-03	80.00	4.84	26.86	2.86	2.02	2.02
JC_g20877.t1	"Dscam1: Down syndrome cell adh	-2.20	2.42E-08	2.25E-06	282.21	796.45	688.35	120.13	95.72	95.72
JC_g15587.t1	Protein of unknown function	-2.21	1.19E-04	3.52E-03	62.42	50.84	8.39	2.86	4.03	4.03
JC_g11427.t1	"l(2)efl: Lethal (2) essential for life,	-2.21	4.45E-08	3.78E-06	76.49	99.25	66.32	11.44	15.11	15.11
JC_g3084.t1	"CG7737: CG7737, isoform A (Dro	-2.22	2.18E-10	3.08E-08	1091.04	698.41	652.25	98.20	175.32	175.32
JC_g9230.t1	Protein of unknown function	-2.23	1.44E-06	8.24E-05	213.64	248.13	78.91	41.00	20.15	20.15
JC_g8202.t1	alpha-Est9: Carboxylic ester hydro	-2.24	4.85E-06	2.28E-04	496.73	371.60	211.54	13.35	69.53	69.53
JC_g7848.t1	Cpr49Ah: Cuticular protein 49Ah (	-2.25	7.08E-05	2.32E-03	115.17	21.79	32.74	1.91	7.05	7.05
JC_g7582.t1	Protein of unknown function	-2.25	1.52E-04	4.28E-03	46.60	12.10	15.11	0.00	2.02	2.02
JC_g18856.t1	26-29-p: 26-29kD-proteinase (Dro	-2.25	1.28E-08	1.31E-06	1316.99	2931.62	1085.41	376.60	260.97	260.97
JC_g4495.t1	CG6083: AT08919p (Drosophila n	-2.27	1.08E-04	3.29E-03	12.31	24.21	26.02	0.00	2.02	2.02
JC_g7179.t1	Protein of unknown function	-2.28	1.59E-04	4.45E-03	28.13	8.47	10.91	0.00	0.00	0.00
JC_g7411.t1	EG:103E12.2: GH18858p (Drosop	-2.28	1.52E-05	6.20E-04	27.25	163.41	73.03	12.39	9.07	9.07
JC_g22823.t1	Protein of unknown function	-2.28	2.19E-10	3.08E-08	817.62	890.86	554.87	77.23	157.19	157.19
JC_g14037.t1	Spn77Ba: Serine protease inhibito	-2.28	1.50E-14	4.62E-12	399.14	593.10	605.24	108.69	92.70	92.70
JC_g22073.t1	CG11005: LD44221p (Drosophila	-2.30	1.24E-06	7.19E-05	65.06	42.36	77.23	13.35	6.05	6.05
JC_g21183.t1	"Dmel\CG9449: CG9449, isoform	-2.30	9.49E-09	1.01E-06	526.62	1047.01	1719.19	156.36	187.42	187.42
JC_g7410.t1	EG:103E12.2: GH18858p (Drosop	-2.30	3.96E-05	1.43E-03	15.82	54.47	47.85	6.67	2.02	2.02
JC_g3190.t1	"unc-13: Unc-13, isoform E (Droso	-2.31	4.24E-09	4.96E-07	166.16	262.66	271.14	20.98	46.35	46.35
JC_g5747.t1	CG6180: CG6180 (Drosophila me	-2.31	7.06E-06	3.15E-04	101.10	959.86	452.46	64.83	59.45	59.45
JC_g22070.t1	CG31548: Uncharacterized protei	-2.31	7.51E-05	2.44E-03	22.86	27.84	13.43	0.00	2.02	2.02
JC_g14328.t1	AttC: Attacin-C (Drosophila melano	-2.32	2.64E-11	4.29E-09	419.36	246.92	324.03	40.04	64.49	64.49
JC_g24092.t1	Dg: Dystroglycan-like protein DG (	-2.32	6.67E-05	2.20E-03	10.55	44.79	21.83	0.95	2.02	2.02
JC_g8572.t1	SP34: CG9372 (Drosophila melan	-2.33	2.19E-12	4.26E-10	896.75	1574.75	1022.45	258.38	172.30	172.30
JC_g8343.t1	Protein of unknown function	-2.33	1.17E-04	3.48E-03	11.43	8.47	31.06	0.00	0.00	0.00
JC_g21451.t1	Protein of unknown function	-2.33	2.01E-05	7.96E-04	60.66	14.52	45.33	3.81	4.03	4.03
JC_g3571.t1	CG11854-RA: IP10429p (Fragme	-2.35	6.38E-05	2.12E-03	24.62	429.70	1124.02	61.02	21.16	21.16
JC_g24784.t1	GEO10169p1 (Fragment) (Drosop	-2.36	4.47E-08	3.78E-06	239.13	820.66	792.44	69.60	99.75	99.75
JC_g14508.t1	CG11961: GH11271p (Drosophila	-2.37	8.98E-05	2.86E-03	23.74	24.21	5.88	0.00	0.00	0.00
JC_g24033.t1	Protein of unknown function	-2.38	2.29E-07	1.65E-05	148.58	458.75	619.51	76.27	44.33	44.33
JC_g5171.t1	CG8952: CG8952 (Drosophila me	-2.39	7.78E-05	2.51E-03	14.95	56.89	5.88	0.00	0.00	0.00
JC_g8478.t1	IP02928p (Fragment) (Drosophila	-2.39	1.28E-11	2.14E-09	155.61	153.72	109.97	22.88	22.17	22.17
JC_g7413.t1	EG:103E12.2: GH18858p (Drosop	-2.40	1.82E-05	7.28E-04	16.70	227.56	152.78	15.25	9.07	9.07
JC_g17688.t1	Protein of unknown function	-2.41	5.64E-06	2.60E-04	291.88	723.83	1997.88	34.32	137.04	137.04
JC_g11428.t1	"Hsp26: Heat shock protein 26, is	-2.41	5.94E-05	2.00E-03	15.82	21.79	10.91	0.95	0.00	0.00
JC_g14528.t1	CG30016: 5-hydroxyisourate hydr	-2.41	2.43E-09	2.96E-07	169.68	418.80	192.23	37.18	38.29	38.29
JC_g22181.t1	CG14905: Uncharacterized protei	-2.43	3.36E-06	1.66E-04	25.50	124.67	81.43	5.72	9.07	9.07
JC_g15589.t1	Protein of unknown function	-2.44	2.39E-06	1.27E-04	29.01	29.05	38.61	3.81	3.02	3.02
JC_g2215.t1	"Mlh1: Mlh1, isoform A (Drosophila	-2.45	1.81E-14	5.30E-12	379.80	378.86	481.84	87.72	54.41	54.41
JC_g20816.t1	pol: Pol protein (Drosophila melan	-2.46	4.69E-05	1.65E-03	11.43	27.84	11.75	0.00	0.00	0.00
JC_g10084.t1	Protein of unknown function	-2.49	1.93E-08	1.85E-06	447.49	156.14	153.62	32.42	32.24	32.24
JC_g4217.t1	Protein of unknown function	-2.49	1.36E-05	5.60E-04	26.37	42.36	13.43	0.95	2.02	2.02
JC_g20798.t1	CG4404: RH45455p (Drosophila r	-2.49	7.60E-06	3.33E-04	27.25	48.42	19.31	0.95	3.02	3.02
JC_g5243.t1	Rpb7: GH11867p (Drosophila mel	-2.50	3.51E-05	1.29E-03	3.52	54.47	137.67	0.00	2.02	2.02
JC_g7414.t1	EG:103E12.2: EG:103E12.2 prot	-2.54	1.32E-05	5.47E-04	14.07	85.94	57.92	0.00	4.03	4.03
JC_g3794.t1	CG11854: Uncharacterized protei	-2.56	3.02E-06	1.53E-04	170.56	311.08	996.42	81.99	18.14	18.14
JC_g11193.t1	"CG3609: CG3609, isoform A (Dro	-2.58	6.00E-09	6.75E-07	958.29	901.76	408.81	38.14	115.88	115.88
JC_g17872.t1	gag-pol: Putative uncharacterized	-2.58	1.91E-05	7.63E-04	6.15	26.63	41.13	0.00	0.00	0.00
JC_g21454.t1	Protein of unknown function	-2.60	4.09E-07	2.78E-05	33.41	71.41	104.93	2.86	8.06	8.06
JC_g921.t1	"Cda5: Chitin deacetylase-like 5, is	-2.62	1.52E-12	3.12E-10	117.81	124.67	99.89	12.39	16.12	16.12
JC_g8173.t1	Protein of unknown function	-2.63	1.07E-07	8.19E-06	270.78	991.33	186.36	36.23	52.40	52.40
JC_g9630.t1	"NT1: Neurotrophin 1, isoform F (D	-2.63	1.17E-06	6.86E-05	23.74	35.10	37.78	0.95	3.02	3.02
JC_g8431.t1	Protein of unknown function	-2.63	6.90E-08	5.53E-06	234.74	66.57	271.98	10.49	23.18	23.18
JC_g16329.t1	CG4572-RC: Carboxypeptidase (D	-2.64	2.45E-06	1.30E-04	21.10	53.26	38.61	4.77	1.01	1.01
JC_g5.t1	Dmel\CG9701: CG9701 (Drosophi	-2.66	3.48E-06	1.70E-04	219.79	39.94	132.63	17.16	2.02	2.02
JC_g4706.t1	Protein of unknown function	-2.67	4.18E-10	5.56E-08	134.51	364.33	224.97	18.12	32.24	32.24
JC_g24099.t1	Protein of unknown function	-2.67	7.55E-10	9.70E-08	72.09	98.04	68.83	12.39	7.05	7.05
JC_g11185.t1	"Nna1: Drosophila Nna1 ortholog,	-2.68	7.51E-09	8.28E-07	147.70	127.09	95.70	3.81	17.13	17.13

JC_g2956.t1	Cyp6g2: Probable cytochrome P4	-2.69	3.78E-06	1.84E-04	12.31	152.51	98.22	7.63	2.02	2.02
JC_g5859.t2	Protein of unknown function	-2.70	4.32E-06	2.04E-04	77.37	21.79	17.63	0.00	2.02	2.02
JC_g13281.t1	MP1: Melanization protease 1 (Dr	-2.74	3.45E-15	1.12E-12	2075.71	1733.31	902.41	174.48	203.54	203.54
JC_g20865.t1	Protein of unknown function	-2.75	4.18E-06	2.00E-04	7.03	633.05	256.87	3.81	10.08	10.08
JC_g3784.t1	CG1124: CG1124 (Drosophila me	-2.75	4.98E-08	4.19E-06	298.04	968.33	1184.46	20.98	92.70	92.70
JC_g11286.t1	Protein of unknown function	-2.76	1.88E-06	1.03E-04	54.51	43.57	68.00	6.67	0.00	0.00
JC_g8904.t1	Obp56d: Odorant-binding protein	-2.77	6.37E-26	5.72E-23	317671.23	474799.38	340985.09	45575.79	52453.28	52452.27
JC_g12365.t1	Protein of unknown function	-2.82	2.79E-06	1.43E-04	14.07	42.36	15.95	0.00	0.00	0.00
JC_g11430.t1	Protein of unknown function	-2.86	5.75E-08	4.74E-06	130.12	639.10	104.09	24.79	17.13	17.13
JC_g3805.t1	CG11854: Uncharacterized protei	-2.87	1.64E-07	1.23E-05	21.10	37.52	55.40	1.91	2.02	2.02
JC_g7958.t1	Protein of unknown function	-2.87	1.72E-06	9.68E-05	69.45	6.05	50.37	0.95	0.00	0.00
JC_g9614.t1	GstE6: Glutathione S transferase	-2.91	7.19E-07	4.48E-05	67.70	136.78	170.41	10.49	0.00	0.00
JC_g23369.t1	obst-E: Protein obstructor-E (Dros	-2.92	8.44E-20	4.11E-17	398.26	544.69	705.97	66.74	58.44	58.44
JC_g7753.t1	Mipp1: Multiple inositol polyphospl	-2.92	3.93E-21	2.19E-18	765.75	574.95	839.45	61.02	92.70	92.70
JC_g20516.t1	Protein of unknown function	-2.93	5.16E-07	3.46E-05	36.92	16.95	33.58	1.91	0.00	0.00
JC_g23610.t1	ssp7: GEO09608p1 (Drosophila m	-2.94	7.09E-07	4.45E-05	134.51	35.10	26.02	3.81	0.00	0.00
JC_g16538.t1	CG5458: AT19426p (Drosophila n	-2.94	6.29E-07	4.06E-05	80.00	88.36	15.95	3.81	0.00	0.00
JC_g14513.t1	Dmel\CG13458: GH20023p (Dros	-2.94	1.03E-06	6.18E-05	5.27	157.35	62.12	0.95	0.00	0.00
JC_g1015.t1	"Cht2: Chitinase 2, isoform B (Dro	-2.95	3.11E-13	7.58E-11	167.92	216.66	256.87	32.42	14.11	14.11
JC_g9809.t1	Tsp42Ed: Tetraspanin (Drosophila	-2.96	4.92E-07	3.32E-05	40.44	499.90	214.90	0.00	10.08	10.08
JC_g6268.t1	Protein of unknown function	-2.96	7.52E-07	4.63E-05	24.62	33.89	13.43	0.00	0.00	0.00
JC_g14988.t1	CG43088: Uncharacterized protei	-2.97	3.74E-07	2.57E-05	21.10	24.21	46.17	1.91	0.00	0.00
JC_g8155.t1	gas: RE48979p (Drosophila melar	-2.97	4.12E-08	3.58E-06	180.23	90.78	28.54	7.63	4.03	4.03
JC_g7856.t1	Acp65Aa: Adult cuticle protein 65	-2.98	1.36E-10	2.03E-08	1094.56	883.60	752.98	19.07	99.75	99.75
JC_g9320.t1	Protein of unknown function	-2.99	5.96E-07	3.89E-05	17.58	48.42	16.79	0.00	0.00	0.00
JC_g1206.t1	"COX7C: Cytochrome c oxidase s	-3.01	9.34E-09	1.00E-06	103.74	58.10	44.49	7.63	2.02	2.02
JC_g10576.t1	"CG2493: CG2493, isoform A (Dro	-3.01	2.89E-07	2.03E-05	31.65	61.73	16.79	1.91	0.00	0.00
JC_g16229.t1	Dmel\CG17687: Uncharacterized	-3.02	2.55E-07	1.83E-05	128.36	233.61	10.91	0.95	4.03	4.03
JC_g4219.t1	Protein of unknown function	-3.04	1.99E-18	8.94E-16	702.45	907.81	838.61	45.76	97.74	97.74
JC_g24207.t1	Phk-3: GEO07322p1 (Drosophila	-3.04	2.61E-14	7.44E-12	179.35	351.02	187.20	27.65	18.14	18.14
JC_g480.t1	Protein of unknown function	-3.04	3.67E-07	2.54E-05	24.62	39.94	14.27	0.00	0.00	0.00
JC_g9233.t1	Protein of unknown function	-3.10	1.77E-13	4.49E-11	134.51	130.72	79.75	11.44	8.06	8.06
JC_g23613.t1	ssp7: GEO09608p1 (Drosophila m	-3.11	1.00E-07	7.74E-06	82.64	53.26	18.47	2.86	0.00	0.00
JC_g8688.t1	GEO04306p1 (Fragment) (Drosop	-3.12	2.25E-07	1.64E-05	255.84	4.84	130.11	0.95	0.00	0.00
JC_g3796.t1	anon-3B1.2: Circadian clock-contr	-3.14	9.48E-12	1.61E-09	259.35	83.52	303.88	15.25	15.11	15.11
JC_g4216.t1	Protein of unknown function	-3.19	9.67E-08	7.58E-06	55.39	41.15	11.75	0.00	0.00	0.00
JC_g10664.t1	Protein of unknown function	-3.21	1.49E-13	3.95E-11	82.64	78.68	94.02	3.81	7.05	7.05
JC_g567.t1	Dmel\CG9701: CG9701 (Drosophi	-3.23	1.51E-10	2.21E-08	1328.42	544.69	329.90	74.37	22.17	22.17
JC_g8201.t1	CG15531: Uncharacterized protei	-3.27	3.13E-17	1.26E-14	680.47	778.30	354.25	30.51	54.41	54.41
JC_g7533.t1	"Pxd: Peroxidase, isoform B (Dros	-3.27	5.32E-17	2.07E-14	110.77	117.41	114.16	9.53	8.06	8.06
JC_g15090.t1	Protein of unknown function	-3.36	1.48E-08	1.47E-06	19.34	71.41	27.70	0.00	0.00	0.00
JC_g20009.t1	arx: Gametocyte-specific factor 1	-3.50	5.53E-12	9.94E-10	115.17	42.36	100.73	1.91	4.03	4.03
JC_g10566.t2	Protein of unknown function	-3.60	1.44E-09	1.79E-07	75.61	331.65	18.47	0.95	0.00	0.00
JC_g14507.t1	CG11961: GH11271p (Drosophila	-3.65	1.86E-10	2.68E-08	104.62	25.42	60.44	1.91	0.00	0.00
JC_g2910.t1	Protein of unknown function	-3.65	3.51E-10	4.72E-08	51.87	25.42	35.26	0.00	0.00	0.00
JC_g16325.t1	Protein of unknown function	-3.73	7.87E-12	1.37E-09	190.78	833.98	108.29	14.30	6.05	6.05
JC_g20110.t1	"Dmel\CG5059: CG5059, isoform	-3.77	8.46E-11	1.28E-08	60.66	24.21	46.17	0.00	0.00	0.00
JC_g4221.t1	Protein of unknown function	-3.84	3.82E-11	6.04E-09	36.92	263.87	52.05	0.00	1.01	1.01
JC_g12364.t1	Protein of unknown function	-3.84	2.58E-21	1.51E-18	209.24	158.56	130.95	8.58	7.05	7.05
JC_g3235.t1	CG5987: AT11276p (Drosophila n	-3.86	2.64E-12	5.06E-10	78.25	43.57	46.17	1.91	0.00	0.00
JC_g4218.t1	Protein of unknown function (Man	-3.93	1.41E-64	8.24E-61	4167.24	3821.28	3478.67	204.99	235.78	235.78
JC_g5125.t1	Protein of unknown function	-3.95	2.02E-35	4.73E-32	2087.14	2725.85	1649.51	143.97	95.72	95.72
JC_g15540.t1	Protein of unknown function	-3.95	4.51E-13	1.08E-10	48.35	125.88	49.53	0.95	1.01	1.01
JC_g21453.t1	Protein of unknown function	-3.99	2.69E-29	3.15E-26	240.01	282.03	268.62	16.21	10.08	10.08
JC_g2214.t1	CG17475: RE05031p (Drosophila	-4.03	1.26E-30	1.83E-27	331.45	457.54	453.30	12.39	22.17	22.17
JC_g4220.t1	Protein of unknown function	-4.08	8.42E-22	5.18E-19	369.25	323.18	167.05	14.30	8.06	8.06
JC_g8445.t1	Sap47: MIP08376p (Drosophila m	-4.09	4.98E-33	8.32E-30	351.67	579.79	511.22	23.84	20.15	20.15
JC_g2381.t1	ORF: ORF (Drosophila melanogas	-4.11	1.93E-27	2.05E-24	212.76	355.86	253.51	10.49	11.08	11.08
JC_g15763.t1	Protein of unknown function	-4.21	8.13E-14	2.21E-11	55.39	60.52	40.29	0.00	0.00	0.00
JC_g4311.t1	Protein of unknown function	-4.24	7.24E-15	2.29E-12	155.61	307.45	62.12	0.00	3.02	3.02
JC_g6589.t1	Protein of unknown function	-4.40	6.50E-17	2.45E-14	80.88	284.45	258.55	0.00	4.03	4.03
JC_g481.t1	Protein of unknown function	-4.44	1.61E-14	4.82E-12	65.06	359.49	71.35	0.00	0.00	0.00
JC_g15695.t1	Nrg-RC: RT01988p (Fragment) (Dr	-4.65	1.78E-66	2.08E-62	6987.60	4592.31	5682.22	210.71	182.38	182.38
JC_g10553.t1	Bug22: Cilia- and flagella-associat	-4.70	1.02E-16	3.61E-14	290.12	1805.94	176.28	0.95	4.03	4.03
JC_g24428.t1	Protein of unknown function	-4.87	1.21E-17	5.06E-15	131.00	508.37	82.27	0.00	0.00	0.00
JC_g14635.t1	Protein of unknown function	-5.25	1.80E-23	1.31E-20	136.27	354.65	133.47	0.00	1.01	1.01
JC_g10555.t1	Protein of unknown function	-5.26	6.50E-22	4.22E-19	298.92	122.25	101.57	0.00	0.00	0.00
JC_g24427.t1	Protein of unknown function	-5.27	2.79E-23	1.92E-20	684.87	1987.50	533.89	0.00	8.06	8.06
JC_g10188.t1	Protein of unknown function	-5.34	5.31E-24	4.44E-21	115.17	147.67	99.89	0.00	0.00	0.00
JC_g2490.t1	Protein of unknown function	-5.61	2.43E-29	3.15E-26	252.32	518.06	201.47	0.00	2.02	2.02
JC_g9248.t1	Protein of unknown function	-6.47	1.04E-34	2.03E-31	927.52	2782.74	685.83	3.81	0.00	0.00
JC_g14783.t1	Protein of unknown function	-6.61	4.75E-38	1.85E-34	247.92	612.47	634.62	0.00	0.00	0.00

Table S11. Differentially expressed transcripts from day 2 pupal wings

Pupal wings, 2 days after pupation					Normalized read counts					
ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g22471.t1	Osi9: FI01546p (Drosophila melar	8.76	5.32E-200	1.52E-196	10.17	28.61	35.77	12706.18	13884.77	19916.18
JC_g22467.t1	Osi9: FI01546p (Drosophila melar	7.29	6.82E-66	3.55E-63	108.97	74.99	221.56	39252.56	55944.47	47849.43
JC_g1499.t1	Dmel\CG33978: Uncharacterized	7.13	0	0	398.10	521.97	376.55	64495.32	70153.34	61314.92
JC_g22472.t1	Osi7: FI03362p (Drosophila melar	6.52	3.53E-259	2.02E-255	374.13	366.07	549.42	39475.30	51663.33	41048.42
JC_g20282.t1	Protein of unknown function	6.46	1.81E-101	2.07E-98	20.34	56.24	56.63	4140.42	7069.91	4488.50
JC_g22468.t1	Osi9: FI01546p (Drosophila melar	6.08	2.22E-79	1.49E-76	10.90	11.84	9.94	648.99	1146.02	1329.30
JC_g2564.t1	Cpr65Ax1: Cuticular protein 65Ax	5.95	2.64E-34	3.77E-32	21.07	56.24	101.34	7982.35	13474.92	9408.80
JC_g24216.t1	Protein of unknown function	5.91	1.42E-29	1.47E-27	0.00	0.00	0.00	114.20	161.49	132.29
JC_g23473.t1	obst-A: LD43683p (Drosophila me	5.74	2.35E-124	3.37E-121	189.61	409.48	258.32	14903.02	19738.49	19266.35
JC_g14980.t1	Cpr56F: Cuticular protein 56F (Dro	5.59	4.09E-67	2.23E-64	6.54	24.67	24.84	1431.40	1257.39	902.78
JC_g21848.t1	Protein of unknown function	5.42	1.61E-53	5.27E-51	10.90	10.85	12.92	377.64	917.71	862.56
JC_g25003.t1	CG17109: Aminoacylase (Drosop	5.17	5.37E-39	9.17E-37	2.91	3.95	7.95	396.86	220.52	247.66
JC_g8911.t1	"mtg: Mind the gap, isoform F (Dro	5.06	3.68E-240	1.40E-236	134.39	129.26	148.04	4692.17	5411.57	4403.83
JC_g24128.t1	"Dmel\CG7201: CG7201, isoform	4.98	1.89E-173	3.61E-170	84.27	81.90	73.52	2822.09	3017.07	2305.10
JC_g22323.t1	"Osi19: Osiris 19, isoform B (Dros	4.96	4.61E-19	2.31E-17	0.00	0.00	0.00	80.28	69.05	59.27
JC_g15251.t1	wat: Fatty acyl-CoA reductase wa	4.95	2.37E-41	4.52E-39	3.63	8.88	11.92	295.10	490.04	296.34
JC_g25301.t1	ninaB: Carotenoid isomerooxyger	4.93	6.48E-62	2.47E-59	17.43	21.71	42.72	1231.27	1082.54	758.84
JC_g11684.t1	CG17443: RE19569p (Drosophila	4.90	6.04E-95	5.76E-92	40.68	32.56	56.63	1226.75	1812.03	1393.86
JC_g25005.t1	ORF: Orf protein (Drosophila mela	4.89	2.67E-80	1.91E-77	93.71	92.75	72.53	4355.24	2331.02	2308.28
JC_g10040.t1	AT12189p (Drosophila melanogas	4.85	1.35E-187	3.10E-184	310.20	339.43	400.39	9860.34	12616.24	9619.42
JC_g4287.t1	Treh: Trehalase (Fragment) (Dros	4.74	6.47E-30	6.86E-28	2.18	1.97	6.95	193.34	167.06	139.70
JC_g24032.t1	Protein of unknown function	4.72	2.56E-33	3.44E-31	4.36	10.85	16.89	612.81	395.37	258.24
JC_g17028.t1	BG:DS01523.2: RE16941p (Dros	4.69	1.83E-22	1.28E-20	79.18	203.26	380.52	10439.23	14325.80	11205.90
JC_g10307.t1	CG4089: CG4089 (Drosophila me	4.69	7.21E-41	1.33E-38	15.26	19.73	28.81	586.80	1174.98	464.62
JC_g8266.t1	hng2: Hinge2 (Drosophila melano	4.60	9.93E-35	1.50E-32	8.72	14.80	19.87	790.32	324.09	378.89
JC_g11247.t1	"stj: Straightjacket, isoform D (Dro	4.58	2.10E-62	8.31E-60	23.97	56.24	37.75	967.83	1370.99	968.40
JC_g9921.t1	pdgy: BcDNA.GH02901 (Drosoph	4.55	1.89E-20	1.08E-18	0.00	2.96	3.97	75.75	171.51	131.24
JC_g4747.t1	Protein of unknown function	4.51	7.92E-22	5.16E-20	1.45	1.97	3.97	160.55	82.42	110.07
JC_g21574.t1	"CG42265: Uncharacterized prote	4.46	6.37E-63	2.60E-60	266.61	245.69	309.98	10546.65	6293.64	4348.79
JC_g15195.t1	polyprotein: Polyprotein (Drosoph	4.40	4.87E-16	1.92E-14	0.00	0.00	1.99	75.75	60.14	52.92
JC_g22463.t1	Osi12: Osiris 12 (Drosophila melar	4.39	6.58E-14	2.15E-12	132.22	339.43	1220.05	80913.39	80068.80	59020.40
JC_g7439.t1	Tret1-2: Facilitated trehalose trans	4.38	5.19E-24	4.01E-22	1.45	3.95	5.96	145.85	148.12	102.66
JC_g24019.t1	"Dhc98D: Dynein heavy chain at	4.36	1.28E-16	5.30E-15	12.35	42.43	33.78	2135.79	1964.61	665.71
JC_g22470.t1	Osi9: FI01546p (Drosophila melar	4.35	1.09E-14	3.84E-13	0.73	0.00	0.00	41.83	51.23	64.56
JC_g18022.t1	Protein of unknown function	4.26	1.25E-22	8.86E-21	2.18	6.91	13.91	339.19	236.11	147.11
JC_g13085.t1	spz4: Protein spaetzle 4 (Drosoph	4.23	9.19E-21	5.48E-19	680.69	866.33	2083.42	43780.79	40932.62	33551.01
JC_g23472.t1	obst-A: LD43683p (Drosophila me	4.21	8.34E-117	1.06E-113	1581.50	1909.28	1241.91	26945.50	35819.52	30967.56
JC_g3147.t1	Protein of unknown function	4.19	1.33E-51	3.64E-49	93.71	204.25	242.42	3736.78	4536.19	3234.34
JC_g20268.t1	Protein of unknown function	4.14	1.21E-49	3.08E-47	169.99	370.02	461.99	7708.73	7059.88	5819.91
JC_g17888.t1	CG13634: Uncharacterized protei	4.06	8.89E-17	3.73E-15	0.00	3.95	3.97	80.28	77.96	106.89
JC_g1343.t1	Protein of unknown function	4.03	5.32E-12	1.45E-10	0.73	0.00	0.00	93.84	31.18	33.87
JC_g2462.t1	dy: Dusky (Drosophila melanogas	4.00	2.16E-19	1.14E-17	1954.90	2597.02	5957.18	97141.53	97073.11	78580.98
JC_g5706.t1	"CG42249: Uncharacterized prote	3.98	3.08E-39	5.34E-37	66.83	85.84	196.72	2127.87	2396.73	2069.09
JC_g5995.t1	polyprotein: Polyprotein (Drosoph	3.96	1.20E-20	7.07E-19	25.43	2.96	7.95	343.72	314.07	246.60
JC_g25074.t1	CG13272: FI02253p (Drosophila	3.96	1.59E-10	3.53E-09	0.00	5.92	11.92	11582.32	17400.79	15826.69
JC_g18879.t1	Dmel\CG4842: CG4842 (Drosoph	3.96	2.59E-14	8.88E-13	2.18	1.97	0.00	64.45	49.00	66.68
JC_g24021.t1	"Dhc98D: Dynein heavy chain at	3.90	4.10E-11	1.01E-09	29.06	10.85	3.97	1653.00	1310.85	424.40
JC_g4247.t1	Protein of unknown function	3.86	7.06E-15	2.53E-13	15.26	44.40	78.49	1115.95	1505.75	1309.19
JC_g16788.t1	Pka-C3: Put. protein kinase DC2 (	3.81	5.80E-49	1.38E-46	197.60	184.51	390.46	4073.71	4704.36	3457.66
JC_g22460.t1	Osi14: SP558 protein (Drosophila	3.79	2.05E-24	1.62E-22	8.72	5.92	6.95	153.77	129.19	125.94
JC_g10328.t1	CG16885: RH04334p (Drosophila	3.77	1.42E-20	8.25E-19	12.35	4.93	16.89	315.45	228.31	132.29
JC_g4865.t1	"Dmel\CG9628: CG9628, isoform	3.76	3.11E-10	6.62E-09	45.04	79.92	380.52	11470.38	14183.25	11903.35
JC_g23477.t1	"Gasp: Gasp, isoform A (Drosoph	3.73	5.45E-10	1.12E-08	0.00	0.00	0.00	35.05	36.75	23.28
JC_g20104.t1	LManII: Alpha-mannosidase (Dros	3.69	2.43E-80	1.85E-77	2076.21	2313.83	1990.03	38260.99	27348.55	22447.78
JC_g22456.t1	"Osi17: Osiris 17, isoform A (Dros	3.68	9.10E-89	7.44E-86	1080.97	1151.49	1587.65	18438.54	18963.34	14412.72
JC_g1774.t1	Protein of unknown function	3.62	1.05E-27	9.81E-26	42.13	15.79	30.80	304.14	545.72	513.30
JC_g23453.t1	Protein of unknown function	3.54	1.07E-09	2.13E-08	1.45	0.00	0.00	29.40	33.41	40.22
JC_g16776.t1	"CG6055: CG6055, isoform A (Dro	3.51	2.35E-52	6.90E-50	3427.42	3445.58	6182.71	58566.22	58879.13	44741.03
JC_g16810.t1	"Fatp: Fatty acid (Long chain) tran	3.49	6.07E-26	5.23E-24	58.12	38.48	68.55	384.42	1013.49	865.74
JC_g10545.t1	dpld: Cyt-b5-PB (Drosophila melar	3.48	7.04E-22	4.69E-20	46.49	50.32	154.00	1435.92	1296.37	836.10
JC_g25054.t1	"CG13282: Uncharacterized prote	3.48	1.53E-11	3.97E-10	1.45	1.97	2.98	50.88	63.48	39.16
JC_g11837.t1	Gs2-RC: Glutamine synthetase (F	3.48	8.87E-72	5.08E-69	1243.69	1479.08	1149.51	12823.76	19750.74	13176.56
JC_g23558.t1	Protein of unknown function	3.47	1.88E-63	7.95E-61	209.22	212.14	296.07	3500.47	2654.00	2342.15
JC_g15934.t1	Protein of unknown function	3.46	5.41E-40	9.53E-38	31.96	28.61	41.73	414.95	502.29	341.85
JC_g11638.t1	b6: B6 (Drosophila melanogaster)	3.45	7.42E-22	4.91E-20	11.62	7.89	25.83	228.39	203.81	192.62
JC_g8672.t1	FucTA: FI20174p1 (Drosophila me	3.44	8.13E-41	1.48E-38	53.76	74.00	120.22	1031.15	1050.24	909.13
JC_g24954.t1	jhamt: Juvenile hormone acid O-m	3.44	6.70E-21	4.08E-19	11.62	14.80	10.93	231.78	174.85	117.48
JC_g11312.t1	"exp: Expansion, isoform B (Dros	3.44	2.10E-14	7.29E-13	148.20	212.14	471.92	4109.89	5465.03	4291.64
JC_g7871.t1	Protein of unknown function	3.42	1.47E-08	2.48E-07	0.73	0.00	0.00	38.44	47.89	13.76
JC_g12508.t1	anon-WO0107627.1: RE46159p	3.41	1.94E-92	1.71E-89	2140.87	2025.71	2292.06	29114.08	23183.23	19399.70

JC_g4255.t1	Cht7: Chitinase 7 (Drosophila mel	3.37	1.96E-10	4.31E-09	708.30	1170.24	3309.43	42479.42	40247.68	28750.30
JC_g3223.t1	Protein of unknown function	3.36	1.10E-16	4.59E-15	4.36	12.83	11.92	134.55	167.06	101.60
JC_g18359.t1	CG9410-RA: IP16416p (Fragmen	3.34	3.72E-09	6.75E-08	0.00	1.97	7.95	136.81	115.83	31.75
JC_g4065.t1	Dmel\CG7458: CG7458 (Drosoph	3.29	1.25E-10	2.81E-09	4.36	2.96	0.99	49.75	76.85	41.28
JC_g19507.t1	CG17636-RA: MIP19773p (Droso	3.28	9.96E-50	2.59E-47	74.83	50.32	77.49	727.00	789.63	612.79
JC_g12814.t1	ChLD3: ChLD3 (Drosophila melan	3.26	5.54E-23	3.99E-21	54.48	86.83	154.00	1512.80	1137.11	746.14
JC_g14082.t1	CG17386: LP19379p (Drosophila	3.25	9.67E-59	3.46E-56	231.01	297.99	404.36	2900.10	3218.66	3271.39
JC_g22474.t1	Protein of unknown function	3.24	4.15E-34	5.87E-32	17105.89	19642.40	39259.16	305994.05	273144.72	225141.35
JC_g7442.t1	"CG17119: Uncharacterized prote	3.23	1.58E-169	2.58E-166	1487.06	1417.90	1374.05	13816.47	14571.94	12660.08
JC_g4344.t1	Protein of unknown function	3.23	3.09E-22	2.15E-20	18.89	35.52	15.90	336.93	242.79	213.79
JC_g22475.t1	Osi3: FI03378p (Drosophila melar	3.17	4.12E-44	8.90E-42	4810.60	5025.30	9221.90	62850.23	61205.69	61756.26
JC_g2221.t1	CG15890-RA: FI18259p1 (Drosop	3.17	1.88E-14	6.57E-13	7.99	5.92	9.94	71.23	128.08	97.37
JC_g15933.t1	GIIIspla2: LD41157p (Fragment) (	3.16	1.05E-32	1.37E-30	37.05	40.46	68.55	462.43	561.32	427.58
JC_g24280.t1	"Cyp49a1: Cyp49a1, isoform E (D	3.16	5.89E-14	1.93E-12	14.53	7.89	3.97	137.94	89.10	113.24
JC_g16510.t1	Zip71B: IP18018p (Drosophila me	3.16	2.62E-20	1.47E-18	17.43	28.61	10.93	192.21	247.25	177.80
JC_g17157.t1	Dmel\CG32206: FI20154p1 (Dros	3.16	1.03E-42	2.15E-40	55.21	59.20	67.56	695.35	593.61	464.62
JC_g7764.t1	"CG5966: CG5966, isoform A (Dr	3.15	7.35E-54	2.47E-51	1241.52	1492.89	1761.52	16472.35	15719.07	10321.11
JC_g7927.t1	Protein of unknown function	3.15	5.63E-11	1.36E-09	3.63	1.97	11.92	98.37	95.78	61.38
JC_g22651.t1	"CG11966: Uncharacterized prote	3.15	3.30E-32	4.11E-30	1235.70	1271.87	2741.14	16403.38	19517.97	15822.45
JC_g11156.t1	Protein of unknown function	3.13	8.36E-11	1.96E-09	8.72	21.71	33.78	502.01	322.98	83.61
JC_g9319.t1	"CG42346: Uncharacterized prote	3.11	4.07E-14	1.37E-12	10.90	4.93	13.91	140.20	134.76	79.38
JC_g23292.t1	CG15255: Metalloendopeptidase	3.11	8.92E-53	2.69E-50	360.32	555.52	580.22	5178.35	4714.38	3848.19
JC_g13088.t1	"SmydA-4: Uncharacterized prote	3.10	2.24E-12	6.43E-11	9.44	3.95	5.96	59.92	84.64	104.78
JC_g11697.t1	Protein of unknown function	3.10	4.15E-37	6.69E-35	165.63	236.81	342.77	2344.96	2675.16	1949.50
JC_g13075.t1	"futsch: Futsch, isoform F (Drosop	3.09	7.86E-22	5.16E-20	18.89	42.43	43.72	427.38	350.82	267.76
JC_g25160.t1	CG15531: Uncharacterized protei	3.09	1.02E-18	5.02E-17	18.89	58.22	54.64	382.16	596.95	379.95
JC_g24759.t1	Eaat2: Amino acid transporter (Dr	3.09	1.75E-53	5.55E-51	74.83	86.83	89.42	833.28	794.08	630.78
JC_g21599.t1	ZnT77C: RE32485p (Drosophila r	3.09	6.09E-15	2.20E-13	26.15	34.53	34.77	617.33	282.89	164.05
JC_g16632.t1	Osi21: Osiris 21 (Drosophila melar	3.08	1.08E-34	1.59E-32	32009.15	34545.63	65047.11	450358.05	444565.44	326561.70
JC_g21717.t1	Mp20: Muscle-specific protein 20	3.08	6.45E-35	9.98E-33	58.84	79.92	92.40	870.60	719.46	537.65
JC_g8910.t1	Protein of unknown function	3.08	2.65E-07	3.70E-06	0.00	0.00	1.99	32.79	21.16	27.52
JC_g11103.t1	Protein of unknown function	3.05	1.04E-11	2.77E-10	136.57	204.25	441.13	3397.58	3559.45	2543.23
JC_g3160.t1	CG15478: SD03340p (Drosophila	3.04	1.55E-07	2.22E-06	1.45	1.97	0.00	33.92	42.32	19.05
JC_g840.t1	polyprotein: Polyprotein (Drosoph	3.04	9.71E-28	9.11E-26	23.97	39.47	41.73	369.72	321.87	272.00
JC_g13086.t1	"Toll-9: Toll-9, isoform B (Drosoph	3.03	2.42E-07	3.40E-06	2.91	0.00	0.00	37.31	32.30	26.46
JC_g21870.t1	Protein of unknown function	3.01	6.83E-24	5.18E-22	21.79	49.34	29.81	275.88	318.52	329.15
JC_g10836.t1	CG15239-RA: FI03431p (Drosoph	2.99	2.01E-98	2.09E-95	5065.59	4147.13	4899.07	36652.08	43566.57	35337.52
JC_g25269.t1	"CG6431-RB: CG6431, isoform B	2.97	6.27E-32	7.48E-30	76.28	123.34	161.94	1005.14	1166.07	910.19
JC_g8908.t1	Protein of unknown function	2.96	4.10E-12	1.14E-10	7.26	3.95	14.90	106.28	93.55	81.49
JC_g13087.t1	SmydA-1: CG8503 (Drosophila m	2.96	6.03E-16	2.37E-14	18.89	16.77	9.94	171.86	103.58	169.34
JC_g3536.t1	ths: Thisbe (Drosophila melanoga	2.95	9.62E-16	3.72E-14	8.72	24.67	29.81	195.60	181.54	220.14
JC_g8417.t1	Oatp33Eb: Organic anion transpo	2.94	1.93E-15	7.28E-14	10.17	35.52	39.74	275.88	278.43	252.95
JC_g1688.t1	Protein of unknown function	2.92	2.68E-06	3.01E-05	0.00	0.00	0.00	18.09	25.62	13.76
JC_g2058.t1	Scr-RC: LD21370p (Fragment) (Dr	2.92	9.36E-08	1.38E-06	0.73	2.96	3.97	28.27	59.03	35.98
JC_g22591.t1	"CG7720: CG7720, isoform A (Dr	2.92	4.55E-10	9.47E-09	6.54	12.83	11.92	140.20	171.51	45.51
JC_g21600.t1	CG17739: GH02025p (Drosophila	2.92	1.25E-10	2.81E-09	3.63	8.88	9.94	109.67	79.07	56.09
JC_g12854.t1	CG10889: LD08718p (Drosophila	2.92	3.92E-27	3.57E-25	1205.92	1300.48	2606.02	17002.62	14834.77	10957.18
JC_g14984.t1	SD26211p (Drosophila melanoga	2.89	8.34E-13	2.50E-11	6.54	27.63	16.89	159.42	193.79	135.47
JC_g23338.t1	Protein of unknown function	2.89	2.25E-09	4.23E-08	3.63	4.93	5.96	70.10	35.64	64.56
JC_g16234.t1	CG8192-RA: CG8192 (Drosophila	2.88	4.49E-32	5.53E-30	167.09	165.77	137.11	826.50	1316.42	1605.53
JC_g24888.t1	"BcDNA:LP08817: Uncharacterize	2.87	2.37E-21	1.49E-19	21.07	22.69	29.81	236.30	213.83	161.93
JC_g9860.t1	Protein of unknown function	2.87	1.85E-16	7.56E-15	12.35	32.56	32.79	183.16	251.70	240.25
JC_g17065.t1	Cngl: CNG channel-like (Drosophi	2.86	3.87E-11	9.56E-10	7.26	4.93	7.95	81.41	60.14	62.44
JC_g7928.t1	Protein of unknown function	2.84	5.25E-08	8.17E-07	1.45	8.88	1.99	47.49	60.14	50.80
JC_g5339.t1	CG2663: RE58223p (Drosophila r	2.83	2.17E-27	1.99E-25	5384.50	6639.56	12758.85	63503.74	69438.33	60044.89
JC_g25461.t1	CG8775: RE62048p (Fragment) (	2.81	2.75E-12	7.81E-11	10.17	5.92	15.90	113.06	81.30	97.37
JC_g21852.t1	polyprotein: Polyprotein (Drosoph	2.81	3.42E-06	3.73E-05	2.91	0.00	0.00	14.70	51.23	30.69
JC_g10546.t1	Cytochrome b5 (Drosophila melan	2.81	4.65E-26	4.04E-24	50.13	33.55	62.59	368.59	437.69	324.92
JC_g18922.t1	Tsp29Fb: Tetraspanin (Drosophila	2.81	7.72E-11	1.83E-09	11.62	14.80	56.63	310.93	258.38	219.08
JC_g23237.t1	Spn88Ea: Serine protease inhibit	2.80	9.92E-77	5.97E-74	2171.38	2830.87	2762.00	19988.65	19044.64	16540.02
JC_g9782.t1	Protein of unknown function	2.78	5.87E-32	7.07E-30	69.74	92.75	105.31	603.76	814.13	554.58
JC_g7485.t1	Dmel\CG10585: GH23839p (Dros	2.76	1.29E-26	1.16E-24	57.39	50.32	97.37	502.01	553.52	463.56
JC_g2219.t1	"Ance: Angiotensin converting en	2.76	1.64E-10	3.65E-09	13.80	12.83	10.93	61.05	183.76	103.72
JC_g13702.t1	Mocs2: Molybdopterin synthase c	2.76	7.04E-46	1.61E-43	1211.73	1463.29	1222.04	9103.94	11570.46	6949.18
JC_g22473.t1	"Osi5: Osiris 5, isoform B (Drosopl	2.75	4.42E-06	4.70E-05	0.00	0.00	3.97	35.05	22.27	35.98
JC_g23454.t1	Rapgap1: RE67551p (Drosophila	2.75	5.67E-24	4.36E-22	338.53	705.50	780.91	5673.57	3728.74	4137.12
JC_g20171.t1	Protein of unknown function	2.73	1.30E-05	0.0001229	0.00	0.00	0.00	47.49	16.71	6.35
JC_g1952.t1	Protein of unknown function	2.73	5.69E-18	2.65E-16	42.86	24.67	27.82	202.39	320.75	211.67
JC_g22465.t1	Osi10: Osiris 10 (Drosophila melar	2.72	3.61E-19	1.86E-17	42.13	36.51	72.53	452.26	397.60	274.11
JC_g3009.t1	"AkhR: Adipokinetic hormone rece	2.71	2.10E-09	3.98E-08	21.07	37.49	3.97	225.00	204.92	148.17
JC_g1051.t1	Dmel\CG12017: FI24008p1 (Dros	2.71	1.51E-08	2.55E-07	372.67	422.31	1231.97	7867.02	7006.42	5012.38
JC_g12075.t1	t: Mutant tan (Drosophila melanog	2.69	1.62E-11	4.19E-10	29.06	40.46	38.75	442.08	112.49	335.50
JC_g16895.t1	atk: Protein artichoke (Drosophila	2.69	1.52E-64	6.97E-62	249.90	259.50	315.94	1998.98	1715.13	1756.87
JC_g10716.t1	"CG31663: Uncharacterized prote	2.68	4.01E-24	3.12E-22	1155.07	1386.32	1604.54	14690.46	8137.97	6331.10

JC_g11024.t1	bbg-RC: MIP21057p (Fragment) (	2.67	4.93E-31	5.54E-29	87.90	126.30	123.20	799.37	898.77	591.62
JC_g4315.t1	"cort: Cortex, isoform B (Drosophil	2.67	2.36E-12	6.75E-11	8.72	26.64	26.83	152.64	142.56	187.33
JC_g2470.t1	"Ance-3: Ance-3, isoform B (Dros	2.67	8.85E-18	4.07E-16	189.61	402.58	499.74	3492.56	2641.75	1755.82
JC_g14004.t1	CG15080: Uncharacterized protei	2.66	7.59E-21	4.60E-19	4107.39	7100.35	11681.87	59930.91	54787.32	45573.96
JC_g4852.t1	Mipp1: Multiple inositol polyphosp	2.65	4.54E-31	5.14E-29	492.54	518.02	622.94	4547.45	4027.22	2386.60
JC_g11949.t1	"fw: Furrowed, isoform A (Drosoph	2.64	9.16E-52	2.56E-49	454.04	469.67	664.67	3388.54	3609.57	3273.50
JC_g22649.t1	CG14866: RE26319p (Drosophila	2.63	8.99E-15	3.20E-13	13.08	19.73	19.87	111.93	144.78	121.71
JC_g13873.t1	"CG45076: Uncharacterized prote	2.62	2.15E-10	4.70E-09	15.26	18.75	56.63	267.96	163.72	284.70
JC_g21803.t1	"Cyp4g15: Cyp4g15, isoform C (D	2.60	1.39E-20	8.15E-19	74.10	95.71	76.50	786.93	454.40	407.47
JC_g23227.t1	CG6746: Very-long-chain (3R)-3-h	2.57	5.77E-64	2.54E-61	798.38	726.22	939.88	5084.51	5500.67	4476.85
JC_g18341.t1	"Ptr: Patched-related, isoform A (D	2.57	6.36E-19	3.16E-17	181.61	236.81	476.89	2177.62	1979.08	1733.59
JC_g4577.t1	yellow-h: Yellow-h (Drosophila me	2.56	2.88E-20	1.59E-18	451.86	470.66	736.20	5129.73	3404.65	2246.89
JC_g13510.t1	MIP02663p (Fragment) (Drosophi	2.56	2.08E-09	3.95E-08	7.26	40.46	40.73	261.18	189.33	231.78
JC_g20075.t1	CG6688-RA: CG6688 (Drosophila	2.56	5.76E-07	7.37E-06	8.72	8.88	1.99	99.50	56.80	34.93
JC_g22464.t1	Osi11: Osiris 11 (Drosophila melan	2.55	3.06E-25	2.52E-23	54387.66	53556.54	104091.67	520851.43	440205.22	374453.46
JC_g24674.t1	Protein of unknown function	2.55	1.11E-07	1.63E-06	7.26	5.92	3.97	56.53	61.25	33.87
JC_g1778.t1	"CG5961: CG5961, isoform A (Dro	2.53	9.67E-10	1.93E-08	24.70	28.61	110.28	342.59	428.78	442.39
JC_g2685.t1	Protein of unknown function	2.52	5.82E-05	0.0004573	0.00	0.00	0.00	18.09	18.93	8.47
JC_g10838.t1	CG34038-RB: MIP24587p (Droso	2.52	4.14E-06	4.43E-05	1.45	5.92	1.99	42.96	31.18	27.52
JC_g9097.t1	"Amph: Amphiphysin, isoform B (D	2.52	9.26E-65	4.42E-62	1719.52	1607.35	1989.04	11394.63	10825.38	9011.92
JC_g11104.t1	"dyl: Dusky-like, isoform A (Drosop	2.52	4.38E-22	3.00E-20	17490.18	17891.98	37893.06	160864.61	160514.04	133973.32
JC_g5382.t1	Dmel\CG42598: Uncharacterized	2.52	1.80E-78	1.15E-75	2152.49	1991.18	2117.20	10987.60	13885.88	11683.22
JC_g2958.t2	Protein of unknown function	2.51	4.39E-05	0.0003556	0.73	1.97	2.98	111.93	8.91	12.70
JC_g1049.t1	Protein of unknown function	2.51	8.34E-07	1.04E-05	46.49	55.26	189.76	957.66	935.53	737.68
JC_g7441.t1	CG4797: CG4797 (Drosophila me	2.49	4.80E-09	8.56E-08	11.62	11.84	5.96	84.80	79.07	53.98
JC_g18112.t1	if: Integrin alpha-PS2 (Drosophila	2.48	2.21E-06	2.50E-05	1729.69	3406.12	7889.59	55342.75	36887.58	28267.69
JC_g7848.t1	Cpr49Ah: Cuticular protein 49Ah (	2.46	5.66E-06	5.83E-05	3.63	1.97	2.98	31.66	22.27	34.93
JC_g11188.t1	Protein of unknown function	2.46	1.85E-06	2.13E-05	5.81	8.88	1.99	71.23	30.07	48.68
JC_g13491.t1	Protein of unknown function	2.45	1.38E-26	1.23E-24	121.32	136.17	186.78	1049.24	818.59	702.75
JC_g2450.t1	Protein of unknown function	2.44	3.70E-08	5.93E-07	8.72	23.68	45.70	267.96	168.17	128.06
JC_g4084.t1	Dmel\CG7458: CG7458 (Drosoph	2.44	1.36E-05	0.0001277	0.73	2.96	4.97	29.40	23.39	40.22
JC_g3648.t1	Protein of unknown function	2.44	2.26E-14	7.80E-13	28.33	22.69	51.66	202.39	198.24	228.61
JC_g22499.t1	Osi2: LP14110p (Drosophila mela	2.43	1.05E-41	2.07E-39	212.13	188.46	237.45	1321.72	1234.00	1001.21
JC_g646.t1	Protein of unknown function	2.42	5.44E-05	0.0004308	48.67	138.14	17.88	511.05	1813.14	653.01
JC_g2442.t1	Protein of unknown function	2.42	1.45E-14	5.06E-13	40.68	43.42	33.78	336.93	192.67	184.15
JC_g3452.t1	"Sb: Stubble, isoform B (Drosophi	2.42	6.74E-24	5.14E-22	841.24	874.22	1421.73	7374.06	6147.74	4382.66
JC_g18930.t1	Protein of unknown function	2.42	3.65E-06	3.95E-05	3.63	3.95	12.92	97.24	44.55	37.04
JC_g10717.t1	NLaz: Neural Lazarillo (Drosophila	2.41	5.18E-22	3.49E-20	1341.04	1559.00	2264.24	12952.66	10016.81	6636.96
JC_g6311.t1	Protein of unknown function	2.41	1.00E-05	9.77E-05	1.45	2.96	11.92	38.44	42.32	75.14
JC_g22458.t1	Osi16: Osiris 16 (Drosophila melan	2.40	3.45E-05	0.0002886	4.36	1.97	0.00	26.00	31.18	24.34
JC_g7786.t1	Timp: Tissue inhibitor of metallopr	2.40	9.05E-35	1.38E-32	317.46	408.50	511.67	2245.46	2542.63	2029.93
JC_g17835.t2	dmp: Multiplexin transcript 10 (Fra	2.40	3.67E-19	1.88E-17	37.78	36.51	42.72	230.65	183.76	256.12
JC_g17835.t1	"Mp: Multiplexin, isoform S (Droso	2.40	2.98E-23	2.23E-21	173.62	358.17	317.93	1590.82	1480.14	1696.55
JC_g19635.t1	"Duox: Dual oxidase, isoform C (D	2.39	1.42E-18	6.95E-17	269.52	332.52	625.92	2754.25	2120.53	2123.07
JC_g23862.t1	wun: Putative phosphatidate pho	2.39	3.49E-42	7.14E-40	223.75	214.12	288.12	1224.49	1451.18	1245.69
JC_g8220.t1	"NT1: Neurotrophin 1, isoform F (D	2.38	1.20E-16	4.96E-15	5741.19	8168.96	14102.10	70241.25	51899.44	38636.42
JC_g10878.t1	CAH1: Carbonic anhydrase 1 (Dro	2.38	2.77E-20	1.54E-18	228.11	464.74	514.65	2508.90	2189.58	2061.68
JC_g11630.t1	"Dmel\CG45057: Uncharacterized	2.37	0.0001064	0.0007777	0.00	1.97	1.99	37.31	7.80	27.52
JC_g7725.t1	"CG13643: Uncharacterized prote	2.37	5.93E-11	1.43E-09	34.87	95.71	110.28	362.94	415.42	687.93
JC_g4687.t1	"IRSp53: IRSp53, isoform A (Dros	2.37	2.28E-30	2.49E-28	1087.51	1176.16	1583.68	8731.96	6665.62	5477.00
JC_g5478.t1	CG30053: IP10855p (Drosophila	2.37	1.40E-11	3.64E-10	30.51	31.57	43.72	318.84	172.63	143.94
JC_g4703.t1	ect-RA: RE17440p (Drosophila me	2.36	3.26E-23	2.43E-21	56944.07	58064.80	109231.17	453898.09	420031.26	352761.35
JC_g17016.t1	Adk1: AT17975p (Drosophila mela	2.36	1.30E-07	1.89E-06	33.42	13.81	18.88	115.33	263.95	78.32
JC_g10282.t1	"Snmp1: Sensory neuron membra	2.36	3.73E-14	1.26E-12	24.70	33.55	22.85	185.43	145.90	134.41
JC_g18235.t1	Protein of unknown function	2.35	5.39E-28	5.14E-26	8276.53	7197.05	12311.77	59673.12	48151.76	41405.09
JC_g10563.t1	Protein of unknown function	2.35	6.56E-13	1.99E-11	33.42	46.38	68.55	394.59	233.88	228.61
JC_g23559.t1	"PsGEF: Protostome-specific GEF	2.35	1.10E-19	5.88E-18	677.78	849.56	411.32	4402.73	3637.42	2620.49
JC_g3632.t1	Dmel\CG8541: CG8541 (Drosoph	2.34	0.0001887	0.0012767	0.00	0.00	0.00	6.78	31.18	9.53
JC_g12234.t1	"Fhos: Formin homology 2 domain	2.34	4.26E-08	6.78E-07	7.26	8.88	10.93	63.32	49.00	63.50
JC_g20579.t1	CG4797: CG4797 (Drosophila me	2.33	7.84E-07	9.83E-06	7.99	6.91	8.94	30.53	75.73	63.50
JC_g25019.t1	CG6142: CG6142 (Drosophila me	2.33	1.16E-32	1.48E-30	1495.78	1337.98	1960.23	9668.14	8844.06	6556.53
JC_g597.t1	"Neto: Neuropilin and tolloid-like, i	2.32	4.44E-09	7.95E-08	23.25	24.67	21.86	87.06	229.43	110.07
JC_g5737.t1	CG6180: CG6180 (Drosophila me	2.32	2.02E-06	2.31E-05	9.44	10.85	10.93	109.67	90.21	26.46
JC_g1010.t1	"CG8213: CG8213, isoform B (Dro	2.32	3.47E-18	1.65E-16	5728.84	7120.08	13375.83	55186.72	47014.65	39115.86
JC_g5175.t1	ORF: Orf protein (Drosophila mela	2.31	2.74E-07	3.80E-06	7.99	6.91	15.90	83.67	73.51	45.51
JC_g4618.t1	T48: GM18993p (Drosophila mela	2.30	2.90E-36	4.60E-34	696.67	538.74	733.22	3965.17	3307.75	2801.47
JC_g16177.t1	"Arr1: Arrestin 1, isoform B (Droso	2.30	7.82E-07	9.82E-06	7.26	8.88	27.82	137.94	84.64	73.03
JC_g21965.t1	Cubn: Cubilin homolog (Drosophil	2.30	4.83E-07	6.30E-06	28.33	27.63	90.41	567.58	256.16	145.00
JC_g5241.t1	Rpb7: GH11867p (Drosophila me	2.29	1.70E-32	2.13E-30	1080.97	998.55	1321.39	7095.92	5694.46	4498.02
JC_g19185.t1	CG14205: RE53177p (Fragment)	2.29	9.27E-05	0.0006893	5.81	0.00	1.99	39.57	30.07	21.17
JC_g4429.t1	Protein of unknown function	2.29	0.0001632	0.0011243	2.18	0.99	0.99	19.22	35.64	8.47
JC_g1783.t1	Protein of unknown function	2.29	6.99E-17	2.99E-15	91.53	111.50	185.79	582.28	849.77	623.37
JC_g7821.t1	lin-28: Protein lin-28 homolog (Dro	2.28	4.01E-19	2.04E-17	194.69	236.81	219.57	1530.89	1156.04	719.68
JC_g19508.t1	Protein of unknown function	2.28	5.11E-05	0.0004066	5.09	0.00	10.93	70.10	47.89	31.75

JC_g1973.t1	FER: Tyrosine-protein kinase Fer	2.28	4.99E-15	1.81E-13	1207.37	1948.75	3195.18	14541.21	10616.00	8646.79
JC_g15377.t1	CG12268-RB: Fatty acyl-CoA redu	2.27	1.40E-06	1.67E-05	5.81	6.91	11.92	36.18	74.62	53.98
JC_g19653.t1	"CG4678: CG4678, isoform I (Dro	2.27	6.72E-45	1.48E-42	1004.69	984.73	1348.21	5321.94	6017.44	5240.99
JC_g882.t1	BEST:CK00459: Sodium/nucleos	2.27	1.31E-05	0.0001238	5.09	3.95	5.96	21.48	57.91	37.04
JC_g10763.t1	Protein of unknown function	2.27	2.76E-12	7.83E-11	47.95	45.39	41.73	141.33	305.16	292.11
JC_g22639.t1	Protein of unknown function	2.26	1.77E-10	3.91E-09	15.26	13.81	21.86	92.71	98.01	92.08
JC_g2968.t1	"futsch: Futsch, isoform F (Drosop	2.26	6.81E-09	1.19E-07	36.32	125.31	132.14	357.28	514.54	822.34
JC_g18019.t1	Protein of unknown function	2.26	2.73E-21	1.71E-19	72.65	76.96	49.68	364.07	339.69	311.16
JC_g12633.t1	"Dmel\CG3961: CG3961, isoform	2.25	2.68E-60	9.89E-58	2666.10	2747.00	3206.11	14983.29	14496.20	12432.53
JC_g7824.t1	Protein of unknown function	2.25	1.23E-06	1.49E-05	11.62	16.77	21.86	176.38	106.92	42.33
JC_g7731.t1	CG33299: HDC01644 (Drosophila	2.25	1.08E-27	9.96E-26	10558.33	11752.68	16969.42	76557.02	66672.96	52313.58
JC_g23623.t1	CG11085: IP01054p (Drosophila	2.25	4.11E-05	0.0003347	3.63	2.96	2.98	23.74	20.05	38.10
JC_g10590.t1	Protein of unknown function	2.25	0.0001907	0.0012876	1.45	1.97	4.97	20.35	8.91	76.20
JC_g5472.t1	Protein of unknown function	2.25	1.14E-08	1.96E-07	13.08	12.83	22.85	113.06	100.23	66.68
JC_g23288.t1	CG10936: RE29777p (Drosophila	2.24	3.87E-41	7.25E-39	3938.12	5077.60	5791.26	26091.87	24223.45	21691.05
JC_g23002.t1	CG4115: CG4115 (Drosophila me	2.24	1.76E-17	7.86E-16	108.24	52.30	82.46	394.59	420.99	426.52
JC_g1734.t1	"cag: Cag, isoform A (Drosophila	2.23	0.0003639	0.0022433	0.00	0.00	0.00	27.14	13.36	4.23
JC_g11172.t1	"nAChRalpha5: Nicotinic acetylch	2.23	2.84E-06	3.15E-05	16.71	58.22	19.87	381.03	134.76	102.66
JC_g13829.t1	CG5639: CG5639 (Drosophila me	2.23	6.46E-17	2.78E-15	3333.71	3848.16	7613.39	29115.21	24589.86	21093.08
JC_g12472.t1	Protein of unknown function	2.22	8.69E-11	2.04E-09	61.02	89.79	167.91	764.32	551.29	383.13
JC_g21297.t1	"Ets98B: Ets at 98B, isoform B (D	2.22	2.35E-19	1.22E-17	2613.79	2653.26	4709.31	20348.20	16590.00	12473.81
JC_g24994.t1	bchs: Blue cheese (Drosophila me	2.21	6.87E-07	8.67E-06	8.72	7.89	12.92	78.01	61.25	40.22
JC_g9418.t1	Dmel\CG14086: Uncharacterized	2.21	4.53E-19	2.28E-17	92.99	77.95	115.25	462.43	583.59	368.31
JC_g2033.t1	Protein of unknown function	2.20	4.88E-09	8.69E-08	16.71	57.23	51.66	273.62	210.49	195.80
JC_g4576.t1	Protein of unknown function	2.19	7.65E-08	1.15E-06	10.17	18.75	13.91	101.76	81.30	57.15
JC_g10149.t1	CG13407: Uncharacterized protei	2.19	4.42E-05	0.0003572	429.34	185.50	169.89	3622.58	1027.97	1213.94
JC_g10886.t1	"CG18304: Uncharacterized prote	2.19	5.43E-13	1.67E-11	138.03	400.60	341.77	1351.12	1734.06	1356.82
JC_g22108.t1	Mob2-RA: RE25560p (Drosophila	2.19	1.09E-10	2.50E-09	22.52	28.61	20.86	154.90	123.62	95.25
JC_g14230.t2	GIP: Copia protein (Drosophila me	2.18	0.0001019	0.0007502	5.81	5.92	21.86	204.65	34.53	38.10
JC_g5302.t1	"Rbp: RIM-binding protein, isofor	2.18	2.69E-08	4.42E-07	15.98	10.85	14.90	66.71	66.82	96.31
JC_g9150.t1	Protein of unknown function	2.18	6.34E-11	1.51E-09	34.87	20.72	22.85	114.20	160.38	131.24
JC_g18932.t1	Pax: LD06038p (Drosophila melan	2.17	6.07E-13	1.86E-11	695.22	530.85	727.26	5247.32	2597.20	1858.48
JC_g21538.t1	"Dmel\CG44836: Uncharacterized	2.17	1.86E-15	7.04E-14	155.46	136.17	90.41	801.63	615.89	441.34
JC_g14003.t1	Protein of unknown function	2.16	2.09E-21	1.34E-19	735.17	1068.60	1428.69	5751.59	5269.02	4253.54
JC_g11946.t1	Protein of unknown function	2.16	1.55E-05	0.0001431	5.81	4.93	6.95	38.44	52.34	25.40
JC_g16825.t1	"ome: Omega, isoform H (Drosoph	2.15	4.29E-30	4.63E-28	1269.12	1143.59	1469.42	7296.04	5948.39	4622.91
JC_g12922.t1	Gk1: GH12641p (Drosophila mela	2.15	6.10E-25	4.95E-23	317.46	445.01	519.61	2194.58	2104.93	1636.22
JC_g20170.t1	Ugt35a: LD21102p (Drosophila m	2.15	0.0005496	0.0031906	0.00	3.95	0.00	40.70	14.48	14.82
JC_g21311.t1	Elo68alpha: Elongation of very lo	2.15	0.0002733	0.001752	0.00	5.92	5.96	58.79	37.87	17.99
JC_g11155.t1	Protein of unknown function	2.14	4.65E-07	6.07E-06	9.44	20.72	25.83	139.07	64.60	104.78
JC_g4314.t1	Protein of unknown function	2.14	5.13E-05	0.0004073	8.72	1.97	3.97	29.40	35.64	41.28
JC_g2576.t1	aos: Protein giant-lens (Drosophil	2.14	5.65E-17	2.44E-15	270.24	301.93	474.91	2112.04	1612.67	1205.47
JC_g18413.t1	MsR2: Peptide receptor GPCR (D	2.11	1.06E-05	0.0001022	7.99	8.88	37.75	136.81	98.01	86.79
JC_g2970.t1	futsch: IP18437p (Fragment) (Dro	2.10	1.30E-06	1.56E-05	16.71	88.80	86.44	296.23	241.68	503.78
JC_g19655.t1	"Sep4: Septin 4, isoform A (Drosc	2.10	7.03E-23	5.03E-21	316.01	188.46	239.44	1178.13	1207.27	963.11
JC_g2684.t1	Protein of unknown function	2.09	0.0008354	0.0045736	0.00	1.97	0.00	24.87	23.39	4.23
JC_g2034.t1	Protein of unknown function	2.09	1.86E-06	2.14E-05	13.08	92.75	92.40	365.20	348.59	359.84
JC_g2541.t1	CrzR: Putative corazonin receptor	2.09	0.0005498	0.0031906	0.00	0.99	7.95	28.27	43.44	24.34
JC_g20794.t1	"CG42594: Uncharacterized prote	2.09	0.0008653	0.0047111	0.73	0.00	0.00	7.91	14.48	11.64
JC_g17306.t1	"Tre1: Trapped in endoderm 1, is	2.09	4.53E-28	4.36E-26	5887.21	4806.25	6996.41	31681.77	24952.94	21354.49
JC_g2250.t1	"CG33098: Uncharacterized prote	2.09	0.0002643	0.0017042	1.45	1.97	5.96	29.40	28.96	16.93
JC_g24167.t1	CG30069: Uncharacterized protei	2.09	1.14E-46	2.67E-44	7963.42	9867.08	7517.01	34168.06	39670.77	36015.93
JC_g10030.t1	Protein of unknown function	2.09	1.93E-06	2.21E-05	12.35	15.79	27.82	154.90	87.98	58.21
JC_g1714.t1	Protein of unknown function	2.08	2.06E-05	0.0001847	5.09	4.93	14.90	42.96	59.03	44.45
JC_g11840.t1	CG34356-RC: IP12866p (Drosopl	2.08	7.82E-18	3.61E-16	132.94	133.21	137.11	594.72	427.67	781.07
JC_g21323.t1	CG7840: Polyprenol reductase (D	2.08	8.39E-26	7.17E-24	3209.49	2780.54	4160.88	17319.20	15537.53	11574.20
JC_g22267.t1	"CT30701: Uncharacterized prote	2.07	0.0002077	0.001385	1.45	5.92	2.98	27.14	22.27	26.46
JC_g17161.t1	Protein of unknown function	2.07	0.0002965	0.0018782	4.36	1.97	1.99	15.83	22.27	29.63
JC_g10692.t1	Protein of unknown function	2.07	0.0003603	0.0022231	2.91	1.97	1.99	19.22	24.50	14.82
JC_g849.t1	CG4734: CG4734 (Drosophila me	2.06	6.43E-31	7.14E-29	855.04	964.01	843.50	4787.15	3243.16	3433.31
JC_g2031.t1	ORF: Orf protein (Drosophila mela	2.06	2.17E-08	3.61E-07	33.42	112.48	140.09	457.91	432.12	493.19
JC_g15354.t1	wat: Fatty acyl-CoA reductase wa	2.06	0.0002131	0.0014158	2.18	1.97	7.95	24.87	33.41	27.52
JC_g9906.t1	Con-RA: RT10551p (Fragment) (D	2.05	0.0003703	0.00228	0.00	5.92	9.94	47.49	33.41	43.39
JC_g1508.t1	vri: FI01009p (Drosophila melano	2.05	6.69E-19	3.31E-17	3946.11	3726.80	7101.72	23269.78	21750.99	19192.27
JC_g9174.t1	Cad96Ca: Tyrosine kinase recept	2.04	3.65E-65	1.82E-62	1708.63	1663.59	1688.00	7289.26	7474.19	6368.14
JC_g4584.t1	yellow-e: RE55542p (Drosophila r	2.04	3.52E-07	4.74E-06	56.66	75.98	259.31	694.22	709.44	535.53
JC_g3696.t1	Jheh1: Epoxide hydrolase (Droso	2.04	2.80E-07	3.87E-06	14.53	15.79	13.91	70.10	94.67	53.98
JC_g8121.t1	CG33110-RA: Elongation of very	2.04	3.82E-07	5.09E-06	18.16	11.84	9.94	65.58	70.16	64.56
JC_g3456.t1	ORF: Orf protein (Drosophila mela	2.04	2.57E-17	1.15E-15	76.28	133.21	119.22	504.27	491.15	424.40
JC_g13182.t1	Protein of unknown function	2.04	0.0006385	0.0036383	1.45	2.96	0.99	20.35	15.59	14.82
JC_g1058.t1	Dmel\CG12009: LP10131p (Dros	2.03	0.0010886	0.0057161	0.00	0.00	0.00	6.78	2.23	48.68
JC_g23474.t1	Peritrophin-A: LD20793p (Drosop	2.03	9.36E-08	1.38E-06	14.53	15.79	12.92	71.23	73.51	62.44
JC_g15375.t2	CG12268-RB: Fatty acyl-CoA redu	2.02	0.0009581	0.0051473	2.91	3.95	0.00	50.88	7.80	20.11
JC_g8557.t1	CG17739: GH02025p (Drosophila	2.02	0.0002693	0.0017318	0.73	9.87	5.96	38.44	31.18	42.33

