THE JOURNAL OF BIOLOGICAL CHEMISTRY
Vol. 277, No. 16, Issue of April 19, pp. 14048–14052, 2002
Printed in U.S.A.

Genome-wide Transcriptional Orchestration of Circadian Rhythms in *Drosophila**$\boxed{\text{S}}$

Received for publication, December 27, 2001, and in revised form, February 15, 2002
Published, JBC Papers in Press, February 19, 2002, DOI 10.1074/jbc.C100765200

Hiroki R. Ueda‡§¶‖, Akira Matsumoto¶, Miho Kawamura§, Masamitsu Iino‡, Teiichi Tanimura**‡‡, and Seiichi Hashimoto§**

*From the ‡Department of Pharmacology, Graduate School of Medicine, The University of Tokyo, Bunkyo-ku, Tokyo 113-0033, §Molecular Medicine Research Laboratories, Institute for Drug Discovery Research, Yamanouchi Pharmaceutical Co., Ltd., 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, and the **Department of Biology, Faculty of Science, Kyushu University, Ropponmatsu, Fukuoka 810-8560, Japan*

Circadian rhythms govern the behavior, physiology, and metabolism of living organisms. Recent studies have revealed the role of several genes in the clock mechanism both in *Drosophila* and in mammals. To study how gene expression is globally regulated by the clock mechanism, we used a high density oligonucleotide probe array (GeneChip) to profile gene expression patterns in *Drosophila* under light-dark and constant dark conditions. We found 712 genes showing a daily fluctuation in mRNA levels under light-dark conditions, and among these the expression of 115 genes was still cycling in constant darkness, *i.e.* under free-running conditions. Unexpectedly the expression of a large number of genes cycled exclusively under constant darkness. We found that cycling in most of these genes was lost in the arrhythmic *Clock* (*Clk*) mutant under light-dark conditions. Expression of periodically regulated genes is coordinated locally on chromosomes where small clusters of genes are regulated jointly. Our findings reveal that many genes involved in diverse functions are under circadian control and reveal the complexity of circadian gene expression in *Drosophila*.

The use of *Drosophila* has been at the forefront of studies of the molecular and genetic basis of circadian rhythms (1). A number of clock genes have been identified in *Drosophila*, and interlocked *per-tim* and *Clk* feedback loops are now thought to underlie the central molecular machinery of circadian rhythms (2, 3). However, we still do not know how expression of the whole genome is orchestrated by the circadian mechanism nor have we identified all the genes involved. One comprehensive way to find out all the rhythmically expressed genes is to utilize microarray. A number of genes regulated in a circadian manner have been identified in *Arabidopsis* and mammalian cultured cells (4, 5). Since information about all the possible transcription units is available in *Drosophila* (6, 7), we can extensively analyze the data for all the genes relating to their function. Functions of identified genes can be analyzed using various genetic tool and databases (9–11) available in *Drosophila*.

EXPERIMENTAL PROCEDURES

Strain and Sample Preparations—$white^{1118}$ was used as a wild-type strain, and Clk^{Jrk} was also used (11). Flies were reared in a regime of 12 h of light followed by 12 h of darkness (LD),[1] and collected every 4 h over 2 days. Total RNA was prepared from 100 heads of 1-week-old adult males and females using the Fast RNA kit (BIO 101, Inc.) followed by DNase treatment. Double-stranded cDNA was synthesized from 10 μg of total RNA using Superscript II reverse transcriptase (Invitrogen) and was used as a template to synthesize biotin-labeled cRNA by *in vitro* transcription using an ENZO BioArray High Yield RNA transcript labeling kit. Amplified cRNA was fragmented and hybridized to GeneChip *Drosophila* arrays (Affymetrix, Santa Clara, CA) for 16 h at 45 °C. Hybridized arrays were washed, stained, and scanned using a Hewlett-Packard GeneArray Scanner. Affymetrix GeneChip software was used to determine the average difference between perfectly matched oligonucleotide probes and single base pair mismatches for each probe set. Data were then scaled globally such that the total intensity of each microarray is equal. The resulting hybridization intensity values reflect the abundance of a given mRNA relative to the total RNA population and were used in all subsequent analyses. Quantitative PCR was performed using the ABI Prism 7700 and SYBR Green reagents (Applied Biosystems).

Analysis of Cycling Genes—We examined gene expression profiles under LD using two successive filters: a periodic filter to extract genes with periodic expression patterns and a deviation filter to identify genes where the changes were above background level.

