Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in *Drosophila*

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ABSTRACT We present a transcriptomic analysis aimed at investigating whether the changes in gene expression that occur under inbreeding generally reduce or enhance inbreeding depression. Discerning between these two alternatives can be addressed only when both changes in expression due to inbreeding and to inbreeding depression are estimated simultaneously. We used Affymetrix 2.0 arrays to study the changes in gene expression associated with both inbreeding and inbreeding depression for fitness in four sets of inbred sublines of *Drosophila melanogaster*. We found that for most genes showing changes in expression associated with inbreeding, the least depressed sublines were those showing the largest departures in expression from that of the outbred control. This suggests a pattern consistent with a protective role of expression changes against inbreeding effects, and would reveal a new dimension of the transcriptomics of inbreeding. The variation in depression observed could then be due not only to the genetic damages primarily originating that depression, but also possibly to differences in the ability to carry out the appropriate adjustments in gene expression to cope with the inbreeding. We also found that these expression changes with a putative protective role against inbreeding effects show a clear specificity on RNA synthesis and splicing and energy derivation functions.

INBREEDING depression, the reduction in fitness observed in the progeny of genetically related individuals, plays a key role in population biology, affecting processes as diverse as the management of livestock and endangered wild species (Keller and Waller 2002; Koenig and Simianer 2006), the evolution of mating systems (Kelly 2005), and the dispersal strategies (Motro 1991; Gandon 1999). The population genetics of this depression is well understood (Lynch 1991; Charlesworth and Charlesworth 1999; Charlesworth and Willis 2009), but the genomic details about the mechanisms causing it are just starting to be unveiled (Paige 2010). In particular, it would be important to determine the relationship between gene regulation and inbreeding, as regulatory variation underlies much of phenotypic diversity (Wilson *et al.* 1974; Carroll 2005; Ranz and Machado 2006). Evidence has been provided for significant intraspecific variation in transcript abundance for a large fraction of the genome (Primig *et al.* 2000; Sandberg *et al.* 2000) and to show that much of such variation is heritable (Cavalieri *et al.* 2000; Karp *et al.* 2000; Jin *et al.* 2001), suggesting that regulatory variation is likely the main mediator of phenotypic divergence in evolution (King and Wilson 1975; Wray *et al.* 2003; Hoekstra and Coyne 2007). Therefore, genetic correlations between expression phenotypes and organismal phenotypes point to the molecular pathways that underlie the organismal phenotypes (Rockman and Kruglyak 2006). Thus, an understanding of the molecular basis of inbreeding depression requires knowledge of variation at the whole-genome level (Ayroles *et al.* 2009).

Using whole-genome cDNA microarrays, which make it possible to study the gene-expression changes associated with inbreeding, Kristensen *et al.* (2005) compared the expression profiles of *Drosophila melanogaster* virgin males taken from inbred and control outbred lines and discovered that many different genes were differentially expressed with inbreeding and that genes involved in metabolism, biological defense, and stress responses were overrepresented among them. Ayroles *et al.* (2009) carried out a comparison between the expressions of inbred lines of *D. melanogaster* differing in their magnitude of inbreeding depression. They set up lines completely homozygous for different third chromosomes derived from a wild population and compared the male gene expression in lines showing strong and weak

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depression for male competitive reproductive success. In their analysis there was not an evaluation of the expression of an outbred control. Again, many genes showed differences in expression between depression levels, those related with metabolism, and stress and defense responses being overrepresented. A comparison of the gene lists showing inbreeding and inbreeding depression effects in both studies found a significant overlap between the two, although there was also a great effect of genetic background on transcriptome patterns (Sarup *et al.* 2011).

The above studies, however, did not allow ascertaining whether the observed expression changes were either a functional, fitness-increasing response to compensate for some physiological inefficiency caused by inbreeding or just a consequence of defective gene regulation (Girardot *et al.* 2004; Kristensen *et al.* 2010). Discerning the changes that alleviate the depression from those that generate it can be addressed only when both the changes in expression due to inbreeding and to inbreeding depression are estimated simultaneously. Here we present a study focused on this objective.

The alternative hypotheses that we try to test are shown in Figure 1. For those genes where inbred lines' expression differs from outbred lines' expression, two patterns are possible. In the first, the most depressed individuals (+D) deviate more from the outbred controls (C) than the least depressed ones (–D). These expression changes could be either dysfunctional (the most depressed individuals change most) or protective (changes are needed to be larger in the individuals suffering most depression). Because of this ambiguity and to be conservative, we denote this pattern as *nonprotective*. For the alternative pattern (*protective*), in which the most depressed individuals deviate less from the outbred control than the least depressed ones, the interpretation is less ambiguous. Genes showing this kind of response could have a role in protecting individuals against the effects of inbreeding, those failing to complete the appropriate changes in expression contributing to the depression.

In this work, we analyzed changes in gene expression in different *D. melanogaster* inbred sublines differing in their magnitudes of inbreeding depression relative to the expression in an outbred control to evaluate the relative importance of protective and deleterious gene-expression changes associated with inbreeding. Our results suggest that most changes in gene expression associated with inbreeding are compatible with a protection against the effects of inbreeding.

Materials and Methods

Base population and culture conditions

The *D. melanogaster* base population was founded in November 2006 from a sample of more than 1000 individuals collected in a wine cellar close to Vigo (Galicia, northwest Spain). The population was maintained in ~30 bottles (30–60 individuals per bottle) with circular mating until the start of the experiment in July 2008. Flies were reared in a culture medium composed of 1 liter water, 100 g brewer's yeast, 100 g sucrose, 12 g agar, 2.5 g NaCl, and 5 ml propionic acid and were handled at room temperature under CO_2 anesthesia. All cultures were incubated in a chamber at 25 ± 1°, 65 ± 5% relative humidity, and maintained under continuous lighting. Virgin males and females were used for mating across the entire experiment.

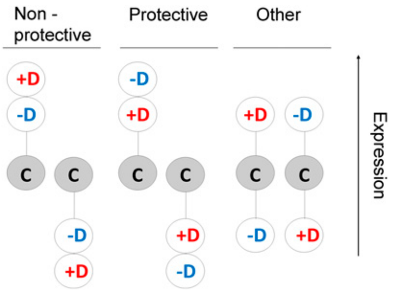


Figure 1 Alternative patterns of expression for genes showing a differential expression under inbreeding. Circles represent the level of expression of genes in an outbred control set (C, shaded circles), in an inbred highly depressed set (+D, in red), and in an inbred lowly depressed set (–D, in blue). Three gene-expression configurations are possible. In the nonprotective configuration, the most depressed set shows an expression that deviates from the outbred control expression more than that for the least depressed set. The opposite occurs in the protective configuration.

Inbred lines and sublines

Four couples were randomly collected from the base population and placed into separate vials to generate four independent lines (Figure 2). From their progeny, 55 full-sib sublines (single brother–sister mating) were initiated for each line. At generation 4, when the expected inbreeding coefficient achieved was 0.5, the number of surviving sublines was 38, 43, 27, and 39 for each of the 4 lines, respectively. To minimize further line losses, from generation 5 to generation 8 the sublines were maintained with two males and two females (full sibs) placed into the same vial. Because of this, the expected inbreeding coefficient at generation 8 ($F = 0.709$) would present a small variance among sublines (0.000512; value obtained by simulating 1000 times the pedigree data of the mating system carried out until generation 8). The numbers of surviving sublines available for analysis in generation 8 in the four lines were 25, 31, 17, and 27.

Productivity evaluation

The character measured to select the most and least depressed sublines was pupa productivity, a composite trait including fecundity and offspring–pupa viability. The trait behaves as a typical fitness trait, showing substantial inbreeding depression (1.2% per 1% increase in inbreeding coefficient) and asymmetrical response to artificial selection (realized heritability 0.05 for upward selection and 0.4 for downward selection) (unpublished data obtained from the same base population). The productivity of the sublines was evaluated at generations 4 and 8. From each subline, three

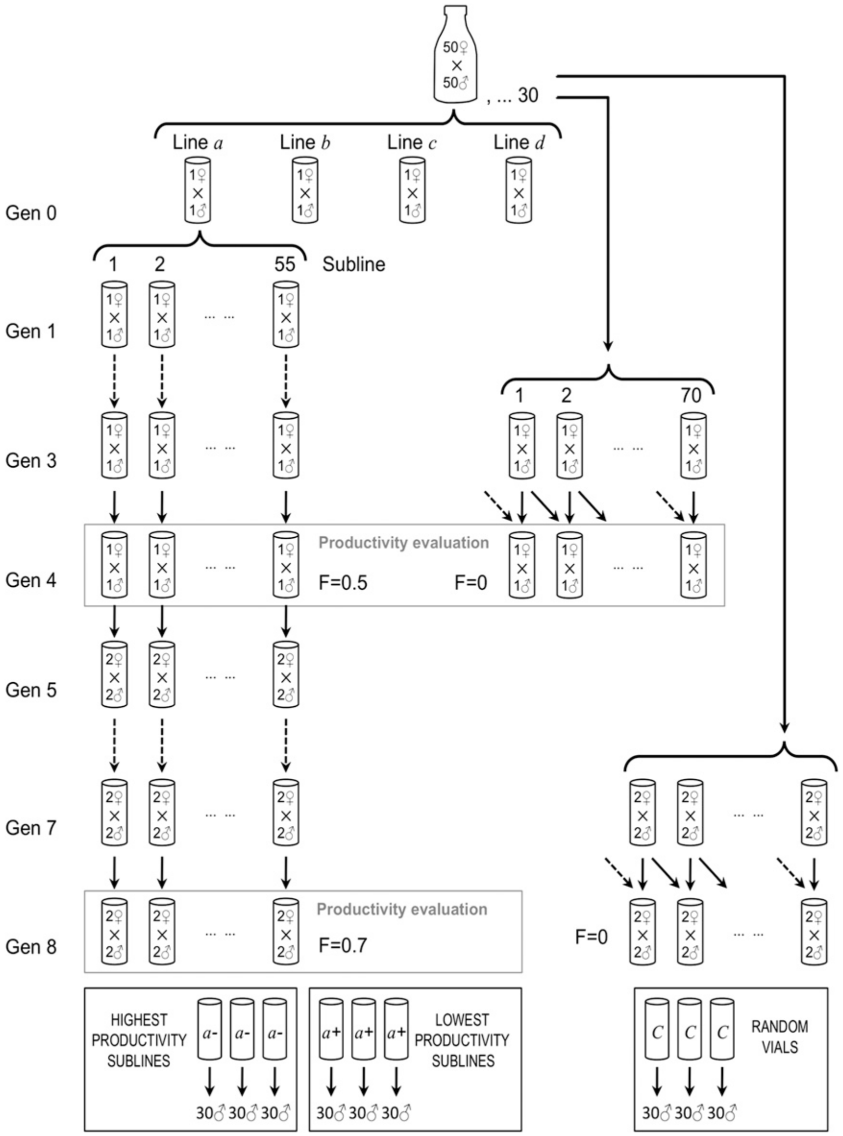


Figure 2 Experimental design to produce four sets of sublines with the highest inbreeding depression (lowest productivity, sublines labeled with +) and sublines with the lowest inbreeding depression (highest productivity, sublines labeled with –). Expression analysis was carried out for these sublines' sets as well as for an outbred control obtained from the base population.

evaluation replicate vials were established using a single virgin couple per vial (generation 4) or two virgin couples per vial (generation 8). At generation 4 an evaluation of the productivity was also carried out for the base population (used as a noninbred control). Seventy virgin couples were randomly collected from the base population and put in single vials simultaneously with the inbred sublines. To evaluate the total productivity of each vial, we counted the number of pupa present after a 14-day incubation period (so that most lifetime pupa production was considered), and the productivity of each subline was computed as the mean value of the three replicates. Since we had only one (at generation 4) or two (at generation 8) laying females per vial, population density was uniformly low in all vials. Mean productivities for each line at generations 4 and 8 as well as for the control base population at generation 4 are shown in Supporting Information, Figure S1. At generation 4, the rate of inbreeding depression was 1.14, 1.02, 0.97, and 1.12% per 1% increase in inbreeding for lines a, b, c, and d, respectively.

For each line, the three sublines showing the lowest productivity and the three sublines showing the highest productivity at generation 8 were chosen for expression analysis, along with the outbred control base population (Figure 3). The number of arrays analyzed was thus 27. The distributions of the productivities of all sublines are shown in Figure 3, and the average productivity of the chosen sublines are shown in Figure 4. Note that the average productivity of the highest productivity sublines was about three times larger than that of the lowest productivity sublines.

Expression arrays

For the expression analysis, 30 males from each selected subline and 3 groups of 30 males from the control (in all cases between 1 and 6 days after adult emergence) were collected at generation 8. These flies were anesthetized with CO_2, frozen in liquid nitrogen, and stored at −80° prior to RNA extraction. Total RNA purification was performed with the RNeasy Mini kit (QIAGEN, Valencia, CA). RNA concentration

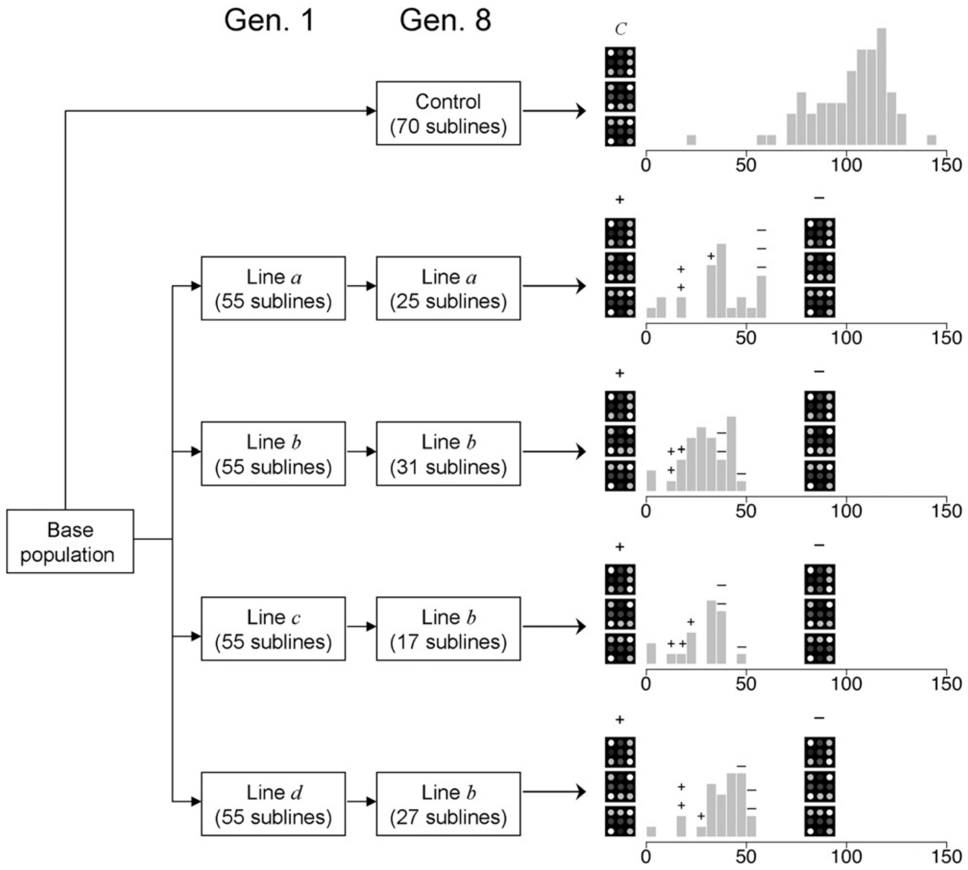


Figure 3 Design for the analysis of arrays. From each full-sib line (*a*, *b*, *c*, *d*), sets of full-sib sublines were established and analyzed for productivity. The distribution of these productivities is shown. Samples from the three sublines with the largest inbreeding depression (with symbol +) and those with the lowest inbreeding depression (with symbol –) with at least 30 males, were analyzed along with three samples from an outbred control. Thus, a total of 27 arrays were analyzed.

was determined using a Thermo Fisher Scientific NanoDrop 1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA). RNA integrity was assessed on an Agilent 2100 Bioanalyzer (Agilent, Palo Alto, CA). cDNA was synthesized with One-Cycle cDNA synthesis kit (Affymetrix) following the Affymetrix Expression Analysis Technical Manual protocol. cRNA was synthesized from this cDNA using the Affymetrix IVT labeling kit and purified with the Affymetrix GeneChip Sample Cleanup Module kit, being eluted in a total volume of 22 μl of RNase-free water. Purified cRNA was quantified spectrophotometrically, and 15 μg of each biotinylated cRNA sample was fragmented and mixed with hybridization buffer (100 mM MES, 1 M NaCl, 20 mM EDTA, 0.01% Tween 20) and loaded into the Affymetrix Drosophila GeneChip Array (v. 2.0). This single array contains 18,500 transcripts with 14 probes per transcript. After hybridization, arrays were washed and stained using Affymetrix fluidic station. Arrays were then scanned using the Affymetrix GeneChip Scanner 3000. The robust multichip average (RMA) method (Bolstad *et al.* 2003) was used for background adjustment, quantile normalization, and probe-level summarization of the microarray samples. RMA expression summary was computed using Partek Genomics Suite v. 7.3.3 (Partek) and the *affy* package in Bioconductor (Gentleman *et al.* 2004). To exclude genes that were not accurately detected in the data analysis probe, sets with less than one present call within at least one of the samples were disregarded.

We used two normalized sets of expression data. The first set includes data of the three control samples and all inbred sublines, to study the effect of inbreeding. The second set includes the inbred sublines only, to study the effect of the line, depression importance, and their interaction. The number of probe sets with some evidence of expression was 9133 in the inbred + control sublines set and 9113 in the only inbred sublines set.

Probe sets associated with phenotypic variation

We used statistic analysis for microarrays (SAM; Tusher *et al.* 2001) to analyze the variation in expression. SAM is a permutation-based multitest statistical procedure that takes into account the correlations between probe sets in the calculation of false discovery rates (FDRs; Storey 2002). In the case of the comparisons between the expression levels in inbred lines and the outbred control (*i.e.*, the analysis of inbreeding effects, Inb, calculated as inbreds' minus controls' average), based on Student's *t*-test, we used the Bioconductor R package *siggenes* (Schwender *et al.* 2006). For the more complex comparisons between the inbred sublines we used a normalized data set including only these sublines' data and applied a mixed model factorial analysis of variance (ANOVA) according to the model $Y = \mu + \text{Lin} + \text{Dep} + \text{Lin} \times \text{Dep} + W$, where μ is the overall mean, Lin the random main effect of line, Dep the fixed main effect of the magnitude of inbreeding depression (calculated as most depressed minus

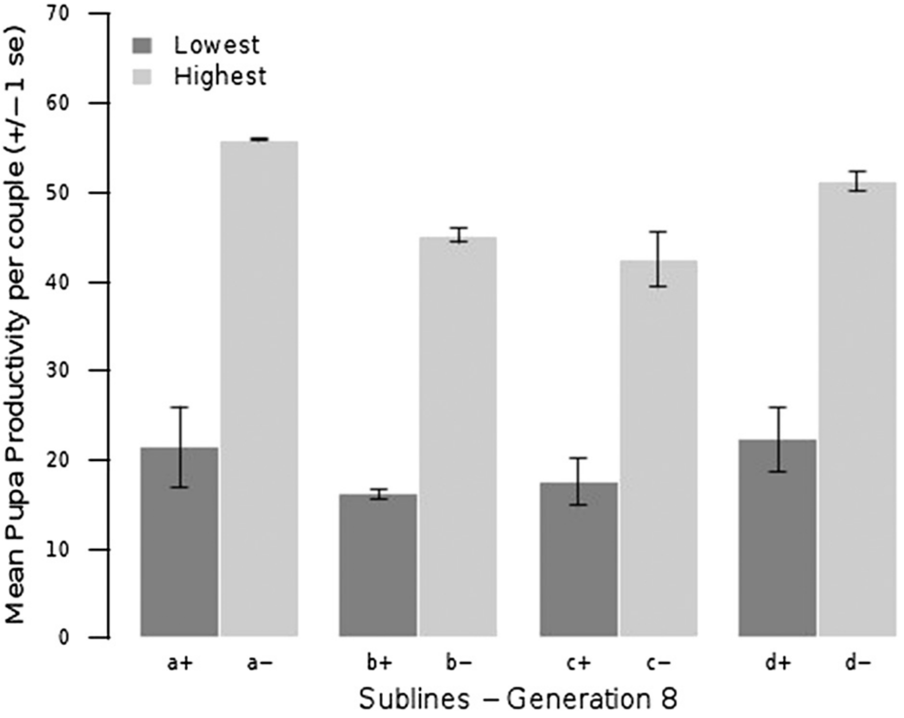


Figure 4 Mean pupa productivity for sublines with the highest and lowest productivity. Mean pupa productivity for the three sublines showing the lowest productivity and the three sublines showing the highest productivity at generation 8, which were chosen for expression analysis. Letters *a*, *b*, *c*, and *d* denote the inbred line code, and + and – denote most depressed (lowest productivity) and least depressed (highest productivity), respectively.

least depressed lines' average), Lin × Dep is the random effect of the line by depression interaction, and *W* is the within-replicate variance. The FDR values for the ANOVA's F's were obtained following Storey and Tibshirani (2003), in a SAM procedure in which the permutation pattern was adapted to each studied factor following the guidelines for mixed models in Anderson and Ter Braak (2003): for the fixed Dep, the Lin residuals were permuted as Dep × Lin units (approximate test). For the random Lin, raw observations were randomized within levels of Dep (exact test). For the interactions, the residuals left after adjusting for the Dep and Lin effects were permuted (approximate test). The R code used for these analyses is available from the authors on request. In every probe set, the fixed Dep mean squares were tested against the Lin × Dep mean squares, and the random Lin, against the error mean squares.

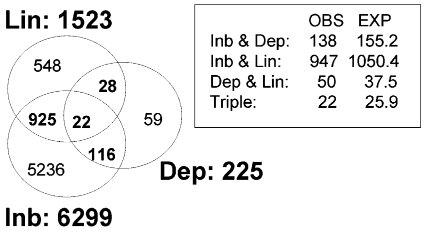
Analysis of gene functions

We used the DAVID Bioinformatics Resources 6.7 (http://david.abcc.ncifcrf.gov/home.jsp; Dennis *et al.* 2003). These programs can use lists of probe sets as input and provide results in terms of the corresponding genes. Our basic tool was the functional annotation clustering, which clusters functionally similar terms in the user's gene list into groups. In all cases, we chose the medium classification stringency and, as recommended by the authors, retained clusters having enrichment scores >1.3. The enrichment score is the geometric mean of all expression analysis systematic explorer (EASE; Hosack *et al.* 2003) scores (*P* values) of each annotation term in the group. Enrichment score 1.3 is equivalent to nonlogarithmic scale 0.05. The DAVID cluster annotation tool enables the user to specify a background list of genes against which to look for relative functional enrichment in a given gene list. We applied this procedure to compare the most significant genes in a gene-expression category against the whole of genes in that category. Because the functional annotation clustering tool has a limit of 3000 genes for the input lists, we used instead the less restrictive functional annotation chart tool (we kept functional terms with $\text{FDR} < 0.1$) for the analysis of the longer gene lists in the more general gene categories in our results. In addition to this large-scale exploratory analysis, we made direct significance tests for genes pinpointed as candidates by different kinds of *a priori* information.

Results

The number of significant probe sets resulting in $\text{FDR} < 0.1$ in the inbreds *vs.* control contrasts (Inb effects) was 6299 (4535 of them upregulated and 1764 downregulated in the inbred lines), 1523 in the variance between lines analyses (Lin effects), 225 in the most depressed *vs.* less depressed contrasts (Dep effects; 95 of them upregulated and 130 downregulated in the most depressed lines), and 2 in the Lin × Dep analysis. The lists of SAM selected probe sets for Inb, Lin, and Dep effects are in File S1.

The lists of SAM-selected probe sets for Inb, Lin, and Dep effects did not show clear nonrandom overlaps. Interestingly, having marked Inb effects did not increase the probability of having Dep effects (Figure 5). However, the distribution of up- and downregulation for the two effects was not independent. In most probe sets showing Inb and Dep effects (138 probes; listed along with their functional annotations in File S2), the most depressed sublines were intermediate in expression between the controls and the least depressed sublines



	OBS	EXP
Inb & Dep:	138	155.2
Inb & Lin:	947	1050.4
Dep & Lin:	50	37.5
Triple:	22	25.9

Figure 5 Numbers of probes differentially expressed in the experiment. Overlap in the lists of probe sets affected by inbreeding (Inb), line (Lin) and depression (Dep) effects. The total numbers of probe sets are shown besides the circles (size not proportional to list length). The inlaid box compares the number of probe sets shared between lists (OBS) with that expected if the overall proportions of probe sets showing a given effect were conserved in the other lists (EXP). No significance tests were applied to these comparisons because the expressions in the probe sets were not independent. The numbers of expressed probe sets were 9133 (in the analysis of Inb effects) and 9113 (in that of Dep and Lin).

(Figure 6), corresponding to the protective configuration of Figure 1. The analysis of the corresponding Inb × Dep contingency table resulted in a $\chi^2_{1\ \mathrm{d.f.}} = 37.008$, $P = 10^{-9}$. However, this test does not consider the lack of independence between the gene expressions in the lists. We complemented it with a randomization test (Westfall and Young 1993) that takes into account the correlations between observations. We randomized the positions of the inbred samples (10000 permutations) in these 12 + 11 + 63 + 39 + 5 + 8 = 138 probe sets. Only 1.94% of randomizations had as many or more than 63 + 39 = 102 probe sets with the most depressed samples in intermediate positions. Thus, the Dep effects were not in general mere extensions of the Inb effects, as would be the case if the most depressed sublines simply showed an intensification of the Inb effects.

The power of the functional enrichment analysis is low when the gene lists used are short (Huang *et al.* 2009), as was the case with the categories shown in Figure 6. For the 39 probes downregulated in the inbreds and having a protective configuration we found two functional clusters with enrichment scores >1.3. The first included GO:0044242, *cellular lipid catabolic process*; GO:0016042, *lipid catabolic process*, and GO:0005811, *lipid particle*, and the second, SP PIR Keywords *ank repeat*; Interpro *ankyrin*, and Smart *ANK*.

We next investigated whether the prevalence of the protective pattern found in the 138 probes significant for Inb and Dep effects (Figure 6) was also apparent for the whole set of analyzed probes. Thus, we carried out a randomization test for the proportion of probes showing a protective *vs.* nonprotective pattern (we excluded from this analysis the pattern called “other” in Figure 1, as these were not relevant for the intended test). Thus, we carried out 1000 permutations of the positions of the inbred samples for all probes. Figure 7 shows the observed proportion of protective patterns found (between 50% and >80%) in comparison with the expected random proportion (50% of each pattern). In this figure, probes are represented according to the absolute value of the Student’s *t*-value for the comparison between the most depressed and the least depressed contrasts (Dep effects). Thus, in the left-hand side of the *x*-axis are represented those probes with little difference in expression between the most depressed and the least depressed sublines, whereas in the right-hand side of the *x*-axis are represented those probes with the largest difference in expression between the most depressed and the least depressed sublines. The figure shows that the prevalence of the protective pattern is a general observation. However, only the three right-hand points had a proportion of protective patterns significantly larger than those obtained at random after randomization (P = 0.00, 0.01 and 0.02, respectively).

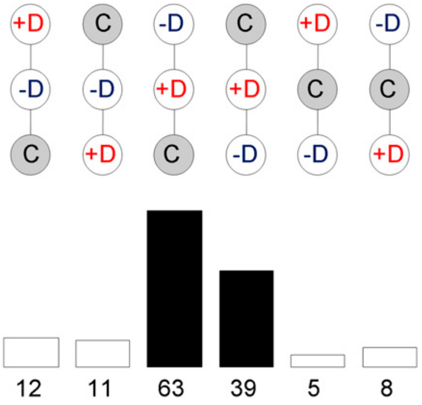


Figure 6 Number of probes SAM-selected for Inb and Dep effects for different patterns of expression. Relative rankings of sublines (C, outbred controls; +D, most depressed; –D, least depressed) expression levels in probe sets showing both inbreeding (Inb) and depression (Dep) effects (FDR < 0.1 in both cases) and their frequencies. The black bars correspond to probes with the most depressed samples in the intermediate positions, corresponding to the protective configuration given in Figure 1.