JC_g11918.t1	Protein of unknown function	2.02	0.0001669	0.0011477	3.63	3.95	3.97	22.61	28.96	23.28
JC_g23177.t1	Tsp39D: Tetraspanin (Drosophila	2.02	1.48E-13	4.69E-12	62.48	113.47	132.14	393.46	474.45	469.91
JC_g4286.t1	Treh: Trehalase (Drosophila melar	2.01	7.15E-33	9.41E-31	403.91	408.50	323.89	1637.17	1721.81	1357.87
JC_g2463.t1	m: Miniature (Drosophila melanog	2.01	3.33E-17	1.46E-15	13041.36	13946.13	23624.05	87229.17	73394.27	55242.06
JC_g9931.t1	ORF: ORF (Drosophila melanogas	2.01	9.03E-07	1.12E-05	29.06	28.61	14.90	179.77	104.69	71.97
JC_g10815.t1	"Asap: ArfGAP with SH3 domain,	2.01	3.09E-15	1.14E-13	47.22	70.06	54.64	271.35	222.74	238.13
JC_g8467.t1	Protein of unknown function	2.01	4.50E-15	1.64E-13	7429.48	9388.53	16394.16	56604.55	46069.10	39459.83
JC_g4619.t1	"Dnai2: Dynein, axonemal, interm	2.00	3.93E-10	8.25E-09	34.87	37.49	51.66	223.87	202.70	124.89
JC_g5335.t1	Protein of unknown function	2.00	1.34E-09	2.61E-08	86.45	43.42	134.13	435.30	409.85	332.32
JC_g10689.t1	Acyl-coenzyme A oxidase (Drosop	1.99	2.21E-07	3.12E-06	21.07	11.84	22.85	106.28	89.10	67.73
JC_g3196.t1	Protein of unknown function	1.99	0.0014608	0.0073212	0.73	0.99	0.00	22.61	6.68	8.47
JC_g238.t1	"Fak: Focal adhesion kinase, isof	1.99	4.04E-42	8.11E-40	1774.73	1867.84	1932.41	8630.20	7613.40	6382.96
JC_g3865.t1	polyprotein: Polyprotein (Drosoph	1.99	0.0014715	0.0073651	0.00	0.00	2.98	13.57	12.25	22.23
JC_g18345.t1	Protein of unknown function	1.98	1.63E-08	2.74E-07	29.78	38.48	41.73	194.47	203.81	95.25
JC_g21003.t1	"v: Tryptophan 2,3-dioxygenase (	1.98	3.67E-18	1.73E-16	254.26	240.76	329.85	1329.64	1280.78	807.53
JC_g2103.t1	Protein of unknown function	1.98	1.08E-06	1.31E-05	13.08	33.55	23.84	113.06	145.90	73.03
JC_g2881.t1	CG14713: IP14232p (Drosophila	1.98	1.66E-31	1.94E-29	13210.62	9858.20	13106.59	54283.34	51337.01	40707.63
JC_g1799.t1	CG31274: LP05795p (Drosophila	1.98	5.55E-10	1.14E-08	42.13	95.71	112.27	361.81	410.96	313.27
JC_g10038.t1	Dmel\CG15020: Uncharacterized	1.98	1.31E-23	9.87E-22	114.05	115.44	151.02	551.75	478.90	519.65
JC_g20993.t1	ESTS:172F5T: LP03571p (Droso	1.98	1.69E-06	1.98E-05	22.52	13.81	19.87	131.15	84.64	55.03
JC_g12638.t1	"for: Foraging, isoform K (Drosoph	1.97	2.26E-21	1.43E-19	5248.65	5632.13	8358.53	30755.77	26239.29	21118.48
JC_g5849.t1	CG11005: LD44221p (Drosophila	1.96	0.0002136	0.0014177	2.18	8.88	4.97	31.66	28.96	33.87
JC_g18018.t1	Protein of unknown function	1.96	1.09E-32	1.41E-30	294.22	354.23	390.46	1322.85	1509.09	1307.07
JC_g23293.t1	CG15255: Metalloendopeptidase	1.96	0.0012409	0.0063727	0.73	3.95	0.99	11.31	20.05	21.17
JC_g16212.t1	rau: GH01721p (Drosophila melar	1.96	4.05E-29	4.10E-27	450.40	375.94	527.56	1657.52	2035.88	1701.84
JC_g15483.t1	"CG3726: CG3726, isoform A (Dr	1.95	1.87E-16	7.61E-15	680.69	701.55	596.12	2646.84	3676.40	1761.11
JC_g21882.t1	CG16786: RE48511p (Drosophila	1.95	4.02E-49	9.79E-47	5827.64	5554.18	4789.79	20886.38	23093.02	19635.72
JC_g23119.t1	"jbug: Jitterbug, isoform M (Droso	1.95	1.07E-31	1.26E-29	6708.10	6458.99	8710.24	31983.65	30247.57	24559.20
JC_g2422.t1	CG4386: CG4386 (Drosophila me	1.94	2.21E-30	2.43E-28	2448.16	2083.93	2825.59	11122.14	9741.72	8144.07
JC_g5250.t1	CG40485: RH03309p (Drosophila	1.94	1.34E-06	1.60E-05	14.53	31.57	56.63	180.90	148.12	136.53
JC_g18020.t1	"d: Dachs, isoform E (Drosophila r	1.94	1.17E-28	1.16E-26	1244.42	1541.24	1762.51	6874.31	5804.72	5183.84
JC_g19178.t1	Protein of unknown function	1.93	0.0009998	0.0053255	7.26	29.60	4.97	232.91	62.37	14.82
JC_g1272.t1	Hex-A: Phosphotransferase (Dros	1.92	0.0001334	0.0009493	7.99	8.88	3.97	30.53	28.96	52.92
JC_g7849.t1	Cpr49Aa: Cuticular protein 49Aa (	1.92	0.0021473	0.0101865	0.73	1.97	0.00	9.05	7.80	24.34
JC_g12721.t1	Protein of unknown function	1.92	0.0005306	0.0030988	2.91	2.96	11.92	46.36	20.05	42.33
JC_g23450.t1	Atac1: Ada2a-containing complex	1.91	2.08E-08	3.45E-07	69.01	253.58	143.07	713.44	623.68	629.72
JC_g3894.t1	mspo: M-spondin (Drosophila mel	1.91	0.0014593	0.0073169	0.00	11.84	13.91	64.45	18.93	123.83
JC_g21573.t1	CG17761: IP03637p (Fragment) (	1.91	1.54E-28	1.50E-26	242.64	257.53	306.01	1127.25	1065.83	908.07
JC_g5936.t1	Gld-RA: FI21568p1 (Drosophila m	1.91	3.22E-05	0.0002715	10.90	32.56	11.92	52.01	114.71	98.43
JC_g25210.t1	beat-IIIa-RA: RT09993p (Fragmer	1.90	0.00163	0.008025	2.18	9.87	0.00	31.66	15.59	55.03
JC_g15153.t1	edl: ETS-domain lacking (Drosoph	1.90	2.81E-10	6.03E-09	45.04	51.31	92.40	288.31	228.31	247.66
JC_g10877.t1	"stl: Stall, isoform C (Drosophila m	1.90	0.0001707	0.0011699	2.91	23.68	11.92	63.32	60.14	76.20
JC_g22466.t1	Osi8: Osiris 8 (Drosophila melano	1.90	1.70E-17	7.67E-16	89294.65	88336.02	154012.35	490544.52	443132.08	359404.67
JC_g11005.t1	CG3376: Sphingomyelin phospho	1.90	1.01E-33	1.38E-31	1146.35	1223.52	1484.33	5566.16	4581.85	4526.60
JC_g18703.t1	"MRP: Multidrug-Resistance like p	1.90	1.63E-49	4.05E-47	1800.16	2166.81	1919.49	7472.43	7820.55	6932.25
JC_g23856.t1	"stl: Stall, isoform C (Drosophila m	1.89	5.73E-20	3.11E-18	2973.39	2248.71	1995.99	6983.99	11054.80	9832.15
JC_g18995.t1	Protein of unknown function	1.89	4.01E-09	7.24E-08	29.78	33.55	41.73	186.56	126.96	116.42
JC_g24923.t1	"CG6431-RB: CG6431, isoform B	1.89	2.69E-06	3.01E-05	17.43	11.84	28.81	99.50	93.55	63.50
JC_g8142.t1	CG5326-RA: Elongation of very lo	1.89	0.0025733	0.0118537	5.81	9.87	7.95	127.76	298.48	5.29
JC_g21781.t1	Protein of unknown function	1.89	0.0025176	0.0116415	19.61	16.77	3.97	671.60	11.14	467.79
JC_g12819.t1	CG15629-RA: MIP05442p (Droso	1.89	3.41E-21	2.12E-19	2887.67	2825.93	4487.75	14596.61	13159.74	11297.97
JC_g19910.t1	"CG42237: Uncharacterized prote	1.88	0.000497	0.0029298	4.36	9.87	3.97	22.61	24.50	56.09
JC_g22663.t1	"Nlg3: Neuroligin 3, isoform B (Dro	1.88	1.59E-05	0.000146	8.72	15.79	8.94	46.36	53.46	51.86
JC_g8124.t1	sit: Elongation of very long chain	1.88	7.25E-05	0.0005557	18.16	20.72	10.93	135.68	69.05	35.98
JC_g11395.t2	"nAChRalpha6: Nicotinic acetylch	1.87	0.0002042	0.0013665	5.09	9.87	4.97	41.83	26.73	32.81
JC_g10814.t1	Asap: SD02805p (Drosophila mel	1.87	3.51E-19	1.82E-17	98.80	141.10	129.16	427.38	465.54	502.72
JC_g5427.t1	FASN3: Fatty acid synthase 3 (Dr	1.87	0.0024522	0.0114107	2.18	3.95	1.99	50.88	2.23	26.46
JC_g25300.t1	ninaB: Carotenoid isomerooxyger	1.87	0.0026567	0.0121741	3.63	4.93	0.00	263.44	10.02	154.52
JC_g222.t1	VGAT: Vesicular GABA transporte	1.86	0.0010365	0.0054979	5.81	4.93	0.99	24.87	16.71	33.87
JC_g11767.t1	"CG2930: CG2930, isoform E (Dr	1.86	2.30E-26	2.04E-24	419.17	437.11	443.11	1892.70	1656.10	1295.43
JC_g10297.t1	DAAM: RE67944p (Drosophila me	1.86	3.08E-15	1.14E-13	254.26	370.02	285.14	1283.28	1369.88	805.41
JC_g9135.t1	Protein of unknown function	1.85	0.0016917	0.0082986	2.91	1.97	5.96	45.23	23.39	8.47
JC_g22269.t1	"CG9990: CG9990, isoform D (Dr	1.85	8.34E-08	1.25E-06	143.84	237.80	507.69	1423.48	1295.26	885.85
JC_g10812.t1	Protein of unknown function	1.85	0.0003227	0.0020197	7.26	14.80	3.97	66.71	28.96	38.10
JC_g10148.t1	"CG4702: CG4702, isoform B (Dr	1.85	2.17E-14	7.52E-13	26733.62	31622.02	53312.58	164334.56	145583.49	113056.99
JC_g10111.t1	Sik2: FI24002p1 (Drosophila mela	1.84	7.14E-30	7.50E-28	1258.95	928.49	1244.89	4321.32	4500.55	3776.22
JC_g10837.t1	"CG34038: Uncharacterized prote	1.84	0.0031616	0.0141647	1.45	1.97	0.00	15.83	21.16	5.29
JC_g17862.t1	"RhoGEF64C: Rho guanine nucle	1.84	2.23E-21	1.42E-19	4808.42	5569.97	6628.80	25896.27	20747.52	16260.61
JC_g8627.t1	Cht5: Cht5 (Drosophila melanoga	1.84	9.17E-34	1.26E-31	6233.00	7307.56	7900.51	29743.85	25657.92	22872.18
JC_g17551.t5	Protein of unknown function	1.84	4.40E-05	0.0003557	12.35	17.76	7.95	76.88	55.69	39.16
JC_g17335.t1	LPCAT: Lysophosphatidylcholine	1.84	1.17E-12	3.47E-11	79.18	79.92	89.42	411.55	284.00	247.66
JC_g9140.t1	"CG14516: Uncharacterized prote	1.84	2.18E-18	1.05E-16	483.09	347.32	545.45	2065.69	1571.46	1465.83
JC_g9139.t1	CG31198: LP07754p (Drosophila	1.83	2.06E-20	1.18E-18	364.68	272.33	407.35	1451.75	1303.05	1084.82
JC_g12051.t1	"Cyp303a1: Cyp303a1, isoform B	1.83	1.35E-10	3.03E-09	464.93	477.57	1103.81	2826.61	2535.94	2434.22

JC_g12643.t1	Protein of unknown function	1.82	1.31E-11	3.43E-10	759.87	682.80	1393.92	4533.88	3516.02	2664.95
JC_g21572.t1	CG11473: RE56564p (Drosophila	1.82	8.49E-52	2.43E-49	2559.31	2300.02	2406.32	8633.60	9327.42	8024.47
JC_g14321.t1	"Dscam3: Down syndrome cell ad	1.82	2.06E-05	0.0001846	22.52	36.51	100.35	299.62	219.40	161.93
JC_g24298.t1	"Pde8: Phosphodiesterase 8, isof	1.82	4.70E-18	2.20E-16	198.32	196.35	215.60	915.82	747.31	572.57
JC_g12511.t1	CG6426: CG6426 (Drosophila me	1.82	1.06E-40	1.90E-38	4099.40	3629.11	4249.31	15896.85	14266.78	12752.16
JC_g12038.t1	"CG9095: CG9095, isoform C (Dr	1.82	2.65E-20	1.48E-18	1067.17	1004.47	1421.73	5199.83	4070.65	3464.01
JC_g23521.t1	Protein of unknown function	1.81	4.70E-21	2.89E-19	748.98	704.51	845.49	2949.85	3315.55	2071.21
JC_g9920.t1	pdgy: BcDNA.GH02901 (Drosoph	1.81	4.39E-07	5.77E-06	23.25	69.07	57.62	223.87	199.36	168.28
JC_g2562.t1	"hwt: Uncharacterized protein, iso	1.81	2.66E-18	1.28E-16	169.99	274.30	260.30	889.82	856.45	810.70
JC_g10519.t1	"hpo: Hippo, isoform B (Drosophila	1.80	2.47E-45	5.54E-43	533.22	516.05	533.52	1960.54	1893.33	1744.17
JC_g10659.t1	Protein of unknown function	1.80	0.0016559	0.0081385	5.81	4.93	12.92	27.14	100.23	13.76
JC_g14535.t1	spz6: RE45222p (Drosophila mela	1.80	4.39E-26	3.83E-24	7075.69	7463.46	9912.40	33152.74	28055.77	25858.86
JC_g21732.t1	Protein of unknown function	1.80	9.34E-06	9.18E-05	59.57	139.13	142.07	172.99	660.44	561.99
JC_g21728.t1	"Rab3-GEF: Rab3 GDP-GTP exch	1.80	8.12E-13	2.44E-11	196.14	280.23	381.51	944.09	1291.92	901.72
JC_g23571.t1	CG34049-RA: IP19912p (Drosopl	1.79	0.0037311	0.0163139	1.45	2.96	0.00	14.70	8.91	19.05
JC_g578.t1	Dmel\CG9701: CG9701 (Drosoph	1.79	0.0025594	0.0118133	3.63	3.95	4.97	39.57	4.45	41.28
JC_g3633.t1	"CG14280: Uncharacterized prote	1.79	0.0037141	0.016252	0.00	4.93	0.99	16.96	18.93	16.93
JC_g7695.t1	"Cpr62Bc: Cuticular protein 62Bc,	1.79	0.0019554	0.0093892	1.45	1.97	10.93	22.61	32.30	31.75
JC_g24417.t1	Protein of unknown function	1.79	2.81E-13	8.76E-12	1556.07	1763.25	3146.50	8848.42	8064.46	6561.82
JC_g14565.t1	Tsp47F: Tetraspanin (Drosophila	1.79	8.83E-55	3.06E-52	997.43	1058.74	983.59	3386.28	3641.87	3569.84
JC_g9632.t1	slo-RI: IP14811p (Drosophila mela	1.78	2.65E-06	2.97E-05	15.98	35.52	36.76	142.46	115.83	87.84
JC_g9629.t1	ORF: Uncharacterized protein (Dr	1.78	1.04E-13	3.37E-12	63.20	63.15	69.55	208.04	270.63	227.55
JC_g10816.t1	"Asap: ArfGAP with SH3 domain,	1.78	5.25E-22	3.51E-20	154.74	133.21	177.84	547.23	526.79	570.46
JC_g5084.t1	CG4576: CG4576 (Drosophila me	1.78	8.75E-11	2.05E-09	80.64	109.52	162.94	509.92	404.28	372.54
JC_g7885.t1	GNBP1: Gram-negative bacteria b	1.78	2.93E-08	4.75E-07	24.70	36.51	29.81	108.54	130.31	101.60
JC_g7732.t1	"CG9328: CG9328, isoform B (Dr	1.77	4.06E-20	2.22E-18	1356.30	1389.28	1392.92	5817.16	5303.54	3470.36
JC_g17332.t1	LPCAT: Lysophosphatidylcholine	1.77	9.19E-11	2.12E-09	913.16	388.76	598.10	2839.05	2266.42	1820.38
JC_g16211.t1	Protein of unknown function	1.77	5.07E-13	1.57E-11	106.06	95.71	156.98	444.34	482.24	358.78
JC_g9108.t1	"CG30497: Uncharacterized prote	1.77	3.97E-25	3.25E-23	794.74	870.28	909.08	3490.30	3109.51	2387.66
JC_g8190.t1	Cyp4d21: GH25251p (Drosophila	1.76	1.39E-05	0.0001302	74.10	37.49	24.84	102.89	229.43	218.02
JC_g13062.t1	"CG7781: CG7781, isoform A (Dr	1.76	4.82E-06	5.11E-05	26.88	14.80	22.85	99.50	60.14	95.25
JC_g1509.t1	"Task6: TWIK-related acid-sensitiv	1.76	6.49E-17	2.78E-15	212.85	199.32	240.43	949.74	743.97	602.21
JC_g17722.t1	"SPH66: CG4998, isoform A (Dros	1.76	3.25E-10	6.90E-09	128.58	229.90	156.98	749.62	701.64	414.88
JC_g12413.t1	pol: RNA-directed DNA polymeras	1.76	0.0032418	0.0144785	13.08	0.99	1.99	65.58	27.84	17.99
JC_g25270.t1	CG17265: GM03282p (Drosophila	1.76	1.08E-34	1.59E-32	849.23	883.10	1007.43	3235.90	3389.06	2787.72
JC_g4745.t1	yellow-b: LD43175p (Drosophila m	1.76	7.38E-13	2.22E-11	302.93	347.32	567.30	1673.35	1477.91	1165.25
JC_g1549.t1	"CG17816: Uncharacterized prote	1.75	5.22E-14	1.74E-12	1253.86	1496.84	2426.19	7152.45	5458.35	5618.82
JC_g9861.t1	Protein of unknown function	1.75	4.87E-20	2.65E-18	131.49	144.06	179.83	526.88	534.59	510.13
JC_g23297.t1	"CG9413: CG9413, isoform A (Dr	1.75	0.0011453	0.0059702	6.54	21.71	16.89	64.45	20.05	138.64
JC_g19923.t1	HDAC4: GH08881p (Drosophila m	1.75	1.02E-20	6.05E-19	1463.81	1553.08	1694.95	6745.42	5388.19	4128.66
JC_g24129.t1	"Pal2: Peptidyl-alpha-hydroxyglyc	1.73	1.34E-05	0.0001265	15.26	15.79	11.92	58.79	55.69	52.92
JC_g7998.t1	Protein of unknown function	1.73	1.92E-31	2.22E-29	350.88	407.51	385.49	1238.05	1412.20	1216.05
JC_g21879.t1	"Fgop2: Fibroblast growth factor r	1.73	6.35E-21	3.89E-19	1261.86	1219.57	1527.05	5187.39	5009.52	3487.29
JC_g1246.t2	ORF: Orf protein (Drosophila mela	1.73	7.05E-07	8.86E-06	56.66	59.20	78.49	334.67	261.72	123.83
JC_g14096.t1	CG17834-RC: FI04485p (Drosoph	1.73	9.88E-07	1.21E-05	30.51	53.28	66.57	125.50	243.91	184.15
JC_g16390.t1	"uzip: Unzipped, isoform B (Droso	1.72	9.31E-26	7.90E-24	2268.00	2241.80	3014.36	8751.18	9090.20	7390.51
JC_g24242.t1	hop: Tyrosine-protein kinase hops	1.71	8.72E-07	1.08E-05	51.58	28.61	83.46	201.25	227.20	170.40
JC_g10711.t1	Protein of unknown function	1.71	0.0004438	0.0026557	5.81	8.88	13.91	27.14	49.00	45.51
JC_g12697.t1	ORF: Orf protein (Drosophila mela	1.71	7.23E-13	2.18E-11	156.19	215.10	145.05	729.27	570.23	465.68
JC_g7825.t1	"Blimp-1: Blimp-1, isoform A (Dros	1.71	2.15E-10	4.70E-09	87.90	86.83	132.14	419.47	380.89	261.41
JC_g15148.t1	CG10175: Carboxylic ester hydrol	1.71	2.92E-18	1.40E-16	1957.08	2290.15	2605.02	9430.70	7811.64	5794.51
JC_g9575.t1	CG6980: CG6980 protein (Fragm	1.71	3.99E-05	0.0003254	10.90	13.81	13.91	54.27	46.78	47.63
JC_g9101.t1	Protein of unknown function	1.70	8.19E-06	8.15E-05	15.26	15.79	18.88	68.97	60.14	57.15
JC_g19577.t1	SD02026p (Drosophila melanoga	1.70	0.0002489	0.0016154	8.72	15.79	7.95	33.92	56.80	42.33
JC_g20394.t1	"Dip-B: Dipeptidase B, isoform A (	1.70	2.29E-06	2.58E-05	21.79	31.57	47.69	92.71	136.99	136.53
JC_g18796.t1	"ImpE1: Ecdysone-inducible gene	1.70	9.16E-11	2.12E-09	514.33	449.94	865.36	2695.45	1970.17	1599.18
JC_g25057.t1	"VGlut: Vesicular glutamate transp	1.69	0.0012017	0.0062074	4.36	17.76	4.97	49.75	41.21	31.75
JC_g7147.t1	Protein of unknown function	1.69	0.002458	0.0114284	2.18	34.53	17.88	136.81	105.80	32.81
JC_g7922.t1	dnc-RG: Phosphodiesterase (Frag	1.69	0.0001572	0.0010913	7.26	17.76	18.88	67.84	61.25	43.39
JC_g11241.t1	"fd96Ca: Forkhead domain 96Ca,	1.69	0.0020112	0.0096326	2.18	7.89	11.92	21.48	32.30	51.86
JC_g10141.t1	Protein of unknown function	1.69	1.58E-15	6.02E-14	96.62	106.56	100.35	345.98	377.55	289.99
JC_g3839.t1	Protein of unknown function	1.69	0.0006498	0.003688	6.54	8.88	5.96	30.53	35.64	25.40
JC_g4385.t1	"unc-4: Unc-4, isoform B (Drosoph	1.69	0.0003341	0.0020807	11.62	10.85	6.95	28.27	42.32	50.80
JC_g9344.t1	qless: FI02023p (Drosophila mela	1.68	1.08E-21	6.97E-20	4620.27	4196.47	6147.94	17410.78	17534.44	14105.80
JC_g277.t1	Cg25C: Collagen alpha-1(IV) chai	1.68	0.0022307	0.0105168	10.17	9.87	1.99	52.01	37.87	17.99
JC_g10037.t1	Protein of unknown function	1.68	0.0011517	0.00599	5.81	8.88	3.97	30.53	25.62	26.46
JC_g2036.t1	Protein of unknown function	1.67	0.0009832	0.0052542	2.91	19.73	19.87	48.62	62.37	70.91
JC_g25273.t1	Protein of unknown function	1.67	5.66E-12	1.53E-10	2262.91	1951.71	3022.30	11036.21	7427.41	5646.34
JC_g10295.t1	"DAAM: Dishevelled associated a	1.67	4.02E-08	6.41E-07	350.88	752.86	746.14	2207.02	2831.08	1309.19
JC_g13930.t1	Protein of unknown function	1.67	0.0006341	0.0036173	7.26	78.94	40.73	141.33	197.13	184.15
JC_g17447.t1	CG13800-RA: MIP13840p (Fragm	1.67	3.09E-16	1.23E-14	1087.51	856.46	702.42	3237.03	3156.29	2282.88
JC_g1836.t1	Protein of unknown function	1.67	0.0002196	0.0014494	10.17	9.87	28.81	62.19	66.82	60.33
JC_g5263.t1	CG6178: CG6178 (Drosophila me	1.66	1.15E-05	0.0001098	17.43	29.60	16.89	84.80	64.60	80.44
JC_g7969.t1	ORF: Orf protein (Drosophila mela	1.66	0.0033851	0.0150018	0.73	11.84	8.94	29.40	34.53	42.33

JC_g24098.t1	Protein of unknown function	1.65	3.57E-13	1.10E-11	201.23	200.30	247.39	922.61	648.19	555.64
JC_g10094.t1	EG:BACR37P7.9: RE15974p (Dro	1.65	5.79E-28	5.48E-26	1928.02	1946.77	2061.57	7009.99	6750.27	5184.90
JC_g1856.t1	Protein of unknown function	1.65	0.0001771	0.0012102	7.26	16.77	17.88	55.40	51.23	50.80
JC_g8207.t1	Protein of unknown function	1.65	3.07E-09	5.66E-08	122.77	217.08	209.63	782.41	617.00	430.75
JC_g8245.t1	Protein of unknown function	1.65	2.50E-12	7.12E-11	147.47	160.83	235.47	682.91	610.32	483.67
JC_g19688.t1	CG15117: Beta-glucuronidase (D	1.65	8.50E-13	2.53E-11	78.46	72.03	62.59	219.34	236.11	242.36
JC_g17570.t1	Sox100B: Sox100B protein (Dros	1.64	0.0008922	0.0048425	7.99	6.91	10.93	41.83	43.44	21.17
JC_g17074.t1	nrv1: FI04125p (Drosophila melar	1.64	0.0001918	0.0012931	23.97	63.15	13.91	151.51	96.89	133.35
JC_g18680.t1	CG8945: CG8945 (Drosophila me	1.64	4.03E-28	3.91E-26	485.27	457.83	401.38	1392.95	1544.73	1329.30
JC_g314.t1	Pepck: Phosphoenolpyruvate car	1.64	1.07E-11	2.84E-10	1357.02	1441.58	2517.59	7056.35	5363.68	4866.33
JC_g3107.t1	DIP-gamma: Dpr-interacting prote	1.63	0.002422	0.011307	3.63	5.92	9.94	38.44	31.18	16.93
JC_g10022.t1	pdgy: BcDNA.GH02901 (Drosoph	1.63	6.45E-06	6.55E-05	27.61	33.55	15.90	92.71	86.87	87.84
JC_g1989.t1	CG7896: CG7896 (Drosophila me	1.63	7.89E-17	3.34E-15	16995.46	20019.32	26973.22	78960.77	67818.97	56706.83
JC_g2262.t1	Cad99C: Cadherin-99C (Drosophi	1.62	7.64E-17	3.25E-15	3080.90	3644.90	5014.32	13709.06	12934.76	10594.17
JC_g12646.t1	"RapGAP1: Rap GTPase activatir	1.62	1.77E-13	5.56E-12	4228.71	4110.63	6809.62	19509.26	15819.30	13125.76
JC_g10518.t1	Protein of unknown function	1.62	1.48E-50	3.94E-48	1388.99	1406.06	1312.45	4299.84	4265.55	4181.57
JC_g7722.t1	CG9798: Elongation of very long	1.62	1.02E-37	1.70E-35	1903.32	1866.85	2045.67	5715.40	6673.42	5682.32
JC_g12698.t1	Protein of unknown function	1.62	0.0006115	0.0035054	16.71	9.87	38.75	115.33	89.10	47.63
JC_g18701.t1	A2bp1: A2bp1-N (Drosophila mela	1.62	4.42E-22	3.01E-20	1110.75	1584.65	1610.50	4546.32	4501.66	4410.18
JC_g13704.t1	CG15161: RE26667p (Drosophila	1.61	4.88E-11	1.19E-09	122.04	125.31	162.94	526.88	464.42	321.74
JC_g15379.t1	CG5065: Fatty acyl-CoA reductas	1.61	4.89E-07	6.36E-06	111.87	318.71	340.78	774.49	878.73	899.60
JC_g12258.t1	"sls: Sallimus, isoform Z (Drosophi	1.61	1.81E-19	9.59E-18	807.09	1021.24	1094.87	3536.65	2562.67	3013.15
JC_g12083.t1	Dmel\CG3967: Alpha-tubulin N-ac	1.60	2.43E-20	1.37E-18	1027.94	961.05	1280.65	3820.45	3488.18	2826.87
JC_g1462.t1	"Ank2: Ankyrin 2, isoform U (Dros	1.60	1.21E-13	3.86E-12	1041.01	1282.72	1591.63	4917.17	4325.70	3017.38
JC_g13703.t1	"tacc: Transforming acidic coiled-c	1.60	6.13E-11	1.47E-09	1355.57	1392.24	2474.87	6850.57	4552.89	5119.28
JC_g24872.t1	"CG7530: CG7530, isoform A (Dr	1.59	6.09E-16	2.38E-14	865.21	654.19	1118.71	2773.47	2894.56	2529.48
JC_g20326.t1	"snk: Snake, isoform B (Drosophil	1.59	3.37E-33	4.48E-31	1797.98	1938.88	1651.24	6056.86	5324.70	5095.99
JC_g3902.t1	"Pif1A: PFTAIRE-interacting facto	1.59	5.62E-16	2.21E-14	7786.89	8885.31	12463.78	35426.46	28816.44	26203.89
JC_g18238.t1	"St4: Sulfotransferase 4, isoform A	1.59	1.21E-20	7.10E-19	758.42	735.10	657.71	2140.31	2640.63	1839.43
JC_g2253.t1	AT07338p (Drosophila melanogas	1.59	0.002373	0.0111051	12.35	3.95	39.74	96.10	59.03	75.14
JC_g10859.t1	"CT30701: Uncharacterized prote	1.58	1.55E-05	0.0001432	219.39	84.86	62.59	395.73	474.45	369.37
JC_g12431.t1	Rho1: Ras-like GTP-binding prote	1.58	4.18E-17	1.83E-15	2926.17	2860.47	2590.12	10404.18	9077.95	6284.53
JC_g10539.t1	ORF: ORF (Drosophila melanogas	1.58	0.0030708	0.0138227	5.81	7.89	7.95	48.62	14.48	28.58
JC_g13345.t1	"Dhc93AB: Dynein heavy chain a	1.58	0.0009669	0.0051866	5.81	9.87	18.88	44.10	38.98	46.57
JC_g24705.t1	"Msp300: Muscle-specific protein	1.58	2.82E-09	5.23E-08	2825.19	6322.82	6611.91	15807.53	14462.79	19417.70
JC_g7432.t1	Protein of unknown function	1.58	6.19E-05	0.0004834	26.15	48.35	73.52	203.52	98.01	202.15
JC_g15485.t1	Protein of unknown function	1.58	1.25E-08	2.13E-07	73.37	51.31	92.40	245.35	248.36	193.68
JC_g16041.t1	"CG42390: Uncharacterized prote	1.58	2.90E-07	3.99E-06	132.94	178.59	232.48	703.26	326.32	716.51
JC_g5722.t1	sea: LD46175p (Drosophila melar	1.58	4.86E-16	1.92E-14	164.18	221.02	209.63	651.25	635.94	531.30
JC_g11902.t1	"CG31100: Uncharacterized prote	1.57	3.09E-05	0.0002632	21.07	40.46	18.88	96.10	80.19	91.02
JC_g10561.t1	Protein of unknown function	1.56	3.51E-11	8.71E-10	6125.49	7008.59	11249.69	31307.53	23646.54	20192.42
JC_g501.t1	"kappaB-Ras: KappaB-Ras, isofo	1.56	4.50E-15	1.64E-13	237.55	232.86	289.12	883.03	811.90	613.85
JC_g17710.t1	Protein of unknown function	1.56	0.0015788	0.0078201	10.17	6.91	9.94	36.18	21.16	46.57
JC_g9372.t1	"uif: Uninflatable, isoform C (Dros	1.56	8.25E-16	3.20E-14	19474.86	28812.86	32471.39	91507.53	80136.74	73154.77
JC_g17241.t1	Orphan GPCR (Drosophila melan	1.56	0.0002774	0.0017741	10.17	18.75	20.86	71.23	43.44	57.15
JC_g11585.t1	CG18547: IP11040p (Drosophila	1.55	2.02E-11	5.13E-10	110.42	165.77	148.04	369.72	511.20	411.70
JC_g21847.t1	CG14196: IP13170p (Drosophila	1.55	0.0024383	0.0113599	11.62	5.92	6.95	19.22	36.75	41.28
JC_g14029.t1	Tmhs: LP10272p (Drosophila mel	1.55	1.24E-10	2.81E-09	476.56	649.25	916.03	2495.33	2077.09	1664.80
JC_g4574.t1	CG10311: RE61190p (Drosophila	1.55	1.31E-08	2.23E-07	616.76	627.55	1026.31	3265.30	2178.44	1565.31
JC_g21730.t1	"CG5160: CG5160, isoform A (Dr	1.55	0.000154	0.0010723	34.14	24.67	26.83	50.88	94.67	145.00
JC_g15010.t1	"ena: Enabled, isoform G (Drosop	1.54	3.00E-07	4.11E-06	81.36	53.28	60.61	149.24	262.84	201.09
JC_g8243.t1	Cad96Ca: Tyrosine kinase recept	1.54	1.96E-11	5.00E-10	414.81	390.74	523.59	1645.09	1458.98	920.77
JC_g1461.t1	"Ank2: Ankyrin 2, isoform AA (Dro	1.54	1.95E-18	9.47E-17	4824.40	5554.18	6215.50	19752.35	16422.94	13229.48
JC_g10854.t1	LpR1: FI11925p (Drosophila mela	1.54	1.23E-41	2.39E-39	6437.86	7020.43	6141.97	19015.17	20202.91	18369.92
JC_g16583.t1	"kkv: Krotzkopf verkehrt, isoform D	1.54	4.37E-34	6.10E-32	5114.26	5885.71	5793.25	16508.53	17830.69	15033.98
JC_g23056.t1	Parg: Poly(ADP-ribose) glycohydr	1.54	0.0016058	0.007923	14.53	42.43	47.69	131.15	42.32	212.73
JC_g23436.t1	"CG42684: Uncharacterized prote	1.54	2.41E-37	3.94E-35	6412.44	6818.15	7428.59	21182.61	20730.82	18663.09
JC_g5284.t1	"Pgam5: Serine/threonine-protein	1.53	6.69E-07	8.48E-06	276.78	684.78	881.26	2100.74	1775.27	1845.78
JC_g24349.t1	"Hmgs: HMG coenzyme A syntha	1.53	1.40E-14	4.91E-13	3496.44	3144.64	4998.43	13470.49	11230.77	9843.79
JC_g23339.t1	"CG43740: Uncharacterized prote	1.52	0.0026515	0.01216	4.36	8.88	17.88	42.96	31.18	42.33
JC_g14836.t1	"RyR: Ryanodine receptor, isofor	1.52	0.0028034	0.0127392	14.53	28.61	42.72	40.70	63.48	221.20
JC_g14046.t1	Tret1-2: Facilitated trehalose trans	1.52	7.01E-11	1.67E-09	932.04	908.76	1725.75	3720.95	3532.73	3408.97
JC_g618.t1	"Hasp: Uncharacterized protein, is	1.52	1.23E-10	2.79E-09	254.26	371.99	269.25	1173.61	739.51	764.13
JC_g4620.t1	"CG30089: Uncharacterized prote	1.52	8.21E-25	6.62E-23	824.53	694.64	721.30	2222.85	2382.25	1933.62
JC_g12828.t1	pgant5: Polypeptide N-acetylgala	1.52	2.22E-21	1.42E-19	2785.96	2817.05	3623.39	9868.26	9298.46	7775.76
JC_g22285.t1	Protein of unknown function	1.52	0.00335	0.0148921	8.72	2.96	14.90	33.92	36.75	31.75
JC_g5592.t1	Cpr92F: RH04437p (Drosophila m	1.51	0.0001232	0.0008857	37.78	45.39	134.13	252.13	208.27	243.42
JC_g24400.t1	"NijC: Ninjurin C, isoform F (Droso	1.51	0.0019166	0.00923	5.81	15.79	9.94	46.36	34.53	31.75
JC_g12259.t1	"sls: Sallimus, isoform P (Drosoph	1.51	5.67E-12	1.53E-10	306.56	451.91	521.60	1255.01	1064.72	1437.25
JC_g2169.t1	TkR86C: Tachykinin-like peptides	1.50	4.86E-06	5.14E-05	104.61	66.11	74.51	267.96	148.12	338.67
JC_g2880.t1	Protein of unknown function	1.49	0.0010724	0.005644	12.35	9.87	12.92	54.27	33.41	32.81
JC_g12548.t2	"CG43707: Uncharacterized prote	1.49	0.0016073	0.0079269	14.53	9.87	6.95	29.40	41.21	40.22
JC_g12829.t1	pgant5: Polypeptide N-acetylgala	1.49	8.79E-21	5.27E-19	1389.71	1463.29	1854.91	4974.83	4422.59	4063.04
JC_g17542.t1	Protein of unknown function	1.49	3.65E-07	4.89E-06	35.60	48.35	57.62	146.98	130.31	143.94

JC_g15331.t1	CG9617: CG9617-PA (Drosophila	1.48	1.97E-14	6.85E-13	1154.34	1868.82	1881.74	4835.76	4722.18	4509.66
JC_g14772.t1	Protein of unknown function	1.48	0.0018915	0.0091358	58.84	58.22	16.89	222.74	51.23	193.68
JC_g22109.t1	"Mob2: Mob2, isoform E (Drosoph	1.48	1.51E-22	1.07E-20	1274.21	1117.94	1371.07	3847.58	3753.24	3057.60
JC_g15269.t1	CG4020: Fatty acyl-CoA reductas	1.48	2.13E-06	2.42E-05	220.84	190.43	325.88	1132.91	606.98	468.85
JC_g16175.t1	"Ggt-1: Gamma-glutamyl transpep	1.48	1.34E-17	6.07E-16	2518.63	1984.27	3057.08	7513.13	7351.68	6617.91
JC_g19926.t1	Rala: Ras-related protein Ral-a (D	1.48	4.13E-21	2.56E-19	3696.21	3354.81	3788.31	11366.36	11039.21	8246.73
JC_g7512.t1	gag-r: F-element protein (Fragmer	1.47	0.0004133	0.0024941	14.53	15.79	11.92	41.83	49.00	45.51
JC_g24933.t1	CG17646: SD03967p (Drosophila	1.47	2.08E-19	1.10E-17	733.72	782.46	566.31	2104.13	1844.32	1936.80
JC_g2038.t1	cysu: CG5873 (Drosophila melanc	1.47	5.14E-11	1.25E-09	557.92	883.10	927.95	2482.89	2552.65	1758.99
JC_g23316.t1	"sick: Sickie, isoform I (Drosophila	1.47	1.25E-19	6.65E-18	3503.70	3815.60	3654.19	12018.74	10739.62	8183.23
JC_g21315.t1	"CG8785: CG8785, isoform A (Dr	1.47	2.63E-09	4.89E-08	122.77	197.34	142.07	547.23	397.60	387.36
JC_g3698.t1	Jheh2: Epoxide hydrolase (Droso	1.47	4.27E-08	6.78E-07	4103.03	3994.19	8652.61	19181.37	16003.07	13599.90
JC_g4575.t1	Protein of unknown function	1.47	0.0002012	0.0013487	53.76	55.26	122.20	368.59	224.97	130.18
JC_g11270.t1	dmrt11E-RA: RT11749p1 (Drosop	1.46	0.000577	0.0033357	12.35	24.67	12.92	47.49	54.57	57.15
JC_g11314.t1	"Dhc93AB: Dynein heavy chain a	1.46	0.0003809	0.0023353	18.89	15.79	17.88	40.70	53.46	71.97
JC_g22910.t1	"CG10407: Uncharacterized prote	1.45	0.0021285	0.0101097	36.32	49.34	6.95	126.63	79.07	107.95
JC_g22402.t1	lost: LD30155p (Drosophila melar	1.45	5.35E-17	2.32E-15	4117.56	4070.17	5943.27	14036.94	13204.29	12235.68
JC_g18309.t1	CLIP-190: Restin homolog (Droso	1.45	1.76E-17	7.86E-16	7392.43	7258.22	9075.86	26576.91	20552.62	18728.71
JC_g16282.t1	"spir: Spire, isoform E (Drosophila	1.44	7.99E-17	3.38E-15	950.93	1076.50	1250.85	3466.55	3125.10	2507.25
JC_g15651.t1	"Plc21C: 1-phosphatidylinositol 4,	1.44	8.40E-05	0.000632	40.68	51.31	20.86	140.20	104.69	96.31
JC_g20071.t1	betaTub56D: Tubulin beta-1 chai	1.44	5.50E-23	3.99E-21	412.63	412.44	496.76	1224.49	1188.34	1222.40
JC_g19861.t1	"Cht6: Cht6, isoform J (Drosophila	1.44	7.93E-22	5.16E-20	1777.64	1727.73	1865.84	5816.03	4672.06	4301.17
JC_g19228.t1	slif: LD37241p (Drosophila melanc	1.44	1.02E-05	9.89E-05	38.50	27.63	29.81	84.80	93.55	103.72
JC_g20761.t1	ORF: Orf protein (Drosophila mela	1.44	0.0021203	0.0100788	13.80	21.71	6.95	58.79	43.44	38.10
JC_g15369.t1	GEO04266p1 (Fragment) (Drosop	1.43	2.78E-12	7.85E-11	946.57	1545.18	1658.19	4092.93	3766.61	3670.39
JC_g12230.t1	wus: LD21896p (Drosophila melar	1.43	1.43E-25	1.18E-23	2042.80	1600.44	1968.17	5214.53	4952.72	5173.25
JC_g11989.t1	side-RB: RT09994p (Fragment) (D	1.43	4.76E-09	8.51E-08	212.13	195.37	327.86	836.68	666.01	561.99
JC_g25147.t1	Protein of unknown function	1.43	1.54E-12	4.50E-11	563.00	470.66	671.62	1899.48	1570.35	1256.27
JC_g2435.t1	Protein of unknown function	1.43	6.38E-15	2.29E-13	4506.21	4633.58	6870.23	15718.21	15027.45	13333.20
JC_g22498.t1	Osi24: Osiris 24 (Drosophila melar	1.43	1.61E-17	7.28E-16	634.20	658.13	644.80	1967.32	1925.62	1413.97
JC_g1007.t1	Dmel\CG10585: GH23839p (Dros	1.42	3.90E-12	1.09E-10	8644.84	8212.37	13875.58	30980.77	28500.14	25305.34
JC_g23434.t1	"CG42684: Uncharacterized prote	1.42	5.63E-14	1.86E-12	256.44	251.61	320.91	871.73	749.53	653.01
JC_g16857.t1	CG31738: RE04201p (Drosophila	1.42	1.52E-05	0.0001413	42.86	38.48	31.79	131.15	115.83	81.49
JC_g7860.t1	Cpr65Av: Cuticular protein 65Av (	1.42	1.81E-09	3.45E-08	135.12	101.63	154.99	428.51	340.80	318.57
JC_g15351.t1	Snx6: Sorting nexin (Drosophila m	1.41	2.68E-07	3.73E-06	431.52	924.55	1127.65	2377.74	2406.75	2185.51
JC_g10709.t1	"bun: Bunched, isoform P (Drosop	1.41	2.85E-26	2.51E-24	4018.03	4090.89	4676.52	12534.32	11586.05	10293.59
JC_g17587.t1	Protein of unknown function	1.41	4.44E-14	1.49E-12	185.97	209.18	204.67	460.17	606.98	563.05
JC_g3728.t1	"Dmel\CG4729: CG4729, isoform	1.41	0.0009435	0.0050849	15.26	51.31	50.67	142.46	140.33	77.26
JC_g2663.t1	CG2509: GH09711p (Drosophila	1.41	8.90E-08	1.33E-06	82.09	123.34	100.35	237.44	358.62	252.95
JC_g187.t1	"btz: Barentsz, isoform D (Drosopl	1.40	2.05E-16	8.30E-15	1675.94	1720.82	1852.93	5742.54	4603.01	3799.51
JC_g2202.t1	"how: Held out wings, isoform E (I	1.40	3.04E-15	1.14E-13	7202.82	7997.27	9567.65	26519.25	22245.48	17986.80
JC_g5748.t1	Protein of unknown function	1.40	1.96E-12	5.65E-11	118.41	130.25	117.24	314.32	361.96	311.16
JC_g13902.t1	CG11151: GEO07753p1 (Drosop	1.39	5.87E-12	1.58E-10	175.08	213.13	217.58	472.61	649.30	511.19
JC_g20631.t1	CG6564: LD27203p (Drosophila r	1.39	3.41E-05	0.0002857	82.09	42.43	49.68	157.16	217.18	125.94
JC_g9123.t1	CG13409-RA: FI19816p1 (Drosop	1.39	0.0027284	0.012458	13.08	7.89	13.91	47.49	33.41	30.69
JC_g3322.t1	"Pez: Pez, isoform A (Drosophila r	1.39	2.23E-09	4.20E-08	371.22	223.00	299.05	903.38	904.34	629.72
JC_g19259.t1	Protein of unknown function	1.39	5.52E-13	1.70E-11	471.47	467.70	617.97	1630.39	1408.86	1135.62
JC_g19349.t1	Trp1: RE23984p (Drosophila mela	1.39	5.81E-20	3.14E-18	5996.18	4979.92	5696.88	14945.98	16816.09	12509.79
JC_g19260.t1	"Dmel\CG16711: Uncharacterized	1.39	8.94E-14	2.90E-12	4740.86	4890.12	6582.11	17393.82	13911.50	12054.70
JC_g1921.t2	Protein of unknown function	1.39	0.0018667	0.0090391	11.62	18.75	36.76	82.54	74.62	48.68
JC_g23584.t1	Vav: Protein vav (Drosophila mela	1.38	2.92E-11	7.33E-10	469.29	443.03	606.05	1637.17	1393.27	1044.60
JC_g5379.t1	CG12123: GH02722p (Drosophila	1.38	4.75E-12	1.30E-10	487.45	708.46	829.59	1702.75	1863.26	1838.37
JC_g4476.t1	"Dscam3: Down syndrome cell ad	1.38	0.0004117	0.0024868	20.34	50.32	28.81	98.37	73.51	116.42
JC_g12274.t1	Mtp: Microsomal triacylglycerol tra	1.37	5.25E-32	6.40E-30	1932.38	1985.26	2125.15	5324.20	5490.65	4911.84
JC_g16439.t1	CG14351-RA: RT10042p (Fragme	1.37	2.89E-13	8.97E-12	13127.81	12542.05	18948.52	43800.01	40171.95	33571.12
JC_g23861.t1	CG10904: RE30687p (Drosophila	1.37	3.99E-09	7.22E-08	128.58	104.59	148.04	405.90	308.50	302.69
JC_g2876.t1	T: Transposase (Drosophila melar	1.36	8.71E-17	3.67E-15	345.79	300.95	366.61	979.14	809.68	864.68
JC_g1776.t1	CG31140-RB: Diacylglycerol kinas	1.36	7.51E-07	9.43E-06	76.28	127.29	151.02	358.41	273.98	323.86
JC_g8454.t1	"Dys: Dystrophin, isoform L (Drosc	1.36	4.35E-08	6.87E-07	401.00	532.82	668.64	1884.78	1374.33	1032.96
JC_g22892.t1	CG12241: LD32196p (Drosophila	1.36	3.92E-15	1.44E-13	1629.44	1353.76	1787.35	4899.08	4124.11	3488.35
JC_g10528.t1	CG1371-RA: FI04003p (Fragmen	1.36	9.22E-17	3.85E-15	1265.49	1375.47	1784.37	4135.90	3791.11	3600.53
JC_g12421.t1	CG5112: CG5112 (Drosophila me	1.36	1.69E-10	3.73E-09	188.15	253.58	282.16	723.61	640.39	540.82
JC_g18158.t1	Protein of unknown function	1.36	1.08E-09	2.13E-08	109.70	126.30	114.26	249.87	338.57	336.56
JC_g21789.t1	"aop: Anterior open, isoform C (Dr	1.36	4.86E-10	1.00E-08	3581.43	2937.43	3953.24	12412.21	8416.40	6816.88
JC_g22644.t1	CG8312: GH04568p (Drosophila	1.35	2.52E-31	2.88E-29	2753.27	2656.22	3015.35	7549.31	7298.22	6859.22
JC_g9023.t1	"BcDNA:GH27361: CG7497, isofo	1.35	1.82E-06	2.11E-05	50.85	69.07	68.55	208.04	141.44	156.64
JC_g218.t1	Ime4: Probable N6-adenosine-me	1.35	3.96E-10	8.29E-09	403.91	245.69	318.92	910.17	917.71	718.63
JC_g22897.t1	CG14694: IP11787p (Drosophila	1.34	3.08E-18	1.47E-16	1833.58	1660.63	1336.29	4404.99	4189.82	3859.83
JC_g16447.t1	"smog: Poor gastrulation, isoform	1.34	2.24E-06	2.54E-05	45.77	67.10	69.55	188.82	150.35	147.11
JC_g11541.t1	gb: GH08870p (Drosophila melan	1.34	1.06E-11	2.82E-10	179.43	199.32	199.70	577.76	512.31	412.76
JC_g15208.t1	"ATP7: ATP7, isoform B (Drosoph	1.34	5.21E-06	5.44E-05	180.89	319.69	197.71	884.16	435.47	553.52
JC_g24983.t1	Cda4: Chitin deacetylase-like 4 (D	1.34	4.06E-14	1.37E-12	614.58	692.67	518.62	1423.48	1851.01	1443.60
JC_g11734.t1	Protein of unknown function	1.34	9.10E-11	2.11E-09	1138.36	1506.70	1819.15	4723.83	3648.55	3235.40
JC_g10584.t1	Unc-89: Obscurin (Drosophila mel	1.34	0.0035897	0.0157801	15.26	36.51	40.73	98.37	41.21	137.59

JC_g23418.t1	brk: Brinker (Drosophila melanoga	1.34	3.71E-24	2.91E-22	979.26	837.72	903.11	2222.85	2483.60	2244.78
JC_g22138.t1	"CG9990: CG9990, isoform A (Dr	1.34	2.95E-15	1.10E-13	1058.45	1236.35	1585.67	3377.23	3396.85	3197.30
JC_g19642.t1	"anon-WO0170980.76: Uncharac	1.34	6.25E-15	2.25E-13	6247.53	4862.50	7013.30	17069.33	16195.74	13338.49
JC_g5650.t1	CG12075-RB: LP09875p (Drosop	1.33	2.68E-14	9.17E-13	2658.11	2349.35	3010.38	8179.08	6843.82	5555.32
JC_g1416.t1	siz: RE02556p (Drosophila melan	1.33	9.61E-06	9.42E-05	92.99	121.37	217.58	448.87	367.53	335.50
JC_g20559.t1	pol: Pol protein (Fragment) (Drosc	1.33	0.0010416	0.0055147	13.08	25.65	18.88	57.66	53.46	51.86
JC_g8691.t1	Jupiter: Microtubule-associated pr	1.33	4.17E-12	1.16E-10	55808.61	53986.74	85188.85	182462.17	171369.49	148140.51
JC_g17539.t1	pip: Heparan sulfate 2-O-sulfotrar	1.33	4.01E-22	2.76E-20	7906.76	8653.43	10110.12	21048.07	24240.15	22563.14
JC_g11654.t2	Protein of unknown function	1.33	2.55E-06	2.87E-05	60.30	89.79	62.59	210.30	204.92	147.11
JC_g10315.t1	"tx: Taxi, isoform B (Drosophila me	1.33	2.62E-09	4.88E-08	91.53	91.76	83.46	252.13	230.54	208.50
JC_g5908.t1	CG31548: Uncharacterized protei	1.33	0.0008462	0.0046281	30.51	15.79	20.86	52.01	75.73	63.50
JC_g9647.t1	gag-pol: Putative uncharacterized	1.33	0.0005233	0.0030625	21.79	27.63	22.85	83.67	70.16	47.63
JC_g13436.t1	Zip42C.1: RE15841p (Drosophila	1.33	0.0001607	0.0011096	62.48	25.65	42.72	119.85	109.14	131.24
JC_g10227.t1	Protein of unknown function	1.32	0.0015495	0.0077087	19.61	54.27	47.69	81.41	91.33	172.51
JC_g69.t1	"CT30701: Uncharacterized prote	1.32	0.0002709	0.0017389	61.02	25.65	63.59	139.07	108.03	166.16
JC_g3605.t1	CG10898: LD28119p (Drosophila	1.32	3.52E-18	1.67E-16	3080.90	2825.93	3184.25	8662.99	8014.34	6334.27
JC_g5652.t1	CG11448: RILP-like protein homo	1.32	3.15E-22	2.19E-20	1755.85	1808.64	1904.59	4701.22	5081.91	4011.18
JC_g18358.t1	"CG2911: CG2911, isoform A (Dr	1.32	0.000218	0.0014408	209.22	205.24	260.30	920.34	678.26	238.13
JC_g19862.t1	CG15313: CG15313-PA (Drosoph	1.31	0.0008783	0.0047754	36.32	25.65	34.77	139.07	69.05	62.44
JC_g9634.t1	slo: Calcium-activated potassium	1.31	6.07E-10	1.24E-08	531.04	920.60	814.69	2161.79	1699.54	1924.10
JC_g10751.t1	"trio: Trio, isoform A (Drosophila m	1.31	6.60E-14	2.15E-12	1028.66	900.86	1280.65	3067.44	2669.59	2388.71
JC_g17946.t1	dm: Diminutive (Fragment) (Drosop	1.31	1.44E-08	2.44E-07	1452.91	2198.39	2819.63	6644.79	5296.86	4670.53
JC_g22101.t1	Protein of unknown function	1.31	5.66E-05	0.0004466	48.67	40.46	80.48	179.77	125.85	145.00
JC_g18098.t1	Protein of unknown function	1.31	1.64E-12	4.78E-11	357.42	410.47	538.49	1115.95	1151.59	1035.07
JC_g1066.t2	Sin3A: SD07795p (Drosophila me	1.30	0.0005882	0.0033954	79.91	74.00	23.84	162.81	145.90	178.86
JC_g17562.t1	Zip48C: CG13189 protein (Drosop	1.30	1.47E-06	1.74E-05	646.55	1173.20	1188.26	1723.10	2676.27	3366.64
JC_g4368.t1	"Act5C: Actin 5C, isoform E (Dros	1.30	0.0031441	0.0141027	30550.43	12591.38	10565.15	55520.26	48283.18	50467.81
JC_g17448.t1	Protein of unknown function	1.30	0.0003782	0.0023213	32.69	25.65	54.64	118.72	77.96	107.95
JC_g23755.t1	pk: Protein prickle (Drosophila me	1.30	0.0002715	0.0017421	23.25	38.48	28.81	75.75	95.78	69.85
JC_g21735.t1	Best1: Bestrophin homolog (Dros	1.29	5.38E-14	1.78E-12	313.10	299.96	340.78	815.19	887.64	676.29
JC_g7921.t1	dnc: Phosphodiesterase (Drosoph	1.29	9.24E-08	1.37E-06	1646.15	2494.40	3024.29	7794.66	5762.40	4610.21
JC_g20144.t1	Sln: RE01051p (Drosophila melar	1.29	1.03E-05	1.00E-04	55.94	80.91	50.67	134.55	160.38	188.39
JC_g20539.t1	"kek6: Kek6, isoform A (Drosophil	1.28	0.0007416	0.0041413	61.75	28.61	51.66	175.25	79.07	130.18
JC_g5956.t1	Protein of unknown function	1.28	4.80E-10	9.91E-09	171.44	190.43	168.90	533.66	407.62	382.07
JC_g16653.t1	"by: Blistery, isoform A (Drosophila	1.28	1.65E-06	1.94E-05	1872.81	2104.65	3669.09	8835.98	5305.77	5281.21
JC_g5340.t1	CG2663: RE58223p (Drosophila	1.28	0.0024965	0.0115792	15.26	59.20	41.73	82.54	112.49	124.89
JC_g3103.t1	ORF: ORF (Drosophila melanogas	1.28	0.0008643	0.0047111	31.24	26.64	25.83	91.58	87.98	46.57
JC_g14071.t1	"nolo: No long nerve cord, isoform	1.28	0.0012844	0.0065667	16.71	41.44	48.68	109.67	82.42	95.25
JC_g284.t1	Protein of unknown function	1.28	0.0007515	0.004186	18.89	24.67	23.84	72.36	53.46	53.98
JC_g5378.t1	CG1440-RC: AT08049p (Drosoph	1.28	2.70E-17	1.19E-15	840.51	988.68	804.76	1914.18	2338.82	2207.74
JC_g1770.t1	Mcm3: DNA helicase (Drosophila	1.27	7.41E-18	3.43E-16	710.48	714.38	823.63	1650.74	2038.11	1809.79
JC_g10749.t1	CG12183: LD43457p (Drosophila	1.27	8.73E-11	2.04E-09	11121.33	11031.40	16908.81	37380.22	31052.79	28040.14
JC_g22369.t1	Tfb4: FI01003p (Drosophila melar	1.27	0.0001175	0.0008503	62.48	57.23	42.72	165.07	165.94	91.02
JC_g23341.t1	CG4331: RE58242p (Drosophila	1.27	0.0002229	0.0014682	57.39	91.76	84.45	281.53	114.71	211.67
JC_g11421.t1	Fic: Adenosine monophosphate-p	1.27	3.65E-08	5.87E-07	264.43	394.68	274.21	880.77	585.82	855.15
JC_g169.t1	"shot: Short stop, isoform O (Dros	1.27	1.83E-05	0.000166	67.56	112.48	139.09	331.28	251.70	227.55
JC_g13592.t1	"atl: Atlastin, isoform C (Drosophila	1.27	4.56E-10	9.48E-09	234.65	283.19	196.72	516.70	672.69	575.75
JC_g21531.t1	"CG6903: CG6903, isoform A (Dr	1.27	1.21E-18	5.94E-17	9899.43	8036.74	9644.15	24410.60	23203.28	19650.54
JC_g10687.t1	Acyl-coenzyme A oxidase (Drosop	1.27	1.46E-07	2.12E-06	327.63	262.46	318.92	1036.80	667.12	566.22
JC_g20741.t1	insc: Inscuteable (Drosophila mela	1.26	1.02E-12	3.03E-11	3412.17	3965.58	5393.85	10518.38	10383.23	10186.70
JC_g14994.t1	so: Protein sine oculis (Drosophila	1.26	0.0028795	0.0130617	18.89	36.51	23.84	46.36	63.48	104.78
JC_g20759.t1	Gycbeta100B: Guanylyl cyclase b	1.26	0.0001457	0.0010197	36.32	76.96	72.53	161.68	129.19	183.10
JC_g6518.t1	AT07338p (Drosophila melanogas	1.25	3.76E-05	0.00031	122.77	144.06	99.35	413.82	321.87	186.27
JC_g18234.t1	Protein of unknown function	1.25	3.33E-09	6.08E-08	43599.78	37567.92	57307.54	143553.32	105588.62	88194.04
JC_g18713.t1	"CG1632: CG1632, isoform A (Dr	1.25	5.38E-09	9.54E-08	2169.93	1403.10	2067.53	5496.06	4754.48	3503.17
JC_g18363.t1	"nemy: No extended memory, isof	1.25	2.63E-17	1.17E-15	4975.50	4174.76	4496.70	12146.51	11347.71	9286.03
JC_g15359.t1	CG9304: LD26991p (Drosophila	1.25	4.07E-06	4.37E-05	308.02	763.71	629.90	1431.40	1352.06	1427.73
JC_g20875.t1	zye: Zye (Drosophila melanogaste	1.24	9.94E-05	0.0007358	34.14	64.14	51.66	108.54	130.31	137.59
JC_g7405.t1	Papss: LD25351p (Drosophila me	1.24	3.90E-12	1.09E-10	3943.94	3690.29	5050.09	12131.81	9745.07	8627.74
JC_g11073.t1	BEST:CK01670: GH09510p (Dros	1.24	0.0006669	0.0037716	29.78	82.88	61.60	180.90	136.99	128.06
JC_g10523.t1	CG1371: LD47325p (Fragment) (I	1.23	2.89E-13	8.97E-12	1370.82	1430.73	1963.21	4007.00	3835.66	3540.21
JC_g25015.t1	"toc: Toucan, isoform A (Drosophi	1.23	1.22E-05	0.0001165	92.26	105.58	147.04	371.98	252.81	222.26
JC_g11020.t1	"nAChRalpha5: Nicotinic acetylch	1.23	0.0008586	0.0046893	42.86	89.79	147.04	295.10	206.04	213.79
JC_g15164.t1	Mdr49: Multidrug resistance prote	1.23	1.33E-10	2.98E-09	355.96	433.16	552.40	1143.08	1072.51	991.68
JC_g11548.t1	"Sh: Shaker, isoform S (Drosophil	1.23	0.0008155	0.0044818	26.88	20.72	22.85	61.05	54.57	65.62
JC_g23224.t1	CG15863: IP05962p (Drosophila	1.23	1.52E-05	0.0001411	212.13	351.27	145.05	518.97	641.50	582.10
JC_g14433.t1	"mim: Missing-in-metastasis, isofo	1.23	2.44E-05	0.000214	333.44	365.08	742.16	1512.80	980.08	1054.12
JC_g5072.t1	Protein of unknown function	1.22	3.01E-07	4.13E-06	1130.37	1184.05	1949.30	2560.91	4018.31	3696.85
JC_g24254.t1	CG13229-RA: AT19640p (Drosop	1.22	0.0004184	0.0025179	230.29	439.09	772.96	1698.23	956.69	963.11
JC_g20739.t1	sqa: GH17420p (Drosophila mela	1.21	1.69E-20	9.76E-19	1932.38	2371.06	2080.44	4869.68	5276.81	4795.42
JC_g11041.t1	Protein of unknown function	1.21	2.53E-10	5.46E-09	146.02	145.05	162.94	329.02	392.03	351.37
JC_g843.t1	"pwn: Pawn, isoform C (Drosophila	1.21	1.32E-06	1.58E-05	2031.90	2098.73	3627.36	8044.53	5780.22	4775.31
JC_g11456.t1	"l(2)efl: Lethal (2) essential for life	1.21	3.09E-09	5.68E-08	4265.76	4117.53	5778.34	14231.41	10120.39	9060.60
JC_g4201.t1	"CG9518-RA: CG9518, isoform A	1.20	1.08E-10	2.49E-09	1747.13	2219.11	2908.05	5546.94	5179.92	5416.68