First, to extract genes with periodic expression pattern, we empirically tested for statistically significant cross-correlation between the temporal expression profiles of each probe set and cosine waves of defined period and phases. We prepared cosine waves of nine test periodicities (τ) from 20 to 28 h in increments of 1 h. Cosine waves of each test period were considered over 60 phases (*i.e.* peaks at 60 equally spaced times in the defined period), yielding a total of 540 test cosine waves. Statistical significance was assessed by an empirical procedure. We generated ~14,000 (the same number of probe sets) normally distributed random expression profiles. Then we calculated correlation between the random profiles and each of the 540 test cosine waves. Standard deviations and averages of cross-correlation were virtually equal for 540 cosine filters despite their different periods and phases. Thus, we searched for the common cut-off correlation of these cosine filters so that 95% of random expression profiles were filtered out after passing 540 parallel cosine filters. We determined this value as 99.8% probable correlation. This analysis is independent of signal strength and imposes no minimal change in amplitude.

Next, to further extract genes whose variation was above background, we determined the noise level associated with a series of ex-

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* This work was performed as a part of a research and development project of the Industrial Science and Technology Program supported by NEDO (New Energy and Industrial Technology Development Organization) and was also supported by grants from the Ministry of Education, Science, Sports and Culture of Japan (to T. T. and A. M.). The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "*advertisement*" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

$\boxed{\text{S}}$ The on-line version of this article (available at http://www.jbc.org) contains Tables I–VIII.

¶ Both authors contributed equally to this work.

‖ To whom correspondence may be addressed. Tel.: 81-298-54-1524; Fax: 81-298-54-1669; E-mail: hiro@m.u- tokyo.ac.jp.

‡‡ To whom correspondence may be addressed. Tel.: 81-92-726-4759; Fax: 81-92-726-4625; E-mail: tanimura@rc.kyushu-u.ac.jp.

[1] The abbreviations used are: LD, 12 h of light followed by 12 h of darkness; DD, constant dark; RT, reverse transcription; GABA, γ-aminobutyric acid.

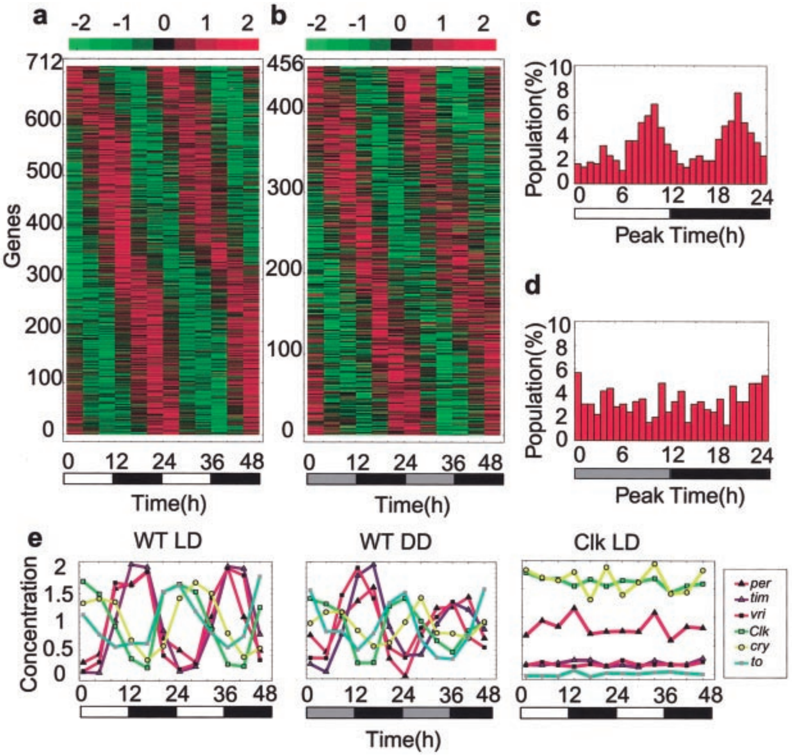

FIG. 1. **Cycling of gene expression in wild-type flies kept under LD and DD and in *Clk*^{Jrk} mutant flies under LD.** *a*, a cluster image of 712 cycling genes under LD. Data were normalized so that the average and the standard deviation of signal intensities of 12 time points are 0.0 and 1.0, respectively. For each gene, the *12 horizontal bars* along the *time axis* represent a 48-h series of data. The genes were ordered by their peak time to help to visualize the extensive pattern of cycling. *Bars* are colored *red* for positive values and *green* for negative values as shown in the *upper color code*. *b*, a cluster image of 456 genes whose expression is free-running under DD. The details of representation are similar to *a*. *c* and *d*, phase distributions of the peak expression times of periodically regulated genes under LD (*c*) and DD (*d*) derived from data on 712 and 456 periodically regulated genes under LD and DD, respectively. Two major populations have peaks at around ZT10 and ZT20 under LD. These peaks are not found in DD. *e*, periodic expression of *per*, *tim*, *vri*, *Clk*, *cry*, and *to* under LD and DD in wild-type and in *Clk*^{Jrk} mutant background flies under LD. Data of LD and DD were normalized so that the average signal intensity of 12 time points was 1.0. For data in *Clk*^{Jrk} background, signal intensities of these genes were divided by the average signal intensities under LD conditions. *WT*, wild type.