We further investigated if a higher proportion of probes with the protective configuration was apparent when all 9133 were ranked according to the Student’s *t*-value for the comparison between inbred and outbred contrasts. This is shown in Figure 8. It is clear that, for probes with large absolute values of *t*, there is again an overrepresentation of the protective configuration (circles) with respect to the nonprotective one (triangles). The same pattern was dominant when the four experimental lines were analyzed separately (Figure S2). However, no significant differences between the observed proportion of protective probes and a random proportion were found in the randomizations for this case (not shown), likely because these differences were less associated with the proportion of protective patterns (compare these proportions’ extreme values in Figure 7 and Figure 8).

The probes’ classification in Figure 8 enabled us to make a larger, more powerful functional analysis distinguishing genes up- and downregulated after inbreeding (see File S3). Genes downregulated in the inbred sublines (solid circles and triangles) were enriched in energy-related terms, those upregulated (opened circles and triangles) in transcription and translation-related terms, and those having

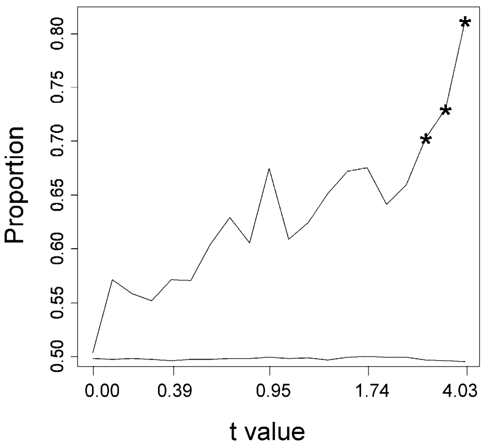


Figure 7 Proportion of probes showing a protective pattern of expression (see Figure 1) after ranking the 9133 expressed probe sets according to their Student's *t* absolute value in the most depressed *vs.* least depressed test and dividing the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure indicates probes where there is a large difference in expression between the most depressed and the least depressed sublines, and those on the left-hand side are probes where this difference is low. The lower line (without symbols) corresponds to the average proportion after 1000 randomizations of the expressions for the inbred sublines. Asterisks indicate a significant difference ($P < 0.05$) between the observed proportion and that obtained after randomization.

intermediate expression in the control lines (squares), in terms related with the production of functional versions of proteins and RNA. It is apparent from the figure that the overrepresentation of probe sets consistent with protective effects (circles) tended to increase as the Student's *t*-values testing the inbreeding effects became more extreme, especially in the case of the inbreeding downregulated probe sets. This supports the interpretation that protective profiles are associated with real changes in gene expression. Furthermore, some of the functional associations seen in Figure 8 are reinforced in the probe sets with extreme *t*-values, especially in those showing protective expression profiles (Table S1). When the analysis was restricted to the probe sets upregulated and with protective expression profiles (open circles), those showing the most extreme upregulation were relatively more enriched in RNA splicing functions. Moreover, when the analysis was restricted to the probe sets downregulated and with protective expression profiles (solid circles), those showing the most extreme downregulation were relatively more enriched in energy derivation related terms.

To conduct a more conservative and robust functional analysis, we looked for enriching terms that appeared for a particular profile (protective, nonprotective, upregulated, or downregulated) in all four inbred lines and did not appear in any line for the other profiles. These are the results given in Figure 9. The inbreeding downregulated genes with protective profiles had a clearly higher degree of similarity and specificity between lines, the number of functional terms coincident in the four lines was as large as 79. These results suggest a precisely regulated transcriptomic response to inbreeding. The other category of protective profiles, that involving upregulated probes, had 14 specific functional terms. No specific terms were found for the nonprotective categories, which suggest a more heterogeneous causation for these expression differences. There were no common functional terms for both protective and nonprotective extreme probe sets (right-hand marginal zero values), but the upregulated categories, and also the downregulated ones, shared some (lower marginal figures), very general functional terms. The inbreeding upregulated probes tended to be related with transcription, and the inbreeding downregulated ones, with energy. The terms in the corresponding protective categories involved similar concepts, but were more restricted, and in the case of the protective downregulation, much more diverse.

Discussion

Inbreeding seems to produce large-scale transcriptomic changes in *Drosophila melanogaster*. About one-half of the expressed genes in our experiment had differences (FDR < 0.1) in expression between inbred lines and outbred controls. Upregulation arising from inbreeding was more frequent than downregulation, and a majority of changes corresponded to expression profiles consistent with protective responses, where the least depressed lines changed in expression more than the most depressed ones. The high frequency of protective-consistent patterns of expression seems to be a robust observation, made in the four independent lines analyzed. According to this interpretation, inbreeding would therefore constitute an organismal challenge requiring the activation or deactivation of a large number of genes to cope with it. For many genes, this change would not be fulfilled, leading to a higher inbreeding depression for individual fitness.

A possible problem with gene-expression measurements using microarray data are sequence mismatches due to sequence heterogeneity among target DNA at many base pairs. In the presence of such sequence mismatches, relative hybridization intensities could reflect both differences in transcript abundance and differences in hybridization kinetics. However, the impact of sequence heterogeneity on the main results of our article is expected, *a priori*, to be modest, because we aimed at highly inbred lines from a single population and a single species. Gene-expression measurements in different species (*D. melanogaster* and *Drosophila simulans*) using single-species Affymetrix arrays did not reveal a consistent variation in signal intensity due to sequence mismatches (Nuzhdin *et al.* 2004), despite that these two species split 2.3 ± 0.3 MYA ago (Li *et al.* 1999).

In any case, the hypothesis that the pervasive protective pattern observed from our data is a consequence of sequence mismatches is difficult to defend because it would imply two contrasting assumptions. We observed that, for a majority of genes, the expressions of the most depressed sublines were intermediate between the expressions of the control and the least depressed sublines, and this happened both for up- and

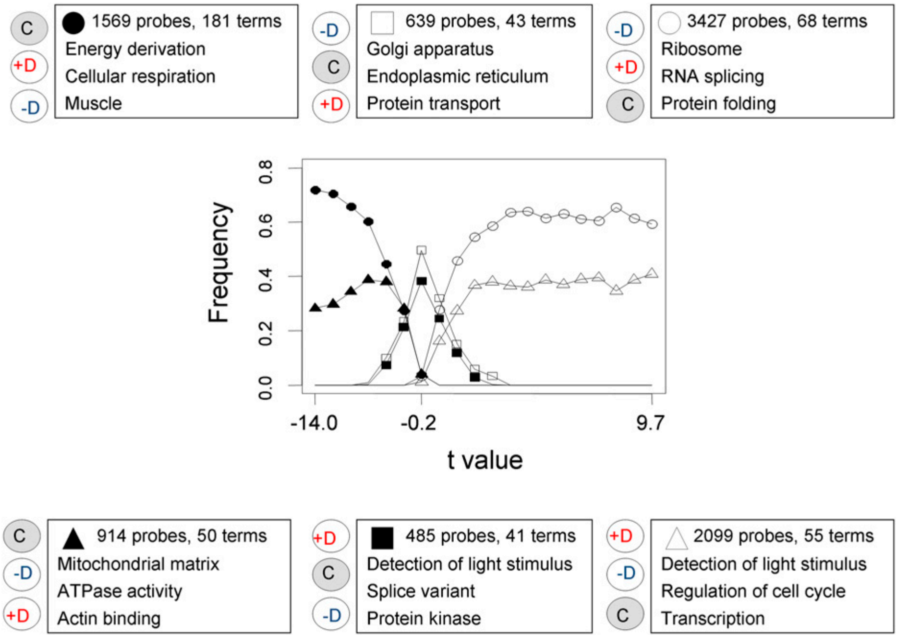


Figure 8 Relative frequencies of probe sets in each gene-expression profile of Figure 5. We ranked the 9133 expressed probe sets according to their Student's *t*-value in the inbreds *vs.* control test, and divided the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure indicates probes upregulated with inbreeding, and those in the left-hand side are probes downregulated with inbreeding. We show the frequencies of the different expression profiles in each tier. The most relevant functional terms enriching the genes in each profile are shown, giving preference to those most informative, significant, and nonredundant.

downregulated genes under inbreeding. It could be hypothesized that the largest heterogeneity in probe mismatch sequence occurred in the most depressed sublines, leading to higher mismatch rates and weaker hybridization signals (*i.e.*, closer to the control ones), as observed in the upregulated genes. But then, to explain the same protective pattern in the downregulated genes, it should be necessary to assume that the largest heterogeneity and weaker hybridization signals (*i.e.*, farther away from the control ones) occurred this time in the least depressed sublines. Thus, it would be hard to explain why mismatches should be more frequent on the most depressed sublines than in the least depressed sublines in the case of upregulated genes and the opposite in the case of downregulated genes.

Nevertheless, a way to obtain indirect information on the effects of sequence variation and other confounding factors on the results of our experiment is to ascertain the agreement between probes of the same gene. We identified the 300 expressed genes displaying more than one probe set in the array. Probes attributed to the same gene would be subject to the same regulation and would be expected to have consistent expression levels. The average Pearson correlation of hybridization signals for the 248 genes with only two probe sets across the 27 microarrays assayed in this experiment was 0.58, a positive value consistent with regulation-caused variation in signal intensity, but not with independent changes in sequence in the two probe sets from the same gene. This large but nonunity correlation would reflect experimental noise, possible sequence mismatches, and alternative splicing. To do a test directly related with the protective variation patterns, we took each of the above 300 genes and assigned values of 1 or 0 to the two probes of each gene depending on whether they showed protective patterns or not, respectively. Thus, for each gene, the two probes could show protective effects (1, 1), one protective and one nonprotective (1, 0), or both nonprotective (0, 0). The *F*-value for the gene effect in an ANOVA was 2.168, with a probability as low as $P = 1.15E\text{-}12$. The calculated intraclass correlation coefficient between the probe values was $t = 0.344$, whereas a test randomizing the probe sets' gene identities found a maximum value of $t = 0.150$ for the coefficient among 999 random replicates. These results therefore suggest a clear hybridization protective variation signal common to both probe sets from the same gene.

The high frequency of genes with protective-consistent expression changes, *i.e.*, those changes most extreme in the least depressed sublines, was not related with an increase in variance in these sublines within probe set. The variance between lines within probe sets was on average (for the 9133 probe sets) very similar for the most (0.043) and the least (0.044) depressed groups of sublines. Moreover, the average variance between sublines within lines was 0.028 for the control sublines, 0.044 for the least depressed sublines, and 0.086 for the most depressed sublines. A larger variance among inbred lines expressions than among outbred control expressions was also found by Kristensen *et al.* (2005).

As explained in *Materials and Methods*, we had to pool the extracts from 30 adult males in every analyzed sample to obtain the mRNA quantities required to run each microarray in the experiment. Appropriate pooling has been shown to improve efficiency for microarray experiments (Peng *et al.* 2003). One study, however (Shih *et al.* 2004), found discordances between the average expression of individual samples and that of a corresponding pool sample, the magnitude of the discordance in each probe set increasing monotonically with its signal in the microarray. In any case, this effect was not associated with our results. When the list of expressed

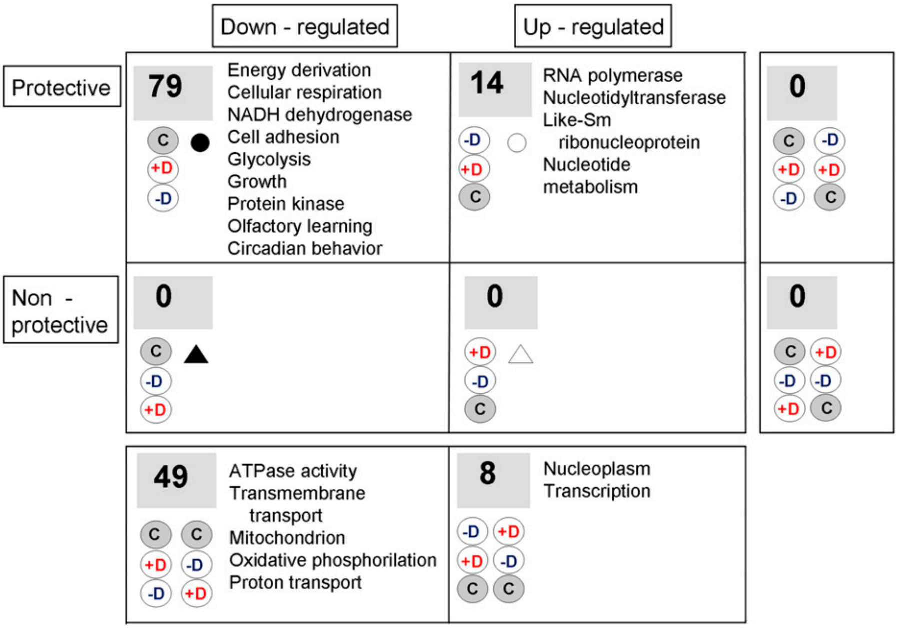


Figure 9 Number of functional terms enriching exclusively each expression profile. Analysis of the functional terms enriching the gene-expression profiles in the four most extreme tiers in each direction in Figure 8 (1824 probe sets in the case of the most negative *t*-values and 1837 in that of the most positive ones). As a conservative analysis, we show the number of terms enriching a particular profile in all four inbred lines and not found in any line for the other profiles. The marginal cells correspond to the terms exclusive to the whole set of protective probes, to the whole set of downregulated ones, etc. The most informative, significant, and nonredundant terms in each cell are shown. See File S4 for complete lists of terms. Triangles and circles help to relate these categories with their values in Figure 8.

probe sets was divided in 20 intervals according to their mean microarray signal, the correlation between the intervals' median of the averages and their proportion of protective expression patterns (the relationship studied in Shih *et al.* 2004) was 0.188 ($P = 0.427$).

Another concern that may be raised regarding our main observation of a pervasive protective-consistent pattern is that the normalization process performed on the data (RMA) could generate some sort of bias in the relative expression changes of the least and most depressed sublines, so that the main result of this study is an artifact of the normalization. To address this concern we analyzed directly the raw data without any adjustment or normalization step, simply averaging in each individual array the perfect match probes in each probe set. In this case, the number of probes with protective, nonprotective, and other patterns (following Figure 1) are 4830, 3045, and 1258, respectively. When only the first step in the RMA sequence of adjustment steps (the probe-position background correction) is made, the numbers are 4993, 2918, and 1222, respectively. These numbers can be compared with the corresponding ones using RMA normalized data, which are 4996, 3013, and 1124, respectively. It is clear that the preponderance of protective patterns over nonprotective ones is equally observed in the raw data. This is also evident by looking at Figure S3, which is equivalent to Figure 8, but considering raw expression data rather than normalized data. Therefore, normalization is not responsible for any artifact causing the observed general patterns.

Protective-consistent changes in expression were more specific in function than nonprotective ones. This would be expected if the first corresponded to functional, established pathways coping with alterations in body condition, whereas the second corresponded to contingent, heterogeneous disruptions in development and metabolism. The functions of protective-consistent genes were diverse but a clear specificity on RNA splicing functions for upregulated probes and on energy generation for downregulated probes was apparent.

The enrichment in energy derivation functions among the downregulated protective-consistent genes suggests physiological measures to save energy. There are to our knowledge no clear expectations about energy use changes in inbred *D. melanogaster*. It has been found (Ketola and Kotiaho 2009) that inbreeding in the insect *Gryllus firmus* had, relative to controls, increased CO_2 production (used as a proxy of respiration and energy use) at rest and decreased under forced exercise (the signs of these differences implied a depression in the capacity to mobilize body resources), but the extrapolation to gene expression at the moment of sampling in our fly populations is not straightforward. In any case, the observation that the reductions in expression were largest in the least depressed sublines suggests that they had a fitness-enhancing role. An inspection of functional annotations for genes involved in these reductions could throw some light on their physiological implications. Among the genes showing the strongest evidence for protective reductions in expression (File S2), in addition to *Dmel\CG6020* and *Dmel\CG12400*, directly involved in energy derivation and respiration, we found *Toll* and *Relish*, involved in the *Toll* pathway, the major regulator of innate immune response in *Drosophila* (De Gregorio *et al.* 2002). The repression of these genes and pathway leads to both the repression of immunity and the activation of insulin signaling, which increases nutrient reserves and growth (Di Angelo *et al.* 2009). In the same list of genes with strong protective reductions in expression is *Ankyrin*, which communicates with the *Toll* pathway (Lemaitre 2004).

These results suggest that inbreeding resulted in a change in the optimum resource allocation to different metabolic pathways. The most productive–least depressed individuals would have improved their energy balance and approached that new optimum not only reducing the expression of both energy derivation and growth regulating genes, but also trading immune competence for growth, which could increase fitness in the isolated laboratory environment. Another interesting gene among the downregulated protective ones is *SNF1A/AMP-activated protein kinase*, which works as an energy sensor, being activated at low levels of the ratio AMP/ATP. It represses the *raptor* branch of the *mTOR* pathway, a key positive regulator of cell growth and proliferation (Sarbassov *et al.* 2005). Thus, the stability of the laboratory environment might have favored genotypes less sensitive to energy availability. All these expression changes in the least depressed sublines suggest that reducing depression was not simply a question of maintaining as much as possible the expression patterns observed in the outbred individuals. Specific adjustments in gene expression were required to maintain individuals functional in an inbreeding situation.

Protective-consistent increases in expression were more numerous and heterogeneous in function than the corresponding decreases. They were enriched in functional terms related with the synthesis of proteins, but also with RNA polymerase, mRNA splicing, and the spliceosome. The latter relationship is specially interesting because it raises the possibility that changes in splicing may be a relevant mechanism of response to inbreeding. Recent studies have shown that alternative splicing determines the binding properties, intracellular localization, enzymatic activity, protein stability, and post-translational modifications of a large number of proteins. The magnitude of the effects ranges from a complete loss of function or acquisition of a new function to very subtle modulations (Stamm *et al.* 2005). Changes in splicing have already been found to contribute to the response to the stress generated by pathogens in *Citrus* trees (Del Carratore *et al.* 2011) and exposition to heavy metals in animals (Jeong *et al.* 2011).

We defined the protective pattern as that in which the expression of the least depressed sublines is more extreme than that of the most depressed sublines and the nonprotective one as that in which the opposite occurs. This is a conservative view though, because changes in expression with a protective role against inbreeding may occur also under the remaining scenarios, as is the case with genes showing more expression in the least depressed sublines than in the controls and in the controls more expression than in the most depressed sublines (open rectangles in Figure 8 and functional enrichment analysis in File S3). These genes tended to be associated with the endoplasmic reticulum and Golgi apparatus, and their functions of protein synthesis, maturation, transport, and localization, and with the synthesis of carbohydrates and their addition to proteins in Glycosylation reactions. The upregulation of these genes in the least depressed sublines and their downregulation in the most depressed ones suggests a special role of this process in the generation of inbreeding depression. Homozygosis could result in polypeptides with abnormal conformations that prevent normal folding or their associations with other subunits or cofactors (Sherman and Goldberg 2001; Pedersen *et al.* 2005; Kristensen *et al.* 2010). Disruptions in cellular homeostasis could be also involved. Successful protein folding requires a tightly controlled environment of substrates that include glucose, calcium, and redox buffers (Sherman and Goldberg 2001). Kristensen *et al.* (2005) had already found that inbreeding affected the expression of protein *Hsp70*, involved in protein quality control, and interestingly, the *protein Hsp70*-annotated gene *Dmel\CG2918* was one of the eight genes included in our Figure 6 that were upregulated in the least depressed and downregulated in the most depressed sublines (listed in File S2). More evidence for a relationship between inbreeding and protein folding can be found in the lists of SAM-selected probe sets related with inbreeding in Kristensen *et al.* (2005). These show that six upregulated probes corresponded to genes in the protein-processing functional category GO:0006511, ubiquitin-dependent protein catabolic process. Ubiquitines are small proteins binding to unneeded proteins and labeling them for destruction in the proteasome (Hochstrasser 2009). Only one of the probe sets in our platform corresponding to these six was significant ($P < 0.05$; 1633951_at, for the gene *Drosophila damage-specific DNA-binding protein-piccolo*-; upregulated in inbreds, nonsignificant for Dep).

Two of the eight genes upregulated in the least depressed and downregulated in the most depressed sublines were related in particular with protein targeting and localization. This function is very stringently regulated. Reumers *et al.* (2005) found that <1% human SNPs changed the subcellular localization of proteins, whereas >50% affected protein folding and stability, indicating that the first changes were far less benign (see also Kohn *et al.* 2006). One of these two genes, *Protein transport protein Sec61 gamma-2 subunit-Sec61γ*-, was already annotated as having cytoprotective effects in *D. melanogaster* (Arsham and Neufeld 2009). A simple and tentative interpretation of the above observations would be that inbreeding reduces the efficiency in the production of functionally matured and located proteins and that the reduction was partially compensated in sublines that increased the expression of genes related with this production.

While both Kristensen *et al.*'s (2005, 2006) and the present study found inbreeding affecting the expression of genes involved in protein processing, the overlap in results was modest at most when considering specific genes (Table S2). Ayroles *et al.* (2009) listed the probe codes of three genes differentially expressed in their three highly depressed lines; *Cecropin B*, AFFYID: 1626530_at; *Hsp70Bc*, AFFYID: 1632841_x_at; and one *gluthatione transferase*, *Dmel\CG6673*, AFFYID: 1638074_at. The first was not expressed in our experiment, and the other two showed no significant Dep effects (the corresponding *F*-values in our analysis were 0.270 and 0.848, respectively). Such limited overlap between the lists of gene expressions affected by inbreeding in different populations of this species might be the most common situation, as was found also by Sarup *et al.*

(2011) in their comparison of published studies. Instead, they found a high degree of overlap between studies made in samples from the same genetic background, even when they involved different sexes and traits. These effects of genetic background suggest that interpretations based on expression changes in individual genes or very specific functional categories might be inappropriately simplistic. Expression traits consistently show complex inheritance, explicable only by multiple underlying loci and interactions among them (Rockman and Kruglyak 2006; Nègre *et al.* 2011) and may be heavily dependent on sex and chromosome context even within the same population (Wayne *et al.* 2007). The total numbers of genes showing changes in expression were also lower in the above experiments. Differences could be related to the culture environment, which is known to affect gene expression (see, for example, Kristensen *et al.* 2006) and the numbers of arrays analyzed and of flies pooled per sample.

Comparisons of our results with those of Kristensen *et al.* (2005, 2006) and Ayroles *et al.* (2009) are restricted to contrast of inbreds *vs.* outbreds in one case and more and less depressed samples in the other. As explained in the introduction, the existence of protective responses could not be detected in these experiments because they did not consider separately the effects of inbreeding and depression. The microarray analysis by Sorensen's *et al.* (2007) of *D. melanogaster* populations artificially selected to withstand different kinds of stress is a valuable source of information about gene-expression protective responses, as changes observed in these selected lines may be considered as adaptations protecting the organism against stressful situations. Similarity between experiment lists of Sorensen *et al.* and our study of Inb and Dep SAM selected genes would indicate that similar expression changes are involved in inbreeding and response to stress. However, the number of coincidences in the corresponding gene lists was very similar to those expected after random sampling of terms (Table S3).

Inbreeding is a whole-organism phenomenon, and it would not be surprising if it were related with genome-wide transcription alterations. Studies like this one, analyzing broad patterns of gene expression and gene function categories, give a picture of the overall consequences of inbreeding that cannot be achieved when searching individual genes contributing to inbreeding depression. Our results seem to provide a new view on the genetics of inbreeding and are compatible with the hypothesis that inbreeding induces large-scale changes in gene regulation that would alleviate the ensuing depression. The between individuals variation in depression would be due not only to differences in the severity of the particular genetic alterations originating that depression, but also to differences in the ability to carry out depression-alleviating adjustments. Nevertheless, further evidence will be needed to confirm the prevalence of a pattern of expression compatible with the protection against inbreeding depression effects. In addition, a more complete understanding of the consequences of inbreeding would require research on the two mechanisms involved: those causing the depression and those reducing its magnitude.

Acknowledgments

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Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in *Drosophila*

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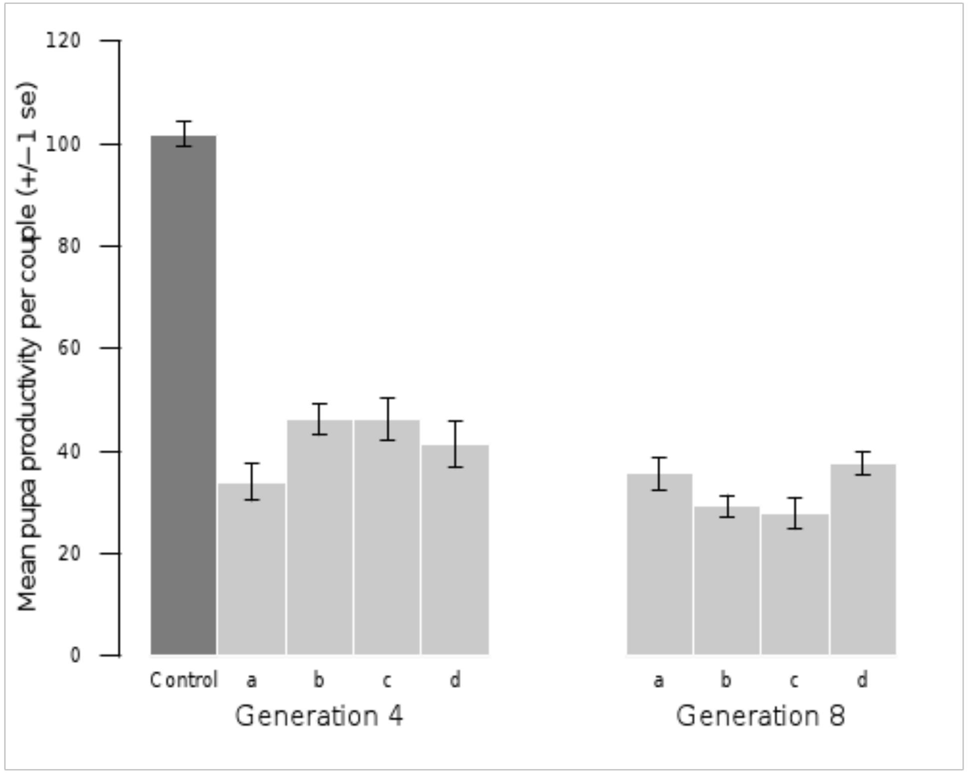

Figure S1 Mean pupa productivity for the four inbred lines and the outbred control at generations 4 and 8. At generation 4, the rate of inbreeding depression was 1.14, 1.02, 0.97 and 1.12% per 1% increased in inbreeding for lines *a*, *b*, *c* and *d*, respectively.