JC_g23271.t1	"Dmel\CG32448: Uncharacterized	1.20	1.67E-07	2.39E-06	297.12	550.58	377.54	1085.42	896.55	921.83
JC_g21285.t1	Prosap: LD13733p (Drosophila m	1.20	2.43E-11	6.16E-10	3593.78	4343.49	5305.43	12102.41	9827.48	9096.59
JC_g23435.t1	Protein of unknown function	1.20	9.08E-09	1.57E-07	165.63	127.29	156.98	381.03	374.21	307.98
JC_g1346.t1	CG10413: GH08340p (Drosophila	1.20	1.51E-12	4.44E-11	481.64	529.86	597.11	1447.22	1193.91	1103.87
JC_g1736.t1	CG10864: Uncharacterized protei	1.20	1.62E-08	2.72E-07	146.02	132.22	115.25	270.22	330.78	325.97
JC_g4467.t1	CG18549: RE35942p (Drosophila	1.20	1.38E-09	2.69E-08	276.05	262.46	390.46	682.91	770.70	719.68
JC_g9707.t1	"Moe: Moesin, isoform L (Drosoph	1.19	1.37E-25	1.15E-23	6548.28	6160.02	6917.92	15354.14	15779.21	14083.57
JC_g2100.t1	CG14304-RB: MIP13644p (Droso	1.19	6.18E-08	9.49E-07	187.43	215.10	309.98	568.71	580.25	519.65
JC_g13494.t1	pnt-RD: FI19015p1 (Drosophila m	1.19	9.95E-07	1.22E-05	282.59	399.62	494.78	1101.25	975.62	698.52
JC_g21929.t1	Rep: Rab proteins geranylgeranyl	1.19	2.75E-16	1.10E-14	12693.38	11513.90	14242.19	32301.36	30806.66	25535.01
JC_g2657.t1	"CG3168: CG3168, isoform A (Dr	1.19	0.0005623	0.0032543	31.24	25.65	32.79	64.45	84.64	70.91
JC_g63.t1	stmA: Protein EFR3 homolog cmp	1.19	1.14E-06	1.38E-05	559.37	638.40	1061.09	2129.00	1687.29	1498.64
JC_g1938.t1	Protein of unknown function	1.19	1.83E-08	3.05E-07	117.69	103.60	127.17	293.97	266.18	252.95
JC_g16373.t1	Protein of unknown function	1.19	0.002775	0.0126422	15.26	22.69	27.82	49.75	55.69	59.27
JC_g18829.t1	Tob: LD04013p (Drosophila melan	1.18	0.0008545	0.004671	33.42	64.14	79.48	184.29	135.87	113.24
JC_g17972.t1	eg: Protein embryonic gonad (Dro	1.18	2.07E-16	8.36E-15	429.34	426.26	376.55	974.61	898.77	960.99
JC_g5451.t1	schlank: LD18904p (Drosophila m	1.18	4.96E-07	6.44E-06	807.82	766.67	1265.75	2777.99	2169.53	1709.25
JC_g15360.t1	PPP1R15: GH11727p (Drosophila	1.18	6.38E-09	1.12E-07	2303.60	3958.67	3695.91	8535.23	7686.91	6922.72
JC_g16068.t1	kst: BetaH spectrin (Fragment) (Dr	1.18	4.06E-12	1.13E-10	2599.26	3324.22	3530.00	8384.85	7204.67	6213.62
JC_g17449.t1	Protein of unknown function	1.18	2.90E-08	4.72E-07	849.95	923.56	1228.00	2937.41	2237.47	1809.79
JC_g2037.t1	CG8417: Mannose-6-phosphate i	1.18	1.35E-10	3.02E-09	246.27	303.91	338.79	725.87	707.21	617.02
JC_g15650.t1	Protein of unknown function	1.18	0.0009464	0.005091	26.15	35.52	37.75	101.76	80.19	61.38
JC_g1785.t1	CG13827: RE30473p (Drosophila	1.18	4.66E-10	9.66E-09	339.26	376.92	463.98	824.24	1063.60	837.16
JC_g13497.t1	"pnt: Pointed, isoform E (Drosoph	1.18	1.07E-14	3.78E-13	1099.13	946.25	1249.86	2750.86	2454.64	2356.96
JC_g18672.t1	CG15211: RE01453p (Drosophila	1.18	3.51E-14	1.19E-12	8376.05	7620.35	9803.12	22823.18	18540.13	17749.72
JC_g2628.t1	"Crag: Calmodulin-binding protein	1.18	5.55E-15	2.01E-13	1088.96	1360.67	1410.81	3035.78	3098.37	2691.40
JC_g20758.t1	CG31559: Glutaredoxin domain-c	1.18	1.15E-09	2.27E-08	1096.22	1262.99	1479.36	3501.60	3073.87	2273.35
JC_g24034.t1	"tamo: Tamo, isoform B (Drosophi	1.17	1.52E-12	4.45E-11	530.31	633.47	677.58	1544.46	1428.91	1222.40
JC_g23324.t1	CG3812: 1-acyl-sn-glycerol-3-pho	1.16	2.36E-09	4.42E-08	385.02	614.72	469.94	1127.25	1187.23	1044.60
JC_g16072.t1	kst: Beta-H spectrin (Fragment) (D	1.16	9.80E-09	1.69E-07	706.12	1031.11	1079.96	2496.46	2184.01	1773.81
JC_g9053.t1	Nurf-38-RA: FI20112p1 (Fragmen	1.16	5.39E-14	1.78E-12	4065.25	3166.35	4264.21	9562.99	8545.59	7993.78
JC_g23179.t1	pck-RC: LD14222p (Fragment) (D	1.16	1.21E-13	3.86E-12	3285.04	4380.00	3153.45	8503.57	8098.98	7891.12
JC_g9698.t1	"Hsc70-4: Heat shock protein cog	1.16	3.78E-19	1.93E-17	719.19	640.37	703.42	1571.59	1603.76	1477.47
JC_g18156.t1	Drak: Death-associated protein ki	1.16	1.11E-24	8.88E-23	2293.43	2412.50	2374.53	5060.76	5684.44	5176.43
JC_g24143.t1	CG15890: RE46682p (Drosophila	1.16	6.62E-06	6.71E-05	233.92	197.34	313.95	760.92	529.02	436.04
JC_g11028.t1	"a: Arc, isoform A (Drosophila mel	1.15	1.57E-09	3.04E-08	3781.94	2667.07	2837.51	8336.24	7102.20	5650.57
JC_g4840.t1	Protein of unknown function	1.15	1.13E-08	1.94E-07	154.74	196.35	217.58	469.22	405.39	415.93
JC_g19052.t1	"Hsepi: Heparan sulfate C5-epime	1.15	2.51E-14	8.64E-13	666.16	553.54	619.96	1501.49	1239.57	1400.21
JC_g3092.t1	Dmel\CG7458: CG7458 (Drosoph	1.15	6.81E-10	1.38E-08	2518.63	2019.79	1524.07	4864.03	4373.59	4488.50
JC_g17586.t1	Psa: LP21249p (Drosophila melan	1.15	1.65E-15	6.24E-14	1995.58	1632.02	1779.40	4320.19	4262.21	3557.14
JC_g15061.t1	"CalpA: Calpain-A, isoform C (Dro	1.15	8.43E-13	2.52E-11	6807.63	5166.40	7491.18	14353.52	15575.40	13870.84
JC_g24110.t1	"Dscam4: Down syndrome cell ad	1.15	0.0003089	0.001943	55.94	102.62	111.27	189.95	168.17	273.06
JC_g2152.t1	"CG7029: CG7029, isoform C (Dr	1.15	5.56E-18	2.60E-16	3070.01	3559.06	3839.98	8092.02	7972.02	7303.73
JC_g25433.t1	Protein of unknown function	1.14	7.80E-10	1.56E-08	414.81	342.39	498.75	855.90	1036.87	925.01
JC_g21529.t1	CrebA: RE64328p (Drosophila me	1.14	5.49E-10	1.13E-08	5028.54	5038.13	7196.11	14854.40	12719.82	11125.46
JC_g17353.t1	Dmel\CG11367: LD47277p (Dros	1.14	1.63E-09	3.14E-08	325.45	274.30	273.22	749.62	667.12	545.05
JC_g24122.t1	Dmel\CG13937: Carbohydrate su	1.14	0.0001037	0.00076	133.67	81.90	96.37	271.35	284.00	167.22
JC_g18110.t1	CG9527: Acyl-coenzyme A oxidas	1.13	2.69E-16	1.08E-14	2979.20	2356.26	2596.08	6353.09	5637.66	5601.89
JC_g11895.t1	"Nep2: Neprilysin 2, isoform A (Dr	1.13	3.63E-16	1.44E-14	27340.94	25436.35	33066.52	67463.26	60377.09	62111.86
JC_g7494.t1	"Lmpt: Limpet, isoform D (Drosoph	1.13	3.25E-11	8.13E-10	355.24	312.79	350.71	711.17	869.82	683.70
JC_g24967.t1	jdp-RB: FI17328p1 (Drosophila m	1.13	6.00E-11	1.44E-09	1701.36	1499.80	1958.24	4383.51	3953.71	3125.33
JC_g15192.t1	CG6904-RA: Glycogen [starch] sy	1.13	1.07E-08	1.84E-07	1143.44	1195.89	1594.61	3480.12	2990.34	2305.10
JC_g13646.t1	AMPdeam: AMP deaminase (Dros	1.13	6.57E-09	1.15E-07	499.08	639.39	806.74	1398.61	1356.51	1575.90
JC_g23067.t1	eEF1alpha2: Elongation factor 1-	1.13	0.0030629	0.0137926	68.29	156.89	216.59	251.00	265.07	534.47
JC_g12061.t1	CG42750: Dipeptidase (Drosophil	1.13	6.97E-07	8.78E-06	160.55	246.68	221.56	388.94	531.25	485.79
JC_g19219.t1	"mtt: Mangetout, isoform G (Drosc	1.12	0.0001605	0.0011092	171.44	243.72	382.51	762.05	428.78	633.96
JC_g12193.t1	CG2812: CG2812 (Drosophila me	1.12	2.21E-20	1.26E-18	5034.35	4156.01	4532.46	9774.42	10284.11	10060.75
JC_g22621.t1	CG31028: Uncharacterized protei	1.12	3.65E-06	3.95E-05	699.58	990.65	896.16	1952.62	1285.23	2564.40
JC_g23404.t1	GIP: Copia protein (Drosophila me	1.12	1.87E-05	0.0001696	193.24	397.64	327.86	797.10	688.28	575.75
JC_g4243.t1	"zip: Zipper, isoform D (Drosophila	1.12	9.75E-20	5.24E-18	7956.88	8713.62	7571.66	16227.00	17722.65	18961.54
JC_g18379.t1	Protein of unknown function	1.12	3.29E-05	0.0002763	95.17	75.98	117.24	244.22	236.11	169.34
JC_g25435.t1	lace: Serine palmitoyl transferase	1.11	1.24E-11	3.26E-10	1340.31	1363.63	1694.95	3190.68	3680.85	2772.90
JC_g14981.t1	hng2: Hinge2 (Drosophila melano	1.11	3.48E-06	3.78E-05	173.62	216.09	206.65	353.89	585.82	388.42
JC_g25295.t1	Cyp4c3: Cytochrome P450 4c3 (D	1.11	0.0001256	0.0009015	100.25	233.85	154.99	362.94	333.00	405.35
JC_g9606.t1	"Snx1: Sorting nexin 1, isoform B	1.11	2.23E-10	4.87E-09	692.31	480.53	591.15	1403.13	1227.32	1238.28
JC_g3791.t1	ORF: Orf protein (Drosophila mela	1.11	0.0009454	0.0050905	49.40	57.23	28.81	115.33	100.23	96.31
JC_g1063.t1	conv: Acid labile subunit (Drosoph	1.11	8.21E-16	3.20E-14	1081.69	1120.90	1197.20	2569.95	2650.66	2170.69
JC_g3646.t1	"CG10019: Uncharacterized prote	1.11	6.15E-13	1.87E-11	722.10	773.58	788.86	1594.21	1920.06	1461.59
JC_g9973.t1	"cyr: Cypher, isoform B (Drosophil	1.11	2.68E-05	0.0002319	15362.39	14727.60	20653.41	53456.84	37727.33	22137.68
JC_g1905.t1	Protein of unknown function	1.10	0.0008309	0.0045532	30.51	57.23	49.68	113.06	94.67	104.78
JC_g9591.t1	Protein of unknown function	1.10	5.20E-14	1.73E-12	956.02	869.29	1022.34	2283.90	2063.73	1829.90
JC_g18351.t1	"EcR: Ecdysone receptor, isoform	1.10	1.79E-13	5.60E-12	704.66	700.56	663.68	1616.82	1589.28	1281.67
JC_g10809.t1	"Gp150: Gp150, isoform E (Drosc	1.10	0.0005499	0.0031906	31.96	36.51	40.73	81.41	82.42	82.55
JC_g16065.t1	"Lrrk: Leucine-rich repeat kinase,	1.10	3.46E-08	5.59E-07	176.53	217.08	197.71	436.43	486.70	366.19

JC_g17076.t1	nrv2: IP16413p (Drosophila melar	1.10	8.07E-05	0.0006094	57.39	67.10	53.65	116.46	125.85	154.52
JC_g11395.t1	"nAChRalpha6: Nicotinic acetylch	1.09	0.0007591	0.0042185	331.99	630.51	227.52	988.18	605.86	1100.69
JC_g15436.t1	"emp: Epithelial membrane protei	1.09	1.27E-08	2.17E-07	4907.94	5079.57	6839.43	14745.86	11991.44	9794.05
JC_g1710.t1	CG6490: Plum (Fragment) (Droso	1.09	5.21E-06	5.44E-05	139.48	157.87	189.76	435.30	356.39	276.23
JC_g16797.t1	Pura: FI18828p1 (Drosophila mel	1.09	2.60E-11	6.56E-10	1133.27	944.28	1086.92	2668.32	2200.71	1956.90
JC_g14095.t1	inaD: Inactivation-no-after-potenti	1.09	5.10E-07	6.60E-06	136.57	187.47	150.02	383.29	348.59	299.52
JC_g8174.t1	Protein of unknown function	1.08	3.55E-05	0.0002958	7233.33	9757.56	12875.10	31150.37	19213.93	15243.53
JC_g3509.t1	"CG32816: Uncharacterized prote	1.08	3.83E-08	6.14E-07	1269.12	953.16	919.01	2363.05	2646.20	1780.16
JC_g19319.t1	Pkc53E: Protein kinase C (Drosop	1.08	1.27E-05	0.0001203	127.13	122.35	121.21	263.44	341.91	205.32
JC_g7752.t1	Rab3: Ras-related protein Rab-3 (	1.08	0.0028012	0.0127344	34.87	23.68	24.84	68.97	62.37	60.33
JC_g10517.t1	Protein of unknown function	1.08	8.29E-06	8.24E-05	106.79	120.38	79.48	236.30	221.63	209.55
JC_g25185.t1	ed: Echinoid (Drosophila melanog	1.08	1.55E-12	4.52E-11	6330.35	5190.08	4852.38	12294.62	12410.20	10215.27
JC_g18124.t1	osp: Protein outspread (Drosophil	1.07	3.38E-10	7.17E-09	5122.98	6386.96	7958.14	14393.10	13213.20	13963.98
JC_g25323.t1	"CG4822-RB: CG4822, isoform A	1.07	1.68E-07	2.41E-06	365.41	402.58	576.24	1056.02	958.91	865.74
JC_g15411.t1	CG5065: Fatty acyl-CoA reductas	1.07	0.001586	0.0078489	32.69	29.60	28.81	67.84	63.48	73.03
JC_g22949.t1	"CG5916: CG5916, isoform A (Dr	1.07	2.47E-10	5.35E-09	1490.69	1378.43	1501.22	3665.55	3167.42	2465.97
JC_g15355.t1	Ets97D: DNA-binding protein Ets9	1.07	8.33E-05	0.0006282	202.68	420.34	455.03	849.11	697.19	795.89
JC_g21316.t1	"CG8785: CG8785, isoform A (Dr	1.06	9.22E-05	0.000686	87.90	80.91	89.42	136.81	230.54	193.68
JC_g5457.t1	"Mer: Merlin, isoform B (Drosophila	1.06	0.0004524	0.0026972	220.84	562.42	614.00	1006.27	911.02	1140.91
JC_g23374.t1	"CG9171: CG9171, isoform C (Dr	1.06	2.35E-19	1.22E-17	2213.51	2524.99	2550.38	5150.08	5157.65	4964.76
JC_g23550.t1	"CG8180: CG8180, isoform B (Dr	1.06	2.63E-10	5.67E-09	1633.80	1672.47	1788.35	3614.67	4263.33	2871.33
JC_g14233.t1	Apoltp: Apolipoprotein lipid transf	1.06	0.0009367	0.0050527	73.37	152.94	199.70	349.37	282.89	300.57
JC_g1735.t1	"Apc: APC-like, isoform A (Drosop	1.05	1.90E-16	7.72E-15	6023.78	6925.70	7519.00	14758.29	14432.72	13636.94
JC_g12463.t1	aPKC: Protein kinase C (Drosoph	1.05	1.35E-11	3.53E-10	1201.56	1254.11	1370.07	3074.22	2700.78	2257.48
JC_g16073.t1	kst: LP04011p (Drosophila melan	1.05	5.52E-08	8.53E-07	733.72	1018.28	1221.04	2212.67	2108.28	1959.02
JC_g4678.t1	CG9896: CG9896 (Drosophila me	1.05	8.59E-07	1.07E-05	998.88	544.66	811.71	1614.56	1790.86	1596.00
JC_g18378.t1	"inaE: Inactivation no afterpotenti	1.05	1.78E-09	3.41E-08	677.06	642.35	881.26	1723.10	1520.23	1384.33
JC_g9585.t1	Protein of unknown function	1.05	3.24E-09	5.93E-08	203.41	214.12	243.41	469.22	492.27	426.52
JC_g12614.t1	"CG33156: Uncharacterized prote	1.05	9.97E-18	4.56E-16	933.50	989.67	991.54	2109.78	2060.39	1897.64
JC_g8776.t1	Spn100A: Serpin 100A (Drosophi	1.05	1.15E-09	2.27E-08	61923.20	57244.85	77064.79	162457.69	132982.84	116083.90
JC_g19254.t1	"Mhc: Myosin heavy chain, isoform	1.05	1.57E-05	0.0001448	527.41	899.88	717.33	2018.20	1299.71	1245.69
JC_g5338.t1	CG2663: RE58223p (Drosophila r	1.05	0.0004835	0.0028603	46.49	66.11	81.47	128.89	129.19	159.81
JC_g1756.t2	Protein of unknown function	1.05	0.0007983	0.0044082	90.81	62.16	48.68	120.98	170.40	149.23
JC_g22078.t1	"Dmel\CG43980: Uncharacterized	1.04	2.16E-06	2.45E-05	648.00	974.87	1216.08	1766.07	2150.60	2076.50
JC_g13059.t1	"CG13868: Uncharacterized prote	1.04	3.46E-12	9.75E-11	616.76	498.29	572.27	1174.74	1245.14	1098.58
JC_g24094.t1	"CT14378: CG8560, isoform A (D	1.04	4.97E-14	1.66E-12	3141.93	3468.28	2906.06	6705.85	7230.28	5848.49
JC_g21784.t1	"pns: Pinstripe, isoform A (Drosop	1.04	9.77E-10	1.94E-08	1792.17	1512.62	1769.47	4163.03	3570.59	2855.45
JC_g14032.t1	Tmhs: LP10272p (Drosophila mel	1.04	5.66E-08	8.73E-07	1600.38	1369.55	1797.29	4053.36	3332.26	2581.34
JC_g5879.t1	CG17365: Bicaudal D-related pro	1.04	1.65E-08	2.77E-07	439.51	389.75	317.93	884.16	804.11	709.10
JC_g2132.t1	"Atg16: Autophagy-related 16, iso	1.04	0.0003899	0.0023765	75.55	56.24	70.54	166.20	160.38	107.95
JC_g21548.t1	Protein of unknown function	1.04	6.46E-05	0.0005019	113.33	107.55	118.23	312.06	222.74	184.15
JC_g3175.t1	mRpS14: LD31543p (Drosophila r	1.03	2.11E-07	2.99E-06	602.96	899.88	771.97	1758.15	1707.34	1273.20
JC_g1825.t1	Protein of unknown function	1.03	5.13E-06	5.38E-05	140.93	189.45	228.51	356.15	417.65	392.65
JC_g17810.t1	Dmel\CG6216: CG6216 (Drosoph	1.03	9.30E-06	9.14E-05	1189.94	716.35	660.69	2012.55	1861.03	1509.22
JC_g22090.t1	"CG9646: CG9646, isoform B (Dr	1.03	2.07E-12	5.96E-11	2130.70	1965.52	2411.29	4065.80	5056.30	4285.29
JC_g23560.t1	pot: GH09980p (Drosophila melar	1.03	6.18E-08	9.49E-07	3140.47	3169.31	4057.56	5624.95	8806.20	7071.95
JC_g12447.t1	Protein of unknown function	1.03	3.23E-08	5.22E-07	718.47	673.92	822.64	1850.86	1504.64	1227.70
JC_g1877.t1	ftz-f1: Nuclear hormone receptor F	1.02	0.0038099	0.0165888	75.55	194.38	284.15	396.86	418.76	385.24
JC_g19003.t1	sni: LD36273p (Drosophila melan	1.02	1.46E-11	3.78E-10	333.44	333.51	297.06	656.90	644.84	675.23
JC_g23241.t1	"nct: Nicastrin, isoform D (Drosoph	1.02	2.19E-09	4.13E-08	2128.52	3022.29	2093.36	5018.93	4707.70	5152.09
JC_g12049.t1	CG12164-RA: FI17860p1 (Fragm	1.02	0.0024042	0.0112332	59.57	55.26	35.77	118.72	126.96	79.38
JC_g21737.t1	SP1173: FI19426p1 (Drosophila r	1.02	1.67E-10	3.70E-09	8914.36	7969.64	11201.01	20850.20	17450.91	19229.31
JC_g9243.t1	CG8483: CG8483 (Drosophila me	1.02	0.0010854	0.0057019	88.63	169.71	234.47	307.54	344.14	392.65
JC_g14823.t1	CG12950: GH14967p (Drosophila	1.01	1.48E-05	0.0001379	108.24	155.90	146.05	241.96	291.80	314.33
JC_g1740.t1	Tango10: HL07962p (Drosophila	1.01	7.28E-12	1.95E-10	1030.12	879.16	1112.75	1949.23	2245.26	1967.49
JC_g9089.t1	CG3386: SD24069p (Drosophila r	1.01	8.43E-05	0.0006333	67.56	63.15	68.55	135.68	126.96	152.40
JC_g11775.t1	Su(P): Putative uncharacterized p	1.01	5.57E-19	2.78E-17	1525.56	1457.37	1421.73	2989.42	3085.01	2855.45
JC_g22559.t1	"CG1103: CG1103, isoform A (Dr	1.01	3.93E-06	4.22E-05	1167.42	951.19	1787.35	2512.29	2809.92	2701.99
JC_g21957.t1	CG18419: Phospholipid-transport	1.01	0.0002952	0.001873	94.44	180.57	136.11	344.85	248.36	261.41
JC_g24725.t1	CG7206: GH28353p (Drosophila	1.00	2.36E-07	3.31E-06	666.89	463.75	450.07	1170.22	976.73	1084.82
JC_g7447.t1	Dmel\CG14079: IP09370p (Drosc	1.00	2.98E-05	0.0002545	152.56	159.85	171.88	298.49	265.07	433.93
JC_g24988.t1	ry: Xanthine dehydrogenase (Dro	1.00	2.01E-05	0.0001806	176.53	190.43	161.94	470.35	297.36	319.62
JC_g14754.t1	Protein of unknown function	1.00	4.46E-11	1.09E-09	4592.66	4542.80	5491.22	11219.38	9859.78	8502.85
JC_g3211.t1	"ari-1: Ariadne 1, isoform C (Drosc	1.00	7.77E-11	1.84E-09	3914.88	2917.70	3486.28	7515.39	7147.87	6199.86
JC_g23594.t1	"Hsc70-3: Heat shock 70-kDa pro	1.00	5.87E-09	1.04E-07	52339.05	49523.86	71200.01	132474.14	108444.20	109635.32
JC_g2898.t1	CG9220: Hexosyltransferase (Dro	1.00	4.66E-10	9.66E-09	294.94	330.55	358.66	634.29	654.87	696.40
JC_g21752.t1	Ten-m: Teneurin-m (Drosophila m	1.00	1.16E-15	4.44E-14	10361.46	11776.36	10393.27	23907.46	20679.59	20766.05
JC_g21257.t1	Protein of unknown function	1.00	0.0002771	0.0017734	83.54	87.82	128.16	249.87	197.13	171.45
JC_g10736.t1	"Mef2: Myocyte enhancer factor 2	1.00	1.49E-18	7.27E-17	1577.86	1650.76	1604.54	3052.74	3365.67	3269.27
JC_g1054.t1	"Dmel\CG13676: Uncharacterized	1.00	6.88E-09	1.20E-07	2103.82	2287.19	2151.98	3411.15	5181.03	4623.97
JC_g11771.t1	AcCoAS: Acetyl-coenzyme A synt	0.99	0.0015639	0.0077667	89.35	135.18	61.60	231.78	208.27	158.75
JC_g18136.t1	CG17544: Acyl-coenzyme A oxida	0.99	3.06E-07	4.18E-06	206.31	224.97	226.52	393.46	526.79	411.70
JC_g2869.t1	CG1105: CG1105 (Drosophila me	0.99	4.35E-06	4.64E-05	544.12	400.60	322.90	828.76	977.85	777.89
JC_g24992.t1	bchs: Blue cheese (Drosophila me	0.99	8.84E-06	8.72E-05	218.66	250.62	239.44	617.33	378.67	445.57

JC_g23727.t1	"chp: Chaoptin, isoform D (Drosop	0.99	7.85E-05	0.000596	85.72	93.74	82.46	214.82	158.15	162.99
JC_g17509.t1	anon-EST:fe3A8: SD03655p (Dro	0.99	1.85E-16	7.56E-15	3259.61	3126.88	3716.78	6791.78	6833.80	6566.05
JC_g12521.t1	beta4GalNAcTA: Beta4GalNAcTA	0.99	3.02E-05	0.0002581	123.50	144.06	200.69	329.02	333.00	288.93
JC_g4753.t1	stet: Rhomboid-like protein (Drosc	0.99	0.0003299	0.0020567	499.08	515.06	1013.40	1766.07	1210.62	1189.59
JC_g7480.t1	spz5: Protein spaetzle 5 (Drosoph	0.99	0.001316	0.0066922	77.73	81.90	79.48	235.17	139.22	121.71
JC_g61.t1	BcDNA.GH05582: BcDNA.GH055	0.98	3.76E-07	5.02E-06	355.96	396.66	394.43	957.66	696.08	653.01
JC_g21407.t1	"kug: Kugelei, isoform E (Drosoph	0.97	4.22E-12	1.17E-10	604.41	715.36	709.38	1354.51	1383.24	1272.15
JC_g11099.t1	"CG2145: CG2145, isoform B (Dro	0.97	0.0008324	0.0045591	85.72	125.31	172.87	255.53	311.84	213.79
JC_g20255.t1	Nup98-96: Nucleoporin 98-96 (Fra	0.97	0.0003923	0.0023884	66.11	84.86	114.26	168.47	190.45	176.75
JC_g8461.t1	"Dys: Dystrophin, isoform L (Drosc	0.97	2.21E-05	0.0001963	448.95	818.97	804.76	1311.55	1531.37	1308.13
JC_g23410.t1	"CG8611: CG8611, isoform C (Dro	0.97	2.04E-11	5.18E-10	744.62	940.33	846.48	1596.47	1759.68	1639.40
JC_g10941.t1	pnut: Protein peanut (Drosophila	0.97	3.17E-15	1.17E-13	4354.38	4220.15	4355.62	8868.77	9026.72	7528.10
JC_g19693.t1	Protein of unknown function	0.97	0.0004757	0.0028168	72.65	120.38	102.33	237.44	190.45	168.28
JC_g4912.t1	tty: Protein tweety homolog (Dros	0.96	0.0003381	0.0021048	228.83	404.55	402.38	807.28	792.97	486.84
JC_g22478.t1	"Dmel\CG8765: CG8765, isoform	0.96	7.86E-05	0.0005966	164.18	186.49	151.02	369.72	395.37	240.25
JC_g16067.t1	"Lrrk: Leucine-rich repeat kinase,	0.96	0.0006935	0.0038951	68.29	131.23	93.39	185.43	214.95	190.50
JC_g9436.t1	Protein of unknown function	0.96	0.0006201	0.0035492	160.55	217.08	300.04	611.68	382.01	372.54
JC_g19931.t1	Usp30: Ubiquitin carboxyl-termina	0.96	4.55E-07	5.96E-06	239.73	243.72	312.96	558.54	464.42	549.29
JC_g9586.t1	Protein of unknown function	0.96	1.58E-12	4.60E-11	1274.93	1132.74	1390.94	2462.54	2623.93	2352.73
JC_g21405.t1	"kug: Kugelei, isoform E (Drosoph	0.96	8.79E-09	1.52E-07	350.15	303.91	378.53	618.46	717.24	694.28
JC_g8464.t1	"Dys: Dystrophin, isoform K (Drosc	0.96	4.27E-06	4.56E-05	2476.49	4230.02	4423.18	7121.93	7771.55	7134.39
JC_g1061.t1	"Ance-3: Ance-3, isoform B (Drosc	0.96	7.07E-05	0.0005438	1072.98	907.77	1766.49	2719.20	2719.71	2027.81
JC_g1792.t1	Cdc16: Cell division cycle 16 orthc	0.95	0.0002326	0.0015212	275.33	512.10	610.02	1026.62	888.75	874.20
JC_g23247.t1	"mTerf5: Transcription termination	0.95	0.0014431	0.0072518	124.95	233.85	103.33	342.59	277.32	313.27
JC_g12235.t1	"Fhos: Formin homology 2 domair	0.95	5.78E-08	8.91E-07	1566.97	1943.81	1994.01	3023.34	4327.92	3448.13
JC_g20067.t1	CG34404: GH12452p (Fragment)	0.95	2.39E-09	4.47E-08	601.51	590.05	720.31	1372.60	1259.62	1105.98
JC_g8274.t1	bnl: Fibroblast growth factor (Dros	0.95	9.16E-05	0.0006832	131.49	227.93	225.53	371.98	399.83	386.30
JC_g12203.t1	"Sugb: Sugar baby, isoform F (Dro	0.95	9.57E-08	1.41E-06	561.55	474.61	383.50	958.79	922.16	903.84
JC_g12749.t1	"CG3625: CG3625, isoform B (Dro	0.94	1.74E-08	2.92E-07	3197.86	2522.03	3347.19	6622.18	6075.35	4956.29
JC_g5310.t1	"CG3711: CG3711, isoform D (Dro	0.94	7.05E-10	1.42E-08	879.01	863.37	1016.38	1975.23	1830.96	1552.61
JC_g7496.t1	Protein of unknown function	0.94	5.03E-08	7.85E-07	231.01	209.18	219.57	448.87	393.14	444.51
JC_g15157.t1	"Usp2: Ubiquitin specific protease	0.94	3.17E-05	0.0002679	331.99	413.43	516.63	1024.36	789.63	662.53
JC_g1737.t1	CG5245: IP01468p (Drosophila m	0.94	2.81E-08	4.60E-07	337.80	316.73	364.62	731.53	672.69	576.81
JC_g12189.t1	Protein of unknown function	0.94	0.0005227	0.0030606	110.42	66.11	86.44	162.81	190.45	170.40
JC_g9975.t1	beta-Spec: Spectrin beta chain (D	0.94	2.83E-09	5.23E-08	21579.41	27991.92	31091.39	54545.65	52930.74	48708.82
JC_g5468.t1	Protein of unknown function	0.94	0.0004103	0.0024808	1184.13	1119.91	2124.16	3830.62	2743.10	2183.39
JC_g21956.t1	CG33298: Phospholipid-transport	0.94	2.34E-07	3.29E-06	353.78	380.87	478.88	866.07	784.06	704.87
JC_g5408.t1	"CG42339: Uncharacterized prote	0.94	2.95E-05	0.0002525	292.76	298.97	304.02	423.99	581.36	746.14
JC_g3122.t1	CG9267-RA: Very-long-chain (3R)	0.94	5.02E-06	5.29E-05	944.39	625.57	601.08	1587.42	1267.42	1380.10
JC_g18407.t1	IP3K1: Kinase (Drosophila melan	0.94	6.10E-13	1.86E-11	1319.25	1295.55	1381.99	2592.57	2794.33	2313.57
JC_g20717.t1	"AdipoR: Adiponectin receptor, is	0.93	1.71E-11	4.38E-10	8445.79	7038.19	8672.48	16924.61	15573.17	14059.23
JC_g5388.t1	wkd: RE26521p (Drosophila mela	0.93	1.52E-07	2.18E-06	544.84	754.83	799.79	1423.48	1334.24	1301.78
JC_g1886.t1	"pre-mod(mdg4)-J: Pre-mod(Mdg4	0.93	0.0029638	0.0134149	48.67	97.68	64.58	151.51	143.67	124.89
JC_g17439.t1	Eip63E: LD27880p (Drosophila m	0.93	1.23E-11	3.23E-10	5526.89	4861.51	5747.54	11026.04	10950.11	9060.60
JC_g13841.t1	spas: Spastin (Drosophila melano	0.93	3.47E-11	8.64E-10	925.51	1006.44	1002.47	2073.60	1892.21	1667.97
JC_g1220.t1	"Cht2: Chitinase 2, isoform B (Dro	0.92	5.37E-07	6.93E-06	650.18	459.81	670.63	1184.91	1201.71	1040.37
JC_g18700.t1	mys: Integrin beta (Drosophila me	0.92	0.0002839	0.0018128	16224.69	11771.43	19725.46	43736.69	27773.99	21488.90
JC_g11407.t1	"Nrg: Neuroglian, isoform G (Dros	0.92	4.18E-09	7.54E-08	7457.08	9896.68	9380.87	18315.30	14790.23	18010.08
JC_g23586.t1	alpha-Spec: Spectrin alpha chain	0.92	4.13E-06	4.42E-05	220.12	194.38	255.34	373.11	431.01	482.61
JC_g15342.t1	egg: Histone-lysine N-methyltrans	0.92	0.0001941	0.0013059	329.81	676.88	575.25	909.04	1037.99	1115.51
JC_g17304.t1	l(2)k01209: Uridine kinase (Drosop	0.91	0.0015009	0.0074929	270.97	117.42	181.82	401.38	397.60	319.62
JC_g21406.t1	"kug: Kugelei, isoform E (Drosoph	0.91	1.33E-09	2.60E-08	940.76	1239.31	1188.26	2105.26	2214.08	2065.92
JC_g23272.t1	CG2885: CG2885 (Drosophila me	0.91	2.97E-10	6.35E-09	1003.96	1068.60	860.39	1998.98	1786.41	1763.22
JC_g1364.t1	"2D9: Uncharacterized protein, isc	0.91	7.74E-10	1.55E-08	817.99	864.36	997.50	1797.72	1748.54	1521.92
JC_g23737.t1	"Taz: Tafazzin, isoform D (Drosop	0.91	9.99E-09	1.72E-07	2963.22	3068.66	3807.19	6982.86	6236.84	5408.21
JC_g23759.t1	Krn: Keren (Drosophila melanoga	0.91	1.79E-07	2.56E-06	751.16	582.16	604.06	1398.61	1202.82	1077.41
JC_g2664.t1	"Ptpmeg2: Protein tyrosine phosp	0.90	1.28E-14	4.51E-13	1704.27	1807.65	1704.89	3450.72	3291.05	3058.66
JC_g9523.t1	"alpha-Man-Ia: Mannosyl-oligosac	0.90	1.46E-06	1.74E-05	956.74	651.23	664.67	1421.22	1555.87	1333.53
JC_g2171.t1	"Pxd: Peroxidase, isoform C (Dros	0.90	0.0030956	0.0139128	77.73	49.34	76.50	122.11	112.49	161.93
JC_g496.t1	Pgi: Glucose-6-phosphate isomer	0.90	8.92E-09	1.54E-07	2271.63	2083.93	2423.21	4988.40	4161.98	3615.35
JC_g2143.t1	CG8516-RA: GM31468p (Fragme	0.90	8.36E-11	1.96E-09	622.57	559.46	578.23	1114.81	1163.84	1027.67
JC_g5074.t1	"EG:103E12.3: CG3655, isoform	0.90	9.72E-08	1.43E-06	9432.32	8750.13	12912.85	20137.90	20274.19	18161.43
JC_g21846.t1	out: BcDNA.LD28120 (Drosophila	0.90	0.0004157	0.0025045	336.35	346.33	315.94	410.42	865.36	636.07
JC_g4514.t1	dmGlut: Dietary and metabolic glu	0.90	0.0005354	0.0031251	1460.91	1095.25	934.91	1374.86	2450.19	2862.86
JC_g14531.t1	spz6: RE45222p (Drosophila mela	0.90	0.0012286	0.0063265	4327.50	4596.09	8725.14	14624.88	11580.48	7742.95
JC_g19353.t1	Protein of unknown function	0.89	1.16E-08	1.98E-07	2155.40	1781.99	2272.19	3681.38	4454.89	3519.04
JC_g10937.t1	ninaC: Neither inactivation nor aft	0.89	2.87E-06	3.18E-05	4762.65	4044.52	5709.79	11347.14	8433.10	7599.01
JC_g1755.t1	"Ppcs: Phosphopantothenoylcyst	0.89	4.76E-08	7.47E-07	278.23	250.62	294.08	532.53	492.27	520.71
JC_g11988.t1	CalpC-RA: FI22009p1 (Drosophila	0.89	6.96E-08	1.06E-06	4730.69	4051.42	5836.96	10208.58	8721.56	8517.67
JC_g4382.t1	CG8146: CG8146 (Fragment) (Dro	0.89	1.19E-11	3.15E-10	3115.05	3875.79	3378.98	6467.28	6789.25	6124.72
JC_g11095.t1	"CG1814-RB: CG1814, isoform B	0.89	0.0022554	0.0106099	68.29	129.26	108.29	191.08	165.94	229.66
JC_g19462.t1	Protein of unknown function	0.89	0.0002322	0.00152	3156.46	2144.12	3719.76	7424.94	4100.72	5626.23
JC_g4914.t1	"St4: Sulfotransferase 4, isoform A	0.89	3.55E-06	3.86E-05	684.32	788.38	984.58	1828.25	1465.66	1325.06
JC_g16915.t1	CG3792: Mannose-P-dolichol utili	0.89	6.11E-09	1.08E-07	1857.55	1609.32	2068.52	3892.81	3160.74	3292.55

JC_g16858.t1	"CG42389: Uncharacterized prote	0.89	1.30E-08	2.21E-07	2360.26	2172.73	2942.82	5079.98	4621.95	4273.65
JC_g3543.t1	Protein of unknown function	0.89	4.53E-10	9.45E-09	9216.56	8150.21	9859.75	19122.58	16665.73	15023.39
JC_g24993.t1	bchs: Blue cheese (Drosophila me	0.89	3.74E-05	0.000309	329.09	320.68	318.92	798.23	495.61	534.47
JC_g4086.t1	Dmel\CG7458: CG7458 (Drosoph	0.88	0.0010943	0.0057356	143.11	170.70	203.67	230.65	317.41	436.04
JC_g17811.t1	Dmel\CG13251: Uncharacterized	0.88	7.78E-05	0.0005922	3048.21	1816.53	1884.72	5153.47	4008.28	3561.38
JC_g11094.t1	"CG2145: CG2145, isoform B (Dr	0.88	0.0004661	0.0027688	89.35	95.71	105.31	174.12	221.63	153.46
JC_g19367.t1	MFS10: FI19708p1 (Drosophila m	0.88	2.39E-05	0.0002105	1145.62	802.19	750.11	1925.49	1783.07	1355.76
JC_g8516.t1	pyd: LP05923p (Drosophila melan	0.88	4.93E-12	1.35E-10	9589.96	8771.83	9657.07	17495.58	19032.39	15421.34
JC_g9447.t1	CG12065: GH15213p (Drosophila	0.88	2.46E-10	5.33E-09	1290.19	1072.55	1232.97	2328.00	2315.43	2029.93
JC_g9562.t1	"Dmel\CG42268: Uncharacterized	0.88	4.92E-06	5.20E-05	7826.85	7492.07	9951.15	19639.28	15177.80	12381.73
JC_g9663.t1	Protein of unknown function	0.88	0.0015938	0.0078739	217.21	174.65	114.26	321.10	390.92	251.89
JC_g4334.t1	Drep4: Caspase-activated DNase	0.88	0.0025694	0.0118453	163.45	95.71	166.91	344.85	265.07	202.15
JC_g3819.t1	"CG9248: CG9248, isoform A (Dr	0.87	4.38E-07	5.76E-06	440.96	526.90	566.31	1059.41	956.69	826.58
JC_g3412.t1	"CG8097: CG8097, isoform A (Dr	0.87	3.73E-07	4.98E-06	366.86	393.70	371.58	793.71	713.90	591.62
JC_g10137.t1	ASPP: RE13301p (Drosophila me	0.87	1.19E-10	2.71E-09	3544.38	3249.23	3206.11	6848.31	6204.54	5396.57
JC_g15139.t1	"ACC: Acetyl-CoA carboxylase, is	0.87	1.11E-07	1.62E-06	828.89	714.38	996.51	1685.79	1528.03	1485.93
JC_g23585.t1	"alpha-Spec: Alpha spectrin, isofo	0.87	9.99E-08	1.47E-06	4622.45	5031.22	6597.01	10732.07	9150.34	10174.00
JC_g9569.t1	Cyp304a1: Probable cytochrome	0.87	2.28E-10	4.96E-09	1200.83	1202.80	1235.95	2268.07	2469.12	1963.25
JC_g17221.t1	CG34352-RA: IP21817p (Fragme	0.87	0.0001414	0.0009949	285.50	374.95	432.18	829.89	679.37	527.06
JC_g3410.t1	bves: BVES (Drosophila melanog	0.87	0.0020835	0.0099207	2739.47	3251.20	5835.97	10399.66	6088.72	5850.60
JC_g5576.t1	cin-RA: MIP27737p (Fragment) (D	0.87	7.70E-05	0.0005871	548.48	429.22	350.71	1011.93	753.99	710.16
JC_g24104.t1	Fpps: Farnesyl pyrophosphate sy	0.87	2.05E-05	0.0001842	1436.21	1396.19	2129.13	3532.13	3131.79	2526.30
JC_g5293.t1	"Mhcl: Myosin heavy chain-like, is	0.86	1.48E-06	1.75E-05	4404.51	4329.67	6577.14	9741.63	9041.19	9460.66
JC_g23055.t1	"Adk3: GTP:AMP phosphotransfe	0.86	0.0013372	0.0067819	124.95	127.29	83.46	218.21	245.02	167.22
JC_g19064.t1	polyprotein: Polyprotein (Drosoph	0.86	2.44E-09	4.56E-08	509.97	567.36	551.41	1052.63	1022.40	904.90
JC_g1800.t1	CG30291: CDK5RAP3-like protein	0.86	1.18E-08	2.02E-07	735.90	753.84	944.84	1469.84	1456.75	1530.39
JC_g19417.t1	pgant9: Putative polypeptide N-ac	0.86	2.84E-05	0.0002447	11013.82	12125.65	13908.36	29939.45	21593.95	16831.07
JC_g15123.t1	"ACC: Acetyl-CoA carboxylase, is	0.86	5.15E-07	6.65E-06	667.61	746.94	953.78	1541.07	1434.47	1366.34
JC_g21522.t1	ome: LD21715p (Drosophila mela	0.86	0.0002782	0.0017782	216.48	239.77	241.43	578.89	355.28	359.84
JC_g19643.t1	"BEST:CK01296: CG5885, isofor	0.86	2.11E-10	4.63E-09	9628.46	8100.87	9854.78	17974.98	17185.84	15196.96
JC_g13513.t1	dzy: Dizzy isoform BI (Drosophila	0.86	1.55E-13	4.88E-12	4109.57	3939.92	3942.31	7557.22	7657.95	6630.61
JC_g650.t1	cora: Protein 4.1 homolog (Drosop	0.86	1.48E-05	0.0001379	15814.97	15500.20	19925.15	40951.92	28000.08	25325.45
JC_g5610.t1	Sep1: RE30523p (Drosophila mel	0.86	5.71E-07	7.34E-06	4565.78	4266.53	5604.48	10249.29	8909.77	7286.80
JC_g8632.t1	"shd: Shade, isoform D (Drosophi	0.85	8.56E-06	8.47E-05	7805.06	7903.53	12223.34	18973.33	16024.23	16232.04
JC_g21592.t1	CycD: Cyclin D (Fragment) (Drosop	0.85	1.02E-10	2.35E-09	3802.28	3734.69	3266.71	6962.50	6810.41	5873.89
JC_g23184.t1	"skap: Succinate--CoA ligase [AD	0.85	6.50E-11	1.55E-09	3643.18	3917.23	3145.50	6832.48	6332.62	6299.35
JC_g9770.t1	"CanB2: Calcineurin B2, isoform E	0.85	5.28E-08	8.20E-07	625.48	778.51	758.06	1342.07	1414.43	1179.01
JC_g9704.t1	alphaTub84B: Tubulin alpha-1 ch	0.85	3.07E-07	4.19E-06	1425.31	1414.94	1772.45	2658.14	2469.12	3284.09
JC_g19057.t1	BTBD9: BTB/POZ domain-contain	0.85	0.0007565	0.004208	112.60	165.77	134.13	286.05	278.43	197.91
JC_g24920.t1	GH20910p (Fragment) (Drosophila	0.85	0.0007535	0.0041933	309.47	398.63	547.43	561.93	876.50	877.38
JC_g1419.t1	"siz: Schizo, isoform D (Drosophila	0.85	1.60E-05	0.0001468	3217.48	3574.84	5213.03	8323.80	6807.07	6767.14
JC_g9939.t1	"EG:25E8.1: CG2918, isoform A (	0.85	2.47E-05	0.0002161	6076.81	9233.61	10795.65	17217.44	15406.11	15026.57
JC_g25205.t1	Syn1: IP02644p (Drosophila mela	0.85	9.13E-06	9.00E-05	193.24	187.47	157.97	326.76	314.07	341.85
JC_g15348.t1	"Nf1: Neurofibromin 1, isoform D (	0.84	0.0004497	0.0026851	198.32	338.44	305.01	417.21	564.66	561.99
JC_g16172.t1	InR-RC: LD06045p1 (Fragment) (I	0.84	9.10E-10	1.81E-08	1195.02	964.01	1137.59	2066.82	1930.08	1968.55
JC_g2649.t1	Protein of unknown function	0.84	0.0015703	0.0077882	120.59	127.29	89.42	262.31	171.51	190.50
JC_g17014.t1	Hs2st: Heparin sulfate O-sulfotran	0.84	2.88E-06	3.19E-05	1281.47	1515.58	1803.25	2832.26	3194.15	2329.45
JC_g11029.t1	CG11339: IP17263p (Drosophila	0.84	1.93E-09	3.67E-08	4780.09	5528.52	6276.10	10625.79	9730.59	9586.61
JC_g23155.t1	botv: Exostosin-3 (Drosophila mel	0.84	6.23E-09	1.09E-07	712.65	630.51	692.49	1236.92	1330.90	1105.98
JC_g14891.t1	Protein of unknown function	0.84	8.21E-07	1.02E-05	4729.24	4623.71	6499.64	10743.38	9013.35	8915.61
JC_g13835.t1	"PP2A-B': PP2A-B', isoform B (Dr	0.84	0.0001229	0.0008845	2327.57	1321.20	1571.76	3706.25	3106.17	2706.22
JC_g4549.t1	Ucp4A: RH64870p (Drosophila me	0.84	6.37E-05	0.0004959	175.08	202.28	252.36	410.42	390.92	341.85
JC_g11986.t1	Protein of unknown function	0.84	3.65E-05	0.0003021	220.12	310.81	315.94	555.15	516.77	463.56
JC_g19377.t1	CG30274: Uncharacterized protei	0.84	3.12E-05	0.0002649	331.99	330.55	461.99	755.27	581.36	703.81
JC_g8984.t1	"CG43427: Uncharacterized prote	0.84	1.80E-08	3.00E-07	13095.84	14253.98	15791.09	29780.03	25627.85	22362.05
JC_g18259.t1	SERCA: Calcium-transporting ATP	0.84	3.56E-10	7.53E-09	7692.45	8455.10	9824.97	16317.45	15492.98	14877.34
JC_g2616.t1	"Fur1: Furin-like protease 1, isofor	0.84	1.17E-10	2.67E-09	2454.70	2877.24	2957.73	5258.62	4923.76	4703.34
JC_g2168.t1	"Pxd: Peroxidase, isoform C (Dros	0.83	4.22E-09	7.59E-08	3081.63	3569.91	3945.29	5901.96	6919.55	6215.74
JC_g1235.t1	qsm: GH08941p (Drosophila mela	0.83	3.17E-11	7.95E-10	20337.89	18372.50	17104.53	32768.32	36135.82	31180.29
JC_g11012.t1	TRAM: Translocating chain-assoc	0.83	1.68E-11	4.33E-10	3304.65	3192.00	3544.90	6399.44	6157.77	5428.32
JC_g1482.t1	p120ctn: Arm repeat protein (Dros	0.83	3.22E-09	5.90E-08	761.33	912.70	788.86	1461.92	1560.32	1393.86
JC_g15370.t1	CG11802: LD30509p (Drosophila	0.83	0.0004591	0.0027328	164.91	233.85	268.25	443.21	331.89	434.99
JC_g8574.t1	"Sema5c: Semaphorin 5c, isoform	0.83	0.0001152	0.0008353	5353.26	7511.81	9261.64	16389.81	12366.77	11271.51
JC_g8601.t1	AnxB9: Annexin (Drosophila mela	0.83	5.03E-12	1.38E-10	14610.51	15931.39	16629.63	30398.49	26137.94	27686.65
JC_g19608.t1	Protein of unknown function	0.83	2.74E-06	3.06E-05	948.75	970.92	1291.58	2210.41	1769.70	1785.45
JC_g2678.t1	"CG42404: Uncharacterized prote	0.82	1.99E-07	2.83E-06	613.13	569.33	709.38	1199.61	1181.66	1001.21
JC_g5110.t1	CAMKIIB: LD14939p (Drosophila	0.82	0.0001575	0.0010921	363.23	452.90	651.75	878.51	893.20	873.15
JC_g21410.t1	Protein of unknown function	0.82	3.53E-05	0.0002948	422.07	629.52	684.54	1014.19	1022.40	1078.47
JC_g16995.t1	Protein of unknown function	0.82	1.67E-09	3.21E-08	632.02	604.85	624.93	1022.10	1187.23	1102.81
JC_g16117.t1	Protein of unknown function	0.82	0.0015576	0.0077447	138.75	236.81	156.98	382.16	309.61	272.00
JC_g21872.t1	CG12769-RB: RE08168p (Drosop	0.82	2.91E-06	3.22E-05	2948.69	2372.05	3245.85	5972.06	5021.77	4302.23
JC_g4280.t1	Protein of unknown function	0.82	0.0006916	0.0038862	1766.74	1094.26	852.44	1977.50	2280.90	2449.04
JC_g24040.t1	"CG4239: CG4239, isoform A (Dr	0.82	0.0032004	0.0143163	106.06	109.52	183.80	232.91	208.27	283.64
JC_g9687.t1	"Ance-3: Ance-3, isoform B (Dros	0.82	4.22E-06	4.52E-05	375.58	405.54	373.57	577.76	680.48	801.18

JC_g12379.t1	"garz: Gartenzwerg, isoform C (Dr	0.82	0.0004715	0.0027964	329.81	371.00	388.47	883.03	583.59	491.08
JC_g22953.t1	Protein of unknown function	0.81	0.0002257	0.0014812	195.42	186.49	289.12	422.86	388.69	389.48
JC_g5724.t1	sea: LD46175p (Drosophila melar	0.81	2.11E-05	0.0001886	191.78	227.93	253.35	414.95	415.42	367.25
JC_g14831.t1	Gk2: FI03690p (Drosophila melan	0.81	1.81E-07	2.58E-06	1140.54	1112.02	1332.32	1804.51	2306.52	2242.66
JC_g14426.t1	"mim: Missing-in-metastasis, isofor	0.81	0.0013307	0.006752	2764.17	3337.05	4303.95	8578.19	6128.81	4021.76
JC_g13708.t1	CG3308: GH08045p (Drosophila	0.81	1.43E-10	3.20E-09	1208.82	1224.50	1361.13	2382.27	2152.82	2157.99
JC_g24259.t1	"Src42A: Src oncogene at 42A, is	0.81	1.19E-10	2.70E-09	5909.73	5810.72	6142.97	11362.97	10882.18	9252.17
JC_g12512.t1	CG17593-RA: FI04424p (Drosopl	0.81	4.20E-08	6.68E-07	3363.50	2611.82	3066.02	5937.01	4980.56	5061.07
JC_g19376.t1	"CG42284: Uncharacterized prote	0.81	0.0027912	0.012694	143.84	163.79	213.61	408.16	226.09	302.69
JC_g24955.t1	"dac: Dachshund, isoform C (Dros	0.81	3.68E-05	0.0003046	201.23	213.13	277.19	409.29	396.48	419.11
JC_g5217.t1	CG17370-RC: RE38540p (Drosop	0.81	3.66E-08	5.88E-07	4844.02	4497.41	5404.78	9873.91	8498.81	7602.19
JC_g16962.t1	trbl: RH69304p (Drosophila melan	0.81	1.17E-07	1.71E-06	2408.21	2008.94	2785.85	4432.12	4048.38	4213.32
JC_g19559.t1	shep: Protein alan shepard (Dros	0.80	9.38E-06	9.21E-05	13292.71	14414.82	20265.93	31843.45	27133.60	25858.86
JC_g11592.t1	CG14234: RE70461p (Drosophila	0.80	3.74E-05	0.0003086	1173.23	741.02	1117.72	1959.41	1776.39	1633.05
JC_g24862.t1	"jvl: Javelin-like, isoform C (Drosop	0.80	2.83E-08	4.62E-07	1083.15	996.58	1189.25	2063.42	1970.17	1705.01
JC_g10246.t1	CG1630: Kinase (Drosophila mela	0.80	0.0021338	0.0101307	302.21	158.86	318.92	502.01	458.85	433.93
JC_g11655.t1	trio: Trio (Drosophila melanogaste	0.80	2.91E-10	6.24E-09	10057.07	10257.82	10936.73	16246.22	20143.89	18266.20
JC_g920.t1	BcDNA:GH10614: IP10737p (Fra	0.80	1.51E-06	1.78E-05	1654.14	1243.25	1542.95	2987.16	2381.14	2422.58
JC_g2154.t1	CG15890-RA: FI18259p1 (Drosop	0.80	2.75E-06	3.07E-05	1949.08	1548.14	1815.17	3718.69	2669.59	2935.89
JC_g23342.t1	Cip4: RE39037p (Drosophila mela	0.80	5.13E-10	1.06E-08	6290.39	6212.31	6795.71	12266.35	11493.61	9942.22
JC_g14075.t1	"CG2004: CG2004, isoform A (Dr	0.80	0.0002567	0.0016623	655.99	577.22	520.61	1377.12	855.34	867.85
JC_g1004.t1	Hr3: FI17818p1 (Drosophila melar	0.79	0.0009863	0.0052659	10982.58	10428.52	15479.13	30525.12	19216.16	15688.04
JC_g10990.t1	"tapas: CG8920, isoform F (Drosc	0.79	1.07E-09	2.12E-08	5614.79	5287.77	6407.25	10796.52	9935.51	9395.05
JC_g10472.t1	CG2556: CG2556 (Drosophila me	0.79	4.56E-06	4.84E-05	6124.76	5505.83	5467.37	11844.62	10308.61	7711.20
JC_g16856.t1	Protein of unknown function	0.79	2.80E-08	4.58E-07	3422.34	3475.19	4357.60	6930.85	6357.12	6259.13
JC_g3411.t1	CG7872: DnaJ homolog subfamily	0.79	0.0001025	0.000753	3132.48	2919.67	4439.07	7455.47	5794.69	5113.99
JC_g2453.t1	"CASK: CASK ortholog, isoform D	0.78	0.0003616	0.0022303	150.38	216.09	183.80	360.68	318.52	283.64
JC_g15219.t1	CG11533: RE74626p (Drosophila	0.78	2.74E-07	3.80E-06	1144.90	1375.47	1520.09	2427.49	2436.82	2146.35
JC_g3321.t1	"Coprox: Coproporphyrinogen oxi	0.78	3.95E-05	0.0003231	650.91	438.10	520.61	1030.02	951.12	829.75
JC_g5332.t1	"PI4KIIIalpha: Phosphatidylinositc	0.78	0.000498	0.0029309	1283.65	2207.27	2472.88	3759.39	3110.62	3573.02
JC_g21256.t1	"C3G: C3G ortholog, isoform L (D	0.78	5.07E-06	5.32E-05	313.10	346.33	345.75	650.12	586.93	508.01
JC_g13020.t1	"Npc1a: Niemann-Pick type C-1a,	0.78	3.87E-08	6.19E-07	6554.10	7281.90	8649.63	13538.33	13294.50	12089.63
JC_g10388.t1	norpA: Phosphoinositide phospho	0.78	5.09E-05	0.000405	358.87	543.68	510.67	872.86	796.31	788.48
JC_g15357.t1	"Zip102B: Zinc/iron regulated tran	0.78	0.0011343	0.0059235	143.11	198.33	191.75	385.55	288.45	260.36
JC_g1065.t1	Hmgcr-RA: 3-hydroxy-3-methylglut	0.78	0.0004052	0.0024582	2371.88	2464.80	3709.82	6151.83	4954.95	3835.49
JC_g10686.t1	Acyl-coenzyme A oxidase (Drosop	0.78	0.0001261	0.0009041	606.59	657.15	665.66	1426.87	1091.45	844.57
JC_g7883.t1	CG5599: Dihydrolipoamide acetyl	0.78	0.0016463	0.0080948	204.86	242.73	219.57	532.53	330.78	307.98
JC_g19066.t1	sprt: GH21160p (Drosophila mela	0.78	2.24E-07	3.16E-06	731.54	662.08	677.58	1312.68	1042.44	1226.64
JC_g9167.t1	Dmel\CG14085: RE61245p (Dros	0.78	0.0009646	0.0051765	206.31	250.62	153.00	391.20	301.82	374.66
JC_g1781.t1	Protein of unknown function	0.78	0.0025956	0.0119323	122.04	148.01	124.19	297.36	178.20	216.96
JC_g19324.t1	Picot-RB: RH11868p (Drosophila	0.78	5.02E-05	0.0004002	492.54	659.12	728.25	1248.23	993.44	1020.26
JC_g16477.t1	CG4502: Ubiquitin-conjugating er	0.78	0.0011525	0.0059915	313.10	181.55	198.71	402.51	423.21	391.59
JC_g5510.t1	CG9503: CG9503-PA (Drosophila	0.78	6.81E-08	1.04E-06	623.30	577.22	611.02	1151.00	1016.83	959.93
JC_g15004.t1	CG18490: RE33713p (Drosophila	0.78	3.39E-10	7.17E-09	1752.94	1930.00	1925.45	2956.63	3323.35	3377.22
JC_g173.t1	"shot: Short stop, isoform J (Drosc	0.78	3.59E-07	4.83E-06	1196.47	1444.54	1563.81	2625.35	2218.53	2409.88
JC_g10632.t1	"CycE: Cyclin E, isoform F (Drosop	0.78	0.0007919	0.0043794	413.35	485.46	527.56	1007.40	918.82	563.05
JC_g17487.t1	"nuf: Nuclear fallout, isoform H (Dr	0.77	1.26E-06	1.52E-05	6933.31	6202.45	8147.90	14009.81	12146.25	10589.93
JC_g4259.t1	HDC07883: HDC07883 (Drosophi	0.77	2.88E-05	0.0002473	373.40	291.08	413.31	576.63	643.73	645.60
JC_g13009.t1	"Clic: Chloride intracellular channe	0.77	7.73E-12	2.06E-10	5064.86	4966.10	5110.70	9056.46	9005.55	7931.34
JC_g22891.t1	MBD-R2: SD10773p (Drosophila r	0.77	9.89E-07	1.21E-05	1395.52	1857.97	1364.11	2572.21	2695.21	2687.17
JC_g2899.t1	Protein of unknown function	0.77	0.000153	0.0010673	190.33	197.34	261.30	350.50	403.17	368.31
JC_g1464.t1	"cdc14: Cell division cycle 14, isof	0.77	0.0001218	0.0008784	368.31	386.79	397.41	802.76	679.37	510.13
JC_g16367.t1	Rgl: LD16082p (Drosophila melan	0.77	5.32E-08	8.24E-07	1804.52	1649.78	1780.40	3307.13	3095.03	2581.34
JC_g15996.t1	ATPCL: ATP-citrate synthase (Dro	0.77	1.73E-10	3.81E-09	2623.24	2942.36	2831.55	4429.86	4898.15	5031.43
JC_g5118.t1	pigs: GAS2-like protein pickled eg	0.77	0.0002301	0.0015069	377.76	457.83	531.54	642.21	760.67	955.70
JC_g4242.t1	CG10184: LD34157p (Drosophila	0.76	0.0004413	0.0026433	2595.63	1842.18	1394.91	2928.37	3482.61	3670.39
JC_g1591.t1	"Sec24CD: Sec24CD ortholog, isc	0.76	4.35E-09	7.80E-08	2142.32	2160.89	2606.02	3983.26	3919.19	3889.47
JC_g24273.t1	"Sema1a: Sema-1a, isoform F (Dr	0.76	0.0001321	0.0009421	343.61	492.37	537.50	842.33	736.17	780.01
JC_g23266.t1	Spn42Da: RE31022p (Drosophila	0.76	1.78E-09	3.41E-08	3589.42	3190.03	3592.59	6463.89	5733.44	5490.76
JC_g22917.t1	CG9893: CG9893 protein (Drosop	0.76	1.14E-06	1.38E-05	1344.67	1768.18	1601.56	3016.56	2533.72	2509.37
JC_g8571.t1	"Dmel\CG5618: CG5618, isoform	0.76	0.0002869	0.0018286	219.39	190.43	258.32	446.60	336.34	367.25
JC_g21867.t1	Liprin-beta: AT31531p (Drosophil	0.76	1.19E-09	2.33E-08	1131.82	1022.23	1114.74	1784.16	1816.48	1968.55
JC_g4754.t1	CG7718: CDP-diacylglycerol--glyc	0.76	0.0010642	0.0056091	1748.58	1841.20	3297.51	4390.29	3687.53	3803.74
JC_g11341.t1	"Klp31E: Kinesin-like protein at 3	0.76	5.36E-11	1.30E-09	2638.49	2644.38	2630.86	4720.44	4625.29	4109.60
JC_g23487.t1	Drip: Aquaporin (Drosophila melar	0.76	1.21E-10	2.74E-09	4596.29	4284.29	4340.71	7469.03	8103.44	6910.02
JC_g10856.t1	"LpR2: Lipophorin receptor 2, isof	0.76	0.0030009	0.0135721	183.07	174.65	317.93	418.34	373.10	377.83
JC_g16920.t1	mys: Integrin beta (Drosophila me	0.76	5.09E-05	0.0004053	379.94	367.06	427.22	807.28	629.25	573.63
JC_g23043.t1	Protein of unknown function	0.76	7.80E-10	1.56E-08	6737.16	6887.22	7136.49	12666.60	12183.00	10437.53
JC_g17451.t1	CG33232-RA: SD07506p (Drosop	0.76	0.0001243	0.0008932	137.30	148.99	156.98	257.79	246.13	254.01
JC_g19934.t1	CG3960: IP18653p (Fragment) (D	0.76	2.25E-08	3.73E-07	24661.77	25769.85	29754.10	50624.58	43192.36	42438.04
JC_g14731.t1	NC2alpha: LD24434p (Drosophila	0.75	2.96E-07	4.08E-06	1014.13	1014.34	1069.03	1664.31	2024.75	1574.84
JC_g22920.t1	"pum: Pumilio, isoform G (Drosopl	0.75	3.18E-07	4.33E-06	28688.52	26291.82	34027.25	56474.53	48538.22	46179.34
JC_g15403.t1	CG42741: Uncharacterized protei	0.75	0.0003034	0.0019134	152.56	188.46	214.60	303.01	337.46	307.98
JC_g10465.t1	Protein of unknown function	0.75	5.74E-07	7.36E-06	378.48	378.90	352.70	632.03	661.55	590.56

JC_g23299.t1	CG17528: Serine/threonine-prote	0.75	3.92E-08	6.26E-07	1769.65	1641.88	1944.33	3267.56	3072.76	2728.45
JC_g15212.t1	"ATP7: ATP7, isoform B (Drosoph	0.75	5.87E-05	0.0004608	286.22	281.21	306.01	589.07	462.19	436.04
JC_g15935.t1	Parp: Poly [ADP-ribose] polymera	0.75	0.0004672	0.0027737	258.62	220.04	245.40	429.64	319.64	488.96
JC_g11633.t1	meigo: Solute carrier family 35 me	0.75	6.69E-07	8.48E-06	759.87	767.66	846.48	1426.87	1440.04	1155.73
JC_g5221.t1	gag: Gag protein (Drosophila mel	0.75	0.0009772	0.0052313	127.13	114.46	144.06	249.87	216.06	193.68
JC_g8551.t1	Protein of unknown function	0.75	1.32E-09	2.58E-08	1515.39	1460.33	1459.49	2365.31	2724.16	2395.06
JC_g17342.t1	l(1)G0320: LD26546p (Drosophila	0.75	6.97E-10	1.41E-08	10977.49	10530.15	12225.33	20139.03	19095.87	17628.01
JC_g21278.t1	nac: GDP-fucose transporter 1 (D	0.75	4.67E-05	0.0003754	227.38	282.20	295.08	451.13	481.13	429.69
JC_g17440.t1	Eip63E-RF: RH42523p (Drosophil	0.74	0.000162	0.001117	172.90	169.71	205.66	339.19	286.23	304.81
JC_g12923.t1	heix: UbiA prenyltransferase dom	0.74	6.57E-08	1.00E-06	3093.25	2919.67	3231.94	5658.87	5426.05	4471.56
JC_g5164.t1	CG16804: Mevalonate kinase (Dr	0.74	1.12E-05	0.0001078	1099.86	1019.27	1323.38	2230.76	1898.90	1679.61
JC_g2577.t1	dsx-c73A: Doublesex cognate 73	0.74	1.35E-05	0.0001275	10883.78	9988.44	13774.24	22782.47	17274.94	18387.91
JC_g4263.t1	"mwh: Multiple wing hairs, isoform	0.74	3.17E-05	0.0002679	1460.18	1018.28	1015.38	1862.17	1954.58	2087.08
JC_g15345.t1	Protein of unknown function	0.74	6.03E-05	0.0004722	316.74	414.42	453.05	650.12	706.10	641.37
JC_g11408.t1	"shf: Shifted, isoform D (Drosophil	0.74	0.001432	0.0072055	2530.25	3486.04	2380.49	4890.03	3269.89	6110.96
JC_g19752.t1	"Samuel: SAM-motif ubiquitously	0.74	2.06E-06	2.34E-05	16660.57	15653.14	18025.53	34019.94	25661.26	24964.55
JC_g19883.t1	Protein of unknown function	0.74	0.0010816	0.0056848	162.00	171.69	122.20	247.61	288.45	238.13
JC_g15969.t1	Gl: Dynactin subunit 1 (Drosophila	0.74	2.81E-08	4.59E-07	923.33	1071.56	1099.83	1718.58	1688.40	1775.92
JC_g7957.t1	"Nc73EF: Neural conserved at 73	0.74	8.42E-08	1.26E-06	3630.11	4464.85	4718.25	7140.02	7294.88	7033.85
JC_g10704.t1	Rab32: FI09421p (Drosophila me	0.74	6.49E-07	8.26E-06	4302.81	3662.66	4454.97	7941.64	6233.50	6654.96
JC_g9584.t1	CG14073: SD21394p (Drosophila	0.74	5.15E-06	5.39E-05	496.17	572.29	542.46	1026.62	802.99	874.20
JC_g5481.t1	Protein of unknown function	0.73	2.38E-05	0.0002097	752.61	867.32	1095.86	1625.87	1523.57	1412.91
JC_g5216.t1	CG14210: GEO07531p1 (Drosop	0.73	4.91E-11	1.20E-09	4420.49	3992.22	4199.63	7343.53	7058.77	6670.83
JC_g20965.t1	"CG13003: Uncharacterized prote	0.73	0.0001466	0.001025	665.43	604.85	895.17	1388.43	1193.91	1064.71
JC_g9616.t1	Protein of unknown function	0.73	0.0016141	0.0079535	17818.54	15389.68	27128.21	42564.22	26229.26	33268.43
JC_g22954.t1	Pcyt2: CTP:phosphocholine cytidy	0.73	1.55E-05	0.0001432	3675.87	3683.38	5118.64	7731.34	6567.62	6586.16
JC_g4341.t1	"stc: Shuttle craft, isoform D (Dros	0.73	8.12E-07	1.01E-05	1388.99	1146.55	1150.50	2188.93	2123.87	1841.54
JC_g9195.t1	sba: TF125 protein (Drosophila m	0.73	0.0002466	0.0016022	508.52	485.46	644.80	1002.88	1022.40	721.80
JC_g649.t1	"Dmel\CG5665: CG5665, isoform	0.73	0.0021391	0.0101521	445.32	367.06	433.18	945.22	506.74	648.77
JC_g19261.t1	CG15118: LD31969p (Drosophila	0.73	3.70E-06	3.99E-05	948.75	893.96	1075.99	1814.68	1648.31	1402.32
JC_g25422.t1	CG11576: Uncharacterized protei	0.73	0.0001283	0.0009178	308.02	300.95	377.54	592.46	593.61	463.56
JC_g10755.t1	"dnt: Doughnut on 2, isoform B (D	0.73	0.0006002	0.0034492	1120.20	904.81	1161.43	1414.44	2353.29	1580.13
JC_g23236.t1	"CG4374: CG4374, isoform B (Dr	0.73	6.85E-07	8.67E-06	2576.74	2524.99	2916.00	5035.89	4450.43	3858.77
JC_g15752.t1	"Slik: Sterile20-like kinase, isoform	0.72	2.39E-08	3.94E-07	2440.90	2674.97	3052.11	4429.86	4582.97	4555.17
JC_g19756.t1	Protein of unknown function	0.72	0.0001368	0.0009706	791.84	797.26	1093.87	1749.11	1432.25	1296.49
JC_g10018.t1	"Actn: Alpha actinin, isoform D (Dr	0.72	1.52E-05	0.0001409	3144.83	3293.63	4332.76	6756.73	5675.53	5483.35
JC_g16322.t1	Gpo-1: Glycerol-3-phosphate deh	0.72	5.42E-06	5.62E-05	1080.24	1243.25	1426.70	2315.56	1931.19	1972.78
JC_g1970.t1	Men: Malic enzyme (Drosophila m	0.72	0.0007702	0.0042697	1468.90	2735.15	2177.81	3481.25	3913.62	3259.74
JC_g23180.t1	sinu: Sinuous (Drosophila melano	0.71	4.07E-06	4.37E-05	4751.76	5376.57	3801.23	8020.79	7794.94	7221.18
JC_g1212.t1	wit: Receptor protein serine/threor	0.71	6.76E-06	6.85E-05	362.50	447.97	423.24	703.26	654.87	677.35
JC_g5113.t1	ImpE3: Ecdysone-inducible gene	0.71	6.08E-06	6.23E-05	19906.38	18681.34	26547.00	37086.25	34675.73	35783.09
JC_g21230.t1	Noa36: Zinc finger protein 330 ho	0.71	1.54E-06	1.82E-05	1391.17	1204.77	1304.50	2463.67	2014.72	1955.85
JC_g8805.t1	nSyb: GH19566p (Drosophila mel	0.71	0.0022247	0.0104971	105.34	145.05	153.00	222.74	231.65	215.91
JC_g23909.t1	CG4972-RA: Nicalin (Drosophila n	0.71	7.04E-06	7.10E-05	778.76	713.39	663.68	1197.35	1329.78	1029.78
JC_g11624.t1	CG10467-RA: MIP04215p (Fragm	0.71	8.93E-05	0.0006672	436.60	423.30	315.94	617.33	681.60	646.66
JC_g16841.t1	CG12547: RE33981p (Drosophila	0.71	2.42E-06	2.72E-05	1766.74	1542.22	1950.29	3067.44	3051.60	2536.88
JC_g11403.t1	SsRbeta: Translocon-associated	0.71	6.94E-08	1.05E-06	6201.04	5894.59	6226.42	11428.55	9106.90	9546.39
JC_g470.t1	GSS: Glutathione synthetase (Dr	0.71	3.12E-05	0.0002646	913.88	1019.27	1050.16	1970.71	1551.41	1391.74
JC_g15772.t1	"CG3744: CG3744, isoform E (Dr	0.71	0.0001574	0.0010918	448.95	363.11	536.50	801.63	726.15	697.46
JC_g16860.t1	Protein of unknown function	0.71	2.41E-05	0.0002117	534.67	553.54	649.77	1065.07	968.94	825.52
JC_g20924.t1	"msps: Mini spindles, isoform B (D	0.71	0.0013007	0.0066342	1684.65	2844.68	3171.33	4305.49	4624.17	3824.91
JC_g5294.t1	"Mhcl: Myosin heavy chain-like, is	0.70	5.19E-05	0.0004114	10362.18	10928.78	15571.52	20226.09	19026.82	21380.95
JC_g4240.t1	"Tmc: Transmembrane channel-lik	0.70	2.35E-05	0.0002068	670.52	542.69	504.71	878.51	1002.35	945.11
JC_g5248.t1	CG32668: Uncharacterized protei	0.70	0.0026685	0.0122233	286.95	228.92	196.72	303.01	444.37	436.04
JC_g16809.t1	"Fatp: Fatty acid (Long chain) tran	0.70	0.0001359	0.0009649	1990.49	1767.19	2042.69	3995.70	2521.47	3030.08
JC_g16048.t1	Tapdelta: GEO05407p1 (Drosoph	0.70	8.31E-08	1.25E-06	6589.69	6146.20	7397.79	11996.13	10612.65	10293.59
JC_g12057.t1	luna: Krueppel-like factor luna (Dr	0.70	2.21E-05	0.0001965	854.31	706.48	993.53	1390.69	1471.23	1320.83
JC_g3783.t1	Toll-7: Toll-like receptor 7 (Drosop	0.70	5.47E-05	0.0004323	8663.00	7874.92	7678.96	16283.53	12914.72	10486.21
JC_g24422.t1	Hil: Hillarin (Drosophila melanogas	0.70	4.71E-05	0.0003772	16187.64	15049.27	22477.52	31686.29	28238.42	28069.77
JC_g23769.t1	CG10283: GH02263p (Drosophila	0.70	9.62E-06	9.42E-05	1196.47	1004.47	1063.07	2021.59	1791.98	1528.27
JC_g15173.t1	"MFS16: Major facilitator superfan	0.70	0.0001227	0.0008836	397.37	460.79	518.62	861.55	737.28	656.18
JC_g20974.t1	Protein of unknown function	0.70	0.0006303	0.0036038	163.45	199.32	213.61	313.19	345.25	286.82
JC_g12446.t1	"f: Forked, isoform I (Drosophila m	0.70	8.59E-06	8.50E-05	25714.40	24485.16	32027.29	51287.13	40794.52	42203.09
JC_g2721.t1	"Fur2: Furin 2, isoform I (Drosophi	0.70	3.12E-06	3.43E-05	1293.09	1712.93	1596.60	2601.61	2357.75	2545.35
JC_g2627.t1	CG4553-RA: MIP05631p (Drosop	0.70	1.20E-07	1.75E-06	751.88	722.27	829.59	1279.89	1217.30	1253.10
JC_g23486.t1	"poe: Purity of essence, isoform E	0.69	5.06E-06	5.32E-05	4497.50	6015.96	5803.18	8102.19	9004.44	9426.80
JC_g19388.t1	"CG9784: CG9784, isoform A (Dr	0.69	0.0001863	0.0012629	227.38	242.73	216.59	408.16	384.23	328.09
JC_g24425.t1	Hil: Hillarin (Drosophila melanogas	0.69	0.000344	0.0021356	933.50	848.57	1313.44	1874.61	1636.06	1536.74
JC_g9699.t1	Vha100-1: V-type proton ATPase	0.69	3.01E-06	3.31E-05	8997.90	9446.74	11807.06	17619.95	16415.15	15031.86
JC_g21866.t1	CG14305: AT25266p (Drosophila	0.69	4.30E-06	4.58E-05	909.52	779.50	763.03	1243.71	1266.30	1470.06
JC_g16055.t1	mura-RC: MIP32849p1 (Fragment	0.69	0.0002347	0.0015328	1383.90	1879.68	1431.67	3045.95	2476.92	2123.07
JC_g8843.t1	"CG43102: Uncharacterized prote	0.69	3.53E-05	0.0002948	1214.64	1545.18	1316.42	1840.69	2349.95	2428.93
JC_g14209.t1	glu: Structural maintenance of chr	0.69	2.82E-06	3.14E-05	928.41	1015.32	925.97	1767.20	1405.52	1478.53
JC_g23408.t1	CG1703: LD35151p (Fragment) (I	0.69	5.84E-09	1.03E-07	3436.87	3274.88	3801.23	5826.21	5750.15	5415.62