perimental procedures for each probe set. Two replicate samples (*i.e.* two sets of 100 fly heads collected independently at the same time of the day) were hybridized to two GeneChips. The standard deviation of the two signal intensities for each probe set was calculated and used as noise deviation (σ) in subsequent analysis. Expression profiles which, over the 12 time points, show a standard deviation (s) greater than noise deviation (σ) with 95% significance are classified as "changing." 95% probability cut-off values are determined from χ^2 (chi-square) distribution with 11 degrees of freedom ($(12 - 1)\ s^2/\sigma^2 > 19.6751$).

To estimate the false positive rate, we generated ~14,000 (the same number of probe sets) random expression profiles that were normally distributed using the noise deviations as determined above. Then we filtered these random expression profiles using two successive filters. Random profiles produced 27 genes classified as "periodically changing." We assume that this estimates the false positive rate (*i.e.* 3.8% of all genes identified would be false positives).

To analyze periodicity of gene expression profiles under constant dark (DD), we used damping cosine curves as test waves. We prepared damping cosine waves of four decay rates (k) from 0.0/h (no damping) to 0.03/h (half-life is 23.0 h) in increments of 0.01/h. Each was considered at nine test periodicities and over 60 phases as described above. We used the same cut-off cross-correlation values and the same deviation filters as in LD analysis.

Phase Analysis—To determine the phase of cycling genes, we tested for correlation between the temporal expression profiles of each gene and 24-h period cosine waves at 60 different phases. We estimated the phase of each cycling gene from the phase of the cosine wave with which it was correlated most closely.

Determination of Statistical Significance for Rhythmic Biological Processes and Periodically Regulated Molecules—We classified the cycling genes by biological process category in the Gene Ontology database (9). For each category, we calculated the probability of finding at least r periodically regulated genes from the category size (n) using the cumulative hypergeometric probability distribution. Probability is given by:

$$\text{Probability} = 1 - \sum_{l=1}^{r-1} \frac{\binom{n}{l}\binom{N-n}{R-l}}{\binom{N}{n}}$$

where N is the total number of genes within the genome, and R is the total number of periodically regulated genes. p values ($-\log_{10}$ (probability)) where the sum of probabilities is below 0.05 were considered significant.

We also performed similar analyses using the LIGAND metabolic database (9). We mapped cycling genes into the metabolic network in *Drosophila* and calculated the probability for observing at least r cycling genes within n enzymes metabolizing the same molecule using the cumulative hypergeometric probability distribution as above.

Analysis of Clk^{Jrk}—For each gene, expression levels in *Clk*^{Jrk} mutants were averaged with those in wild-type flies. Both were kept in LD conditions, and equivalent points in the light-dark cycle were compared. Genes were classified as "up-regulated" if expression was at least 2 times higher in the mutant and "down-regulated" if expression was least 2 times lower in the mutant. Otherwise genes were classified as "unchanged."

Mapping of Periodically Regulated Genes and Calculation of Chromosome Correlation Maps—Among 14,010 probes on the GeneChip, 44 probes are for control, and 299 probes map to multiple genes. The other 13,667 probes map to single genes. Among these, there are several redundant probe sets that map to the same gene, leaving 13,282 nonredundant probes. 12,795 of these match in FlyBase ID (10) to identified genes from Release 2 *Drosophila* genomic sequences (6, 7). We identified the chromosomal positions of all 12,795 genes using the BLASTN algorithm. Using the chromosomal positions obtained above, we mapped the genes belonging to each Class I, II, and III on chromosomes. To detect co-regulated regions, we calculated the correlation between expression patterns under LD conditions of genes on the same chromosome as described elsewhere (12). To identify significantly co-regulated regions, we calculated the average correlation of six adjacent genes and compared it with the average correlation of six nonadjacent genes as background. There were 140 chromosomal regions where the average correlation of the six adjacent genes was more than 3.5 standard deviations from background, *i.e.* the mean average correlation of six nonadjacent genes. This analysis showed that a substantial number of adjacent sets have correlated expression patterns in comparison with 25 expected co-regulated regions derived from a control set of nonadjacent genes. Similar results were obtained from analysis of 2–10 adjacent genes. Among 140 chromosomal regions, 38 clusters of genes included periodically regulated genes. We also analyzed co-expressed region under the DD condition and obtained similar results to the LD condition.