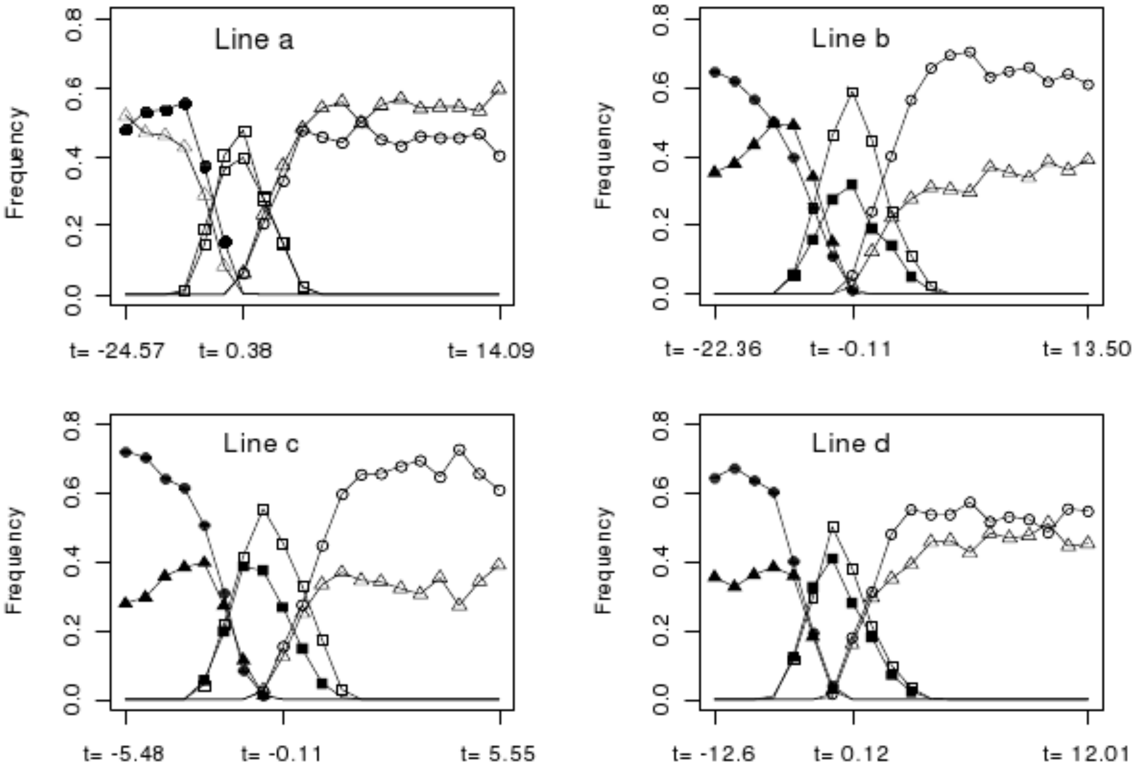

Figure S2 Relative frequencies of probe sets in each of the gene expression profiles shown in Figure 5 of the main text for each inbred line. We ranked the 9133 expressed probe sets according to their Student's *t* value in the inbreds *vs.* control test, and divided the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure includes probes up-regulated with inbreeding, and those in the left-hand side are probes down-regulated with inbreeding.

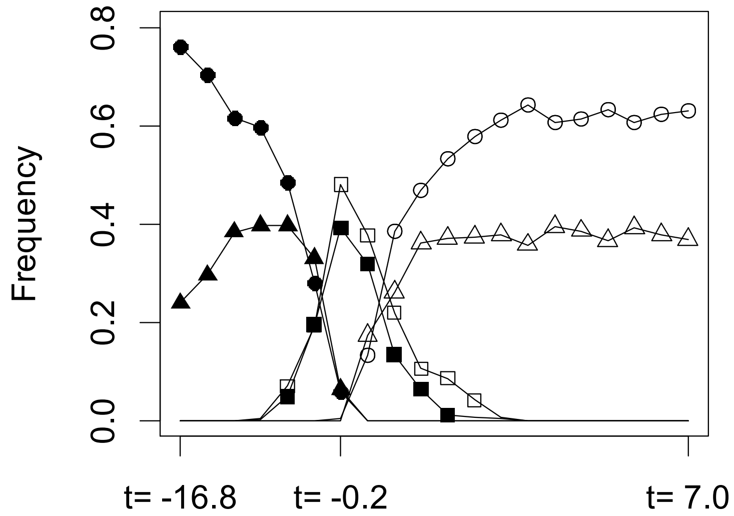

Figure S3 Relative frequencies of probe sets in each of the gene expression profiles shown in Figure 5 of the main text for each inbred line. Profiles in this figure correspond to raw gene expressions, i.e., the average of the perfect match probes in each probe set. We ranked the 9133 expressed probe sets according to their Student's *t* value in the inbreds *vs.* control test, and divided the rank in 20 tiers of size 456 (except the last one, of size 469). Thus, the right-hand part of the figure includes probes up-regulated with inbreeding, and those in the left-hand side are probes down-regulated with inbreeding.

Table S1

Category	Cluster	Classification	Term's name	Number of genes
Inbreds up-regulated, protective configuration	Cluster 1, ES: 2.25	GOTERM_BP_FAT	RNA processing	60
		KEGG_PATHWAY	Spliceosome	40
		GOTERM_CC_FAT	Small nuclear ribonucleoprotein complex	22
	Cluster 2: ES: 2.04	GOTERM_BP_FAT	RNA localization	20
		GOTERM_BP_FAT	Nucleocytoplasmic transport	19
		GOTERM_BP_FAT	mRNA export from nucleus	11
	Cluster 3: ES: 1.76	GOTERM_CC_FAT	Extracellular region	46
		UP_SEQ_FEATURE	Signal peptide	44
		SP_PIR_KEYWORDS	Glycoprotein	25
	Cluster 4, ES: 1.44	GOTERM_BP_FAT	Cell surface receptor linked signal transduction	24
		GOTERM_MF_FAT	Hormone activity	16
		GOTERM_BP_FAT	G-protein coupled receptor protein signaling pathway	11
Inbreds down-regulated, protective configuration	Cluster 1, ES: 2.36	GOTERM_BP_FAT	Phosphate metabolic process	121
		GOTERM_CC_FAT	Mitochondrion	116
		GOTERM_BP_FAT	Energy derivation by oxidation of organic compounds	55
	Cluster 2, ES: 2.03	GOTERM_MF_FAT	Nucleotide binding	149
		GOTERM_MF_FAT	ATP binding	101
		INTERPRO	Protein kinase, ATP binding site	40
	Cluster 3, ES: 1.44	GOTERM_BP_FAT	Protein amino acid phosphorylation	50
		INTERPRO	Serine/threonine protein kinase-related	35
		UP_SEQ_FEATURE	Active site:Proton acceptor	25

Table S1 (cont.)

Inbreds up-regulated, non-protective configuration	Cluster 1, ES: 1.35	SMART	JHBP	5
		INTERPRO	Hormone binding	5
		INTERPRO	Odorant binding protein	5

Cluster annotation analysis of the probe sets showing the most extreme Student’s *t* values in the test of inbreds’ *vs.* controls’ expression (1846 and 1860 probes for the positive and negative *t* values respectively), using as background all probes in the same expression pattern. The lists of functional terms shown are not exhaustive, we chose three informative and less redundant terms in each cluster. No significant clusters were found in the analysis of down-regulated probes having non-protective configurations. ES: Enrichment Score.

Table S2 Comparison with Kristensen et al gene lists

	Number of probe sets in the Kristensen et al. list	Correspon-dences in our platform	Expressed in this experiment	*Inb* effects OBS	*Inb* effects EXP	*Inb* same dir. OBS	*Inb* same dir. EXP	*Dep* effects OBS	*Dep* effects EXP	*Dep* same dir. OBS	*Dep* same dir. EXP
Fast+	60	38	35	14	14.70	13	9.8	4	5.60	2	2.80
Fast-	13	15	11	4	4.62	3	1.2	4	1.76	2	1.20
Slow+	113	76	69	42	28.98	32	29.4	12	11.4	5	8.40
Slow-	41	20	19	7	7.98	4	2.1	4	3.04	3	1.20
Joint+	9	9	8	5	3.36	4	3.5	3	1.28	2	2.10
Joint-	12	12	12	9	5.04	8	2.7	2	1.92	1	0.60
25º+	5	5	5	3	2.10	2	2.1	2	0.80	1	1.40
25º-	7	7	7	5	2.94	1	1.5	1	1.12	0	0.3
Total	**260**	**182**	**166**	**89**	**69.72**	**67**	**52.3**	**32**	**26.92**	**16**	**18**
χ^2 (7 d.f.)				5.09, P = 0.649		9.53, P = 0.217		5.73, P = 0.572		5.96, P = 0.544	

Inb and *Dep* effects for the probe sets listed as SAM-selected in the Fast and Slow inbreeding treatments and the Joint analysis in Kristensen et al. [2005] and in the 25ºC treatment in Kristensen et al. [2006]. Plus and minus signs indicate over and down regulated probe sets in the inbred samples, respectively. Because their results correspond to the older Affymetrix Drosophila Genome Array Version 1, we show the number of equivalent probe sets in our Version 2 Array (note that the equivalences were not one to one); of these, the number expressed in the current experiment; the number of *Inb* or *Dep* significant, and the number showing these effects in the same direction. The expected numbers of probe sets showing *Inb* and *Dep* effects were calculated as: number of Kristensen et al.'s SAM-selected probe sets expressed in our experiment × our overall proportion of probe sets showing *Inb* or *Dep* effects (0.42 and 0.16). The expected counts in the same direction were calculated as: number of expressed probe sets showing *Inb* or *Dep* effects x overall proportion of up or down regulated genes in our experiment (0.7 and 03 for *Inb* and 0.41 and 0.59 for *Dep*).

Table S3 Comparison with Sorensen et al. gene lists

Selected line	In Sorensen's list	Expressed in this experiment	*Inb* effects OBS	*Inb* effects EXP	*Inb* same dir. OBS	*Inb* same dir. EXP	*Dep* effects OBS	*Dep* effects EXP	*Dep* same dir. OBS	*Dep* same dir. EXP
Heat survival	94	78	28	33.12	6	-	12	12.76	5	
Starvation	230	176	74	74.73	19	22.20	20	28.80	12	11.80
Longevity	64	54	27	22.92	8	8.10	9	8.83	2	5.31
Heat knock down	21	16	4	6.79	3	2.80	8	2.62	8	3.28
Dessication	262	154	53	65.39	20	15.9	21	25.20	11	12.39
Constant 30º C	12	10	4	4.25	2	3.00	0	1.64	0	-
Combined	262	245	108	104.03	51	75.6	46	40.08	24	18.86
Goodness-of-fit χ^2			4.82, P = 0.566, 6 d.f.		6.35, P = 0.273, 5 d.f.		17.44, P = 0.008, 6 d.f.		8.93, P = 0.063, 4 d.f.	

Numbers of genes differentially expressed in the Sorensen et al. (2003) stress selection lines; number of these genes expressed in our experiment (only the counts in the *Inb* analysis lists are shown; the counts difference with the *Dep* analysis lists was never greater than two); of these, numbers showing *Inb* or *Dep* effects ($P < 0.05$ in *t* test and ANOVA respectively); of these, numbers with expression changed in the same direction as in the Sorensen's et al experiment. The expected numbers of *Inb* and *Dep* effects genes were calculated as: number of Sorensen's et al. significant genes expressed in this experiment × our overall proportion of genes showing *Inb* or *Dep* effects (0.42 and 0.16). The expected counts in the same direction were calculated using the number of expressed genes with *Inb* or *Dep* effects × overall proportion of up- or down-regulated genes in our experiment (0.7 and 0.3 for *Inb* and 0.41 and 0.59 for *Dep*). All genes in each selected line list showed changes in the same direction, with the exception of Heat survival, for which we calculated no expected direction changes. Combined: genes differentially expressed in a joint analysis of all selected lines versus controls in Sorensen's et al. experiment.

File S1

Lists of probe sets showing (FDR<0.1) *Inb*, *Lin*, *Dep* and *Lin* x *Dep* effects

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Inb Effects UP regulated FDR < 0.1

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Dep Effects UP regulated FDR < 0.1

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1641506_at

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Dep Effects DOWN regulated FDR < 0.1

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Lin x Dep Effects FDR < 0.1

1632492_at

1628404_at

File S2

Functional annotations for probe sets in Figure 6, showing both *Inb* and *Dep* effects

For each pattern we give the list of probe sets and their functional information as provided by the *Functional annotation table* tool in the DAVID web page.

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+D

C

-D

Probe sets:

1624717_s_at
1625430_at
1625840_at
1631385_at
1631527_at
1632623_at
1635581_at
1636896_a_at
1637193_at
1637940_s_at
1641126_at
1641381_s_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1632623_at	Cytochrome b5-related	Drosophila melanogaster	GO:0006631~fatty acid metabolic process,GO:0006633~fatty acid biosynthetic process,GO:0008610~lipid biosynthetic process,GO:0016053~organic acid biosynthetic process,GO:0046394~carboxylic acid biosynthetic process,GO:0055114~oxidation reduction,	GO:0005739~mitochondrion,GO:0005811~lipid particle,	GO:0005506~iron ion binding,GO:0009055~electron carrier activity,GO:0016717~oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water,GO:0020037~heme binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046906~tetrapyrrole binding,GO:0046914~transition metal ion binding,	IPR001199:Cytochrome b5,IPR005804:Fatty acid desaturase, type 1,IPR012171:Fatty acid/sphingolipid desaturase,IPR018506:Cytochrome b5, heme-binding site,		PIRSF015921:fatty acid desaturase/sphingolipid desaturase,PIRSF015921:FA_sphinglp_des,		complete proteome, heme,iron,metal-binding,metalloprotein,	chain:Cytochrome b5-related protein,domain:Cytochrome b5 heme-binding,metal ion-binding site:Iron (heme axial ligand),sequence conflict,sequence variant,
1636896_a_at	Dmel_CG12576	Drosophila melanogaster								complete proteome,	
1641381_s_at	Dmel_CG13213	Drosophila melanogaster				IPR001810:Cyclin-like F-box,IPR018483:Carbohydrate kinase, FGGY, conserved site,		PIRSF036853:conserved protein with F-box/LRR-repeat, AtFBL11 type,	SM00256:FBOX,	complete proteome,	
1625430_at	Dmel_CG14022	Drosophila melanogaster			GO:0003998~acylphosphatase activity,	IPR001792:Acylphosphatase,IPR001792:Acylphosphatase-like,	dme00620:Pyruvate metabolism,	PIRSF001266:acylphosphatase,		complete proteome,hydrolase,	
1631385_at	Dmel_CG2889	Drosophila melanogaster			GO:0008270~zinc ion binding,GO:0043167~ion						

binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR007087:Zinc finger, C2H2-type,IPR012934:Zinc finger, AD-type,IPR015880:Zinc finger, C2H2-like, SM00355:ZnF_C2H2, complete proteome,

1624717_s_at Dmel_CG32647 Drosophila melanogaster IPR001007:von Willebrand factor, type C,IPR002052:N-6 adenine-specific DNA methylase, conserved site, SM00214:VWC, complete proteome,methyltransferase,transferase,

1635581_at Dmel_CG8300 Drosophila melanogaster complete proteome,

1637193_at Eukaryotic translation initiation factor 3 subunit C Drosophila melanogaster GO:0006412~translation,GO:0006413~translational initiation, GO:0005829~cytosol,GO:0005852~eukaryotic translation initiation factor 3 complex, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR000717:Proteasome component region PCI,IPR008905:Eukaryotic translation initiation factor 3 subunit 8, N-terminal,IPR011991:Winged helix repressor DNA-binding, PIRSF017001:eukaryotic translation initiation factor 3, subunit 8, SM00088:PINT, complete proteome,cytoplasm,Initiation factor,phosphoprotein,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit C,domain:PCI,modified residue,sequence conflict,

1631527_at Eukaryotic translation initiation factor 3 subunit L Drosophila melanogaster GO:0006412~translation, GO:0003743~translation initiation factor activity,GO:0008135~translation factor activity, nucleic acid binding, IPR019382:RNA polymerase I-associated factor PAF67, complete proteome,cytoplasm,Initiation factor,protein biosynthesis, chain:Eukaryotic translation initiation factor 3 subunit L,

1641126_at Protein LSM12 homolog A Drosophila melanogaster IPR019181:RNA-processing, Lsm domain, complete proteome, chain:Protein LSM12 homolog A,

1625840_at Uncharacterized protein CG12001 Drosophila melanogaster complete proteome,rna editing, chain:Uncharacterized protein CG12001,sequence variant,

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C

-D

+D

Probe sets:

1624185_at
1628296_at
1628598_s_at
1628938_at
1633463_s_at
1636337_s_at
1636762_a_at
1637778_a_at
1638335_at
1640241_at
1640332_at

Functional annotation table:

ID Gene Name Species COG_ONTOLOGY GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SMART SP_PIR_KEYWORDS UP_SEQ_FEATURE

1624185_at Dmel_CG1041 Drosophila melanogaster GO:0005739~mitochondrion,GO:0005777~peroxisome,GO:0042579~microbody, GO:0004092~carnitine O-acetyltransferase activity,GO:0008374~O-acyltransferase activity,GO:0016406~carnitine O-acyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016413~O-acetyltransferase activity, IPR000542:Acyltransferase ChoActase/COT/CPT, PIRSF000430:carnitine O-acetyltransferase, Acyltransferase,complete proteome,transferase,

1628938_at Dmel_CG10882 Drosophila melanogaster GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0034613~cellular protein localization,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0070727~cellular macromolecule localization, GO:0005794~Golgi apparatus,GO:0005811~lipid particle,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane,

GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0008270~zinc ion binding,GO:0017171~serine hydrolase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000183:Orn/DAP/Arg decarboxylase 2,IPR000276:7TM GPCR, rhodopsin-like,IPR006031:XYPPX repeat,IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, complete proteome,hydrolase,protein transport,transport,

1628598_s_at Dmel_CG1250 Drosophila melanogaster Intracellular trafficking and secretion, GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval development,GO:0003002~regionalization,GO:0006886~intracellular protein transport,GO:0006888~ER to Golgi vesicle-mediated transport,GO:0007030~Golgi organization,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based cuticle,GO:0007592~protein-based cuticle development,GO:0008104~protein localization,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0010721~negative regulation of cell development,GO:0010769~regulation of cell morphogenesis involved in differentiation,GO:0010975~regulation of neuron projection development,GO:0015031~protein transport,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle process,GO:0022604~regulation of cell morphogenesis,GO:0031344~regulation of cell projection organization,GO:0031345~negative regulation of cell projection organization,GO:0034613~cellular protein localization,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting,GO:0045184~establishment of protein localization,GO:0045596~negative regulation of cell differentiation,GO:0045664~regulation of neuron differentiation,GO:0046907~intracellular transport,GO:0048193~Golgi vesicle transport,GO:0048814~regulation of dendrite morphogenesis,GO:0050767~regulation of neurogenesis,GO:0050768~negative regulation of neurogenesis,GO:0050773~regulation of dendrite development,GO:0050774~negative regulation of dendrite morphogenesis,GO:0051129~negative regulation of cellular component organization,GO:0051960~regulation of nervous system development,GO:0060284~regulation of cell development,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0012505~endomembrane system,GO:0012506~vesicle membrane,GO:0012507~ER to Golgi transport vesicle membrane,GO:0016023~cytoplasmic membrane-bounded vesicle,GO:0030117~membrane coat,GO:0030120~vesicle coat,GO:0030127~COPII vesicle coat,GO:0030133~transport vesicle,GO:0030134~ER to Golgi transport vesicle,GO:0030135~coated vesicle,GO:0030658~transport vesicle membrane,GO:0030659~cytoplasmic vesicle membrane,GO:0030662~coated vesicle membrane,GO:0031090~organelle membrane,GO:0031410~cytoplasmic vesicle,GO:0031982~vesicle,GO:0031988~membrane-bounded vesicle,GO:0044431~Golgi apparatus part,GO:0044433~cytoplasmic vesicle part,GO:0048475~coated membrane, GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding ,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR006895:Zinc finger, Sec23/Sec24-type,IPR006896:Sec23/Sec24 trunk region,IPR006900:Sec23/Sec24 helical region,IPR007123:Gelsolin region,IPR012990:Sec23/Sec24 beta-sandwich, PIRSF003206:SEC23 protein, protein transport,transport,

1638335_at Dmel_CG18493 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR008758:Peptidase S28, PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2, complete proteome,

1640332_at Dmel_CG6972 Drosophila melanogaster complete proteome,

1640241_at Dmel_CG7008 Drosophila melanogaster GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0010629~negative regulation of gene expression,GO:0016246~RNA interference,GO:0016441~posttranscriptional gene silencing,GO:0016458~gene silencing,GO:0031047~gene silencing by RNA,GO:0035194~posttranscriptional gene silencing by RNA,GO:0040029~regulation of gene expression, epigenetic, GO:0005811~lipid particle,GO:0016442~RNA-induced silencing complex,GO:0030529~ribonucleoprotein complex,GO:0031332~RNAi effector complex, GO:0003712~transcription cofactor activity,GO:0003713~transcription coactivator activity,GO:0008134~transcription factor binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity, IPR002999:Tudor domain,IPR006021:Staphylococcal nuclease (SNase-like),IPR008191:Maternal tudor protein,IPR016685:RNA-induced silencing complex, nuclease component Tudor-SN,IPR018351:Tudor subgroup, PIRS F017179:RISC-Tudor-SN, SM00318:SNc,SM00333:TUDOR, complete proteome,hydrolase, 1637778_a_at Probable glucosamine 6-phosphate N-acetyltransferase Drosophila melanogaster GO:0004343~glucosamine 6-phosphate N-acetyltransferase activity,GO:0008080~N-acetyltransferase activity,GO:0016407~acetyltransferase activity,GO:0016410~N-acyltransferase activity,GO:0042802~identical protein binding, IPR000182:GCN5-related N-acetyltransferase,IPR016181:Acyl-CoA N-acyltransferase, dme00520:Amino sugar and nucleotide sugar metabolism, Acyltransferase,complete proteome,transferase, binding site:Substrate,chain:Probable glucosamine 6-phosphate N- acetyltransferase,domain:N-acetyltransferase,region of interest:Acetyl-CoA binding,region of interest:Substrate binding,

1633463_s_at Putative polypeptide N-acetylgalactosaminyltransferase 9 Drosophila melanogaster GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, alternative splicing,calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:Putative polypeptide N- acetylgalactosaminyltransferase 9,compositionally biased region:Gly-rich,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...) ,region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,splice variant,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1628296_at polypeptide GalNAc transferase 4 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransferase 4,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636337_s_at polypeptide GalNAc transferase 6 Drosophila melanogaster GO:0009311~oligosaccharide metabolic process,GO:0009312~oligosaccharide biosynthetic process,GO:0016051~carbohydrate biosynthetic process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity,GO:0005509~calcium ion binding,GO:0005529~sugar binding,GO:0008376~acetylgalactosaminyltransferase activity,GO:0030145~manganese ion binding,GO:0030246~carbohydrate binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR000772:Ricin B lectin,IPR001173:Glycosyl transferase, family 2, dme00512:O-Glycan biosynthesis, SM00458:RICIN, calcium,complete proteome,disulfide bond,glycoprotein,glycosyltransferase,golgi apparatus,Lectin,manganese,membrane,Signal-anchor,transferase,transmembrane, chain:N-acetylgalactosaminyltransfer ase 6,disulfide bond,domain:Ricin B-type lectin,glycosylation site:N-linked (GlcNAc...),region of interest:Catalytic subdomain A,region of interest:Catalytic subdomain B,sequence conflict,topological domain:Cytoplasmic,topological domain:Lumenal,transmembrane region,

1636762_a_at supercoiling factor Drosophila melanogaster Signal transduction mechanisms / Cytoskeleton / Cell division and chromosome partitioning / General function prediction only, GO:0006325~chromatin organization,GO:0007549~dosage compensation,GO:0009047~dosage compensation, by hyperactivation of X chromosome,GO:0040029~regulation of gene expression, epigenetic,GO:0051276~chromosome organization, GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0003677~DNA binding,GO:0003916~DNA topoisomerase activity,GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2, SM00054:EFh, calcium,

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-D

+D

C

Probe sets:

1622935_at
1623032_at
1623766_at
1623783_at
1623928_at
1624158_at
1624699_s_at
1624840_at
1624888_at
1624984_at
1625027_a_at
1625375_at
1625814_at
1626075_at
1626222_at
1626503_at
1626811_at
1627078_at
1627459_at
1627888_at
1628376_x_at
1628634_at
1629391_at
1629476_at
1629718_at
1629955_at
1630131_at
1631200_at
1631627_at
1631648_at
1631877_a_at
1631909_at
1631998_at
1632318_at
1632374_at
1632583_at
1633810_at
1634575_at
1634697_at
1635305_s_at
1635821_at
1635983_a_at
1635987_at
1636014_at
1636131_at
1636711_at
1636829_at
1636921_at
1637124_at
1637547_at
1638217_at
1638224_at
1638272_at
1638350_at
1638970_at
1639071_a_at
1639152_at
1639341_at
1639993_at
1640824_at
1640826_at
1641201_at
1641568_a_at

Functional annotation table:

ID	Gene Name	Species	COG_ONTOLOGY	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE

1624840_at Accessory gland-specific peptide 29AB Drosophila melanogaster GO:0007320~insemination,GO:0007321~sperm displacement,GO:0007610~behavior,GO:0007618~mating,GO:0007620~copulation,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0045297~post-mating behavior,GO:0046692~sperm competition,GO:0046693~sperm storage,GO:0048609~reproductive process in a multicellular organism, GO:0005576~extracellular region, GO:0005179~hormone activity,GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like,IPR018378:C-type lectin, conserved site, SM00034:CLECT, behavior,complete proteome,disulfide bond,glycoprotein,Lectin,polymorphism,Secreted,signal, chain:Accessory gland protein Acp29AB,disulfide bond,domain:C-type lectin,glycosylation site:N-linked (GlcNAc...),sequence variant,signal peptide,

1631200_at Accessory gland-specific peptide 32CD Drosophila melanogaster GO:0007610~behavior,GO:0007617~mating behavior,GO:0007618~mating,GO:0007621~negative regulation of female receptivity,GO:0019098~reproductive behavior,GO:0032504~multicellular organism reproduction,GO:0033057~reproductive behavior in a multicellular organism,GO:0045297~post-mating behavior,GO:0045434~negative regulation of female receptivity, post-mating,GO:0045924~regulation of female receptivity,GO:0046008~regulation of female receptivity, post-mating,GO:0048609~reproductive process in a multicellular organism,GO:0051705~behavioral interaction between organisms,GO:0060180~female mating behavior, GO:0005576~extracellular region, GO:0005179~hormone activity, alternative initiation,behavior,complete proteome,polymorphism,Secreted,signal, chain:Accessory gland protein Acp32CD,compositionally biased region:Arg-rich,compositionally biased region:Gly-rich,sequence variant,signal peptide,splice variant,

1628634_at Adenosine 3'-phospho 5'-phosphosulfate transporter 2 Drosophila melanogaster GO:0015858~nucleoside transport,GO:0015860~purine nucleoside transport,GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport,GO:0046963~3'-phosphoadenosine 5'-phosphosulfate transport, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0005337~nucleoside transmembrane transporter activity,GO:0015211~purine nucleoside transmembrane transporter activity,GO:0015932~nucleobase, nucleoside, nucleotide and nucleic acid transmembrane transporter activity,GO:0046964~3'-phosphoadenosine 5'-phosphosulfate transmembrane transporter activity, IPR013657:UAA transporter, PIRSF017416:solute carrier family 35, member B type,PIRSF500839:solute carrier family 35, member B3, complete proteome,developmental protein,glycoprotein,golgi apparatus,membrane,phosphoprotein,transmembrane,transport, chain:Adenosine 3'-phospho 5'-phosphosulfate transporter 2,glycosylation site:N-linked (GlcNAc...),modified residue,transmembrane region,

1624699_s_at	Beadex	Drosophila melanogaster	GO:0002165~instar larval or pupal development,GO:0003002~regionalization,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007389~pattern specification process,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0007610~behavior,GO:0007622~rhythmic behavior,GO:0007623~circadian rhythm,GO:0007626~locomotory behavior,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0010033~response to organic substance,GO:0010324~membrane invagination,GO:0014070~response to organic cyclic substance,GO:0014073~response to tropane,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0035107~appendage morphogenesis,GO:0035108~limb morphogenesis,GO:0035110~leg morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035218~leg disc development,GO:0035220~wing disc development,GO:0035282~segmentation,GO:0035285~appendage segmentation,GO:0035286~leg segmentation,GO:0042220~response to cocaine,GO:0043279~response to alkaloid,GO:0045475~locomotor rhythm,GO:0048511~rhythmic process,GO:0048512~circadian behavior,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0060173~limb development,	GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,	IPR001781:Zinc finger, LIM-type,	SM00132:LIM,	complete proteome,LIM domain,metal-binding,zinc,
1636131_at	DNA ligase III	Drosophila melanogaster	GO:0006259~DNA metabolic process,GO:0006260~DNA replication,GO:0006281~DNA repair,GO:0006310~DNA recombination,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,	GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003677~DNA binding,GO:0003909~DNA ligase activity,GO:0003910~DNA ligase (ATP) activity,GO:0005524~ATP binding,GO:0016886~ligase activity, forming phosphoric ester bonds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding,	IPR000977:ATP-dependent DNA ligase,IPR001357:BRCT,IPR012308:DNA ligase, N-terminal,IPR012309:ATP dependent DNA ligase, C-terminal,IPR012310:ATP dependent DNA ligase, central,IPR012340:Nucleic acid-binding, OB-fold,IPR016059:ATP-dependent DNA		

ligase, conserved site, dme03410:Base excision repair, SM00292:BRCT, atp-binding,complete proteome,DNA damage,dna recombination,dna repair,dna replication,ligase,nucleotide-binding,