JC_g20923.t1	msps: Protein mini spindles (Dros	0.69	0.0025276	0.0116809	1516.12	2829.88	2970.64	4074.84	3906.94	3978.37
JC_g14140.t1	"brp: Bruchpilot, isoform J (Drosop	0.68	0.003184	0.0142539	140.21	212.14	178.83	332.41	270.63	263.53
JC_g12124.t1	path: Proton-coupled amino acid	0.68	2.71E-06	3.02E-05	3378.75	3911.31	4320.84	6684.37	6519.73	5568.02
JC_g9031.t1	"Arp10: Actin-related protein 10, i	0.68	8.53E-06	8.46E-05	2358.08	2654.24	3257.77	4652.60	4194.28	4516.01
JC_g9862.t1	Protein of unknown function	0.68	2.60E-05	0.0002264	40050.31	34628.52	45596.86	76457.53	60284.65	57823.40
JC_g4694.t1	"CtsB1: Cathepsin B1, isoform A (	0.68	6.62E-05	0.0005126	1176.13	980.79	1147.52	2026.11	1879.96	1445.72
JC_g15397.t1	CG10011: SD03956p (Drosophila	0.68	0.0003046	0.0019192	344.34	445.01	512.66	695.35	670.46	738.73
JC_g21729.t1	Aats-gln: Probable glutamine--tRN	0.68	3.45E-07	4.66E-06	2167.02	2216.15	2645.76	3962.91	3715.38	3623.82
JC_g9124.t1	CG11955: GH07390p (Drosophila	0.68	0.0020493	0.0097785	324.73	408.50	282.16	473.74	679.37	495.31
JC_g18996.t1	"CG8578: CG8578, isoform A (Dr	0.68	0.0021728	0.010285	1095.50	910.73	1575.73	2334.78	1760.79	1714.54
JC_g21472.t1	CG1827: Putative N(4)-(beta-N-ac	0.68	2.33E-06	2.63E-05	493.26	443.03	511.67	776.75	767.35	783.19
JC_g24467.t1	"ITP: Ion transport peptide, isofor	0.68	0.0001594	0.0011024	430.79	323.64	392.44	555.15	658.21	638.19
JC_g23433.t1	"Rop: Ras opposite, isoform B (Dr	0.68	1.68E-06	1.97E-05	3235.64	3042.02	3686.97	5926.83	5274.59	4804.95
JC_g8531.t1	GEO09824p1 (Fragment) (Drosop	0.67	2.74E-05	0.0002365	615.31	539.73	516.63	940.70	966.71	785.30
JC_g16167.t1	Stam: Jak pathway signal transdu	0.67	1.05E-05	0.0001017	852.13	807.13	727.26	1454.01	1211.73	1172.66
JC_g15174.t1	"pen-2: Presenilin enhancer, isofo	0.67	7.29E-06	7.33E-05	1907.68	1814.56	2064.55	3416.81	3275.46	2598.27
JC_g24276.t1	Pka-R2: cAMP-dependent protein	0.67	1.73E-06	2.01E-05	2568.75	2225.03	2362.60	4311.14	3752.13	3410.03
JC_g11352.t1	"Rab6: Rab6, isoform B (Drosoph	0.67	4.97E-06	5.24E-05	11995.99	8888.27	10631.72	18090.30	16692.46	15722.97
JC_g7897.t1	rictor: FI03615p (Drosophila melan	0.67	0.0009913	0.0052852	988.71	1474.14	1638.32	2479.50	2207.40	1923.04
JC_g5450.t1	schlank: LD18904p (Drosophila m	0.67	0.0011947	0.0061795	1872.81	2547.68	3200.15	4839.16	3717.60	3730.71
JC_g21824.t1	CG1397: Protein quiver (Drosoph	0.67	0.0001798	0.0012258	704.66	691.68	685.53	1320.59	1144.91	880.55
JC_g9442.t1	Protein of unknown function	0.67	3.94E-05	0.0003227	14237.83	14243.13	17109.50	29458.92	21634.05	22029.72
JC_g13457.t1	"mthl10: Methuselah-like 10, isofo	0.67	3.08E-05	0.0002622	476.56	557.49	486.83	907.91	782.95	741.91
JC_g10494.t1	"CdGAPr: Cd GTPase activating p	0.67	1.43E-09	2.76E-08	5478.21	5081.55	5456.44	7989.13	8724.90	8805.54
JC_g12390.t1	garz: AT08349p (Drosophila mela	0.67	0.0002477	0.0016085	334.90	359.16	466.96	641.08	605.86	611.73
JC_g23483.t1	"poe: Purity of essence, isoform E	0.67	6.74E-05	0.0005196	316.74	396.66	371.58	568.71	612.55	551.40
JC_g17996.t1	"lola: Longitudinals lacking protein	0.66	1.37E-06	1.63E-05	3222.56	3088.40	3856.87	5785.50	5357.00	5068.48
JC_g18600.t1	spoon: GM14014p (Drosophila m	0.66	1.48E-07	2.14E-06	7448.36	7456.55	8556.24	13538.33	12246.48	11549.86
JC_g9197.t1	"CG13775: Uncharacterized prote	0.66	2.63E-07	3.68E-06	3538.57	3328.17	4039.67	5638.52	6155.54	5548.97
JC_g17311.t1	"CG2938: CG2938, isoform B (Dr	0.66	0.0007044	0.0039528	240.46	208.20	259.31	417.21	388.69	327.03
JC_g4235.t1	"FoxK: Forkhead box K, isoform N	0.66	1.30E-09	2.56E-08	1652.69	1620.17	1697.94	2647.97	2572.70	2662.83
JC_g13158.t1	His2B: Histone H2B (Drosophila m	0.66	0.0015831	0.0078384	168.54	152.94	165.92	220.48	285.11	275.17
JC_g17025.t1	"CG31678: Uncharacterized prote	0.66	8.38E-06	8.31E-05	476.56	495.33	572.27	799.37	831.95	820.23
JC_g24861.t1	Protein of unknown function	0.66	1.35E-07	1.97E-06	1850.29	1762.26	1952.28	2945.33	3165.20	2712.57
JC_g15177.t1	Protein of unknown function	0.66	0.000728	0.004073	446.77	481.51	536.50	831.02	903.23	603.26
JC_g23703.t1	"crb: Crumbs, isoform C (Drosophi	0.66	0.0002215	0.0014604	2596.36	3122.93	3908.53	4459.26	5537.42	5310.84
JC_g10609.t1	CG17082-RC: RE22750p (Fragm	0.66	7.00E-05	0.0005384	730.09	693.66	919.01	1135.17	1238.46	1344.11
JC_g25034.t1	Protein of unknown function	0.65	0.0003579	0.0022121	234.65	247.66	295.08	417.21	437.69	379.95
JC_g7474.t1	ko: FI21431p1 (Drosophila melan	0.65	0.0001078	0.0007856	509.97	586.10	631.88	973.48	780.72	986.39
JC_g17763.t1	Protein of unknown function	0.65	0.001235	0.0063563	2852.07	3321.26	4418.21	6900.32	5258.99	4717.10
JC_g5615.t1	CG2025-RA: CG2025 (Drosophila	0.65	6.21E-05	0.0004845	1653.42	1262.99	1670.12	2435.41	2671.82	2163.28
JC_g25395.t1	mv: Mauve (Drosophila melanoga	0.65	2.45E-05	0.0002144	1585.86	1713.91	2168.87	3017.69	2862.27	2772.90
JC_g10661.t1	Dmel\CG11370: RE13370p (Dros	0.65	7.66E-06	7.65E-05	737.35	802.19	727.26	1284.41	1245.14	1054.12
JC_g9317.t1	"CG7675: CG7675, isoform B (Dr	0.65	0.003298	0.0146839	747.52	881.13	1271.71	1864.43	1420.00	1338.82
JC_g348.t1	CG34348: LP13185p (Drosophila	0.65	0.0019635	0.0094239	1169.60	1417.90	1646.27	2834.52	2204.06	1698.66
JC_g23379.t1	CG9551: LD35051p (Drosophila r	0.65	0.000545	0.0031746	2963.94	2777.58	3304.47	6021.81	4650.90	3685.20
JC_g11269.t1	Lig4: FI02888p (Drosophila melar	0.65	1.69E-05	0.0001546	732.27	653.20	605.06	1123.86	954.46	1071.06
JC_g5287.t1	"fabp: Fatty acid bindin protein, is	0.65	5.08E-07	6.58E-06	38193.48	35854.01	44485.10	66169.80	60990.75	59530.53
JC_g16323.t1	Spase25: CG1751-PA (Drosophila	0.65	1.56E-05	0.0001438	5152.03	4156.01	3892.63	7229.34	7277.06	6307.81
JC_g10070.t1	mbt-RA: FI05259p (Drosophila me	0.64	5.16E-06	5.39E-05	714.83	618.67	720.31	1118.21	1088.11	1017.08
JC_g24503.t1	Spp: SD07518p (Drosophila mela	0.64	1.66E-06	1.95E-05	4643.51	4618.78	5412.73	8328.32	7750.39	6924.84
JC_g5305.t1	CG3823: CG3823 (Drosophila me	0.64	0.0002132	0.0014158	1048.28	1013.35	1230.98	2063.42	1624.92	1478.53
JC_g20371.t1	"PAPLA1: Phosphatidic acid phos	0.64	1.65E-06	1.94E-05	1503.77	1666.55	1613.49	2756.51	2443.51	2275.47
JC_g16553.t1	"mib1: Mind bomb 1, isoform B (D	0.64	0.0031947	0.0142963	693.04	447.97	463.98	899.99	931.07	702.75
JC_g21231.t1	"Graf: GRAF ortholog, isoform A (	0.64	0.0004346	0.0026113	932.04	731.15	1139.57	1430.26	1492.39	1474.29
JC_g23274.t1	raw: RAW (Drosophila melanogas	0.63	1.16E-06	1.40E-05	1290.19	1473.16	1566.79	2308.77	2207.40	2234.19
JC_g13098.t1	"Sec31: Sec31 ortholog, isoform I	0.63	9.94E-07	1.22E-05	4794.62	4676.01	5762.45	8205.08	7817.21	7727.07
JC_g5140.t1	coro: Coronin (Drosophila melano	0.63	2.76E-05	0.0002386	2080.57	2165.82	2700.40	3964.04	3507.11	3376.16
JC_g11214.t1	ptc: Protein patched (Drosophila r	0.63	3.62E-06	3.92E-05	1837.21	1836.26	2197.68	2808.52	3194.15	3152.85
JC_g23303.t1	"dare-RA: NADPH:adrenodoxin o	0.63	5.20E-08	8.11E-07	1880.07	1820.48	1783.38	2961.16	2925.75	2653.30
JC_g3155.t1	Pka-C3: Put. protein kinase DC2 (	0.63	6.72E-05	0.0005184	1405.69	1425.79	1515.13	2272.59	1875.51	2638.49
JC_g3229.t1	"Myo28B1: Myosin 28B1, isoform	0.63	1.28E-05	0.0001213	2631.95	3232.46	3416.73	5169.30	4803.48	4493.79
JC_g961.t1	"PIP5K59B: Phosphatidylinositol	0.63	0.0003539	0.0021898	1739.14	1670.50	2331.80	3298.09	3106.17	2564.40
JC_g1786.t1	CG6729: Protein SMG8 (Drosoph	0.63	0.0010629	0.005607	300.03	293.05	379.53	446.60	576.91	497.43
JC_g8907.t1	"ss: Spineless, isoform C (Drosopl	0.63	1.93E-05	0.0001743	6535.93	6862.55	8397.28	12594.24	10668.34	10668.25
JC_g8530.t1	Protein of unknown function	0.63	0.0001375	0.0009735	1281.47	1407.05	1279.66	2479.50	1739.63	1968.55
JC_g883.t1	didum: Myosin V (Drosophila mela	0.63	0.0035018	0.015453	213.58	285.16	335.81	476.00	394.26	436.04
JC_g23698.t1	crb: Protein crumbs (Drosophila m	0.63	1.71E-05	0.0001565	1380.27	1642.87	1821.13	2631.01	2427.91	2467.03
JC_g11348.t1	krz: Kurtz arrestin (Drosophila mel	0.63	5.98E-06	6.14E-05	2543.33	2663.12	2979.58	4677.47	4244.39	3776.22
JC_g7467.t1	Sec61alpha: DSec61alpha (Dros	0.62	3.07E-05	0.0002612	11851.42	11119.21	15105.56	20974.57	19217.27	18867.35
JC_g21817.t1	"Bx: Beadex, isoform A (Drosophi	0.62	3.95E-05	0.0003231	915.34	920.60	1119.70	1686.92	1467.89	1427.73
JC_g20978.t1	"Hipk: Homeodomain interacting p	0.62	2.90E-05	0.0002492	2988.64	3511.69	3994.97	5856.73	5406.01	5006.03
JC_g13860.t1	"CD98hc: CD98 heavy chain, isof	0.62	0.0004914	0.0028983	3480.46	2520.05	3046.15	5643.04	4329.04	4094.79
JC_g24079.t1	"Ih: I[[h]] channel, isoform B (Dros	0.62	2.43E-08	4.00E-07	2283.98	2295.08	2213.57	3710.77	3396.85	3384.63

JC_g9227.t1	twr: Signal peptidase complex cat	0.62	7.11E-08	1.08E-06	3276.32	2924.60	3184.25	4842.55	5059.64	4595.39
JC_g14138.t1	RYBP: GEO03726p1 (Drosophila	0.62	1.81E-05	0.0001643	1129.64	1031.11	1201.17	1931.14	1718.47	1554.73
JC_g12990.t1	CCHa1-R: Neuropeptide CCHamic	0.62	0.0013067	0.006657	310.20	260.49	248.38	450.00	363.07	462.50
JC_g3513.t1	"CG8468: CG8468, isoform A (Dr	0.62	0.0030223	0.0136422	1094.77	1998.08	1526.06	2548.47	2421.23	2222.55
JC_g15393.t1	CG7706: CG7706 (Drosophila me	0.62	0.0004463	0.0026666	812.18	1129.78	1183.29	1542.20	1559.21	1733.59
JC_g24279.t1	Galphao: G protein alpha o subu	0.62	2.29E-07	3.23E-06	4598.47	4414.53	5129.57	7556.09	7373.95	6860.28
JC_g22256.t1	"dsd: Distracted, isoform B (Droso	0.62	2.27E-05	0.0002009	836.88	852.52	920.00	1441.57	1414.43	1170.54
JC_g18036.t1	TBPH: GH09868p (Drosophila me	0.62	1.87E-06	2.15E-05	1195.75	1058.74	1252.84	1858.78	1755.23	1789.68
JC_g11011.t1	Protein of unknown function	0.62	0.0001835	0.0012467	9172.97	8102.85	11272.54	16827.37	13850.24	13401.99
JC_g23034.t1	CG1418-RA: PRA1 family protein	0.61	3.24E-05	0.0002723	1312.71	1641.88	1701.91	2427.49	2496.96	2244.78
JC_g23475.t1	obst-B: BcDNA.GH02976 (Drosop	0.61	7.81E-06	7.79E-05	4804.06	3760.34	4704.34	6868.66	6554.25	6999.98
JC_g16753.t1	"Nha1: Na[ ]/H[ ] hydrogen antipo	0.61	0.0003706	0.0022808	406.82	436.12	467.95	754.14	698.30	570.46
JC_g23494.t1	Protein of unknown function	0.61	0.0001389	0.0009807	1983.23	1760.29	2436.12	3424.72	3239.82	2863.92
JC_g11006.t1	"LRP1: LDL receptor protein 1, is	0.61	0.0002206	0.0014555	1537.91	1697.14	1676.08	3070.83	2355.52	2144.23
JC_g23692.t1	Protein of unknown function	0.61	0.0003069	0.001931	381.39	419.35	492.79	607.16	692.73	690.05
JC_g815.t1	ORF: ORF (Drosophila melanogas	0.61	0.0003035	0.0019134	400.28	477.57	543.46	731.53	750.65	702.75
JC_g18941.t1	Ero1L: Ero1-like protein (Drosoph	0.61	2.29E-05	0.000202	1135.45	1008.42	1081.95	1763.80	1744.09	1440.43
JC_g21767.t1	"CG8086: CG8086, isoform N (Dr	0.61	2.11E-05	0.0001885	1756.57	1588.60	1671.11	2363.05	2375.57	2951.76
JC_g23014.t1	RasGAP1: GTPase-activating pro	0.61	2.18E-05	0.000194	2440.17	2567.41	2933.88	4562.15	3934.78	3674.62
JC_g5247.t1	Gos28: Golgi SNAP receptor com	0.61	7.36E-06	7.38E-05	671.25	588.08	648.77	964.44	960.03	999.09
JC_g17654.t1	Msr-110: EN protein binding prote	0.61	4.12E-05	0.0003355	9216.56	8662.31	10359.49	12940.22	13535.06	16803.55
JC_g24281.t1	Galphao: G protein alpha o subu	0.61	3.20E-06	3.51E-05	3571.26	3394.28	3974.10	5985.63	5698.91	5055.78
JC_g23446.t1	Protein of unknown function	0.61	5.72E-07	7.34E-06	11976.37	10781.76	12627.71	18787.91	18581.33	16708.30
JC_g23496.t1	"CG42748: Uncharacterized prote	0.61	2.05E-05	0.0001842	2694.43	2506.24	3195.18	4625.46	4223.23	4000.59
JC_g839.t1	"Cdk4: Cyclin-dependent kinase 4	0.61	0.0014347	0.0072124	331.99	312.79	384.49	534.79	604.75	442.39
JC_g11154.t1	"Oatp30B: Organic anion transpo	0.60	1.01E-05	9.82E-05	3454.30	3771.20	3929.39	6379.09	5061.87	5579.66
JC_g14244.t1	exu: AT02443p (Drosophila melar	0.60	0.0011471	0.0059743	3075.09	3074.58	4201.62	5898.57	5704.48	4256.72
JC_g10626.t1	"OstDelta: Oligosaccharide transf	0.60	3.59E-06	3.89E-05	8109.44	7802.89	9798.15	13037.45	12992.68	13162.80
JC_g24560.t1	"CG1885: CG1885, isoform A (Dr	0.60	0.0003427	0.0021285	621.85	462.77	587.17	889.82	870.93	798.00
JC_g15170.t1	CG7639: LD18146p (Drosophila r	0.60	2.08E-05	0.0001864	576.08	590.05	623.93	935.04	962.26	832.93
JC_g5462.t1	"svr: Silver, isoform N (Drosophila	0.60	8.15E-05	0.000615	2450.34	3131.81	3420.71	4618.68	4637.54	4482.15
JC_g10178.t1	spri: Protein sprint (Drosophila me	0.60	0.0004732	0.0028049	3626.47	4194.50	5198.13	7569.66	6459.59	5874.95
JC_g1472.t1	p120ctn-RA: RE55335p (Drosoph	0.60	8.83E-06	8.72E-05	694.49	694.64	780.91	1059.41	1156.04	1090.11
JC_g21668.t1	CG2827-RA: Transaldolase (Dros	0.60	3.66E-07	4.90E-06	8340.45	7952.87	8851.32	13194.61	13383.59	11658.87
JC_g22257.t1	CG5634: LD07466p (Fragment) (I	0.60	3.78E-05	0.0003113	580.44	511.11	507.69	852.51	807.45	776.83
JC_g1447.t1	Fim: Fimbrin (Drosophila melanoga	0.60	1.84E-05	0.0001666	3124.49	3750.48	3736.65	5617.04	5724.53	4799.65
JC_g23278.t1	"CG6769: CG6769, isoform A (Dr	0.60	0.0002221	0.0014637	762.78	998.55	759.05	1343.20	1208.39	1288.02
JC_g21202.t1	Protein of unknown function	0.60	0.0037427	0.016352	702.48	562.42	575.25	1204.14	802.99	808.59
JC_g5574.t1	cin: Molybdenum cofactor synthes	0.60	0.0010982	0.0057507	722.10	504.21	636.85	1056.02	926.62	860.45
JC_g7486.t1	"Dmel\CG9674: CG9674, isoform	0.59	4.88E-05	0.0003905	2402.39	2658.19	3220.02	4308.88	4270.01	3993.19
JC_g5506.t1	CG45065: RE28171p (Drosophila	0.59	6.41E-05	0.0004988	2758.36	2339.48	3137.55	4488.66	4041.70	3972.02
JC_g3202.t1	Protein kish (Fragment) (Drosophi	0.59	0.0005968	0.0034366	1224.81	900.86	864.37	1590.82	1531.37	1428.78
JC_g5295.t1	AP-1-2beta: AP complex subunit	0.59	2.77E-05	0.0002393	5243.57	5681.46	6660.59	9050.80	8064.46	9516.76
JC_g14623.t1	CG5004-RD: SD11546p (Drosoph	0.59	1.14E-05	0.0001091	1258.95	1469.21	1413.79	1907.40	2198.49	2160.11
JC_g23760.t1	Protein of unknown function	0.59	0.0015767	0.0078133	285.50	221.02	260.30	358.41	409.85	399.00
JC_g20551.t1	Protein of unknown function	0.59	7.97E-05	0.0006027	14244.37	11807.93	12455.83	22541.65	18736.14	17054.38
JC_g4094.t1	Mocs1: Molybdenum cofactor bios	0.59	0.0034942	0.0154254	219.39	234.84	206.65	308.67	298.48	397.94
JC_g16458.t1	qua-RB: AT02619p (Drosophila m	0.59	0.00132	0.0067098	9629.19	10604.15	14724.05	19311.40	15441.75	18176.24
JC_g12275.t1	"CalpB: Calpain-B, isoform B (Dro	0.58	1.39E-05	0.0001307	2462.69	2632.54	2691.46	4417.43	3786.65	3529.62
JC_g4604.t1	"oys: Oysgedart, isoform A (Drosc	0.58	0.0006839	0.0038507	362.50	465.73	486.83	664.82	672.69	646.66
JC_g8080.t1	"CG9536: CG9536, isoform A (Dr	0.58	0.0017896	0.0087282	2315.95	2553.60	2992.50	4835.76	3951.48	3107.34
JC_g17523.t1	p130CAS: GH02705p (Drosophila	0.58	2.10E-06	2.38E-05	4225.80	4536.88	4236.39	6203.84	7222.49	6127.89
JC_g24874.t1	Cad88C: Cadherin 88C (Drosophi	0.58	0.0012266	0.0063239	1957.08	1637.94	1277.67	2245.46	2700.78	2417.29
JC_g10684.t1	Acyl-coenzyme A oxidase (Drosop	0.58	0.0005966	0.0034366	2552.04	1904.35	2681.53	3922.20	3644.10	3185.66
JC_g25035.t1	"GlyP: Alpha-1,4 glucan phospho	0.58	0.0001408	0.0009909	1317.07	1539.26	1544.93	2305.38	2423.46	1888.11
JC_g11740.t1	"per: Period, isoform B (Drosophila	0.58	7.17E-05	0.0005507	2241.85	1736.61	1847.96	2789.30	3105.06	2841.69
JC_g9395.t1	Galphaq: G protein alpha q subu	0.57	5.63E-05	0.0004439	686.50	637.41	651.75	1051.50	1021.28	886.90
JC_g5003.t1	"CG6972-RA: CG6972, isoform A	0.57	3.22E-05	0.0002712	1144.90	968.95	1115.73	1487.93	1682.83	1659.51
JC_g7543.t1	"vn: Vein, isoform C (Drosophila m	0.57	0.0007499	0.0041792	3352.60	3499.85	3731.68	6410.75	5243.40	4212.27
JC_g16764.t1	BG:DS01368.1: RE25285p (Dros	0.57	1.66E-05	0.0001525	3094.71	3009.46	3319.37	5265.41	4599.67	4217.56
JC_g18626.t1	"Dp1: Dodeca-satellite-binding pro	0.57	3.82E-06	4.12E-05	20295.03	18550.11	22103.96	32536.54	30078.28	28401.04
JC_g25428.t1	Rtnl1: Reticulon-like protein (Dros	0.57	4.74E-06	5.03E-05	6414.62	5469.32	6752.00	9229.45	9338.56	9241.58
JC_g11318.t1	"PRL-1: PRL-1 phosphatase, isof	0.57	7.58E-08	1.15E-06	22849.25	20879.73	22255.96	33073.59	34083.23	31182.41
JC_g23294.t1	"C3G: C3G ortholog, isoform G (D	0.57	9.06E-05	0.0006764	1737.69	1870.80	2110.25	3168.06	2832.19	2540.06
JC_g5507.t1	Protein of unknown function	0.57	0.0003293	0.0020542	1088.96	876.20	1163.42	1702.75	1481.25	1490.17
JC_g12036.t1	"Mical: Molecule interacting with C	0.57	6.16E-05	0.0004815	2505.55	3039.06	3122.65	4606.24	4374.70	3926.51
JC_g5479.t1	Atx2: Ataxin-2 homolog (Drosophi	0.57	0.0017209	0.0084219	834.70	924.55	1195.21	1662.05	1437.81	1313.42
JC_g20313.t1	CG30105: Uncharacterized protei	0.57	0.0011752	0.0060926	250.63	285.16	290.11	433.04	375.32	422.28
JC_g5134.t1	CG4572-RC: Carboxypeptidase (I	0.57	4.21E-07	5.56E-06	1484.88	1532.36	1510.16	2322.34	2178.44	2219.38
JC_g17495.t1	Pdi: Protein disulfide-isomerase (D	0.56	5.41E-06	5.61E-05	33886.32	31749.30	38227.88	54400.93	51466.20	48265.36
JC_g4367.t1	"Dmel\CG7368: CG7368, isoform	0.56	0.0002254	0.0014802	2229.50	2380.93	2969.65	3985.52	3840.11	3439.66
JC_g9115.t1	CG6015: CG6015 (Drosophila me	0.56	0.0008965	0.0048637	1787.81	1229.44	1474.39	2359.65	2295.38	2033.11
JC_g3261.t1	CG1105: CG1105 (Drosophila me	0.56	0.0003871	0.0023646	1230.62	1112.02	1386.96	2058.90	1894.44	1591.77
JC_g956.t1	"ced-6: Ced-6, isoform F (Drosoph	0.56	5.69E-06	5.86E-05	4069.61	3937.95	4224.47	6579.22	6018.55	5463.24

JC_g18857.t1	fng: Fringe glycosyltransferase (D	0.55	1.35E-05	0.0001269	3388.92	3309.42	3442.57	5614.78	4724.41	4619.73
JC_g23690.t1	"Sec16: Sec16 ortholog, isoform I	0.55	0.0008655	0.0047111	2703.87	2802.25	3901.57	4551.97	4753.36	4609.15
JC_g16387.t1	"mxt: Mextli, isoform G (Drosophila	0.55	0.0002116	0.0014077	8895.47	8864.58	11177.16	16040.44	13490.51	13211.48
JC_g22927.t1	DNApol-alpha180: DNA polymera	0.55	0.0001858	0.0012599	825.98	891.00	756.07	1304.76	1264.07	1082.70
JC_g10708.t1	Cog3: Conserved oligomeric Golg	0.55	0.0001488	0.0010383	1241.52	987.69	1230.98	1795.46	1642.74	1670.09
JC_g10747.t1	"CG8771: CG8771, isoform C (Dr	0.55	1.76E-06	2.04E-05	8921.62	8669.22	9430.54	14446.24	12749.89	12597.64
JC_g17726.t1	Pdk1: FI19402p1 (Drosophila mel	0.55	5.15E-05	0.0004087	17011.45	16672.40	18014.60	28269.49	26228.15	21678.35
JC_g5609.t1	Protein of unknown function	0.55	3.12E-05	0.0002647	3674.42	3988.27	4548.36	6398.31	5937.25	5648.46
JC_g23705.t1	"crb: Crumbs, isoform D (Drosophi	0.55	0.0025935	0.0119307	1451.46	1672.47	1917.50	1948.10	2758.69	2745.38
JC_g13584.t1	Stt3B: Oligosaccharyl transferase	0.55	0.0009798	0.0052409	5876.31	6302.10	7374.94	10321.65	10815.35	7727.07
JC_g17452.t1	"c62E-11: Uncharacterized protei	0.55	3.44E-05	0.000288	9005.89	10204.53	11246.71	16158.03	14260.09	14391.55
JC_g1773.t1	CG3534: CG3534 (Drosophila me	0.55	0.001239	0.0063688	1652.69	1826.40	2332.80	3227.99	2679.61	2666.00
JC_g2342.t1	CG33635: Vesicle transport prote	0.55	0.0014329	0.0072068	1878.62	1425.79	1528.04	2564.30	1966.83	2603.56
JC_g19737.t1	flil: Protein flightless-1 (Drosophila	0.55	0.0001344	0.0009553	1035.93	1079.46	1227.00	1818.08	1540.28	1557.90
JC_g302.t1	"Dysb: Dysbindin, isoform B (Dros	0.55	0.0010777	0.0056669	876.83	699.58	799.79	1345.47	1139.34	1020.26
JC_g3.t1	CG43313: Hexosyltransferase (Dr	0.55	0.0012275	0.0063239	613.13	557.49	783.89	954.26	966.71	958.87
JC_g1342.t1	"Mitf: Mitf, isoform D (Drosophila m	0.55	0.002638	0.0121041	199.05	203.26	185.79	282.66	285.11	299.52
JC_g17581.t1	scny: Ubiquitin carboxyl-terminal h	0.55	4.92E-06	5.20E-05	1606.20	1585.64	1620.44	2320.08	2532.60	2204.56
JC_g17310.t1	Spt-I: RE58623p (Drosophila mela	0.55	8.39E-05	0.0006312	2030.45	1668.52	1859.88	2863.92	2842.22	2458.57
JC_g1795.t1	put: Serine/threonine-protein kina	0.55	0.0019095	0.0092032	956.02	1118.93	1420.74	1580.64	1836.53	1727.24
JC_g19880.t1	AnxB10: Annexin B10 (Drosophila	0.55	6.43E-06	6.54E-05	6200.31	5184.16	5951.22	8591.76	8641.37	8165.23
JC_g9396.t1	Galphaq: G protein alpha q subu	0.55	0.0018906	0.0091354	619.67	440.07	555.38	844.59	762.90	770.48
JC_g22452.t1	"CG5447: CG5447, isoform A (Dr	0.54	0.0019106	0.009205	1446.38	1094.26	1374.05	2121.09	2050.36	1584.36
JC_g18194.t1	"cta: Concertina, isoform B (Drosc	0.54	3.64E-05	0.0003014	1258.95	1329.10	1306.49	2050.99	1943.44	1702.90
JC_g13488.t1	sec10-RA: FI22538p1 (Drosophila	0.54	0.0001731	0.0011849	733.72	639.39	671.62	1083.16	927.73	983.21
JC_g4806.t1	Chd64: Transgelin (Drosophila me	0.54	3.23E-05	0.0002721	2550.59	2631.55	2344.72	3269.82	3856.82	3876.77
JC_g7735.t1	"ca: Claret, isoform A (Drosophila	0.54	0.0008186	0.0044962	459.85	565.38	558.36	840.07	718.35	757.78
JC_g15978.t1	fbl: Fumble (Drosophila melanoga	0.54	0.0007237	0.0040547	1309.80	1310.35	1726.75	2299.73	2049.25	2008.76
JC_g15155.t1	CG8924: CG8924 (Drosophila me	0.54	0.0034165	0.0151176	455.49	467.70	589.16	845.72	730.60	639.25
JC_g3284.t1	"klar: Klarsicht, isoform E (Drosopl	0.54	7.31E-06	7.34E-05	2201.16	2255.61	2308.95	3463.16	3410.22	2994.10
JC_g4613.t1	Dmel\CG13671: GH24192p (Dros	0.54	1.21E-06	1.46E-05	2062.41	2004.99	2022.82	3032.39	3043.80	2800.42
JC_g22097.t1	Ptp10D: Tyrosine-protein phospha	0.54	0.0003591	0.002217	3406.36	3566.95	4484.77	5333.25	6112.11	5291.79
JC_g5368.t1	Ald: Fructose-bisphosphate aldola	0.54	0.0002653	0.0017087	3656.99	3937.95	4911.99	5995.80	5844.81	6420.00
JC_g12683.t1	"CG9864: CG9864, isoform A (Dr	0.54	1.02E-05	9.89E-05	1681.02	1826.40	1812.19	2454.63	2782.08	2511.48
JC_g3644.t1	EG:22E5.9: CG4025 (Drosophila	0.54	0.0032363	0.0144598	223.75	199.32	202.68	323.36	296.25	297.40
JC_g5390.t1	Pp2C1: LD34192p (Drosophila me	0.54	0.0004079	0.0024706	1697.73	1453.42	1736.68	2709.02	2322.11	2102.96
JC_g8435.t1	mas: LP06006p (Drosophila mela	0.54	0.0006001	0.0034492	3263.97	2803.24	3948.27	5142.17	4554.01	4923.48
JC_g23107.t1	TMS1: Membrane protein TMS1d	0.54	0.0004111	0.0024848	1564.79	1619.19	2031.76	2603.87	2325.45	2677.65
JC_g23238.t1	CG17337: RE11562p (Drosophila	0.54	9.95E-07	1.22E-05	9401.81	8215.33	9091.75	13097.38	12930.31	12833.65
JC_g13499.t1	"sip3: Septin interacting protein 3	0.54	0.0025864	0.0119047	948.03	680.83	946.83	1162.30	1211.73	1390.68
JC_g15380.t1	"Pex19: Peroxin 19, isoform A (Dr	0.54	0.0009272	0.0050089	1333.78	1601.43	1914.52	2374.35	2439.05	2257.48
JC_g9702.t1	"DCTN4-p62: Dynactin 4, p62 sub	0.53	0.0006439	0.0036636	921.15	956.12	1041.21	1621.34	1415.54	1215.00
JC_g20361.t1	Invadolysin: Leishmanolysin-like p	0.53	9.78E-06	9.57E-05	1260.40	1232.40	1367.09	1859.91	1937.88	1808.73
JC_g1000.t1	"Np: Notopleural, isoform A (Drosc	0.53	0.0004394	0.0026378	25450.70	25726.44	33704.36	44184.43	41518.43	37822.55
JC_g16482.t1	CG7382: CG7382 (Drosophila me	0.53	0.0033341	0.0148332	318.91	301.93	356.68	543.84	425.44	454.04
JC_g1974.t1	eIF4B: Eukaryotic initiation factor	0.53	0.0002188	0.0014454	9767.22	8533.05	11535.82	14508.42	14889.35	13841.21
JC_g23329.t1	Ctr1A-RA: MIP12854p (Drosophila	0.53	0.0004209	0.0025315	1038.11	1018.28	1178.32	1751.37	1552.53	1383.27
JC_g24478.t1	"CG1718: CG1718, isoform D (Dr	0.53	0.0020293	0.0096951	616.76	834.75	725.27	1111.42	928.84	1116.57
JC_g15152.t1	hoe1: RE09889p (Drosophila mel	0.53	0.00074	0.0041341	401.00	414.42	427.22	580.02	663.78	556.70
JC_g12684.t1	"RhoGAP92B: Rho GTPase activ	0.53	5.96E-06	6.13E-05	3989.70	3492.95	3891.64	5389.78	5722.30	5316.13
JC_g1547.t1	"dop: Drop out, isoform A (Drosop	0.52	0.0031555	0.0141431	794.74	974.87	1124.67	1517.32	1463.43	1209.70
JC_g1969.t1	"Doa: Darkener of apricot, isoform	0.52	5.27E-06	5.48E-05	2991.55	3287.71	3450.51	4764.53	4627.51	4628.20
JC_g5259.t1	"AsnRS: Asparaginyl-tRNA synthe	0.52	7.22E-05	0.0005542	4698.00	4136.28	5223.96	6965.90	6859.41	6445.40
JC_g22913.t1	"CG2016-RB: CG2016, isoform B	0.52	6.12E-06	6.26E-05	33190.37	33833.23	31553.38	51573.19	43780.40	46649.25
JC_g2293.t1	"CG42342: Uncharacterized prote	0.52	0.000963	0.0051703	605.87	760.75	722.29	1014.19	914.37	1084.82
JC_g19640.t1	CG14767: SD02746p (Drosophila	0.52	0.0005799	0.003351	2939.97	2479.60	3444.55	4068.06	4341.29	4382.66
JC_g14618.t1	Spred: SD10629p (Drosophila me	0.52	5.80E-05	0.0004558	3776.85	3600.50	4290.04	5939.27	5694.46	5160.55
JC_g21845.t1	"CG8034: CG8034, isoform A (Dr	0.52	0.0024244	0.0113104	2687.16	2178.65	2348.69	2851.48	4141.93	3422.73
JC_g19055.t1	PGAP3: Post-GPI attachment to p	0.52	0.0019254	0.0092606	398.10	399.62	339.79	577.76	572.45	492.14
JC_g2843.t1	epsilonCOP: BcDNA.LD29885 (Dr	0.52	3.83E-05	0.0003148	4165.50	3514.65	3639.28	5420.31	5695.57	5124.57
JC_g15929.t1	CG5214: CG5214 (Drosophila me	0.51	0.0002922	0.0018583	1694.82	1478.09	1940.36	2455.76	2410.09	2474.44
JC_g13877.t1	ZnT86D: LD23375p (Drosophila n	0.51	0.000404	0.0024524	1489.96	1201.81	1466.44	2136.92	1971.29	1854.24
JC_g23734.t1	"Dmel\CG6479: CG6479, isoform	0.51	0.002239	0.0105471	922.60	742.00	737.20	991.57	1220.64	1238.28
JC_g11525.t1	CG5284-RB: Chloride channel pro	0.51	7.93E-05	0.0006015	3136.12	3325.21	3482.31	4712.52	5245.63	4275.77
JC_g16989.t1	sky: LD10117p (Drosophila melan	0.51	0.0002107	0.0014025	2522.26	2571.36	3157.42	4108.76	3958.17	3746.59
JC_g15167.t1	CG6475: UDP-glucuronosyltransfe	0.51	0.0001798	0.0012258	1019.22	1078.47	1117.72	1650.74	1578.14	1373.75
JC_g12202.t1	"CG18659: Uncharacterized prote	0.51	0.0002172	0.0014374	708.30	692.67	776.94	1077.50	1076.97	962.05
JC_g10259.t1	"mnb: Minibrain, isoform H (Drosop	0.51	0.0031209	0.01401	1497.95	2017.82	1868.82	2944.20	2590.52	2184.45
JC_g17408.t1	tud: Maternal protein tudor (Drosc	0.51	7.35E-05	0.0005622	13137.98	12001.33	13806.03	20584.50	18091.30	16983.47
JC_g24935.t1	"CG9664: CG9664, isoform D (Dr	0.51	9.10E-05	0.0006793	2131.43	2059.26	2148.00	3247.21	3150.72	2660.71
JC_g15941.t1	Protein of unknown function	0.51	0.001363	0.0068916	1281.47	1089.33	1244.89	1977.50	1725.16	1474.29
JC_g24986.t1	"Tango1: Transport and golgi org	0.51	4.16E-05	0.000338	2775.07	2863.43	2998.46	4537.27	3964.85	3830.20
JC_g16440.t1	CG31935: Rab3 GTPase-activatin	0.51	0.0009082	0.0049248	547.75	517.03	530.54	819.72	795.20	667.82
JC_g23300.t1	"CG9596: CG9596, isoform B (Dr	0.51	0.0001278	0.0009147	1345.40	1331.07	1311.45	2112.04	1852.12	1730.42

JC_g14946.t1	BcDNA.LD23634: BcDNA.LD2362	0.51	0.0010427	0.0055183	2508.46	3411.05	3389.91	4437.78	4257.76	4607.03
JC_g16998.t1	"Dlic: Dynein light intermediate ch	0.51	0.0003246	0.0020296	1300.36	1215.62	1321.39	2018.20	1852.12	1603.41
JC_g4327.t1	wash: Washout (Drosophila melan	0.50	0.0005719	0.0033081	1919.30	2450.00	2282.13	2854.88	3265.43	3352.88
JC_g5178.t1	Jon65Aiii: GH01508p (Drosophila	0.50	0.001104	0.0057759	1589.49	2059.26	2131.11	2911.41	2606.11	2706.22
JC_g1772.t1	Sf3a1: GH03554p (Drosophila me	0.50	0.0019281	0.0092696	2354.45	1914.21	2432.15	2723.72	3604.00	3214.23
JC_g22926.t1	CG7065: Uncharacterized protein	0.50	6.54E-05	0.0005067	2280.35	2078.99	1972.15	2791.56	3077.21	3116.86
JC_g5158.t1	CG5745: CG5745 (Drosophila me	0.50	0.0002065	0.0013783	2387.14	2700.62	2943.82	3973.08	3912.50	3511.63
JC_g23415.t1	CG11880-RA: FI05260p (Drosopl	0.50	0.0006141	0.0035184	778.76	763.71	653.74	1084.29	966.71	1067.88
JC_g11990.t1	roq: LD12033p (Drosophila melan	0.50	0.0021493	0.0101876	655.26	735.10	846.48	1160.04	954.46	1061.53
JC_g19267.t1	"AP-2mu: Adaptor protein comple	0.50	0.0001015	0.0007485	4932.64	4397.76	5064.99	7392.15	6809.30	6206.21
JC_g11315.t1	"Khc-73: Kinesin heavy chain 73,	0.50	2.51E-05	0.0002192	3690.40	4335.59	4190.69	5862.39	5672.19	5749.00
JC_g4316.t1	Protein of unknown function	0.50	1.43E-05	0.0001342	2181.55	2045.45	2080.44	2805.13	3105.06	3012.09
JC_g807.t1	rhea: SD07967p (Drosophila mela	0.49	0.0002298	0.001506	3322.09	4206.34	4085.38	5585.38	5392.64	5448.43
JC_g1820.t1	Protein of unknown function	0.49	0.0027666	0.0126121	283.32	285.16	312.96	399.12	436.58	410.64
JC_g21664.t1	eas: Ethanolamine kinase (Droso	0.49	0.0011513	0.00599	414.08	462.77	413.31	639.94	604.75	577.86
JC_g23413.t1	"shi: Shibire, isoform L (Drosophila	0.49	7.97E-05	0.0006027	2427.09	2450.98	2667.62	3460.90	3872.41	3308.43
JC_g9439.t1	mub: LD32520p (Drosophila mela	0.49	0.0015416	0.0076726	740.99	669.97	737.20	1161.17	950.00	923.95
JC_g22541.t1	"CG7920: CG7920, isoform A (Dr	0.49	0.0001026	0.0007531	3250.90	2923.62	3553.84	4386.90	4571.83	4743.56
JC_g22169.t1	knk: Knickkopf (Drosophila melan	0.49	9.76E-05	0.0007235	2579.65	2513.15	2946.80	3638.41	3999.37	3678.85
JC_g4371.t1	"Act5C: Actin 5C, isoform E (Dros	0.49	0.0030612	0.0137924	120055.75	98875.05	150414.79	173639.76	169968.42	177089.78
JC_g11127.t1	"yki: Yorkie, isoform G (Drosophila	0.49	0.0001328	0.0009453	5111.35	4730.28	5237.87	7396.67	7533.21	6272.89
JC_g12940.t1	TER94: LP12034p (Drosophila m	0.49	0.0037556	0.0163903	293.49	277.26	317.93	444.34	398.71	408.53
JC_g25014.t1	GABPI: Palmitoyltransferase (Dros	0.48	0.0009839	0.0052554	1195.75	1070.58	1075.99	1786.42	1486.82	1427.73
JC_g4459.t1	GATAd: GATA factor d (Drosophil	0.48	0.0003887	0.0023704	612.40	607.81	593.13	793.71	892.09	858.33
JC_g21864.t1	"Edem1: alpha-1,2-Mannosidase	0.48	0.0002413	0.0015731	2873.14	2533.87	2628.87	4143.81	3705.35	3422.73
JC_g10033.t1	Protein of unknown function	0.48	2.50E-05	0.0002181	3821.16	3682.39	3950.26	5704.10	5353.66	4990.16
JC_g8503.t1	Fbxl7: F-box and leucine-rich repe	0.48	6.51E-05	0.0005048	1186.30	1261.01	1257.80	1802.25	1754.11	1634.10
JC_g9113.t1	Protein of unknown function	0.48	0.0014111	0.0071129	628.39	642.35	630.89	966.70	926.62	773.66
JC_g5456.t1	CG2691-RA: LD23114p (Fragmer	0.48	0.0004159	0.0025045	1536.46	1818.50	1906.58	2528.12	2335.47	2504.08
JC_g23936.t1	CG6089: AT01533p (Drosophila r	0.48	3.54E-05	0.0002948	3175.34	2985.78	3000.45	4579.11	4212.10	4012.24
JC_g11404.t1	CG11210: RE44586p (Drosophila	0.48	1.08E-05	0.0001037	3362.04	3068.66	3183.26	4444.56	4372.47	4600.68
JC_g3931.t1	Ext2: Exostosin-2 (Drosophila mel	0.48	0.0005284	0.0030894	696.67	689.71	617.97	973.48	896.55	929.24
JC_g11769.t1	CG5880-RA: Palmitoyltransferase	0.47	0.000194	0.0013059	855.04	851.53	952.79	1241.45	1226.21	1239.34
JC_g7484.t1	Tet: DNA N6-methyl adenine dem	0.47	0.0012782	0.0065377	966.91	1232.40	1193.22	1637.17	1503.52	1590.71
JC_g24257.t1	Src42A-RB: Tyrosine-protein kinas	0.47	0.0030114	0.0136091	1156.52	1001.51	1344.24	1707.27	1714.02	1467.94
JC_g12125.t1	RN-tre: LD38355p (Drosophila me	0.47	0.0010214	0.0054333	1431.12	1323.18	1368.08	2122.22	1976.86	1649.98
JC_g12931.t1	"CG31688: Uncharacterized prote	0.47	0.0015676	0.0077815	3548.74	3521.56	4081.40	5735.76	5434.96	4369.96
JC_g23772.t1	"Eps-15: Epidermal growth factor	0.47	0.0003458	0.002144	1205.19	1251.15	1410.81	1854.26	1844.32	1681.73
JC_g11826.t1	"fax: Failed axon connections, isc	0.47	2.44E-05	0.0002138	42840.63	42382.07	46810.95	57487.59	64656.00	61296.93
JC_g20553.t1	Protein of unknown function	0.47	0.0016321	0.0080322	1347.58	1293.57	1337.29	2127.87	1820.94	1590.71
JC_g10551.t1	"CG7461: CG7461, isoform B (Dr	0.47	0.0001325	0.0009437	5125.88	4419.47	5301.45	6623.31	7046.52	6947.06
JC_g5330.t1	Bet3: Blocked early in transport 3	0.47	0.00288	0.0130617	778.04	973.88	999.49	1244.84	1195.02	1384.33
JC_g16093.t1	CG3061: CG3061 (Drosophila me	0.47	0.0008061	0.00444	1373.73	1225.49	1493.27	1941.32	2006.93	1738.88
JC_g18642.t1	ine: Transporter (Drosophila melar	0.47	0.0018237	0.0088722	1159.43	1174.18	1140.57	1865.56	1562.55	1402.32
JC_g18828.t1	crol: CROL ALPHA (Drosophila m	0.47	0.0008859	0.0048129	3850.22	3288.70	3403.82	5265.41	5140.94	4244.02
JC_g17341.t1	bc10: Bc10 (Drosophila melanoga	0.47	0.0003886	0.0023704	851.41	855.48	753.09	1163.43	1143.79	1109.16
JC_g10032.t1	"Dip-C: Dipeptidase C, isoform A (	0.47	0.0005117	0.0030036	2161.94	1844.16	2104.29	3105.88	2711.91	2664.95
JC_g5138.t1	Dmel\CG12025: RH22148p (Dros	0.47	0.0022005	0.0104	1945.45	1929.01	2116.21	3070.83	2953.59	2293.46
JC_g17725.t1	Protein of unknown function	0.47	6.66E-05	0.0005145	10820.58	10122.64	11323.21	15976.00	14855.93	13857.08
JC_g17470.t1	Nhe2: Sodium/hydrogen exchang	0.46	0.0010503	0.0055497	1201.56	1093.27	1101.82	1707.27	1621.58	1380.10
JC_g5321.t1	CG4078: Regulator of telomere e	0.46	0.0006307	0.0036046	1009.05	1163.33	1074.00	1370.34	1552.53	1571.66
JC_g21944.t1	Tsp74F: Tetraspanin (Drosophila	0.46	2.26E-05	0.0002	2002.12	1861.92	1952.28	2712.41	2645.09	2687.17
JC_g1436.t1	Fim: Fimbrin (Drosophila melanog	0.46	0.0005981	0.0034403	2621.06	2479.60	2449.04	3511.78	3883.55	3059.71
JC_g12553.t1	Dmel\CG33290: HDC11369 (Dros	0.46	0.0035796	0.0157477	2773.61	3272.91	3506.15	5158.00	3937.01	4146.65
JC_g16273.t1	"Patronin: Patronin, isoform L (Dr	0.46	0.0002342	0.00153	3514.60	3701.14	4284.08	5421.44	5313.57	5160.55
JC_g21549.t1	eIF5B: IF2 protein (Drosophila me	0.46	3.73E-05	0.0003082	7211.54	6357.36	7237.83	9661.35	9652.63	9408.80
JC_g4938.t1	"CG3409-RA: CG3409, isoform A	0.46	0.002764	0.0126055	2968.30	2806.20	3624.38	4893.43	4019.42	4085.26
JC_g20576.t1	"Kr-h2: Kruppel homolog 2, isofor	0.46	0.0001377	0.0009745	4982.77	4191.54	4897.09	6580.35	6391.65	6448.58
JC_g2425.t1	"Glut1: Glucose transporter 1, iso	0.46	0.000182	0.00124	3352.60	3138.72	3197.17	4694.43	4675.40	4001.65
JC_g11598.t1	whd: LD31742p (Drosophila mela	0.46	0.0001134	0.0008239	7379.35	7320.39	8547.30	11076.92	10693.96	10296.77
JC_g3336.t1	"cib: Ciboulot, isoform A (Drosoph	0.46	0.0002921	0.0018583	27861.08	24778.21	29491.81	41267.37	35820.63	36222.31
JC_g1391.t1	PMCA: Calcium-transporting ATPa	0.46	0.0001722	0.0011794	4433.57	4569.44	5262.70	6814.39	6356.01	6488.79
JC_g19073.t1	CG40191: LD12604p (Drosophila	0.46	0.0008203	0.0045038	2868.05	2268.44	2665.63	3765.04	3392.40	3605.83
JC_g17061.t1	fwe: Calcium channel flower (Dros	0.46	0.0023473	0.0109894	2026.82	1795.81	2400.36	2833.39	3066.08	2686.11
JC_g1460.t1	BcDNA:LD05303: Cation-transpor	0.45	0.0022602	0.0106251	427.88	445.99	395.42	572.11	598.07	575.75
JC_g15486.t1	eRF1-RC: LD01551p (Drosophila	0.45	0.0021196	0.0100788	13920.37	12419.69	11542.78	16950.61	19945.64	15188.50
JC_g9728.t1	Nrx-IV: FI12817p (Drosophila mel	0.45	0.0015099	0.0075345	1941.09	2530.91	2352.67	2987.16	3177.45	3199.42
JC_g4046.t1	Protein of unknown function	0.45	0.0014705	0.0073634	1672.30	1556.04	1344.24	2223.98	2119.41	1933.62
JC_g15424.t1	Fas3: Fasciclin-3 (Drosophila mela	0.45	0.0021977	0.0103911	7039.37	7122.06	8083.32	11522.39	10352.04	8640.44
JC_g8364.t1	"CycJ: Cyclin J, isoform A (Drosop	0.45	0.0025129	0.0116315	846.32	827.85	881.26	1269.71	1230.66	1005.44
JC_g23185.t1	g: AP-3 complex subunit delta (Dr	0.45	0.0001893	0.0012799	3661.34	3088.40	3490.26	4744.18	4719.95	4554.12
JC_g18788.t1	CG10674: Protein Asterix (Drosop	0.45	0.0010714	0.0056412	1155.79	1098.21	1239.92	1755.89	1564.78	1465.83
JC_g18849.t1	"Cen: Centrocortin, isoform A (Dro	0.45	0.0025141	0.0116326	4077.60	3466.31	4265.20	6152.96	4964.97	5048.37
JC_g2110.t1	VhaM8.9: LD30634p (Drosophila	0.45	9.80E-05	0.0007263	4612.28	4108.65	4039.67	5991.28	5726.76	5720.43

JC_g22827.t1	Nmda1: GH12715p (Drosophila m	0.44	0.0010407	0.0055128	995.97	992.63	877.28	1360.16	1345.38	1209.70
JC_g4699.t1	Spase12-RA: GM01169p (Fragme	0.44	0.0004056	0.0024591	3172.44	2724.30	2735.18	4157.38	3771.06	3853.48
JC_g5226.t1	Protein of unknown function	0.44	0.0010264	0.0054521	1851.74	2067.15	2181.78	2975.85	2836.65	2511.48
JC_g7873.t1	CG13220: GEO09659p1 (Drosop	0.44	0.0033614	0.0149314	1436.21	1151.49	1115.73	1750.24	1729.61	1582.25
JC_g829.t1	"ergic53: Ergic53, isoform A (Dros	0.44	0.001829	0.0088873	11486.01	10746.24	13706.68	17890.18	16032.03	15094.30
JC_g817.t1	"rhea: Rhea, isoform H (Drosophil	0.44	0.0013111	0.0066731	2630.50	2925.59	3139.54	4388.03	3822.29	3637.58
JC_g12231.t1	Egfr: Receptor protein-tyrosine kir	0.44	0.0011264	0.0058851	8049.14	8666.26	8882.12	13100.77	11583.82	10178.23
JC_g3146.t1	"Cbp80: Cap binding protein 80, i	0.44	0.0009268	0.0050089	1378.09	1132.74	1225.02	1667.70	1727.38	1694.43
JC_g1470.t1	lgs: Protein BCL9 homolog (Drosc	0.44	0.0001405	0.0009904	4905.76	4941.43	5401.80	7057.48	7208.01	6440.11
JC_g1449.t1	Dyrk3: Putative dual specificity tyr	0.44	0.0030948	0.0139128	828.16	898.89	953.78	1366.95	1156.04	1121.86
JC_g24934.t1	CG5853: SD06390p (Drosophila r	0.44	0.0016644	0.008177	585.52	646.29	586.18	859.29	826.38	784.24
JC_g5482.t1	Vps45: SD10846p (Drosophila me	0.44	0.0011438	0.005965	1747.86	1661.62	1885.71	2633.27	2385.59	2173.87
JC_g24558.t1	CG17321: RH30783p (Drosophila	0.44	0.0009908	0.0052849	966.91	1062.68	1068.04	1295.72	1416.65	1488.05
JC_g7760.t1	"CG13643: Uncharacterized prote	0.43	0.0003977	0.002419	2168.47	1983.28	2369.56	2958.89	2930.20	2952.82
JC_g3246.t1	"Dhc64C: Dynein heavy chain, cy	0.43	0.0021958	0.0103863	9796.27	12197.68	13192.03	16231.52	15674.52	15833.04
JC_g1779.t1	"AP-1sigma: Adaptor protein com	0.43	0.0001825	0.0012421	4180.03	4242.84	4637.78	5692.79	6295.87	5696.08
JC_g21794.t1	"Drp1: Dynamin related protein 1,	0.43	0.003032	0.0136788	3009.71	2412.50	2746.10	3852.10	3974.87	3253.39
JC_g20555.t1	"EG:65F1.1: CG4293, isoform A (	0.43	0.001896	0.0091537	1941.09	1618.20	1721.78	2612.92	2354.41	2191.86
JC_g21766.t1	"Pvr: PDGF-and VEGF-receptor re	0.43	0.0009768	0.0052313	1864.82	1876.72	1555.86	2343.82	2434.60	2395.06
JC_g10649.t1	"X11Lbeta: X11Lbeta, isoform E	0.43	0.0006911	0.0038854	1205.19	1294.56	1414.78	1792.07	1789.75	1710.31
JC_g16278.t1	mop: Myopic (Drosophila melanog	0.43	2.24E-05	0.0001984	3755.06	3904.40	3780.36	5093.55	5256.77	5097.05
JC_g17196.t1	Protein of unknown function	0.43	0.0024506	0.0114078	590.61	589.06	541.47	829.89	736.17	763.08
JC_g17496.t1	"Dmel\CG3529: CG3529, isoform	0.43	0.0002995	0.001893	1237.16	1225.49	1283.63	1671.09	1768.59	1616.11
JC_g25097.t1	Ufd4: CG5604 (Drosophila melan	0.43	0.000192	0.0012938	7573.32	8268.61	8850.33	11093.88	11456.86	10758.21
JC_g12181.t1	"CG4928: CG4928, isoform C (Dr	0.43	0.0018747	0.0090702	1922.21	1802.72	1754.57	2262.42	2337.70	2785.60
JC_g5315.t1	Chc: Clathrin heavy chain (Drosop	0.42	0.0002289	0.0015016	11749.72	12179.92	13762.32	16456.52	17347.33	16918.91
JC_g1956.t1	beta-PheRS: Phenylalanine--tRN/	0.42	0.0005608	0.0032472	1642.52	1675.43	1834.05	2448.97	2182.89	2300.87
JC_g18306.t1	"Syx1A: Syntaxin 1A, isoform B (D	0.42	0.0001294	0.0009239	2599.99	2765.74	2682.52	3802.36	3520.47	3497.87
JC_g3300.t1	cathD: CathD (Drosophila melano	0.42	0.0007856	0.0043488	5340.19	5675.54	5534.93	6584.87	8119.03	7548.21
JC_g5212.t1	AMPKalpha: Non-specific serine/t	0.42	0.0004523	0.0026972	1641.07	1670.50	1586.66	2217.19	2324.34	2037.34
JC_g9455.t1	Fas1: FI05280p (Drosophila mela	0.42	0.0012669	0.006491	743.89	820.94	839.53	1068.46	1069.17	1086.93
JC_g8533.t1	"osa: Osa, isoform E (Drosophila r	0.42	0.0007256	0.0040638	3735.44	3564.98	4158.90	4753.23	5358.12	5260.04
JC_g2567.t1	Ell: AT31092p (Fragment) (Drosop	0.42	0.0037572	0.0163903	2466.32	2116.49	2748.09	3265.30	3508.22	3059.71
JC_g22951.t1	Karybeta3: FI07923p (Drosophila	0.42	0.0022521	0.0106004	15700.19	14563.81	18452.75	20685.13	23518.46	21023.23
JC_g23309.t1	tyn: RE15579p (Drosophila melan	0.41	0.0001917	0.001293	62080.12	63285.48	70170.72	90295.48	83100.35	87462.72
JC_g7514.t1	CG3098: LP04564p (Drosophila r	0.41	0.0020289	0.0096951	5969.30	5046.02	6328.76	8216.39	7575.54	7364.06
JC_g20894.t1	"CG11168: Uncharacterized prote	0.41	0.0002106	0.0014025	2772.16	2621.68	2664.64	3598.84	3742.11	3398.39
JC_g12149.t1	NUCB1: IP03868p (Drosophila me	0.41	0.0001437	0.0010094	6345.60	5932.09	5940.29	7648.81	8283.86	8320.81
JC_g18586.t1	BI-1: Bax inhibitor 1 (Drosophila m	0.41	0.0004022	0.0024439	7639.42	6853.67	7544.83	10263.98	9913.24	9128.34
JC_g9727.t1	Nrx-IV: FI12817p (Drosophila mel	0.41	0.0002696	0.0017326	1726.79	1849.09	1849.94	2445.58	2346.61	2419.41
JC_g3244.t1	"Dhc64C: Dynein heavy chain 64	0.41	0.003594	0.015787	8917.26	11277.09	11579.54	13748.63	13760.03	14750.34
JC_g19071.t1	Protein of unknown function	0.41	0.0021139	0.0100575	3184.06	3860.99	3300.49	4453.61	4921.54	4377.37
JC_g22542.t1	"Vha55: Vacuolar H[ ]-ATPase 55	0.41	0.0024886	0.0115473	8738.55	7121.07	9113.61	10758.08	11077.08	11355.12
JC_g11659.t1	Tudor-SN: LD20211p (Drosophila	0.40	0.0014748	0.0073787	23929.50	21418.47	26607.61	33273.72	32165.40	30109.23
JC_g11764.t1	magu: LD30894p (Drosophila mel	0.40	0.0006377	0.0036351	3038.04	2639.44	2800.75	3881.50	3590.64	3777.28
JC_g21862.t1	wgn: Tumor necrosis factor recept	0.40	0.0034595	0.0152839	741.71	839.69	786.87	1069.59	968.94	1103.87
JC_g16568.t1	Mtpalpha: BcDNA.GH12558 (Dros	0.40	0.0005018	0.002949	10318.60	9403.33	11139.41	13519.11	13961.62	13403.05
JC_g3730.t1	"CG8654-RA: CG8654, isoform A	0.40	0.0013516	0.0068488	841.24	888.04	913.05	1164.56	1134.88	1194.89
JC_g3422.t1	CG6040-RA: MIP19203p (Drosop	0.40	0.0014662	0.0073452	4912.30	4401.70	5307.41	6480.85	6083.15	6777.73
JC_g23429.t1	"ND-ASHI: NADH dehydrogenase	0.40	0.0016696	0.0081991	1070.07	1038.02	1177.33	1487.93	1470.11	1387.51
JC_g14115.t1	CG8399: Putative ferric-chelate re	0.40	0.0025671	0.0118396	2179.37	2239.83	2027.79	2531.51	3082.78	2903.08
JC_g8452.t1	"Dys: Dystrophin, isoform K (Drosc	0.40	0.0023304	0.0109283	7655.40	8986.94	9240.78	12347.76	11058.14	10778.32
JC_g17044.t1	"NFAT: NFAT homolog, isoform G	0.40	0.0012909	0.0065909	3522.59	3989.26	3936.35	4799.58	5466.15	4847.28
JC_g19696.t1	Slmap: LD47843p (Drosophila me	0.39	0.0031234	0.0140154	1550.99	1605.37	1853.92	2290.68	2254.17	2059.56
JC_g12378.t1	Usp16-45: Ubiquitinyl hydrolase 1	0.39	0.0023949	0.0111988	3598.87	3345.93	4109.22	5116.16	4820.19	4631.38
JC_g9601.t1	PyK: Pyruvate kinase (Drosophila	0.39	0.0022707	0.0106704	7174.49	5813.68	7054.03	8532.97	9066.81	8814.01
JC_g3606.t1	"CG7218: CG7218, isoform B (Dr	0.39	0.0030616	0.0137924	1445.65	1491.90	1687.01	1967.32	2181.78	1933.62
JC_g11901.t1	"eIF4G1: Eukaryotic translation in	0.39	0.0002035	0.0013623	19861.34	20540.30	22041.36	27237.21	28153.77	26595.48
JC_g16272.t1	Protein of unknown function	0.39	0.0016921	0.0082986	2356.63	2490.45	2762.99	3206.51	3267.66	3513.75
JC_g4319.t1	Manf: Mesencephalic astrocyte-de	0.39	0.0011645	0.0060452	6345.60	5650.88	5815.10	8397.29	7672.43	7296.32
JC_g23105.t1	Protein of unknown function	0.39	0.002472	0.0114891	3334.44	2979.86	3638.29	4153.99	4343.51	4555.17
JC_g11876.t1	"Edem2: alpha-1,2-Mannosidase	0.38	0.0008043	0.0044346	2217.15	2209.24	2374.53	2828.87	3098.37	2949.64
JC_g18222.t1	rl-RE: Mitogen-activated protein ki	0.38	0.001833	0.0088986	3754.33	3593.59	3975.10	5281.24	4934.90	4521.31
JC_g5225.t1	Osbp: Oxysterol-binding protein (D	0.37	0.0003831	0.0023437	3529.13	3459.40	3683.99	4469.44	4659.81	4735.09
JC_g25072.t1	CG7806: CG7806 (Drosophila me	0.37	0.0035158	0.015503	1359.93	1525.45	1406.83	2008.02	1758.57	1812.97
JC_g12780.t1	"CG30460: Uncharacterized prote	0.37	0.0018134	0.0088333	1928.02	1968.48	1867.83	2595.96	2598.31	2294.52
JC_g2223.t1	CG13321: RE03883p (Drosophila	0.37	0.002507	0.0116092	6416.80	5316.38	5863.79	8000.44	7474.19	7371.46
JC_g11731.t1	Flo1: Flotillin-1 (Drosophila melanc	0.37	0.0009463	0.005091	3965.73	4210.28	4371.51	5215.66	5691.12	5321.42
JC_g4486.t1	KdelR: ER lumen protein-retaining	0.37	0.0030916	0.0139056	8166.10	7242.44	8068.42	10845.14	10321.97	9183.37
JC_g2719.t1	Scamp: Secretory carrier-associat	0.37	0.0003542	0.0021906	3792.83	3876.78	3851.90	5134.25	4855.83	4888.56
JC_g2182.t1	Protein of unknown function	0.37	0.0011459	0.0059702	1720.98	1774.10	1864.85	2338.17	2326.56	2252.19
JC_g12827.t1	"CG33181: Uncharacterized prote	0.36	0.0034046	0.0150764	1000.33	925.53	929.94	1206.40	1270.76	1208.65
JC_g2830.t1	hrp48: Heterogeneous nuclear rib	0.36	0.0014532	0.0072929	22823.10	21994.71	23659.82	30851.88	30522.66	26835.73
JC_g4585.t1	"Usp15-31: Ubiquitin specific prot	0.36	0.003383	0.0149981	841.24	864.36	878.28	1104.64	1144.91	1078.47