RESULTS AND DISCUSSION

We have examined temporal patterns of gene expression under LD and under DD using a GeneChip (Affymetrix) representing the entire genome (more than 13,500 genes) of *Dro-*

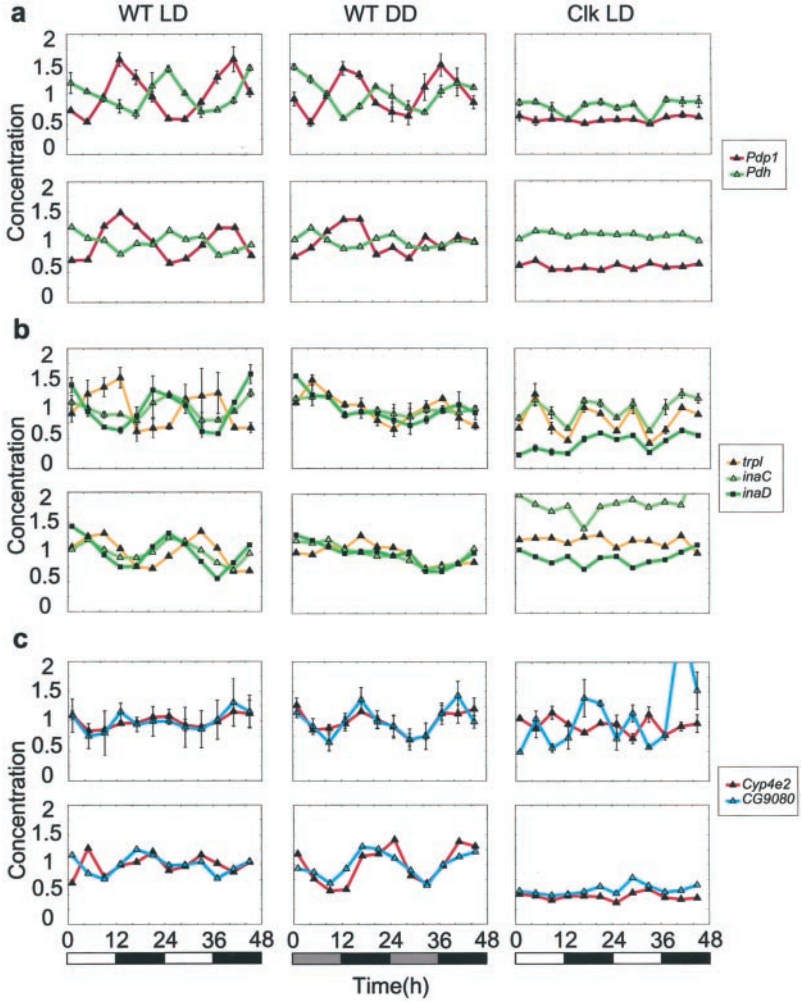

FIG. 2. **Three classes of periodically regulated genes and validation of GeneChip data by quantitative RT-PCR using wild-type flies (*WT*) under LD and DD and Clk^{Jrk} (*Clk*) mutant flies under LD.** *a*, Class I genes cycling both in LD and DD; *b*, Class II genes cycling only in LD; *c*, genes cycling in DD but not in LD. In each class, data are shown for two to three genes, the rhythmic expression of which was found in this study. *Upper curves* in *a*, *b*, and *c* are based on the GeneChip analyses; *lower curves* are based on the quantitative PCR analyses. *Pdp1*, PAR domain protein encoding a transcription factor; *Pdh*, photoreceptor dehydrogenase; *trpl*, transient receptor potential-like encoding a Ca^{2+} channel; *inaC*, inactivation no after-potential C encoding a protein kinase C; *inaD*, inactivation no after-potential D encoding a structural protein containing a PDZ domain; *Cyp4e2*, cytochrome P450-4e2.