1639071_a_at Death related ced-3/Nedd2-like protein Drosophila melanogaster GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003006~reproductive developmental process,GO:0006508~proteolysis,GO:0006915~apoptosis,GO:0006952~defense response,GO:0006955~immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0008219~cell death,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0012501~programmed cell death,GO:0016265~death,GO:0016485~protein processing,GO:0019953~sexual reproduction,GO:0031328~positive regulation of cellular biosynthetic process,GO:0032504~multicellular organism reproduction,GO:0042742~defense response to bacterium,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0050829~defense response to Gram-negative bacterium,GO:0051604~protein maturation,GO:0051605~protein maturation by peptide bond cleavage, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008047~enzyme activator activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO:0016504~peptidase activator activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001309:Peptidase C14, ICE, catalytic subunit p20,IPR002138:Peptidase C14, caspase non-catalytic subunit p10,IPR002398:Peptidase C14, caspase precursor p45,IPR011600:Peptidase C14, caspase catalytic,IPR015917:Peptidase C14, caspase precursor p45, core,IPR016129:Peptidase C14, ICE, catalytic subunit p20, active site, SM00115:CASc, alternative splicing,Apoptosis,complete proteome,cytoplasm,hydrolase,immune response,Protease,thiol protease,zymogen, chain:Caspase-8 subunit p10,chain:Caspase-8 subunit p15,sequence conflict,splice variant, 1634575_at Dmel_CG11037 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, SM00020:Tryp_SPc, complete proteome,hydrolase,

1640824_at Dmel_CG11306 Drosophila melanogaster GO:0000026~alpha-1,2-mannosyltransferase activity,GO:0000030~mannosyltransferase activity, IPR001296:Glycosyl transferase, group 1, dme00510:N-Glycan biosynthesis, complete proteome,glycosyltransferase,transferase,

1626075_at Dmel_CG11664 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,

1641568_a_at Dmel_CG11790 Drosophila melanogaster GO:0019725~cellular homeostasis,GO:0042592~homeostatic process,GO:0045454~cell redox homeostasis, IPR012335:Thioredoxin fold,IPR013766:Thioredoxin domain, complete proteome,

1635987_at Dmel_CG12116 Drosophila melanogaster Secondary metabolites biosynthesis, transport, and catabolism / General function prediction only, GO:0055114~oxidation reduction, GO:0004757~sepiapterin reductase activity, IPR002198:Short-chain dehydrogenase/reductase SDR,IPR016040:NAD(P)-binding domain, dme00790:Folate biosynthesis, complete proteome,oxidoreductase,

1632318_at Dmel_CG12773 Drosophila melanogaster GO:0006865~amino acid transport,GO:0015837~amine transport,GO:0015849~organic acid transport,GO:0046942~carboxylic acid transport, GO:0005275~amine transmembrane transporter activity,GO:0008509~anion transmembrane transporter activity,GO:0008511~sodium:potassium:chloride symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015296~anion:cation symporter activity,GO:0015377~cation:chloride symporter activity, IPR004841:Amino acid permease-associated region, complete proteome,

1622935_at Dmel_CG12828 Drosophila melanogaster complete proteome,

1629955_at	Dmel_CG13309	Drosophila melanogaster	GO:0005976~polysaccharide metabolic process,GO:0006022~aminoglycan metabolic process,GO:0006030~chitin metabolic process, GO:0005576~extracellular region, GO:0001871~pattern binding,GO:0008061~chitin binding,GO:0030246~carbohydrate binding,GO:0030247~polysaccharide binding, IPR002557:Chitin binding protein, peritrophin-A, SM00494:ChtBD2, complete proteome,
1632583_at	Dmel_CG13539	Drosophila melanogaster	IPR009961:Protein of unknown function DUF1487, complete proteome,
1628376_x_at	Dmel_CG13947	Drosophila melanogaster	complete proteome,
1623766_at	Dmel_CG14054	Drosophila melanogaster	complete proteome,
1624158_at	Dmel_CG14481	Drosophila melanogaster	complete proteome,
1638970_at	Dmel_CG14543	Drosophila melanogaster	IPR019398:Pre-rRNA-processing protein TSR2, conserved region, complete proteome,
1639341_at	Dmel_CG14971	Drosophila melanogaster	GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, IPR004853:Protein of unknown function DUF250, complete proteome,membrane,transmembrane,
1629391_at	Dmel_CG1656	Drosophila melanogaster	GO:0005529~sugar binding,GO:0005534~galactose binding,GO:0030246~carbohydrate binding,GO:0048029~monosaccharide binding, IPR001304:C-type lectin,IPR016186:C-type lectin-like, SM00034:CLECT, complete proteome,
1629718_at	Dmel_CG16727	Drosophila melanogaster	GO:0015101~organic cation transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1, complete proteome,transmembrane,
1625027_a_at	Dmel_CG17035	Drosophila melanogaster	GO:0006644~phospholipid metabolic process,GO:0016042~lipid catabolic process,GO:0019637~organophosphate metabolic process, GO:0005576~extracellular region, GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004623~phospholipase A2 activity,GO:0005509~calcium ion binding,GO:0016298~lipase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR010711:Phospholipase A2, group XII secretory,IPR013090:Phospholipase A2, active site, dme00564:Glycerophospholipid

									metabolism,dme00565:Ether lipid metabolism,dme00590:Arachidonic acid metabolism,dme00591:Linoleic acid metabolism,dme00592:alpha-Linolenic acid metabolism,	complete proteome,hydrolase,
1639152_at	Dmel_CG18243	Drosophila melanogaster	GO:0000902~cell morphogenesis,GO:0000904~cell morphogenesis involved in differentiation,GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006928~cell motion,GO:0007409~axonogenesis,GO:0007411~axon guidance,GO:0016311~dephosphorylation,GO:0030030~cell projection organization,GO:0030182~neuron differentiation,GO:0031175~neuron projection development,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0048666~neuron development,GO:0048667~cell morphogenesis involved in neuron differentiation,GO:0048812~neuron projection morphogenesis,GO:0048858~cell projection morphogenesis,		GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity,	IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type,IPR000387:Dual-specific/protein-tyrosine phosphatase, conserved region,IPR000387:Protein-tyrosine phosphatase,IPR000572:Oxidoreductase, molybdopterin binding,IPR003961:Fibronectin, type III,IPR008957:Fibronectin, type III-like fold,IPR016130:Protein-tyrosine phosphatase, active site,		SM00060:FN3,SM00194:PTPc,		hydrolase,
1626503_at	Dmel_CG2254	Drosophila melanogaster	GO:0055114~oxidation reduction,	GO:0005811~lipid particle,		IPR002198:Short-chain dehydrogenase/reductase SDR,IPR002347:Glucose/ribitol dehydrogenase,IPR016040:NAD(P)-binding domain,	PIRSF000126:11beta-hydroxysteroid dehydrogenase,			complete proteome,oxidoreductase,
1623032_at	Dmel_CG2336	Drosophila melanogaster	GO:0055114~oxidation reduction,			IPR009961:Protein of unknown function DUF1487,				complete proteome,oxidoreductase,
1636711_at	Dmel_CG31265	Drosophila melanogaster	GO:0006508~proteolysis,		GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site,	PIRSF001135:trypsin,	SM00020:Tryp_SPc,		complete proteome,hydrolase,Protease,Serine protease,
1636014_at	Dmel_CG31419	Drosophila melanogaster								complete proteome,

1636829_at Dmel_CG31902 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR000215:Protease inhibitor I4, serpin, SM00093:SERPIN, complete proteome,

1625375_at Dmel_CG32201 Drosophila melanogaster GO:0006575~cellular amino acid derivative metabolic process,GO:0018208~peptidyl-proline modification,GO:0018401~peptidyl-proline hydroxylation to 4-hydroxy-L-proline,GO:0019471~4-hydroxyproline metabolic process,GO:0055114~oxidation reduction, GO:0005783~endoplasmic reticulum,GO:0016222~procollagen-proline 4-dioxygenase complex,GO:0044432~endoplasmic reticulum part, GO:0004656~procollagen-proline 4-dioxygenase activity,GO:0005506~iron ion binding,GO:0016706~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors,GO:0019798~procollagen-proline dioxygenase activity,GO:0019842~vitamin binding,GO:0031406~carboxylic acid binding,GO:0031418~L-ascorbic acid binding,GO:0031543~peptidyl-proline dioxygenase activity,GO:0031545~peptidyl-proline 4-dioxygenase activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR005123:Oxoglutarate and iron-dependent oxygenase,IPR006620:Prolyl 4-hydroxylase, alpha subunit, dme00330:Arginine and proline metabolism, SM00702:P4Hc, oxidoreductase,

1638224_at Dmel_CG32250 Drosophila melanogaster GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,GO:0005779~integral to peroxisomal membrane,GO:0016021~integral to membrane,GO:0019866~organelle inner membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031231~intrinsic to peroxisomal membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0031903~microbody membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0042579~microbody,GO:0044429~mitochondrial part,GO:0044438~microbody part,GO:0044439~peroxisomal part, IPR001993:Mitochondrial substrate carrier,IPR002113:Adenine nucleotide translocator 1,IPR018108:Mitochondrial substrate/solute carrier, complete proteome,membrane,repeat,transmembrane,transport,

1634697_at Dmel_CG32667 Drosophila melanogaster IPR001007:von Willebrand factor, type C, SM00214:VWC, complete proteome, 1640826_at Dmel_CG3947 Drosophila melanogaster GO:0007031~peroxisome organization, IPR013919:Peroxisome membrane protein, Pex16, complete proteome,

1626222_at Dmel_CG4812 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, PIRSF001135:trypsin, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease,

1641201_at Dmel_CG5267 Drosophila melanogaster IPR013032:EGF-like region, conserved site,IPR018453:Protease inhibitor I8, cysteine-rich trypsin inhibitor-like subgroup, complete proteome,

1631627_at Dmel_CG5335 Drosophila melanogaster GO:0005529~sugar binding,GO:0030246~carbohydrate binding, IPR001079:Galectin, carbohydrate recognition domain,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, SM00276:GLECT, complete proteome,Lectin,

1626811_at Dmel_CG5510 Drosophila melanogaster IPR005052:Legume-like lectin,IPR013320:Concanavalin A-like lectin/glucanase, subgroup, PIRSF017635:L-type lectin, animal type,PIRSF500265:vesicular integral-membrane protein VIP36, complete proteome,

1623928_at Dmel_CG5910 Drosophila melanogaster complete proteome,

1630131_at Dmel_CG6567 Drosophila melanogaster GO:0004091~carboxylesterase activity,GO:0004620~phospholipase activity,GO:0004622~lysophospholipase activity,GO:0016298~lipase activity, IPR003140:Phospholipase/carboxylesterase, complete proteome,hydrolase,

1627888_at Dmel_CG6672 Drosophila melanogaster GO:0006811~ion transport,GO:0006812~cation transport, GO:0005385~zinc ion transmembrane transporter activity,GO:0015082~di-, tri-valent inorganic cation transmembrane transporter activity,GO:0022890~inorganic cation transmembrane transporter activity,GO:0046873~metal ion transmembrane transporter activity,GO:0046915~transition metal ion transmembrane transporter activity, IPR002524:Cation efflux protein, complete proteome, 1632374_at Dmel_CG6769 Drosophila melanogaster GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR003604:Zinc finger, U1-type,IPR007087:Zinc finger, C2H2-type,IPR015880:Zinc finger, C2H2-like, SM00355:ZnF_C2H2,SM00451:ZnF_U1, complete proteome,

1637124_at Dmel_CG6773 Drosophila melanogaster GO:0002164~larval development,GO:0002165~instar larval or pupal development,GO:0002168~instar larval development,GO:0003002~regionalization,GO:0006900~membrane budding,GO:0007389~pattern specification process,GO:0007591~molting cycle, chitin-based cuticle,GO:0007592~protein-based cuticle development,GO:0008363~larval chitin-based cuticle development,GO:0009791~post-embryonic development,GO:0016044~membrane organization,GO:0016050~vesicle organization,GO:0016192~vesicle-mediated transport,GO:0018988~molting cycle, protein-based cuticle,GO:0022404~molting cycle process,GO:0035017~cuticle pattern formation,GO:0035293~chitin-based larval cuticle pattern formation,GO:0040003~chitin-based cuticle development,GO:0042303~molting cycle,GO:0042335~cuticle development,GO:0042336~protein-based cuticle development during molting,GO:0042337~chitin-based cuticle development during molting, IPR001680:WD40 repeat,IPR015943:WD40/YVTN repeat-like,IPR017986:WD40 repeat, region,IPR019781:WD40 repeat, subgroup,IPR019782:WD40 repeat 2, SM00320:WD40, complete proteome,repeat,wd repeat,

1624888_at Dmel_CG7081 Drosophila melanogaster GO:0007031~peroxisome organization, GO:0005777~peroxisome,GO:0005778~peroxisomal membrane,GO:0031090~organelle membrane,GO:0031903~microbody membrane,GO:0042579~microbody,GO:0044438~microbody part,GO:0044439~peroxisomal part, GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR001841:Zinc finger, RING-type,IPR006845:Pex, N-terminal,IPR017907:Zinc finger, RING-type, conserved site,IPR018957:Zinc finger, C3HC4 RING-type, SM00184:RING, complete proteome,metal-binding,zinc,zinc-finger,

1629476_at Dmel_CG7542 Drosophila melanogaster GO:0006508~proteolysis, GO:0004175~endopeptidase activity,GO:0004252~serine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR001254:Peptidase S1 and S6, chymotrypsin/Hap,IPR001314:Peptidase S1A, chymotrypsin,IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site, SM00020:Tryp_SPc, complete proteome,hydrolase,Protease,Serine protease, 1624984_at Dmel_CG8021 Drosophila melanogaster GO:0000166~nucleotide binding,GO:0003723~RNA binding,GO:0003729~mRNA binding, IPR000504:RNA recognition motif, RNP-1,IPR012677:Nucleotide-binding, alpha-beta plait, SM00360:RRM, complete proteome,

1637547_at Dmel_CG8199 Drosophila melanogaster Energy production and conversion, GO:0006637~acyl-CoA metabolic process,GO:0006732~coenzyme metabolic process,GO:0009108~coenzyme biosynthetic process,GO:0046949~acyl-CoA biosynthetic process,GO:0051186~cofactor metabolic process,GO:0051188~cofactor biosynthetic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0017086~3-methyl-2-oxobutanoate dehydrogenase (lipoamide) complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003863~3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity,GO:0016624~oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, IPR001017:Dehydrogenase, E1 component, dme00280:Valine, leucine and isoleucine degradation, PIRSF000152:pyruvate dehydrogenase (lipoamide) alpha chain, complete proteome,oxidoreductase,

1623783_at Dmel_CG8489 Drosophila melanogaster GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007283~spermatogenesis,GO:0007286~spermatid development,GO:0007291~sperm individualization,GO:0007349~cellularization,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048232~male gamete generation,GO:0048515~spermatid differentiation,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, complete proteome,developmental protein,differentiation,glycoprotein,spermatogenesis, chain:Male-specific protein scotti,glycosylation site:N-linked (GlcNAc...),

1633810_at Dmel_CG8793 Drosophila melanogaster complete proteome,

1625814_at Dymeclin Drosophila melanogaster IPR019142:Dymeclin, complete proteome,lipoprotein,myristate,phosphoprotein, chain:Dymeclin,lipid moiety-binding region:N-myristoyl glycine,modified residue,

1631877_a_at Histidyl-tRNA synthetase Drosophila melanogaster Translation, ribosomal structure and biogenesis, GO:0006399~tRNA metabolic process,GO:0006412~translation,GO:0006418~tRNA aminoacylation for protein translation,GO:0006427~histidyl-tRNA aminoacylation,GO:0034660~ncRNA metabolic process,GO:0043038~amino acid activation,GO:0043039~tRNA aminoacylation, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004812~aminoacyl-tRNA ligase activity,GO:0004821~histidine-tRNA ligase activity,GO:0005524~ATP binding,GO:0016875~ligase activity, forming carbon-oxygen bonds,GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000738:WHEP-TRS,IPR002314:Aminoacyl-tRNA synthetase, class II (G, H, P and S), conserved region,IPR004154:Anticodon-binding,IPR004516 :Histidyl-tRNA synthetase, class IIa,IPR006195:Aminoacyl-tRNA synthetase, class II, conserved region,IPR009068:S15/NS1, RNA-binding,IPR015807:Histidyl-tRNA synthetase, class IIa, subgroup, dme00970:Aminoacyl-tRNA biosynthesis, PIRSF001549:His-tRNA_synth,PIRSF001549:histidyl-tRNA synthetase, Aminoacyl-tRNA synthetase,complete proteome,ligase,

1635821_at Mediator complex subunit 28 Drosophila melanogaster GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0045449~regulation of transcription,GO:0051252~regulation of RNA metabolic process, GO:0005654~nucleoplasm,GO:0016592~Srb-mediator complex,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043233~organelle lumen,GO:0044451~nucleoplasm part,GO:0070013~intracellular organelle lumen, GO:0003702~RNA polymerase II transcription factor activity,GO:0016251~general RNA polymerase II transcription factor activity,GO:0016455~RNA polymerase II transcription mediator activity,GO:0030528~transcription regulator activity, activator,coiled coil,complete proteome,nucleus,Transcription,transcription regulation,chain:Mediator of RNA polymerase II transcription subunit 28,compositionally biased region:Pro-rich,

1627459_at N(6)-adenine-specific DNA methyltransferase 2 homolog Drosophila melanogaster GO:0006730~one-carbon metabolic process,GO:0032259~methylation, IPR002052:N-6 adenine-specific DNA methylase, conserved site,IPR019369:N-6 adenine-specific DNA methylase-related, eukaryotic, complete proteome,methyltransferase,transferase, chain:N(6)-adenine-specific DNA methyltransferase 2 homolog,sequence conflict,

1627078_at Organic anion transporting polypeptide 58Dc Drosophila melanogaster GO:0006811~ion transport,GO:0006820~anion transport,GO:0015711~organic anion transport, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane, GO:0008509~anion transmembrane transporter activity,GO:0008514~organic anion transmembrane transporter activity,GO:0015347~sodium-independent organic anion transmembrane transporter activity, IPR002350:Proteinase inhibitor I1, Kazal,IPR004156:Organic anion transporter polypeptide OATP,IPR011497:Protease inhibitor, Kazal-type, SM00280:KAZAL, 1638217_at Probable dolichol-phosphate mannosyltransferase Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005783~endoplasmic reticulum, GO:0000030~mannosyltransferase activity,GO:0004582~dolichyl-phosphate beta-D-mannosyltransferase activity, IPR001173:Glycosyl transferase, family 2, dme00510:N-Glycan biosynthesis, PIRSF005860:dolichyl-phosphate beta-D-mannosyltransferase, complete proteome,endoplasmic reticulum,glycosyltransferase,transferase, chain:Probable dolichol-phosphate mannosyltransferase,

1638350_at Probable ribosome production factor 1 Drosophila melanogaster GO:0006364~rRNA processing,GO:0006396~RNA processing,GO:0016072~rRNA metabolic process,GO:0022613~ribonucleoprotein complex biogenesis,GO:0034470~ncRNA processing,GO:0034660~ncRNA metabolic process,GO:0042254~ribosome biogenesis, GO:0005730~nucleolus,GO:0031974~membrane-enclosed lumen,GO:0031981~nuclear lumen,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0043233~organelle lumen,GO:0070013~intracellular organelle lumen, GO:0003723~RNA binding,GO:0019843~rRNA binding, IPR007109:Brix domain, PIRSF015949:U3 small nucleolar ribonucleoprotein (snoRNP) complex, Imp4p subunit, complete proteome,nucleus,ribosome biogenesis,rna-binding,rrna processing,rrna-binding, chain:Probable ribosome production factor 1,domain:Brix,region of interest:RNA-binding,

1639993_at Protein RFT1 homolog Drosophila melanogaster GO:0006869~lipid transport,GO:0010876~lipid localization, GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0005319~lipid transporter activity, IPR007594:RFT1, dme00510:N-Glycan biosynthesis, complete proteome,membrane,transmembrane, chain:Protein RFT1 homolog,transmembrane region,

1631648_at Signal recognition particle 9 kDa protein Drosophila melanogaster GO:0006417~regulation of translation,GO:0006448~regulation of translational elongation,GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0009890~negative regulation of biosynthetic process,GO:0010558~negative regulation of macromolecule biosynthetic process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010608~posttranscriptional regulation of gene expression,GO:0015031~protein transport,GO:0017148~negative regulation of translation,GO:0031327~negative regulation of cellular biosynthetic process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein

			localization,GO:0045900~negative regulation of translational elongation,GO:0046907~intracellular transport,GO:0051248~negative regulation of protein metabolic process,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0003729~mRNA binding,GO:0008312~7S RNA binding, IPR008832:Signal recognition particle, SRP9 subunit,IPR009018:Signal recognition particle, SRP9/SRP14 subunit, dme03060:Protein export, PIRSF017029:signal recognition particle, 9 kDa protein,PIRSF017029:Signal_recog_particle_SRP9, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 9 kDa protein,
1638272_at	Signal recognition particle protein 19	Drosophila melanogaster	GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0008104~protein localization,GO:0015031~protein transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization, GO:0005786~signal recognition particle, endoplasmic reticulum targeting,GO:0030529~ribonucleoprotein complex,GO:0048500~signal recognition particle, GO:0003723~RNA binding,GO:0008312~7S RNA binding, IPR002778:Signal recognition particle, SRP19 subunit, dme03060:Protein export, PIRSF006433:Signal recognition particle 19 kDa protein,PIRSF500827:Eukaryota signal recognition particle 19 kDa protein, complete proteome,cytoplasm,ribonucleoprotein,rna-binding,signal recognition particle, chain:Signal recognition particle 19 kDa protein,compositionally biased region:Poly-Gly,region of interest:Basic region, potentially involved in RNA-binding,sequence conflict,
1635305_s_at	Trithorax-like	Drosophila melanogaster	GO:0000087~M phase of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0002165~instar larval or pupal development,GO:0006323~DNA packaging,GO:0006325~chromatin organization,GO:0006333~chromatin assembly or disassembly,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO:0006357~regulation of transcription from RNA polymerase II promoter,GO:0006461~protein complex assembly,GO:0007049~cell cycle,GO:0007067~mitosis,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007444~imaginal disc development,GO:0007472~wing disc morphogenesis,GO:0007476~imaginal disc-derived wing morphogenesis,GO:0007549~dosage compensation,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0009791~post-embryonic development,GO:0009886~post-embryonic

morphogenesis,GO:0009891~positive regulation of biosynthetic process,GO:0010557~positive regulation of macromolecule biosyntheti c process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene expression,GO:0016568~chromatin modification,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031497~chromatin assembly,GO:0032504~multicellular organism reproduction,GO:0033301~cell cycle comprising mitosis without cytokinesis,GO:0035107~appendage morphogenesis,GO:0035114~imaginal disc-derived appendage morphogenesis,GO:0035120~post-embryonic appendage morphogenesis,GO:0035186~syncytial blastoderm mitotic cell cycle,GO:0035220~wing disc development,GO:0040029~regulation of gene expression, epigenetic,GO:0043933~macromolecular complex subunit organization,GO:0045448~mitotic cell cycle, embryonic,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0048285~organelle fission,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048707~instar larval or pupal morphogenesis,GO:0048736~appendage development,GO:0048737~imaginal disc-derived appendage development,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process,GO:0051259~protein oligomerization,GO:0051276~chromosome organization,GO:0051301~cell division,GO:0065003~macromolecular complex assembly,GO:0070271~protein complex biogenesis, GO:0000775~chromosome, centromeric region,GO:0000785~chromatin,GO:0000791~euchromatin,GO:0000792~heterochromatin,GO:0005694~chromosome,GO:0005700~polytene chromosome,GO:0005721~centromeric heterochromatin,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membr ane-bounded organelle,GO:0044427~chromosomal part,

GO:0003677~DNA binding,GO:0003702~RNA polymerase II transcription factor activity,GO:0003704~specific RNA polymerase II transcription factor activity,GO:0008270~zinc ion binding,GO:0016563~transcription activator activity,GO:0030528~transcription regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0046982~protein heterodimerization activity,GO:0046983~protein dimerization activity,

IPR000210:BTB/POZ-like,IPR007087:Zinc finger, C2H2-type,IPR011333:BTB/POZ fold,IPR013069:BTB/POZ,IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding,IPR015318:Zinc finger, GAGAG binding factor,IPR015880:Zinc finger, C2H2-like, SM00225:BTB,SM00355:ZnF_C2H2, 3d-structure,activator,alternative splicing,cell cycle,cell division,chromatin regulator,complete proteome,developmental protein,differentiation,direct protein sequencing,DNA binding,dna-binding,metal-binding,mitosis,nucleus,oogenesis,phosphoprotein,repressor,Transcription,transcription factor,transcription regulation,zinc,zinc-finger, chain:Transcription factor GAGA,compositionally biased region:Gln-rich,domain:BTB,helix,modified residue,region of interest:Interaction with E(bx),sequence conflict,splice variant,strand,turn,zinc finger region:C2H2-type; degenerate,

1631998_at Ubiquitin carrier protein Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR016135:Ubiquitin-conjugating enzyme/RWD-like, dme04120:Ubiquitin mediated proteolysis, PIRSF001567:ubiquitin-protein ligase E2, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1631909_at baiser Drosophila melanogaster GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007276~gamete generation,GO:0007281~germ cell development,GO:0007292~female gamete generation,GO:0007308~oocyte construction,GO:0007309~oocyte axis specification,GO:0007310~oocyte dorsal/ventral axis specification,GO:0007311~maternal specification of dorsal/ventral axis, oocyte, germ-line encoded,GO:0007389~pattern specification process,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0009994~oocyte differentiation,GO:0016192~vesicle-mediated transport,GO:0019953~sexual reproduction,GO:0021700~developmental maturation,GO:0032504~multicellular organism reproduction,GO:0048469~cell maturation,GO:0048477~oogenesis,GO:0048599~oocyte development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process, GO:0005794~Golgi apparatus,GO:0005795~Golgi stack,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0044431~Golgi apparatus part, IPR000348:emp24/gp25L/p24,IPR009038:GOLD,IPR015720:TMP21 related, PIRSF005359:conserved hypothetical protein YHR110w, complete proteome,membrane,transmembrane,

1636921_at lethal (2) 06496 Drosophila melanogaster GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement, GO:0005856~cytoskeleton,GO:0005869~dynactin complex,GO:0005875~microtubule associated complex,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,

complete proteome,

1635983_a_at no mechanoreceptor potential B Drosophila melanogaster GO:0000902~cell morphogenesis,GO:0007017~microtubule-based process,GO:0007018~microtubule-based movement,GO:0007600~sensory perception,GO:0007605~sensory perception of sound,GO:0009296~flagellum assembly,GO:0010970~microtubule-based transport,GO:0030030~cell projection organization,GO:0030031~cell projection assembly,GO:0030705~cytoskeleton-dependent intracellular transport,GO:0032989~cellular component morphogenesis,GO:0032990~cell part morphogenesis,GO:0035058~sensory cilium assembly,GO:0042073~intraflagellar transport,GO:0042384~cilium assembly,GO:0043064~flagellum organization,GO:0046907~intracellular transport,GO:0048858~cell projection morphogenesis,GO:0050877~neurological system process,GO:0050890~cognition,GO:0050954~sensory perception of mechanical stimulus,GO:0060271~cilium morphogenesis,

IPR001440:Tetratricopeptide TPR-1,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR019734:Tetratricopeptide repeat, SM00028:TPR, complete proteome,receptor,repeat,tpr repeat,

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C

+D

-D

Probe sets:

1623693_a_at
1624042_at
1624943_at
1625264_s_at
1625433_at
1625830_a_at
1626178_s_at
1626566_at
1627270_at
1627376_at
1627651_a_at
1629357_s_at
1629839_a_at
1629843_s_at
1630280_s_at
1630824_a_at
1630968_at
1631243_s_at