JC_g22807.t1	"Stt3A: CG1518, isoform A (Drosc	0.36	0.0009334	0.0050375	5359.07	5489.06	5315.36	6656.10	7394.00	6712.11
JC_g13590.t1	"atl: Atlastin, isoform C (Drosophila	0.36	0.0025544	0.0118002	1720.25	1605.37	1695.95	2283.90	2124.98	2044.75
JC_g4841.t1	"ckn: Caskin, isoform D (Drosophil	0.36	0.0005194	0.0030446	5722.30	5944.92	5600.50	7482.60	7573.31	7117.46
JC_g9406.t1	rdx: Protein roadkill (Drosophila m	0.36	0.0036528	0.016002	3861.12	3684.37	3612.46	4397.07	5270.13	4671.59
JC_g20919.t1	gag-pol: Putative uncharacterized	0.36	0.0036108	0.0158423	3630.83	3347.90	3974.10	4910.39	4654.24	4492.73
JC_g16991.t1	"c11.1: C11.1, isoform A (Drosoph	0.35	0.0034065	0.0150788	1223.35	1282.72	1165.41	1589.69	1592.62	1514.51
JC_g17977.t1	Sec71: LD29171p (Drosophila me	0.35	0.0014836	0.0074142	2085.66	1953.68	1970.16	2616.31	2501.42	2561.23
JC_g11527.t1	beta'COP: Coatomer subunit beta	0.34	0.0012377	0.0063647	9921.95	8991.87	9790.20	12438.21	12158.50	11836.68
JC_g13434.t1	Snap25: Synaptosomal-associate	0.32	0.0025942	0.0119307	4125.55	4342.50	4090.34	5389.78	5326.93	5001.80
JC_g21880.t1	"Spase22-23: Spase 22/23-subu	0.32	0.0015289	0.0076159	4738.68	4574.38	4579.16	5752.72	5921.66	5689.73
JC_g18636.t1	Nipped-B: Nipped-B protein (Dros	0.31	0.0016038	0.0079166	5940.24	5748.56	5933.33	7158.11	7445.23	7325.96
JC_g22099.t1	"NAT1: NAT1, isoform D (Drosoph	0.30	0.0034559	0.0152739	15717.63	15008.82	15950.06	18413.67	19822.02	19206.03
JC_g9216.t1	RpL24: GEO07624p1 (Drosophila	-0.30	0.0037007	0.0162056	47699.90	44205.50	43321.69	36196.43	36855.28	36954.69
JC_g4614.t1	"nudE: NudE, isoform C (Drosoph	-0.32	0.0035887	0.0157801	1819.05	1833.30	1767.48	1432.53	1435.59	1451.01
JC_g11201.t1	imd: GH20785p (Drosophila melan	-0.33	0.0020485	0.0097785	8246.74	7710.14	7451.44	6172.18	6047.51	6374.49
JC_g23767.t1	Dmel\CG10565: LD23875p (Dros	-0.33	0.0019087	0.0092032	3564.72	3311.39	3458.46	2758.77	2687.41	2751.73
JC_g24991.t1	"numb: Numb, isoform D (Drosoph	-0.33	0.003512	0.0154919	5314.76	4674.04	4929.87	3819.31	3915.85	4089.50
JC_g4548.t1	drk: Protein enhancer of sevenles	-0.34	0.0033355	0.0148334	5180.37	4604.97	4832.51	3640.67	3910.28	3993.19
JC_g3121.t1	"PIP4K: Phosphatidylinositol 5-ph	-0.34	0.0037412	0.0163517	2213.51	2123.40	1978.11	1693.70	1650.54	1637.28
JC_g24159.t1	CG2852: Peptidyl-prolyl cis-trans i	-0.34	0.0012915	0.0065909	26924.68	26950.94	25277.28	19604.23	21103.91	21670.94
JC_g9408.t1	"Mapmodulin: Mapmodulin, isofor	-0.34	0.0015875	0.0078501	7143.98	6424.46	6541.37	5256.36	5402.66	5167.96
JC_g12501.t1	mts: Serine/threonine-protein pho	-0.35	0.003215	0.0143757	7518.83	6471.82	7473.30	5482.49	5746.80	5625.17
JC_g17906.t1	Uba2: Ubiquitin-like protein activa	-0.35	0.0011394	0.0059472	5112.81	5294.68	4910.00	3907.51	4155.30	3964.61
JC_g17535.t1	SRPK: SD09672p (Fragment) (Dr	-0.35	0.0010578	0.005585	8100.00	7269.08	7884.62	6129.22	6076.47	6017.82
JC_g19612.t1	BcDNA.LD34475: BcDNA.LD3447	-0.35	0.0026382	0.0121041	1437.66	1370.54	1419.75	1082.03	1102.58	1118.68
JC_g5324.t1	"bi: Bifid, isoform G (Drosophila m	-0.35	0.0011911	0.0061636	5357.62	5462.42	5288.54	3921.07	4395.86	4257.77
JC_g17732.t1	"CT30663: Uncharacterized prote	-0.36	0.0019068	0.009198	4036.92	3928.08	3722.74	2801.74	3147.38	3127.45
JC_g3263.t1	IntS3: Integrator complex subunit	-0.36	0.0027379	0.0124912	2762.72	2657.20	2389.43	1944.71	2079.32	2027.81
JC_g17041.t1	HP1b: FI06908p (Drosophila mela	-0.37	0.000939	0.0050631	8100.00	7602.59	7386.86	5609.12	6104.31	6159.64
JC_g19650.t1	Ref1: LD24793p (Drosophila mela	-0.37	0.0026897	0.0123105	6903.52	6674.09	6004.87	4670.69	5137.60	5339.42
JC_g3120.t1	CG11981: Proteasome subunit b	-0.37	0.0014808	0.0074051	5226.13	4783.56	4604.00	3709.64	3637.42	3950.85
JC_g21345.t1	CG9776-RA: MIP13067p (Fragme	-0.37	0.0018574	0.0090013	3102.70	3497.88	3184.25	2393.57	2538.17	2625.79
JC_g9581.t1	"Kul: Kuzbanian-like, isoform A (D	-0.37	0.0013628	0.0068916	9011.70	9869.05	10377.37	7938.25	7241.42	7385.22
JC_g893.t1	"gem: Gemini, isoform F (Drosoph	-0.38	0.0026887	0.0123105	6347.06	6755.99	6247.29	5208.88	4408.11	5263.22
JC_g21863.t1	CycA: G2/mitotic-specific cyclin-A	-0.38	0.0025002	0.0115914	1763.11	1663.59	1572.75	1217.70	1338.69	1284.85
JC_g23225.t1	Protein of unknown function	-0.38	0.0007674	0.0042583	15095.05	14781.87	14072.30	10530.82	11120.51	12100.21
JC_g8561.t1	GEO04306p1 (Fragment) (Drosop	-0.38	0.0009927	0.0052904	2738.02	2441.12	2577.21	2009.15	1956.81	1990.77
JC_g4757.t1	Protein of unknown function	-0.38	0.0006626	0.0037509	3800.10	4083.98	4021.79	3207.64	3002.59	2922.13
JC_g11838.t1	dod: Putative peptidyl-prolyl cis-tra	-0.38	0.000617	0.0035332	4766.28	4350.40	4271.17	3396.45	3385.71	3488.35
JC_g13623.t1	Arl2: ADP-ribosylation factor-like p	-0.38	0.0012355	0.0063565	2235.31	2149.05	1978.11	1607.78	1633.83	1630.93
JC_g24648.t1	CG5861: CG5861 (Drosophila me	-0.38	0.0024355	0.011356	2132.88	2439.14	2404.33	1893.83	1728.50	1712.42
JC_g5314.t1	Ufd1-like: Ubiquitin fusion degrada	-0.38	0.0030036	0.013579	2961.77	2780.54	2628.87	1925.49	2214.08	2261.71
JC_g13484.t1	Max: GEO11490p1 (Drosophila m	-0.38	0.0017349	0.0084795	2117.62	2115.50	2010.90	1473.23	1706.22	1590.71
JC_g20885.t1	Sox102F: LD16247p (Drosophila	-0.39	0.0005562	0.0032223	4867.26	4638.51	5092.81	3640.67	3592.87	3916.98
JC_g3050.t1	CG33691-RB: MIP08166p (Droso	-0.39	0.0018441	0.0089472	5187.63	4253.70	4767.93	3602.23	3689.76	3539.15
JC_g12034.t1	CG9135: CG9135 protein (Drosop	-0.39	0.002305	0.0108181	7934.36	7316.44	7208.03	5241.66	6372.72	5475.95
JC_g24131.t1	Prosalpha3: Proteasome subunit	-0.39	0.0004992	0.0029349	5476.03	5195.02	4810.65	3889.41	3867.96	4024.94
JC_g56.t1	"CG12929: Uncharacterized prote	-0.39	0.0037294	0.0163125	1486.33	1290.61	1350.20	982.53	1033.53	1119.74
JC_g23035.t1	CG3732: Zinc finger Ran-binding	-0.39	0.0010451	0.0055259	3244.36	3266.00	2908.05	2270.33	2509.22	2373.90
JC_g24721.t1	Protein of unknown function	-0.39	0.0008277	0.0045398	16226.87	14331.93	16285.87	11515.61	12673.04	11385.82
JC_g24939.t1	Protein of unknown function	-0.39	0.0031039	0.0139445	1294.55	1247.20	1166.40	1013.06	904.34	897.49
JC_g23097.t1	ebi-RA: FI17838p1 (Drosophila m	-0.40	0.0008885	0.0048249	4080.51	3756.40	3596.56	2729.37	2907.93	3032.20
JC_g3490.t1	BcDNA.GH03108: BcDNA.GH031	-0.40	0.0020574	0.0098091	2302.87	2045.45	2000.96	1499.23	1648.31	1664.80
JC_g11929.t1	BcDNA:GH04978: BcDNA.GH049	-0.40	0.0004085	0.002473	2629.77	2826.92	2574.22	1997.85	2020.29	2063.80
JC_g13192.t1	Rpb7: IP02321p (Drosophila mela	-0.40	0.0023315	0.0109292	1185.58	1317.26	1327.35	978.01	1004.58	914.42
JC_g3257.t1	Protein of unknown function	-0.40	0.0010397	0.00551	2885.49	2720.35	2531.50	2101.87	1933.42	2120.95
JC_g21607.t1	"Nrt: Neurotactin, isoform C (Dros	-0.40	0.0032932	0.014668	7839.20	7432.87	8165.79	5051.72	6264.69	6381.90
JC_g14598.t1	"sm: Smooth, isoform U (Drosophi	-0.40	0.0002983	0.0018889	6170.53	5900.51	5650.18	4307.75	4362.45	4721.34
JC_g25045.t1	"HIP-R: Hsc/Hsp70-interacting pro	-0.40	0.0003465	0.0021474	7192.65	6471.82	6633.77	4853.85	5176.58	5306.61
JC_g3471.t1	Protein of unknown function	-0.40	0.0006404	0.0036473	57432.24	55888.13	49613.68	38453.20	43057.60	41500.34
JC_g9566.t1	Dis3: SD10981p (Drosophila mela	-0.40	0.0018285	0.0088873	1303.26	1291.60	1394.91	956.52	975.62	1077.41
JC_g13388.t1	"flfl: Falafel, isoform E (Drosophila	-0.40	0.0003259	0.0020362	4358.74	4475.71	4136.05	3209.90	3452.54	3113.69
JC_g20633.t1	CG4975-RB: SD16468p1 (Drosop	-0.40	0.0010227	0.0054348	1991.22	2122.41	1936.38	1449.49	1477.91	1628.81
JC_g25088.t1	Protein of unknown function	-0.41	0.0008081	0.0044452	3070.73	2900.92	2823.60	2040.81	2202.94	2367.55
JC_g24066.t1	Amy-p: Alpha-amylase A (Drosoph	-0.41	0.0004001	0.0024326	3330.81	3490.97	3628.36	2453.50	2672.93	2727.39
JC_g21708.t1	CCT2: CG7033 (Drosophila melan	-0.41	0.0002142	0.0014199	15900.69	14130.65	14654.50	11145.89	10765.23	11683.22
JC_g1335.t1	"l(2)efl: Lethal (2) essential for life	-0.41	0.003251	0.0145085	802.74	792.33	899.14	624.12	612.55	635.01
JC_g21007.t1	Bap111: Brahma associated prot	-0.41	0.0020538	0.009796	8639.75	8160.08	8196.59	5392.04	6819.32	6554.41
JC_g22219.t1	tex: GM21396p (Drosophila melan	-0.41	0.0032919	0.0146679	664.71	679.84	675.60	474.87	517.88	518.60
JC_g17929.t1	snf: U1 small nuclear ribonucleopr	-0.41	0.002875	0.0130494	2024.64	1725.75	1620.44	1337.55	1316.42	1366.34
JC_g2568.t1	CG12168: GH04826p (Drosophila	-0.41	0.0001002	0.0007398	7165.77	7274.01	7125.56	5086.77	5401.55	5666.45
JC_g349.t1	MED25: Mediator of RNA polymer	-0.41	0.0010058	0.0053524	3030.78	2612.80	2851.42	2004.63	2086.00	2262.77
JC_g17489.t1	Protein of unknown function	-0.42	0.0012643	0.0064814	3264.70	3044.98	2884.20	2131.26	2226.33	2514.66
JC_g22321.t1	"Ent2: Equilibrative nucleoside tra	-0.42	0.0033283	0.0148129	3323.54	3621.22	4122.14	2773.47	2994.80	2496.67

JC_g22625.t1	"Nlp: Nucleoplasmin, isoform B (D	-0.42	0.000548	0.0031848	7052.45	6485.63	6728.15	4654.86	4983.91	5510.87
JC_g12691.t1	CG16935-RA: FI19911p1 (Drosop	-0.42	0.002731	0.0124647	1106.39	1032.10	971.67	781.27	712.78	822.34
JC_g19601.t1	Dmel\CG12091: RE06653p (Dros	-0.42	0.0011978	0.0061931	1396.98	1407.05	1256.81	948.61	1051.35	1020.26
JC_g4774.t1	"U2af50: U2 small nuclear ribopro	-0.42	0.0001294	0.0009239	6934.03	6836.90	6536.40	4734.01	5021.77	5345.77
JC_g16517.t1	LysRS: Lysine--tRNA ligase (Dros	-0.42	3.97E-05	0.0003242	4451.00	4445.12	4597.04	3437.16	3275.46	3323.24
JC_g2039.t1	Pfdn6: GEO08974p1 (Drosophila	-0.42	0.002396	0.0111992	2481.58	2071.10	2036.73	1745.71	1554.76	1593.89
JC_g15852.t1	CG11247: SD02478p (Drosophila	-0.42	0.0026992	0.0123394	844.87	779.50	820.65	636.55	555.75	622.31
JC_g20426.t1	"Dmel\CG3689: CG3689, isoform	-0.43	0.0020489	0.0097785	3086.72	2418.42	2570.25	1968.45	2012.50	2000.30
JC_g17466.t1	Dmel\CG32066: GH09096p (Dros	-0.43	0.0004384	0.002633	20169.35	16711.87	19284.33	14280.03	14054.06	13280.28
JC_g19885.t1	CG6459: CG6459 protein (Drosop	-0.43	0.0032809	0.0146306	1759.48	1723.78	1495.26	1100.12	1219.53	1358.93
JC_g24531.t1	CG10175: Carboxylic ester hydrol	-0.43	0.0001866	0.001264	4474.25	4092.86	3918.46	3077.61	2993.68	3167.67
JC_g21791.t1	Grip84: Gamma-tubulin complex c	-0.43	0.002598	0.0119385	1199.38	1049.86	1051.15	741.70	836.41	860.45
JC_g18361.t1	CG8545-RA: CG8545 (Drosophila	-0.43	0.0004898	0.0028914	3290.85	3113.06	3111.72	2524.73	2118.30	2384.48
JC_g4847.t1	su(r): Dihydropyrimidine dehydrog	-0.43	0.0010591	0.0055892	2394.40	2211.21	2025.80	1553.50	1581.48	1758.99
JC_g18584.t1	CG6962: CG6962 (Drosophila me	-0.43	0.0014839	0.0074142	1390.44	1332.06	1199.19	893.21	1007.92	990.62
JC_g18395.t1	"CG42672: Uncharacterized prote	-0.44	0.0001158	0.000839	5303.14	4830.92	5360.07	3631.63	3856.82	3939.21
JC_g18777.t1	"cold: Coiled, isoform A (Drosophi	-0.44	0.0007521	0.0041873	1280.02	1354.75	1199.19	936.17	983.42	905.95
JC_g17905.t1	CG7650: Phosducin-like protein (I	-0.44	0.0003798	0.0023299	3417.98	3485.05	2983.56	2368.70	2390.05	2524.18
JC_g12500.t1	Protein of unknown function	-0.44	0.0005385	0.0031418	25198.62	21321.77	20502.39	16627.25	16924.12	15807.64
JC_g19932.t1	eIF6: Eukaryotic translation initiati	-0.44	0.0012511	0.006422	2481.58	2061.23	2163.90	1544.46	1751.88	1641.51
JC_g12306.t1	"CG3436: CG3436, isoform A (Dr	-0.44	0.0019753	0.0094765	901.53	816.01	783.89	602.63	599.18	639.25
JC_g22126.t1	Non2: LD45195p (Drosophila mel	-0.44	0.0003171	0.0019911	24755.48	21885.18	21922.14	15414.07	16787.13	18113.80
JC_g2460.t1	"Karl: Karl, isoform A (Drosophila	-0.44	0.0011436	0.005965	1144.90	1070.58	996.51	785.80	747.31	822.34
JC_g7621.t1	Protein of unknown function	-0.44	0.0037918	0.0165162	1566.97	1203.78	1310.46	939.57	1050.24	998.03
JC_g18588.t1	CG8939: Putative rRNA methyltra	-0.44	8.38E-05	0.0006307	2296.33	2397.70	2243.38	1707.27	1741.86	1637.28
JC_g3426.t1	"CG1416: CG1416, isoform A (Dr	-0.44	0.0014072	0.0070963	3519.68	2743.05	3315.39	2266.94	2416.78	2330.50
JC_g652.t1	"Vps28: Vacuolar protein sorting 2	-0.44	0.0013228	0.0067178	2493.93	2240.81	2325.84	1920.96	1528.03	1718.77
JC_g1643.t1	CG10340: GM04207p (Drosophila	-0.45	0.0004403	0.0026414	1656.32	1585.64	1550.89	1239.19	1075.86	1191.71
JC_g12955.t1	CG9890: CG9890 (Drosophila me	-0.45	0.0003273	0.0020438	1287.28	1195.89	1195.21	922.61	883.18	884.79
JC_g25126.t1	"nonA: No on or off transient A, is	-0.45	2.24E-05	0.0001982	32312.09	30492.24	32184.26	21789.77	24122.10	23600.33
JC_g17628.t1	"Gdap1: Gdap1, isoform A (Drosc	-0.45	0.0003731	0.0022937	18904.59	18895.46	16672.35	11967.86	13657.57	14195.76
JC_g14306.t1	Myb: LD22943p (Drosophila mela	-0.45	0.0007422	0.0041426	1997.03	1950.72	1881.74	1260.67	1532.48	1465.83
JC_g16381.t1	"jub: Ajuba LIM protein, isoform C	-0.45	2.91E-05	0.0002496	3045.31	3118.00	2977.60	2233.02	2171.76	2280.76
JC_g18934.t1	CSN5: COP9 signalosome comple	-0.45	0.0017112	0.0083781	3053.30	2498.34	2534.48	1983.15	1799.77	2119.89
JC_g10012.t1	Galactosylgalactosylxylosylprotein	-0.45	0.0009881	0.0052733	2086.38	1804.69	1717.81	1297.98	1433.36	1359.99
JC_g5751.t1	GEO12753p1 (Fragment) (Drosop	-0.45	0.0004147	0.0025013	1054.09	994.60	1061.09	732.66	776.26	759.90
JC_g10151.t1	Protein of unknown function	-0.45	0.0013627	0.0068916	2635.59	2214.17	2088.39	1664.31	1771.93	1619.29
JC_g7507.t1	"akirin: Akirin, isoform C (Drosophi	-0.45	0.0002003	0.001344	9982.25	8666.26	8946.70	6177.84	6910.64	7005.27
JC_g16394.t1	"CG7358: CG7358, isoform A (Dr	-0.45	0.0001391	0.0009816	7562.42	6826.05	6925.87	5403.35	4743.34	5372.23
JC_g9278.t1	"SKIP: Shal K[ ] channel interacti	-0.45	0.0023337	0.0109348	5056.14	5559.11	4754.02	3148.84	3806.70	4204.86
JC_g3673.t1	Rab4: Rab4 protein (Drosophila m	-0.46	0.0006617	0.0037478	3803.73	3384.41	3072.97	2354.00	2625.04	2479.73
JC_g4559.t1	CG13096-RA: FI17503p1 (Drosop	-0.46	0.0009829	0.0052542	976.36	850.54	866.35	650.12	654.87	651.95
JC_g15083.t1	Protein of unknown function	-0.46	0.0002297	0.001506	2939.97	2833.83	2744.12	1934.53	2263.08	1992.89
JC_g801.t1	Protein of unknown function	-0.46	6.23E-06	6.37E-05	4401.60	4456.96	4392.38	3171.46	3220.88	3243.87
JC_g16813.t1	Zw-RA: Glucose-6-phosphate 1-d	-0.46	0.0002169	0.0014366	4139.35	3797.84	3954.23	3170.33	2720.82	2748.56
JC_g16853.t1	"CG9967: CG9967, isoform A (Dr	-0.46	0.0002236	0.0014721	1966.52	2005.98	1790.33	1428.00	1438.93	1316.60
JC_g17753.t1	fidipidine: Fidipidine (Drosophila m	-0.46	0.0001435	0.0010087	2348.64	2270.42	2107.27	1563.68	1715.13	1600.24
JC_g16034.t1	ATPsynE: 9 kD basic protein (Dro	-0.46	0.0021734	0.010285	4158.97	3393.29	3422.70	2996.21	2527.03	2423.64
JC_g19681.t1	Nle: Protein Notchless (Drosophila	-0.46	0.0006339	0.0036173	1214.64	1158.40	1083.94	810.67	798.54	895.37
JC_g17642.t1	"Dmel\CG17233: Uncharacterized	-0.46	3.62E-05	0.0003003	10529.27	9578.96	9204.02	6902.58	7183.51	7173.55
JC_g19532.t1	RnpS1: LD23870p (Drosophila m	-0.46	6.79E-05	0.0005232	2488.12	2361.19	2371.55	1712.93	1675.04	1845.78
JC_g24511.t1	"Nup44A: Nucleoporin at 44A, isc	-0.46	0.0010959	0.0057414	871.75	840.68	776.94	632.03	563.54	604.32
JC_g16337.t1	CG6947-RA: MIP31231p (Fragme	-0.46	0.0015211	0.0075805	2402.39	2095.77	2399.36	1533.15	1549.19	1899.75
JC_g24788.t1	CG14043-RA: FI18232p1 (Drosop	-0.47	0.000451	0.0026914	2282.53	2029.66	1863.85	1521.85	1454.52	1482.76
JC_g19491.t1	lwr: SUMO-conjugating enzyme (D	-0.47	2.06E-05	0.0001846	9791.19	8982.99	9131.49	6366.66	6748.04	7029.61
JC_g16814.t1	Protein of unknown function	-0.47	0.0023454	0.0109851	866.66	861.40	712.36	556.28	600.30	601.15
JC_g16339.t1	CG9246: Nucleolar complex prote	-0.47	0.0002867	0.0018284	1182.67	1349.82	1304.50	932.78	909.91	922.89
JC_g4508.t1	Rpn5: GH11341p (Drosophila me	-0.47	0.0003513	0.0021748	9663.33	8729.41	8487.69	6299.95	5884.91	7192.60
JC_g7626.t1	CG15432-RA: GEO11163p1 (Dro	-0.47	0.002502	0.0115923	857.22	839.69	815.68	537.06	687.17	584.21
JC_g254.t1	Mtr3: FI01414p (Drosophila melar	-0.47	0.0020001	0.0095875	862.30	961.05	792.83	584.54	628.14	669.94
JC_g16850.t1	"TfIIS: RNA polymerase II elongat	-0.47	0.0003181	0.0019964	4636.98	4331.65	3936.35	2965.68	2939.11	3388.86
JC_g23973.t1	Aatf: Protein Aatf (Drosophila mel	-0.47	0.0014319	0.0072055	824.53	845.61	788.86	531.40	593.61	643.48
JC_g4338.t1	SC35: LD32469p (Drosophila mel	-0.47	8.43E-05	0.0006335	12955.64	12251.95	11909.39	8043.40	9288.44	9406.69
JC_g1043.t1	D12: D12 (Drosophila melanogast	-0.47	0.0022293	0.0105145	768.59	689.71	759.05	480.52	583.59	530.24
JC_g4843.t1	mof: Males-absent on the first pro	-0.47	6.17E-05	0.0004815	2459.06	2337.51	2277.16	1624.74	1791.98	1677.50
JC_g2987.t1	CG1890: Tubulin-specific chaperc	-0.47	3.87E-05	0.0003175	2863.69	2724.30	2763.99	2117.70	1903.35	1993.95
JC_g21017.t1	"Sbf: SET domain binding factor,	-0.47	0.0007495	0.0041789	2507.73	2329.62	2915.00	1805.64	1778.61	1987.60
JC_g13904.t1	Art1: Arginine methyltransferase 1	-0.47	0.0010909	0.0057218	1741.32	1656.68	1928.43	1248.23	1151.59	1425.61
JC_g25345.t1	Rbbp5: Retinoblastoma-binding p	-0.47	0.0006055	0.0034742	934.95	893.96	866.35	602.63	683.83	650.89
JC_g18898.t1	"Mi-2: Mi-2, isoform B (Drosophila	-0.47	0.0016087	0.0079307	24483.06	18938.87	21308.14	13709.06	15501.89	17258.65
JC_g2764.t1	Protein of unknown function	-0.47	0.0001826	0.0012421	4828.03	4273.43	4084.38	2958.89	3210.86	3307.37
JC_g3596.t1	CCT8: CG8258 (Drosophila melar	-0.47	3.19E-05	0.0002696	15112.49	14089.20	13863.65	9638.74	10274.08	11040.79
JC_g4776.t1	mRpS23: Mitochondrial ribosomal	-0.47	0.0022078	0.0104304	673.43	679.84	675.60	434.17	541.27	478.38
JC_g12628.t1	Pde11: Phosphodiesterase (Dros	-0.47	0.000945	0.0050905	3237.09	2770.68	3164.38	1919.83	2416.78	2241.60

JC_g19700.t1	su(Hw): Protein suppressor of hai	-0.47	0.0004842	0.0028628	1929.47	1674.44	1625.41	1293.46	1171.64	1288.02
JC_g1131.t1	Dhfr-RB: FI15873p1 (Drosophila r	-0.48	0.001148	0.0059758	1269.85	1135.70	1035.25	791.45	879.84	793.77
JC_g24089.t1	"Fs: Follistatin, isoform A (Drosop	-0.48	0.0027889	0.0126888	6479.27	8293.28	6595.02	4538.40	5861.52	4866.33
JC_g24421.t1	"Dys: Dystrophin, isoforms A/C/F/	-0.48	0.0031829	0.0142539	1952.72	1869.81	2567.27	1595.34	1438.93	1529.33
JC_g16363.t1	CG8142: CG8142 (Drosophila me	-0.48	0.0010643	0.0056091	736.63	654.19	755.08	529.14	502.29	501.66
JC_g1042.t1	"da: Daughterless, isoform B (Dro	-0.48	0.0010729	0.005644	2390.04	2605.90	2862.35	1811.29	2117.19	1680.67
JC_g19709.t1	IP11908p (Fragment) (Drosophila	-0.48	0.0020205	0.0096685	1295.27	999.54	1043.20	783.54	811.90	787.42
JC_g23157.t1	"pita: Pita, isoform B (Drosophila r	-0.48	0.0001555	0.0010816	5409.20	4881.24	4977.56	3507.26	3374.58	4029.17
JC_g17867.t1	"CG7457-RA: CG7457, isoform B	-0.48	0.0007931	0.0043838	1608.38	1770.15	1433.66	1104.64	1238.46	1087.99
JC_g7627.t1	CG10217-RA: LD32918p (Drosop	-0.48	4.66E-05	0.0003749	5117.89	5317.37	4683.48	3484.64	3833.43	3469.30
JC_g12333.t1	lark: RNA-binding protein lark (Dro	-0.48	0.000154	0.0010723	9342.24	7991.35	8742.03	5615.91	6364.92	6611.56
JC_g7633.t1	jumu: DOMINA protein (Drosophila	-0.48	0.0001174	0.0008501	4174.95	4153.05	3672.07	2678.50	3080.55	2793.01
JC_g5252.t1	GLaz-RA: MIP34477p1 (Drosophi	-0.48	1.08E-05	0.0001037	3490.63	3552.15	3317.38	2567.69	2405.64	2415.17
JC_g12477.t1	Daxx: Daxx-like protein (Drosophil	-0.48	0.0035199	0.0155147	447.50	396.66	438.14	323.36	292.91	295.28
JC_g4557.t1	"rempA: Reduced mechanorecep	-0.49	0.0004407	0.0026418	793.29	798.25	733.22	567.58	553.52	533.41
JC_g23152.t1	CG9125: CG9125-PA (Drosophila	-0.49	0.0018219	0.0088669	659.62	602.88	565.32	455.65	404.28	439.22
JC_g8914.t1	dod: Putative peptidyl-prolyl cis-tra	-0.49	0.0006648	0.0037617	1685.38	1485.00	1438.62	988.18	1185.00	1102.81
JC_g9250.t1	Rel: Nuclear factor NF-kappa-B p	-0.49	9.31E-05	0.0006914	3939.58	3332.11	3401.83	2451.24	2583.83	2556.99
JC_g18305.t1	Ran: GTP-binding nuclear protein	-0.49	1.55E-05	0.0001431	16715.05	16123.80	15422.50	10552.30	11718.58	12054.70
JC_g10213.t1	"CoRest: CoRest, isoform K (Dros	-0.49	0.0002649	0.0017072	2353.72	2556.56	2508.65	1571.59	1946.79	1747.35
JC_g19387.t1	geminin: Geminin (Drosophila mel	-0.49	0.0036405	0.0159605	1907.68	1514.60	1393.92	1034.54	1252.94	1125.03
JC_g1034.t1	"YME1L: CG3499, isoform D (Dro	-0.49	3.64E-05	0.0003014	3733.26	3310.41	3671.08	2409.40	2641.75	2558.05
JC_g11212.t1	CG3356: CG3356 (Drosophila me	-0.49	0.0029263	0.0132608	2088.56	1900.40	2036.73	1157.78	1676.15	1428.78
JC_g10466.t1	GEO11442p1 (Fragment) (Drosop	-0.49	0.0010437	0.0055208	1933.10	2133.26	1982.08	1668.83	1305.28	1304.96
JC_g24505.t1	Protein of unknown function	-0.49	0.0029031	0.0131611	2215.69	2245.75	1609.51	1361.30	1485.70	1441.48
JC_g3419.t1	Protein of unknown function	-0.49	0.0027754	0.0126422	1325.78	1254.11	1653.23	1032.28	1071.40	885.85
JC_g8267.t1	"CG11980: Uncharacterized prote	-0.49	3.10E-05	0.0002635	1590.21	1575.77	1510.16	1063.94	1137.11	1109.16
JC_g8439.t1	Protein of unknown function	-0.49	0.0009284	0.0050128	655.26	756.81	692.49	483.92	475.56	526.00
JC_g21936.t1	Rrp1: DNA-(apurinic or apyrimidini	-0.49	0.0002911	0.001853	939.31	921.59	868.34	654.64	601.41	673.12
JC_g20443.t1	CG11247: SD02478p (Drosophila	-0.50	0.0037804	0.016473	1046.82	1075.51	934.91	581.15	792.97	777.89
JC_g18710.t1	"Dmel\CG32264: Uncharacterized	-0.50	0.0003882	0.0023703	3263.97	3313.37	3135.57	1958.28	2343.27	2550.64
JC_g16684.t1	Oseg4: LD29485p (Drosophila me	-0.50	0.0001186	0.000857	3343.16	2834.81	3104.77	2014.81	2256.40	2278.65
JC_g16531.t1	CG12129: LD21545p (Drosophila	-0.50	0.0006342	0.0036173	735.90	820.94	780.91	582.28	505.63	558.81
JC_g16786.t1	Tgt: Queuine tRNA-ribosyltransfer	-0.50	0.0005535	0.0032096	2459.78	2311.86	1963.21	1526.37	1497.96	1723.01
JC_g11060.t1	PGAP5: Metallophosphoesterase	-0.50	0.0006948	0.0039007	1607.65	1715.89	1360.14	1161.17	1114.84	1024.49
JC_g946.t1	vlc: RE52822p (Drosophila melan	-0.50	7.95E-05	0.0006022	4084.14	3762.32	4354.62	2799.47	2692.98	3108.40
JC_g22147.t1	"S: Star, isoform B (Drosophila me	-0.50	0.0013729	0.0069355	1532.10	1603.40	1408.82	975.75	1249.60	971.57
JC_g16588.t1	"CG12264: Probable cysteine des	-0.50	0.0005946	0.0034276	1400.61	1239.31	1181.30	910.17	815.24	965.22
JC_g22255.t1	"Eip93F: Ecdysone-induced prote	-0.50	0.0006092	0.0034939	21870.72	25399.84	23027.93	14042.60	18787.37	16638.45
JC_g18983.t1	"CG14442: Uncharacterized prote	-0.50	0.0009246	0.0049995	1200.11	993.61	1088.90	711.17	745.08	849.86
JC_g12679.t1	"CG5846: CG5846, isoform A (Dro	-0.50	0.0012527	0.0064275	1116.56	968.95	1002.47	693.08	652.64	822.34
JC_g24045.t1	HnRNP-K: Heterogeneous nuclea	-0.50	1.05E-05	0.0001017	6622.38	6622.78	6747.03	4313.41	5036.25	4708.64
JC_g16988.t1	CG8185: LD40680p (Drosophila r	-0.51	0.0005974	0.003438	722.10	653.20	666.66	452.26	507.86	472.03
JC_g21576.t1	Vamp7: RH15778p (Drosophila m	-0.51	0.0018113	0.0088268	2981.38	2579.25	3172.33	1679.01	2212.97	2222.55
JC_g4348.t1	dwg: Deformed wings (Drosophila	-0.51	0.0013293	0.0067481	695.95	712.40	837.54	540.45	550.18	481.55
JC_g22380.t1	Pbp95: LD18233p (Drosophila me	-0.51	0.0012032	0.0062126	778.76	660.11	649.77	515.57	466.65	480.49
JC_g5655.t1	Dlish: SH3 domain-containing pro	-0.51	0.0002054	0.0013723	7467.98	6835.91	5898.56	4365.42	4934.90	4853.63
JC_g10114.t1	CG31950: IP06106p (Drosophila	-0.51	0.0008397	0.0045944	796.20	702.54	751.11	477.13	570.23	527.06
JC_g2113.t1	Protein of unknown function	-0.51	0.0002138	0.0014177	1465.99	1327.12	1222.04	897.73	942.21	972.63
JC_g11696.t1	CG6287: CG6287 (Drosophila me	-0.51	0.0013967	0.0070464	5076.48	3891.58	3840.97	2823.22	2794.33	3327.48
JC_g13544.t1	CG17565: LD36454p (Drosophila	-0.51	4.23E-05	0.0003433	1781.27	1620.17	1629.38	1182.65	1225.09	1112.33
JC_g21663.t1	UQCR-Q: AT13736p (Drosophila r	-0.51	0.000262	0.0016933	3994.06	3297.58	3227.96	2380.01	2332.13	2639.55
JC_g11051.t1	"CG8272: CG8272, isoform A (Dro	-0.51	0.0005401	0.0031481	717.01	636.43	657.71	462.43	493.38	448.74
JC_g16774.t1	"mTTF: Transcription termination f	-0.51	0.0035275	0.0155423	662.53	602.88	565.32	367.46	488.92	419.11
JC_g24801.t1	CG6766-RA: CG6766 (Drosophila	-0.51	0.0026328	0.012089	3043.86	2460.85	2025.80	1692.57	1804.23	1749.47
JC_g23068.t1	GCC185: FI04457p (Drosophila m	-0.51	4.35E-05	0.0003529	1952.72	1843.17	1697.94	1258.41	1245.14	1332.47
JC_g3466.t1	"Letm1: LETM1 and EF-hand dor	-0.51	8.00E-06	7.97E-05	3306.83	2969.00	3292.54	2275.99	2169.53	2238.43
JC_g21283.t1	Oseg6: Outer segment 6 (Drosop	-0.51	0.0030839	0.0138762	1763.11	1715.89	1479.36	927.13	1181.66	1339.88
JC_g9265.t1	"CG12320: Uncharacterized prote	-0.51	0.001773	0.0086546	538.30	459.81	461.99	327.89	337.46	351.37
JC_g10020.t1	CG14407: RH03087p (Drosophila	-0.51	0.0033759	0.0149723	532.49	431.19	426.22	327.89	324.09	315.39
JC_g11339.t1	lft: Protein limb expression 1 hom	-0.51	0.0012674	0.006491	44394.52	36857.49	35125.10	22369.79	29826.58	28782.05
JC_g2963.t1	CG32758: LD13361p (Drosophila	-0.51	0.0020212	0.0096685	2332.65	2570.37	2599.06	2129.00	1502.41	1584.36
JC_g24669.t1	Prx5: LD45324p (Drosophila mela	-0.52	0.0002177	0.00144	10569.95	8247.89	8411.19	6229.85	6138.83	6592.51
JC_g10522.t1	BcDNA:RE26825: MIP04739p (Dr	-0.52	1.84E-06	2.12E-05	5980.92	5418.01	5663.10	4014.92	3845.68	4039.75
JC_g21611.t1	"CG6907: CG6907, isoform B (Dro	-0.52	0.0006052	0.0034742	865.21	808.11	740.18	518.97	603.64	556.70
JC_g17514.t1	CIAPIN1: Anamorsin homolog (Dr	-0.52	0.0005474	0.0031842	3930.86	3769.22	3630.34	2165.18	2815.49	2896.73
JC_g13285.t1	MP1: Melanization protease 1 (Dr	-0.52	0.0001336	0.0009498	11371.96	10951.47	10440.96	6591.65	7656.84	8542.01
JC_g5765.t1	PhKgamma: GH28523p (Drosoph	-0.52	5.46E-05	0.000432	1978.14	1910.27	2115.22	1271.97	1466.77	1438.31
JC_g8019.t1	CG8858: Proteasome-associated	-0.52	0.0025708	0.0118471	2451.07	3162.40	3711.81	2283.90	2094.91	2087.08
JC_g25086.t1	"emb: Embargoed, isoform B (Dro	-0.52	1.17E-05	0.0001117	8562.02	8334.72	7824.01	5243.93	5867.09	6098.26
JC_g11268.t1	"CG8950: CG8950, isoform A (Dr	-0.52	0.0025591	0.0118133	815.81	631.49	660.69	509.92	510.08	443.45
JC_g25338.t1	"Hexo1: Hexosaminidase 1, isofo	-0.52	0.0004158	0.0025045	16314.05	14809.50	13533.80	8955.83	10293.02	11770.00
JC_g12490.t1	Ku80: ATP-dependent DNA helic	-0.52	0.0015961	0.0078821	637.10	642.35	537.50	452.26	385.35	422.28
JC_g8629.t1	CG9322: GH13441p (Drosophila	-0.52	0.001512	0.0075416	12944.74	10358.46	8775.81	6999.82	7327.18	7910.17

JC_g11211.t1	LamC: Lamin-C (Drosophila melar	-0.52	0.0008612	0.0047001	15236.71	13816.87	14767.76	8112.37	10900.00	11380.53
JC_g11686.t1	Uch-L5: Ubiquitin carboxyl-termina	-0.52	5.15E-05	0.0004087	4748.12	3910.32	4403.30	3049.35	2862.27	3164.49
JC_g7640.t1	mRpL47: AT29239p (Drosophila r	-0.52	0.0006785	0.0038296	1111.48	1093.27	916.03	713.44	663.78	784.24
JC_g11170.t1	cdc2rk-RA: GM29110p (Fragment	-0.52	0.0002252	0.00148	4169.86	3604.44	3350.17	2381.14	2817.72	2510.43
JC_g19651.t1	"CG6379-RB: CG6379, isoform B	-0.52	0.0001022	0.0007517	5751.36	5258.17	4697.39	3451.86	3473.70	3962.49
JC_g16555.t1	l(2)37Cb: LD25692p (Drosophila r	-0.52	0.000518	0.003038	1026.48	856.46	909.08	621.85	700.53	611.73
JC_g17831.t1	RIOK1: Serine/threonine-protein k	-0.52	8.86E-05	0.0006627	1214.64	1299.49	1277.67	954.26	854.22	819.17
JC_g12150.t1	"Taf7: TBP-associated factor 7, is	-0.52	0.0001782	0.0012164	3237.09	2779.56	2606.02	1835.03	2064.84	2074.38
JC_g22553.t1	Mes-4: Probable histone-lysine N-	-0.53	0.0014556	0.0073018	1811.78	1820.48	2103.29	1104.64	1305.28	1548.38
JC_g14852.t1	"rst: Roughest, isoform B (Drosop	-0.53	4.39E-05	0.0003557	3433.96	3661.67	3113.71	2249.98	2545.97	2264.89
JC_g25201.t1	Trf: TBP-related factor (Drosophila	-0.53	0.00027	0.0017343	903.71	824.89	767.00	558.54	596.95	569.40
JC_g23038.t1	Sulf1: FI12873p (Drosophila mela	-0.53	0.0001645	0.0011317	40426.61	36527.93	30937.39	22933.98	26131.25	25426.00
JC_g10884.t1	Dbp73D: Probable ATP-depende	-0.53	0.0001546	0.001076	1136.91	1165.30	1013.40	708.91	790.74	789.54
JC_g1696.t1	"CG3168: CG3168, isoform A (Dr	-0.53	0.0027783	0.0126463	5285.70	5419.99	5341.19	3109.27	3230.91	4703.34
JC_g24402.t1	"EbpIII: Ejaculatory bulb protein III	-0.53	5.03E-05	0.0004007	3886.55	3577.80	3393.88	2340.43	2388.93	2760.20
JC_g12458.t1	Faa: Fumarylacetoacetase (Droso	-0.53	0.0035484	0.0156227	1635.25	1548.14	1390.94	926.00	905.46	1310.25
JC_g15991.t1	CG5390: SD23103p (Drosophila r	-0.53	0.0005456	0.0031765	5619.87	4949.33	4364.56	2995.08	3806.70	3480.94
JC_g23637.t1	Protein of unknown function	-0.53	0.00043	0.002585	1881.52	1792.85	1648.26	1061.67	1213.96	1389.62
JC_g8109.t1	CG1542: Probable rRNA-processi	-0.53	0.0007658	0.0042511	1601.11	1676.42	1476.38	1265.19	1073.63	933.47
JC_g12182.t1	PGRP-SB2-RA: MIP14408p (Frag	-0.53	0.0015699	0.0077882	431.52	443.03	445.10	329.02	307.39	270.94
JC_g22250.t1	Tsp3A: Tetraspanin (Drosophila m	-0.53	0.0008649	0.0047111	1837.21	1893.49	1703.90	1084.29	1483.48	1170.54
JC_g17009.t1	MED15: Mediator of RNA polymer	-0.53	0.0005842	0.003374	1620.73	2019.79	2083.42	1183.78	1376.56	1375.87
JC_g8390.t1	CG1234: Nucleolar complex prote	-0.53	0.0012711	0.006507	716.29	745.95	730.24	516.70	423.21	566.22
JC_g18154.t1	"CG7882: CG7882, isoform A (Dr	-0.53	0.0002772	0.0017734	1211.73	1128.79	966.70	743.96	761.79	769.43
JC_g7995.t1	Sh3beta: SH3 domain-binding glu	-0.53	0.0002533	0.0016419	4421.94	4561.55	5105.73	3737.91	3039.35	2900.96
JC_g21466.t1	Nle: Protein Notchless (Drosophila	-0.53	1.04E-05	0.0001005	2328.29	2275.35	2082.43	1483.40	1611.56	1506.04
JC_g17743.t1	TfIIA-L: Transcription initiation fac	-0.53	0.0002355	0.0015368	4567.96	3786.00	3497.21	2526.99	2776.51	2838.52
JC_g1001.t1	Protein of unknown function	-0.53	0.0006866	0.0038624	918.97	848.57	885.23	533.66	694.96	591.62
JC_g11396.t1	Protein of unknown function	-0.54	0.0033698	0.0149626	1049.00	916.65	740.18	680.65	623.68	549.29
JC_g9803.t1	mRRF1: CG4447 (Drosophila mela	-0.54	0.0011197	0.0058529	1322.15	1224.50	1067.05	710.04	839.75	927.12
JC_g16784.t1	NC2beta: Protein Dr1 (Drosophila	-0.54	0.00091	0.0049324	1261.13	1199.84	992.53	705.52	796.31	865.74
JC_g24649.t1	CG15141: LD24839p (Drosophila	-0.54	0.0004632	0.0027544	3911.24	4385.92	5187.20	2744.07	3275.46	3225.88
JC_g17975.t1	"Bub3: Bub3, isoform A (Drosoph	-0.54	0.0014227	0.0071679	3130.30	2306.92	2379.49	1649.61	2009.15	1696.55
JC_g17808.t1	Dmel\CG15877: IP09724p (Droso	-0.54	0.0031502	0.0141246	1223.35	1270.88	1001.47	818.59	649.30	921.83
JC_g18927.t1	Ubc2: RE74673p (Drosophila mel	-0.54	2.30E-05	0.0002032	5928.62	4806.25	5168.32	3572.83	3685.31	3658.74
JC_g20206.t1	Uba4: Adenylyltransferase and su	-0.54	0.0037448	0.0163553	807.09	722.27	610.02	421.73	477.79	561.99
JC_g4349.t1	"crol: Crooked legs, isoform G (Dr	-0.54	0.0007312	0.0040891	750.43	905.80	932.92	633.16	592.50	545.05
JC_g9303.t1	GEO08308p1 (Fragment) (Drosop	-0.54	0.0001643	0.001131	1791.44	1462.30	1476.38	1027.76	1109.27	1102.81
JC_g17612.t1	Dmel\CG5567: CG5567 (Drosoph	-0.54	0.0015616	0.0077586	497.62	432.18	425.23	289.44	306.27	330.21
JC_g925.t1	CG4449-RA: RE23302p (Drosoph	-0.54	0.0013619	0.0068916	611.68	545.65	482.85	355.02	389.80	375.72
JC_g24125.t1	Rab19: RE48347p (Drosophila me	-0.54	0.0011571	0.0060126	1054.82	1143.59	996.51	670.47	863.13	647.72
JC_g8816.t1	Protein of unknown function	-0.54	0.0001195	0.0008628	1625.08	1404.09	1395.90	981.40	951.12	1095.40
JC_g7833.t1	Orc3: Origin recognition complex s	-0.54	1.99E-05	0.0001792	1678.84	1489.93	1486.31	1087.68	1063.60	1035.07
JC_g3264.t1	rump: FI21236p1 (Drosophila mel	-0.54	1.38E-06	1.64E-05	6339.06	6097.86	5908.50	3896.20	4304.53	4361.49
JC_g3953.t1	"Dmel\CG7519: CG7519, isoform	-0.54	0.0026297	0.0120796	1123.83	1505.72	1341.26	742.83	945.55	1012.85
JC_g3157.t1	rha: RADHA protein (Drosophila m	-0.55	0.0019505	0.0093692	603.69	655.17	612.01	394.59	373.10	503.78
JC_g13830.t1	Hph: GH23732p (Drosophila mela	-0.55	0.0011	0.0057577	1218.27	958.09	895.17	688.56	728.37	674.17
JC_g19741.t1	"HmgZ: HMG protein Z, isoform C	-0.55	8.96E-07	1.11E-05	39460.42	35955.64	36198.11	24006.96	26981.02	25228.08
JC_g12682.t1	Ate1: Arginyl-tRNA--protein transf	-0.55	0.0008057	0.00444	1036.65	808.11	914.04	570.98	682.71	624.43
JC_g16659.t1	tefu: Serine/threonine-protein kina	-0.55	3.49E-05	0.0002919	1112.93	1218.58	1117.72	753.01	766.24	830.81
JC_g20703.t1	Nup58: Probable nucleoporin Nup	-0.55	0.0016431	0.0080826	1446.38	1318.24	1274.69	720.22	990.10	1030.84
JC_g24970.t1	"cos: Costa, isoform B (Drosophila	-0.55	0.0020273	0.0096934	1460.18	1330.08	1076.98	887.56	988.98	742.97
JC_g17928.t1	CG3430: Mini-chromosome mainte	-0.55	0.0001473	0.0010292	1449.28	1585.64	1251.84	988.18	997.89	923.95
JC_g10313.t1	ird5: Inhibitor of nuclear factor kap	-0.55	1.59E-05	0.0001464	1170.32	1161.36	1118.71	786.93	818.59	739.79
JC_g25068.t1	Protein of unknown function	-0.55	0.0004564	0.0027195	3664.98	3370.59	3625.37	1937.92	2629.50	2658.60
JC_g4603.t1	Patsas: Palmitoyltransferase (Dros	-0.55	3.83E-05	0.0003146	1423.86	1363.63	1257.80	845.72	946.66	953.58
JC_g7630.t1	BcDNA:RE67573: Transcription e	-0.55	0.0007276	0.0040725	472.20	456.85	416.29	290.58	304.05	316.45
JC_g8525.t1	Atu: Another transcription unit pro	-0.55	6.83E-06	6.91E-05	2063.86	1861.92	1848.95	1258.41	1305.28	1356.82
JC_g25048.t1	"CG4324: CG4324, isoform A (Dr	-0.55	1.69E-06	1.98E-05	6379.02	6036.68	7068.93	4382.38	4398.09	4449.34
JC_g1494.t1	Protein of unknown function	-0.55	4.45E-05	0.0003595	905.17	932.44	897.15	663.69	591.39	599.03
JC_g11237.t1	pr: 6-pyruvoyl tetrahydrobiopterin	-0.55	0.0003849	0.0023537	3487.72	3075.57	3298.50	2076.99	2652.89	1946.32
JC_g9555.t1	Protein of unknown function	-0.55	1.10E-05	0.000106	1416.59	1435.66	1282.64	924.87	927.73	952.52
JC_g5665.t1	Spt3: RE50415p (Drosophila mela	-0.55	0.0011696	0.0060662	347.97	377.91	350.71	251.00	239.45	237.07
JC_g25082.t1	Protein of unknown function	-0.55	2.68E-05	0.0002322	2299.24	2032.62	1917.50	1476.62	1406.63	1354.70
JC_g21923.t1	Protein of unknown function	-0.55	0.0024801	0.0115218	790.39	614.72	570.28	457.91	410.96	465.68
JC_g18173.t1	Protein of unknown function	-0.56	0.0002331	0.0015239	1863.36	1652.74	1926.45	1413.30	1134.88	1135.62
JC_g19222.t1	Protein of unknown function	-0.56	1.60E-05	0.0001467	8653.56	8068.31	7826.00	4882.12	5869.31	5884.47
JC_g7634.t1	Protein of unknown function	-0.56	0.0001017	0.0007489	1756.57	1666.55	1567.78	1158.91	986.76	1232.99
JC_g20969.t1	Protein of unknown function	-0.56	0.0006017	0.0034557	1875.71	1367.58	1593.61	1049.24	1183.89	1035.07
JC_g2467.t1	HP1c: Heterochromatin protein 1c	-0.56	0.0001381	0.0009763	1811.78	1568.87	1527.05	1071.85	1017.94	1227.70
JC_g10157.t1	CG42240-RA: LD32923p (Drosop	-0.56	0.0001835	0.0012467	2392.95	2097.74	2667.62	1511.67	1531.37	1789.68
JC_g25039.t1	"CG6115: CG6115, isoform A (Dr	-0.56	0.0001287	0.00092	1109.30	1012.36	902.12	671.60	707.21	662.53
JC_g4908.t1	CG7044-RA: CG7044 (Drosophila	-0.56	8.54E-05	0.0006402	1503.77	1391.26	1197.20	929.39	916.59	915.48
JC_g10470.t1	"Meics: Meiotic central spindle, isc	-0.56	0.0027057	0.0123643	289.13	309.83	268.25	188.82	192.67	201.09

JC_g23481.t1	Txl: AT08565p (Drosophila melan	-0.56	7.63E-06	7.64E-05	3676.60	3228.51	3090.86	2195.71	2215.19	2335.80
JC_g18372.t1	"CG10395: Uncharacterized prote	-0.56	0.0003003	0.0018972	3170.26	3361.71	2936.86	1862.17	1990.22	2521.01
JC_g12919.t1	Protein of unknown function	-0.56	0.0001014	0.000748	1081.69	937.37	1030.29	729.27	624.80	699.57
JC_g19706.t1	Protein of unknown function	-0.56	0.001817	0.0088471	166981.97	156692.19	112883.37	81794.17	105655.45	105413.53
JC_g12998.t1	Protein of unknown function	-0.56	0.0006469	0.0036788	542.66	472.63	462.98	336.93	312.96	343.97
JC_g23638.t1	Protein of unknown function	-0.57	0.0001058	0.0007739	19318.67	15782.39	17965.92	10710.59	11325.44	13634.83
JC_g620.t1	Protein of unknown function	-0.57	0.0016963	0.0083157	632.02	525.92	687.52	459.04	367.53	409.58
JC_g25125.t1	mei-9: FI21265p1 (Drosophila me	-0.57	0.0008078	0.0044452	975.63	1160.37	951.80	620.72	645.96	802.24
JC_g22868.t1	srp-RA: GH11649p1 (Drosophila r	-0.57	6.16E-05	0.0004815	1201.56	1226.48	1392.92	780.14	876.50	904.90
JC_g11178.t1	CG15506: AT15667p (Drosophila	-0.57	0.0001458	0.00102	1864.09	1461.31	1758.54	1062.81	1115.95	1225.58
JC_g16638.t1	slmo: RH14110p (Drosophila mela	-0.57	0.0036119	0.0158423	12227.73	11594.81	11310.29	9308.59	5427.17	8679.60
JC_g25040.t1	"Syt1: Synaptotagmin 1, isoform I	-0.57	0.0017704	0.0086456	349.43	339.43	302.03	222.74	207.15	231.78
JC_g16986.t1	ast: Protein asteroid (Drosophila r	-0.57	0.0012398	0.0063699	1270.57	920.60	1005.45	629.77	738.40	766.25
JC_g22095.t1	"loqs: Loquacious, isoform D (Dro	-0.57	0.0012753	0.0065257	1330.87	1230.42	1067.05	663.69	816.36	940.88
JC_g18753.t1	Nop17l: Protein kintoun (Drosoph	-0.57	3.96E-05	0.0003233	1635.98	1339.95	1449.55	974.61	946.66	1036.13
JC_g17904.t1	SmF: Small nuclear ribonucleopro	-0.58	0.0001942	0.0013059	2798.31	2734.17	2208.61	1529.76	1727.38	1900.81
JC_g10010.t1	Fas2: Fasciclin-2 (Drosophila mela	-0.58	6.18E-07	7.88E-06	10598.28	10071.33	10350.55	6601.83	6545.34	7569.38
JC_g10608.t1	Nup43: Nucleoporin 43kD (Drosop	-0.58	0.0001276	0.000914	590.61	603.87	540.48	392.33	374.21	389.48
JC_g22433.t1	Prx3: Peroxiredoxin 3 (Drosophila	-0.58	0.0004636	0.0027556	2679.90	2354.29	2067.53	1478.88	1409.97	1836.25
JC_g21008.t1	Protein of unknown function	-0.58	0.0010335	0.0054846	555.01	470.66	561.34	394.59	345.25	315.39
JC_g11000.t1	grh: Protein grainyhead (Drosoph	-0.58	4.71E-05	0.0003772	37653.00	36458.86	36288.52	21118.17	23771.28	28655.05
JC_g23150.t1	Protein of unknown function	-0.58	1.55E-05	0.0001431	1696.28	1669.51	1458.50	1009.66	1122.63	1083.76
JC_g4755.t1	CG7860: CG7860-PA (Drosophila	-0.58	9.99E-05	0.0007384	1567.69	1283.71	1446.57	862.68	958.91	1038.25
JC_g23918.t1	"CG34401: Uncharacterized prote	-0.58	0.0006796	0.0038341	3752.88	2835.80	2902.09	1807.90	2405.64	2081.79
JC_g20320.t1	Protein of unknown function	-0.58	0.0024247	0.0113104	833.97	657.15	568.30	483.92	466.65	413.82
JC_g11144.t1	shn: Zinc finger protein (Drosophil	-0.58	2.20E-06	2.50E-05	5742.64	6054.44	5240.85	3485.77	3888.00	3956.14
JC_g25066.t1	Tsp97E: LD03691p (Drosophila m	-0.59	1.32E-05	0.000125	2496.11	2382.90	2346.71	1403.13	1738.52	1651.04
JC_g18308.t1	Rpb11-RA: MIP32452p1 (Drosopl	-0.59	0.0037028	0.0162087	1429.67	1138.66	917.02	663.69	747.31	886.90
JC_g22376.t1	"CG7987: CG7987, isoform A (Dr	-0.59	0.0002627	0.0016968	659.62	633.47	597.11	383.29	397.60	468.85
JC_g24891.t1	"Ask1: Apoptotic signal-regulating	-0.59	0.0034512	0.0152589	629.11	640.37	640.82	309.80	487.81	459.33
JC_g969.t1	Ephrin: Ephrin (Drosophila melanc	-0.59	0.0004813	0.002849	709.75	721.28	655.73	507.66	484.47	385.24
JC_g14872.t1	Cbl: Cbl protein (Drosophila melar	-0.59	9.91E-07	1.22E-05	6558.45	5717.97	5850.87	3748.08	4095.16	4162.52
JC_g25344.t1	"bab2: Bric a brac 2, isoform B (D	-0.59	0.0006727	0.0038028	704.66	589.06	544.45	378.77	435.47	399.00
JC_g20335.t1	CG5245: IP01468p (Drosophila m	-0.59	3.61E-05	0.0002999	1098.40	1088.34	994.52	633.16	713.90	754.61
JC_g18940.t1	Tsp42Ee: Tetraspanin (Drosophila	-0.59	0.0001386	0.0009794	12190.68	9240.52	8731.10	6472.94	6595.46	6831.70
JC_g12808.t1	PIF1: ATP-dependent DNA helica	-0.59	0.0011775	0.0061016	794.02	661.09	716.33	386.68	537.93	503.78
JC_g10071.t1	"CG9213: CG9213, isoform B (Dr	-0.59	3.06E-05	0.0002609	1256.77	1095.25	1046.18	777.88	725.03	740.85
JC_g25343.t1	SpdS: RE01362p (Fragment) (Dro	-0.59	4.50E-06	4.79E-05	3253.07	2914.74	2850.42	1884.78	1907.81	2164.34
JC_g22814.t1	"Cdep: Chondrocyte-derived ezrin	-0.59	0.0028622	0.0129962	1195.02	1468.22	1612.49	851.37	1173.86	776.83
JC_g18335.t1	Mipp2: GH13296p (Drosophila me	-0.59	0.0034819	0.0153771	367.59	409.48	393.44	226.13	224.97	314.33
JC_g1345.t1	GEO12573p1 (Fragment) (Drosop	-0.60	2.42E-05	0.0002121	3060.56	2850.60	2772.93	1731.02	1797.55	2186.57
JC_g3003.t1	MIP02663p (Fragment) (Drosophi	-0.60	2.59E-05	0.0002253	1559.70	1577.75	1291.58	967.83	937.75	1007.56
JC_g15404.t1	CG3045: tRNA pseudouridine syn	-0.60	0.0001263	0.000905	996.70	863.37	856.42	533.66	652.64	597.97
JC_g12020.t1	"BtbVII: BTB-protein-VII, isoform I	-0.60	0.0019034	0.0091858	374.13	406.52	460.00	235.17	266.18	309.04
JC_g3236.t1	Cdk7: Cyclin-dependent kinase 7	-0.60	1.63E-06	1.92E-05	1630.90	1499.80	1448.56	1006.27	982.30	1023.43
JC_g22363.t1	Dr: Muscle segmentation homeob	-0.60	0.0015903	0.0078603	544.12	668.00	649.77	327.89	446.60	441.34
JC_g22328.t1	CG5510: CG5510 (Drosophila me	-0.60	6.40E-06	6.52E-05	4383.44	5195.02	5125.60	2996.21	3506.00	3144.38
JC_g24063.t1	"Hnf4: Hepatocyte nuclear factor	-0.60	0.0027785	0.0126463	278.23	280.23	265.27	159.42	206.04	171.45
JC_g24509.t1	Protein of unknown function	-0.60	6.72E-05	0.0005184	1110.03	1090.31	900.13	638.81	694.96	696.40
JC_g16596.t1	"Phlpp: PH domain leucine-rich re	-0.60	9.58E-05	0.0007106	1828.49	1664.58	1767.48	1034.54	1048.01	1353.64
JC_g18677.t1	"r: Rudimentary, isoform D (Drosop	-0.61	0.0012544	0.0064333	5922.80	5593.65	4102.27	3123.97	2962.50	4078.91
JC_g5884.t1	CBP: BcDNA.GH12350 (Drosophi	-0.61	9.90E-05	0.0007327	8323.02	7286.84	6478.78	4163.03	4819.07	5437.84
JC_g20097.t1	Sd-RanGAP: Truncated Ran GTP	-0.61	0.0001452	0.0010174	523.78	469.67	477.89	315.45	335.23	310.10
JC_g20786.t1	"lilli: Lilliputian, isoform H (Drosoph	-0.61	0.0002924	0.0018588	855.04	648.27	735.21	462.43	483.36	514.36
JC_g15029.t1	otk: Tyrosine-protein kinase-like o	-0.61	0.0002609	0.001687	928.41	972.89	968.69	528.01	608.09	733.44
JC_g1713.t1	glo: AT27789p (Drosophila melan	-0.61	5.61E-06	5.78E-05	973.45	950.20	947.82	622.98	663.78	589.51
JC_g10752.t1	Protein of unknown function	-0.61	0.000458	0.002728	2095.10	2031.63	2086.40	1054.89	1613.78	1373.75
JC_g11934.t1	"ap: Apterous, isoform C (Drosoph	-0.61	0.0001775	0.0012123	996.70	1022.23	877.28	539.32	642.62	702.75
JC_g16389.t1	Protein of unknown function	-0.61	0.0011675	0.006058	429.34	372.98	455.03	243.09	308.50	264.59
JC_g17754.t1	CG30493-RB: FI05339p (Drosoph	-0.61	6.44E-05	0.0005008	2184.46	1920.13	1656.21	1153.26	1317.53	1280.61
JC_g21671.t1	"CG5921: CG5921, isoform E (Dr	-0.61	2.73E-05	0.0002363	1913.49	1550.12	1739.66	1024.36	1182.77	1182.19
JC_g16983.t1	Protein of unknown function	-0.61	0.0005241	0.0030655	1155.07	1290.61	999.49	636.55	733.94	865.74
JC_g19579.t1	"CG43658: Uncharacterized prote	-0.61	0.0015188	0.0075724	1332.32	1402.11	1382.99	665.95	896.55	1102.81
JC_g18919.t1	Nsun5: LD16340p (Drosophila me	-0.61	0.002245	0.010571	1447.10	928.49	1099.83	853.64	655.98	739.79
JC_g9721.t1	"CG5044: 3-hydroxyisobutyryl-CoA	-0.61	0.0001443	0.0010115	1145.62	1085.38	951.80	625.25	653.75	788.48
JC_g9152.t1	ash2: Set1/Ash2 histone methyltr	-0.61	0.0019236	0.0092556	590.61	558.48	590.15	304.14	467.76	353.49
JC_g3405.t1	Slu7-RA: FI05206p (Drosophila m	-0.61	2.03E-06	2.31E-05	2918.90	2749.96	2781.87	1726.49	1729.61	2046.86
JC_g11187.t1	CG11513-RB: IP15135p (Drosopl	-0.61	1.43E-05	0.0001336	2923.99	2588.14	2326.84	1572.73	1795.32	1731.47
JC_g1045.t1	Protein of unknown function	-0.61	0.0003853	0.0023547	881.92	793.31	1009.42	670.47	531.25	538.70
JC_g23420.t1	CG3527: Ribosomal RNA small su	-0.61	1.02E-05	9.89E-05	1913.49	1588.60	1571.76	1085.42	1092.56	1121.86
JC_g9334.t1	"CG12096: Uncharacterized prote	-0.61	5.59E-05	0.0004412	2249.11	1971.44	1676.08	1234.66	1248.48	1346.23
JC_g10791.t1	"mRpL42: Mitochondrial ribosoma	-0.61	0.0014501	0.0072803	764.23	602.88	544.45	444.34	433.24	359.84
JC_g1032.t1	"CG3107: CG3107, isoform D (Dr	-0.61	1.80E-06	2.08E-05	3345.33	3300.54	3313.41	2040.81	2005.81	2427.87
JC_g22818.t1	Gnf1: Replication factor C subunit	-0.62	1.93E-05	0.0001743	1479.07	1350.80	1227.00	806.15	897.66	930.30