sophila melanogaster. Flies were collected every 4 h over 2 days both in LD and DD, and biotin-labeled probes made from cDNA from 100 heads were used for hybridization. We estimate that the expression of 6,061 genes (43.4% of all genes) was detected on GeneChip. The number of genes detected here is thought to be delimited by the detection method using GeneChip, and there should be additional cycling genes expressed at a lower level or in a small number of cells. Data were analyzed through two sequential statistical filters, and 712 genes (5.3% of the whole genome) were classified as periodically regulated genes in LD (Fig. 1*a*). This is likely to be a minimum number for the genes that are periodically regulated; the number may increase if a different filtration analysis was applied. Our analyses might not detect genes that cycle in some cells but not in others, and moreover, it is technically difficult to monitor genes with very low levels of transcription. The number of periodically regulated genes in *Drosophila* is similar to that reported from *Arabidopsis* under constant light (4), in which 6% of genes investigated are rhythmic, but is in contrast to cyanobacteria, in which nearly all genes are expressed periodically (13). We found that genes implicated in circadian rhythms, including *period* (*per*) (14), *timeless* (*tim*) (15), *Clock* (*Clk*) (11), *vrille* (*vri*) (16), *cryptochrome* (*cry*) (17), and *takeout* (*to*) (18), cycled with high amplitude and in similar phase, as previously reported, validating our experimental and statistic procedures (Fig. 1*e*). We analyzed the phase of periodically regulated genes at a resolution of 0.4 h and found two peaks around ZT10 and ZT20 (Fig. 1*c*). The peaks may reflect the after-effect of the change from dark to light and light to dark since significant peaks were absent under the constant dark condition (Fig. 1*d*). The peak phases of the clock genes, *Clk*, *cry*, *per*, *vri*, *tim*, and *to*, were not at these times. We then analyzed the gene expression under DD (Fig. 1*b*) and found that 115 genes of 712 were still periodically regulated in the free-running condition (Class I, periodically regulated both in LD and DD). The remaining 597 genes were judged to be periodically regulated only in LD (Class II). Surprisingly 341 genes that were not judged as periodically regulated under LD were, however, periodically regulated under DD (Class III). Their cyclings might have been suppressed or masked under LD as suggested from behavioral experiments (19). In our classification of genes we should note that because we used a strict filter to identify periodically regulated genes, genes judged to be not cycling might in fact cycle with low amplitude. Lists of all genes in each class may be found in Supplemental Tables I–III. After completion of our work two similar works using GeneChip were published (20, 21). Their findings are similar to ours, but there are several differences, specifically the Class II and III genes were not mentioned in other studies. We think that the major differences are the numbers of sampling and statistical analyses. We analyzed data for 2 days both under LD and DD, while the previous studies analyzed data only for 1 day in each light condition. Several interesting periodically regulated genes were identified from the three classes, I, II, and III (Fig. 2). The reliability of GeneChip data was assessed by quantitative RT-PCR analyses, which confirmed that both methods yielded similar data. A novel candidate of clock genes, *Pdp1*, showing a robust cycling (Fig. 2*a*), encodes a transcription factor with

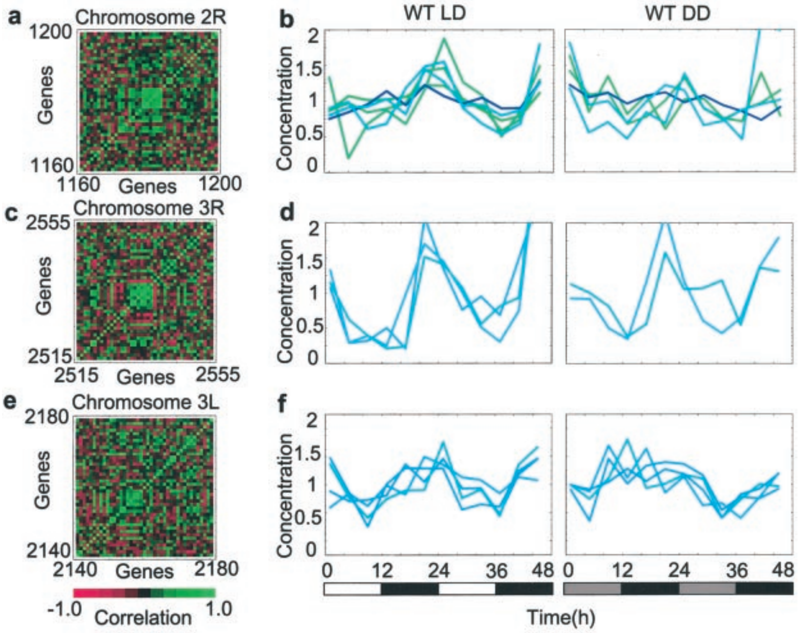

FIG. 3. **Global chromosomal profiles of periodic gene expression.** *a*, correlation map for gene clusters that included the Class I genes on the right arm of the second chromosome. The *green block* at the *center* indicates the group of six adjacent co-expressing genes, including cytochrome P450, *Cyp6a17* (Class I), *Cyp6a23*, *Cyp6a19*, *Cyp6a9*, *Cyp6a20*, and *Cyp6a21*. The *numbers* along the matrix represent the gene number along the chromosome. *Green squares* indicates a positive correlation; *red squares* indicate a negative correlation. *b*, the six cytochrome P450 genes that are periodically co-regulated under LD and DD. *Cyp6a17* is represented by the *green line* with the highest peak at a time point of 25 h. *c*, correlation map for gene clusters that included the Class I genes but that have no functional relatedness to each other. *d*, three genes on the third chromosome (CG11891, which belongs to Class I, CG11889, and CG10513) showed similar rhythmic expressions in LD, and periodic expression of these genes also persists under DD. Data for CG11889 under DD is not shown here as they included a few negative values. *e*, correlation map for gene clusters that included the three Class II genes on the left arm of the third chromosome. *f*, CG7646, CG7654, and CG7433 are Class II genes, and their neighboring gene, neurocalcin, showed a similar expression pattern in LD. *WT*, wild type.