1631426_at
1632916_at
1633965_at
1634707_s_at
1634869_at
1634877_at
1635202_s_at
1635619_a_at
1635711_s_at
1636423_at
1636521_at
1636591_at
1636682_at
1638050_s_at
1638186_a_at
1638727_at
1638994_at
1639321_s_at
1640224_s_at
1640754_at
1641506_at

Functional annotation table:

ID Gene Name Species COG_ONTOLOGY GOTERM_BP_FAT GOTERM_CC_FAT GOTERM_MF_FAT INTERPRO KEGG_PATHWAY PIR_SUPERFAMILY SMART SP_PIR_KEYWORDS UP_SEQ_FEATURE

1635711_s_at Ankyrin Drosophila melanogaster GO:0007010~cytoskeleton organization,GO:0007016~cytoskeletal anchoring at plasma membrane,GO:0008104~protein localization,GO:0032507~maintenance of protein location in cell,GO:0045185~maintenance of protein location,GO:0051235~maintenance of location,GO:0051651~maintenance of location in cell, GO:0005886~plasma membrane,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0045169~fusome,GO:0045170~spectrosome, GO:0005198~structural molecule activity,GO:0005200~structural constituent of cytoskeleton,GO:0008092~cytoskeletal protein binding, IPR000488:Death,IPR000906:ZU5,IPR002110:Ankyrin, SM00005:DEATH,SM00218:ZU5,SM00248:ANK, ank repeat,complete proteome,repeat,

1625264_s_at Cysteine proteinase-1 Drosophila melanogaster GO:0002165~instar larval or pupal development,GO:0006508~proteolysis,GO:0007431~salivary gland development,GO:0007435~salivary gland morphogenesis,GO:0007552~metamorphosis,GO:0007559~histolysis,GO:0007586~digestion,GO:0008219~cell death,GO:0009057~macromolecule catabolic process,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0012501~programmed cell death,GO:0016265~death,GO:0016271~tissue death,GO:0022612~gland morphogenesis,GO:0030163~protein catabolic process,GO:0035070~salivary gland histolysis,GO:0035071~salivary gland cell autophagic cell death,GO:0035272~exocrine system development,GO:0048102~autophagic cell death,GO:0048707~instar larval or pupal morphogenesis,GO:0048732~gland development, GO:0000323~lytic vacuole,GO:0005764~lysosome,GO:0005773~vacuole, GO:0004175~endopeptidase activity,GO:0004197~cysteine-type endopeptidase activity,GO:0008233~peptidase activity,GO:0008234~cysteine-type peptidase activity,GO: 0070011~peptidase activity, acting on L-amino acid peptides, IPR000169:Peptidase, cysteine peptidase active site,IPR000668:Peptidase C1A, papain C-terminal,IPR013128:Peptidase C1A, papain,IPR013201:Proteinase inhibitor I29, cathepsin propeptide, dme04142:Lysosome, PIRSF001182:papain, SM00645:Pept_C1, alternative splicing,complete proteome,developmental protein,digestion,disulfide bond,glycoprotein,hydrolase,lysosome,Protease,signal,thiol protease,zymogen, chain:Cathepsin L heavy chain,chain:Cathepsin L light chain,disulfide bond,glycosylation site:N-linked (GlcNAc...),propeptide:Activation peptide,sequence conflict,signal peptide,splice variant,

1638994_at Dmel_CG10627 Drosophila melanogaster GO:0000287~magnesium ion binding,GO:0004610~phosphoacetylglucosamine mutase activity,GO:0016866~intramolecular transferase activity,GO:0016868~intramolecular transferase activity, phosphotransferases,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR005843:Alpha-D-phosphohexomutase, C-terminal,IPR005844:Alpha-D-phosphohexomutase, alpha/beta/alpha domain I,IPR005845:Alpha-D-phosphohexomutase, alpha/beta/alpha domain II,IPR016055:Alpha-D-phosphohexomutase, alpha/beta/alpha I, II and III,IPR016066:Alpha-D-phosphohexomutase, conserved site,IPR016657:Phosphoacetylglucosamine mutase, dme00520:Amino sugar and nucleotide sugar metabolism, PIRSF016408:PAGM,PIRSF016408:phosphoacetylglucosamine mutase, complete proteome,Isomerase,magnesium,metal-binding,

1641506_at Dmel_CG12400 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain,

			GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0050136~NADH dehydrogenase (quinone) activity, IPR009423:NADH:ubiquinone oxidoreductase, subunit b14.5b, dme00190:Oxidative phosphorylation, PIRSF017834:NADH-UbQ_OxRdtase_b14.5b, complete proteome,oxidoreductase,
1640224_s_at	Dmel_CG13796	Drosophila melanogaster	GO:0006836~neurotransmitter transport, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part, GO:0005275~amine transmembrane transporter activity,GO:0005326~neurotransmitter transporter activity,GO:0005328~neurotransmitter:sodium symporter activity,GO:0015171~amino acid transmembrane transporter activity,GO:0015175~neutral amino acid transmembrane transporter activity,GO:0015187~glycine transmembrane transporter activity,GO:0015293~symporter activity,GO:0015294~solute:cation symporter activity,GO:0015370~solute:sodium symporter activity, IPR000175:Sodium:neurotransmitter symporter,IPR000792:Transcription regulator LuxR, C-terminal, SM00421:HTH_LUXR, Symport,transmembrane,transport,
1630968_at	Dmel_CG13907	Drosophila melanogaster	GO:0008028~monocarboxylic acid transmembrane transporter activity,GO:0015355~secondary active monocarboxylate transmembrane transporter activity, IPR011701:Major facilitator superfamily MFS-1, complete proteome,
1634877_at	Dmel_CG15546	Drosophila melanogaster	complete proteome,
1624943_at	Dmel_CG1636	Drosophila melanogaster	complete proteome,
1636521_at	Dmel_CG1981	Drosophila melanogaster	GO:0006259~DNA metabolic process,GO:0006281~DNA repair,GO:0006289~nucleotide-excision repair,GO:0006298~mismatch repair,GO:0006974~response to DNA damage stimulus,GO:0033554~cellular response to stress,GO:0034984~cellular response to DNA damage stimulus, GO:0000700~mismatch base pair DNA N-glycosylase activity,GO:0003677~DNA binding,GO:0003690~double-stranded DNA binding,GO:0008263~pyrimidine-specific mismatch base pair DNA N-glycosylase activity,GO:0016799~hydrolase activity, hydrolyzing N-glycosyl compounds,GO:0019104~DNA N-glycosylase

activity,GO:0043566~structure-specific DNA binding, IPR005122:Uracil-DNA glycosylase-like,IPR015637:DNA glycosylase, G/T mismatch,IPR017956:AT hook, DNA-binding, conserved site, dme03410:Base excision repair, SM00384:AT_hook, complete proteome,

1632916_at Dmel_CG31357 Drosophila melanogaster General function prediction only, IPR006594:LisH dimerisation motif,IPR006595:CTLH, C-terminal to LisH motif,IPR013144:Ran binding protein-like, CRA domain, SM00667:LisH,SM00668:CTLH,SM00757:CRA, complete proteome,

1636682_at Dmel_CG31778 Drosophila melanogaster GO:0004857~enzyme inhibitor activity,GO:0004866~endopeptidase inhibitor activity,GO:0004867~serine-type endopeptidase inhibitor activity,GO:0030414~peptidase inhibitor activity, IPR002223:Proteinase inhibitor I2, Kunitz metazoa, SM00131:KU, complete proteome,

1626178_s_at Dmel_CG32149 Drosophila melanogaster GO:0004427~inorganic diphosphatase activity, IPR000198:RhoGAP,IPR008162:Inorganic pyrophosphatase, SM00324:RhoGAP, complete proteome,hydrolase,

1631426_at Dmel_CG32412 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0016603~glutaminyl-peptide cyclotransferase activity,GO:0016755~transferase activity, transferring amino-acyl groups, IPR007484:Peptidase M28, Acyltransferase,complete proteome,hydrolase,transferase,

1630824_a_at Dmel_CG33145 Drosophila melanogaster GO:0006486~protein amino acid glycosylation,GO:0009100~glycoprotein metabolic process,GO:0009101~glycoprotein biosynthetic process,GO:0043413~biopolymer glycosylation,GO:0070085~glycosylation, GO:0005794~Golgi apparatus,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0008378~galactosyltransferase activity,GO:0008499~UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity,GO:0035250~UDP-galactosyltransferase activity,GO:0048531~beta-1,3-galactosyltransferase activity, IPR002659:Glycosyl transferase, family 31, complete proteome,glycosyltransferase,golgi apparatus,membrane,transferase,transmembrane,

1623693_a_at Dmel_CG3365 Drosophila melanogaster GO:0032012~regulation of ARF protein signal transduction,GO:0032312~regulation of ARF GTPase activity,GO:0032318~regulation of Ras GTPase activity,GO:0043087~regulation of GTPase activity,GO:0046578~regulation of Ras protein signal transduction,GO:0051056~regulation of small GTPase mediated signal transduction,GO:0051336~regulation of hydrolase activity, GO:0005083~small GTPase regulator activity,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0008060~ARF GTPase activator activity,GO:0008270~zinc ion binding,GO:0030695~GTPase regulator activity,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0060589~nucleoside-triphosphatase regulator activity, IPR001164:Arf GTPase activating protein, SM00105:ArfGap, complete proteome,

1627270_at Dmel_CG42240 Drosophila melanogaster complete proteome,

1630280_s_at Dmel_CG42353; Dmel_CG42354 Drosophila melanogaster complete proteome,

1634869_at Dmel_CG4581 Drosophila melanogaster GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0016507~fatty acid beta-oxidation multienzyme complex,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0003988~acetyl-CoA C-acyltransferase activity,GO:0016408~C-acyltransferase activity,GO:0016509~long-chain-3-hydroxyacyl-CoA dehydrogenase activity, IPR002155:Thiolase,IPR016038:Thiolase-like, subgroup, dme00062:Fatty acid elongation in mitochondria,dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation, PIRSF000429:Ac-CoA_Ac_transf, Acyltransferase,complete proteome,oxidoreductase,transferase,

1635202_s_at Dmel_CG5640 Drosophila melanogaster IPR001440:Tetratricopeptide TPR-1,IPR003347:Transcription factor jumonji/aspartyl beta-hydroxylase,IPR011990:Tetratricopeptide-like helical,IPR013026:Tetratricopeptide region,IPR013129:Transcription factor jumonji,IPR019734:Tetratricopeptide repeat, SM00028:TPR,SM00558:JmjC, complete proteome,repeat,tpr repeat,

1633965_at Dmel_CG6020 Drosophila melanogaster GO:0006091~generation of precursor metabolites and energy,GO:0006119~oxidative phosphorylation,GO:0006120~mitochondrial electron transport, NADH to ubiquinone,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0015980~energy derivation by oxidation of organic compounds,GO:0016310~phosphorylation,GO:0022900~electron transport chain,GO:0022904~respiratory electron transport chain,GO:0042773~ATP synthesis coupled electron transport,GO:0042775~mitochondrial ATP synthesis coupled electron transport,GO:0045333~cellular respiration,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005740~mitochondrial envelope,GO:0005743~mitochondrial inner membrane,GO:0005746~mitochondrial respiratory chain,GO:0005747~mitochondrial respiratory chain complex I,GO:0019866~organelle inner membrane,GO:0030964~NADH

			dehydrogenase complex,GO:0031090~organelle membrane,GO:0031966~mitochondrial membrane,GO:0031967~organelle envelope,GO:0031975~envelope ,GO:0044429~mitochondrial part,GO:0044455~mitochondrial membrane part,GO:0045271~respiratory chain complex I,GO:0070469~respiratory chain, GO:0003954~NADH dehydrogenase activity,GO:0008137~NADH dehydrogenase (ubiquinone) activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor,GO:0048037~cofactor binding,GO:0050136~NADH dehydrogenase (quinone) activity,GO:0050662~coenzyme binding, IPR001509:NAD-dependent epimerase/dehydratase,IPR016040:NAD(P)-binding domain, dme00190:Oxidative phosphorylation, complete proteome,oxidoreductase,
1636423_at	Dmel_CG8012	Drosophila melanogaster	complete proteome,
1636591_at	Dmel_CG8881	Drosophila melanogaster	Posttranslational modification, protein turnover, chaperones, GO:0006508~proteolysis,GO:0006511~ubiquitin-dependent protein catabolic process,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process, IPR001232:SKP1 component,IPR011333:BTB/POZ fold,IPR016072:SKP1 component, dimerisation,IPR016073:SKP1 component, POZ,IPR016897:E3 ubiquitin ligase, SCF complex, Skp subunit, dme04120:Ubiquitin mediated proteolysis,dme04310:Wnt signaling pathway,dme04350:TGF-beta signaling pathway, PIRSF028729:E3_ubiquit_lig_SCF_Skp, SM00512:Skp1, complete proteome,
1638727_at	Dmel_CG9821	Drosophila melanogaster	complete proteome,
1629839_a_at	G protein gamma 1	Drosophila melanogaster	GO:0007010~cytoskeleton organization,GO:0007015~actin filament organization,GO:0007155~cell adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007405~neuroblast proliferation,GO:0007507~heart development,GO:0007584~response to nutrient,GO:0007610~behavior,GO:0007635~chemosensory behavior,GO:0007637~proboscis extension reflex,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008283~cell proliferation,GO:0008360~regulation of cell shape,GO:0009991~response to extracellular stimulus,GO:0017145~stem cell division,GO:0022604~regulation of cell morphogenesis,GO:0022610~biological adhesion,GO:0030029~actin filament-based process,GO:0030036~actin cytoskeleton organization,GO:0031667~response to nutrient levels,GO:0035050~embryonic heart tube development,GO:0035295~tube

development,GO:0045165~cell fate commitment,GO:0045176~apical protein localization,GO:0048103~somatic stem cell division,GO:0051301~cell division,GO:0051780~behavioral response to nutrient,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060004~reflex,

GO:0005834~heterotrimeric G-protein complex,GO:0005886~plasma membrane,GO:0009898~internal side of plasma membrane,GO:0019897~extrinsic to plasma membrane,GO:0019898~extrinsic to membrane,GO:0044459~plasma membrane part, GO:0003924~GTPase activity, IPR001770:G-protein, gamma subunit,IPR015898:G-protein, gamma-like subunit, PIRSF002398:GTP-binding regulatory protein gamma chain, SM00224:GGL, cell membrane,complete proteome,GTP binding,lipoprotein,membrane,methylated carboxyl end,methylation,prenylated cysteine,prenylation,transducer, chain:Guanine nucleotide-binding protein subunit gamma-1,lipid moiety-binding region:S-geranylgeranyl cysteine,modified residue,propeptide:Removed in mature form,

1624042_at G protein-coupled receptor kinase 2 Drosophila melanogaster GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0007166~cell surface receptor linked signal transduction,GO:0007186~G-protein coupled receptor protein signaling pathway,GO:0007224~smoothened signaling pathway,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0016310~phosphorylation,GO:0019953~sexual reproduction,GO:0032504~multicellular organism reproduction,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism, GO:0005886~plasma membrane, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004703~G-protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000239:GPCR kinase,IPR000342:Regulator of G protein signalling,IPR000719:Protein kinase, core,IPR000961:AGC-kinase, C-terminal,IPR002290:Serine/threonine protein kinase,IPR008271:Serine/threonine protein kinase, active site,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related, dme04144:Endocytosis,

SM00133:S_TK_X,SM00220:S_TKc,SM00315:RGS, ATP,atp-binding,complete proteome,developmental protein,differentiation,kinase,membrane,nucleotide-binding,oogenesis,phosphoprotein,phosphotransferase,repeat,serine/threonine-protein kinase,serine/threonine-specific protein kinase,transferase, active site:Proton acceptor,binding site:ATP,chain:G protein-coupled receptor kinase 2,compositionally biased region:Asn-rich,domain:AGC-kinase C-terminal,domain:Protein kinase,domain:RGS 1,domain:RGS 2,modified residue,nucleotide phosphate-binding region:ATP,region of interest:N-terminal,sequence conflict, 1634707_s_at Glutamine:fructose-6-phosphate aminotransferase 1 Drosophila melanogaster Cell envelope biogenesis, outer membrane, GO:0016051~carbohydrate biosynthetic process, GO:0004360~glutamine-fructose-6-phosphate transaminase (isomerizing) activity,GO:0005529~sugar binding,GO:0008483~transaminase activity,GO:0016769~transferase activity, transferring nitrogenous groups,GO:0030246~carbohydrate binding, IPR000583:Glutamine amidotransferase, class-II,IPR001347:Sugar isomerase (SIS),IPR005855:Glucosamine-fructose-6-phosphate aminotransferase, isomerising,IPR017932:Glutamine amidotransferase, type II, dme00250:Alanine, aspartate and glutamate metabolism,dme00520:Amino sugar and nucleotide sugar metabolism, Aminotransferase,complete proteome,transferase,

1626566_at Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial Drosophila melanogaster Lipid metabolism, GO:0006631~fatty acid metabolic process,GO:0006635~fatty acid beta-oxidation,GO:0009062~fatty acid catabolic process,GO:0016042~lipid catabolic process,GO:0016054~organic acid catabolic process,GO:0019395~fatty acid oxidation,GO:0030258~lipid modification,GO:0034440~lipid oxidation,GO:0044242~cellular lipid catabolic process,GO:0046395~carboxylic acid catabolic process,GO:0055114~oxidation reduction, GO:0005739~mitochondrion,GO:0005759~mitochondrial matrix,GO:0005811~lipid particle,GO:0031974~membrane-enclosed lumen,GO:0031980~mitochondrial lumen,GO:0043233~organelle lumen,GO:0044429~mitochondrial part,GO:0070013~intracellular organelle lumen, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0003995~acyl-CoA dehydrogenase activity,GO:0009055~electron carrier activity,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding ,GO:0048037~cofactor binding,GO:0050660~FAD binding,GO:0050662~coenzyme binding, IPR006089:Acyl-CoA dehydrogenase, conserved site,IPR006090:Acyl-CoA oxidase/dehydrogenase, type 1,IPR006091:Acyl-CoA oxidase/dehydrogenase, central region,IPR006092:Acyl-CoA dehydrogenase, N-terminal,IPR013764:Acyl-CoA oxidase/dehydrogenase, type1/2, C-terminal,IPR013786:Acyl-CoA dehydrogenase/oxidase, N-terminal, dme00071:Fatty acid metabolism,dme00280:Valine, leucine and isoleucine degradation,dme00410:beta-Alanine metabolism,dme00640:Propanoate metabolism, PIRSF000182:acyl-CoA dehydrogenase, complete proteome,FAD,fatty acid metabolism,Flavoprotein,lipid metabolism,mitochondrion,oxidoreductase,transit peptide, active site:Proton acceptor,binding site:Substrate; via amide nitrogen,binding site:Substrate; via carbonyl oxygen,chain:Probable medium-chain specific acyl-CoA dehydrogenase, mitochondrial,nucleotide phosphate-binding region:FAD,region of interest:Substrate binding,transit peptide:Mitochondrion, 1638186_a_at Protein fem-1 homolog B Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0031396~regulation of protein ubiquitination,GO:0031399~regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051340~regulation of ligase activity,GO:0051438~regulation of ubiquitin-protein ligase activity,GO:0051603~proteolysis involved in cellular protein catabolic process, GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR002110:Ankyrin, SM00248:ANK, alternative splicing,ank repeat,complete proteome,repeat,ubl conjug ation pathway, chain:Protein fem-1 homolog B,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,repeat:ANK 6,repeat:ANK 7,splice variant,

1627376_at Relish Drosophila melanogaster GO:0002684~positive regulation of immune system process,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002813~regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0006350~transcription,GO:0006355~regulation of transcription, DNA-dependent,GO: 0006357~regulation of transcription from RNA polymerase II promoter,GO:0006952~defense response,GO:0006955~immune response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006964~positive regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007166~cell surface receptor linked signal transduction,GO:0008063~Toll signaling pathway,GO:0009267~cellular response to starvation,GO:0009617~response to bacterium,GO:0009891~positive regulation of biosynthetic process,GO:0009991~response to extracellular stimulus,GO:0010551~regulation of specific transcription from RNA polymerase II promoter,GO:0010552~positive regulation of specific transcription from RNA polymerase II promoter,GO:0010557~positive regulation of macromolecule biosynthetic process,GO:0010604~positive regulation of macromolecule metabolic process,GO:0010628~positive regulation of gene expression,GO:0019730~antimicrobial humoral response,GO:0031328~positive regulation of cellular biosynthetic process,GO:0031349~positive regulation of defense response,GO:0031667~response to nutrient levels,GO:0031668~cellular response to extracellular stimulus,GO:0031669~cellular response to nutrient levels,GO:0032583~regulation of gene-specific transcription,GO:0033554~cellular response to stress,GO:0034198~cellular response to amino acid starvation,GO:0042594~response to starvation,GO:0042742~defense response to bacterium,GO:0043193~positive regulation of gene-specific transcription,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045089~positive regulation of innate immune response,GO:0045428~regulation of nitric oxide biosynthetic process,GO:0045429~positive regulation of nitric oxide biosynthetic process,GO:0045449~regulation of transcription,GO:0045893~positive regulation of transcription, DNA-dependent,GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process,GO:0045941~positive regulation of transcription,GO:0045944~positive regulation of transcription from RNA polymerase II promoter,GO:0048584~positive regulation of response to stimulus,GO:0050778~positive regulation of immune response,GO:0050829~defense response to Gram-negative bacterium,GO:0051173~positive regulation of nitrogen compound metabolic process,GO:0051252~regulation of RNA metabolic process,GO:0051254~positive regulation of RNA metabolic process, GO:0003677~DNA binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity, IPR000451:NF-kappa-B/Rel/dorsal,IPR002110:Ankyrin,IPR002909:Cell surface receptor IPT/TIG,IPR011539:Rel homology,IPR013783:Immunoglobulin-like fold, SM00248:ANK,SM00429:IPT,activator,alternative splicing,ank repeat,complete proteome,cytoplasm,direct protein sequencing,immune response,innate immunity,nucleus,phosphoprotein,repeat,Transcription,transcription regulation, chain:Nuclear factor NF-kappa-B p110 subunit,chain:Nuclear factor NF-kappa-B p49 subunit,chain:Nuclear factor NF-kappa-B p68 subunit,domain:RHD,modified residue,mutagenesis site,repeat:ANK 1,repeat:ANK 2,repeat:ANK 3,repeat:ANK 4,repeat:ANK 5,sequence conflict,sequence variant,short sequence motif:Nuclear localization signal,site:Cleavage (when cotranslationally processed),splice variant,

1629357_s_at SNF1A/AMP-activated protein kinase Drosophila melanogaster GO:0000278~mitotic cell cycle,GO:0000902~cell morphogenesis,GO:0006468~protein amino acid phosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0007049~cell cycle,GO:0007163~establishment or maintenance of cell polarity,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0016310~phosphorylation,GO:0032989~cellular component morphogenesis,GO:0035088~establishment or maintenance of apical/basal cell polarity,GO:0045197~establishment or maintenance of epithelial cell apical/basal polarity, GO:0031588~AMP-activated protein kinase complex, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0004672~protein kinase activity,GO:0004674~protein serine/threonine kinase activity,GO:0004679~AMP-activated protein kinase activity,GO:0004703~G-protein coupled receptor kinase activity,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR000719:Protein kinase, core,IPR002290:Serine/threonine protein kinase,IPR008271:Serine/threonine protein kinase, active site,IPR015741:Snf1-like protein AMPK,IPR017441:Protein kinase, ATP binding site,IPR017442:Serine/threonine protein kinase-related, dme04140:Regulation of autophagy,dme04150:mTOR signaling pathway, PIRSF000590:Snf1/AMPK-type protein kinases, catalytic subunits, SM00220:S_TKc, atp-binding,complete proteome,kinase,nucleotide-binding,serine/threonine-protein kinase,transferase,

1625433_at Sarcoplasmic calcium-binding protein 1 Drosophila melanogaster GO:0005783~endoplasmic reticulum,GO:0016528~sarcoplasm,GO:0016529~sarcoplasmic reticulum, GO:0005509~calcium ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding, IPR002048:Calcium-binding EF-hand,IPR011992:EF-Hand type,IPR018247:EF-HAND 1,IPR018248:EF hand,IPR018249:EF-HAND 2, SM00054:EFh, calcium,

1638050_s_at Sox box protein 14 Drosophila melanogaster GO:0006350~transcription,GO:0045449~regulation of transcription, GO:0003677~DNA binding,GO:0003700~transcription factor activity,GO:0030528~transcription regulator activity, IPR000910:High mobility group, HMG1/HMG2, SM00398:HMG, complete proteome,DNA binding,dna-binding,nucleus,Transcription,transcription regulation, chain:Putative transcription factor SOX-14,compositionally biased region:Poly-Ala,compositionally biased region:Poly-Asn,DNA-binding region:HMG box,sequence conflict,

1639321_s_at Toll Drosophila melanogaster Function unknown,GO:0000578~embryonic axis specification,GO:0000910~cytokinesis,GO:0002520~immune system development,GO:0002697~regulation of immune effector process,GO:0002700~regulation of production of molecular mediator of immune response,GO:0002759~regulation of antimicrobial humoral response,GO:0002784~regulation of antimicrobial peptide production,GO:0002786~regulation of antibacterial peptide production,GO:0002788~regulation of antifungal peptide production,GO:0002805~regulation of antimicrobial peptide biosynthetic process,GO:0002807~positive regulation of antimicrobial peptide biosynthetic process,GO:0002808~regulation of antibacterial peptide biosynthetic process,GO:0002810~regulation of antifungal peptide biosynthetic process,GO:0002831~regulation of response to biotic stimulus,GO:0002920~regulation of humoral immune response,GO:0003002~regionalization,GO:0006952~defense response,GO:0006955~immune response,GO:0006959~humoral immune response,GO:0006963~positive regulation of antibacterial peptide biosynthetic process,GO:0006967~positive regulation of antifungal peptide biosynthetic process,GO:0007155~cell adhesion,GO:0007166~cell surface receptor linked signal transduction,GO:0007352~zygotic determination of dorsal/ventral axis,GO:0007389~pattern specification process,GO:0007416~synaptogenesis,GO:0008063~Toll signaling pathway,GO:0008283~cell proliferation,GO:0009617~response to bacterium,GO:0009620~response to fungus,GO:0009798~axis specification,GO:0009880~embryonic pattern specification,GO:0009891~positive regulation of biosynthetic process,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0019730~antimicrobial humoral response,GO:0019732~antifungal humoral response,GO:0022610~biological adhesion,GO:0030097~hemopoiesis,GO:0031328~positive regulation of cellular biosynthetic process,GO:0035007~regulation of melanization defense response,GO:0035172~hemocyte proliferation,GO:0042742~defense response to bacterium,GO:0043062~extracellular structure organization,GO:0043455~regulation of secondary metabolic process,GO:0043900~regulation of multi-organism process,GO:0045087~innate immune response,GO:0045088~regulation of innate immune response,GO:0045610~regulation of hemocyte differentiation,GO:0048534~hemopoietic or lymphoid organ development,GO:0050808~synapse organization,GO:0050830~defense response to Gram-positive bacterium,GO:0050832~defense response to fungus,GO:0051301~cell division, GO:0005886~plasma membrane,GO:0005887~integral to plasma membrane,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,GO:0031226~intrinsic to plasma membrane,GO:0044459~plasma membrane part,

GO:0019955~cytokine binding,GO:0042802~identical protein binding, IPR000157:Toll-Interleukin receptor,IPR000372:Leucine-rich repeat, cysteine-rich flanking region, N-terminal,IPR000483:Cysteine-rich flanking region, C-terminal,IPR001611:Leucine-rich repeat,IPR003591:Leucine-rich repeat, typical subtype,IPR004075:Interleukin-1 receptor, type I/Toll precursor, SM00013:LRRNT,SM00082:LRRCT,SM00255:TIR,SM00369:LRR_TYP, cell adhesion,cell membrane,complete proteome,developmental protein,disulfide bond,glycoprotein,leucine-rich repeat,membrane,polymorphism,repeat,signal,transmembrane,transmembrane protein, chain:Protein toll,domain:TIR,glycosylation site:N-linked (GlcNAc...),repeat:LRR 1,repeat:LRR 10,repeat:LRR 11,repeat:LRR 12,repeat:LRR 13,repeat:LRR 14,repeat:LRR 15,repeat:LRR 16,repeat:LRR 17,repeat:LRR 18,repeat:LRR 19,repeat:LRR 2,repeat:LRR 20,repeat:LRR 21,repeat:LRR 3,repeat:LRR 4,repeat:LRR 5,repeat:LRR 6,repeat:LRR 7,repeat:LRR 8,repeat:LRR 9,sequence conflict,sequence variant,signal peptide,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