JC_g2112.t1	CG5013: CG5013 (Drosophila me	-0.62	0.0002426	0.0015796	1203.01	1279.76	1063.07	636.55	802.99	856.21
JC_g17684.t1	Fancl: AT07283p (Drosophila mel	-0.62	0.0002853	0.0018204	1227.71	956.12	904.11	622.98	676.03	699.57
JC_g24512.t1	Grip71: Grip71 (Drosophila melan	-0.62	0.0030149	0.0136192	406.82	438.10	298.06	252.13	248.36	236.01
JC_g24351.t1	CG8679: CG8679 (Drosophila me	-0.62	0.0022141	0.010456	726.46	589.06	469.94	361.81	412.08	377.83
JC_g9335.t1	"CG6693: CG6693, isoform B (Dr	-0.62	9.90E-06	9.68E-05	1457.27	1396.19	1198.19	872.86	852.00	901.72
JC_g22799.t1	CG6678: CG6678 (Drosophila me	-0.62	0.0001848	0.0012543	450.40	505.19	497.76	287.18	333.00	318.57
JC_g25115.t1	"baf: Barrier to autointegration fac	-0.62	1.75E-05	0.0001595	918.97	967.96	906.10	551.75	593.61	662.53
JC_g9331.t1	BubR1: Bub1-related kinase (Dros	-0.62	3.46E-05	0.0002893	2278.17	2732.19	2026.79	1508.28	1531.37	1514.51
JC_g13521.t1	Cbs: Cystathionine beta-synthase	-0.62	1.70E-05	0.0001553	4886.15	4073.13	3996.95	2549.60	2744.21	3094.64
JC_g8255.t1	Protein of unknown function	-0.62	1.19E-05	0.0001133	1118.02	1266.93	1117.72	713.44	821.93	728.15
JC_g2356.t1	CG40451-RA: MIP28909p (Fragm	-0.62	0.0006824	0.003844	1716.62	1272.85	1322.38	819.72	865.36	1090.11
JC_g13903.t1	CG12540: GEO12540p1 (Drosop	-0.62	1.57E-08	2.65E-07	39876.68	36242.77	41652.56	24968.01	25074.33	26197.54
JC_g21701.t1	CG30338: IP09963p (Drosophila	-0.62	0.0013584	0.0068802	555.74	567.36	440.13	280.40	370.87	352.43
JC_g23529.t1	fzr: GH07620p (Drosophila melan	-0.62	0.001979	0.0094904	740.99	549.60	504.71	341.45	413.19	397.94
JC_g21282.t1	ArgRS-m: RE18459p (Drosophila	-0.62	0.0029354	0.0132968	553.56	415.40	413.31	286.05	253.93	346.08
JC_g22826.t1	rgr: GH19651p (Drosophila melan	-0.62	7.84E-05	0.000596	838.33	1048.87	1053.14	591.33	659.32	641.37
JC_g8774.t1	Spn55B: SD11922p (Drosophila r	-0.62	3.18E-06	3.49E-05	3120.86	3282.78	2819.63	1804.51	1983.54	2163.28
JC_g1016.t1	Protein of unknown function	-0.63	5.59E-06	5.77E-05	843.42	889.02	940.87	548.36	584.70	589.51
JC_g12131.t1	scu: 3-hydroxyacyl-CoA dehydrog	-0.63	0.0001075	0.000785	1704.27	1457.37	1323.38	838.94	1035.76	1009.67
JC_g919.t1	inv: Homeobox protein invected (I	-0.63	1.74E-05	0.0001583	1624.36	1532.36	1311.45	892.08	963.37	1020.26
JC_g25046.t1	mRpL38: Mitochondrial ribosomal	-0.63	2.21E-05	0.0001963	1598.21	1491.90	1380.01	849.11	960.03	1066.83
JC_g4837.t1	Dmel\CG32202: GEO10739p1 (D	-0.63	0.0001753	0.0011997	459.12	501.25	450.07	331.28	287.34	286.82
JC_g11279.t1	"Oat: Ornithine aminotransferase,	-0.63	0.0001073	0.0007841	546.30	581.17	491.80	325.63	364.19	349.26
JC_g3195.t1	Protein of unknown function	-0.63	7.49E-05	0.0005716	720.65	730.16	601.08	461.30	428.78	427.58
JC_g9719.t1	CHKov1: GH03753p (Drosophila r	-0.63	0.0001038	0.0007603	1093.32	964.01	817.67	604.89	598.07	642.42
JC_g9506.t1	"Gpdh: Glycerol-3-phosphate deh	-0.63	0.0003384	0.0021052	5229.04	3628.13	3587.62	2745.20	2454.64	2763.37
JC_g17640.t1	"Mtor: Megator, isoform B (Drosop	-0.63	7.94E-07	9.93E-06	15819.33	15190.37	15744.40	9031.58	9650.40	11335.02
JC_g5337.t1	CG2663: RE58223p (Drosophila r	-0.63	0.002437	0.0113583	20133.03	19194.43	23345.86	14499.38	9026.72	16365.39
JC_g13083.t1	"ball: Ballchen, isoform B (Drosop	-0.63	2.53E-06	2.84E-05	2013.01	2098.73	1798.28	1192.83	1228.44	1369.52
JC_g16609.t1	CG12007: LD31216p (Drosophila	-0.63	3.81E-05	0.0003137	1410.05	1181.09	1342.25	880.77	731.72	905.95
JC_g22887.t1	Protein of unknown function	-0.63	0.0003479	0.0021548	121390.25	135060.59	125436.57	61133.91	85125.10	97622.96
JC_g25228.t1	"crol: Crooked legs, isoform F (Dro	-0.63	0.0021555	0.0102126	278.23	310.81	253.35	183.16	197.13	155.58
JC_g2629.t1	EG:25E8.3: CG3071 (Drosophila	-0.64	2.99E-05	0.0002555	717.74	728.19	673.61	404.77	481.13	468.85
JC_g17903.t1	Tgs1: Trimethylguanosine synthas	-0.64	2.67E-05	0.0002319	1948.36	2094.78	1605.54	1251.62	1246.25	1113.39
JC_g19571.t1	Protein of unknown function	-0.64	1.59E-05	0.0001464	2002.12	1757.33	1972.15	1067.33	1226.21	1369.52
JC_g18928.t1	CG7747: CG7747 (Drosophila me	-0.64	0.0008019	0.0044239	1273.48	842.65	897.15	630.90	642.62	643.48
JC_g8777.t1	Spn42Da: Serpin 4 (Drosophila m	-0.64	0.0001842	0.0012509	519.42	528.88	446.09	290.58	338.57	322.80
JC_g3602.t1	CG2046: CG2046 (Drosophila me	-0.64	0.0002452	0.0015947	642.91	627.55	500.74	365.20	358.62	403.23
JC_g21702.t1	"APC4: Anaphase promoting com	-0.64	1.53E-05	0.0001414	949.48	867.32	778.92	539.32	557.97	557.75
JC_g16610.t1	CG9247-RA: RE72821p1 (Drosop	-0.64	4.01E-05	0.0003266	933.50	857.45	734.22	521.23	533.47	552.46
JC_g11886.t1	Dhc16F: Dynein heavy chain at 1	-0.64	0.0019211	0.0092477	334.17	298.97	322.90	161.68	221.63	221.20
JC_g18003.t1	"CG7102: CG7102, isoform A (Dr	-0.64	4.61E-07	6.03E-06	3874.20	3486.04	3390.90	2090.56	2329.91	2428.93
JC_g10192.t1	feo: Fascetto (Drosophila melano	-0.64	0.0010898	0.0057199	935.68	1067.62	847.48	460.17	709.44	632.90
JC_g10583.t1	"UbcE2M: Ubiquitin conjugating e	-0.65	0.0012854	0.0065689	538.30	394.68	518.62	341.45	310.73	265.65
JC_g5461.t1	CG7289: CG7289 (Drosophila me	-0.65	0.000539	0.0031432	653.08	583.14	532.53	310.93	427.67	381.01
JC_g15094.t1	CG14286: UPF0488 protein CG1	-0.65	0.0024172	0.0112889	543.39	397.64	381.51	244.22	277.32	313.27
JC_g1022.t1	Protein of unknown function	-0.65	4.58E-05	0.0003688	9264.51	9079.69	12297.86	6136.00	7120.02	6182.93
JC_g24082.t1	CG15440: RE72132p (Drosophila	-0.65	0.0016881	0.0082862	486.00	397.64	334.82	235.17	275.09	259.30
JC_g25324.t1	pgant2: Polypeptide N-acetylgala	-0.65	0.0001252	0.0008994	457.67	492.37	465.96	265.70	325.21	304.81
JC_g19631.t1	Protein of unknown function	-0.65	3.37E-06	3.68E-05	34671.62	38055.35	33289.07	19121.45	23615.36	24529.57
JC_g10132.t1	"fend: Forked end, isoform C (Dro	-0.65	0.0001478	0.001032	7002.32	5254.22	5595.54	3506.13	3322.23	4455.69
JC_g17391.t1	Top2: DNA topoisomerase 2 (Dros	-0.65	4.54E-05	0.0003663	9271.77	11377.73	11019.19	5718.80	6462.93	7854.08
JC_g22233.t1	"CG1208: CG1208, isoform B (Dr	-0.65	0.0018292	0.0088873	459.12	371.99	354.69	204.65	278.43	263.53
JC_g7792.t1	BG4-RA: FI16833p1 (Drosophila r	-0.65	0.0001084	0.00079	979.26	860.41	720.31	533.66	522.34	563.05
JC_g18791.t1	Drice: Caspase (Drosophila melan	-0.65	1.75E-06	2.03E-05	4201.83	3376.51	3458.46	2421.84	2273.11	2300.87
JC_g11136.t1	"Corin: Corin, isoform B (Drosophi	-0.65	0.0030328	0.0136788	48419.82	54054.82	47388.19	24586.98	25017.53	44390.72
JC_g23925.t1	Spn42Da: RE31022p (Drosophila	-0.65	0.0008557	0.0046753	4485.87	3991.23	3895.61	1956.01	2491.40	3338.06
JC_g17494.t1	anon-WO0118547.713: IP09210p	-0.65	0.002458	0.0114284	481.64	407.51	439.14	210.30	286.23	336.56
JC_g17757.t1	Rpd3: Histone deacetylase Rpd3	-0.65	4.39E-08	6.92E-07	6024.51	5982.41	5781.32	3405.50	4046.15	3817.50
JC_g12673.t1	CG3226: CG3226 (Drosophila me	-0.65	1.90E-06	2.18E-05	2697.34	2409.54	2303.99	1452.88	1511.32	1723.01
JC_g3045.t1	Xpd: Xeroderma pigmentosum D	-0.65	1.75E-06	2.03E-05	1035.93	1030.12	915.04	630.90	641.50	612.79
JC_g16851.t1	ORF: Orf protein (Drosophila mela	-0.65	0.0033715	0.0149628	1555.34	936.39	1032.27	633.16	874.27	699.57
JC_g5336.t1	CG9436: CG9436 (Drosophila me	-0.66	0.0005054	0.0029683	13624.70	11464.56	13249.66	6323.69	7445.23	10314.76
JC_g24552.t1	IKKepsilon: SD10041p (Drosophil	-0.66	0.0007614	0.0042291	1090.41	951.19	1024.32	496.35	630.37	796.94
JC_g11262.t1	"rn: Rotund, isoform F (Drosophila	-0.66	6.63E-05	0.0005128	847.05	867.32	917.02	486.18	648.19	521.77
JC_g18744.t1	"milt: Milton, isoform E (Drosophila	-0.66	9.19E-07	1.14E-05	14465.94	15238.72	14281.93	8113.50	9085.74	10510.55
JC_g10232.t1	Dmel\CG7372: CG7372 (Drosoph	-0.66	1.47E-05	0.0001372	1163.78	1061.70	957.76	733.79	629.25	640.31
JC_g5616.t1	Sas-4: Spindle assembly abnorma	-0.66	0.0007912	0.0043774	421.35	459.81	401.38	230.65	249.47	321.74
JC_g12693.t1	Protein of unknown function	-0.66	0.0001607	0.0011096	432.97	370.02	391.45	245.35	239.45	264.59
JC_g19859.t1	tra2: Transformer-2 sex-determinir	-0.66	7.00E-06	7.07E-05	6757.50	5478.20	6189.66	3333.14	4124.11	4124.42
JC_g22237.t1	Nop56: FI04781p (Drosophila me	-0.66	0.0007382	0.0041258	7675.02	6040.63	4902.05	3642.93	4646.45	3340.18
JC_g22027.t1	Protein of unknown function	-0.66	0.0003025	0.0019089	770.04	777.53	654.73	391.20	438.81	547.17
JC_g535.t1	pcs: SH3 domain-binding protein	-0.66	2.82E-05	0.000243	1983.95	1696.15	1989.04	1092.20	1075.86	1386.45
JC_g1660.t1	SPARC: BM-40 (Drosophila melar	-0.66	0.0021031	0.0100101	2430.00	2646.35	2500.70	1033.41	1814.25	1870.12

JC_g14257.t1	Protein of unknown function	-0.66	6.43E-05	0.0005003	613.86	596.96	538.49	322.23	385.35	388.42
JC_g8000.t1	Rheb: Putative uncharacterized p	-0.66	0.0007592	0.0042185	590.61	595.97	760.05	450.00	436.58	328.09
JC_g20016.t1	spo: FI18637p1 (Drosophila mela	-0.66	3.33E-06	3.65E-05	16859.62	14242.14	17308.21	11244.25	10196.12	8942.07
JC_g2660.t1	CG10050: RE31178p (Drosophila	-0.66	0.0006478	0.0036804	500.53	390.74	388.47	261.18	243.91	294.22
JC_g10248.t1	Protein of unknown function	-0.66	0.003355	0.0149088	4871.62	3165.36	5109.70	3267.56	1994.68	2904.13
JC_g20031.t1	CG2202: CG2202 (Drosophila me	-0.66	9.31E-07	1.15E-05	1877.17	1938.88	1910.55	1352.25	1115.95	1125.03
JC_g15431.t1	"crol: Crooked legs, isoform D (Dro	-0.66	0.0003718	0.0022871	422.80	412.44	383.50	266.83	280.66	213.79
JC_g20078.t1	Cf2: Chorion transcription factor C	-0.66	0.0002566	0.0016623	680.69	733.12	584.19	459.04	439.92	349.26
JC_g23151.t1	mus101-RA: FI23710p1 (Fragmer	-0.67	1.99E-06	2.27E-05	1707.17	1832.32	1651.24	966.70	1086.99	1198.06
JC_g8082.t1	CG2974: NAD(P)H-hydrate epime	-0.67	0.0035452	0.0156146	1448.56	1719.83	1683.03	1407.65	827.50	772.60
JC_g11280.t1	"CG3609: CG3609, isoform A (Dro	-0.67	0.0032889	0.0146604	964.01	1134.71	762.03	423.99	686.05	661.47
JC_g12743.t1	"Arp5: Actin-related protein 5, isof	-0.67	3.61E-05	0.0002998	1333.78	1001.51	1091.88	696.48	757.33	687.93
JC_g23277.t1	Protein of unknown function	-0.67	5.69E-05	0.0004484	1622.91	1316.27	1425.71	935.04	765.13	1024.49
JC_g1013.t1	Dmel\CG10907: RE08109p (Dros	-0.67	5.32E-06	5.52E-05	1338.86	1203.78	1351.19	723.61	901.00	809.64
JC_g1150.t1	Protein of unknown function	-0.67	0.0017094	0.0083728	273.15	282.20	247.39	151.51	149.24	196.85
JC_g20749.t1	"CFIm-68k: CG7185, isoform B (D	-0.67	0.0002947	0.0018708	15659.51	19859.47	19683.73	8738.75	12039.33	13568.15
JC_g3769.t1	Ark-RB: SD15113p (Drosophila m	-0.67	1.99E-06	2.27E-05	2825.92	2887.11	2334.78	1568.20	1791.98	1663.74
JC_g22365.t1	Dr: Muscle segmentation homeob	-0.67	7.98E-05	0.0006028	2713.32	2676.94	2615.95	1279.89	1830.96	1871.18
JC_g10753.t1	Protein of unknown function	-0.67	0.0018538	0.0089878	281.14	252.60	263.28	146.98	198.24	148.17
JC_g19499.t1	rad50-RB: FI13085p (Fragment) (	-0.68	2.75E-07	3.81E-06	2416.20	2033.61	2323.86	1345.47	1385.47	1484.88
JC_g17670.t1	Dmel\CG33260: tRNA-splicing end	-0.68	0.0017825	0.0086977	1359.20	1093.27	807.74	610.55	608.09	791.65
JC_g641.t1	"Dmel\CG10681: Uncharacterized	-0.68	0.0004904	0.0028939	1054.09	865.34	979.62	701.00	456.63	635.01
JC_g12546.t1	"bowl: Brother of odd with entrails	-0.68	0.0003229	0.0020197	2732.21	2370.07	2225.50	1141.95	1597.08	1792.86
JC_g917.t1	en: Segmentation polarity homeo	-0.68	6.91E-05	0.0005322	1166.69	1065.64	1025.32	576.63	639.28	802.24
JC_g3237.t1	abo: Abnormal oocyte (Drosophila	-0.68	3.57E-07	4.81E-06	1071.52	964.01	1010.42	618.46	652.64	622.31
JC_g14867.t1	Cbl: Cbl protein (Drosophila melan	-0.68	5.24E-08	8.16E-07	3713.65	3103.20	3555.83	2124.48	2119.41	2199.27
JC_g21268.t1	drd: Drop dead (Drosophila melan	-0.68	0.0003448	0.0021395	2582.55	2364.15	1893.66	1094.46	1569.23	1555.79
JC_g21667.t1	CG2681-RA: E3 ubiquitin-protein	-0.68	2.40E-06	2.70E-05	9003.71	7526.61	6722.19	4548.58	5009.52	4840.93
JC_g2999.t1	lute: FI18038p1 (Drosophila mela	-0.68	3.13E-05	0.0002654	645.09	626.56	601.08	435.30	340.80	381.01
JC_g20338.t1	Snx16: HL01025p (Drosophila me	-0.68	1.43E-05	0.0001336	1442.02	1180.10	1137.59	788.06	827.50	706.98
JC_g18340.t1	Rif1: Putative uncharacterized pro	-0.69	1.37E-07	1.99E-06	3186.97	2979.86	2720.27	1768.33	1741.86	1984.42
JC_g15976.t1	Protein of unknown function	-0.69	5.89E-06	6.05E-05	1056.27	853.50	894.17	563.06	591.39	576.81
JC_g8090.t1	CG3704: CG3704-PA (Fragment)	-0.69	0.0002638	0.0017025	1051.18	1336.00	1206.14	805.02	827.50	571.51
JC_g24235.t1	Protein of unknown function	-0.69	0.0001703	0.001168	456.94	495.33	385.49	278.14	252.81	289.99
JC_g12293.t1	CG30403-RB: FI12833p (Fragme	-0.69	0.0028538	0.0129635	300.03	243.72	222.55	127.76	168.17	170.40
JC_g19224.t1	Protein of unknown function	-0.69	0.0008064	0.00444	444.59	467.70	499.74	218.21	338.57	303.75
JC_g15058.t1	Protein of unknown function	-0.69	0.00222	0.0104791	2168.47	1659.64	1584.67	742.83	1245.14	1302.84
JC_g21840.t1	CG4797: CG4797 (Drosophila me	-0.69	8.60E-05	0.0006436	4287.55	3590.63	3326.32	1832.77	2661.80	2363.31
JC_g22030.t1	CRIF: CR6-interacting factor (Dros	-0.69	0.0004699	0.0027886	401.00	329.56	359.66	195.60	213.83	256.12
JC_g11897.t1	"pico: Pico, isoform B (Drosophila	-0.69	0.0005459	0.0031767	2615.25	2292.12	2695.43	1091.07	1719.59	1825.67
JC_g11765.t1	Ppn: Papilin (Drosophila melanog	-0.69	0.0005481	0.0031848	465.66	409.48	350.71	221.61	241.68	284.70
JC_g160.t1	Protein of unknown function	-0.70	0.0009775	0.0052313	504.89	620.64	714.34	298.49	385.35	434.99
JC_g18360.t1	CG17266: Peptidyl-prolyl cis-trans	-0.70	0.000681	0.0038403	616.04	460.79	499.74	277.01	300.70	383.13
JC_g12692.t1	Protein of unknown function	-0.70	1.85E-06	2.13E-05	2094.38	2020.78	1640.31	1163.43	1129.31	1230.87
JC_g1573.t1	"CG11200: Carbonyl reductase, is	-0.70	1.26E-05	0.0001196	1248.78	960.07	1006.44	688.56	645.96	631.84
JC_g17926.t1	CG4933: Probable tRNA N6-adenr	-0.70	0.0008614	0.0047001	1877.89	3284.75	2102.30	1397.48	1550.30	1459.48
JC_g17899.t1	Hpr1: Hpr1 (Drosophila melanoga	-0.70	1.70E-06	1.98E-05	2014.47	1845.14	1643.29	1035.67	1236.23	1093.28
JC_g23542.t1	"CG43861: Uncharacterized prote	-0.70	5.04E-06	5.30E-05	2998.81	3223.57	2733.19	1543.33	1859.92	2065.92
JC_g24971.t1	Dmel\CG13295: RE27477p (Dros	-0.70	0.0005548	0.0032156	714.83	659.12	488.81	371.98	427.67	332.32
JC_g12281.t1	"Dmel\CG3919: CG3919, isoform	-0.70	2.03E-05	0.0001829	854.31	716.35	658.71	442.08	445.49	470.97
JC_g16479.t1	Tango6: Transport and Golgi orga	-0.70	1.93E-05	0.0001743	642.19	546.64	541.47	370.85	329.66	353.49
JC_g13622.t1	Pnn: Pinin (Drosophila melanogas	-0.71	0.0003279	0.0020464	1239.34	1310.35	1120.70	815.19	863.13	545.05
JC_g17876.t1	Dmel\CG12012: IP05517p (Drosc	-0.71	4.24E-09	7.62E-08	2495.38	2307.91	2337.77	1446.09	1539.16	1373.75
JC_g19535.t1	lok: Ovarian-specific serine/threon	-0.71	0.0008786	0.0047754	349.43	364.10	289.12	169.60	235.00	201.09
JC_g4439.t1	"CG1213: CG1213, isoform A (Dro	-0.71	0.0003301	0.0020573	334.90	294.04	265.27	183.16	181.54	176.75
JC_g3409.t1	Protein of unknown function	-0.71	1.34E-05	0.0001266	1057.00	984.73	887.22	509.92	609.21	657.24
JC_g13289.t1	Dmel\CG14353: IP21091p (Drosc	-0.71	0.0037562	0.0163903	349.43	321.67	254.34	141.33	183.76	229.66
JC_g21006.t1	IP10959p (Drosophila melanogas	-0.71	0.0008015	0.0044234	1270.57	761.74	965.71	669.34	611.43	527.06
JC_g19858.t1	Aats-val-RA: FI22042p1 (Drosoph	-0.71	3.64E-05	0.0003014	3992.61	2686.81	2941.83	1875.74	1925.62	2021.46
JC_g20118.t1	Brd8: SD08060p (Drosophila mela	-0.71	2.57E-05	0.000224	2035.53	1931.97	2419.23	1518.45	1105.93	1239.34
JC_g25047.t1	"lid: Little imaginal discs, isoform C	-0.71	1.76E-08	2.94E-07	3197.86	2830.87	2680.53	1729.89	1818.71	1739.94
JC_g2901.t1	"Gld2: Gld2, isoform C (Drosophila	-0.71	1.73E-05	0.0001578	597.87	738.06	699.44	417.21	374.21	438.16
JC_g16012.t1	Protein of unknown function	-0.71	0.0004067	0.0024643	578.26	388.76	492.79	307.54	298.48	273.06
JC_g3838.t1	Protein of unknown function	-0.72	0.0002721	0.0017452	1335.23	1056.76	865.36	566.45	712.78	678.41
JC_g24120.t1	Protein of unknown function	-0.72	0.0017337	0.0084777	408.27	372.98	322.90	177.51	280.66	202.15
JC_g24898.t1	Sp7: Serine protease 7 (Drosophi	-0.72	0.0013777	0.0069563	8968.84	8668.23	6906.00	3573.97	4337.95	6757.62
JC_g10876.t1	Protein of unknown function	-0.72	1.13E-05	0.0001082	3667.88	3473.21	2934.87	1815.81	1849.89	2399.30
JC_g1961.t1	CG34458: Uncharacterized protei	-0.72	0.0013017	0.0066342	693.04	571.30	481.86	271.35	426.56	345.02
JC_g8568.t1	"RhoGAP71E: Rho GTPase activ	-0.72	8.78E-08	1.31E-06	3167.35	4002.09	3629.35	2138.05	2123.87	2252.19
JC_g2044.t1	"CREG: Cellular repressor of E1A	-0.72	0.0026562	0.0121741	230.29	209.18	159.96	124.37	116.94	115.36
JC_g3242.t1	Ubi-p63E: AT20865p (Drosophila	-0.72	3.65E-07	4.89E-06	16311.14	13109.40	13702.70	8314.75	7970.91	9642.70
JC_g17100.t1	CG15211: RE01453p (Drosophila	-0.73	7.59E-06	7.60E-05	6975.44	5815.66	5569.70	4169.81	3056.05	3777.28
JC_g17672.t1	c62E-15: Purine nucleoside phos	-0.73	0.0010506	0.0055497	327.63	378.90	304.02	175.25	175.97	248.71
JC_g9832.t1	Protein of unknown function	-0.73	0.0007726	0.0042809	1093.32	713.39	663.68	452.26	506.74	511.19

JC_g18816.t1	Fuca: Putative alpha-L-fucosidase	-0.73	0.002483	0.0115306	626.93	459.81	545.45	303.01	237.22	425.46
JC_g11263.t1	Protein of unknown function	-0.73	0.0008742	0.0047559	722.10	585.12	595.12	309.80	492.27	328.09
JC_g20278.t1	Dmel\CG11247: FI01120p (Droso	-0.73	0.0012095	0.006242	1300.36	1101.17	753.09	533.66	596.95	740.85
JC_g8118.t1	"CG16791: Uncharacterized prote	-0.73	1.82E-06	2.11E-05	1781.27	2202.33	2149.99	1375.99	1136.00	1159.96
JC_g23678.t1	bif: Protein phosphatase 1-bindin	-0.73	9.17E-05	0.0006835	558.65	540.72	703.42	327.89	406.51	339.73
JC_g17312.t1	CG7220: AT19555p (Drosophila r	-0.73	4.28E-08	6.78E-07	2999.54	3620.23	3621.40	1934.53	2101.59	2096.61
JC_g10944.t1	Protein of unknown function	-0.73	0.0008101	0.004454	685.05	797.26	462.98	371.98	386.46	394.77
JC_g2211.t1	Mcm2: DNA replication licensing fa	-0.73	0.0015736	0.0078013	375.58	398.63	250.37	198.99	189.33	216.96
JC_g20386.t1	Protein of unknown function	-0.73	0.001616	0.0079597	440.96	380.87	652.75	289.44	267.29	313.27
JC_g10239.t1	CG9650: LD11946p (Drosophila r	-0.73	0.000137	0.0009711	4218.54	3945.85	4184.73	1899.48	2234.13	3193.07
JC_g18747.t1	Protein of unknown function	-0.74	0.000722	0.0040472	231.01	193.39	207.65	116.46	123.62	133.35
JC_g4762.t1	CG10959: LD12075p (Drosophila	-0.74	4.52E-06	4.81E-05	893.54	976.84	1109.77	531.40	590.27	649.83
JC_g15338.t1	Protein of unknown function	-0.74	0.0017424	0.0085129	212.85	291.08	228.51	160.55	149.24	120.65
JC_g19844.t1	Nprl2: Nitrogen permease regulat	-0.74	2.16E-07	3.05E-06	900.08	945.27	1046.18	564.19	602.52	554.58
JC_g23317.t1	Protein of unknown function	-0.74	7.01E-06	7.08E-05	1145.62	1006.44	900.13	533.66	635.94	644.54
JC_g5816.t1	Protein of unknown function	-0.74	1.28E-09	2.50E-08	1604.02	1661.62	1579.71	912.43	999.01	978.98
JC_g2418.t1	"escl: Escl, isoform A (Drosophila	-0.74	4.30E-07	5.67E-06	1223.35	1325.15	1116.72	659.17	771.81	749.32
JC_g25044.t1	kek3: IP22191p (Drosophila mela	-0.74	4.36E-05	0.0003536	504.16	631.49	607.04	306.40	386.46	338.67
JC_g13019.t1	Protein of unknown function	-0.74	5.49E-06	5.69E-05	541.94	513.09	481.86	305.27	282.89	323.86
JC_g5862.t1	"slgA: Sluggish A, isoform F (Dros	-0.74	3.02E-07	4.13E-06	3112.87	2588.14	2628.87	1495.84	1632.72	1821.43
JC_g9225.t1	CG10979: LD10772p (Drosophila	-0.74	2.90E-05	0.0002489	1207.37	1106.10	906.10	544.97	709.44	651.95
JC_g20971.t1	Nf-YA: LD21748p (Drosophila me	-0.74	0.0001107	0.0008053	935.68	614.72	726.27	439.82	455.51	449.80
JC_g12785.t1	pgant3: Polypeptide N-acetylgala	-0.74	7.86E-05	0.0005966	427.88	444.02	383.50	209.17	268.41	263.53
JC_g21269.t1	"CT21630: Uncharacterized prote	-0.74	0.0036018	0.0158151	6849.76	7977.53	8730.11	3569.44	3225.34	6946.00
JC_g13354.t1	CG43320: Uncharacterized protei	-0.75	9.50E-07	1.17E-05	2240.39	1900.40	2133.10	1311.55	1052.47	1345.17
JC_g17980.t1	CG6171: Aprataxin and PNK-like	-0.75	0.0009722	0.0052103	1067.89	599.92	714.34	500.88	428.78	464.62
JC_g25168.t1	"CG4291-RA: CG4291, isoform A	-0.75	1.02E-05	9.89E-05	1287.28	1130.77	948.82	651.25	603.64	727.09
JC_g2108.t1	Protein of unknown function	-0.75	0.0015876	0.0078501	2658.11	1757.33	1320.40	1072.98	999.01	1268.97
JC_g24130.t1	Use1: Vesicle transport protein US	-0.75	0.0001037	0.00076	626.21	784.43	572.27	338.06	443.26	381.01
JC_g695.t1	CG5181: SOSS complex subunit	-0.75	0.001037	0.0054983	1043.92	644.32	611.02	399.12	467.76	472.03
JC_g11180.t1	Protein of unknown function	-0.75	4.29E-06	4.58E-05	10750.84	8923.79	8238.31	4790.54	6416.15	5187.01
JC_g4332.t1	peng: Protein penguin (Drosophila	-0.76	2.64E-07	3.69E-06	1066.44	1095.25	1021.34	555.15	690.51	626.55
JC_g5591.t1	HP1b: GM01918p (Drosophila me	-0.76	4.54E-12	1.25E-10	10392.70	9884.84	9595.47	5641.91	5751.26	6228.44
JC_g23964.t1	GstD7: Glutathione S-transferase	-0.76	0.0001885	0.0012763	576.81	513.09	427.22	284.92	346.37	255.06
JC_g2991.t1	Mat89Ba: Nucleolar protein 6 (Dro	-0.76	3.98E-07	5.28E-06	1385.35	1347.84	1264.76	851.37	672.69	824.46
JC_g20008.t1	"CG6073: CG6073, isoform B (Dro	-0.76	1.70E-05	0.0001553	576.81	562.42	549.42	388.94	299.59	299.52
JC_g10182.t1	GILT1: GILT-like protein 1 (Droso	-0.76	2.27E-05	0.0002004	1368.65	971.91	1330.33	740.57	644.84	760.96
JC_g23330.t1	CG10959: LD12075p (Drosophila	-0.76	0.0001583	0.0010969	613.86	483.49	432.18	333.54	275.09	283.64
JC_g1268.t1	Sip1: GH04176p (Drosophila mela	-0.76	2.18E-07	3.08E-06	4130.64	3275.87	3640.28	1948.10	2157.28	2373.90
JC_g19027.t1	CG11318: RE14222p (Drosophila	-0.76	0.0021732	0.010285	2332.65	2347.38	2412.28	818.59	1396.61	1880.70
JC_g8474.t1	Ugt86Di: UDP-glucuronosyltransfe	-0.76	0.0020033	0.0095988	436.60	430.20	353.70	161.68	242.79	299.52
JC_g12313.t1	"dgo: Diego, isoform A (Drosophila	-0.77	1.02E-05	9.89E-05	3468.83	3133.78	3181.27	1455.14	2088.23	2152.70
JC_g1659.t1	His2Av: Histone H2A (Drosophila	-0.77	8.11E-08	1.22E-06	31874.76	30357.06	28231.03	15085.05	17611.28	20149.02
JC_g17883.t1	Protein of unknown function	-0.77	2.99E-06	3.30E-05	1003.96	1015.32	782.90	554.02	562.43	515.42
JC_g11278.t1	CG43346-RA: LD39232p2 (Droso	-0.77	3.46E-06	3.77E-05	722.82	693.66	667.65	377.64	467.76	366.19
JC_g18844.t1	"E2f2: E2F transcription factor 2,	-0.77	7.71E-06	7.70E-05	968.37	856.46	703.42	478.26	474.45	515.42
JC_g20358.t1	Snm1: LD28027p (Drosophila me	-0.77	0.0008627	0.0047049	317.46	334.49	305.01	132.29	204.92	212.73
JC_g14506.t1	tup: Tailup (Drosophila melanogas	-0.77	0.0004446	0.002659	217.21	226.94	234.47	118.72	152.58	119.59
JC_g8517.t1	Protein of unknown function	-0.77	9.20E-05	0.0006854	462.03	349.29	369.59	227.26	211.61	244.48
JC_g18052.t1	Protein of unknown function	-0.77	0.0022787	0.0106993	185.25	154.91	197.71	84.80	121.40	101.60
JC_g24987.t1	ry: Xanthine dehydrogenase (Dro	-0.77	0.0034357	0.0151964	163.45	219.05	274.21	113.06	141.44	119.59
JC_g3723.t1	"RfC38: Replication factor C 38kD	-0.77	0.0013223	0.0067178	642.91	504.21	506.70	322.23	220.52	405.35
JC_g20743.t1	Dmel\CG14985: FI11682p (Droso	-0.77	3.41E-07	4.61E-06	799.10	920.60	922.99	476.00	503.40	553.52
JC_g14889.t1	Protein of unknown function	-0.77	0.000207	0.001381	378.48	371.00	386.48	189.95	191.56	272.00
JC_g17516.t1	Protein of unknown function	-0.78	0.0002686	0.0017281	2207.70	2451.97	2025.80	864.94	1466.77	1503.93
JC_g13627.t1	Ser: Protein serrate (Drosophila m	-0.78	6.04E-09	1.07E-07	11924.07	13320.56	13747.41	6596.18	8056.66	7934.51
JC_g3522.t1	Protein of unknown function	-0.78	0.0006779	0.0038281	309.47	237.80	236.46	151.51	169.29	127.00
JC_g12784.t1	"CG9323: CG9323, isoform A (Dro	-0.78	1.34E-06	1.60E-05	771.50	640.37	767.00	387.81	449.94	415.93
JC_g2308.t1	Cad89D: Cadherin-89D (Drosophi	-0.78	0.0006297	0.003602	19532.25	13782.34	19575.43	6609.74	11847.77	11657.81
JC_g135.t1	MrgBP: MRG/MORF4L binding pro	-0.79	7.59E-05	0.0005788	1035.93	1230.42	1012.40	465.83	667.12	736.62
JC_g1095.t1	CG6654: CG6654 (Drosophila me	-0.79	7.14E-06	7.19E-05	995.25	954.15	901.13	434.17	571.34	623.37
JC_g20625.t1	CG12006: GPI mannosyltransfera	-0.79	0.0003194	0.0020037	5521.07	7187.18	6119.12	2458.02	3552.77	4675.83
JC_g1021.t1	MED16: Mediator of RNA polymer	-0.79	0.0001593	0.0011024	1059.17	954.15	1244.89	465.83	772.92	612.79
JC_g15586.t1	CG4927: CG4927 (Drosophila me	-0.79	2.57E-07	3.59E-06	1460.91	1391.26	1174.35	775.62	698.30	831.87
JC_g17892.t1	tos: Exonuclease 1 (Drosophila m	-0.79	9.97E-05	0.0007374	694.49	928.49	697.45	400.25	535.70	382.07
JC_g24084.t1	XK-related protein (Drosophila me	-0.80	1.11E-05	0.0001065	2537.51	2808.17	2047.66	1140.82	1574.80	1492.28
JC_g9346.t1	spn-F: Protein spindle-F (Drosoph	-0.80	6.92E-07	8.74E-06	499.08	488.42	494.78	269.09	272.86	303.75
JC_g16365.t1	l(2)35Bd: mRNA cap guanine-N7	-0.80	0.0004855	0.002869	309.47	314.76	391.45	225.00	200.47	147.11
JC_g18715.t1	Protein of unknown function	-0.80	3.86E-07	5.14E-06	1734.78	1540.25	1418.75	765.45	943.32	963.11
JC_g14865.t1	"rst: Roughest, isoform B (Drosop	-0.80	0.0006816	0.0038419	5353.26	4882.23	5012.34	1815.81	2805.47	3949.79
JC_g1302.t1	CG4797: CG4797 (Drosophila me	-0.80	1.21E-05	0.0001149	3186.24	2672.99	2272.19	1309.29	1474.57	1825.67
JC_g3500.t1	smt3: Small ubiquitin-related modi	-0.80	7.50E-10	1.51E-08	4409.59	3651.81	3682.01	2166.31	2244.15	2285.00
JC_g11904.t1	Cat: Catalase (Drosophila melano	-0.80	0.0004101	0.0024808	23938.21	20345.92	12029.61	9056.46	11534.82	11043.97
JC_g24174.t1	"GatB: Glutamyl-tRNA(Gln) amido	-0.81	2.30E-06	2.60E-05	6955.83	5827.50	5102.75	2802.87	3600.66	3720.13

JC_g7454.t1	CG12102: IP04009p (Fragment) (	-0.81	1.13E-07	1.65E-06	6181.42	4856.58	5887.63	2926.11	3044.92	3630.17
JC_g23952.t1	"CG5180: CG5180, isoform B (Dr	-0.81	0.0027099	0.0123785	200.50	174.65	205.66	75.75	113.60	133.35
JC_g16961.t1	ND-51: GM14163p (Drosophila m	-0.81	0.0005224	0.0030601	2673.36	2055.31	4224.47	1662.05	1626.03	1725.12
JC_g23195.t1	CG12938: IP04234p (Fragment) (	-0.81	0.0003941	0.0023981	342.16	365.08	250.37	174.12	203.81	158.75
JC_g2129.t1	Protein of unknown function	-0.81	0.0002766	0.0017716	700.30	496.31	421.25	298.49	286.23	322.80
JC_g19011.t1	BCL7-like: BCL7-like (Drosophila r	-0.81	0.000281	0.0017947	1651.24	877.18	1323.38	670.47	727.26	759.90
JC_g19743.t2	Hip1: Huntingtin interacting protei	-0.81	2.93E-05	0.000251	2912.37	2070.11	2313.92	1300.24	1133.77	1671.15
JC_g25186.t1	"capu: Cappuccino, isoform G (Dr	-0.81	4.33E-08	6.85E-07	9324.08	8184.74	9404.71	4246.70	5452.78	5529.92
JC_g19933.t1	CG13442: AT03090p (Drosophila	-0.81	0.0006598	0.0037389	837.61	1052.82	721.30	347.11	628.14	481.55
JC_g14163.t1	Protein of unknown function	-0.81	5.53E-06	5.71E-05	1660.68	1328.11	1228.99	753.01	697.19	926.06
JC_g24914.t1	"Sfmbt: Scm-related gene contain	-0.81	3.00E-08	4.86E-07	1289.46	1300.48	1339.27	637.68	779.61	803.29
JC_g11501.t1	Protein of unknown function	-0.81	0.0032507	0.0145085	403.18	546.64	394.43	152.64	322.98	266.71
JC_g22163.t1	Protein of unknown function	-0.81	4.53E-07	5.94E-06	1592.39	1661.62	1569.77	968.96	1015.71	736.62
JC_g11446.t1	"CG7280: Probable sulfite oxidas	-0.81	0.0001531	0.0010676	621.85	412.44	423.24	279.27	258.38	278.35
JC_g8003.t1	Protein of unknown function	-0.81	1.44E-10	3.21E-09	60410.72	57699.72	52690.63	29345.86	31643.06	35573.53
JC_g21706.t1	Sema2a: Semaphorin-2A (Drosop	-0.82	0.0006769	0.0038247	4266.48	4230.02	4205.59	1383.91	2730.85	2944.35
JC_g19287.t1	tum: FI24033p1 (Drosophila mela	-0.82	0.0032221	0.0144019	719.92	444.02	370.59	269.09	355.28	221.20
JC_g2655.t1	CSP1: GEO08457p1 (Drosophila	-0.82	2.31E-09	4.33E-08	1279.29	1263.97	1195.21	638.81	710.55	755.67
JC_g1090.t1	BcDNA:GH10229: BcDNA.GH102	-0.82	1.92E-06	2.20E-05	2388.59	2044.46	3042.18	1312.68	1426.68	1451.01
JC_g20599.t1	"Dmel\CG4074: CG4074, isoform	-0.82	0.0004408	0.0026418	1054.09	1583.67	1388.95	517.83	802.99	912.30
JC_g2986.t1	Protein of unknown function	-0.82	2.00E-05	0.0001804	3390.38	3308.43	2699.41	2136.92	1332.01	1783.33
JC_g537.t1	Protein of unknown function	-0.82	0.0001147	0.0008323	583.35	491.38	729.25	359.54	273.98	370.43
JC_g5116.t1	CG13618: RE08075p (Drosophila	-0.82	0.0025604	0.0118135	439.51	256.54	294.08	152.64	160.38	231.78
JC_g7415.t1	CG9917-RA: GM03616p (Drosopl	-0.82	0.002985	0.0135058	138.75	143.07	154.99	88.19	57.91	93.14
JC_g11086.t1	Protein of unknown function	-0.82	4.17E-07	5.51E-06	746.80	825.87	836.55	384.42	472.22	488.96
JC_g25227.t1	beat-VII-RD: RT09811p (Fragmen	-0.83	0.0002668	0.001718	536.13	408.50	359.66	196.73	249.47	275.17
JC_g22798.t1	Art7: Protein arginine N-methyltra	-0.84	1.51E-07	2.17E-06	1667.22	1890.53	1754.57	881.90	1166.07	900.66
JC_g9572.t1	"pll: Pelle, isoform B (Drosophila n	-0.84	5.16E-06	5.39E-05	1675.94	1124.85	1401.86	850.24	775.15	700.63
JC_g10335.t1	Protein of unknown function	-0.84	0.0002933	0.001863	223.02	282.20	217.58	115.33	130.31	150.29
JC_g24108.t1	CG7741: CWF19-like protein 1 ho	-0.84	2.23E-05	0.0001975	1123.10	945.27	1028.30	454.52	720.58	531.30
JC_g13310.t1	"Dhap-at: Dihydroxyacetone phos	-0.84	2.57E-05	0.0002236	460.57	408.50	352.70	195.60	228.31	248.71
JC_g5579.t1	"sti: Sticky, isoform B (Drosophila	-0.84	0.0013838	0.0069843	281.14	409.48	334.82	126.63	202.70	226.49
JC_g11724.t1	sca: Protein scabrous (Drosophila	-0.84	0.0007845	0.0043445	701.03	908.76	599.10	272.49	513.43	412.76
JC_g18746.t1	Protein of unknown function	-0.85	0.0001904	0.0012863	272.42	308.84	288.12	119.85	177.08	176.75
JC_g24065.t1	cv: Crossveinless (Drosophila mela	-0.85	6.07E-06	6.22E-05	3585.79	4059.32	3925.42	1764.94	2741.98	1840.48
JC_g21692.t1	CG17493: RE19335p (Drosophila	-0.85	3.91E-05	0.000321	424.25	305.88	367.60	194.47	188.22	218.02
JC_g22608.t1	"CT30701: Uncharacterized prote	-0.85	1.19E-06	1.44E-05	1572.78	1384.35	1192.23	676.13	886.52	717.57
JC_g5872.t1	CG5255: CG5255 (Drosophila me	-0.85	3.54E-08	5.72E-07	4134.99	3840.27	4201.62	1833.90	2538.17	2334.74
JC_g19079.t1	"CG31869: Uncharacterized prote	-0.85	0.0001402	0.0009892	20005.18	22270.99	19822.82	7091.40	13815.72	12917.26
JC_g10366.t1	Npc2a: Protein NPC2 homolog (D	-0.85	1.99E-07	2.83E-06	3784.84	3059.78	2731.20	1675.61	1945.67	1642.57
JC_g18618.t1	tnc: Tenectin isoform 1 (Drosophil	-0.85	6.11E-05	0.0004777	71195.70	96838.48	77639.05	36024.57	37757.40	60189.89
JC_g18118.t1	mRpL50: GM06185p (Drosophila	-0.85	5.48E-07	7.05E-06	723.55	742.00	622.94	345.98	366.41	431.81
JC_g4475.t1	Protein of unknown function	-0.85	3.69E-06	3.99E-05	1035.93	874.22	836.55	433.04	467.76	601.15
JC_g10808.t1	wdp: Protein windpipe (Drosophila	-0.85	6.31E-07	8.03E-06	2053.69	2166.81	1524.07	989.31	1134.88	1022.37
JC_g20602.t1	Dim1: Dim1 (Drosophila melanoga	-0.85	0.0001323	0.0009432	760.60	772.59	727.26	277.01	446.60	502.72
JC_g9002.t1	CG5886: CG5886 (Drosophila me	-0.85	4.48E-05	0.0003611	1870.63	1125.83	1189.25	739.44	775.15	764.13
JC_g22142.t1	Protein of unknown function	-0.85	3.62E-06	3.92E-05	3434.69	3018.34	3076.95	1286.67	1975.74	1942.09
JC_g15572.t1	BcDNA:LD13269: IP12536p (Dros	-0.85	7.49E-09	1.31E-07	1470.35	1297.52	1544.93	710.04	798.54	857.27
JC_g19573.t1	prage: EG:131F2.2 protein (Dros	-0.86	2.32E-05	0.0002047	1028.66	801.21	1020.35	393.46	552.41	601.15
JC_g11141.t1	nmdyn-D7: FI21821p1 (Drosophil	-0.86	4.29E-07	5.66E-06	1328.69	1063.67	987.56	557.41	642.62	643.48
JC_g10341.t1	Protein of unknown function	-0.86	0.0001442	0.0010114	257.89	277.26	234.47	118.72	129.19	167.22
JC_g17934.t1	CG12106: RE09151p (Drosophila	-0.86	0.0001364	0.0009677	219.39	185.50	188.77	104.02	114.71	101.60
JC_g538.t1	"qkr54B: Quaking related 54B, iso	-0.86	4.24E-11	1.04E-09	10115.19	8520.22	9361.99	4688.78	5009.52	5586.01
JC_g18991.t1	CG17683: Probable cytosolic Fe-S	-0.86	0.0033724	0.0149628	800.56	365.08	717.33	286.05	270.63	440.28
JC_g25446.t1	CG17124: GEO07393p1 (Drosop	-0.87	4.77E-09	8.51E-08	10391.24	8905.04	7923.37	4479.61	4956.06	5382.81
JC_g16536.t1	CG11030-RA: FI04466p (Drosoph	-0.87	3.02E-10	6.45E-09	1329.42	1180.10	1383.98	688.56	740.62	692.17
JC_g19996.t1	"crol: Crooked legs, isoform H (Dro	-0.87	1.98E-05	0.0001786	722.82	495.33	520.61	297.36	338.57	303.75
JC_g22125.t1	"l(3)07882: Lethal (3) 07882, isof	-0.87	1.18E-05	0.0001124	1162.33	1020.26	740.18	521.23	571.34	486.84
JC_g24114.t1	Rpb5: RE34924p (Drosophila mel	-0.87	6.53E-07	8.30E-06	1375.18	1294.56	1150.50	568.71	809.68	692.17
JC_g10769.t1	MED30: Mediator of RNA polymer	-0.87	1.74E-06	2.03E-05	743.89	620.64	628.90	314.32	418.76	346.08
JC_g20327.t1	Rab5: Drab5 (Drosophila melanog	-0.87	3.92E-05	0.0003215	291.31	327.59	253.35	139.07	168.17	161.93
JC_g18988.t1	"Fign: CG3326, isoform B (Drosop	-0.87	0.0012101	0.0062427	181.61	153.93	165.92	90.45	66.82	109.01
JC_g21357.t1	CG7137: Ribosomal RNA-process	-0.87	0.0003818	0.0023385	600.78	475.59	411.32	254.39	341.91	198.97
JC_g11183.t1	nw: MIP03875p (Drosophila melan	-0.87	2.70E-08	4.44E-07	558918.65	497203.14	542382.45	254950.01	259879.18	351159.00
JC_g19544.t1	Sas-6: Spindle assembly abnorma	-0.87	7.04E-06	7.10E-05	305.84	343.37	300.04	163.94	159.26	187.33
JC_g1139.t1	CG8736: CG8736 (Drosophila me	-0.87	0.0013147	0.0066884	227.38	268.38	410.33	174.12	130.31	174.63
JC_g23117.t1	"CG42260: Uncharacterized prote	-0.87	6.50E-05	0.0005043	548.48	842.65	690.50	312.06	356.39	445.57
JC_g20062.t1	Dmel\CG13025: RE72625p (Dros	-0.87	0.0001947	0.0013081	488.18	557.49	436.16	348.24	201.58	240.25
JC_g12889.t1	HLHmgamma: Enhancer of split m	-0.87	7.80E-05	0.000594	887.73	821.93	754.09	326.76	407.62	582.10
JC_g8320.t1	anon-EST:fe1A11: CG7492 (Dros	-0.88	0.0008304	0.0045527	499.80	823.90	578.23	301.88	451.06	254.01
JC_g21720.t1	CycD: Cyclin D (Fragment) (Droso	-0.88	3.39E-09	6.18E-08	727.18	817.98	712.36	399.12	410.96	409.58
JC_g8778.t1	Spn27A: Serine protease inhibito	-0.88	8.19E-06	8.15E-05	3864.03	3389.34	2978.59	1368.08	1883.30	2236.31
JC_g14249.t1	Prosalpha5: Proteasome subunit	-0.88	0.0008211	0.004506	2056.60	1540.25	983.59	594.72	919.93	905.95
JC_g7993.t1	Parp: Poly [ADP-ribose] polymera	-0.88	4.20E-12	1.16E-10	3447.77	3570.90	3899.59	2060.03	1789.75	2047.92

JC_g15415.t1	Nnp-1: Ribosomal RNA processing	-0.88	7.92E-06	7.90E-05	1390.44	1356.72	1344.24	530.27	768.47	889.02
JC_g25445.t1	BcDNA.GH10711: BcDNA.GH107	-0.88	0.0011835	0.0061272	650.18	597.95	464.97	211.43	253.93	436.04
JC_g25064.t1	CG15544: LP06141p (Drosophila	-0.88	4.86E-05	0.000389	3996.97	4180.68	3417.73	1377.12	2222.99	2570.75
JC_g2846.t1	Dmel\CG11360: LD09246p1 (Dro	-0.89	0.0024495	0.0114073	2066.77	1975.39	1585.67	473.74	1255.16	1205.47
JC_g12524.t1	Protein of unknown function	-0.89	2.61E-05	0.0002268	487.45	643.33	427.22	265.70	253.93	307.98
JC_g22779.t1	CG4573-RA: FI07227p (Fragmen	-0.89	0.000651	0.0036925	239.73	395.67	410.33	167.34	218.29	162.99
JC_g17254.t1	"mars: Mars, isoform B (Drosophila	-0.89	2.83E-05	0.0002441	689.41	913.69	582.21	329.02	415.42	414.88
JC_g19687.t1	Mmp2: Matrix metalloproteinase-2	-0.89	8.94E-08	1.33E-06	2290.52	2871.32	2407.31	1118.21	1490.16	1437.25
JC_g3118.t1	pyd3: Beta-alanine synthase (Dro	-0.89	0.0002019	0.0013523	11052.32	10019.03	8428.08	3584.14	4559.58	7422.27
JC_g8113.t1	CG12970: Uncharacterized protei	-0.89	6.31E-12	1.69E-10	1923.66	1804.69	1694.95	905.65	1003.46	999.09
JC_g13645.t1	Protein of unknown function	-0.89	0.0004041	0.0024524	971.27	1096.23	819.66	537.06	661.55	317.51
JC_g24913.t1	AGO2 (Fragment) (Drosophila me	-0.89	4.83E-08	7.56E-07	7152.70	6654.36	6897.05	2970.20	4427.04	3637.58
JC_g4626.t1	"pst: Pastrel, isoform E (Drosophil	-0.89	3.45E-11	8.60E-10	2629.05	2747.98	2461.96	1262.93	1546.96	1381.16
JC_g5543.t1	MIP02663p (Fragment) (Drosophi	-0.89	0.0001219	0.0008786	1417.32	965.00	742.16	498.61	584.70	560.93
JC_g19546.t1	Dmel\CG13248: FI04531p (Droso	-0.89	0.0001408	0.0009909	582.62	396.66	491.80	206.91	240.56	325.97
JC_g18616.t1	Protein of unknown function	-0.89	5.72E-05	0.0004507	924.78	1405.07	1139.57	492.96	555.75	777.89
JC_g2622.t1	CG3823: CG3823 (Drosophila me	-0.89	0.0002239	0.0014733	194.69	194.38	245.40	99.50	131.42	101.60
JC_g13038.t1	"GstS1: Glutathione S transferase	-0.90	1.31E-09	2.57E-08	31908.90	30055.13	26408.90	14060.69	14818.07	18220.69
JC_g20131.t1	CG6654: CG6654 (Drosophila me	-0.90	0.0002118	0.0014082	296.39	278.25	370.59	210.30	149.24	135.47
JC_g22925.t1	Spn85F: Serpin 85F (Drosophila r	-0.90	0.0003581	0.0022121	1014.13	1000.52	749.12	308.67	503.40	629.72
JC_g14534.t1	Protein of unknown function	-0.90	2.49E-06	2.80E-05	286.95	313.77	291.10	167.34	147.01	154.52
JC_g8985.t1	wtrw: HL04706p (Drosophila mela	-0.91	5.50E-06	5.69E-05	1167.42	1151.49	1286.62	584.54	493.38	811.76
JC_g19999.t1	"CG7987: CG7987, isoform A (Dr	-0.91	9.26E-06	9.12E-05	765.69	576.24	728.25	440.95	340.80	300.57
JC_g12292.t1	CG6175-RB: RE65945p1 (Drosop	-0.91	2.89E-06	3.20E-05	1445.65	1428.75	1183.29	532.53	755.10	831.87
JC_g23682.t1	Protein of unknown function	-0.92	6.25E-06	6.38E-05	1191.39	1051.83	1503.20	511.05	689.39	750.38
JC_g14528.t1	CG30016: 5-hydroxyisourate hydr	-0.92	0.0023822	0.0111441	193.96	278.25	167.91	137.94	112.49	75.14
JC_g16335.t1	"Su(H): Suppressor of hairless, iso	-0.92	3.56E-06	3.87E-05	8283.79	8361.36	7673.00	2939.67	4626.40	5103.40
JC_g20312.t1	Protein of unknown function	-0.92	0.0003782	0.0023213	221.57	206.22	176.85	81.41	129.19	100.54
JC_g10766.t1	Protein of unknown function	-0.92	8.46E-05	0.000635	521.60	419.35	460.00	174.12	306.27	243.42
JC_g20053.t1	Ccs: Superoxide dismutase [Cu-Z	-0.92	0.0018746	0.0090702	2945.06	2849.61	2738.16	2412.79	929.96	989.56
JC_g5758.t1	Gba1b: Glucosylceramidase (Dros	-0.92	0.0018314	0.0088942	243.36	253.58	346.74	166.20	175.97	85.73
JC_g16239.t1	"CycB3: Cyclin B3, isoform B (Dro	-0.92	0.0001105	0.0008044	946.57	936.39	582.21	334.67	517.88	414.88
JC_g15949.t1	modSP: Modular serine protease	-0.92	0.0013014	0.0066342	124.95	185.50	155.98	88.19	60.14	87.84
JC_g19081.t1	"CG17127: Uncharacterized prote	-0.93	0.0018875	0.0091242	1187.76	612.75	680.56	469.22	259.50	526.00
JC_g13035.t1	"GstS1: Glutathione S transferase	-0.93	2.50E-10	5.40E-09	3093.98	3182.13	2442.09	1500.36	1481.25	1564.25
JC_g15271.t1	plx: FI17814p1 (Drosophila melan	-0.93	7.82E-05	0.000595	241.18	215.10	220.56	111.93	95.78	139.70
JC_g20430.t1	Dmel\CG6034: CG6034 (Drosoph	-0.93	0.0006858	0.0038593	142.39	204.25	142.07	72.36	85.76	89.96
JC_g8896.t1	Protein of unknown function	-0.93	3.68E-07	4.92E-06	2738.74	2785.48	2190.72	1061.67	1358.74	1575.90
JC_g3425.t1	CG3902: GH07925p (Drosophila	-0.93	7.23E-05	0.0005543	1577.14	1559.99	899.14	828.76	600.30	635.01
JC_g21320.t1	CG12325: LD10780p (Drosophila	-0.93	3.01E-06	3.31E-05	1711.53	1570.84	1704.89	812.93	1105.93	647.72
JC_g2992.t1	"l(1)G0156: Probable isocitrate de	-0.93	3.01E-06	3.31E-05	3263.25	3293.63	2664.64	1772.85	1133.77	1834.13
JC_g10768.t1	Dmel\CG14984: GEO10764p1 (D	-0.94	7.41E-05	0.0005664	25099.82	14725.63	18370.29	7699.68	13241.04	8745.21
JC_g21804.t1	"ovo: Ovo, isoform E (Drosophila r	-0.94	1.58E-09	3.05E-08	104936.73	82668.37	90046.20	48275.10	40907.00	54502.27
JC_g22337.t1	CG6654: CG6654 (Drosophila me	-0.94	6.84E-08	1.04E-06	505.61	505.19	582.21	246.48	272.86	300.57
JC_g20891.t1	"CG4393: CG4393, isoform B (Dr	-0.94	0.0001944	0.0013069	834.70	837.72	609.03	247.61	418.76	485.79
JC_g21426.t1	"CG3106: CG3106, isoform A (Dr	-0.95	0.0002631	0.0016988	159.09	160.83	146.05	75.75	93.55	65.62
JC_g11210.t1	MESR6: LD22716p (Drosophila m	-0.95	3.30E-07	4.48E-06	428.61	387.78	395.42	180.90	230.54	207.44
JC_g5115.t1	Protein of unknown function	-0.95	0.0010222	0.0054346	199.05	144.06	117.24	76.88	72.39	80.44
JC_g9544.t1	Ppn-RC: GH25513p (Fragment) (D	-0.95	0.0013445	0.006816	10822.76	9000.75	6994.42	2118.83	5700.03	5489.70
JC_g24037.t1	Cib2: CIB2 ortholog (Drosophila m	-0.95	0.0020683	0.0098525	104.61	119.39	103.33	40.70	69.05	51.86
JC_g1525.t1	"rn: Rotund, isoform F (Drosophila	-0.95	2.83E-08	4.61E-07	10997.83	10170.99	9699.79	4055.62	6202.32	5491.82
JC_g16121.t1	modSP: Modular serine protease	-0.95	9.27E-06	9.12E-05	2176.47	1748.45	1823.12	673.86	1030.19	1205.47
JC_g9371.t1	CG17928: IP12339p (Drosophila	-0.95	0.0032548	0.0145199	204.13	185.50	135.12	75.75	57.91	123.83
JC_g15432.t1	"Meics: Meiotic central spindle, iso	-0.96	5.07E-06	5.32E-05	419.17	517.03	428.21	209.17	281.77	198.97
JC_g19850.t1	"CG12911: Uncharacterized prote	-0.96	0.0010321	0.0054798	3606.13	4031.69	3812.16	935.04	1882.19	2844.87
JC_g195.t1	"CT30701: Uncharacterized prote	-0.96	0.001809	0.0088191	788.21	666.03	549.42	165.07	356.39	462.50
JC_g19843.t1	Ppcdc: LD37882p2 (Drosophila m	-0.96	7.87E-07	9.86E-06	319.64	322.65	291.10	142.46	170.40	158.75
JC_g21640.t1	"CG1628: CG1628, isoform C (Dr	-0.96	5.07E-05	0.0004038	305.11	268.38	239.44	128.89	167.06	111.13
JC_g15977.t1	Protein of unknown function	-0.96	6.79E-10	1.38E-08	995.97	806.14	898.15	429.64	484.47	456.15
JC_g16438.t1	CG7373: LD27273p (Drosophila r	-0.97	8.57E-05	0.0006416	449.68	438.10	332.83	142.46	227.20	238.13
JC_g9074.t1	PVRAP: PVR adaptor protein (Dro	-0.97	0.0004755	0.0028168	589.88	340.41	390.46	160.55	208.27	283.64
JC_g17909.t1	Protein of unknown function	-0.97	0.0009683	0.0051918	541.21	1161.36	639.83	284.92	495.61	368.31
JC_g1523.t1	Protein of unknown function	-0.97	1.44E-07	2.09E-06	1289.46	1167.28	1040.22	511.05	719.46	530.24
JC_g22128.t1	"gatA-RA: Glutamyl-tRNA(Gln) am	-0.97	4.60E-05	0.0003701	787.48	664.05	453.05	263.44	315.18	369.37
JC_g22129.t1	"BOD1: CG5514, isoform A (Dros	-0.97	8.27E-11	1.95E-09	3456.48	2642.40	2704.38	1463.05	1457.86	1528.27
JC_g16957.t1	mRNA-cap: mRNA-capping enzym	-0.97	2.30E-07	3.23E-06	1840.12	1514.60	2430.16	932.78	1003.46	964.16
JC_g22298.t1	Protein of unknown function	-0.97	3.83E-09	6.94E-08	8853.33	11215.91	10343.59	4161.90	5316.91	5816.74
JC_g4524.t1	stg1: GH12419p1 (Drosophila me	-0.98	8.00E-08	1.21E-06	1349.03	1690.23	1160.44	619.59	764.01	714.39
JC_g22940.t1	Protein of unknown function	-0.98	2.97E-07	4.09E-06	1280.74	1047.88	823.63	491.83	534.59	545.05
JC_g23967.t1	Protein of unknown function	-0.98	1.14E-05	0.0001096	796.20	833.77	707.39	319.97	522.34	314.33
JC_g19074.t1	CG14764: LD39211p (Drosophila	-0.98	0.0009166	0.0049635	517.24	354.23	438.14	169.60	144.78	320.68
JC_g830.t1	Protein of unknown function	-0.99	0.0005295	0.0030943	127.13	100.64	115.25	62.19	51.23	52.92
JC_g10917.t1	Protein of unknown function	-0.99	5.18E-05	0.0004109	768.59	1122.87	662.68	312.06	442.15	495.31
JC_g1595.t1	CG3838: LD21447p (Drosophila r	-0.99	5.04E-07	6.54E-06	584.80	599.92	429.20	258.92	287.34	251.89

JC_g10593.t1	Protein of unknown function	-0.99	0.0009212	0.0049834	115.51	102.62	113.26	64.45	41.21	53.98
JC_g4494.t1	CG6083: AT08919p (Drosophila r	-0.99	1.35E-05	0.0001269	699.58	611.76	503.72	241.96	265.07	384.18
JC_g3753.t1	Toll-6: Toll-like receptor 6 (Drosop	-0.99	0.000251	0.001628	835.43	830.81	729.25	298.49	273.98	589.51
JC_g24105.t1	Fpps: Farnesyl pyrophosphate sy	-0.99	4.41E-10	9.21E-09	9432.32	9211.91	7913.43	3585.27	4705.47	4909.72
JC_g1216.t1	"CG8170: CG8170, isoform B (Dr	-0.99	1.48E-05	0.0001379	1012.68	843.64	887.22	332.41	400.94	610.67
JC_g3879.t1	"Dmel\CG7470: CG7470, isoform	-0.99	2.77E-14	9.44E-13	1780.55	1790.87	1962.21	855.90	986.76	913.36
JC_g21438.t1	MSBP: LD12946p (Drosophila me	-1.00	0.0001683	0.0011563	301.48	192.41	248.38	110.80	101.35	148.17
JC_g24123.t1	CG4406: Putative GPI-anchor tra	-1.00	6.10E-11	1.46E-09	1283.65	1334.03	1093.87	568.71	669.35	600.09
JC_g2185.t1	MIP02663p (Fragment) (Drosophi	-1.00	1.75E-05	0.0001591	446.04	426.26	284.15	198.99	164.83	198.97
JC_g1388.t1	EG:63B12.6: GM08325p (Drosop	-1.00	3.22E-06	3.53E-05	291.31	290.09	252.36	124.37	123.62	158.75
JC_g10703.t1	st-RA: FI22360p1 (Drosophila me	-1.00	0.0001768	0.001209	250.63	265.42	166.91	126.63	91.33	111.13
JC_g5018.t1	Cyp9f2: Probable cytochrome P4	-1.01	2.83E-05	0.0002437	415.53	457.83	508.69	168.47	200.47	299.52
JC_g8112.t1	"Gie: GTPase indispensable for e	-1.01	0.0002172	0.0014374	6341.24	8325.84	8879.14	5622.69	3439.17	2220.44
JC_g13356.t1	CG5285: CG5285 (Drosophila me	-1.01	4.65E-07	6.07E-06	347.97	344.36	340.78	185.43	138.10	179.92
JC_g17344.t1	CG10802: LD13611p (Drosophila	-1.01	0.0001144	0.0008301	324.00	607.81	551.41	205.78	219.40	284.70
JC_g22349.t1	Protein of unknown function	-1.02	1.12E-10	2.55E-09	2340.64	2003.02	1721.78	978.01	1051.35	936.65
JC_g1218.t1	"CG8170: CG8170, isoform B (Dr	-1.02	0.0001026	0.000753	937.86	881.13	810.72	262.31	388.69	602.21
JC_g16686.t1	CG3831: CG3831-PA (Drosophila	-1.02	1.33E-07	1.94E-06	971.27	970.92	674.60	379.90	451.06	433.93
JC_g24510.t1	KP78a: KP78a (Drosophila melan	-1.03	3.81E-05	0.0003137	304.39	456.85	286.14	185.43	173.74	139.70
JC_g14593.t1	Cpr50Cb: Cuticular protein 50Cb (	-1.03	0.0001701	0.0011676	602.96	508.15	684.54	365.20	165.94	318.57
JC_g17256.t1	"NetA: Netrin-A, isoform B (Drosop	-1.03	6.49E-08	9.92E-07	1726.79	1989.20	1585.67	652.38	895.43	1007.56
JC_g24713.t1	Protein of unknown function	-1.03	0.0004421	0.0026468	305.11	570.32	745.14	231.78	295.14	232.84
JC_g11261.t1	"CG9555: CG9555, isoform A (Dr	-1.03	0.0003058	0.0019253	1213.18	957.11	1082.94	430.78	788.52	309.04
JC_g16975.t1	"pirk: Poor Imd response upon kn	-1.03	0.0020121	0.0096329	99.52	144.06	127.17	40.70	80.19	49.74
JC_g8898.t1	Protein of unknown function	-1.03	8.44E-08	1.26E-06	974.91	920.60	705.40	385.55	377.55	486.84
JC_g16028.t1	O-fut2: GDP-fucose protein O-fuc	-1.03	4.45E-07	5.84E-06	584.80	406.52	510.67	234.04	267.29	219.08
JC_g4917.t1	CG15093: 3-hydroxyisobutyrate d	-1.03	1.47E-07	2.12E-06	4522.92	3465.32	3360.10	1432.53	1769.70	2241.60
JC_g20298.t1	Cpr47Ea: Cuticular protein 47Ea (	-1.03	8.60E-06	8.50E-05	853.59	785.42	670.63	249.87	390.92	458.27
JC_g3779.t1	in: Protein inturned (Drosophila m	-1.03	8.49E-06	8.43E-05	1907.68	1694.18	974.65	733.79	760.67	682.64
JC_g20035.t1	Protein of unknown function	-1.03	0.0006473	0.003679	177.26	256.54	134.13	80.28	77.96	105.84
JC_g12634.t1	Protein of unknown function	-1.04	0.000383	0.0023437	215.76	127.29	184.80	78.01	70.16	98.43
JC_g11536.t1	Protein of unknown function	-1.04	0.0010694	0.0056337	2405.30	1783.97	1892.67	428.51	924.39	1453.13
JC_g10089.t1	Protein of unknown function	-1.04	0.0004128	0.0024922	4058.72	3224.56	3069.99	758.66	1963.49	2093.43
JC_g18901.t1	Rad51D: Rad51C (Drosophila me	-1.04	9.76E-07	1.20E-05	522.32	401.59	439.14	175.25	219.40	254.01
JC_g5954.t1	sand: CG8713 (Drosophila melan	-1.04	0.0036436	0.0159681	161.27	337.45	454.04	158.29	90.21	182.04
JC_g3521.t1	Kaz1-ORFB: KAZ1-type serine pr	-1.05	0.0034034	0.0150764	1070.07	1079.46	815.68	154.90	532.36	648.77
JC_g22199.t1	Rpt4-RA: LP16188p (Fragment) (	-1.05	8.37E-05	0.0006306	7980.13	4351.38	4294.02	1776.24	3220.88	2763.37
JC_g5586.t1	Protein of unknown function	-1.05	0.0029584	0.013396	351.61	140.11	156.98	79.15	106.92	106.89
JC_g14228.t1	CG11136-RA: RT10113p (Fragme	-1.05	7.31E-15	2.61E-13	6527.94	7778.22	7950.19	3419.07	3348.96	3860.89
JC_g12012.t1	"Strn-Mlck: Stretchin-Mlck, isoform	-1.05	1.38E-05	0.0001295	817.99	817.98	583.20	236.30	414.30	387.36
JC_g4535.t1	dmGlut: Dietary and metabolic glu	-1.05	2.04E-09	3.87E-08	2820.83	2495.38	2369.56	1034.54	1108.15	1501.81
JC_g20133.t1	Sra-1: Cytoplasmic FMR1-interacti	-1.06	0.0003399	0.0021132	1604.02	1776.07	2063.55	1363.56	586.93	546.11
JC_g3498.t1	LBR: Lamin-B receptor (Drosophil	-1.06	3.40E-09	6.19E-08	1544.45	1406.06	1253.83	533.66	669.35	776.83
JC_g12013.t1	Protein of unknown function	-1.06	0.0001054	0.0007713	363.23	384.82	292.10	110.80	223.86	143.94
JC_g18987.t1	DNApol-eta: DNA polymerase eta	-1.06	0.0005927	0.0034195	499.80	251.61	411.32	143.59	133.65	250.83
JC_g5760.t1	CG9164: CG9164-PA (Fragment)	-1.07	0.0001002	0.0007398	151.83	165.77	189.76	73.49	98.01	61.38
JC_g15871.t1	His2B: Histone H2B (Drosophila m	-1.07	2.10E-05	0.0001877	388.65	467.70	367.60	125.50	221.63	218.02
JC_g3047.t1	CG8132: CG8132 (Drosophila me	-1.07	5.65E-08	8.73E-07	533.22	405.54	433.18	193.34	213.83	234.96
JC_g19993.t1	crol: CROL ALPHA (Drosophila m	-1.07	1.45E-07	2.10E-06	990.89	738.06	766.01	392.33	458.85	313.27
JC_g21347.t1	CG1789: Probable U3 small nucle	-1.07	4.13E-05	0.0003357	597.15	670.96	523.59	249.87	387.58	184.15
JC_g24101.t1	Protein of unknown function	-1.07	9.43E-06	9.25E-05	350.15	306.87	279.18	105.15	152.58	173.57
JC_g229.t1	Gclm: GH03051p (Drosophila mel	-1.08	1.71E-06	2.00E-05	1181.95	1634.98	1467.44	454.52	743.97	782.13
JC_g20091.t1	CG12258: LD33178p (Drosophila	-1.08	0.0002957	0.0018751	2403.12	2271.40	2178.80	1725.36	702.76	672.06
JC_g10963.t1	l(2)k05911: AT19278p (Drosophil	-1.08	1.51E-05	0.0001407	1104.21	1086.37	900.13	287.18	588.05	540.82
JC_g11088.t1	"a: Arc, isoform A (Drosophila mel	-1.08	1.22E-12	3.59E-11	3664.25	3474.20	3831.03	1408.78	1902.24	1820.38
JC_g18408.t1	ncd: Kinesin-like protein (Drosoph	-1.08	3.05E-05	0.0002602	709.75	1082.42	627.91	261.18	392.03	449.80
JC_g24350.t1	"CG7997: CG7997, isoform A (Dr	-1.08	4.41E-05	0.0003565	552.83	525.92	390.46	143.59	282.89	242.36
JC_g17257.t1	NetB: GH10173p (Drosophila mel	-1.09	2.91E-09	5.36E-08	4560.70	5171.34	4827.54	1757.02	2161.73	2827.93
JC_g10607.t1	CG9752: CG9752 (Drosophila me	-1.09	1.09E-07	1.60E-06	2472.13	2346.39	2039.71	741.70	1187.23	1235.10
JC_g24885.t1	Cad86C: Cadherin-86C (Drosophi	-1.09	4.08E-07	5.40E-06	8426.18	8149.22	9085.79	2744.07	3755.47	5302.37
JC_g15688.t1	"CG5390-RA: CG5390, isoform A	-1.09	2.55E-05	0.0002224	346.52	305.88	266.26	94.97	167.06	155.58
JC_g18978.t1	GEO05059p1 (Fragment) (Drosop	-1.09	6.43E-06	6.54E-05	1400.61	786.41	1123.68	446.60	427.67	637.13
JC_g941.t1	Protein of unknown function	-1.09	1.58E-06	1.86E-05	2140.14	1781.99	2165.89	868.33	651.53	1262.62
JC_g6.t1	Dmel\CG9701: CG9701 (Drosoph	-1.10	0.0007462	0.0041627	104.61	82.88	76.50	42.96	34.53	39.16
JC_g11281.t1	Protein of unknown function	-1.10	3.77E-11	9.34E-10	988.71	840.68	838.54	371.98	464.42	394.77
JC_g5542.t1	Protein of unknown function	-1.10	3.25E-05	0.0002731	419.89	320.68	227.52	127.76	148.12	160.87
JC_g7503.t1	"eIF4E1: Eukaryotic initiation fact	-1.10	1.28E-06	1.54E-05	807.09	557.49	643.80	264.57	260.61	389.48
JC_g5587.t1	"CG8501-RA: CG8501, isoform A	-1.10	7.41E-05	0.0005663	253.53	248.65	151.02	88.19	94.67	110.07
JC_g20094.t1	Irp-1A: Aconitate hydratase (Dros	-1.10	0.0001427	0.0010032	1376.64	1477.10	1516.12	1051.50	416.53	478.38
JC_g8437.t1	Protein of unknown function	-1.11	1.54E-13	4.86E-12	1962.16	1939.87	1719.79	740.57	905.46	936.65
JC_g10681.t1	Galk: GH11113p (Drosophila mela	-1.11	0.0002425	0.0015796	429.34	520.98	367.60	101.76	249.47	227.55
JC_g19252.t1	Mipp1: Multiple inositol polyphosp	-1.11	0.000123	0.0008849	366.13	347.32	200.69	98.37	151.47	153.46
JC_g24779.t1	Protein of unknown function	-1.12	0.0001586	0.0010986	390.83	450.93	227.52	114.20	194.90	160.87
JC_g12932.t1	"CG5080: CG5080, isoform A (Dr	-1.12	1.50E-07	2.15E-06	4192.38	4114.57	3766.46	1204.14	2005.81	2224.67