homology to *vri* (16). Most of the genes we found to cycle could be classified according to the category of their "biological process" as defined in the Gene Ontology database (8) (Supplemental Tables IV and V). Phototransduction is one such category, which includes a significant number of periodically regulated genes. Two of these were Class I genes. Photoreceptor dehydrogenase, *Pdh*, also showed a clear cyclical expression (Fig. 2). One retinoid-binding protein (CG5958) was periodically expressed with peak at dusk, while the other retinoid-binding protein (CG10657) belonging to Class II was cycling with almost opposite phases. A number of genes belonged to Class II. Three opsins, *Rh3*, *Rh4*, and *Rh6*, which express in the central rhabdomeres of the compound eye's ommatidia, showed rhythmic expression. Another opsin, *Rh5*, belonged to Class III. The *ninaA* gene encoding cyclophilin, which transports opsins from endoplasmic reticulum to microvilli membrane, also showed rhythmic expression. Molecules associating with Ca^{2+} signal transduction in the photoreceptors, *inaC*, *inaD*, and *trpl*, also cycled (Fig. 2*b*). The expression of most genes listed above peaked in the morning, whereas *Rh6* and *trpl* peaked in the evening. Visual sensitivity is controlled by a circadian rhythm in insects (22), and it would therefore be interesting to know how cyclical changes in these genes influence photoreceptor structure and function.

We also used the LIGAND metabolic database (9) to examine the functional significance of periodically regulated genes (Supplemental Tables VI and VII). Enzymes and transporters involved in metabolism or function of glutamate and GABA were periodically regulated. *Eaat1*, CG5618, and CG7470 are Class I genes, and *Gdh*, *black*, CG4233, and CG7433 are Class II genes. *Gs1* belongs to Class III. All genes except CG4233 showed robust rhythmicity with peaks in the dark phase. In mammals, glutamate (23) and GABA (24) are neurotransmitters associated with clock function. These molecules mimic the dark pulse to a circadian rhythm in the optic lobe of *Musca* (25). In *Drosophila*, one type of glutamate receptor is highly enriched in pacemaker neurons (26), and our data suggest glutamate and GABA might have a role in the circadian mechanism. In the light of a recent finding that the redox state of NAD cofactors is involved in circadian rhythms (27), it is interesting that many enzymes related to NAD^+, NADH, $NADP^+$, and NADPH metabolism were periodically regulated. There are 16 periodically regulated genes directly associated to the synthesis of these nicotinamide nucleotides. Three are in Class I, and the remaining 13 are in Class II. Their peaks expression occurred in three phases under LD: noon, dusk, and night.

We next examined the cycling of gene expression in the arrhythmic mutant of the *Clock* (*Clk*) gene (11) under LD. Our study showed that many genes are cycling only in LD, and we then asked whether the cyclings of the Class II genes are merely a reflection of light responses. Homozygous Clk^{Jrk} mutants show completely arrhythmic locomotor behavior under DD (11). CLK is a transcription factor and activates clock-regulated genes (1, 2, 11). In the *Clk* mutant, periodically expression of all the clock genes disappeared (Fig. 1*e*), and only a few genes were judged to cycle under LD (7, 16, and 23 genes in Class I, II, and III, respectively; Supplemental Table VIII). It is possible that the cycling genes in the Clk^{Jrk} mutant may represent genes controlled by a possible CLK-independent mechanism. We did not analyze the cycling pattern with two peaks in a day. If cycling is simply controlled by light-on and -off, it shows a pattern with dual peaks in a day. We did not investigate this possibility, but genes belonging to the Class III may have such a property. Further studies are necessary to investigate this possibility.

Our results suggest that the cycling of the Class II genes is not merely a result of light exposure during LD but is under circadian control. Under LD, the expression levels of *per*, *tim*, *vri*, and *to* were decreased relative to *Clk* (Fig. 1*e*), whereas *Clk* and *cry* continue to express at a high level as previously shown (11, 17). Fig. 2 shows the expression patterns of seven genes in Clk^{Jrk}. If the transcription level of a gene is lowered in Clk^{Jrk}, the gene might be up-regulated by *Clk*, whereas if the level is not affected, the gene might be regulated by a CLK-independent mechanism. The expression of about 6% of genes was decreased, while in about 3% of genes it was increased. In the latter case, their transcription might normally be down-regulated by genes controlled by CLK. These results indicate that CLK regulates transcription in many genes, but there are other genes in which transcription is not directly controlled by CLK. In addition some genes might be negatively regulated by CLK. We do not think that these changes are caused by the genetic background differences as we dealt with genes whose expression level changed over 2-fold or one-half. Our study thus shows that a single mutation in such a central gene regulator results in global but differential changes of gene expression.