1629843_s_at Ubiquitin carrier protein Drosophila melanogaster GO:0006508~proteolysis,GO:0009057~macromolecule catabolic process,GO:0016567~protein ubiquitination,GO:0019941~modification-dependent protein catabolic process,GO:0030163~protein catabolic process,GO:0032446~protein modification by small protein conjugation,GO:0043632~modification-dependent macromolecule catabolic process,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0070647~protein modification by small protein conjugation or removal,

GO:0004842~ubiquitin-protein ligase activity,GO:0016879~ligase activity, forming carbon-nitrogen bonds,GO:0016881~acid-amino acid ligase activity,GO:0019787~small conjugating protein ligase activity, IPR000608:Ubiquitin-conjugating enzyme, E2,IPR015581:Ubiquitin-conjugating enzyme,IPR016135:Ubiquitin-conjugating enzyme/RWD-like,

dme04120:Ubiquitin mediated proteolysis, SM00212:UBCc, complete proteome,ligase,ubl conjugation pathway,

1640754_at brummer Drosophila melanogaster GO:0006638~neutral lipid metabolic process,GO:0006639~acylglycerol metabolic process,GO:0006641~triglyceride metabolic process,GO:0006642~triglyceride mobilization,GO:0006662~glycerol ether metabolic process,GO:0007568~aging,GO:0008340~determination of adult life span,GO:0010259~multicellular organismal aging,GO:0016042~lipid catabolic process,GO:0018904~organic ether metabolic process,GO:0019433~triglyceride catabolic process,GO:0044242~cellular lipid catabolic process,GO:0044269~glycerol ether catabolic process,GO:0046461~neutral lipid catabolic process,GO:0046464~acylglycerol catabolic process,GO:0046486~glycerolipid metabolic process,GO:0046503~glycerolipid catabolic process,GO:0005811~lipid particle, GO:0004091~carboxylesterase activity,GO:0004806~triacylglycerol lipase activity,GO:0016298~lipase activity, IPR002641:Patatin, complete proteome,hydrolase,lipid degradation,

1635619_a_at centrosomin Drosophila melanogaster GO:0000087~M phase of mitotic cell cycle,GO:0000226~microtubule cytoskeleton organization,GO:0000278~mitotic cell cycle,GO:0000279~M phase,GO:0000280~nuclear division,GO:0007010~cytoskeleton organization,GO:0007017~microtubule-based process,GO:0007049~cell cycle,GO:0007051~spindle organization,GO:0007052~mitotic spindle organization,GO:0007059~chromosome segregation,GO:0007067~mitosis,GO:0007098~centrosome cycle,GO:0007126~meiosis,GO:0007143~female meiosis,GO:0007422~peripheral nervous system development,GO:0007494~midgut development,GO:0016321~female meiosis chromosome segregation,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0031023~microtubule organizing center organization,GO:0045132~meiotic chromosome segregation,GO:0048285~organelle fission,GO:0048565~gut development,GO:0051297~centrosome organization,GO:0051301~cell division,GO:0051321~meiotic cell cycle,GO:0051327~M phase of meiotic cell cycle,

GO:0000242~pericentriolar material,GO:0005813~centrosome,GO:0005815~microtubule organizing center,GO:0005856~cytoskeleton,GO:0005875~microtubule associated complex,GO:0005929~cilium,GO:0005932~microtubule basal body,GO:0015629~actin cytoskeleton,GO:0015630~microtubule cytoskeleton,GO:0016459~myosin

			complex,GO:0019861~flagellum,GO:0042995~cell projection,GO:0043228~non-membrane-bounded organelle,GO:0043232~intracellular non-membrane-bounded organelle,GO:0044430~cytoskeletal part,GO:0044450~microtubule organizing center part,GO:0044463~cell projection part, GO:0008017~microtubule binding,GO:0008092~cytoskeletal protein binding,GO:0015631~tubulin binding,GO:0016887~ATPase activity,GO:0042624~ATPase activity, uncoupled, IPR012943:Spindle associated, alternative splicing,cell cycle,cell division,cell projection,cilium,coiled coil,complete proteome,cytoplasm,cytoskeleton,developmental protein,flagellum,hydrolase,leucine zipper,meiosis,mitosis,phosphoprotein, chain:Centrosomin,modified residue,sequence conflict,short sequence motif:Nuclear localization signal,splice variant,
1631243_s_at	lethal (3) 05822	Drosophila melanogaster	IPR000108:Neutrophil cytosol factor 2,IPR001452:Src homology-3 domain, SM00326:SH3, complete proteome,sh3 domain,
1627651_a_at	locomotion defects	Drosophila melanogaster	GO:0000902~cell morphogenesis,GO:0001885~endothelial cell development,GO:0002009~morphogenesis of an epithelium,GO:0002064~epithelial cell development,GO:0003002~regionalization,GO:0003006~reproductive developmental process,GO:0007010~cytoskeleton organization,GO:0007043~cell-cell junction assembly,GO:0007163~establishment or maintenance of cell polarity,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007300~ovarian nurse cell to oocyte transport,GO:0007303~cytoplasmic transport, nurse cell to oocyte,GO:0007389~pattern specification process,GO:0007405~neuroblast proliferation,GO:0007419~ventral cord development,GO:0008069~dorsal/ventral axis specification, ovarian follicular epithelium,GO:0008104~protein localization,GO:0008105~asymmetric protein localization,GO:0008277~regulation of G-protein coupled receptor protein signaling pathway,GO:0008283~cell proliferation,GO:0009798~axis specification,GO:0009950~dorsal/ventral axis specification,GO:0009953~dorsal/ventral pattern formation,GO:0010001~glial cell differentiation,GO:0014045~establishment of endothelial blood-brain barrier,GO:0016333~morphogenesis of follicular epithelium,GO:0016334~establishment or maintenance of polarity of follicular epithelium,GO:0016482~cytoplasmic transport,GO:0017145~stem cell division,GO:0019953~sexual reproduction,GO:0019991~septate junction assembly,GO:0021782~glial cell development,GO:0030029~actin filament-based process,GO:0030036~actin cytoskeleton organization,GO:0030707~ovarian follicle cell development,GO:0030855~epithelial cell differentiation,GO:0030865~cortical cytoskeleton organization,GO:0030866~cortical actin cytoskeleton organization,GO:0032504~multicellular organism reproduction,GO:0032989~cellular component morphogenesis,GO:0034329~cell junction assembly,GO:0034330~cell junction organization,GO:0042063~gliogenesis,GO:0043297~apical junction assembly,GO:0045165~cell fate commitment,GO:0045216~cell-cell junction

organization,GO:0045446~endothelial cell differentiation,GO:0046907~intracellular transport,GO:0048103~somatic stem cell division,GO:0048477~oogenesis,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048729~tissue morphogenesis,GO:0051301~cell division,GO:0055057~neuroblast division,GO:0055059~asymmetric neuroblast division,GO:0060429~epithelium development,

GO:0005886~plasma membrane,GO:0005938~cell cortex,GO:0044448~cell cortex part,GO:0045177~apical part of cell,GO:0045179~apical cortex,

GO:0001965~G-protein alpha-subunit binding,GO:0005096~GTPase activator activity,GO:0008047~enzyme activator activity,GO:0030695~GTPase regulator activity,GO:0060589~nucleoside-triphosphatase regulator activity,

IPR000342:Regulator of G protein signalling,IPR001478:PDZ/DHR/GLGF,IPR003109:GoLoco motif,IPR003116:Raf-like Ras-binding,IPR006020:Phosphotyrosine interaction region,

SM00228:PDZ,SM00315:RGS,SM00390:GoLoco,SM00455:RBD,SM00462:PTB, complete proteome,

1625830_a_at scruin like at the midline Drosophila melanogaster IPR006652:Kelch repeat type 1,IPR015915:Kelch-type beta propeller,

SM00612:Kelch, complete proteome,

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+D

C

-D

Probe sets:

1625199_s_at 1633654_s_at 1634814_at 1638325_at 1638875_at

Functional annotation table:

-D C +D

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1638875_at	Egg-derived tyrosine phosphatase	Drosophila melanogaster	GO:0006470~protein amino acid dephosphorylation,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016311~dephosphorylation,		GO:0004721~phosphoprotein phosphatase activity,GO:0004725~protein tyrosine phosphatase activity,GO:0016791~phosphatase activity,	IPR016130:Protein-tyrosine phosphatase, active site,			complete proteome,hydrolase,	
1638325_at	Henna	Drosophila melanogaster	GO:0006558~L-phenylalanine metabolic process,GO:0006559~L-phenylalanine catabolic process,GO:0006575~cellular amino acid derivative metabolic process,GO:0006576~biogenic amine metabolic process,GO:0006586~indolalkylamine metabolic process,GO:0006726~eye pigment biosynthetic process,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0009063~cellular amino acid catabolic process,GO:0009072~aromatic amino acid family metabolic process,GO:0009074~aromatic amino acid family catabolic process,GO:0009309~amine biosynthetic process,GO:0009310~amine catabolic process,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016054~organic acid catabolic process,GO:0016192~vesicle-mediated transport,GO:0018130~heterocycle biosynthetic process,GO:0019439~aromatic compound catabolic process,GO:0042398~cellular amino acid derivative biosynthetic process,GO:0042401~biogenic amine biosynthetic process,GO:0042427~serotonin biosynthetic process,GO:0042428~serotonin metabolic process,GO:0042430~indole and derivative metabolic process,GO:0042434~indole derivative metabolic process,GO:0042435~indole derivative biosynthetic process,GO:0042440~pigment metabolic process,GO:0042441~eye pigment metabolic process,GO:0043473~pigmentation,GO:0044271~nitrogen compound biosynthetic process,GO:0046148~pigment biosynthetic process,GO:0046219~indolalkylamine biosynthetic process,GO:0046395~carboxylic acid catabolic process,GO:0048066~pigmentation during development,GO:0048069~eye pigmentation,GO:0055114~oxidation reduction,	GO:0005811~lipid particle,	GO:0004505~phenylalanine 4-monooxygenase activity,GO:0004510~tryptophan 5-monooxygenase activity,GO:0005506~iron ion binding,GO:0016597~amino acid binding,GO:0016714~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen,GO:0031406~carboxylic acid binding,GO:0043167~ion binding,GO:0043169~cation					

binding,GO:0043176~amine binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding, IPR001273:Aromatic amino acid hydroxylase,IPR002912:Amino acid-binding ACT,IPR005961:Phenylalanine-4-hydroxylase, tetrameric form,IPR018301:Aromatic amino acid hydroxylase, iron/copper binding site,IPR019773:Tyrosine 3-monooxygenase-like,IPR019774:Aromatic amino acid hydroxylase, C-terminal, dme00360:Phenylalanine metabolism,dme00400:Phenylalanine, tyrosine and tryptophan biosynthesis, PIRSF000336:TH,PIRSF000336:tyrosine 3-monooxygenase, allosteric enzyme,biopterin,complete proteome,iron,metal-binding,metalloprotein,Monooxygenase,oxidoreductase,phenylalanine catabolism,phenylketonuria,phosphoprotein,serotonin biosynthesis, chain:Protein henna,domain:ACT,metal ion-binding site:Iron,modified residue,sequence conflict,

1633654_s_at Inositol 1,4,5-triphosphate kinase 2 Drosophila melanogaster GO:0006020~inositol metabolic process,GO:0006793~phosphorus metabolic process,GO:0006796~phosphate metabolic process,GO:0016310~phosphorylation,GO:0019751~polyol metabolic process,GO:0046835~carbohydrate phosphorylation,GO:0046853~inositol and derivative phosphorylation, GO:0004428~inositol or phosphatidylinositol kinase activity,GO:0005516~calmodulin binding,GO:0008440~inositol trisphosphate 3-kinase activity,GO:0048306~calcium-dependent protein binding,GO:0051766~inositol trisphosphate kinase activity, IPR005522:Inositol polyphosphate kinase, dme00562:Inositol phosphate metabolism,dme04070:Phosphatidylinositol signaling system, complete proteome,kinase,transferase,

1634814_at UPF0183 protein CG7083 Drosophila melanogaster IPR005373:Uncharacterised protein family UPF0183, PIRSF015809:hypothetical protein, Caenorhabditis elegans T01G9.2b type, complete proteome, chain:UPF0183 protein CG7083,

1625199_s_at dacapo Drosophila melanogaster GO:0000079~regulation of cyclin-dependent protein kinase activity,GO:0000082~G1/S transition of mitotic cell cycle,GO:0000278~mitotic cell cycle,GO:0001709~cell fate determination,GO:0002165~instar larval or pupal development,GO:0003006~reproductive developmental process,GO:0007049~cell cycle,GO:0007050~cell cycle arrest,GO:0007090~regulation of S phase of mitotic cell cycle,GO:0007276~gamete generation,GO:0007292~female gamete generation,GO:0007293~germarium-derived egg chamber formation,GO:0007294~germarium-derived oocyte fate determination,GO:0007346~regulation of mitotic cell cycle,GO:0007423~sensory organ development,GO:0007424~open tracheal system development,GO:0007444~imaginal disc development,GO:0007488~histoblast morphogenesis,GO:0007552~metamorphosis,GO:0007560~imaginal disc morphogenesis,GO:0008356~asymmetric cell division,GO:0009791~post-embryonic development,GO:0009886~post-embryonic morphogenesis,GO:0009994~oocyte differentiation,GO:0010563~negative r egulation of phosphorus metabolic process,GO:0010564~regulation of cell cycle process,GO:0010605~negative regulation of macromolecule metabolic process,GO:0010948~negative regulation of cell cycle process,GO:0019220~regulation of phosphate metabolic process,GO:0019953~sexual reproduction,GO:0022402~cell cycle process,GO:0022403~cell cycle phase,GO:0030706~germarium-derived oocyte differentiation,GO:0030716~oocyte fate determination,GO:0031399~regulation of protein modification process,GO:0031400~negative regulation of protein modification process,GO:0032268~regulation of cellular protein metabolic process,GO:0032269~negative regulation of cellular protein metabolic process,GO:0032504~multicellular organism reproduction,GO:0033261~regulation of S phase,GO:0035303~regulation of dephosphorylation,GO:0035304~regulation of protein amino acid dephosphorylation,GO:0035305~negative regulation of dephosphorylation,GO:0035308~negative regulation of protein amino acid dephosphorylation,GO:0042325~regulation of phosphor ylation,GO:0043549~regulation of kinase activity,GO:0045035~sensory organ precursor cell division,GO:0045165~cell fate commitment,GO:0045749~negative regulation of S phase of mitotic cell cycle,GO:0045786~negative regulation of cell cycle,GO:0045859~regulation of protein kinase activity,GO:0045930~negative regulation of mitotic cell cycle,GO:0045936~negative regulation of phosphate metabolic process,GO:0048477~oogenesis,GO:0048563~post-embryonic organ morphogenesis,GO:0048569~post-embryonic organ development,GO:0048609~reproductive process in a multicellular organism,GO:0048610~reproductive cellular process,GO:0048707~instar larval or pupal morphogenesis,GO:0051174~regulation of phosphorus metabolic process,GO:0051248~negative regulation of protein metabolic process,GO:0051301~cell division,GO:0051318~G1 phase,GO:0051325~interphase,GO:0051329~interphase of mitotic cell cycle,GO:0051338~regulation of transferase activity,GO:0051726~regulation of cell cycle,GO:0060541~respiratory system development, GO:000485 7~enzyme inhibitor activity,GO:0004860~protein kinase inhibitor activity,GO:0004861~cyclin-dependent protein kinase inhibitor activity,GO:0016538~cyclin-dependent protein kinase regulator activity,GO:0019207~kinase regulator activity,GO:0019210~kinase inhibitor activity,GO:0019887~protein kinase regulator activity,GO:0030291~protein serine/threonine kinase inhibitor activity, IPR003175:Cyclin-dependent kinase inhibitor,

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Probe sets:

1625519_at
1628429_at
1632834_a_at
1639762_at
1628194_at
1635065_at
1635491_s_at
1636639_at

Functional annotation table:

ID	Gene Name	Species	GOTERM_BP_FAT	GOTERM_CC_FAT	GOTERM_MF_FAT	INTERPRO	KEGG_PATHWAY	PIR_SUPERFAMILY	SMART	SP_PIR_KEYWORDS	UP_SEQ_FEATURE
1635491_s_at	Dmel_CG11642	Drosophila melanogaster	GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006886~intracellular protein transport,GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0008104~protein localization,GO:0010324~membrane invagination,GO:0015031~protein transport,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0070727~cellular macromolecule localization,	GO:0005783~endoplasmic reticulum,GO:0005811~lipid particle,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,		IPR006634:TRAM, LAG1 and CLN8 homology,IPR013599:TRAM1-like protein,IPR016447:Translocation associated membrane protein,		PIRSF005449:translocation associated membrane protein,PIRSF005449:Translocation_assoc_membrane,	SM00724:TLC,	membrane,transmembrane,	

1628194_at Dmel_CG2918 Drosophila melanogaster GO:0006457~protein folding, GO:0005811~lipid particle, GO:0000166~nucleotide binding,GO:0001882~nucleoside binding,GO:0001883~purine nucleoside binding,GO:0005524~ATP binding,GO:0017076~purine nucleotide binding,GO:0030554~adenyl nucleotide binding,GO:0032553~ribonucleotide binding,GO:0032555~purine ribonucleotide binding,GO:0032559~adenyl ribonucleotide binding, IPR001023:Heat shock protein Hsp70,IPR013126:Heat shock protein 70,IPR018181:Heat shock protein 70, conserved site, atp-binding,complete proteome,nucleotide-binding,

1639762_at Dmel_CG3734 Drosophila melanogaster GO:0006508~proteolysis, GO:0008233~peptidase activity,GO:0008236~serine-type peptidase activity,GO:0017171~serine hydrolase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR008758:Peptidase S28, PIRSF016539:Lysosomal Pro-X carboxypeptidase / Dipeptidyl-peptidase 2, complete proteome,

1632834_a_at Dmel_CG5946 Drosophila melanogaster GO:0006897~endocytosis,GO:0006909~phagocytosis,GO:0006911~phagocytosis, engulfment,GO:0010324~membrane invagination,GO:0016044~membrane organization,GO:0016192~vesicle-mediated transport,GO:0055114~oxidation reduction, GO:0004128~cytochrome-b5 reductase activity,GO:0009055~electron carrier activity,GO:0016651~oxidoreductase activity, acting on NADH or NADPH,GO:0016653~oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor, IPR001433:Oxidoreductase FAD/NAD(P)-binding,IPR001709:Flavoprotein pyridine nucleotide cytochrome reductase,IPR001834:NADH:cytochrome b5 reductase (CBR),IPR008333:Oxidoreductase FAD-binding region,IPR017927:Ferredoxin reductase-type FAD-binding domain, dme00520:Amino sugar and nucleotide sugar metabolism, PIRSF000206:cytochrome-b5 reductase, complete proteome,FAD,Flavoprotein,nad,oxidoreductase,

1625519_at Dmel_CG6453 Drosophila melanogaster GO:0005783~endoplasmic reticulum,GO:0017177~alpha-glucosidase II complex,GO:0044432~endoplasmic reticulum part, GO:0004558~alpha-glucosidase activity,GO:0015926~glucosidase activity, IPR002172:Low density lipoprotein-receptor, class A, cysteine-rich,IPR012913:Glucosidase II beta subunit-like,IPR018247:EF-HAND 1, PIRSF017177:uncharacterized conserved protein, SM00192:LDLa, complete proteome,glycosidase,hydrolase,

1635065_at Dmel_CG7025 Drosophila melanogaster GO:0006508~proteolysis, GO:0004180~carboxypeptidase activity,GO:0004181~metallocarboxypeptidase activity,GO:0008233~peptidase activity,GO:0008235~metalloexopeptidase activity,GO:0008237~metallopeptidase activity,GO:0008238~exopeptidase activity,GO:0008270~zinc ion binding,GO:0043167~ion binding,GO:0043169~cation binding,GO:0046872~metal ion binding,GO:0046914~transition metal ion binding,GO:0070011~peptidase activity, acting on L-amino acid peptides, IPR000834:Peptidase M14, carboxypeptidase A, SM00631:Zn_pept, carboxypeptidase,complete proteome,hydrolase,

1628429_at Protein transport protein Sec61 gamma-2 subunit Drosophila melanogaster GO:0006605~protein targeting,GO:0006612~protein targeting to membrane,GO:0006613~cotranslational protein targeting to membrane,GO:0006614~SRP-dependent cotranslational protein targeting to membrane,GO:0006616~SRP-dependent cotranslational protein targeting to membrane, translocation,GO:0006886~intracellular protein transport,GO:0007033~vacuole organization,GO:0007040~lysosome organization,GO:0008104~protein localization,GO:0009894~regulation of catabolic process,GO:0009895~negative regulation of catabolic process,GO:0010506~regulation of autophagy,GO:0010507~negative regulation of autophagy,GO:0015031~protein transport,GO:0031329~regulation of cellular catabolic process,GO:0031330~negative regulation of cellular catabolic process,GO:0033365~protein localization in organelle,GO:0034613~cellular protein localization,GO:0045047~protein targeting to ER,GO:0045184~establishment of protein localization,GO:0046907~intracellular transport,GO:0055085~transmembrane transport,GO:0065002~intracellular protein transmembrane transport,GO:0070727~cellular macromolecule localization, GO:0005783~endoplasmic reticulum,GO:0005784~translocon complex,GO:0005789~endoplasmic reticulum membrane,GO:0005791~rough endoplasmic reticulum,GO:0012505~endomembrane system,GO:0016021~integral to membrane,GO:0030176~integral to endoplasmic reticulum membrane,GO:0030867~rough endoplasmic reticulum membrane,GO:0031090~organelle membrane,GO:0031224~intrinsic to membrane,GO:0031227~intrinsic to endoplasmic reticulum membrane,GO:0031300~intrinsic to organelle membrane,GO:0031301~integral to organelle membrane,GO:0042175~nuclear envelope-endoplasmic reticulum network,GO:0044432~endoplasmic reticulum part, GO:0008320~protein transmembrane transporter activity,GO:0008565~protein transporter activity,GO:0015399~primary active transmembrane transporter activity,GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity,GO:0015450~P-P-bond-hydrolysis-driven protein transmembrane transporter activity,GO:0022884~macromolecule transmembrane transporter activity, IPR001901:Protein secE/sec61-gamma protein,IPR008158:Protein translocase SEC61 complex gamma subunit, PIRSF005525:preprotein translocase Sec, SecE/Sec61-gamma subunit,PIRSF500209:preprotein translocase Sec, Sec61-gamma subunit, complete proteome,endoplasmic reticulum,membrane,protein transport,translocation,transmembrane,transport, chain:Protein transport protein Sec61 gamma-2 subunit,topological domain:Cytoplasmic,topological domain:Extracellular,transmembrane region,

1636639_at	Signal peptide protease	Drosophila melanogaster	GO:0006508~proteolysis,GO:0007424~open tracheal system development,GO:0009057~macromolecule catabolic process,GO:0030163~protein catabolic process,GO:0033619~membrane protein proteolysis,GO:0044257~cellular protein catabolic process,GO:0044265~cellular macromolecule catabolic process,GO:0051603~proteolysis involved in cellular protein catabolic process,GO:0060541~respiratory system development,	GO:0005783~endoplasmic reticulum,GO:0016021~integral to membrane,GO:0031224~intrinsic to membrane,	GO:0004175~endopeptidase activity,GO:0004190~aspartic-type endopeptidase activity,GO:0008233~peptidase activity,GO:0042500~aspartic endopeptidase activity, intramembrane cleaving,GO:0070001~aspartic-type peptidase activity,GO:0070011~peptidase activity, acting on L-amino acid peptides,	IPR006639:Peptidase A22, presenilin signal peptide,IPR007369:Peptidase A22B, signal peptide peptidase,	SM00730:PSN,	complete proteome,hydrolase,Protease,

File S3

Functional annotations for the probe sets classified in Figure 8

Functional terms enriching the lists of probe sets in each expression pattern, obtained with the DAVID *Functional annotation chart* tool

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Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	SP_PIR_KEYWORDS	alternative splicing	RT		167	11.5	1.4E-31	1.9E-28
	GOTERM_BP_FAT	generation of precursor metabolites and energy	RT		85	5.8	5.4E-27	9.5E-24
	GOTERM_BP_FAT	energy derivation by oxidation of organic compounds	RT		58	4.0	2.4E-25	4.3E-22
	UP_SEQ_FEATURE	splice variant	RT		165	11.3	5.1E-25	8.3E-22
	GOTERM_BP_FAT	cellular respiration	RT		54	3.7	6.9E-24	1.2E-20
	GOTERM_CC_FAT	respiratory chain	RT		46	3.2	3.6E-19	5.1E-16
	GOTERM_BP_FAT	electron transport chain	RT		44	3.0	1.9E-18	3.3E-15
	GOTERM_BP_FAT	phosphorus metabolic process	RT		131	9.0	2.7E-18	4.7E-15

GOTERM_BP_FAT	phosphate metabolic process	RT	131	9.0	2.7E-18	4.7E-15
GOTERM_CC_FAT	mitochondrial respiratory chain	RT	44	3.0	3.7E-18	5.2E-15
GOTERM_BP_FAT	respiratory electron transport chain	RT	39	2.7	8.3E-18	1.5E-14
GOTERM_BP_FAT	phosphorylation	RT	109	7.5	9.8E-18	1.7E-14
KEGG_PATHWAY	Oxidative phosphorylation	RT	58	4.0	5.2E-17	5.7E-14
GOTERM_BP_FAT	mitochondrial ATP synthesis coupled electron transport	RT	36	2.5	8.3E-17	1.9E-13
GOTERM_BP_FAT	oxidative phosphorylation	RT	52	3.6	9.2E-17	1.9E-13
GOTERM_BP_FAT	ATP synthesis coupled electron transport	RT	37	2.5	1.0E-16	1.9E-13
GOTERM_CC_FAT	mitochondrial membrane part	RT	55	3.8	6.0E-16	7.9E-13
GOTERM_CC_FAT	mitochondrial inner membrane	RT	68	4.7	1.0E-14	1.4E-11
GOTERM_CC_FAT	mitochondrion	RT	137	9.4	1.2E-14	1.7E-11
GOTERM_CC_FAT	organelle inner membrane	RT	70	4.8	7.6E-14	1.1E-10
GOTERM_BP_FAT	mitochondrial electron transport, NADH to ubiquinone	RT	22	1.5	1.7E-12	3.0E-9
GOTERM_CC_FAT	mitochondrial membrane	RT	72	4.9	2.2E-12	3.1E-9
GOTERM_CC_FAT	mitochondrial envelope	RT	75	5.2	3.1E-12	4.5E-9
GOTERM_CC_FAT	mitochondrial part	RT	103	7.1	3.7E-12	5.2E-9
GOTERM_MF_FAT	cytoskeletal protein binding	RT	64	4.4	1.3E-11	2.0E-8
GOTERM_BP_FAT	epithelium development	RT	63	4.3	3.2E-11	5.6E-8
SP_PIR_KEYWORDS	phosphoprotein	RT	148	10.2	4.2E-11	5.7E-8
GOTERM_CC_FAT	mitochondrial respiratory chain complex I	RT	25	1.7	4.1E-11	5.9E-8
GOTERM_CC_FAT	NADH dehydrogenase complex	RT	25	1.7	4.1E-11	5.9E-8