JC_g11098.t1	CG1814-RA: RH26605p (Drosoph	-1.12	0.0025181	0.0116415	305.84	328.57	437.15	113.06	267.29	74.09
JC_g16590.t1	Protein of unknown function	-1.13	3.55E-05	0.0002958	367.59	225.96	207.65	120.98	118.05	114.30
JC_g12681.t1	"CG9864: CG9864, isoform A (Dr	-1.13	3.18E-07	4.33E-06	5920.63	6360.32	4570.22	1842.95	2342.16	3335.94
JC_g3084.t1	"CG7737: CG7737, isoform A (Dr	-1.13	6.97E-07	8.78E-06	298.57	405.54	339.79	124.37	174.85	165.10
JC_g20117.t1	Protein of unknown function	-1.13	1.66E-12	4.82E-11	3805.91	3364.67	2941.83	1533.15	1318.65	1712.42
JC_g18896.t1	"Duox: Dual oxidase, isoform C (D	-1.13	0.000462	0.002749	378.48	543.68	391.45	134.55	124.74	304.81
JC_g11193.t1	"CG3609: CG3609, isoform A (Dr	-1.13	0.0004454	0.0026623	523.05	701.55	846.48	185.43	485.58	216.96
JC_g8394.t1	Protein of unknown function	-1.14	0.0006488	0.0036842	173.62	306.87	165.92	68.97	129.19	76.20
JC_g19512.t1	Protein of unknown function	-1.14	0.0002044	0.0013667	108.97	123.34	107.30	47.49	61.25	37.04
JC_g11537.t1	"Eip78C: Ecdysone-induced prote	-1.14	0.0002249	0.0014785	25641.76	17939.34	17305.23	4044.31	8986.62	13060.14
JC_g14012.t1	Dmel\CG6321: CG6321 (Drosoph	-1.14	0.0002398	0.0015642	109.70	152.94	109.29	57.66	61.25	40.22
JC_g3724.t1	CG17283: Uncharacterized protei	-1.15	2.50E-11	6.31E-10	1928.02	1883.63	1503.20	739.44	702.76	920.77
JC_g13281.t1	MP1: Melanization protease 1 (Dr	-1.15	0.000144	0.0010105	1125.28	1936.91	1623.42	343.72	888.75	774.72
JC_g20851.t1	"Dmel\CG7974: CG7974, isoform	-1.15	5.92E-09	1.05E-07	744.62	534.80	728.25	292.84	265.07	330.21
JC_g15584.t1	"snk: Snake, isoform B (Drosophil	-1.15	0.0002435	0.0015844	140.21	154.91	119.22	39.57	59.03	77.26
JC_g23715.t1	"Eip74EF: Ecdysone-induced pro	-1.15	2.36E-05	0.0002078	5000.20	5261.13	5051.08	1136.30	2439.05	3035.37
JC_g20311.t1	"CG2017: CG2017, isoform B (Dr	-1.16	5.30E-08	8.23E-07	2018.10	1556.04	1241.91	563.06	749.53	789.54
JC_g20781.t1	l(1)G0020: RNA cytidine acetyltra	-1.16	6.29E-05	0.0004901	350.15	176.62	225.53	102.89	99.12	118.54
JC_g11137.t1	CG6785: GH27293p (Drosophila	-1.16	8.87E-11	2.06E-09	524.50	513.09	540.48	214.82	208.27	268.82
JC_g4362.t1	CG5245: IP01468p (Drosophila m	-1.17	3.49E-08	5.64E-07	832.52	1181.09	1444.59	507.66	525.68	467.79
JC_g13274.t1	Protein of unknown function	-1.17	7.26E-06	7.30E-05	2073.31	1564.92	884.24	619.59	624.80	693.22
JC_g13822.t1	Protein of unknown function	-1.17	0.0018813	0.009098	212.13	113.47	89.42	39.57	71.28	58.21
JC_g8083.t1	CG6765: RH15369p (Drosophila	-1.17	1.89E-05	0.0001713	594.24	844.62	907.09	461.30	324.09	212.73
JC_g14522.t1	"Nox: NADPH oxidase, isoform B	-1.18	2.76E-08	4.53E-07	514.33	802.19	661.69	271.35	321.87	258.24
JC_g904.t1	Start1: Steroidogenic acute regul	-1.18	6.25E-06	6.38E-05	1609.10	1660.63	1142.55	473.74	913.25	482.61
JC_g4230.t1	Protein of unknown function	-1.18	0.0007965	0.0044002	69.74	64.14	98.36	31.66	28.96	33.87
JC_g21350.t1	betaCOP: Coatomer subunit beta	-1.19	4.85E-05	0.0003883	2892.03	2448.02	3011.38	937.30	1876.62	677.35
JC_g233.t1	CG18065-RA: GH13245p1 (Dros	-1.19	4.99E-07	6.47E-06	828.89	1039.00	953.78	258.92	441.03	495.31
JC_g24936.t1	Protein of unknown function	-1.19	0.0001622	0.0011175	2572.38	1847.12	1482.34	539.32	1340.92	551.40
JC_g21629.t1	btv: Beethoven (Drosophila melar	-1.19	2.02E-08	3.36E-07	1462.36	1519.53	1340.27	429.64	632.59	778.95
JC_g9545.t1	"AdamTS-A: ADAM metallopeptid	-1.19	1.36E-06	1.63E-05	2983.56	3093.33	2731.20	714.57	1509.09	1492.28
JC_g2834.t1	CG10026: AT17811p (Drosophila	-1.20	4.68E-05	0.0003759	271.69	255.56	175.85	65.58	120.28	105.84
JC_g4583.t1	yellow-d2: RH49821p (Drosophila	-1.21	6.76E-07	8.56E-06	986.53	976.84	786.87	264.57	357.50	526.00
JC_g21560.t1	CG13510-RA: MIP04282p (Droso	-1.21	3.38E-05	0.0002834	357.42	549.60	307.00	122.11	150.35	225.43
JC_g2150.t1	tau: Microtubule-associated prote	-1.21	3.80E-10	8.00E-09	6339.79	4820.07	4909.01	2279.38	1748.54	2759.14
JC_g23719.t1	Protein of unknown function	-1.21	0.0001564	0.0010872	1155.79	1018.28	1185.28	189.95	537.93	629.72
JC_g12677.t1	"Swip-1: Swiprosin-1, isoform B (D	-1.22	1.83E-07	2.61E-06	2071.86	1768.18	1491.28	508.79	731.72	977.92
JC_g19853.t1	GEO12660p1 (Fragment) (Drosop	-1.22	0.0003164	0.0019879	666.16	404.55	381.51	212.56	272.86	95.25
JC_g10350.t1	AOX1: Aldehyde oxidase 1 (Dros	-1.22	6.49E-05	0.0005037	2181.55	3409.08	2276.17	528.01	1104.81	1546.26
JC_g18513.t1	CG5390: SD23103p (Drosophila	-1.22	0.0021483	0.0101871	74.10	68.08	48.68	15.83	26.73	30.69
JC_g1468.t1	CG12171: RE01652p (Drosophila	-1.23	0.0002959	0.0018756	94.44	81.90	83.46	39.57	24.50	39.16
JC_g14144.t1	"Mctp: Multiple C2 domain and tra	-1.23	2.65E-05	0.00023	405.36	273.32	230.50	163.94	106.92	96.31
JC_g3816.t1	"CG4630: CG4630, isoform A (Dr	-1.24	6.93E-11	1.65E-09	5447.70	5877.82	3667.10	2034.03	2279.79	1901.87
JC_g12558.t1	ppk26: Pickpocket 26 (Drosophila	-1.24	0.0015382	0.0076591	69.74	62.16	57.62	15.83	23.39	32.81
JC_g15147.t1	Protein of unknown function	-1.25	0.0001093	0.0007959	500.53	445.99	245.40	96.10	208.27	166.16
JC_g16092.t1	CG15436: LD32747p (Drosophila	-1.25	0.0002063	0.0013775	103.88	81.90	100.35	28.27	34.53	48.68
JC_g12887.t1	Protein of unknown function	-1.25	2.69E-06	3.01E-05	6093.52	7026.35	5241.84	1319.46	3020.41	3037.49
JC_g11326.t1	"BG:DS00797.2: CG9008, isoform	-1.25	3.49E-09	6.34E-08	31719.30	25964.23	22587.80	7611.49	12028.20	13117.29
JC_g22018.t1	CG13532: RE31221p (Drosophila	-1.26	1.47E-05	0.0001369	772.95	650.24	526.57	141.33	330.78	302.69
JC_g16831.t1	Ror-RA: MIP23956p (Drosophila r	-1.26	1.45E-05	0.0001355	1796.53	1990.19	1599.58	343.72	906.57	882.67
JC_g3835.t1	BcDNA:RH39779: GEO09635p1	-1.26	0.0011591	0.0060202	121.32	148.99	81.47	24.87	66.82	40.22
JC_g7916.t1	Cpr66Ca: MIP24917p (Drosophila	-1.27	2.22E-05	0.0001975	1157.97	861.40	693.48	266.83	550.18	247.66
JC_g11084.t1	"a: Arc, isoform D (Drosophila mel	-1.27	1.31E-08	2.22E-07	3510.24	3448.54	2916.99	862.68	1649.42	1463.71
JC_g7854.t1	Cpr65Av: Cuticular protein 65Av (	-1.27	6.44E-06	6.55E-05	1960.71	1740.55	1165.41	445.47	515.65	957.81
JC_g19616.t1	"EG:103E12.3: CG3655, isoform	-1.28	9.76E-09	1.68E-07	16300.97	15070.98	12805.55	3834.01	6387.19	7448.72
JC_g25164.t1	Protein of unknown function	-1.28	0.0030401	0.0137061	231.74	161.82	230.50	37.31	36.75	148.17
JC_g8432.t1	"nab: Nab, isoform D (Drosophila	-1.29	1.12E-13	3.58E-12	1289.46	1433.69	1134.61	431.91	554.63	568.34
JC_g18885.t1	Nos: Nitric oxide synthase (Drosop	-1.29	3.72E-06	4.01E-05	358.87	267.40	299.05	93.84	95.78	170.40
JC_g21630.t1	Protein of unknown function	-1.30	0.0003019	0.0019063	177.26	172.67	182.81	29.40	73.51	95.25
JC_g8016.t1	"CG9667: CG9667, isoform A (Dr	-1.30	2.74E-07	3.80E-06	378.48	461.78	547.43	238.57	168.17	135.47
JC_g14545.t1	"CG8668: CG8668, isoform A (Dr	-1.30	2.27E-08	3.76E-07	4867.99	5520.63	8101.21	3070.83	2385.59	1797.09
JC_g8438.t1	Naam: LD05707p (Drosophila me	-1.30	1.24E-05	0.0001178	318.91	352.25	279.18	102.89	79.07	180.98
JC_g13311.t1	CG6701: LD17208p (Fragment) (I	-1.31	2.55E-05	0.0002224	2415.47	1541.24	753.09	580.02	559.09	650.89
JC_g2949.t1	Cyp6g2: Probable cytochrome P4	-1.31	0.0031116	0.0139733	195.42	369.03	225.53	140.20	22.27	111.13
JC_g23514.t1	"Gasp: Gasp, isoform A (Drosoph	-1.31	1.34E-06	1.60E-05	22206.34	20488.00	14490.57	4547.45	6621.08	10891.56
JC_g10580.t1	Oatp26F: Solute carrier organic a	-1.31	2.91E-05	0.0002494	844.87	847.58	721.30	137.94	427.67	345.02
JC_g823.t1	BcDNA:GH10614: IP10737p (Fra	-1.32	3.00E-07	4.11E-06	1561.88	1356.72	1062.08	332.41	496.72	702.75
JC_g12498.t1	MFS3: Major facilitator superfamily	-1.32	5.39E-06	5.59E-05	488.91	463.75	240.43	175.25	157.03	119.59
JC_g17327.t1	CG14314: AT04491p (Drosophila	-1.32	5.69E-07	7.31E-06	237.55	371.99	370.59	109.67	108.03	155.58
JC_g8157.t1	gas: RE48979p (Drosophila melar	-1.33	6.86E-06	6.94E-05	1054.09	1536.30	1559.84	816.32	419.87	327.03
JC_g5039.t1	beat-Vc: Beat-Vc (Drosophila mel	-1.33	1.01E-05	9.81E-05	246.27	386.79	351.71	85.93	178.20	103.72
JC_g21636.t1	Protein of unknown function	-1.33	6.91E-10	1.40E-08	595.69	446.98	455.03	154.90	212.72	209.55
JC_g5013.t1	Cyp9f2: Probable cytochrome P4	-1.33	7.31E-05	0.0005595	247.72	201.29	110.28	73.49	79.07	52.92
JC_g4469.t1	Protein of unknown function	-1.34	1.57E-06	1.85E-05	493.99	453.89	407.35	97.24	199.36	213.79

JC_g2993.t1	Vps33B: Vacuolar protein sorting	-1.34	9.19E-07	1.14E-05	920.42	966.97	744.15	476.00	201.58	315.39
JC_g11885.t1	CG6083: AT08919p (Drosophila r	-1.34	1.02E-05	9.89E-05	112.60	148.01	126.18	36.18	51.23	56.09
JC_g2019.t1	"CG3355: CG3355, isoform A (Dr	-1.34	0.0003418	0.0021242	85.72	116.43	56.63	31.66	27.84	32.81
JC_g11055.t1	RE40670p (Drosophila melanoga	-1.35	2.84E-09	5.25E-08	763.51	750.88	724.28	214.82	250.59	386.30
JC_g17369.t1	GNBP3: SD21560p (Fragment) (D	-1.35	8.92E-13	2.65E-11	18420.77	18016.30	16002.72	5208.88	6301.44	8651.02
JC_g14532.t1	Dmel\CG12016: SD05789p2 (Dro	-1.35	8.20E-07	1.02E-05	321.09	599.92	417.28	205.78	162.60	131.24
JC_g19857.t1	CG12795: LD41381p (Drosophila	-1.35	1.26E-06	1.51E-05	445.32	277.26	242.42	100.63	124.74	134.41
JC_g11284.t1	Protein of unknown function	-1.35	0.0003203	0.0020078	324.73	371.00	336.81	55.40	219.40	89.96
JC_g8482.t1	CG31272: FI03320p (Drosophila	-1.35	0.000157	0.0010902	183.07	211.16	155.98	31.66	65.71	98.43
JC_g20630.t1	Zw10: Centromere/kinetochore pr	-1.36	2.47E-05	0.0002161	390.83	538.74	397.41	84.80	149.24	245.54
JC_g17374.t1	GNBP3-RA: LP12732p (Fragmen	-1.37	1.09E-06	1.33E-05	215.03	362.12	220.56	82.54	110.26	100.54
JC_g1534.t1	CG31954: IP09792p (Drosophila	-1.37	0.000191	0.0012892	66.83	64.14	78.49	22.61	20.05	30.69
JC_g4495.t1	CG6083: AT08919p (Drosophila r	-1.37	1.02E-07	1.50E-06	417.71	455.86	306.01	120.98	123.62	191.56
JC_g19384.t1	CG30259: Uncharacterized protei	-1.37	1.52E-06	1.80E-05	785.30	539.73	606.05	154.90	349.71	202.15
JC_g13284.t1	MP1: Melanization protease 1 (Dr	-1.38	0.0020624	0.0098287	82.09	54.27	31.79	15.83	21.16	17.99
JC_g2771.t1	"snk: Snake, isoform B (Drosophil	-1.38	3.16E-05	0.0002674	194.69	148.01	110.28	39.57	70.16	51.86
JC_g14428.t1	CG9737: CG9737 (Drosophila me	-1.38	2.66E-07	3.70E-06	2644.30	2817.05	2379.49	551.75	1407.74	908.07
JC_g15289.t1	Protein of unknown function	-1.39	0.0009119	0.0049401	119.87	59.20	66.57	15.83	36.75	28.58
JC_g9987.t1	"moody: Moody, isoform B (Droso	-1.40	3.17E-06	3.48E-05	947.30	684.78	665.66	208.04	181.54	429.69
JC_g5736.t1	Protein of unknown function	-1.40	0.0022355	0.0105351	50.85	84.86	86.44	22.61	8.91	38.10
JC_g14431.t1	MP1: Melanization protease 1 (Dr	-1.40	4.12E-06	4.42E-05	1133.27	993.61	727.26	167.34	422.10	420.17
JC_g9712.t1	Protein of unknown function	-1.41	1.88E-09	3.58E-08	323.27	377.91	307.99	91.58	132.53	141.82
JC_g3198.t1	Protein of unknown function	-1.41	1.77E-05	0.0001609	82.82	119.39	131.15	42.96	40.09	32.81
JC_g9156.t1	"BEST:HL01355: Uncharacterized	-1.41	0.0002991	0.0018915	57.39	74.00	73.52	29.40	14.48	24.34
JC_g18179.t1	"Dmel\CG7991: CG7991, isoform	-1.41	0.0037725	0.0164509	4198.20	3192.00	2790.81	349.37	1236.23	1469.00
JC_g22140.t1	Protein of unknown function	-1.42	4.73E-08	7.42E-07	2541.87	2058.27	2205.63	465.83	1100.36	869.97
JC_g21626.t1	btv: Beethoven (Drosophila melar	-1.42	2.86E-07	3.94E-06	714.11	662.08	659.70	131.15	277.32	313.27
JC_g20309.t1	gag-pol: Putative uncharacterized	-1.42	6.11E-07	7.80E-06	848.50	742.00	509.68	159.42	233.88	347.14
JC_g22326.t1	CG6749-RA: RT10189p (Fragmer	-1.43	1.06E-13	3.40E-12	955.29	1200.82	1015.38	347.11	472.22	329.15
JC_g1056.t1	anon-WO0107627.1: RE46159p	-1.43	0.0012001	0.0062021	143.11	100.64	100.35	10.18	46.78	50.80
JC_g8176.t1	Cpr67B: Cuticular protein 67B (Dr	-1.43	9.49E-11	2.19E-09	5818.92	7139.82	7907.47	3428.11	1961.26	2080.73
JC_g22034.t1	"CG7742: CG7742, isoform A (Dr	-1.43	0.0014481	0.0072735	42.13	60.19	110.28	15.83	17.82	31.75
JC_g11265.t1	CG9186: Lipid droplet-associated	-1.44	5.77E-05	0.0004537	297.85	182.54	329.85	67.84	147.01	57.15
JC_g20193.t1	Protein of unknown function	-1.44	0.002583	0.0118935	58.84	51.31	33.78	22.61	6.68	13.76
JC_g3460.t1	"Tsf1: Transferrin 1, isoform A (Dr	-1.44	6.25E-08	9.58E-07	1185.58	1061.70	818.67	212.56	432.12	432.87
JC_g15597.t1	"snk: Snake, isoform B (Drosophil	-1.44	0.0010912	0.0057218	98.80	60.19	41.73	13.57	20.05	28.58
JC_g21632.t1	btv: Beethoven (Drosophila melar	-1.45	1.17E-05	0.000112	1178.31	1275.81	1049.16	168.47	399.83	618.08
JC_g11448.t1	T: Transposable element P transp	-1.45	0.0003214	0.0020139	245.54	116.43	139.09	50.88	26.73	83.61
JC_g5690.t1	"CG2663: CG2663, isoform A (Dr	-1.45	0.0003758	0.0023092	58.12	42.43	58.62	15.83	20.05	14.82
JC_g8483.t1	CG31272: FI03320p (Drosophila	-1.45	4.78E-06	5.06E-05	464.93	363.11	309.98	65.58	160.38	159.81
JC_g2998.t1	CG10793-RA: FI21292p1 (Drosop	-1.46	3.67E-08	5.89E-07	408.27	431.19	295.08	148.11	90.21	155.58
JC_g3049.t1	"crol: Crooked legs, isoform G (Dr	-1.46	3.35E-23	2.48E-21	1246.60	1238.32	1177.33	409.29	413.19	493.19
JC_g1046.t1	Protein of unknown function	-1.46	5.02E-06	5.29E-05	268.06	203.26	224.54	41.83	98.01	95.25
JC_g5473.t1	Protein of unknown function	-1.46	1.01E-06	1.24E-05	484.55	555.52	274.21	105.15	185.99	156.64
JC_g20101.t1	Protein of unknown function	-1.47	0.0007702	0.0042697	66.11	47.36	70.54	14.70	30.07	11.64
JC_g5329.t1	Adgf-A: Adenosine deaminase-re	-1.47	5.33E-11	1.29E-09	1509.58	1668.52	1274.69	460.17	395.37	699.57
JC_g9897.t1	InR: Receptor protein-tyrosine kin	-1.47	0.0002012	0.0013487	130.04	97.68	95.38	20.35	56.80	25.40
JC_g8604.t1	"Atg8a: Autophagy-related 8a, iso	-1.47	1.71E-06	2.00E-05	260.07	196.35	186.78	56.53	55.69	103.72
JC_g9187.t1	PGRP-SA: Peptidoglycan-recogni	-1.48	2.46E-09	4.59E-08	935.68	859.42	694.47	191.08	284.00	379.95
JC_g14056.t1	"Incenp: Inner centromere protein	-1.48	1.27E-13	4.04E-12	1137.63	887.05	748.12	298.49	358.62	310.10
JC_g24629.t1	"Syx1A: Syntaxin 1A, isoform C (D	-1.49	0.000102	0.0007502	352.33	358.17	238.45	39.57	165.94	95.25
JC_g14227.t1	IP04203p (Fragment) (Drosophila	-1.49	0.0023249	0.0109069	50.13	32.56	39.74	19.22	8.91	6.35
JC_g10660.t1	Protein of unknown function	-1.50	8.82E-08	1.32E-06	623.30	430.20	382.51	104.02	175.97	198.97
JC_g8178.t1	Protein of unknown function	-1.51	1.31E-11	3.43E-10	268.06	353.24	287.13	97.24	111.37	99.49
JC_g8434.t1	Klp61F: Kinesin-like protein Klp61	-1.51	9.33E-14	3.02E-12	762.05	978.81	689.51	229.52	298.48	300.57
JC_g11264.t1	Protein of unknown function	-1.52	0.0014283	0.0071931	4016.58	2733.18	3234.92	550.62	1695.08	520.71
JC_g4252.t1	Protein of unknown function	-1.52	1.43E-11	3.71E-10	27993.30	27903.12	34242.85	10240.24	6616.62	13346.95
JC_g17337.t1	CG2608: CG2608 (Drosophila me	-1.53	0.0013658	0.0069025	29.78	88.80	84.45	23.74	10.02	22.23
JC_g13373.t1	Fmo-1: Flavin-containing monooxy	-1.53	2.73E-06	3.05E-05	573.17	478.55	356.68	104.02	103.58	242.36
JC_g20798.t1	CG4404: RH45455p (Drosophila r	-1.53	0.0025024	0.0115923	36.32	35.52	19.87	7.91	6.68	9.53
JC_g8994.t1	modSP: Modular serine protease	-1.53	0.0006322	0.0036114	66.11	49.34	38.75	13.57	21.16	9.53
JC_g14432.t1	"CG9733: CG9733, isoform B (Dr	-1.53	4.90E-05	0.000392	843.42	676.88	511.67	85.93	371.98	165.10
JC_g22146.t1	"CG34355: Uncharacterized prote	-1.54	3.36E-07	4.54E-06	213.58	351.27	202.68	71.23	105.80	69.85
JC_g2101.t1	CG14301-RB: FI17806p1 (Drosop	-1.54	3.10E-07	4.22E-06	2217.15	1415.93	1035.25	326.76	711.67	456.15
JC_g20111.t1	Protein of unknown function	-1.54	2.00E-12	5.77E-11	572.45	592.02	497.76	237.44	163.72	150.29
JC_g3042.t1	"bgcn: Benign gonial cell neoplas	-1.55	9.78E-12	2.60E-10	1577.86	1537.29	1649.25	334.67	651.53	582.10
JC_g672.t1	Protein of unknown function	-1.55	0.0017068	0.0083636	2167.75	976.84	771.97	161.68	444.37	424.40
JC_g13323.t1	RE04396p (Drosophila melanoga	-1.55	3.26E-05	0.0002738	308.74	224.97	99.35	52.01	62.37	77.26
JC_g19488.t1	CG4797: SD10060p (Drosophila r	-1.57	0.0001321	0.0009421	82.09	230.89	95.38	29.40	44.55	44.45
JC_g10290.t1	CG42288-RA: MIP14249p (Fragm	-1.57	0.0002606	0.0016861	61.75	117.42	75.51	38.44	13.36	20.11
JC_g21635.t1	Protein of unknown function	-1.57	7.30E-08	1.10E-06	1673.03	1445.53	1483.33	243.09	496.72	706.98
JC_g24192.t1	"EbpIII: Ejaculatory bulb protein II	-1.58	0.0006561	0.0037197	140.93	97.68	115.25	6.78	42.32	46.57
JC_g7592.t1	Protein of unknown function	-1.59	1.87E-20	1.08E-18	5796.40	5420.97	7545.83	1963.93	1827.62	2330.50
JC_g16569.t1	Ddc-RC: LP11638p (Drosophila m	-1.59	7.87E-09	1.37E-07	183.07	305.88	272.23	72.36	92.44	74.09

JC_g20862.t1	CG5731: CG5731 (Drosophila me	-1.60	1.42E-08	2.41E-07	618.21	438.10	560.35	101.76	168.17	231.78
JC_g24119.t1	"sha: Shavenoid, isoform B (Dros	-1.60	1.61E-09	3.11E-08	27129.54	25120.60	20847.15	4057.88	9541.25	9245.82
JC_g22694.t1	"Nlg4: Neuroligin 4, isoform B (Dro	-1.60	7.01E-10	1.41E-08	539.76	308.84	403.37	156.03	110.26	125.94
JC_g3046.t1	CG11236: GH12548p (Drosophila	-1.61	0.0001181	0.0008537	80.64	118.40	121.21	18.09	18.93	51.86
JC_g8059.t1	nec: Spn43Ac (Fragment) (Drosop	-1.61	9.24E-05	0.0006875	58.12	154.91	195.72	35.05	33.41	45.51
JC_g7904.t1	Protein of unknown function	-1.61	4.96E-05	0.0003963	77.73	105.58	52.66	19.22	20.05	27.52
JC_g16533.t1	sens: Zinc finger protein sens (Dro	-1.62	8.86E-05	0.0006627	68.29	85.84	92.40	12.44	36.75	19.05
JC_g2947.t1	Protein of unknown function	-1.62	0.0001976	0.0013269	217.94	409.48	227.52	134.55	22.27	74.09
JC_g1522.t1	Protein of unknown function	-1.62	4.66E-17	2.03E-15	1786.36	1424.81	1479.36	385.55	598.07	495.31
JC_g25221.t1	CG17110: Aminoacylase (Drosop	-1.63	0.0036122	0.0158423	18.89	16.77	39.74	7.91	4.45	3.18
JC_g7729.t1	"CG9914: CG9914, isoform A (Dro	-1.63	7.02E-14	2.28E-12	1039.56	1857.97	1614.48	461.30	441.03	501.66
JC_g11258.t1	"rost: Rolling stone, isoform B (Dro	-1.64	0.0002897	0.0018452	159.82	124.33	107.30	32.79	60.14	9.53
JC_g8522.t1	Protein of unknown function	-1.64	5.03E-06	5.29E-05	281.14	336.47	248.38	63.32	43.44	140.76
JC_g19778.t1	"mthl15: Methuselah-like 15, isofo	-1.64	1.30E-05	0.0001229	201.96	138.14	130.15	36.18	71.28	25.40
JC_g1336.t1	Protein of unknown function	-1.65	3.92E-05	0.0003215	160.55	115.44	108.29	14.70	37.87	52.92
JC_g4271.t1	CG4404: RH45455p (Drosophila	-1.65	2.37E-12	6.76E-11	260.80	256.54	230.50	67.84	70.16	89.96
JC_g13427.t1	ea: Serine protease easter (Drosc	-1.65	2.88E-10	6.17E-09	464.93	423.30	333.82	84.80	124.74	158.75
JC_g11460.t1	"l(2)efl: Lethal (2) essential for life	-1.66	2.15E-38	3.62E-36	35636.35	37977.40	31463.96	11875.15	10691.73	10296.77
JC_g20319.t1	"Coq2: 4-hydroxybenzoate polypr	-1.66	2.55E-10	5.49E-09	201.96	244.70	180.82	54.27	60.14	73.03
JC_g17832.t1	"b: Black, isoform A (Drosophila m	-1.67	0.0009501	0.0051085	26.88	94.72	34.77	11.31	12.25	12.70
JC_g1459.t1	GEO07170p1 (Fragment) (Drosop	-1.67	2.80E-06	3.11E-05	743.17	575.25	567.30	68.97	179.31	281.52
JC_g24180.t1	Phk-3: GEO07322p1 (Drosophila	-1.67	0.0015581	0.0077447	26.15	42.43	25.83	4.52	4.45	11.64
JC_g20090.t1	CG5245: CG5245 (Drosophila me	-1.67	4.69E-07	6.12E-06	244.09	337.45	231.49	111.93	41.21	78.32
JC_g7595.t1	Protein of unknown function	-1.68	6.84E-09	1.20E-07	208.49	244.70	248.38	56.53	96.89	50.80
JC_g21459.t1	Protein of unknown function	-1.69	0.0001689	0.0011597	91.53	66.11	33.78	13.57	17.82	16.93
JC_g4351.t1	CG2202: CG2202 (Drosophila me	-1.70	1.96E-24	1.56E-22	1109.30	1226.48	1442.60	358.41	361.96	418.05
JC_g4729.t1	CG12163-RB: FI18603p1 (Drosop	-1.70	6.63E-12	1.78E-10	778.04	711.42	502.72	139.07	232.77	211.67
JC_g14547.t1	BcDNA.GH05741: Carboxylic este	-1.70	6.54E-06	6.63E-05	126.40	82.88	135.12	23.74	46.78	22.23
JC_g2329.t1	"lab: Labial, isoform B (Drosophila	-1.70	0.0005947	0.0034276	79.18	34.53	28.81	9.05	10.02	13.76
JC_g20112.t1	Protein of unknown function	-1.71	1.93E-06	2.21E-05	666.16	761.74	622.94	341.45	118.05	98.43
JC_g16922.t1	mys: Integrin beta (Drosophila me	-1.72	2.45E-08	4.04E-07	178.71	110.51	150.02	38.44	44.55	40.22
JC_g6485.t1	Protein of unknown function	-1.73	1.41E-06	1.68E-05	664.71	260.49	240.43	126.63	99.12	86.79
JC_g10228.t1	Protein of unknown function	-1.73	3.22E-20	1.77E-18	1598.93	1367.58	1428.69	332.41	432.12	518.60
JC_g4862.t1	Protein of unknown function	-1.74	0.0021211	0.0100788	47.22	67.10	72.53	1.13	27.84	5.29
JC_g4199.t1	beta4GalNAcTB: Beta4GalNAcTE	-1.75	2.98E-07	4.10E-06	339.98	393.70	260.30	40.70	122.51	102.66
JC_g14156.t1	Rcd6: LD20239p (Drosophila mela	-1.76	4.10E-07	5.43E-06	994.52	1083.41	804.76	106.28	232.77	422.28
JC_g3782.t1	sxc: LD16758p (Drosophila melan	-1.76	2.23E-09	4.20E-08	623.30	498.29	270.24	143.59	124.74	112.19
JC_g2213.t1	CG14434: CG14434-PA (Drosoph	-1.77	1.39E-15	5.34E-14	1949.08	1499.80	1053.14	400.25	426.56	443.45
JC_g4870.t1	Protein of unknown function	-1.78	0.0022775	0.0106978	23.97	26.64	11.92	5.65	2.23	2.12
JC_g14254.t1	Protein of unknown function	-1.78	1.44E-05	0.0001346	69.74	130.25	173.87	44.10	18.93	28.58
JC_g8187.t1	Protein of unknown function	-1.78	1.07E-35	1.67E-33	40054.66	45729.97	44175.12	14067.47	10588.15	12506.62
JC_g2331.t1	CG2604: AT14148p (Drosophila	-1.81	0.0003222	0.0020174	6443.67	3628.13	3511.12	351.63	985.64	1497.58
JC_g11428.t1	"Hsp26: Heat shock protein 26, is	-1.81	0.0035917	0.0157828	51.58	21.71	18.88	0.00	8.91	0.00
JC_g5715.t1	Protein of unknown function	-1.81	0.0013097	0.0066692	87.17	33.55	54.64	22.61	1.11	6.35
JC_g15327.t1	pol: Truncated pol protein (Drosop	-1.81	0.0037781	0.0164692	2.18	32.56	25.83	2.26	0.00	2.12
JC_g21460.t1	Protein of unknown function	-1.82	0.0035694	0.0157091	868.12	150.97	85.44	11.31	64.60	19.05
JC_g17820.t1	alpha-Est9: Carboxylic ester hydro	-1.83	2.12E-07	3.01E-06	363.96	301.93	203.67	49.75	50.12	117.48
JC_g10558.t1	CG7154: CG7154 (Drosophila me	-1.84	1.42E-29	1.47E-27	1249.51	1067.62	1032.27	274.75	329.66	313.27
JC_g2731.t1	RTase: F-element protein (Drosop	-1.84	4.47E-08	7.02E-07	209.22	125.31	173.87	28.27	42.32	57.15
JC_g11452.t1	"TppII: Tripeptidyl-peptidase II, iso	-1.84	6.18E-07	7.88E-06	216.48	117.42	98.36	28.27	34.53	42.33
JC_g23145.t1	Protein of unknown function	-1.85	0.0019484	0.0093632	75.55	15.79	19.87	1.13	3.34	10.58
JC_g4496.t1	"34F4T: CG6084, isoform C (Dros	-1.85	3.17E-09	5.82E-08	127.13	138.14	104.32	33.92	26.73	32.81
JC_g20419.t1	ORF: ORF protein (Drosophila me	-1.85	0.003017	0.0136234	48.67	5.92	13.91	0.00	4.45	1.06
JC_g6165.t1	Protein of unknown function	-1.86	0.0001115	0.0008105	239.00	82.88	53.65	16.96	38.98	22.23
JC_g4736.t1	pol: RNA-directed DNA polymeras	-1.86	0.0026919	0.012311	2.91	12.83	19.87	0.00	0.00	0.00
JC_g7179.t1	Protein of unknown function	-1.86	0.0026919	0.012311	19.61	3.95	9.94	0.00	0.00	0.00
JC_g2824.t1	"snk: Snake, isoform B (Drosophil	-1.90	8.05E-07	1.01E-05	328.36	208.20	106.31	36.18	62.37	49.74
JC_g5269.t1	CG6178: CG6178 (Drosophila me	-1.90	0.002485	0.0115354	13.80	15.79	4.97	0.00	0.00	1.06
JC_g15696.t1	Protein of unknown function	-1.91	0.002256	0.0106099	42.86	20.72	8.94	0.00	0.00	5.29
JC_g8445.t1	Sap47: MIP08376p (Drosophila m	-1.92	0.0012872	0.0065751	571.00	538.74	467.95	21.48	23.39	158.75
JC_g17181.t1	Protein of unknown function	-1.92	0.0017219	0.0084231	26.15	14.80	14.90	0.00	4.45	1.06
JC_g12710.t2	ORF: Orf protein (Drosophila mela	-1.93	0.0010007	0.0053278	32.69	20.72	27.82	0.00	3.34	7.41
JC_g4309.t1	CG10581: IP06602p (Drosophila	-1.93	8.15E-21	4.91E-19	446.04	412.44	485.83	117.59	93.55	128.06
JC_g12568.t1	Dmel\CG33290: HDC11369 (Dros	-1.93	1.85E-06	2.13E-05	214.30	99.66	104.32	26.00	45.66	20.11
JC_g8114.t1	CG12970: Uncharacterized protei	-1.93	5.61E-12	1.53E-10	15607.20	19331.58	18934.61	6934.24	3551.66	2601.44
JC_g3206.t1	Protein of unknown function	-1.94	0.0018602	0.0090111	26.15	18.75	4.97	2.26	1.11	0.00
JC_g9614.t1	GstE6: Glutathione S transferase	-1.95	0.001183	0.0061272	18.89	21.71	17.88	0.00	4.45	2.12
JC_g1055.t1	CG13675: CG13675 protein (Frag	-1.95	0.0003671	0.0022614	61.02	71.04	51.66	0.00	16.71	12.70
JC_g7180.t1	SD27140p (Drosophila melanoga	-1.95	0.0018446	0.0089472	14.53	7.89	19.87	0.00	2.23	0.00
JC_g19657.t1	ORF: Orf protein (Drosophila mela	-1.96	1.10E-06	1.34E-05	249.90	173.66	181.82	15.83	42.32	71.97
JC_g1337.t1	Protein of unknown function	-1.98	0.000392	0.002388	70.47	42.43	20.86	4.52	13.36	2.12
JC_g20010.t1	shu: Inactive peptidyl-prolyl cis-tra	-1.98	4.97E-05	0.0003968	165.63	184.51	189.76	75.75	11.14	12.70
JC_g23399.t1	Protein of unknown function	-1.98	9.17E-08	1.36E-06	201.96	146.03	148.04	15.83	47.89	44.45
JC_g1074.t1	RabX1: LD47384p (Drosophila m	-1.98	5.03E-09	8.95E-08	279.69	218.06	235.47	26.00	61.25	77.26

JC_g10326.t1	"Nep5: Neprilysin 5, isoform D (Dr	-1.99	0.0007194	0.004035	285.50	54.27	7.95	15.83	13.36	14.82
JC_g5360.t1	Protein of unknown function	-1.99	0.0014956	0.0074693	60.30	17.76	5.96	4.52	0.00	0.00
JC_g17780.t1	CG2640: GH28833p (Drosophila	-2.00	0.0003814	0.0023371	40.68	28.61	15.90	2.26	6.68	3.18
JC_g1015.t1	"Cht2: Chitinase 2, isoform B (Dro	-2.00	4.40E-08	6.93E-07	364.68	273.32	268.25	24.87	86.87	84.67
JC_g7649.t1	Cpr66Cb: Cuticular protein 66Cb (	-2.00	8.34E-09	1.45E-07	244.09	174.65	166.91	22.61	45.66	60.33
JC_g5280.t1	CG4830: CG4830 (Drosophila me	-2.01	4.36E-08	6.88E-07	254.99	544.66	296.07	67.84	44.55	122.77
JC_g5859.t2	Protein of unknown function	-2.02	5.77E-05	0.0004537	24.70	45.39	39.74	6.78	5.57	6.35
JC_g24784.t1	GEO10169p1 (Fragment) (Drosop	-2.02	0.0011128	0.0058194	2570.93	573.28	261.30	29.40	150.35	92.08
JC_g20882.t1	epsilonTry: Trypsin epsilon (Droso	-2.03	0.0009582	0.0051473	35.60	18.75	10.93	0.00	4.45	1.06
JC_g9306.t1	Protein of unknown function	-2.03	0.0012271	0.0063239	43.59	21.71	1.99	0.00	0.00	2.12
JC_g24774.t1	CG17739: GH02025p (Drosophila	-2.04	6.10E-05	0.0004777	96.62	90.78	30.80	6.78	22.27	7.41
JC_g16331.t1	CG4572-RC: Carboxypeptidase ([	-2.04	0.0001615	0.0011142	19.61	41.44	27.82	4.52	3.34	5.29
JC_g4032.t2	pol: Retrovirus-related Pol polypro	-2.04	6.69E-05	0.0005165	927.69	1041.96	660.69	44.10	223.86	169.34
JC_g8034.t1	Protein of unknown function	-2.04	9.34E-05	0.0006935	67.56	64.14	28.81	13.57	10.02	2.12
JC_g9172.t1	CG11284: LD36568p (Drosophila	-2.05	5.55E-05	0.0004387	85.72	50.32	72.53	4.52	5.57	24.34
JC_g1223.t1	"Cht2: Chitinase 2, isoform B (Dro	-2.05	1.18E-06	1.42E-05	59.57	53.28	68.55	14.70	7.80	12.70
JC_g24099.t1	Protein of unknown function	-2.07	0.0001372	0.0009717	81.36	90.78	79.48	2.26	30.07	4.23
JC_g20850.t1	Protein of unknown function	-2.07	0.0009184	0.0049709	26.88	11.84	3.97	0.00	0.00	0.00
JC_g21685.t1	Protein of unknown function	-2.07	0.0003144	0.0019763	92.26	50.32	24.84	0.00	12.25	8.47
JC_g4339.t1	CG5435: AT11334p (Drosophila r	-2.07	7.45E-05	0.0005689	58.12	39.47	22.85	4.52	4.45	9.53
JC_g14328.t1	AttC: Attacin-C (Drosophila melan	-2.09	0.0006436	0.0036636	1365.74	309.83	132.14	20.35	70.16	60.33
JC_g4519.t1	CG9645: RH19136p (Drosophila r	-2.10	6.13E-10	1.25E-08	324.00	317.72	195.72	38.44	89.10	44.45
JC_g1129.t2	Protein of unknown function	-2.11	0.0002986	0.0018892	82.09	40.46	15.90	3.39	11.14	1.06
JC_g1960.t1	Protein of unknown function	-2.12	0.0004979	0.0029309	44.31	26.64	8.94	0.00	4.45	2.12
JC_g22497.t1	Protein of unknown function	-2.13	0.0004976	0.0029309	26.15	21.71	25.83	0.00	5.57	0.00
JC_g24450.t2	"CG42346: Uncharacterized prote	-2.13	6.06E-12	1.63E-10	785.30	526.90	343.76	89.32	151.47	100.54
JC_g3813.t1	ORF: ORF (Drosophila melanogas	-2.15	0.0004857	0.002869	31.24	12.83	25.83	4.52	0.00	0.00
JC_g2732.t1	Protein of unknown function	-2.15	6.46E-08	9.88E-07	75.55	70.06	85.44	14.70	8.91	19.05
JC_g8155.t1	gas: RE48979p (Drosophila melar	-2.16	1.74E-06	2.03E-05	198.32	239.77	261.30	80.28	28.96	10.58
JC_g15697.t2	RTase: F-element protein (Drosop	-2.17	0.000499	0.0029349	21.07	21.71	7.95	0.00	0.00	2.12
JC_g22878.t1	Gr64a: Gustatory receptor for sug	-2.17	0.0005175	0.0030366	5.09	26.64	27.82	0.00	2.23	0.00
JC_g19551.t1	IP16913p (Drosophila melanogas	-2.18	2.97E-05	0.0002539	61.02	31.57	32.79	6.78	2.23	8.47
JC_g6468.t1	Protein of unknown function	-2.19	3.19E-05	0.0002696	91.53	48.35	66.57	1.13	18.93	8.47
JC_g12365.t1	Protein of unknown function	-2.20	3.49E-05	0.0002917	23.97	37.49	56.63	6.78	6.68	2.12
JC_g9297.t1	Protein of unknown function	-2.22	3.28E-07	4.45E-06	95.89	125.31	44.71	14.70	14.48	14.82
JC_g21454.t1	Protein of unknown function	-2.23	0.0002094	0.0013951	130.04	31.57	13.91	1.13	11.14	2.12
JC_g15448.t1	Protein of unknown function	-2.24	7.22E-05	0.0005542	63.93	44.40	97.37	2.26	1.11	19.05
JC_g8201.t1	CG15531: Uncharacterized protei	-2.25	1.07E-06	1.31E-05	85.72	198.33	160.95	45.23	12.25	11.64
JC_g14325.t1	AttA: Attacin A (Fragment) (Droso	-2.26	4.05E-11	9.98E-10	1204.47	1030.12	687.52	88.19	294.02	149.23
JC_g12570.t1	Protein of unknown function	-2.27	1.72E-05	0.0001568	51.58	33.55	37.75	1.13	8.91	5.29
JC_g20106.t1	Skp2: RE15215p (Drosophila mel	-2.28	1.02E-05	9.89E-05	29.78	41.44	38.75	2.26	6.68	5.29
JC_g12364.t1	Protein of unknown function	-2.29	1.39E-07	2.02E-06	111.87	118.40	64.58	24.87	14.48	7.41
JC_g2717.t1	Protein of unknown function	-2.29	3.21E-07	4.36E-06	77.00	92.75	45.70	13.57	13.36	6.35
JC_g24449.t1	"CG42346: Uncharacterized prote	-2.29	6.49E-13	1.97E-11	655.99	453.89	270.24	62.19	99.12	88.90
JC_g14310.t1	AttA: Attacin-A (Drosophila melan	-2.30	0.0002457	0.0015973	64.65	11.84	5.96	0.00	0.00	2.12
JC_g14307.t1	Protein of unknown function	-2.34	0.0001822	0.0012407	66.11	5.92	13.91	0.00	2.23	0.00
JC_g22775.t1	CG34384: Diacylglycerol kinase ([	-2.38	0.0001201	0.0008666	26.88	18.75	11.92	0.00	2.23	0.00
JC_g14635.t1	Protein of unknown function	-2.39	3.61E-07	4.84E-06	36.32	59.20	68.55	7.91	5.57	8.47
JC_g2214.t1	CG17475: RE05031p (Drosophila	-2.43	0.0001076	0.0007851	606.59	506.18	312.96	22.61	0.00	7.41
JC_g8477.t1	Ugt86Di: UDP-glucuronosyltransfe	-2.45	1.55E-05	0.0001432	98.07	42.43	45.70	3.39	0.00	12.70
JC_g2776.t1	"snk: Snake, isoform B (Drosophil	-2.45	1.42E-09	2.76E-08	297.12	196.35	118.23	13.57	40.09	34.93
JC_g21432.t1	Protein of unknown function	-2.46	8.53E-05	0.0006402	82.82	5.92	6.95	0.00	0.00	0.00
JC_g4221.t1	Protein of unknown function	-2.47	7.96E-05	0.0006023	9.44	14.80	23.84	0.00	0.00	0.00
JC_g3048.t1	CG8132: CG8132 (Drosophila me	-2.48	6.01E-08	9.24E-07	498.35	293.05	190.76	12.44	32.30	82.55
JC_g9679.t1	ORF: Orf protein (Drosophila mela	-2.48	1.77E-11	4.54E-10	249.90	175.63	184.80	14.70	49.00	27.52
JC_g24925.t1	Protein of unknown function	-2.48	3.80E-06	4.09E-05	47.95	38.48	45.70	0.00	6.68	6.35
JC_g20154.t1	Protein of unknown function	-2.48	6.01E-05	0.0004709	56.66	89.79	663.68	13.57	10.02	10.58
JC_g22806.t1	Protein of unknown function	-2.50	2.10E-15	7.87E-14	220.84	416.39	454.04	42.96	70.16	56.09
JC_g19461.t1	nos-RA: RE53469p1 (Drosophila	-2.51	2.16E-05	0.0001923	14.53	67.10	50.67	2.26	0.00	6.35
JC_g10554.t1	"hpo: Hippo, isoform B (Drosophila	-2.53	1.34E-17	6.07E-16	871.02	1008.42	1384.97	174.12	92.44	239.19
JC_g22181.t1	CG14905: Uncharacterized protei	-2.55	1.13E-06	1.37E-05	51.58	41.44	206.65	7.91	14.48	7.41
JC_g25202.t1	gag-r: F-element protein (Fragmer	-2.55	4.57E-05	0.000368	21.79	14.80	11.92	0.00	0.00	0.00
JC_g8202.t1	alpha-Est9: Carboxylic ester hydro	-2.56	3.97E-07	5.28E-06	56.66	152.94	139.09	26.00	6.68	4.23
JC_g11462.t1	CG7706: LD06275p (Drosophila r	-2.57	4.18E-05	0.0003396	20.34	13.81	13.91	0.00	0.00	0.00
JC_g21453.t1	Protein of unknown function	-2.59	9.45E-07	1.17E-05	325.45	74.99	55.64	16.96	21.16	5.29
JC_g10557.t1	Hey: Hairy/enhancer-of-split relate	-2.59	3.56E-05	0.0002959	15.98	8.88	30.80	0.00	0.00	0.00
JC_g11286.t1	Protein of unknown function	-2.64	1.75E-05	0.0001592	30.51	36.51	9.94	0.00	2.23	0.00
JC_g20013.t1	nvd: Neverland (Drosophila melan	-2.64	3.97E-10	8.30E-09	108.24	132.22	108.29	26.00	6.68	9.53
JC_g3235.t1	CG5987: AT11276p (Drosophila r	-2.65	6.13E-06	6.27E-05	30.51	32.56	17.88	0.00	2.23	2.12
JC_g14783.t1	Protein of unknown function	-2.66	2.20E-05	0.0001955	66.83	221.02	557.37	0.00	0.00	0.00
JC_g9837.t1	gag-pol: Putative uncharacterized	-2.67	5.22E-06	5.44E-05	46.49	39.47	14.90	0.00	3.34	2.12
JC_g23431.t1	"CG1315: CG1315, isoform B (Dr	-2.69	5.39E-07	6.95E-06	43.59	36.51	29.81	1.13	3.34	4.23
JC_g15587.t1	Protein of unknown function	-2.70	1.32E-05	0.0001247	24.70	33.55	8.94	0.00	0.00	1.06
JC_g19487.t1	Protein of unknown function	-2.72	2.96E-06	3.27E-05	100.98	917.64	453.05	30.53	36.75	20.11

JC_g7050.t1	gag-pol: Putative uncharacterized	-2.74	1.19E-05	0.0001137	31.96	18.75	9.94	0.00	0.00	0.00
JC_g10556.t1	Protein of unknown function	-2.74	5.27E-06	5.48E-05	25.43	15.79	26.83	1.13	1.11	0.00
JC_g2741.t1	ORF: Orf protein (Drosophila mela	-2.78	1.46E-06	1.73E-05	35.60	28.61	22.85	0.00	2.23	2.12
JC_g2807.t2	ORF: Orf protein (Drosophila mela	-2.79	7.36E-06	7.38E-05	5.81	148.01	21.86	2.26	0.00	0.00
JC_g593.t1	Protein of unknown function	-2.84	3.42E-06	3.73E-05	64.65	23.68	11.92	0.00	0.00	2.12
JC_g4220.t1	Protein of unknown function	-2.87	9.86E-11	2.27E-09	112.60	71.04	57.62	6.78	8.91	7.41
JC_g7582.t1	Protein of unknown function	-2.88	1.67E-06	1.96E-05	34.14	23.68	20.86	0.00	2.23	0.00
JC_g2215.t1	"Mlh1: Mlh1, isoform A (Drosophila	-3.00	4.30E-19	2.18E-17	509.97	525.92	287.13	56.53	23.39	58.21
JC_g19516.t1	Protein of unknown function	-3.01	1.95E-09	3.72E-08	83.54	96.70	95.38	0.00	5.57	13.76
JC_g1806.t1	CG30291: CDK5RAP3-like protein	-3.05	8.94E-08	1.33E-06	54.48	35.52	20.86	2.26	1.11	1.06
JC_g6268.t1	Protein of unknown function	-3.08	5.90E-07	7.55E-06	26.15	23.68	17.88	0.00	0.00	0.00
JC_g18954.t1	Protein of unknown function	-3.12	1.91E-07	2.73E-06	117.69	18.75	41.73	0.00	0.00	4.23
JC_g3672.t1	pol: Pol protein (Drosophila melan	-3.13	3.60E-07	4.84E-06	23.25	21.71	23.84	0.00	0.00	0.00
JC_g14050.t1	vanin-like: Vanin-like protein 1 (Dr	-3.15	5.06E-11	1.23E-09	165.63	127.29	45.70	4.52	8.91	9.53
JC_g4219.t1	Protein of unknown function	-3.16	4.02E-17	1.76E-15	722.82	844.62	713.35	18.09	101.35	79.38
JC_g4786.t1	"Cpr47Ef: Cuticular protein 47Ef,	-3.31	1.91E-11	4.88E-10	46.49	307.85	234.47	13.57	12.25	7.41
JC_g23655.t1	ORF: ORF (Drosophila melanogas	-3.33	4.91E-08	7.68E-07	21.07	32.56	26.83	0.00	0.00	0.00
JC_g14317.t1	Protein of unknown function	-3.33	6.60E-08	1.01E-06	72.65	36.51	9.94	0.00	0.00	0.00
JC_g4218.t1	Protein of unknown function	-3.34	5.09E-22	3.45E-20	1756.57	1175.17	648.77	49.75	118.05	117.48
JC_g2773.t1	"snk: Snake, isoform B (Drosophil	-3.38	5.74E-14	1.89E-12	150.38	109.52	79.48	2.26	6.68	11.64
JC_g6589.t1	Protein of unknown function	-3.46	5.99E-10	1.22E-08	29.06	99.66	150.02	0.00	2.23	6.35
JC_g481.t1	Protein of unknown function	-3.50	2.98E-09	5.50E-08	34.14	24.67	45.70	0.00	0.00	1.06
JC_g24428.t1	Protein of unknown function	-3.54	7.34E-10	1.48E-08	31.96	37.49	55.64	2.26	0.00	0.00
JC_g8431.t1	Protein of unknown function	-3.57	5.12E-23	3.76E-21	331.99	332.52	202.68	9.05	17.82	29.63
JC_g20877.t1	"Dscam1: Down syndrome cell ad	-3.65	1.05E-15	4.06E-14	210.67	123.34	495.77	6.78	12.25	21.17
JC_g20865.t1	Protein of unknown function	-3.73	8.82E-11	2.06E-09	30.51	58.22	219.57	3.39	0.00	2.12
JC_g20516.t1	Protein of unknown function	-3.75	3.79E-10	7.99E-09	47.95	37.49	24.84	0.00	0.00	0.00
JC_g7958.t1	Protein of unknown function	-3.76	2.62E-11	6.59E-10	44.31	135.18	51.66	0.00	0.00	4.23
JC_g2490.t1	Protein of unknown function	-3.88	1.50E-15	5.74E-14	79.91	85.84	102.33	0.00	6.68	2.12
JC_g6811.t1	gag-pol: Putative uncharacterized	-3.90	4.45E-12	1.23E-10	81.36	54.27	31.79	1.13	0.00	1.06
JC_g10188.t1	Protein of unknown function	-4.07	3.95E-12	1.10E-10	50.85	34.53	45.70	0.00	0.00	0.00
JC_g5264.t1	CG9993: CG9993 (Drosophila me	-4.27	2.16E-13	6.75E-12	78.46	45.39	38.75	0.00	0.00	0.00
JC_g2369.t1	Protein of unknown function	-4.41	1.33E-16	5.47E-15	247.72	81.90	78.49	4.52	1.11	0.00
JC_g2774.t1	"snk: Snake, isoform B (Drosophil	-4.44	3.73E-15	1.37E-13	222.30	74.00	41.73	1.13	1.11	0.00
JC_g24427.t1	Protein of unknown function	-4.52	5.46E-30	5.84E-28	186.70	226.94	370.59	11.31	4.45	6.35
JC_g10566.t1	Protein of unknown function	-4.87	5.38E-23	3.92E-21	136.57	97.68	161.94	4.52	0.00	0.00
JC_g2283.t1	ORF: ORF (Drosophila melanogas	-5.10	1.26E-25	1.06E-23	130.76	115.44	132.14	0.00	1.11	2.12
JC_g2381.t1	ORF: ORF (Drosophila melanogas	-5.37	2.38E-29	2.43E-27	242.64	174.65	142.07	0.00	0.00	4.23
JC_g9248.t1	Protein of unknown function	-5.72	3.79E-43	8.04E-41	272.42	266.41	408.34	3.39	3.34	2.12
JC_g10555.t1	Protein of unknown function	-5.80	1.38E-28	1.36E-26	125.68	158.86	153.00	0.00	0.00	0.00
JC_g10566.t2	Protein of unknown function	-5.94	1.28E-34	1.85E-32	257.17	162.81	242.42	0.00	0.00	2.12
JC_g3809.t2	Protein of unknown function	-6.03	4.08E-29	4.10E-27	388.65	315.75	93.39	0.00	0.00	0.00
JC_g10553.t1	Bug22: Cilia- and flagella-associa	-6.55	7.47E-53	2.31E-50	430.06	380.87	379.53	2.26	0.00	2.12

Table S12. Differentially expressed transcripts from day 6 pupal wings

Pupal wings, 6 days after pupation					Normalized read counts					
ID	BLAST (*D. melanogaster*)	logFC	P value	Adj P Value	WT R1	WT R2	WT R3	*ivory*$^{\Delta 17kb}$ R1	*ivory*$^{\Delta 17kb}$ R2	*ivory*$^{\Delta 17kb}$ R3
JC_g7862.t1	Cpr65Av: Cuticular protein 65Av (	3.91	1.31E-18	7.45E-16	0.94	0.00	0.00	95.06	90.45	69.91
JC_g23371.t1	obst-E: Protein obstructor-E (Dros	3.34	3.65E-18	1.86E-15	8.44	2.10	12.76	154.23	168.90	144.82
JC_g23370.t1	obst-E: Protein obstructor-E (Dros	3.22	8.21E-27	9.33E-24	46.91	23.13	61.68	480.16	570.38	604.25
JC_g4315.t1	"cort: Cortex, isoform B (Drosophil	3.11	1.17E-13	3.92E-11	8.44	10.51	0.00	100.88	173.51	131.84
JC_g13970.t1	CG6472: CG6472 (Drosophila me	3.04	1.92E-11	4.29E-09	91.01	24.18	127.61	3820.93	2289.81	1658.94
JC_g1007.t1	Dmel\CG10585: GH23839p (Dros	3.01	1.58E-19	1.01E-16	110.71	106.19	51.04	498.59	1240.43	1356.32
JC_g5463.t1	CG11005: LD44221p (Drosophila	2.64	1.65E-08	1.74E-06	0.00	1.05	1.06	70.81	24.00	37.95
JC_g782.t1	qvr: Protein quiver (Drosophila me	2.55	4.41E-16	1.80E-13	93.82	108.29	99.96	532.54	507.62	1245.45
JC_g13200.t2	Polyprotein (Drosophila melanoga	2.54	1.10E-10	1.96E-08	15.01	18.93	4.25	117.37	108.91	152.81
JC_g9980.t1	Dat: Dopamine N-acetyltransferas	2.43	1.96E-11	4.29E-09	30.96	16.82	22.33	244.45	108.91	199.75
JC_g16119.t1	Protein of unknown function	2.40	1.35E-07	1.19E-05	0.94	4.21	3.19	60.14	37.84	42.95
JC_g10193.t1	CG14770-RA: GEO13396p1 (Dro	2.34	3.43E-08	3.41E-06	15.01	6.31	10.63	136.77	143.98	40.95
JC_g2024.t1	SP39: CG4914 (Drosophila melan	2.28	3.66E-09	4.45E-07	69.43	76.75	12.76	259.97	550.07	389.52
JC_g9716.t1	Protein of unknown function	2.26	3.91E-12	1.08E-09	45.97	72.55	46.79	329.81	476.24	210.74
JC_g21730.t1	"CG5160: CG5160, isoform A (Dr	2.23	8.72E-11	1.62E-08	81.62	168.22	190.36	547.09	1551.46	665.17
JC_g5027.t1	"Pdh: Photoreceptor dehydrogen	2.22	6.98E-19	4.20E-16	136.04	111.45	84.01	580.08	613.75	557.31
JC_g23845.t1	Cpr65Eb: Cuticular protein 65Eb (	2.21	3.70E-08	3.60E-06	13.13	7.36	8.51	68.87	79.37	76.90
JC_g9478.t1	mamo-RC: FI17807p1 (Drosophila	2.21	6.58E-16	2.57E-13	94.76	64.14	107.41	588.81	431.01	427.47
JC_g6093.t1	ORF: Uncharacterized protein (Dr	2.18	6.50E-07	4.75E-05	7.51	6.31	4.25	33.95	61.84	79.90
JC_g11434.t1	Protein of unknown function	2.18	1.97E-11	4.29E-09	191.39	82.01	88.27	431.66	812.18	839.96
JC_g20722.t1	Protein of unknown function	2.17	2.07E-09	2.68E-07	25.33	24.18	11.70	148.41	120.90	116.85
JC_g2744.t1	"Fur2: Furin 2, isoform I (Drosophi	2.16	9.48E-08	8.58E-06	26.27	4.21	36.16	153.26	167.97	165.79
JC_g14716.t1	Protein of unknown function	2.15	1.88E-06	0.00011576	4.69	4.21	2.13	45.59	35.99	44.94
JC_g2031.t1	ORF: Orf protein (Drosophila mela	2.10	1.94E-07	1.65E-05	30.96	13.67	6.38	106.70	131.98	113.86
JC_g862.t1	CG5493: RH34904p (Drosophila	2.09	5.35E-06	0.00027915	366.84	59.93	103.15	1715.01	2136.60	2275.17
JC_g23774.t1	CG9447: CG9447 (Drosophila me	2.09	9.71E-06	0.00047071	0.00	0.00	4.25	32.01	26.77	50.94
JC_g15275.t1	Protein of unknown function	2.08	2.14E-07	1.80E-05	7.51	16.82	28.71	81.48	119.06	152.81
JC_g7885.t1	GNBP1: Gram-negative bacteria b	2.02	1.77E-06	0.00011116	80.69	13.67	10.63	199.83	244.58	294.63
JC_g5339.t1	CG2663: RE58223p (Drosophila	2.00	8.02E-07	5.50E-05	21.58	24.18	27.65	298.77	91.37	78.90
JC_g11393.t1	Protein of unknown function	1.99	1.33E-05	0.00060465	3.75	5.26	4.25	42.68	71.99	20.97
JC_g22482.t1	Protein of unknown function	1.98	9.69E-06	0.00047071	7.51	5.26	3.19	52.38	30.46	55.93
JC_g21161.t1	Protein of unknown function	1.97	2.31E-21	1.82E-18	1440.15	2099.66	1658.96	7236.39	6563.01	8164.86
JC_g3155.t1	Pka-C3: Put. protein kinase DC2 (	1.92	4.60E-06	0.00024629	13.13	6.31	11.70	86.33	64.61	46.94
JC_g8415.t1	Oatp33Eb: Organic anion transpo	1.90	5.62E-05	0.00189728	1.88	0.00	1.06	29.10	11.08	42.95
JC_g24238.t1	CG8054: GH23453p (Drosophila	1.90	4.39E-09	5.22E-07	69.43	71.50	41.47	210.50	232.58	396.51
JC_g3293.t1	Protein of unknown function	1.90	1.19E-13	3.92E-11	126.66	164.02	148.88	486.95	775.27	572.29
JC_g1010.t1	"CG8213: CG8213, isoform B (Dr	1.89	1.65E-14	5.83E-12	117.28	112.50	105.28	541.27	397.79	444.45
JC_g10759.t1	Protein of unknown function	1.85	3.11E-07	2.56E-05	29.08	47.31	29.78	94.09	227.04	187.77
JC_g4583.t1	yellow-d2: RH49821p (Drosophila	1.84	7.57E-17	3.52E-14	12575.71	15049.81	9409.28	39805.96	51175.02	53002.17
JC_g2896.t1	"CG7675: CG7675, isoform B (Dr	1.83	9.92E-05	0.00300296	0.00	0.00	4.25	111.55	12.92	15.98
JC_g19178.t1	Protein of unknown function	1.80	0.00010663	0.00319833	0.00	0.00	0.00	9.70	47.07	14.98
JC_g16985.t1	Drice: Caspase (Drosophila melan	1.79	5.07E-06	0.00026705	12.20	12.62	20.21	88.27	70.14	66.92
JC_g864.t1	"CG5493-RA: CG5493, isoform A	1.76	0.00015428	0.00428804	167.00	41.00	23.40	674.17	598.06	773.04
JC_g7695.t1	"Cpr62Bc: Cuticular protein 62Bc,	1.76	1.96E-06	0.00011877	46.91	22.08	19.14	151.32	144.90	103.87
JC_g8423.t1	"c-SP18: CG1299, isoform B (Dro	1.75	0.00011317	0.00336478	9.38	3.15	5.32	29.10	43.38	51.94
JC_g8052.t1	"BcDNA:RE33542: Uncharacteriz	1.74	2.12E-11	4.52E-09	321.80	419.51	377.52	966.15	1289.34	1906.63
JC_g12570.t1	Protein of unknown function	1.74	0.00017916	0.00484778	7.51	6.31	2.13	25.22	25.84	80.90
JC_g5367.t1	ORF: Orf protein (Drosophila mela	1.72	0.00024614	0.00611055	1.88	0.00	0.00	19.40	20.30	21.97
JC_g20726.t1	"Dmel\CG7264: CG7264, isoform	1.72	6.97E-05	0.00224653	9.38	10.51	5.32	50.44	45.22	45.94
JC_g21723.t1	Protein of unknown function	1.72	0.00020738	0.0053972	8.44	0.00	17.01	76.63	85.83	36.95
JC_g23926.t1	Spn42Da: Serpin 4 (Drosophila m	1.72	0.00018797	0.00499374	5.63	4.21	4.25	21.34	49.84	33.96
JC_g5106.t1	PPO2: Phenoloxidase 2 (Drosoph	1.69	5.21E-07	3.95E-05	116.34	91.47	57.43	213.41	310.11	532.34
JC_g5755.t1	CG5363: CG5363-PA (Drosophila	1.68	2.68E-08	2.73E-06	148.24	162.97	212.69	1012.71	484.54	464.42
JC_g19396.t1	Amy-d: Alpha-amylase B (Drosoph	1.68	2.36E-06	0.00013974	35.65	33.64	26.59	93.12	115.37	185.77
JC_g24936.t1	Protein of unknown function	1.68	5.67E-06	0.00029433	154.80	86.22	55.30	246.39	286.11	713.11
JC_g9645.t1	"qm: Quemao, isoform A (Drosoph	1.67	1.31E-09	1.77E-07	132.29	202.92	159.52	748.86	616.52	413.49
JC_g2825.t1	"snk: Snake, isoform B (Drosophil	1.66	2.22E-06	0.00013302	128.53	68.34	36.16	356.97	230.73	346.57
JC_g5232.t1	PPO2: Phenoloxidase 2 (Drosoph	1.65	1.98E-10	3.21E-08	193.27	216.59	144.63	496.65	642.36	786.02
JC_g4577.t1	yellow-h: Yellow-h (Drosophila me	1.63	8.76E-10	1.19E-07	109.77	177.69	165.90	495.68	624.83	437.46
JC_g2874.t1	Protein of unknown function	1.62	5.45E-05	0.00184613	129.47	84.11	82.95	86.33	554.69	659.18
JC_g14328.t1	AttC: Attacin-C (Drosophila melan	1.61	3.01E-06	0.00016984	250.50	85.16	152.07	702.30	327.64	816.99
JC_g14481.t1	gd: Serine protease gd (Drosophi	1.61	2.79E-06	0.00016113	54.42	58.88	24.46	156.17	155.98	206.74
JC_g2824.t1	"snk: Snake, isoform B (Drosophil	1.61	9.79E-09	1.06E-06	127.60	138.79	90.39	377.34	323.03	525.35
JC_g13966.t1	Nup133: Nup133 (Drosophila mel	1.61	0.00034918	0.00811685	14.07	3.15	8.51	60.14	56.30	29.96
JC_g5505.t1	Protein of unknown function	1.61	9.09E-06	0.00044697	33.78	17.87	32.97	128.04	111.68	89.89
JC_g5504.t1	"CG9518-RA: CG9518, isoform A	1.60	3.38E-11	6.79E-09	287.09	237.62	255.22	964.21	985.70	631.22