We mapped the chromosomal locations of genes belonging to each class (I, II, and III) and found that they were not randomly distributed but clustered on chromosomes. There were 15 clusters where periodically regulated genes occupied a highly condensed chromosome interval. This suggests that temporal gene expression might be locally regulated on chromosomes. To confirm this possibility, we calculated the correlation of temporal expression pattern along the neighboring genes on all chromosomes and found 140 chromosomal regions where neighboring genes are expressed with a similar pattern to each other. Among them, 38 regions contained at least one periodically regulated gene. There were six genes in Class I, 24 in Class II, and eight in Class III. For example, the expression patterns of six neighboring genes belonging to the cytochrome P450 family, located on the right arm of the second chromosome, are similar (Fig. 3, *a* and *b*). There is a region where genes are co-regulated, but their functions are unknown (Fig. 3, *c* and *d*). Moreover, we found that functionally unrelated genes are co-regulated (Fig. 3, *e* and *f*). These results suggest that the temporal expression of neighboring genes is influenced by a periodically regulated gene. Searches of each class of periodically regulated genes so far failed to reveal any common motifs in the nucleic acid sequence along the putative regulatory region of each class of cycling genes. We found that the co-regulation of temporal expression occurs even more globally. The co-regulated regions were observed along the fourth chromosome at intervals of about 5–10 genes (data not shown). The regular spacing suggests control at the level of higher order chromatin structure as previously reported in suprachiasmatic nuclei neurons (28). These results suggest that gene expression on chromosomes is globally regulated by circadian mechanisms, although we still do not know their molecular bases. Coordinated gene regulation at the chromatin level might be an economical way in remodeling chromosome structures.

Our study thus reveals the complex transcriptional orchestration of genes under LD and DD conditions in *Drosophila*. Although cycling gene expression is not always essential for circadian function, in clock genes such as *cyc* (29) and *doubletime* (30) our study has established the candidacy of many candidate genes that might be implicated in circadian mechanisms. Further work using genetic tools available in *Drosophila* should help to explore the function of these genes with the prospect of leading to a greater understanding of the molecular basis of circadian rhythms in all organisms.

Acknowledgments—We are grateful to Michael Rosbash and Jeffrey C. Hall for the Clk^{Jrk} strain. We thank Shigeru Iwase for computational analysis; Satoko Hayashi, Tomoko Kojima, Toshie Katakura, Yuko Mitsuiki, and Makiko Haruta for technical assistance; and Masami Horikoshi and Takashi Umehara for hospitality in the use of their laboratory. We also thank Hideo Iwasaki and Kenji Tomioka for discussion and Jennifer Hallinan and Ian Meinerzhagen for comments on the manuscript.

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Table 1: Drosophila Genes Rhythmically Expressed Both in Light-Dark and Constant Dark Conditions.

Accession #	Gene Name	Correlation(LD+DD)	Phase(LD)	Phase(DD)	mRNA Levels in *Clk* (*Clk*/*wt*)
FBgn0014396	timeless	1.9689	14.8	15.2	Down (0.19061)
FBgn0040900	CG17777	1.94301	21.2	21.6	Down (0.133756)
FBgn0016076	vrille	1.90589	13.6	12.4	Down (0.1759)
FBgn0024290	Slowpoke binding protein	1.90238	14.4	12.4	Not Changed (1.17702)
FBgn0023076	Clock	1.89791	2.	2.	Not Changed (1.61517)
FBgn0026314	UDP-glycosyltransferase 35b	1.88243	2.	0.8	Not Changed (0.937727)
FBgn0025680	cryptochrome	1.87782	5.2	5.2	Not Changed (1.6446)
FBgn0039324	CG10553	1.87508	19.6	19.6	Not Changed (0.918862)
FBgn0032167	CG5853	1.87215	16.	18.8	Not Changed (0.510791)
FBgn0031326	CG5156	1.85227	2.8	2.4	Down (0.403719)
FBgn0038184	CG9285	1.84608	1.6	0.4	Not Changed (1.01046)
FBgn0032022	CG14275	1.84465	14.	13.2	Not Changed (1.06334)
FBgn0036992	CG11796	1.82834	4.	1.2	Not Changed (1.20056)
FBgn0030422	CG15723	1.8223	21.6	20.8	Not Changed (0.668471)
FBgn0034115	CG16796	1.80734	20.8	0.4	Not Changed (0.548936)
FBgn0038862	CG5798	1.80607	12.4	12.	Down (0.429404)
FBgn0032886	CG9328	1.79906	22.	20.8	Not Changed (1.57588)
FBgn0038966	CG13848	1.7974	0.4	24.	Not Changed (0.585615)
FBgn0031913	CG5958	1.79351	10.4	11.2	Not Changed (1.28367)
FBgn0003068	period	1.7928	13.6	13.6	Not Changed (0.823371)
FBgn0039298	takeout	1.78783	23.6	23.2	Down (0.00711846)
FBgn0011693	Photoreceptor dehydrogenase	1.7863	2.8	1.6	Not Changed (1.09725)
FBgn0034390	CG15093	1.78341	3.2	5.6	Not Changed (0.75899)
FBgn0033289	CG2121	1.77377	12.	12.	Not Changed (1.33584)
FBgn0031428	CG9886	1.7695	19.6	20.	Not Changed (0.948965)
FBgn0034108	CG3767	1.76112	23.2	1.6	Not Changed (1.18085)
FBgn0023548	msta	1.76079	22.4	20.8	Not Changed (1.21929)
FBgn0016694	PAR-domain protein 1	1.76031	14.	14.	Not Changed (0.578511)
FBgn0033464	CG1441	1.75884	22.4	21.6	Not Changed (0.724898)
FBgn0024289	Sorbitol dehydrogenase 1	1.75587	10.4	13.2	Not Changed (1.43016)
FBgn0010383	Cytochrome P45-18a1	1.75318	17.6	15.6	Down (0.4171)
FBgn0036975	CG5618	1.74869	22.	24.	Down (0.465337)
LD15411.3prime-hit	CG17100	1.74559	13.2	13.6	Not Changed (0.839869)