GOTERM_CC_FAT	respiratory chain complex I	RT	25	1.7	4.1E-11	5.9E-8
GOTERM_MF_FAT	NADH dehydrogenase activity	RT	24	1.6	5.8E-11	9.2E-8
GOTERM_BP_FAT	cellular component morphogenesis	RT	106	7.3	2.5E-10	4.3E-7
GOTERM_CC_FAT	organelle envelope	RT	86	5.9	4.0E-10	5.6E-7
GOTERM_CC_FAT	envelope	RT	86	5.9	4.6E-10	6.6E-7
GOTERM_BP_FAT	cell morphogenesis	RT	94	6.5	3.8E-10	6.7E-7
GOTERM_BP_FAT	establishment or maintenance of cell polarity	RT	37	2.5	7.0E-10	1.2E-6
GOTERM_BP_FAT	transmission of nerve impulse	RT	53	3.6	1.1E-9	1.9E-6
GOTERM_BP_FAT	morphogenesis of an epithelium	RT	58	4.0	1.1E-9	1.9E-6
GOTERM_BP_FAT	actin cytoskeleton organization	RT	43	3.0	1.6E-9	2.8E-6
INTERPRO	PDZ/DHR/GLGF	RT	28	1.9	1.7E-9	2.9E-6
GOTERM_MF_FAT	oxidoreductase activity, acting on NADH or NADPH	RT	25	1.7	1.9E-9	3.0E-6
GOTERM_BP_FAT	actin filament-based process	RT	43	3.0	2.0E-9	3.6E-6
GOTERM_BP_FAT	morphogenesis of embryonic epithelium	RT	38	2.6	3.5E-9	6.2E-6
GOTERM_CC_FAT	lipid particle	RT	66	4.5	5.6E-9	8.0E-6
INTERPRO	Src homology-3 domain	RT	29	2.0	5.2E-9	8.7E-6
GOTERM_BP_FAT	post-embryonic morphogenesis	RT	77	5.3	6.0E-9	1.1E-5
GOTERM_BP_FAT	tissue morphogenesis	RT	60	4.1	6.3E-9	1.1E-5
GOTERM_BP_FAT	metamorphosis	RT	78	5.4	8.4E-9	1.5E-5
GOTERM_CC_FAT	septate junction	RT	15	1.0	1.5E-8	2.1E-5
GOTERM_BP_FAT	instar larval or pupal morphogenesis	RT	75	5.2	1.5E-8	2.6E-5

SMART	PDZ	RT	28	1.9	2.0E-8	2.7E-5
GOTERM_BP_FAT	apical junction assembly	RT	16	1.1	2.1E-8	3.8E-5
GOTERM_BP_FAT	synaptic transmission	RT	49	3.4	2.2E-8	3.8E-5
UP_SEQ_FEATURE	compositionally biased region:Gln-rich	RT	48	3.3	2.8E-8	4.5E-5
GOTERM_MF_FAT	NADH dehydrogenase (quinone) activity	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_MF_FAT	oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_MF_FAT	NADH dehydrogenase (ubiquinone) activity	RT	19	1.3	3.0E-8	4.7E-5
GOTERM_BP_FAT	cell-cell junction organization	RT	18	1.2	3.5E-8	6.1E-5
SP_PIR_KEYWORDS	muscle protein	RT	12	0.8	5.1E-8	7.0E-5
GOTERM_BP_FAT	neuron differentiation	RT	83	5.7	4.6E-8	8.0E-5
GOTERM_BP_FAT	cell-cell signaling	RT	52	3.6	4.6E-8	8.0E-5
GOTERM_BP_FAT	open tracheal system development	RT	42	2.9	4.7E-8	8.2E-5
GOTERM_BP_FAT	respiratory system development	RT	42	2.9	4.7E-8	8.2E-5
SMART	SH3	RT	29	2.0	6.1E-8	8.2E-5
GOTERM_BP_FAT	dorsal closure	RT	31	2.1	5.9E-8	1.0E-4
GOTERM_BP_FAT	cell junction organization	RT	18	1.2	5.9E-8	1.0E-4
GOTERM_BP_FAT	cell-cell junction assembly	RT	16	1.1	7.7E-8	1.3E-4
GOTERM_BP_FAT	exocrine system development	RT	39	2.7	8.2E-8	1.4E-4
GOTERM_BP_FAT	salivary gland development	RT	39	2.7	8.2E-8	1.4E-4
GOTERM_BP_FAT	cell adhesion	RT	45	3.1	9.7E-8	1.7E-4
SP_PIR_KEYWORDS	calcium	RT	41	2.8	1.3E-7	1.7E-4

GOTERM_CC_FAT	cell junction	RT	41	2.8	1.2E-7	1.8E-4
GOTERM_BP_FAT	instar larval or pupal development	RT	83	5.7	1.2E-7	2.2E-4
GOTERM_BP_FAT	salivary gland morphogenesis	RT	34	2.3	1.4E-7	2.4E-4
GOTERM_BP_FAT	gland morphogenesis	RT	34	2.3	1.4E-7	2.4E-4
GOTERM_CC_FAT	contractile fiber part	RT	13	0.9	1.7E-7	2.4E-4
GOTERM_BP_FAT	cell junction assembly	RT	16	1.1	1.4E-7	2.4E-4
GOTERM_BP_FAT	regulation of tube size	RT	14	1.0	1.5E-7	2.6E-4
GOTERM_BP_FAT	cofactor catabolic process	RT	17	1.2	1.6E-7	2.7E-4
GOTERM_CC_FAT	organelle membrane	RT	94	6.5	2.1E-7	2.9E-4
GOTERM_BP_FAT	regulation of small GTPase mediated signal transduction	RT	30	2.1	1.7E-7	3.0E-4
GOTERM_BP_FAT	neurotransmitter transport	RT	36	2.5	1.7E-7	3.1E-4
GOTERM_BP_FAT	regulation of tube size, open tracheal system	RT	13	0.9	1.8E-7	3.2E-4
GOTERM_BP_FAT	regulation of neurotransmitter levels	RT	33	2.3	1.8E-7	3.2E-4
SP_PIR_KEYWORDS	developmental protein	RT	97	6.7	2.5E-7	3.4E-4
SP_PIR_KEYWORDS	atp-binding	RT	103	7.1	2.7E-7	3.7E-4
KEGG_PATHWAY	Citrate cycle (TCA cycle)	RT	21	1.4	3.6E-7	3.9E-4
GOTERM_MF_FAT	small GTPase regulator activity	RT	34	2.3	2.5E-7	4.0E-4
INTERPRO	EGF-like	RT	26	1.8	2.4E-7	4.0E-4
SP_PIR_KEYWORDS	nucleotide-binding	RT	124	8.5	3.0E-7	4.1E-4
GOTERM_BP_FAT	acetyl-CoA metabolic process	RT	17	1.2	2.6E-7	4.5E-4
GOTERM_BP_FAT	post-embryonic development	RT	84	5.8	3.2E-7	5.6E-4

GOTERM_BP_FAT	neurotransmitter secretion	RT	31	2.1	3.4E-7	6.0E-4
INTERPRO	Pleckstrin homology-type	RT	33	2.3	3.6E-7	6.1E-4
GOTERM_BP_FAT	acetyl-CoA catabolic process	RT	16	1.1	4.1E-7	7.1E-4
GOTERM_BP_FAT	tricarboxylic acid cycle	RT	16	1.1	4.1E-7	7.1E-4
GOTERM_MF_FAT	GTPase regulator activity	RT	40	2.7	4.8E-7	7.5E-4
GOTERM_BP_FAT	generation of a signal involved in cell-cell signaling	RT	31	2.1	4.3E-7	7.6E-4
GOTERM_CC_FAT	cell-cell junction	RT	23	1.6	5.5E-7	7.8E-4
GOTERM_BP_FAT	autophagic cell death	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_BP_FAT	salivary gland cell autophagic cell death	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_BP_FAT	salivary gland histolysis	RT	24	1.6	5.3E-7	9.2E-4
GOTERM_CC_FAT	occluding junction	RT	15	1.0	6.6E-7	9.4E-4
SP_PIR_KEYWORDS	cytoplasm	RT	81	5.6	6.9E-7	9.5E-4
GOTERM_BP_FAT	coenzyme catabolic process	RT	16	1.1	6.7E-7	1.2E-3
GOTERM_CC_FAT	apical junction complex	RT	19	1.3	8.6E-7	1.2E-3
GOTERM_BP_FAT	regulation of Ras protein signal transduction	RT	26	1.8	7.2E-7	1.3E-3
GOTERM_BP_FAT	muscle cell differentiation	RT	25	1.7	7.2E-7	1.3E-3
GOTERM_CC_FAT	contractile fiber	RT	13	0.9	9.0E-7	1.3E-3
GOTERM_MF_FAT	nucleoside-triphosphatase regulator activity	RT	40	2.7	8.6E-7	1.3E-3
GOTERM_BP_FAT	neuron development	RT	70	4.8	7.8E-7	1.4E-3
GOTERM_BP_FAT	tissue death	RT	24	1.6	9.5E-7	1.7E-3
GOTERM_BP_FAT	histolysis	RT	24	1.6	9.5E-7	1.7E-3

GOTERM_BP_FAT	biological adhesion	RT	45	3.1	1.0E-6	1.8E-3
GOTERM_BP_FAT	regulation of tube architecture, open tracheal system	RT	17	1.2	1.0E-6	1.8E-3
GOTERM_BP_FAT	aerobic respiration	RT	16	1.1	1.1E-6	1.9E-3
GOTERM_BP_FAT	programmed cell death	RT	39	2.7	1.2E-6	2.1E-3
GOTERM_BP_FAT	cell motion	RT	63	4.3	1.3E-6	2.3E-3
GOTERM_BP_FAT	negative regulation of cell communication	RT	30	2.1	1.5E-6	2.6E-3
GOTERM_CC_FAT	sarcomere	RT	11	0.8	1.9E-6	2.7E-3
SMART	EGF	RT	26	1.8	2.0E-6	2.8E-3
GOTERM_CC_FAT	actin cytoskeleton	RT	29	2.0	1.9E-6	2.8E-3
GOTERM_MF_FAT	actin binding	RT	35	2.4	1.8E-6	2.8E-3
SP_PIR_KEYWORDS	actin-binding	RT	18	1.2	2.3E-6	3.1E-3
GOTERM_BP_FAT	vesicle-mediated transport	RT	75	5.2	2.2E-6	3.8E-3
GOTERM_BP_FAT	gland development	RT	40	2.7	2.3E-6	4.1E-3
INTERPRO	Variant SH3	RT	11	0.8	2.5E-6	4.2E-3
GOTERM_BP_FAT	septate junction assembly	RT	11	0.8	2.6E-6	4.6E-3
GOTERM_BP_FAT	secretion by cell	RT	32	2.2	3.2E-6	5.7E-3
GOTERM_CC_FAT	apicolateral plasma membrane	RT	19	1.3	4.4E-6	6.2E-3
GOTERM_CC_FAT	myofibril	RT	11	0.8	4.6E-6	6.5E-3
GOTERM_BP_FAT	striated muscle cell differentiation	RT	22	1.5	3.8E-6	6.7E-3
GOTERM_BP_FAT	negative regulation of signal transduction	RT	29	2.0	3.8E-6	6.7E-3
INTERPRO	Pleckstrin homology	RT	25	1.7	4.0E-6	6.7E-3

GOTERM_BP_FAT	regulation of cell morphogenesis	RT	32	2.2	3.9E-6	6.8E-3
SP_PIR_KEYWORDS	sh3 domain	RT	18	1.2	6.2E-6	8.5E-3
GOTERM_BP_FAT	cell death	RT	39	2.7	5.2E-6	9.1E-3
GOTERM_BP_FAT	chitin-based embryonic cuticle biosynthetic process	RT	11	0.8	5.3E-6	9.2E-3
GOTERM_BP_FAT	cell proliferation	RT	33	2.3	5.9E-6	1.0E-2
GOTERM_BP_FAT	cytoskeleton organization	RT	84	5.8	5.9E-6	1.0E-2
GOTERM_BP_FAT	death	RT	39	2.7	6.1E-6	1.1E-2
SP_PIR_KEYWORDS	oxidoreductase	RT	94	6.5	8.3E-6	1.1E-2
GOTERM_BP_FAT	neurological system process	RT	95	6.5	6.7E-6	1.2E-2
GOTERM_CC_FAT	plasma membrane part	RT	83	5.7	8.8E-6	1.2E-2
GOTERM_MF_FAT	calcium ion binding	RT	54	3.7	1.0E-5	1.6E-2
GOTERM_BP_FAT	synaptic vesicle transport	RT	26	1.8	1.0E-5	1.7E-2
GOTERM_BP_FAT	secretion	RT	32	2.2	1.2E-5	2.0E-2
SP_PIR_KEYWORDS	transit peptide	RT	29	2.0	1.7E-5	2.4E-2
GOTERM_BP_FAT	muscle cell development	RT	17	1.2	1.4E-5	2.4E-2
GOTERM_BP_FAT	striated muscle cell development	RT	17	1.2	1.4E-5	2.4E-2
GOTERM_MF_FAT	protein serine/threonine kinase activity	RT	47	3.2	1.5E-5	2.4E-2
GOTERM_BP_FAT	protein amino acid phosphorylation	RT	53	3.6	1.4E-5	2.4E-2
GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	34	2.3	1.6E-5	2.5E-2
INTERPRO	Serine/threonine protein kinase	RT	31	2.1	1.5E-5	2.6E-2
INTERPRO	EGF-like, type 3	RT	20	1.4	1.6E-5	2.6E-2

SP_PIR_KEYWORDS	mitochondrion	RT	40	2.7	2.2E-5	3.0E-2
SP_PIR_KEYWORDS	kinase	RT	44	3.0	2.3E-5	3.2E-2
GOTERM_MF_FAT	monovalent inorganic cation transmembrane transporter activity	RT	28	1.9	2.1E-5	3.3E-2
SP_PIR_KEYWORDS	ubl conjugation pathway	RT	26	1.8	2.4E-5	3.3E-2
INTERPRO	Protein kinase, ATP binding site	RT	43	3.0	2.0E-5	3.3E-2
GOTERM_BP_FAT	oxidation reduction	RT	103	7.1	2.0E-5	3.5E-2
GOTERM_CC_FAT	plasma membrane	RT	138	9.5	2.6E-5	3.7E-2
SMART	PH	RT	25	1.7	2.8E-5	3.8E-2
GOTERM_CC_FAT	myosin II complex	RT	7	0.5	2.8E-5	4.0E-2
GOTERM_BP_FAT	cellular protein complex assembly	RT	24	1.6	2.3E-5	4.1E-2
GOTERM_BP_FAT	membrane organization	RT	61	4.2	2.5E-5	4.4E-2
GOTERM_BP_FAT	skeletal muscle organ development	RT	19	1.3	2.7E-5	4.6E-2
GOTERM_MF_FAT	hydrogen ion transmembrane transporter activity	RT	27	1.9	4.1E-5	6.4E-2
GOTERM_BP_FAT	myofibril assembly	RT	9	0.6	3.7E-5	6.5E-2
SP_PIR_KEYWORDS	egf-like domain	RT	17	1.2	4.8E-5	6.6E-2
INTERPRO	EF-Hand type	RT	28	1.9	4.2E-5	7.0E-2
SP_PIR_KEYWORDS	transmembrane protein	RT	21	1.4	5.2E-5	7.1E-2
GOTERM_BP_FAT	cuticle development	RT	20	1.4	4.2E-5	7.4E-2
SP_PIR_KEYWORDS	ATP	RT	20	1.4	5.9E-5	8.1E-2
UP_SEQ_FEATURE	mutagenesis site	RT	48	3.3	5.0E-5	8.2E-2
GOTERM_BP_FAT	post-embryonic organ morphogenesis	RT	55	3.8	4.7E-5	8.3E-2

	GOTERM_BP_FAT	imaginal disc morphogenesis	RT		55	3.8	4.7E-5	8.3E-2
	GOTERM_BP_FAT	regulation of cell shape	RT		26	1.8	4.9E-5	8.5E-2
	GOTERM_BP_FAT	protein kinase cascade	RT		19	1.3	5.7E-5	1.0E-1
	GOTERM_CC_FAT	cytoskeleton	RT		71	4.9	7.2E-5	1.0E-1
	GOTERM_CC_FAT	synapse	RT		33	2.3	7.4E-5	1.0E-1

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Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	Golgi apparatus part	RT		23	3.6	1.9E-10	2.6E-7
	GOTERM_CC_FAT	endoplasmic reticulum part	RT		26	4.1	7.8E-10	1.0E-6
	GOTERM_CC_FAT	endoplasmic reticulum	RT		43	6.8	1.3E-9	1.7E-6
	GOTERM_CC_FAT	Golgi-associated vesicle	RT		12	1.9	2.3E-9	3.1E-6
	GOTERM_CC_FAT	rough endoplasmic reticulum	RT		10	1.6	6.1E-9	8.0E-6
	GOTERM_CC_FAT	endoplasmic reticulum membrane	RT		20	3.2	1.0E-8	1.3E-5

GOTERM_CC_FAT	Golgi apparatus	RT	30	4.7	1.0E-8	1.4E-5
GOTERM_CC_FAT	organelle membrane	RT	54	8.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	endomembrane system	RT	35	5.5	1.5E-8	1.9E-5
GOTERM_CC_FAT	nuclear envelope-endoplasmic reticulum network	RT	20	3.2	1.6E-8	2.1E-5
GOTERM_BP_FAT	cotranslational protein targeting to membrane	RT	10	1.6	2.4E-8	3.9E-5
GOTERM_CC_FAT	rough endoplasmic reticulum membrane	RT	9	1.4	3.0E-8	3.9E-5
GOTERM_CC_FAT	Golgi membrane	RT	14	2.2	1.3E-7	1.7E-4
GOTERM_BP_FAT	protein targeting to ER	RT	9	1.4	2.7E-7	4.4E-4
GOTERM_BP_FAT	SRP-dependent cotranslational protein targeting to membrane	RT	9	1.4	2.7E-7	4.4E-4
GOTERM_MF_FAT	exopeptidase activity	RT	21	3.3	3.1E-7	4.6E-4
GOTERM_BP_FAT	protein targeting to membrane	RT	11	1.7	2.9E-7	4.7E-4
GOTERM_BP_FAT	retrograde vesicle-mediated transport, Golgi to ER	RT	7	1.1	6.0E-7	1.0E-3
GOTERM_BP_FAT	intracellular protein transport	RT	25	3.9	8.5E-7	1.4E-3
GOTERM_CC_FAT	Golgi-associated vesicle membrane	RT	8	1.3	1.8E-6	2.3E-3
GOTERM_BP_FAT	cellular protein localization	RT	25	3.9	1.4E-6	2.4E-3
GOTERM_CC_FAT	COPI coated vesicle membrane	RT	7	1.1	1.9E-6	2.5E-3
GOTERM_CC_FAT	COPI vesicle coat	RT	7	1.1	1.9E-6	2.5E-3
GOTERM_CC_FAT	vesicle coat	RT	9	1.4	2.0E-6	2.6E-3
GOTERM_BP_FAT	protein transport	RT	32	5.1	2.5E-6	4.1E-3
GOTERM_CC_FAT	COPI-coated vesicle	RT	7	1.1	4.4E-6	5.9E-3
GOTERM_BP_FAT	establishment of protein localization	RT	32	5.1	4.2E-6	6.9E-3

GOTERM_CC_FAT	coated vesicle membrane	RT	9	1.4	1.2E-5	1.6E-2
GOTERM_MF_FAT	aminopeptidase activity	RT	12	1.9	1.1E-5	1.7E-2
GOTERM_BP_FAT	intracellular transport	RT	33	5.2	1.1E-5	1.8E-2
GOTERM_BP_FAT	protein localization	RT	38	6.0	1.4E-5	2.3E-2
GOTERM_CC_FAT	cytoplasmic vesicle part	RT	9	1.4	1.7E-5	2.3E-2
GOTERM_CC_FAT	cytoplasmic vesicle membrane	RT	9	1.4	1.7E-5	2.3E-2
GOTERM_BP_FAT	Golgi vesicle transport	RT	11	1.7	1.6E-5	2.6E-2
GOTERM_CC_FAT	translocon complex	RT	6	0.9	2.3E-5	3.1E-2
GOTERM_BP_FAT	hexose metabolic process	RT	15	2.4	2.3E-5	3.8E-2
GOTERM_BP_FAT	monosaccharide metabolic process	RT	16	2.5	2.6E-5	4.2E-2
GOTERM_BP_FAT	protein targeting	RT	17	2.7	2.7E-5	4.4E-2
GOTERM_MF_FAT	vitamin binding	RT	17	2.7	3.7E-5	5.4E-2
GOTERM_BP_FAT	mannose metabolic process	RT	6	0.9	3.8E-5	6.2E-2
GOTERM_BP_FAT	protein localization in organelle	RT	15	2.4	5.0E-5	8.3E-2
GOTERM_CC_FAT	vesicle membrane	RT	9	1.4	6.5E-5	8.5E-2
SP_PIR_KEYWORDS	transport	RT	42	6.6	8.2E-5	1.0E-1

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Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	ribonucleoprotein complex	RT		176	5.3	2.6E-25	3.8E-22
	SP_PIR_KEYWORDS	ribonucleoprotein	RT		88	2.6	6.5E-24	9.0E-21
	GOTERM_CC_FAT	cytosolic part	RT		82	2.5	2.9E-23	4.2E-20
	GOTERM_CC_FAT	cytosolic ribosome	RT		66	2.0	1.6E-22	2.2E-19
	GOTERM_MF_FAT	structural constituent of ribosome	RT		95	2.9	1.3E-18	2.1E-15
	GOTERM_CC_FAT	ribosome	RT		97	2.9	4.0E-18	5.7E-15
	KEGG_PATHWAY	Ribosome	RT		67	2.0	5.4E-18	6.1E-15
	GOTERM_CC_FAT	ribosomal subunit	RT		89	2.7	4.3E-18	6.1E-15
	GOTERM_BP_FAT	RNA processing	RT		129	3.9	2.0E-17	3.5E-14
	GOTERM_BP_FAT	ribonucleoprotein complex biogenesis	RT		57	1.7	8.7E-17	2.0E-13
	GOTERM_CC_FAT	cytosolic large ribosomal subunit	RT		41	1.2	5.7E-15	8.3E-12
	SP_PIR_KEYWORDS	ribosomal protein	RT		85	2.6	9.6E-15	1.3E-11
	GOTERM_BP_FAT	ribosome biogenesis	RT		42	1.3	4.1E-14	7.2E-11
	GOTERM_CC_FAT	large ribosomal subunit	RT		54	1.6	1.4E-10	2.0E-7
	GOTERM_BP_FAT	protein folding	RT		55	1.7	1.5E-10	2.6E-7
	GOTERM_BP_FAT	intracellular transport	RT		112	3.4	2.9E-10	5.1E-7

GOTERM_BP_FAT	mitotic spindle elongation	RT	42	1.3	3.2E-10	5.7E-7
GOTERM_BP_FAT	spindle elongation	RT	42	1.3	5.4E-10	9.5E-7
GOTERM_BP_FAT	mRNA metabolic process	RT	85	2.6	6.2E-10	1.1E-6
GOTERM_BP_FAT	RNA splicing	RT	64	1.9	7.1E-10	1.3E-6
GOTERM_CC_FAT	membrane-enclosed lumen	RT	191	5.8	1.9E-9	2.8E-6
KEGG_PATHWAY	Spliceosome	RT	65	2.0	2.6E-9	2.9E-6
SP_PIR_KEYWORDS	rna-binding	RT	67	2.0	3.6E-9	4.9E-6
GOTERM_BP_FAT	ncRNA metabolic process	RT	58	1.7	3.4E-9	6.0E-6
GOTERM_BP_FAT	mRNA processing	RT	76	2.3	3.5E-9	6.1E-6
GOTERM_BP_FAT	ncRNA processing	RT	45	1.4	3.6E-9	6.4E-6
GOTERM_BP_FAT	post-mating behavior	RT	17	0.5	4.8E-9	8.4E-6
GOTERM_CC_FAT	intracellular organelle lumen	RT	184	5.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	organelle lumen	RT	184	5.5	1.1E-8	1.5E-5
GOTERM_CC_FAT	nuclear lumen	RT	137	4.1	1.3E-8	1.9E-5
GOTERM_CC_FAT	spliceosome	RT	39	1.2	2.1E-8	3.0E-5
GOTERM_BP_FAT	nucleocytoplasmic transport	RT	37	1.1	2.2E-8	3.9E-5
GOTERM_BP_FAT	nuclear transport	RT	37	1.1	2.2E-8	3.9E-5
GOTERM_BP_FAT	mitotic spindle organization	RT	73	2.2	5.2E-8	9.1E-5
SMART	Sm	RT	15	0.5	7.1E-8	9.5E-5
GOTERM_BP_FAT	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	RT	53	1.6	7.6E-8	1.3E-4
GOTERM_BP_FAT	nuclear mRNA splicing, via spliceosome	RT	53	1.6	7.6E-8	1.3E-4

GOTERM_BP_FAT	RNA splicing, via transesterification reactions	RT	53	1.6	1.0E-7	1.8E-4
GOTERM_CC_FAT	cytosolic small ribosomal subunit	RT	25	0.8	1.4E-7	1.9E-4
GOTERM_CC_FAT	small ribosomal subunit	RT	36	1.1	1.7E-7	2.5E-4
SP_PIR_KEYWORDS	protein biosynthesis	RT	47	1.4	2.4E-7	3.3E-4
GOTERM_BP_FAT	spindle organization	RT	79	2.4	4.0E-7	7.0E-4
GOTERM_CC_FAT	non-membrane-bounded organelle	RT	277	8.3	5.1E-7	7.3E-4
GOTERM_CC_FAT	intracellular non-membrane-bounded organelle	RT	277	8.3	5.1E-7	7.3E-4
SP_PIR_KEYWORDS	ribosome	RT	19	0.6	9.2E-7	1.3E-3
SP_PIR_KEYWORDS	mrna splicing	RT	23	0.7	1.0E-6	1.4E-3
COG_ONTOLOGY	Translation, ribosomal structure and biogenesis	RT	34	1.0	2.2E-6	2.0E-3
INTERPRO	Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core	RT	15	0.5	1.2E-6	2.2E-3
INTERPRO	Like-Sm ribonucleoprotein, core	RT	15	0.5	1.2E-6	2.2E-3
GOTERM_MF_FAT	mRNA binding	RT	72	2.2	1.5E-6	2.4E-3
SP_PIR_KEYWORDS	mrna processing	RT	28	0.8	1.8E-6	2.5E-3
GOTERM_BP_FAT	rRNA processing	RT	23	0.7	1.6E-6	2.7E-3
GOTERM_BP_FAT	microtubule-based process	RT	123	3.7	2.0E-6	3.5E-3
GOTERM_BP_FAT	rRNA metabolic process	RT	23	0.7	2.7E-6	4.8E-3
GOTERM_CC_FAT	small nuclear ribonucleoprotein complex	RT	39	1.2	3.7E-6	5.3E-3
GOTERM_BP_FAT	RNA export from nucleus	RT	16	0.5	4.2E-6	7.3E-3
GOTERM_BP_FAT	nuclear export	RT	19	0.6	5.0E-6	8.8E-3
GOTERM_CC_FAT	nucleoplasm part	RT	86	2.6	6.1E-6	8.8E-3

	GOTERM_BP_FAT	microtubule cytoskeleton organization	RT		94	2.8	6.2E-6	1.1E-2
	GOTERM_BP_FAT	translation	RT		148	4.5	8.0E-6	1.4E-2
	GOTERM_CC_FAT	nucleoplasm	RT		92	2.8	1.2E-5	1.7E-2
	GOTERM_BP_FAT	ribonucleoprotein complex assembly	RT		20	0.6	1.0E-5	1.8E-2
	GOTERM_BP_FAT	oxidation reduction	RT		171	5.1	1.1E-5	1.9E-2
	GOTERM_BP_FAT	tRNA metabolic process	RT		38	1.1	2.0E-5	3.6E-2
	SMART	RRM	RT		50	1.5	3.8E-5	5.1E-2
	GOTERM_MF_FAT	unfolded protein binding	RT		34	1.0	3.9E-5	6.2E-2
	GOTERM_BP_FAT	mRNA export from nucleus	RT		14	0.4	4.2E-5	7.4E-2
	GOTERM_BP_FAT	sulfur amino acid metabolic process	RT		11	0.3	5.7E-5	1.0E-1

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Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_CC_FAT	mitochondrial matrix	RT		38	4.3	5.9E-9	8.0E-6