JC_g1961.t1	CG34458: Uncharacterized protei	1.59	7.91E-10	1.09E-07	773.08	485.75	431.76	1432.73	1983.39	2184.29
JC_g16893.t1	Tmem18: GEO10750p1 (Drosoph	1.58	2.96E-05	0.00112255	147.30	104.09	436.01	448.15	957.09	1295.39
JC_g9682.t1	CG6564: LD27203p (Drosophila r	1.58	4.48E-07	3.44E-05	13624.62	8153.64	5401.19	17203.40	40417.26	37169.84
JC_g22478.t1	"Dmel\CG8765: CG8765, isoform	1.56	8.85E-05	0.00274164	24.39	39.95	42.54	207.59	52.61	180.78
JC_g4534.t1	l(2)01810: Lethal (2) 01810 (Dros	1.56	2.67E-05	0.00103086	29.08	18.93	28.71	116.40	68.30	108.86
JC_g11112.t1	"GLS: Glutaminase, isoform B (Dr	1.55	0.00028284	0.00683886	34.71	15.77	7.44	57.23	74.76	135.83
JC_g20821.t1	Protein of unknown function	1.54	0.00029294	0.00699593	12.20	22.08	6.38	77.60	59.99	46.94
JC_g19551.t1	IP16913p (Drosophila melanogas	1.54	1.39E-05	0.00061732	52.54	27.34	38.28	161.02	172.59	94.88
JC_g17953.t1	Protein of unknown function	1.53	3.39E-10	5.02E-08	237.37	158.76	193.55	652.83	668.21	526.35
JC_g19027.t1	CG11318: RE14222p (Drosophila	1.53	2.94E-06	0.00016713	243.00	194.51	122.30	316.23	780.80	814.99
JC_g5107.t1	PPO2: Phenoloxidase 2 (Drosoph	1.52	1.55E-05	0.00067979	153.87	252.34	73.38	676.11	708.82	315.61
JC_g6411.t1	SD02026p (Drosophila melanoga	1.51	0.00023607	0.00594707	8.44	21.03	19.14	50.44	70.14	78.90
JC_g15793.t1	MED28: Mediator of RNA polymer	1.51	0.00014163	0.00402388	22.52	17.87	21.27	45.59	91.37	102.87
JC_g14536.t1	Protein of unknown function	1.50	1.34E-05	0.00060465	52.54	63.08	129.74	388.01	192.89	266.67
JC_g18208.t1	Protein of unknown function	1.50	4.12E-08	3.90E-06	152.93	167.17	194.61	724.61	380.25	513.36
JC_g7846.t1	"Edg78E: Ecdysone-dependent g	1.50	0.00040668	0.0091018	29.08	6.31	52.11	143.56	148.59	80.90
JC_g2873.t1	Ncc69: GH27027p (Drosophila me	1.49	2.70E-05	0.00103715	485.99	318.58	314.78	407.41	1511.77	1972.55
JC_g111.t1	CHKov1: GH03753p (Drosophila r	1.49	0.00030708	0.00723682	14.07	16.82	10.63	51.41	71.07	45.94
JC_g3294.t1	Protein of unknown function	1.49	8.31E-06	0.00041264	45.97	41.00	58.49	111.55	211.35	163.80
JC_g23293.t1	CG15255: Metalloendopeptidase	1.47	2.29E-06	0.00013622	454.09	446.85	1176.16	2007.95	2746.66	1879.67
JC_g8777.t1	Spn42Da: Serpin 4 (Drosophila m	1.46	1.68E-11	3.90E-09	1047.98	840.07	657.20	2469.68	2434.71	2507.89
JC_g2025.t1	"CG11836: Uncharacterized prote	1.45	0.00011542	0.00342174	30.02	18.93	19.14	81.48	72.91	84.89
JC_g1354.t1	CT31491: RE68558p (Drosophila	1.44	2.63E-09	3.28E-07	577.00	513.09	426.44	1053.45	1672.36	1715.87
JC_g12553.t1	Dmel\CG33290: HDC11369 (Dros	1.44	1.99E-08	2.07E-06	124.78	103.04	93.58	301.68	314.72	333.59
JC_g17689.t1	Protein of unknown function	1.43	1.35E-05	0.00060607	71.30	67.29	47.85	254.15	125.52	212.74
JC_g1792.t1	Cdc16: Cell division cycle 16 ortho	1.43	5.65E-05	0.0018973	121.03	41.00	51.04	177.51	275.04	253.68
JC_g22912.t1	CG3246: RH02901p (Drosophila r	1.42	4.95E-05	0.00173231	42.22	31.54	26.59	88.27	126.44	112.86
JC_g18937.t1	Protein of unknown function	1.42	4.79E-06	0.00025358	59.11	94.63	111.66	328.84	290.73	195.76
JC_g1061.t1	"Ance-3: Ance-3, isoform B (Dros	1.42	0.00035098	0.00813303	53.48	31.54	21.27	77.60	95.06	211.74
JC_g18353.t1	"CG7763: CG7763, isoform A (Dr	1.42	7.62E-07	5.32E-05	56.29	68.34	67.00	182.36	203.05	185.77
JC_g9337.t1	hh: Protein hedgehog (Drosophila	1.41	5.92E-06	0.00030452	104.14	49.42	97.84	236.69	303.65	229.71
JC_g10287.t1	Protein of unknown function	1.41	5.45E-05	0.00184613	869.72	1210.17	2914.88	8572.11	3888.33	3531.61
JC_g4519.t1	CG9645: RH19136p (Drosophila r	1.40	0.00015352	0.00427835	66.61	32.59	60.62	175.57	92.29	265.67
JC_g19778.t1	"mthl15: Methuselah-like 15, isofo	1.40	6.43E-06	0.00032883	68.49	59.93	54.24	134.83	195.66	221.72
JC_g15586.t1	CG4927: CG4927 (Drosophila me	1.39	1.24E-05	0.00056996	570.43	226.05	187.16	982.64	985.70	1021.73
JC_g11180.t1	Protein of unknown function	1.39	3.48E-07	2.80E-05	84.44	104.09	87.20	317.20	247.35	233.71
JC_g20715.t1	"Etf-QO: Electron transfer flavopro	1.38	1.21E-05	0.00056009	561.05	443.69	164.83	1080.61	1113.99	1318.36
JC_g15296.t1	MAPk-Ak2: LD26767p (Drosophila	1.37	4.78E-09	5.55E-07	425.95	530.96	447.71	1016.59	1224.74	1631.97
JC_g7535.t1	"Pxd: Peroxidase, isoform B (Dros	1.36	2.13E-08	2.20E-06	322.74	389.02	418.99	886.60	1366.87	874.91
JC_g22913.t1	"CG2016-RB: CG2016, isoform B	1.35	3.48E-06	0.00019215	1563.05	612.97	1129.37	4072.17	2838.95	2480.92
JC_g18680.t1	CG8945: CG8945 (Drosophila me	1.34	0.00037505	0.00854338	29.08	45.21	35.09	68.87	178.13	102.87
JC_g5379.t1	CG12123: GH02722p (Drosophila	1.34	5.71E-06	0.00029507	299.29	373.25	489.18	1675.23	749.42	862.93
JC_g15351.t1	Snx6: Sorting nexin (Drosophila m	1.33	1.52E-07	1.32E-05	496.31	835.87	927.32	2299.93	2251.97	1604.01
JC_g23127.t1	Protein of unknown function	1.33	3.30E-10	4.96E-08	353.70	430.02	396.66	1168.88	910.94	1045.70
JC_g9638.t1	"qm: Quemao, isoform A (Drosoph	1.33	2.94E-10	4.56E-08	1757.26	1334.23	1801.46	4465.03	3596.69	4838.99
JC_g15377.t1	CG12268-RB: Fatty acyl-CoA redu	1.31	1.57E-06	9.97E-05	238.30	293.34	501.94	991.37	1028.15	797.01
JC_g14206.t1	Mco1: FI03373p (Drosophila mela	1.31	2.41E-05	0.0009469	588.26	215.54	306.27	960.33	1363.18	812.99
JC_g23616.t1	shakB: Innexin shaking-B (Drosop	1.31	0.00035147	0.00813303	31.90	39.95	26.59	83.42	139.36	77.90
JC_g20197.t1	Galt: Galactose-1-phosphate urid	1.31	0.00015604	0.00432525	60.05	47.31	37.22	93.12	183.66	149.81
JC_g5649.t1	"CG14395: Uncharacterized prote	1.30	0.00024064	0.00601183	28.15	38.90	31.90	100.88	114.44	76.90
JC_g23925.t1	Spn42Da: RE31022p (Drosophila	1.30	6.41E-05	0.00209619	61.92	50.47	49.98	107.67	170.74	181.77
JC_g24456.t1	CG12964: IP14311p (Drosophila	1.29	3.22E-08	3.23E-06	2589.45	2032.37	1774.88	4148.80	5717.60	6816.53
JC_g10489.t1	XRCC1: FI04011p (Drosophila me	1.29	2.46E-05	0.00096205	58.17	58.88	58.49	165.87	188.28	128.84
JC_g3053.t1	"Cyp6a14: Cyp6a14, isoform E (F	1.29	5.24E-05	0.00179804	64.74	42.06	87.20	190.12	181.82	168.79
JC_g4219.t1	Protein of unknown function	1.29	0.00011758	0.00345562	824.68	396.38	259.48	1232.90	957.09	2017.49
JC_g2325.t1	Cpr31A: Cuticular protein 31A (Dr	1.28	6.78E-05	0.00219459	1582.75	427.92	1224.02	3496.94	3176.75	2371.06
JC_g2458.t1	kal-1-RA: RT10464p (Fragment) (I	1.28	5.16E-05	0.00177608	69.43	78.86	65.93	128.04	216.89	246.69
JC_g22514.t1	Protein of unknown function	1.28	0.00035719	0.00820981	31.90	35.75	30.84	93.12	71.99	122.85
JC_g10282.t1	"Snmp1: Sensory neuron membra	1.27	0.00041636	0.00923754	62.86	25.23	37.22	120.28	109.83	134.83
JC_g23278.t1	"CG6769: CG6769, isoform A (Dr	1.25	4.36E-07	3.40E-05	312.42	396.38	525.34	1097.10	1198.90	848.95
JC_g22904.t1	"CG10407: Uncharacterized prote	1.24	6.92E-07	5.02E-05	16937.43	23404.27	11461.72	49738.06	44324.98	36928.14
JC_g5497.t1	CG9521: CG9521 (Drosophila me	1.22	4.22E-05	0.00149743	705.53	1048.25	1634.50	3437.77	3536.69	1792.77
JC_g10704.t1	Rab32: FI09421p (Drosophila me	1.21	1.17E-05	0.00055066	155.74	108.29	119.10	256.09	394.09	317.61
JC_g5449.t1	schlank: LD18904p (Drosophila m	1.21	8.29E-05	0.00260077	278.65	132.48	282.87	827.43	510.38	458.43
JC_g11247.t1	"stj: Straightjacket, isoform D (Dro	1.20	1.20E-05	0.00055749	123.84	151.40	181.85	278.40	453.16	416.48
JC_g12521.t1	beta4GalNAcTA: Beta4GalNAcTA	1.20	3.01E-05	0.00112878	108.83	95.68	67.00	238.63	251.96	199.75
JC_g23179.t1	pck-RC: LD14222p (Fragment) (D	1.20	1.50E-06	9.69E-05	614.52	578.27	1014.52	1783.88	2083.99	1549.08
JC_g11421.t1	Fic: Adenosine monophosphate-p	1.20	9.86E-06	0.00047349	238.30	142.99	176.53	447.18	569.45	374.53
JC_g9550.t1	"CG3168: CG3168, isoform A (Dr	1.20	0.00021733	0.00559911	110.71	142.99	89.33	181.39	275.04	440.45
JC_g10328.t1	CG16885: RH04334p (Drosophila	1.19	0.0001012	0.0030534	2086.57	1585.52	3247.73	6170.33	8405.19	3121.12

JC_g7607.t1	BcDNA.GH04922: BcDNA.GH049	1.19	0.00030184	0.0071796	50.66	69.39	43.60	117.37	176.28	131.84
JC_g25262.t1	"CG4630: CG4630, isoform A (Dr	1.18	4.78E-07	3.65E-05	1062.05	1303.74	934.76	2125.33	2385.79	3436.73
JC_g17722.t1	"SPH66: CG4998, isoform A (Dros	1.17	1.67E-05	0.00071797	2796.79	3372.91	4630.20	5810.45	8021.25	12501.47
JC_g21257.t1	Protein of unknown function	1.14	1.11E-05	0.00052514	207.34	197.66	132.93	496.65	407.02	375.53
JC_g23550.t1	"CG8180: CG8180, isoform B (Dr	1.13	9.37E-05	0.00286883	1922.38	1871.50	1305.90	4370.93	5743.44	2146.33
JC_g18144.t1	"Hml: Hemolectin, isoform B (Dros	1.13	8.38E-06	0.00041407	2450.59	1851.52	1167.65	3808.32	4866.65	4123.88
JC_g11521.t1	CG13646: Uncharacterized protei	1.12	1.43E-05	0.000635	319.93	222.90	292.44	465.61	720.81	767.05
JC_g1227.t1	"Pdk: Pyruvate dehydrogenase ki	1.11	1.18E-07	1.06E-05	2753.63	2013.44	2092.84	4891.84	4563.92	6046.49
JC_g23775.t1	CG1561: HL08023p (Drosophila r	1.11	0.00020322	0.00532951	172.63	136.68	118.04	220.20	452.24	343.57
JC_g19813.t1	"Dmel\CG5150: CG5150, isoform	1.10	6.68E-05	0.00216784	292.72	547.78	468.98	704.24	1113.99	1209.50
JC_g15257.t1	CG8299: CG8299 (Drosophila me	1.09	0.00042726	0.00945899	688.64	1368.93	571.07	1252.30	2411.63	2572.80
JC_g14289.t1	CG9518: RE11240p (Drosophila r	1.09	2.54E-10	4.04E-08	8634.31	9475.26	9987.79	19837.02	20440.29	21172.70
JC_g10494.t1	"CdGAPr: Cd GTPase activating p	1.08	5.53E-07	4.10E-05	934.45	627.69	674.22	1619.94	1723.12	1608.00
JC_g7848.t1	Cpr49Ah: Cuticular protein 49Ah (	1.08	1.78E-05	0.00075042	28202.47	20205.90	14827.49	50620.78	35825.65	56120.30
JC_g9626.t1	"spz: Spatzle, isoform J (Drosophi	1.08	5.77E-05	0.00192196	144.48	141.94	112.72	293.92	247.35	364.55
JC_g10008.t1	"CG8586-RA: CG8586, isoform A	1.08	2.04E-05	0.00083986	176.38	230.26	199.93	407.41	388.56	564.30
JC_g13281.t1	MP1: Melanization protease 1 (Dr	1.07	0.00034854	0.00811685	344.32	405.84	215.88	940.92	438.40	856.94
JC_g12049.t1	CG12164-RA: FI17860p1 (Fragm	1.07	7.28E-07	5.21E-05	2499.38	2502.34	3147.77	7427.48	5429.64	5010.78
JC_g23514.t1	"Gasp: Gasp, isoform A (Drosoph	1.07	6.81E-06	0.00034659	1320.99	854.79	1573.89	2530.80	2939.55	2809.51
JC_g11020.t1	"nAChRalpha5: Nicotinic acetylch	1.06	0.00023232	0.00588154	882.85	626.64	530.65	1749.93	880.48	1984.54
JC_g11352.t1	"Rab6: Rab6, isoform B (Drosoph	1.05	3.19E-06	0.00017901	3179.58	3628.40	5182.12	8620.62	9951.11	7521.66
JC_g1006.t1	CG11601: AT02829p (Drosophila	1.05	0.00028901	0.00694403	67.55	74.65	74.44	150.35	158.75	178.78
JC_g11895.t1	"Nep2: Neprilysin 2, isoform A (Dr	1.04	1.30E-05	0.00059253	5946.35	3987.98	3915.57	7711.70	12357.20	9900.70
JC_g4082.t1	Protein of unknown function	1.03	0.00010803	0.00323078	2475.93	2139.61	4211.21	7924.14	6696.83	4756.09
JC_g10627.t1	RnrS: Ribonucleoside-diphosphat	1.03	0.00018451	0.00492743	134.16	182.94	245.65	473.37	430.09	335.58
JC_g882.t1	BEST:CK00459: Sodium/nucleos	1.03	0.00038132	0.00864782	222.35	158.76	158.45	255.12	447.62	497.38
JC_g25336.t1	Ndg-RA: RE69505p (Drosophila n	1.03	1.10E-05	0.00052202	281.46	254.44	239.27	449.12	632.21	583.28
JC_g23341.t1	CG4331: RE58242p (Drosophila r	1.03	2.11E-05	0.0008599	17183.24	15357.87	21813.20	39953.41	50155.17	27031.43
JC_g16921.t1	mys: Integrin beta (Drosophila me	1.02	0.00043126	0.00952677	87.25	90.42	63.81	183.33	166.13	183.77
JC_g23271.t1	"Dmel\CG32448: Uncharacterized	1.02	0.00013542	0.00390157	158.56	155.61	243.53	367.64	476.24	363.55
JC_g12363.t1	"CT39634: Uncharacterized prote	1.01	5.40E-05	0.00184408	6203.42	5506.21	5139.59	10725.57	17111.25	8227.78
JC_g13285.t1	MP1: Melanization protease 1 (Dr	1.01	3.51E-05	0.00128254	1414.81	1395.21	880.53	1980.79	3003.24	2888.41
JC_g2470.t1	"Ance-3: Ance-3, isoform B (Dros	1.00	2.71E-05	0.00103835	993.56	608.76	858.19	1659.71	2074.76	1446.20
JC_g11155.t1	Protein of unknown function	1.00	5.08E-05	0.00176783	467.23	453.16	715.69	1319.23	1212.74	920.86
JC_g22907.t1	CG14661: IP07792p (Drosophila	0.98	7.49E-07	5.28E-05	2663.57	2296.27	2110.92	4601.80	5553.31	4273.69
JC_g4287.t1	Treh: Trehalase (Fragment) (Dros	0.98	7.72E-05	0.00243856	691.46	827.46	1278.25	2115.63	1642.83	2070.43
JC_g16869.t1	"Hydr2: Alpha/beta hydrolase2, is	0.98	2.92E-06	0.00016713	1257.20	917.88	1157.02	2001.16	2586.07	2237.22
JC_g3995.t1	Protein of unknown function	0.98	0.00012802	0.00371752	310.55	448.95	379.65	671.26	656.21	1045.70
JC_g23189.t1	"CG7627-RA: CG7627, isoform A	0.97	3.35E-06	0.00018697	1456.10	1360.52	1051.74	2307.69	2948.78	2613.75
JC_g9352.t1	"Dmel\CG8519: CG8519, isoform	0.97	0.0003568	0.00820981	289.91	220.80	362.63	683.87	710.66	427.47
JC_g875.t1	CG5726: CG5726 (Drosophila me	0.96	0.0001492	0.00420387	274.89	218.69	161.64	424.87	464.24	466.42
JC_g17379.t1	GNBP1: Gram-negative bacteria b	0.95	0.00025562	0.00633053	113.52	135.63	170.15	288.10	289.80	283.65
JC_g10259.t1	"mnb: Minibrain, isoform H (Drosop	0.95	3.68E-05	0.0013271	450.34	401.64	313.71	696.48	912.78	753.06
JC_g1277.t1	Pur-alpha: LD15002p (Drosophila	0.95	0.00020144	0.00529652	266.45	186.10	238.21	559.70	474.39	374.53
JC_g5206.t1	CG6763: Metalloendopeptidase (	0.93	9.83E-06	0.00047349	282.40	292.29	321.16	567.46	613.75	593.26
JC_g11628.t1	"trol: Terribly reduced optic lobes,	0.93	2.98E-05	0.00112458	3617.72	2860.87	2633.07	4647.39	7166.61	6237.25
JC_g7726.t1	Lkb1: GM01569p (Drosophila mel	0.91	0.00013997	0.0040101	369.65	516.24	619.98	1022.41	859.25	1085.65
JC_g10250.t1	"mnb: Minibrain, isoform I (Drosop	0.91	0.00018181	0.0048936	374.34	284.93	342.43	532.54	825.11	620.23
JC_g5695.t1	"CG2663: CG2663, isoform A (Dr	0.91	0.0001733	0.00470167	2592.26	4222.44	4686.56	8531.37	6201.21	7869.23
JC_g1364.t1	"2D9: Uncharacterized protein, iso	0.90	0.00020923	0.00541783	449.40	432.13	382.84	879.81	1008.77	591.27
JC_g1735.t1	"Apc: APC-like, isoform A (Drosop	0.89	0.00034549	0.00808624	3711.54	1950.36	2064.13	5334.17	5050.31	4675.19
JC_g17332.t1	LPCAT: Lysophosphatidylcholine	0.89	0.00015802	0.00434479	334.94	251.29	236.08	581.05	511.31	501.38
JC_g24898.t1	Sp7: Serine protease 7 (Drosophi	0.89	0.00015765	0.00434479	2688.90	3503.28	2083.27	4239.98	6141.22	5640.99
JC_g23241.t1	"nct: Nicastrin, isoform D (Drosoph	0.89	0.00016108	0.00441135	811.55	907.36	1165.53	1774.18	2331.34	1471.17
JC_g14935.t1	Syx17: GH06387p (Drosophila me	0.88	4.82E-05	0.00169258	2146.61	1832.60	2740.48	4566.88	4723.59	3575.56
JC_g11407.t1	"Nrg: Neuroglian, isoform G (Dros	0.87	0.00014965	0.00420489	3628.04	2562.27	2191.74	4475.70	5938.18	5527.14
JC_g22891.t1	MBD-R2: SD10773p (Drosophila r	0.86	8.93E-05	0.00276037	819.99	827.46	627.43	1373.56	1704.66	1218.49
JC_g9591.t1	Protein of unknown function	0.86	0.00020797	0.00539883	443.77	549.88	336.05	816.76	869.41	832.97
JC_g4328.t1	dome: Cytokine receptor (Drosoph	0.85	0.00012459	0.00364081	547.91	619.28	414.74	904.06	1026.31	1032.72
JC_g16212.t1	rau: GH01721p (Drosophila melan	0.85	6.98E-05	0.00224653	559.17	599.30	583.83	1284.31	1056.76	901.88
JC_g7728.t1	Lkb1: GM01569p (Drosophila mel	0.84	7.44E-05	0.00236188	348.07	345.91	416.87	734.31	665.44	654.19
JC_g21256.t1	"C3G: C3G ortholog, isoform L (D	0.83	0.00026388	0.00651927	455.97	417.41	331.79	807.06	626.67	796.01
JC_g22890.t1	Prosbeta1: Proteasome subunit b	0.83	2.42E-05	0.0009469	3256.51	2615.90	2977.62	6218.83	5138.91	4793.05
JC_g24680.t1	wap: LD15927p (Drosophila mela	0.82	0.00044722	0.00981587	327.43	333.30	279.68	607.24	463.31	651.19
JC_g23408.t1	CG1703: LD35151p (Fragment) (I	0.81	0.00010346	0.00311221	1590.26	1657.01	1790.83	2526.92	3714.82	2842.47
JC_g24237.t1	CG30345: IP12271p (Drosophila	0.80	0.00038971	0.00877954	23620.27	24228.57	14370.21	35005.31	37057.77	39935.40
JC_g20593.t1	Klp68D: Kinesin-like protein (Dros	0.79	0.00019561	0.00516978	3219.92	2840.90	3529.55	5781.35	6859.27	4485.43
JC_g12922.t1	Gk1: GH12641p (Drosophila mela	0.78	0.00015207	0.00424975	805.92	912.62	915.62	1805.22	1555.15	1302.38
JC_g16591.t1	amd-RA: FI18657p1 (Drosophila r	0.77	0.00038538	0.0087012	16503.04	18693.98	25288.51	36517.58	40289.90	29943.81
JC_g7764.t1	"CG5966: CG5966, isoform A (Dr	0.77	0.00014098	0.00401646	1202.78	1318.46	1168.72	1861.48	2553.77	2048.46

JC_g20551.t1	Protein of unknown function	0.76	2.08E-05	0.00085172	3664.63	3791.37	3287.08	6527.30	6373.80	5704.91
JC_g23379.t1	CG9551: LD35051p (Drosophila r	0.76	6.11E-05	0.0020154	945.71	1013.55	1142.13	1690.75	1898.48	1795.77
JC_g3521.t1	Kaz1-ORFB: KAZ1-type serine pr	0.76	6.24E-05	0.00204538	1028.27	856.89	995.38	1673.29	1737.89	1587.03
JC_g2622.t1	CG3823: CG3823 (Drosophila me	0.76	0.00018164	0.0048936	1244.06	1427.81	1747.23	2626.83	2717.13	2350.08
JC_g11341.t1	"Klp31E: Kinesin-like protein at 31	0.75	0.0001279	0.00371752	1502.07	1319.51	1134.69	2415.36	2275.04	2135.35
JC_g23294.t1	"C3G: C3G ortholog, isoform G (D	0.75	9.32E-05	0.0028636	1735.68	1612.85	1394.16	2966.34	2722.66	2482.92
JC_g18266.t1	"laccase2: Laccase 2, isoform D (	0.75	0.0002797	0.00678449	612.65	506.78	533.85	1056.36	941.40	861.93
JC_g5332.t1	"PI4KIIIalpha: Phosphatidylinositol	0.75	0.00028881	0.00694403	876.28	891.59	671.03	1483.17	1281.96	1448.20
JC_g15380.t1	"Pex19: Peroxin 19, isoform A (Dr	0.75	0.00035651	0.00820981	772.14	994.63	965.60	1346.40	1748.04	1619.99
JC_g9055.t1	Cow: Proteoglycan Cow (Drosoph	0.74	0.00018298	0.00490383	683.01	660.28	782.69	1112.62	1262.58	1250.45
JC_g20717.t1	"AdipoR: Adiponectin receptor, iso	0.72	0.00031701	0.00743656	4357.03	4905.85	4105.93	6406.05	8862.04	7212.04
JC_g2134.t1	neo: GH22837p (Drosophila mela	0.70	0.00021866	0.00561599	722.42	666.59	698.68	1203.80	1087.22	1181.53
JC_g2619.t1	CrebA: RE64328p (Drosophila me	-0.66	0.00027062	0.00663763	2577.25	2286.81	2499.08	1587.93	1441.63	1551.07
JC_g8079.t1	Lk6: LD17393p (Drosophila melan	-0.66	0.00014792	0.0041908	33974.31	34348.34	31793.55	18905.80	21074.35	22307.30
JC_g15742.t1	"uex: Unextended, isoform E (Dro	-0.69	0.00039561	0.00889287	4926.52	4899.55	3837.94	2852.84	2939.55	2509.88
JC_g24105.t1	Fpps: Farnesyl pyrophosphate sy	-0.69	4.06E-05	0.00144824	15107.93	14016.28	14346.82	8770.00	8674.69	9087.71
JC_g636.t1	GEO11434p1 (Fragment) (Drosop	-0.70	0.00020733	0.0053972	11334.46	15201.21	13829.99	8162.76	8430.11	7734.39
JC_g5718.t1	"fabp: Fatty acid bindin protein, is	-0.70	0.00021716	0.00559911	2182.27	2436.10	2589.47	1355.13	1375.18	1604.01
JC_g12488.t1	Thor: 4E-binding protein THOR (D	-0.70	0.0002687	0.00660627	1726.30	1868.35	1925.88	1018.53	1257.04	1036.71
JC_g18309.t1	CLIP-190: Restin homolog (Droso	-0.71	4.28E-05	0.00151624	11254.72	10104.00	10669.46	5997.67	6766.97	6469.96
JC_g22647.t1	RpL35A: GEO07455p1 (Drosoph	-0.71	0.00044537	0.00979619	10839.09	16320.96	12822.91	8299.54	7825.58	7642.51
JC_g25064.t1	CG15544: LP06141p (Drosophila	-0.72	9.53E-05	0.0029025	14400.52	16582.76	16640.65	10573.28	9255.21	8586.34
JC_g3808.t1	Toll-7: Toll-like receptor 7 (Drosop	-0.73	0.00027992	0.00678449	4064.31	3746.16	3061.63	2249.49	1872.64	2292.15
JC_g17758.t1	Rm62: LP18603p (Drosophila me	-0.73	0.0001928	0.00510877	38519.92	45390.20	40046.88	22360.06	21456.44	29080.88
JC_g11422.t1	CG32512: LD23009p (Drosophila	-0.74	2.84E-05	0.00107871	5870.35	6345.23	6539.07	3430.01	3967.71	3599.53
JC_g12333.t1	lark: RNA-binding protein lark (Dro	-0.75	2.22E-05	0.00088649	3133.61	3298.26	3271.13	2025.41	1771.12	1839.72
JC_g10315.t1	"tx: Taxi, isoform B (Drosophila me	-0.76	9.41E-05	0.00287249	15139.83	20528.68	17193.64	10897.27	9172.15	10438.04
JC_g4547.t1	sta: 40S ribosomal protein SA (Dr	-0.77	1.95E-05	0.00080618	13598.36	14538.83	12452.84	8458.62	7768.36	7149.12
JC_g17926.t1	CG4933: Probable tRNA N6-ader	-0.79	0.0004528	0.00991709	807.80	1048.25	1202.75	567.46	631.29	514.36
JC_g5382.t1	Dmel\CG42598: Uncharacterized	-0.79	3.00E-05	0.00112779	2893.43	3381.32	3012.71	1639.34	1959.40	1658.94
JC_g5340.t1	CG2663: RE58223p (Drosophila r	-0.80	0.00030351	0.00718586	2508.76	1969.28	3258.37	1404.60	1473.93	1426.23
JC_g16269.t1	"Tctp: Translationally controlled tu	-0.80	8.35E-05	0.00261276	36150.95	47628.64	44564.36	28059.93	20407.06	23205.18
JC_g7463.t1	Protein of unknown function	-0.80	8.14E-06	0.00040637	189776.52	########	175345.75	106437.01	88300.16	108378.40
JC_g17538.t1	"Gbs-76A: Glycogen binding subu	-0.80	0.0004148	0.00923754	2496.57	2606.43	1736.59	1020.47	1341.95	1412.25
JC_g494.t1	CG13404: Uncharacterized protei	-0.82	0.0004547	0.00993722	463.47	560.40	667.84	336.60	278.73	305.62
JC_g17706.t1	CT15908: CG4962 (Drosophila m	-0.82	1.51E-06	9.74E-05	1094949.05	########	#########	631427.40	611161.57	680756.54
JC_g24108.t1	CG7741: CWF19-like protein 1 ho	-0.84	0.00036968	0.00843997	324.62	383.76	347.74	189.15	175.36	201.75
JC_g13627.t1	Ser: Protein serrate (Drosophila m	-0.85	9.21E-07	6.24E-05	7845.28	7610.07	8450.06	4193.42	4262.12	4555.34
JC_g11364.t1	Protein of unknown function	-0.86	1.92E-06	0.00011715	5075.69	6012.98	5888.25	3157.43	2822.34	3133.11
JC_g16106.t1	"34F4T: CG6084, isoform D (Dros	-0.87	5.30E-06	0.00027817	3606.46	4629.34	3699.69	2023.47	2182.75	2162.31
JC_g22905.t1	CG1124: CG1124 (Drosophila me	-0.88	0.00035829	0.0082165	895.05	1642.29	1431.39	621.79	751.27	687.15
JC_g13005.t1	"CG9331: CG9331, isoform B (Dr	-0.88	0.00026793	0.00660326	14789.88	17536.38	14233.03	5164.42	9658.54	9273.48
JC_g24066.t1	Amy-p: Alpha-amylase A (Drosoph	-0.89	2.93E-06	0.00016713	7446.54	9379.58	10084.57	4745.36	4708.83	4686.18
JC_g24067.t1	"CG3907: CG3907, isoform A (Dr	-0.90	9.15E-06	0.00044783	1557.42	1249.07	1561.12	702.30	727.27	836.96
JC_g5461.t1	CG7289: CG7289 (Drosophila me	-0.90	0.00014058	0.00401631	394.98	393.23	367.95	175.57	185.51	229.71
JC_g3323.t1	"CycK: Cyclin K, isoform A (Drosop	-0.91	0.00017221	0.00468444	668.00	888.44	529.59	372.49	336.87	347.57
JC_g13436.t1	Zip42C.1: RE15841p (Drosophila	-0.91	1.61E-05	0.00069826	2425.26	2590.66	2116.24	975.85	1251.50	1428.23
JC_g21883.t1	CG31954: IP09792p (Drosophila	-0.92	0.0004611	0.01005566	11204.05	22210.93	16919.27	10987.48	6809.43	7387.82
JC_g15853.t1	Dmel\CG7372: CG7372 (Drosoph	-0.92	0.00022095	0.00563561	377.16	337.50	294.57	194.01	151.36	160.80
JC_g25160.t1	CG15531: Uncharacterized protei	-0.92	0.00030272	0.0071838	2114.72	3447.56	4465.37	1774.18	1435.17	1790.78
JC_g19631.t1	Protein of unknown function	-0.93	0.00011626	0.00343663	8512.34	9717.08	5890.37	3981.95	3137.06	4984.81
JC_g2408.t1	"CG18428: Uncharacterized prote	-0.93	1.94E-05	0.00080618	791.85	717.06	633.81	406.44	343.33	335.58
JC_g842.t1	Protein of unknown function	-0.93	0.00016131	0.00441135	10515.41	10700.15	9640.05	5081.96	6982.02	3358.83
JC_g5338.t1	CG2663: RE58223p (Drosophila r	-0.93	3.32E-05	0.00122696	1028.27	1565.54	1358.01	733.34	668.21	590.27
JC_g20556.t1	anon-WO0118547.633: FI16105p	-0.94	1.83E-05	0.00076919	1172.76	1113.44	1598.34	712.97	611.91	626.22
JC_g20599.t1	"Dmel\CG4074: CG4074, isoform	-0.94	3.62E-05	0.00130994	469.10	570.91	585.95	299.74	238.12	272.66
JC_g23473.t1	obst-A: LD43683p (Drosophila me	-0.96	1.87E-05	0.00078224	4126.23	6191.72	5604.31	3001.26	2101.53	2763.57
JC_g16686.t1	CG3831: CG3831-PA (Drosophila	-0.96	2.52E-05	0.00097605	402.49	369.04	386.03	196.92	178.13	192.76
JC_g24016.t1	CG34010: Uncharacterized protei	-0.98	0.00015683	0.00433514	619.22	493.11	820.97	381.22	273.19	269.67
JC_g4745.t1	yellow-b: LD43175p (Drosophila n	-0.98	7.87E-06	0.00039476	2218.86	2834.59	1865.27	971.00	1211.82	1184.53
JC_g2562.t1	"hwt: Uncharacterized protein, iso	-0.99	0.00031346	0.00737017	1968.36	1783.18	947.52	557.76	815.88	838.96
JC_g12767.t1	Protein of unknown function	-0.99	6.97E-06	0.00035304	3780.03	4139.38	5982.89	2303.81	2041.54	2383.04
JC_g2318.t1	Protein of unknown function	-1.00	3.58E-05	0.00130148	2385.86	1982.95	3545.50	1151.42	1162.90	1453.20
JC_g13643.t1	Protein of unknown function	-1.01	3.28E-05	0.00122112	375.28	471.03	360.50	174.60	212.28	181.77
JC_g8191.t1	"Cyp4g15: Cyp4g15, isoform C (D	-1.01	5.07E-05	0.00176783	2290.16	1977.69	3099.92	863.32	1089.07	1497.14
JC_g25265.t1	CG42399: LP02990p (Drosophila	-1.02	0.00018663	0.00497101	259.88	281.78	307.33	131.92	98.75	160.80
JC_g10368.t1	"EG:BACR19J1.2: CG5254, isofo	-1.02	7.46E-07	5.28E-05	986.05	1059.82	1267.62	560.67	499.31	517.36
JC_g24400.t1	"NijC: Ninjurin C, isoform F (Drosop	-1.02	3.37E-05	0.00123987	3724.68	5925.72	6002.03	2305.75	3088.15	1881.66
JC_g17720.t1	Protein of unknown function	-1.02	2.29E-05	0.00090869	2502.19	3184.71	1705.75	1000.10	1205.36	1237.46
JC_g22215.t1	"CG1607: CG1607, isoform A (Dr	-1.03	4.03E-05	0.00144009	1301.29	1118.69	1301.65	371.52	700.51	645.20

JC_g18111.t1	"CG9109: CG9109, isoform A (Dr	-1.03	1.56E-05	0.00067979	987.93	1078.74	739.09	453.97	503.92	344.57
JC_g10182.t1	GILT1: GILT-like protein 1 (Drosoj	-1.04	9.42E-07	6.34E-05	2258.26	1865.19	2064.13	1177.61	880.48	827.97
JC_g10233.t1	CG8300: CG8300 (Drosophila me	-1.05	5.66E-05	0.0018973	2023.71	1889.37	1769.56	1256.18	706.05	610.24
JC_g7592.t1	Protein of unknown function	-1.05	0.00043249	0.00953349	3248.07	4000.60	1287.82	1261.03	1234.89	1247.45
JC_g12508.t1	anon-WO0107627.1: RE46159p	-1.06	0.00038496	0.0087012	239.24	427.92	384.96	189.15	164.28	104.87
JC_g10108.t1	CG14194: SD22372p (Drosophila	-1.08	0.00024547	0.00610873	1146.49	974.65	643.38	527.69	235.35	434.46
JC_g8172.t1	qjt: CG13732 protein (Drosophila	-1.08	0.00028922	0.00694403	520.70	338.55	744.41	287.13	233.50	169.79
JC_g1045.t1	Protein of unknown function	-1.09	0.00021991	0.00562312	201.71	237.62	314.78	96.03	88.60	138.83
JC_g5013.t1	Cyp9f2: Probable cytochrome P45	-1.09	7.82E-07	5.40E-05	1099.58	1076.64	806.08	473.37	393.17	472.41
JC_g21346.t1	Nep1: GH03315p (Drosophila me	-1.09	0.00041178	0.00919581	1002.94	1250.12	848.62	208.56	463.31	635.21
JC_g1090.t1	BcDNA:GH10229: BcDNA.GH102	-1.11	7.11E-05	0.00227916	2520.02	2900.83	2221.52	1151.42	603.60	1520.11
JC_g10107.t1	CG13842: Uncharacterized protei	-1.11	3.59E-05	0.00130148	365.90	320.68	244.59	127.07	119.98	154.81
JC_g16395.t1	"CG2200: CG2200, isoform B (Dr	-1.12	1.39E-05	0.00061732	805.92	1049.30	985.81	443.30	509.46	269.67
JC_g4351.t1	CG2202: CG2202 (Drosophila me	-1.12	5.43E-11	1.05E-08	1126627.57	########	#########	549301.17	536348.29	517060.84
JC_g13283.t1	CG34114-RB: RT02067p (Fragme	-1.13	0.00022886	0.0058124	299.29	219.74	414.74	106.70	173.51	101.87
JC_g8183.t1	sec8-RA: FI22107p1 (Drosophila	-1.14	3.71E-06	0.0002019	567.61	409.00	513.64	252.21	197.51	184.77
JC_g19086.t1	rho-6: Rhomboid-like protein (Dros	-1.15	6.71E-08	6.18E-06	2472.17	3299.31	2403.37	1286.25	1007.85	1238.46
JC_g24467.t1	"ITP: Ion transport peptide, isofor	-1.15	0.00021908	0.00561599	622.03	1882.01	1587.71	435.54	600.83	615.24
JC_g11237.t1	pr: 6-pyruvoyl tetrahydrobiopterin	-1.15	5.34E-07	3.99E-05	5903.19	5384.24	4920.52	3070.13	1784.96	2072.43
JC_g14094.t1	inaD-RA: MIP15238p (Drosophila	-1.15	5.79E-05	0.00192399	780.59	371.15	703.99	202.74	262.11	297.63
JC_g14548.t1	CG4797: CG4797 (Drosophila me	-1.16	5.15E-05	0.00177608	1350.08	1075.59	1775.94	451.06	399.63	859.93
JC_g11730.t1	CG4670: Sulfhydryl oxidase (Dros	-1.16	1.69E-05	0.00072308	670.82	553.04	1033.66	268.70	278.73	383.52
JC_g18983.t1	"CG14442: Uncharacterized prote	-1.17	2.29E-05	0.00090869	580.75	526.75	748.66	229.90	178.13	351.56
JC_g18203.t1	CG17633-RA: FI04406p (Fragme	-1.21	6.15E-05	0.002023	12957.56	33456.75	17304.24	10960.32	8113.54	5700.92
JC_g19351.t1	Dmel\CG11796: 4-hydroxyphenylp	-1.21	5.11E-05	0.00177331	331.19	859.00	585.95	219.23	219.66	251.69
JC_g23411.t1	B-H1: Homeobox protein B-H1 (Dr	-1.21	2.17E-06	0.0001306	474.73	522.55	440.26	239.60	195.66	141.82
JC_g12789.t1	CG10348: IP08802p (Drosophila	-1.21	4.03E-07	3.17E-05	654.87	908.41	993.25	340.48	293.49	400.50
JC_g16851.t1	ORF: Orf protein (Drosophila mela	-1.22	0.00016536	0.00451007	556.36	303.86	240.34	157.14	91.37	163.80
JC_g22506.t1	"CG8420: CG8420, isoform A (Dr	-1.22	4.23E-06	0.00022897	389.36	444.74	497.69	220.20	124.60	180.78
JC_g8014.t1	Protein of unknown function	-1.23	1.70E-05	0.00072422	477.55	359.58	583.83	254.15	146.75	150.81
JC_g3779.t1	in: Protein inturned (Drosophila m	-1.23	4.34E-09	5.22E-07	723.36	698.13	622.11	280.34	280.57	267.67
JC_g21199.t1	Dmel\CG11306: HL02815p (Dros	-1.23	5.74E-05	0.00191937	510.38	865.31	1120.86	254.15	458.70	230.71
JC_g14545.t1	"CG8668: CG8668, isoform A (Dr	-1.24	3.22E-07	2.64E-05	1560.24	1297.43	1681.29	485.98	513.15	807.00
JC_g11041.t1	Protein of unknown function	-1.24	1.03E-05	0.00049025	3428.20	4010.06	1922.69	885.63	1098.30	1631.97
JC_g11264.t1	Protein of unknown function	-1.24	9.86E-05	0.00299174	1565.87	1204.91	808.21	689.69	235.35	405.50
JC_g941.t1	Protein of unknown function	-1.25	4.45E-05	0.00156944	178.26	175.58	214.81	56.26	94.14	62.92
JC_g12692.t1	Protein of unknown function	-1.26	7.23E-05	0.00230968	1143.67	1827.34	3577.40	764.38	599.91	1037.71
JC_g5510.t1	CG9503: CG9503-PA (Drosophila	-1.27	0.00020549	0.00537524	167.00	113.55	178.66	76.63	47.99	37.95
JC_g14435.t1	CG5721: Armadillo repeat-contair	-1.27	2.48E-05	0.00096574	614.52	1064.02	981.55	234.75	249.19	503.37
JC_g19996.t1	"crol: Crooked legs, isoform H (Dr	-1.28	0.00015026	0.00421043	386.54	222.90	153.13	108.64	66.45	94.88
JC_g14144.t1	"Mctp: Multiple C2 domain and tra	-1.28	0.0002341	0.005912	82.56	168.22	178.66	55.29	47.99	45.94
JC_g19462.t1	Protein of unknown function	-1.28	0.00012936	0.00373767	187.64	234.46	181.85	36.86	87.68	88.89
JC_g20736.t1	mesh: Protein mesh (Drosophila n	-1.28	1.81E-06	0.0001126	2121.28	1906.20	3080.77	1268.79	720.81	693.14
JC_g24143.t1	CG15890: RE46682p (Drosophila	-1.28	4.96E-10	7.14E-08	3216.17	2947.09	2567.14	975.85	1344.72	1103.63
JC_g5128.t1	Protein of unknown function	-1.28	4.77E-06	0.00025358	1373.53	1092.41	2005.64	702.30	610.06	354.56
JC_g8478.t1	IP02928p (Fragment) (Drosophila	-1.29	0.0003046	0.00719498	122.90	186.10	164.83	85.36	42.46	32.96
JC_g9614.t1	GstE6: Glutathione S transferase	-1.31	2.21E-05	0.00088649	837.82	472.08	971.98	220.20	189.20	401.50
JC_g10558.t1	CG7154: CG7154 (Drosophila me	-1.32	0.00039664	0.00889658	183.89	499.42	127.61	98.94	82.14	80.90
JC_g8167.t1	"CG7675: CG7675, isoform B (Dr	-1.33	1.91E-06	0.00011678	2009.64	1950.36	4323.93	1038.90	896.17	1056.69
JC_g17717.t1	Protein of unknown function	-1.34	2.69E-08	2.73E-06	118113.54	########	123189.52	42944.00	67666.06	46440.32
JC_g22747.t1	ORF: ORF (Drosophila melanogas	-1.35	6.04E-05	0.00199786	307.73	222.90	130.80	75.66	53.53	90.89
JC_g6746.t1	MIP02663p (Fragment) (Drosophi	-1.35	0.00027334	0.00665742	61.92	93.58	78.69	24.25	25.84	22.97
JC_g20112.t1	Protein of unknown function	-1.36	3.78E-05	0.00135733	257.07	383.76	621.05	120.28	202.12	96.88
JC_g16480.t1	CG16798: RE22905p (Drosophila	-1.36	1.39E-08	1.48E-06	428.76	424.77	517.89	190.12	146.75	159.80
JC_g3949.t2	Protein of unknown function	-1.37	1.10E-05	0.00052202	372.47	518.34	656.14	131.92	267.65	122.85
JC_g10545.t1	dpld: Cyt-b5-PB (Drosophila melar	-1.37	1.85E-06	0.00011458	5929.46	12963.82	4972.63	2863.52	2515.00	2863.44
JC_g4415.t1	"CG9518-RA: CG9518, isoform A	-1.39	6.10E-08	5.67E-06	3082.01	4853.28	4368.60	1074.79	1278.27	1975.55
JC_g3629.t1	AsnS: Asparagine synthetase (Dr	-1.39	1.28E-05	0.00058574	1002.94	3747.21	2725.59	802.21	858.33	810.99
JC_g2714.t1	Cpr30F: Cuticular protein 30F (Dr	-1.39	2.04E-07	1.72E-05	579.81	326.99	467.91	148.41	151.36	177.78
JC_g17016.t1	Adk1: AT17975p (Drosophila mela	-1.42	3.36E-06	0.00018697	189.52	226.05	290.32	100.88	71.99	58.93
JC_g1314.t1	"daw: Dawdle, isoform A (Drosoph	-1.42	0.00037758	0.00858199	90.07	386.92	213.75	36.86	48.92	104.87
JC_g10388.t1	norpA: Phosphoinositide phospho	-1.42	7.65E-07	5.32E-05	1838.88	991.47	825.23	364.73	341.49	509.37
JC_g4309.t1	CG10581: IP06602p (Drosophila	-1.43	0.00019973	0.00526502	161.37	57.83	190.36	32.01	46.15	38.95
JC_g18510.t1	CG15661: UDP-glucuronosyltrans	-1.43	4.25E-11	8.35E-09	732.74	646.61	665.71	212.44	256.58	247.69
JC_g7533.t1	"Pxd: Peroxidase, isoform B (Dros	-1.44	2.24E-09	2.86E-07	109193.08	73232.45	65413.03	21835.27	33524.77	29728.08
JC_g14528.t1	CG30016: 5-hydroxyisourate hydr	-1.44	3.32E-05	0.00122696	106.02	292.29	185.04	56.26	58.15	62.92
JC_g3552.t1	CG32603: RE22786p (Drosophila	-1.44	3.73E-08	3.60E-06	359172.39	########	648683.37	228102.46	210660.39	177858.11
JC_g5858.t1	Protein of unknown function	-1.44	0.00024049	0.00601183	91.94	56.78	84.01	25.22	25.84	12.98
JC_g17351.t1	Protein of unknown function	-1.45	3.49E-05	0.00128082	199.84	179.79	278.62	34.92	103.37	59.93
JC_g5553.t1	ORF: ORF (Drosophila melanogas	-1.45	0.00041552	0.00923754	61.92	68.34	52.11	21.34	9.23	16.98

JC_g12246.t1	"MESK2: Misexpression suppress	-1.46	3.79E-08	3.62E-06	974.80	937.85	567.87	272.58	212.28	331.59
JC_g1388.t1	EG:63B12.6: GM08325p (Drosop	-1.47	0.00011985	0.00351238	72.24	119.86	237.15	46.56	39.69	31.96
JC_g12885.t1	E(spl)mbeta-HLH: Enhancer of sp	-1.47	1.82E-10	3.01E-08	836.88	817.99	641.25	230.87	238.12	303.62
JC_g2451.t1	Protein of unknown function	-1.48	8.12E-09	9.03E-07	3659.00	3488.56	3823.05	710.06	1503.46	1385.28
JC_g3425.t1	CG3902: GH07925p (Drosophila	-1.48	1.38E-10	2.39E-08	5541.98	9584.61	7311.12	2555.05	2134.75	2806.51
JC_g21377.t1	Protein of unknown function	-1.48	5.93E-08	5.56E-06	407.18	636.10	591.27	151.32	231.66	142.82
JC_g8435.t1	mas: LP06006p (Drosophila mela	-1.49	8.46E-05	0.00263855	86.31	107.24	97.84	14.55	38.76	25.97
JC_g2054.t1	pb: Homeotic protein probosciped	-1.49	0.00027197	0.00665478	69.43	287.03	367.95	29.10	57.22	93.88
JC_g20853.t1	CG12795: LD41381p (Drosophila	-1.50	1.37E-09	1.82E-07	583.56	530.96	388.15	154.23	163.36	171.79
JC_g23380.t1	KFase: Kynurenine formamidase	-1.51	2.58E-11	5.27E-09	3722.80	4597.79	5602.18	1668.44	1183.21	1702.89
JC_g19376.t1	"CG42284: Uncharacterized prote	-1.52	0.00014852	0.00419637	380.91	115.65	119.10	28.13	50.76	76.90
JC_g9644.t1	"qm: Quemao, isoform A (Drosoph	-1.52	0.00036697	0.00839669	42.22	51.52	102.09	21.34	9.23	13.98
JC_g13311.t1	CG6701: LD17208p (Fragment) (I	-1.52	5.61E-09	6.38E-07	2360.53	1328.98	2766.00	788.63	630.37	626.22
JC_g15649.t1	CG9238-RB: MIP07493p (Fragme	-1.53	1.75E-05	0.00073792	361.21	298.60	116.98	96.03	59.07	59.93
JC_g20359.t1	Protein of unknown function	-1.54	2.82E-12	8.23E-10	4521.21	5449.43	5501.16	2074.88	1284.73	1632.97
JC_g2730.t1	"Nmdmc: Bifunctional methylenete	-1.54	5.92E-07	4.36E-05	582.63	361.68	577.45	83.42	179.97	188.77
JC_g21626.t1	btv: Beethoven (Drosophila melar	-1.54	0.00029344	0.00699593	377.16	82.01	248.84	14.55	95.06	47.94
JC_g24694.t1	"santa-maria: Scavenger receptor	-1.55	0.00029022	0.00695167	366.84	43.11	176.53	27.16	65.53	34.96
JC_g10041.t1	CG12542: RE55639p (Drosophila	-1.56	3.37E-12	9.58E-10	683.95	719.16	931.57	246.39	255.65	236.71
JC_g3401.t1	Protein of unknown function	-1.56	0.00013582	0.00390205	41.28	151.40	190.36	36.86	24.00	28.96
JC_g12248.t1	MESK2: Misexpression suppressc	-1.56	3.07E-05	0.00114608	169.82	225.00	86.14	60.14	26.77	37.95
JC_g20614.t1	Protein of unknown function	-1.57	3.93E-07	3.12E-05	291.78	241.82	511.51	80.51	100.60	119.85
JC_g19377.t1	CG30274: Uncharacterized protei	-1.58	1.75E-05	0.00073792	611.71	157.71	223.32	87.30	79.37	92.88
JC_g12935.t1	Protein of unknown function	-1.58	2.62E-06	0.00015422	422.19	395.33	180.78	66.93	130.13	78.90
JC_g17511.t1	ORF: ORF (Drosophila melanogas	-1.58	7.30E-08	6.67E-06	1768.52	1014.61	881.59	389.95	228.89	449.44
JC_g20001.t1	"CG3285: CG3285, isoform A (Dr	-1.60	2.36E-05	0.0009314	776.83	196.61	298.83	83.42	72.91	161.80
JC_g7650.t1	"Cpr62Bb: Cuticular protein 62Bb	-1.60	1.82E-07	1.57E-05	847.20	1169.16	1077.26	347.27	393.17	136.83
JC_g2213.t1	CG14434: CG14434-PA (Drosoph	-1.60	2.05E-05	0.00084048	98.51	302.80	267.99	84.39	38.76	43.95
JC_g8114.t1	CG12970: Uncharacterized protei	-1.62	8.18E-12	1.99E-09	16670.98	18843.28	28886.12	7483.75	6423.64	5404.29
JC_g23360.t1	CG6385-RA: FI21471p1 (Fragme	-1.62	9.54E-07	6.38E-05	325.56	501.52	297.76	105.73	51.68	144.82
JC_g14449.t1	CG9645: RH19136p (Drosophila r	-1.63	7.43E-06	0.00037424	149.17	530.96	445.58	98.94	59.07	124.84
JC_g7697.t1	"Cpr62Bc: Cuticular protein 62Bc,	-1.63	4.39E-07	3.40E-05	267.39	551.99	607.22	117.37	88.60	179.78
JC_g14437.t1	CG5721: Armadillo repeat-contair	-1.64	1.50E-06	9.69E-05	662.37	1487.74	1379.28	165.87	232.58	518.36
JC_g7916.t1	Cpr66Ca: MIP24917p (Drosophila	-1.65	8.61E-05	0.00267746	135.10	189.25	99.96	7.76	56.30	23.97
JC_g4885.t1	Protein of unknown function	-1.65	4.56E-06	0.00024549	989.81	1756.90	315.84	259.00	228.89	273.66
JC_g21630.t1	Protein of unknown function	-1.66	0.00024099	0.00601183	110.71	25.23	57.43	3.88	14.77	12.98
JC_g6268.t1	Protein of unknown function	-1.68	0.00027338	0.00665742	11.26	15.77	28.71	0.00	0.00	0.00
JC_g10391.t1	crol: CROL ALPHA (Drosophila m	-1.68	0.00034817	0.00811685	11.26	33.64	28.71	2.91	0.00	0.00
JC_g4882.t1	MIP02663p (Fragment) (Drosophi	-1.69	0.00022902	0.0058124	31.90	49.42	23.40	3.88	3.69	6.99
JC_g942.t1	Protein of unknown function	-1.71	7.47E-15	2.73E-12	136711.60	########	137258.78	43842.24	52780.93	35863.46
JC_g17458.t1	Dmel\CG8281: CG8281 (Drosoph	-1.71	2.19E-05	0.00088315	64.74	75.70	71.25	8.73	21.23	13.98
JC_g2329.t1	"lab: Labial, isoform B (Drosophila	-1.71	0.00018315	0.00490383	52.54	54.67	23.40	1.94	7.38	8.99
JC_g7700.t1	"Cpr62Bc: Cuticular protein 62Bc,	-1.72	1.20E-06	7.86E-05	122.90	201.87	361.57	59.17	42.46	60.92
JC_g3782.t1	sxc: LD16758p (Drosophila melan	-1.73	1.45E-10	2.47E-08	366.84	375.35	293.51	71.78	107.06	98.88
JC_g21355.t1	CG7137: Ribosomal RNA-process	-1.73	9.12E-05	0.00280886	34.71	75.70	61.68	3.88	8.31	15.98
JC_g20753.t1	Protein of unknown function	-1.73	0.00023753	0.00596928	41.28	17.87	22.33	1.94	0.92	4.00
JC_g1951.t1	Protein of unknown function	-1.73	2.76E-06	0.00016011	98.51	262.85	152.07	31.04	31.38	53.93
JC_g14480.t1	Protein of unknown function	-1.73	5.41E-05	0.00184408	34.71	116.71	120.17	13.58	9.23	25.97
JC_g22740.t1	polyprotein: Polyprotein (Drosoph	-1.74	3.67E-08	3.60E-06	1741.31	1068.23	700.80	185.27	287.96	409.49
JC_g16295.t1	Edg84A: Pupal cuticle protein Ed	-1.74	0.0001283	0.00371752	84.44	90.42	73.38	20.37	14.77	0.00
JC_g10554.t1	"hpo: Hippo, isoform B (Drosophila	-1.75	3.60E-06	0.00019806	235.49	806.43	197.80	113.49	72.91	83.90
JC_g1068.t1	"Sin3A: Sin3A, isoform J (Drosoph	-1.75	0.0001169	0.00344553	28.15	36.80	75.50	4.85	3.69	10.99
JC_g10559.t1	Protein of unknown function	-1.75	7.58E-05	0.00239883	72.24	180.84	32.97	25.22	8.31	11.99
JC_g22456.t1	"Osi17: Osiris 17, isoform A (Dros	-1.78	6.07E-09	6.82E-07	254.25	197.66	181.85	61.11	39.69	55.93
JC_g18635.t1	Protein of unknown function	-1.78	1.56E-05	0.00067979	57.23	65.19	108.47	7.76	20.30	14.98
JC_g20877.t1	"Dscam1: Down syndrome cell ad	-1.79	3.71E-06	0.0002019	580.75	104.09	548.73	94.09	67.37	93.88
JC_g4871.t1	Sec15: Exocyst complex compone	-1.80	9.72E-07	6.45E-05	375.28	722.32	206.31	51.41	135.67	92.88
JC_g16375.t1	"CG6870: CG6870, isoform A (Dr	-1.81	8.27E-05	0.00260077	1973.05	13308.68	8622.34	800.27	932.17	1302.38
JC_g22844.t1	CG11158: RH22417p (Drosophila	-1.81	1.15E-06	7.58E-05	107.89	150.35	196.74	50.44	18.46	26.97
JC_g7531.t1	"Pxd: Peroxidase, isoform B (Dros	-1.81	6.62E-05	0.00215526	41.28	38.90	39.35	8.73	4.61	2.00
JC_g16051.t1	"CT12789: CG3819, isoform A (D	-1.82	9.27E-12	2.20E-09	1155.87	1462.50	1124.05	236.69	248.27	453.44
JC_g6114.t1	gag-pol: Putative uncharacterized	-1.82	0.00011148	0.00332418	28.15	30.49	25.52	3.88	0.00	0.00
JC_g19657.t1	ORF: Orf protein (Drosophila mela	-1.83	7.25E-05	0.00230976	130.41	157.71	106.34	0.97	40.61	4.99
JC_g5860.t1	ast: Protein asteroid (Drosophila r	-1.85	7.32E-11	1.39E-08	801.23	914.72	1739.78	238.63	322.11	271.66
JC_g21632.t1	btv: Beethoven (Drosophila melar	-1.89	7.07E-07	5.09E-05	573.24	214.49	437.07	32.98	140.29	60.92
JC_g8187.t1	Protein of unknown function	-1.89	6.06E-13	1.82E-10	449.40	523.60	739.09	159.08	123.67	124.84
JC_g3549.t1	CG32603: RE22786p (Drosophila	-1.90	2.33E-09	2.94E-07	71873.13	########	202648.42	46333.27	41040.24	27585.74
JC_g24909.t1	CG13606: GEO09712p1 (Drosop	-1.90	3.46E-13	1.11E-10	7296.43	8762.41	7958.76	1111.65	2004.62	2565.81
JC_g10039.t1	CG12542: RE55639p (Drosophila	-1.94	1.57E-18	8.46E-16	706.47	841.12	914.56	188.18	213.20	188.77
JC_g2702.t1	Cpr30F: Cuticular protein 30F (Dr	-1.94	5.96E-12	1.52E-09	537.59	909.47	727.39	224.08	143.06	120.85

JC_g8064.t1	CG15528-RA: IP21249p (Drosopl	-1.94	5.35E-09	6.15E-07	343.38	162.97	337.11	43.65	52.61	77.90
JC_g16917.t1	TTLL3A: Tubulin glycylase 3A (Dr	-1.95	4.66E-09	5.48E-07	9610.04	16699.46	17575.41	1780.00	1794.19	5431.25
JC_g5715.t1	Protein of unknown function	-1.97	2.13E-05	0.00086482	35.65	22.08	63.81	2.91	1.85	5.99
JC_g14588.t1	ImpL2: Neural/ectodermal develo	-1.98	2.79E-05	0.00106592	68.49	778.04	572.13	28.13	15.69	30.96
JC_g20539.t1	"kek6: Kek6, isoform A (Drosophil	-2.00	1.50E-05	0.0006634	103.20	55.72	40.41	5.82	0.00	11.99
JC_g20935.t1	Protein of unknown function	-2.00	2.19E-05	0.00088315	40.34	38.90	10.63	0.00	0.00	2.00
JC_g21560.t1	CG13510-RA: MIP04282p (Droso	-2.00	7.25E-12	1.81E-09	738.37	2028.16	1435.64	299.74	303.65	283.65
JC_g9679.t1	ORF: Orf protein (Drosophila mela	-2.00	8.23E-07	5.61E-05	120.09	101.99	111.66	8.73	33.23	9.99
JC_g2540.t1	ORF: Orf protein (Drosophila mela	-2.02	1.64E-05	0.00070919	3.75	69.39	43.60	0.00	0.00	1.00
JC_g2215.t1	"Mlh1: Mlh1, isoform A (Drosophila	-2.04	1.19E-05	0.00055445	50.66	77.80	172.28	19.40	0.00	4.00
JC_g14521.t1	Protein of unknown function	-2.04	3.60E-13	1.11E-10	8187.72	8070.58	4387.74	1045.69	1216.43	2047.46
JC_g16331.t1	CG4572-RC: Carboxypeptidase (D	-2.05	1.36E-05	0.00060994	6.57	119.86	45.73	0.97	2.77	4.00
JC_g11804.t1	Protein of unknown function	-2.06	2.83E-09	3.48E-07	197.96	471.03	363.70	95.06	53.53	39.95
JC_g11337.t1	Protein of unknown function	-2.06	1.19E-08	1.28E-06	104.14	170.33	121.23	28.13	14.77	25.97
JC_g11846.t1	"zyd: Zydeco, isoform G (Drosoph	-2.07	8.24E-09	9.06E-07	334.94	395.33	388.15	104.76	22.15	69.91
JC_g15823.t1	CG6178: CG6178 (Drosophila me	-2.12	1.54E-06	9.84E-05	35.65	358.53	282.87	31.04	34.15	8.99
JC_g4159.t1	Protein of unknown function	-2.14	1.75E-06	0.00011023	147.30	103.04	171.21	4.85	34.15	2.00
JC_g16229.t1	Dmel\CG17687: Uncharacterized	-2.14	3.90E-07	3.11E-05	94.76	57.83	63.81	5.82	14.77	5.99
JC_g7707.t1	Cpr66Cb: Cuticular protein 66Cb (	-2.17	2.65E-06	0.0001551	2512.52	3442.30	14235.16	607.24	456.85	394.51
JC_g21840.t1	CG4797: CG4797 (Drosophila me	-2.29	5.57E-10	7.92E-08	360.27	1425.70	1042.17	211.47	70.14	114.86
JC_g15270.t1	wat: Fatty acyl-CoA reductase wa	-2.29	5.35E-07	3.99E-05	113.52	47.31	29.78	2.91	1.85	7.99
JC_g14254.t1	Protein of unknown function	-2.30	2.88E-07	2.39E-05	20.64	424.77	273.30	24.25	16.61	18.98
JC_g14518.t1	Protein of unknown function	-2.31	6.79E-16	2.57E-13	2398.99	2702.11	1261.24	271.61	322.11	478.41
JC_g16970.t1	Protein of unknown function	-2.31	1.20E-19	8.20E-17	1046.10	1105.03	741.22	214.38	159.67	133.83
JC_g1694.t1	CG31106: RE45749p (Drosophila	-2.36	3.75E-26	3.83E-23	2813.68	3973.26	3015.91	696.48	527.00	499.38
JC_g2381.t1	ORF: ORF (Drosophila melanogas	-2.38	3.34E-07	2.71E-05	30.02	42.06	47.85	1.94	0.00	3.00
JC_g17716.t1	Protein of unknown function	-2.40	1.29E-16	5.71E-14	131697.83	########	123902.02	30063.03	33779.50	19228.12
JC_g21344.t1	Gnmt: Glycine N-methyltransferas	-2.43	1.41E-07	1.23E-05	14.07	348.01	152.07	3.88	11.08	11.99
JC_g10227.t1	Protein of unknown function	-2.44	2.57E-10	4.04E-08	107.89	82.01	133.99	13.58	7.38	15.98
JC_g21685.t1	Protein of unknown function	-2.45	1.31E-07	1.17E-05	30.02	80.96	38.28	3.88	1.85	0.00
JC_g14516.t1	Ir: IP03029p (Fragment) (Drosoph	-2.55	4.52E-10	6.60E-08	296.47	71.50	183.97	15.52	9.23	25.97
JC_g4862.t1	Protein of unknown function	-2.55	1.64E-10	2.75E-08	179.20	331.19	85.07	10.67	22.15	24.97
JC_g19015.t1	Dmel\CG7272: Sugar transporter	-2.56	2.30E-22	1.96E-19	3741.56	3618.94	6090.30	446.21	790.03	704.13
JC_g7173.t1	polyprotein: Polyprotein (Drosoph	-2.71	2.55E-11	5.27E-09	92.88	88.32	96.77	7.76	11.08	3.00
JC_g2219.t1	"Ance: Angiotensin converting en	-2.71	1.95E-09	2.56E-07	72.24	146.15	110.60	1.94	0.00	12.98
JC_g24911.t1	Dmel\CG9701: CG9701 (Drosoph	-2.91	6.21E-10	8.70E-08	27.21	80.96	36.16	0.00	0.00	0.00
JC_g5699.t1	"CG2663: CG2663, isoform A (Dr	-2.91	1.11E-10	1.96E-08	53.48	135.63	173.34	10.67	1.85	0.00
JC_g21666.t1	GIP: Copia protein (Drosophila me	-2.92	1.11E-10	1.96E-08	28.15	216.59	193.55	2.91	1.85	9.99
JC_g14041.t1	Jheh1: Epoxide hydrolase (Droso	-2.92	3.12E-10	4.76E-08	67.55	28.39	61.68	1.94	0.00	0.00
JC_g8054.t1	Cpr66D: Cuticular protein 66D (Dr	-3.00	3.96E-27	5.06E-24	2795.85	3879.68	5044.94	542.24	382.10	253.68
JC_g10566.t1	Protein of unknown function	-3.17	5.84E-12	1.52E-09	60.05	103.04	30.84	0.00	0.92	1.00
JC_g2266.t2	Protein of unknown function	-3.19	5.29E-12	1.42E-09	52.54	144.04	34.03	0.00	1.85	0.00
JC_g18634.t1	Protein of unknown function	-3.24	1.27E-37	2.17E-34	911.00	885.28	1351.63	89.24	107.06	79.90
JC_g5125.t1	Protein of unknown function	-3.24	1.20E-27	1.76E-24	1454.22	803.27	1456.91	141.62	89.52	64.92
JC_g5054.t1	"Esp: Epidermal stripes and patch	-3.34	4.14E-55	1.06E-51	3932.02	4807.02	3144.58	331.75	355.33	338.58
JC_g10566.t2	Protein of unknown function	-3.78	1.34E-16	5.71E-14	94.76	138.79	39.35	0.00	0.00	0.00
JC_g2214.t1	CG17475: RE05031p (Drosophila	-3.78	3.03E-17	1.47E-14	47.85	145.09	112.72	0.00	0.00	2.00
JC_g14473.t1	Protein of unknown function	-3.97	5.06E-20	3.70E-17	92.88	212.38	119.10	4.85	0.00	0.00
JC_g17672.t1	c62E-15: Purine nucleoside phos	-4.26	2.35E-62	8.01E-59	5664.89	8691.96	10947.01	329.81	273.19	419.48
JC_g3632.t1	Dmel\CG8541: CG8541 (Drosoph	-4.31	4.11E-83	4.20E-79	47566.10	46923.15	56385.52	2534.68	1497.93	2244.21
JC_g3809.t2	Protein of unknown function	-4.56	1.64E-25	1.53E-22	105.08	100.93	191.42	0.00	0.00	0.00
JC_g23205.t1	"CG5789-RA: CG5789, isoform A	-4.93	6.54E-81	3.34E-77	1864.21	1674.89	1168.72	35.89	43.38	32.96
JC_g10555.t1	Protein of unknown function	-5.81	4.44E-46	9.08E-43	255.19	662.39	316.90	0.97	0.00	0.00