GOTERM_CC_FAT	mitochondrial lumen	RT		38	4.3	5.9E-9	8.0E-6
GOTERM_MF_FAT	ATPase activity, coupled to movement of substances	RT		32	3.6	1.2E-8	1.8E-5
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of substances	RT		32	3.6	1.2E-8	1.8E-5
GOTERM_CC_FAT	mitochondrion	RT		88	10.0	1.4E-8	1.9E-5
GOTERM_MF_FAT	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	RT		32	3.6	1.7E-8	2.5E-5
GOTERM_CC_FAT	mitochondrial part	RT		69	7.8	2.9E-8	3.9E-5
GOTERM_MF_FAT	primary active transmembrane transporter activity	RT		34	3.9	3.3E-8	5.0E-5
GOTERM_MF_FAT	P-P-bond-hydrolysis-driven transmembrane transporter activity	RT		34	3.9	3.3E-8	5.0E-5
GOTERM_MF_FAT	ATPase activity	RT		54	6.1	4.8E-7	7.3E-4
GOTERM_MF_FAT	actin binding	RT		27	3.1	7.2E-7	1.1E-3
GOTERM_CC_FAT	vacuolar membrane	RT		14	1.6	1.3E-6	1.8E-3
GOTERM_CC_FAT	vacuolar part	RT		14	1.6	1.3E-6	1.8E-3
GOTERM_BP_FAT	purine nucleoside triphosphate biosynthetic process	RT		20	2.3	1.2E-6	2.0E-3
GOTERM_BP_FAT	purine ribonucleoside triphosphate biosynthetic process	RT		20	2.3	1.2E-6	2.0E-3
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	RT		20	2.3	1.5E-6	2.3E-3
GOTERM_CC_FAT	vacuolar proton-transporting V-type ATPase complex	RT		13	1.5	1.8E-6	2.4E-3
GOTERM_BP_FAT	ribonucleoside triphosphate biosynthetic process	RT		20	2.3	1.5E-6	2.5E-3
GOTERM_BP_FAT	nucleoside triphosphate biosynthetic process	RT		20	2.3	1.5E-6	2.5E-3
GOTERM_BP_FAT	ribonucleotide biosynthetic process	RT		23	2.6	1.5E-6	2.6E-3
GOTERM_CC_FAT	proton-transporting V-type ATPase complex	RT		14	1.6	1.9E-6	2.6E-3
GOTERM_CC_FAT	mitochondrial ribosome	RT		21	2.4	2.2E-6	3.0E-3

GOTERM_CC_FAT	organellar ribosome	RT	21	2.4	2.2E-6	3.0E-3
GOTERM_BP_FAT	ATP biosynthetic process	RT	19	2.2	2.4E-6	4.1E-3
GOTERM_BP_FAT	purine ribonucleotide biosynthetic process	RT	22	2.5	2.6E-6	4.4E-3
GOTERM_MF_FAT	ATPase activity, coupled	RT	47	5.3	3.0E-6	4.6E-3
GOTERM_BP_FAT	purine ribonucleoside triphosphate metabolic process	RT	20	2.3	3.1E-6	5.2E-3
GOTERM_BP_FAT	purine nucleoside triphosphate metabolic process	RT	20	2.3	3.1E-6	5.2E-3
GOTERM_MF_FAT	ATPase activity, coupled to transmembrane movement of ions	RT	20	2.3	3.5E-6	5.3E-3
GOTERM_BP_FAT	ribonucleotide metabolic process	RT	23	2.6	3.4E-6	5.8E-3
GOTERM_BP_FAT	ATP metabolic process	RT	19	2.2	3.6E-6	6.1E-3
GOTERM_BP_FAT	ribonucleoside triphosphate metabolic process	RT	20	2.3	3.7E-6	6.3E-3
GOTERM_BP_FAT	nucleoside triphosphate metabolic process	RT	20	2.3	4.4E-6	7.5E-3
GOTERM_BP_FAT	purine ribonucleotide metabolic process	RT	22	2.5	5.8E-6	9.8E-3
SP_PIR_KEYWORDS	transmembrane	RT	104	11.8	1.0E-5	1.3E-2
GOTERM_MF_FAT	inorganic cation transmembrane transporter activity	RT	25	2.8	2.0E-5	3.0E-2
SP_PIR_KEYWORDS	actin-binding	RT	13	1.5	2.8E-5	3.7E-2
GOTERM_CC_FAT	organelle membrane	RT	63	7.1	2.9E-5	4.0E-2
SP_PIR_KEYWORDS	nucleotide-binding	RT	78	8.8	3.4E-5	4.5E-2
GOTERM_BP_FAT	generation of precursor metabolites and energy	RT	32	3.6	3.9E-5	6.6E-2
GOTERM_BP_FAT	transmembrane transport	RT	21	2.4	4.1E-5	6.9E-2
INTERPRO	Major facilitator superfamily MFS-1	RT	22	2.5	4.4E-5	7.1E-2
SMART	AAA	RT	21	2.4	6.8E-5	8.5E-2

GOTERM_BP_FAT proton transport RT 15 1.7 5.0E-5 8.5E-2

SP_PIR_KEYWORDS mitochondrion RT 28 3.2 7.1E-5 9.3E-2

GOTERM_MF_FAT solute:cation symporter activity RT 18 2.0 6.3E-5 9.5E-2

GOTERM_MF_FAT hydrogen-exporting ATPase activity, phosphorylative mechanism RT 14 1.6 6.4E-5 9.6E-2

GOTERM_BP_FAT energy coupled proton transport, down electrochemical gradient RT 14 1.6 5.7E-5 9.7E-2

GOTERM_BP_FAT ATP synthesis coupled proton transport RT 14 1.6 5.7E-5 9.7E-2

GOTERM_BP_FAT hydrogen transport RT 15 1.7 6.1E-5 1.0E-1

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+D

C

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Functional annotation chart:

Sublist Category Term RT Genes Count % P-Value FDR

SP_PIR_KEYWORDS alternative splicing RT 51 10.7 2.9E-8 3.7E-5

GOTERM_BP_FAT phototransduction RT 13 2.7 5.3E-8 8.9E-5

GOTERM_BP_FAT phosphate metabolic process RT 47 9.8 1.3E-7 2.2E-4

GOTERM_BP_FAT phosphorus metabolic process RT 47 9.8 1.3E-7 2.2E-4

GOTERM_BP_FAT	detection of light stimulus	RT	13	2.7	2.4E-7	4.0E-4
GOTERM_BP_FAT	detection of external stimulus	RT	14	2.9	2.6E-7	4.4E-4
GOTERM_BP_FAT	detection of abiotic stimulus	RT	13	2.7	7.2E-7	1.2E-3
SP_PIR_KEYWORDS	phosphoprotein	RT	57	11.9	1.1E-6	1.4E-3
UP_SEQ_FEATURE	splice variant	RT	51	10.7	1.4E-6	2.0E-3
GOTERM_CC_FAT	cell projection	RT	16	3.3	9.0E-6	1.2E-2
GOTERM_BP_FAT	response to radiation	RT	16	3.3	1.7E-5	2.8E-2
GOTERM_BP_FAT	phosphorylation	RT	35	7.3	1.7E-5	2.8E-2
GOTERM_BP_FAT	response to light stimulus	RT	15	3.1	1.7E-5	2.9E-2
SP_PIR_KEYWORDS	rna editing	RT	9	1.9	2.3E-5	2.9E-2
GOTERM_CC_FAT	axon	RT	8	1.7	2.7E-5	3.6E-2
GOTERM_BP_FAT	regulation of cell development	RT	17	3.6	2.6E-5	4.3E-2
GOTERM_BP_FAT	vesicle-mediated transport	RT	32	6.7	4.9E-5	8.2E-2
SP_PIR_KEYWORDS	zinc	RT	40	8.4	7.5E-5	9.6E-2
SP_PIR_KEYWORDS	metal-binding	RT	50	10.5	9.6E-5	1.2E-1
GOTERM_BP_FAT	detection of stimulus	RT	14	2.9	7.7E-5	1.3E-1
GOTERM_BP_FAT	protein amino acid phosphorylation	RT	24	5.0	8.9E-5	1.5E-1
SP_PIR_KEYWORDS	vision	RT	10	2.1	1.2E-4	1.5E-1
GOTERM_BP_FAT	neurological system process	RT	39	8.2	1.2E-4	1.9E-1
GOTERM_CC_FAT	rhabdomere	RT	7	1.5	2.1E-4	2.8E-1
GOTERM_BP_FAT	oogenesis	RT	38	7.9	1.9E-4	3.2E-1

GOTERM_CC_FAT	extrinsic to plasma membrane	RT	8	1.7	2.5E-4	3.3E-1
GOTERM_BP_FAT	visual perception	RT	11	2.3	2.4E-4	3.9E-1
GOTERM_BP_FAT	female gamete generation	RT	38	7.9	2.5E-4	4.1E-1
INTERPRO	Protein kinase, core	RT	21	4.4	2.8E-4	4.2E-1
GOTERM_MF_FAT	protein kinase activity	RT	25	5.2	3.0E-4	4.3E-1
GOTERM_BP_FAT	sensory perception of light stimulus	RT	11	2.3	2.7E-4	4.4E-1
GOTERM_BP_FAT	rhodopsin mediated signaling pathway	RT	6	1.3	2.9E-4	4.9E-1
GOTERM_BP_FAT	regulation of cellular protein metabolic process	RT	15	3.1	3.2E-4	5.3E-1
GOTERM_BP_FAT	response to abiotic stimulus	RT	20	4.2	3.7E-4	6.1E-1
SP_PIR_KEYWORDS	kinase	RT	19	4.0	5.2E-4	6.7E-1
GOTERM_BP_FAT	instar larval or pupal morphogenesis	RT	27	5.6	4.9E-4	8.1E-1
GOTERM_BP_FAT	membrane invagination	RT	22	4.6	5.9E-4	9.8E-1
GOTERM_BP_FAT	endocytosis	RT	22	4.6	5.9E-4	9.8E-1
SP_PIR_KEYWORDS	zinc-finger	RT	24	5.0	7.7E-4	9.9E-1
GOTERM_BP_FAT	post-embryonic morphogenesis	RT	27	5.6	6.3E-4	1.1E0

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Functional annotation chart:

Sublist	Category	Term	RT	Genes	Count	%	P-Value	FDR
	GOTERM_BP_FAT	macromolecule catabolic process	RT		73	3.6	4.7E-8	8.3E-5
	GOTERM_BP_FAT	sensory perception of light stimulus	RT		29	1.4	8.7E-8	1.5E-4
	GOTERM_CC_FAT	cell fraction	RT		39	1.9	1.3E-7	1.9E-4
	GOTERM_CC_FAT	rhabdomere	RT		16	0.8	1.5E-7	2.2E-4
	GOTERM_CC_FAT	insoluble fraction	RT		38	1.9	1.9E-7	2.7E-4
	GOTERM_BP_FAT	detection of external stimulus	RT		26	1.3	1.8E-7	3.1E-4
	GOTERM_CC_FAT	chromosome	RT		77	3.8	2.5E-7	3.5E-4
	GOTERM_BP_FAT	visual perception	RT		28	1.4	2.5E-7	4.4E-4
	GOTERM_BP_FAT	detection of light stimulus	RT		23	1.1	3.3E-7	5.8E-4
	GOTERM_BP_FAT	detection of abiotic stimulus	RT		24	1.2	5.3E-7	9.2E-4
	GOTERM_CC_FAT	membrane fraction	RT		36	1.8	6.9E-7	9.8E-4
	SP_PIR_KEYWORDS	phosphoprotein	RT		173	8.5	1.2E-6	1.6E-3
	SP_PIR_KEYWORDS	metal-binding	RT		169	8.3	1.6E-6	2.1E-3
	GOTERM_CC_FAT	extrinsic to membrane	RT		45	2.2	2.5E-6	3.5E-3
	GOTERM_BP_FAT	regulation of cell cycle	RT		47	2.3	2.0E-6	3.5E-3
	GOTERM_BP_FAT	transcription from RNA polymerase II promoter	RT		33	1.6	2.1E-6	3.7E-3
	GOTERM_BP_FAT	chromosome organization	RT		69	3.4	2.2E-6	3.9E-3

GOTERM_BP_FAT	phototransduction	RT	20	1.0	3.1E-6	5.5E-3
GOTERM_CC_FAT	nucleoplasm	RT	66	3.3	4.0E-6	5.7E-3
GOTERM_BP_FAT	modification-dependent protein catabolic process	RT	47	2.3	3.4E-6	6.0E-3
GOTERM_BP_FAT	protein localization	RT	88	4.3	3.5E-6	6.2E-3
GOTERM_BP_FAT	modification-dependent macromolecule catabolic process	RT	47	2.3	4.1E-6	7.1E-3
GOTERM_BP_FAT	cellular macromolecule catabolic process	RT	57	2.8	6.4E-6	1.1E-2
GOTERM_BP_FAT	detection of light stimulus involved in sensory perception	RT	13	0.6	8.5E-6	1.5E-2
GOTERM_MF_FAT	general RNA polymerase II transcription factor activity	RT	31	1.5	9.5E-6	1.5E-2
GOTERM_BP_FAT	intracellular signaling cascade	RT	69	3.4	1.5E-5	2.6E-2
GOTERM_BP_FAT	proteolysis involved in cellular protein catabolic process	RT	48	2.4	1.5E-5	2.6E-2
GOTERM_BP_FAT	cellular protein catabolic process	RT	48	2.4	1.5E-5	2.6E-2
INTERPRO	Snf7	RT	8	0.4	1.6E-5	2.8E-2
GOTERM_BP_FAT	macromolecular complex subunit organization	RT	66	3.3	1.6E-5	2.8E-2
GOTERM_BP_FAT	protein catabolic process	RT	51	2.5	1.8E-5	3.1E-2
GOTERM_CC_FAT	nucleoplasm part	RT	59	2.9	2.2E-5	3.1E-2
SP_PIR_KEYWORDS	vision	RT	22	1.1	2.3E-5	3.2E-2
GOTERM_CC_FAT	microsome	RT	29	1.4	2.5E-5	3.6E-2
GOTERM_CC_FAT	vesicular fraction	RT	29	1.4	2.5E-5	3.6E-2
SP_PIR_KEYWORDS	nucleus	RT	175	8.6	2.7E-5	3.7E-2
INTERPRO	Cytochrome P450, C-terminal region	RT	30	1.5	2.3E-5	3.8E-2
GOTERM_BP_FAT	establishment of protein localization	RT	66	3.3	2.6E-5	4.5E-2

INTERPRO	Cytochrome P450	RT	30	1.5	2.9E-5	4.9E-2
GOTERM_CC_FAT	spindle	RT	24	1.2	3.7E-5	5.3E-2
SP_PIR_KEYWORDS	zinc-finger	RT	75	3.7	4.0E-5	5.4E-2
COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catabolism	RT	32	1.6	6.2E-5	5.6E-2
GOTERM_BP_FAT	phosphate metabolic process	RT	111	5.5	3.2E-5	5.7E-2
GOTERM_BP_FAT	phosphorus metabolic process	RT	111	5.5	3.2E-5	5.7E-2
SP_PIR_KEYWORDS	microsome	RT	27	1.3	4.3E-5	5.9E-2
GOTERM_BP_FAT	detection of light stimulus involved in visual perception	RT	12	0.6	3.4E-5	5.9E-2
GOTERM_BP_FAT	transcription initiation from RNA polymerase II promoter	RT	23	1.1	3.7E-5	6.5E-2
GOTERM_MF_FAT	transition metal ion binding	RT	255	12.6	4.3E-5	6.8E-2
GOTERM_BP_FAT	protein transport	RT	64	3.2	4.2E-5	7.4E-2
UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	RT	34	1.7	4.8E-5	7.8E-2
SP_PIR_KEYWORDS	chromosomal protein	RT	18	0.9	5.8E-5	7.9E-2
GOTERM_BP_FAT	detection of visible light	RT	13	0.6	4.5E-5	8.0E-2
SP_PIR_KEYWORDS	heme	RT	34	1.7	6.1E-5	8.3E-2
GOTERM_BP_FAT	macromolecular complex assembly	RT	58	2.9	5.0E-5	8.8E-2
SP_PIR_KEYWORDS	Monooxygenase	RT	31	1.5	7.1E-5	9.7E-2

File S4

Lists of functional terms common and exclusive to each of the expression patterns shown in Figure 9

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Common and exclusive to all down regulated protective

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 [1,] "GOTERM_BP_FAT "   "energy derivation by oxidation of organic compounds "
 [2,] "GOTERM_BP_FAT "   "cellular respiration "
 [3,] "GOTERM_CC_FAT "   "respiratory chain "
 [4,] "GOTERM_BP_FAT "   "electron transport chain "
 [5,] "GOTERM_CC_FAT "   "mitochondrial respiratory chain "
 [6,] "GOTERM_BP_FAT "   "respiratory electron transport chain "
 [7,] "GOTERM_BP_FAT "   "ATP synthesis coupled electron transport "
 [8,] "GOTERM_BP_FAT "   "mitochondrial ATP synthesis coupled electron transport "
 [9,] "GOTERM_CC_FAT "   "mitochondrial membrane part "
[10,] "GOTERM_BP_FAT "   "mitochondrial electron transport, NADH to ubiquinone "
[11,] "GOTERM_CC_FAT "   "NADH dehydrogenase complex "
[12,] "GOTERM_CC_FAT "   "respiratory chain complex I "
[13,] "GOTERM_CC_FAT "   "mitochondrial respiratory chain complex I "
[14,] "GOTERM_MF_FAT "   "NADH dehydrogenase activity "
[15,] "GOTERM_MF_FAT "   "oxidoreductase activity, acting on NADH or NADPH "
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[16,] "GOTERM_MF_FAT "   "NADH dehydrogenase (quinone) activity "
[17,] "GOTERM_MF_FAT "   "NADH dehydrogenase (ubiquinone) activity "
[18,] "GOTERM_MF_FAT "   "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor "
[19,] "GOTERM_BP_FAT "   "cofactor catabolic process "
[20,] "GOTERM_BP_FAT "   "acetyl-CoA metabolic process "
[21,] "GOTERM_BP_FAT "   "tricarboxylic acid cycle "
[22,] "GOTERM_BP_FAT "   "acetyl-CoA catabolic process "
[23,] "GOTERM_BP_FAT "   "coenzyme catabolic process "
[24,] "GOTERM_BP_FAT "   "aerobic respiration "
[25,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex "
[26,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex "
[27,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex, coupling factor F(o) "
[28,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) "
[29,] "GOTERM_BP_FAT "   "glucose metabolic process "
[30,] "GOTERM_BP_FAT "   "hexose metabolic process "
[31,] "GOTERM_BP_FAT "   "glycolysis "
[32,] "GOTERM_BP_FAT "   "cellular carbohydrate catabolic process "
[33,] "GOTERM_BP_FAT "   "monosaccharide metabolic process "
[34,] "GOTERM_BP_FAT "   "carbohydrate catabolic process "
[35,] "GOTERM_BP_FAT "   "hexose catabolic process "
[36,] "GOTERM_BP_FAT "   "glucose catabolic process "
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[37,] "GOTERM_BP_FAT "   "alcohol catabolic process "

[38,] "GOTERM_BP_FAT "   "monosaccharide catabolic process "

[39,] "GOTERM_BP_FAT "   "regulation of cellular component size "

[40,] "GOTERM_BP_FAT "   "cell growth "

[41,] "GOTERM_BP_FAT "   "regulation of cell size "

[42,] "GOTERM_BP_FAT "   "growth "

[43,] "GOTERM_BP_FAT "   "developmental growth "

[44,] "GOTERM_BP_FAT "   "developmental cell growth "

[45,] "GOTERM_BP_FAT "   "protein amino acid phosphorylation "

[46,] "INTERPRO "        "Protein kinase, ATP binding site "

[47,] "GOTERM_MF_FAT "   "protein serine/threonine kinase activity "

[48,] "SMART "           "S_TKc "

[49,] "INTERPRO "        "Serine/threonine protein kinase "

[50,] "SP_PIR_KEYWORDS " "kinase "

[51,] "SP_PIR_KEYWORDS " "serine/threonine-protein kinase "

[52,] "INTERPRO "        "Serine/threonine protein kinase-related "

[53,] "GOTERM_MF_FAT "   "protein kinase activity "

[54,] "INTERPRO "        "Protein kinase, core "

[55,] "INTERPRO "        "Serine/threonine protein kinase, active site "

[56,] "SP_PIR_KEYWORDS " "atp synthesis "

[57,] "GOTERM_CC_FAT "   "mitochondrial proton-transporting ATP synthase complex, catalytic core F(1) "
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[58,] "GOTERM_CC_FAT "   "proton-transporting ATP synthase complex, catalytic core F(1) "

[59,] "SMART "          "EGF "

[60,] "INTERPRO "       "EGF-like "

[61,] "INTERPRO "       "EGF-like, type 3 "

[62,] "SP_PIR_KEYWORDS " "egf-like domain "

[63,] "GOTERM_BP_FAT "   "olfactory learning "

[64,] "GOTERM_BP_FAT "   "learning or memory "

[65,] "GOTERM_BP_FAT "   "chemosensory behavior "

[66,] "GOTERM_BP_FAT "   "learning "

[67,] "GOTERM_BP_FAT "   "olfactory behavior "

[68,] "GOTERM_BP_FAT "   "circadian rhythm "

[69,] "GOTERM_BP_FAT "   "rhythmic process "

[70,] "GOTERM_BP_FAT "   "circadian behavior "

[71,] "GOTERM_BP_FAT "   "rhythmic behavior "

[72,] "GOTERM_BP_FAT "   "locomotor rhythm "

[73,] "GOTERM_BP_FAT "   "epithelial tube morphogenesis "

[74,] "INTERPRO "       "Pleckstrin homology-type "

[75,] "GOTERM_BP_FAT "   "chitin-based embryonic cuticle biosynthetic process "

[76,] "GOTERM_BP_FAT "   "cuticle development "

[77,] "GOTERM_BP_FAT "   "chitin-based cuticle development "

[78,] "GOTERM_BP_FAT "   "organic acid catabolic process "
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[79,] "GOTERM_BP_FAT "   "carboxylic acid catabolic process "
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Common and exclusive to all up regulated protective

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 [1,] "GOTERM_MF_FAT "   "RNA polymerase activity "
 [2,] "GOTERM_MF_FAT "   "DNA-directed RNA polymerase activity "
 [3,] "GOTERM_CC_FAT "   "RNA polymerase complex "
 [4,] "GOTERM_CC_FAT "   "DNA-directed RNA polymerase complex "
 [5,] "GOTERM_CC_FAT "   "nuclear DNA-directed RNA polymerase complex "
 [6,] "GOTERM_MF_FAT "   "nucleotidyltransferase activity "
 [7,] "KEGG_PATHWAY "    "RNA polymerase "
 [8,] "GOTERM_CC_FAT "   "DNA-directed RNA polymerase II, core complex "
 [9,] "SP_PIR_KEYWORDS " "nucleotidyltransferase "
[10,] "KEGG_PATHWAY "    "Pyrimidine metabolism "
[11,] "KEGG_PATHWAY "    "Purine metabolism "
[12,] "SMART "           "Sm "
[13,] "INTERPRO "        "Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core "
[14,] "INTERPRO "        "Like-Sm ribonucleoprotein, core "
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Common and exclusive to all down regulated non-protective

None

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Common and exclusive to all up regulated non-protective

None

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Common and exclusive to all protective

None

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Common and exclusive to all non-protective

None

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Common and exclusive to all down regulated

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 [1,] "GOTERM_MF_FAT "   "ATPase activity "
 [2,] "GOTERM_CC_FAT "   "mitochondrial part "
 [3,] "GOTERM_CC_FAT "   "mitochondrion "
 [4,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of substances "
 [5,] "GOTERM_MF_FAT "   "ATPase activity, coupled to movement of substances "
 [6,] "GOTERM_MF_FAT "   "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances "
 [7,] "GOTERM_MF_FAT "   "P-P-bond-hydrolysis-driven transmembrane transporter activity "
 [8,] "GOTERM_MF_FAT "   "primary active transmembrane transporter activity "
 [9,] "GOTERM_BP_FAT "   "ribonucleotide biosynthetic process "
[10,] "GOTERM_BP_FAT "   "purine nucleoside triphosphate biosynthetic process "
[11,] "GOTERM_BP_FAT "   "purine ribonucleoside triphosphate biosynthetic process "
[12,] "GOTERM_BP_FAT "   "ribonucleotide metabolic process "
[13,] "GOTERM_BP_FAT "   "purine ribonucleotide biosynthetic process "
[14,] "GOTERM_BP_FAT "   "nucleoside triphosphate biosynthetic process "
[15,] "GOTERM_BP_FAT "   "ribonucleoside triphosphate biosynthetic process "
[16,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism "
[17,] "GOTERM_BP_FAT "   "cation transport "
[18,] "GOTERM_BP_FAT "   "purine ribonucleotide metabolic process "
[19,] "GOTERM_BP_FAT "   "purine nucleoside triphosphate metabolic process "
[20,] "GOTERM_BP_FAT "   "purine ribonucleoside triphosphate metabolic process "
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[21,] "GOTERM_BP_FAT "   "ATP biosynthetic process "
[22,] "SP_PIR_KEYWORDS " "Hydrogen ion transport "
[23,] "GOTERM_BP_FAT "   "ribonucleoside triphosphate metabolic process "
[24,] "GOTERM_BP_FAT "   "nucleoside triphosphate metabolic process "
[25,] "GOTERM_MF_FAT "   "ATPase activity, coupled to transmembrane movement of ions "
[26,] "GOTERM_BP_FAT "   "ATP metabolic process "
[27,] "GOTERM_BP_FAT "   "ion transport "
[28,] "GOTERM_BP_FAT "   "purine nucleotide biosynthetic process "
[29,] "GOTERM_MF_FAT "   "ATPase activity, coupled "
[30,] "GOTERM_BP_FAT "   "purine nucleotide metabolic process "
[31,] "GOTERM_MF_FAT "   "hydrogen-exporting ATPase activity, phosphorylative mechanism "
[32,] "GOTERM_BP_FAT "   "nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process "
[33,] "GOTERM_BP_FAT "   "nucleobase, nucleoside and nucleotide biosynthetic process "
[34,] "GOTERM_BP_FAT "   "monovalent inorganic cation transport "
[35,] "GOTERM_BP_FAT "   "nucleotide biosynthetic process "
[36,] "GOTERM_BP_FAT "   "proton transport "
[37,] "GOTERM_BP_FAT "   "hydrogen transport "
[38,] "GOTERM_BP_FAT "   "ATP synthesis coupled proton transport "
[39,] "GOTERM_BP_FAT "   "energy coupled proton transport, down electrochemical gradient "
[40,] "GOTERM_BP_FAT "   "ion transmembrane transport "
[41,] "GOTERM_MF_FAT "   "inorganic cation transmembrane transporter activity "
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[42,] "GOTERM_CC_FAT "   "proton-transporting two-sector ATPase complex "

[43,] "GOTERM_CC_FAT "   "proton-transporting two-sector ATPase complex, catalytic domain "

[44,] "GOTERM_MF_FAT "   "monovalent inorganic cation transmembrane transporter activity "

[45,] "GOTERM_MF_FAT "   "hydrogen ion transmembrane transporter activity "

[46,] "GOTERM_BP_FAT "   "transmembrane transport "

[47,] "KEGG_PATHWAY "    "Oxidative phosphorylation "

[48,] "GOTERM_BP_FAT "   "oxidative phosphorylation "

[49,] "GOTERM_CC_FAT "   "proton-transporting two-sector ATPase complex, proton-transporting domain "
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[1,] "GOTERM_CC_FAT " "nucleoplasm part "

[2,] "GOTERM_BP_FAT " "transcription from RNA polymerase II promoter "

[3,] "GOTERM_BP_FAT " "transcription, DNA-dependent "

[4,] "GOTERM_BP_FAT " "RNA biosynthetic process "

[5,] "GOTERM_CC_FAT " "nucleoplasm "

[6,] "GOTERM_CC_FAT " "DNA-directed RNA polymerase II, holoenzyme "

[7,] "GOTERM_BP_FAT " "transcription "

[8,] "GOTERM_CC_FAT " "nuclear lumen "
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