LD29569.3prime-hit	CG12790	1.74397	21.6	22.	Not Changed (1.15495)
FBgn0000723	Fps oncogene analog	1.74169	17.2	1.2	Not Changed (1.28634)
FBgn0034229	CG4847	1.74157	6.	5.2	Not Changed (1.1628)
FBgn0032739	CG15171	1.73872	14.4	12.	Not Changed (0.904992)
FBgn0040491	Buffy	1.73788	9.6	23.6	Not Changed (1.58313)
FBgn0038211	CG9649	1.73656	2.4	1.6	Not Changed (1.83911)
FBgn0039309	CG11891	1.73006	22.	21.2	Not Changed (0.801263)
FBgn0011768	Formaldehyde dehydrogenase	1.72598	9.6	11.6	Not Changed (0.832379)
FBgn0035282	CG13936	1.72321	9.6	12.4	Down (0.244055)
FBgn0037290	CG1124	1.72075	7.6	7.6	Not Changed (0.790751)
FBgn0015872	Drip	1.71802	9.2	4.4	Not Changed (1.46769)
FBgn0015714	Cyp6a17	1.71544	23.6	0.8	Not Changed (1.01577)
FBgn0033821	CG10799	1.71527	19.6	22.	Not Changed (0.857952)
FBgn0034934	CG2827	1.71292	9.6	10.8	Down (0.467347)
GH1265.3prime-hit	CG12397	1.71054	18.8	21.2	Not Changed (0.894984)
FBgn0039084	CG10175	1.70787	17.6	19.2	Not Changed (0.866168)
FBgn0037865	CG18578	1.70703	4.4	2.4	Not Changed (1.20009)
FBgn0033675	CG8889	1.70439	2.8	23.6	Not Changed (1.2497)
FBgn0027593	BcDNA:GH03693	1.70365	17.6	10.	Up (2.52465)
FBgn0031971	CG7224	1.70198	18.8	17.2	Not Changed (1.1274)
FBgn0031808	CG9507	1.70127	18.4	17.2	Not Changed (1.659)
FBgn0036673	CG11915	1.69733	1.2	24.	Not Changed (1.26821)
FBgn0027055	COP9 complex homolog subunit 3	1.69635	18.	3.6	Not Changed (0.828713)
FBgn0038212	CG9645	1.6946	4.4	2.8	Not Changed (1.14215)
FBgn0035985	CG3672	1.68791	23.6	0.4	Not Changed (0.750775)
FBgn0034706	CG11275	1.68698	21.6	23.2	Not Changed (0.578001)
FBgn0041001	CG14403	1.6842	22.8	22.4	Not Changed (1.03193)
LP11629.3prime-hit	CG3451	1.68388	18.	19.2	Not Changed (1.22562)
FBgn0038972	CG7054	1.68145	11.2	10.8	Not Changed (1.81932)
SD1469.3prime-hit	CG8468	1.68036	13.2	10.4	Not Changed (1.18721)
FBgn0037607	CG8036	1.67872	8.8	12.	Not Changed (0.983286)
FBgn0037515	CG3066	1.67825	0.4	24.	Not Changed (0.81568)
FBgn0036659	CG9701	1.67813	21.6	16.8	Not Changed (1.29681)
FBgn0039001	CG4919	1.67624	11.2	12.8	Not Changed (0.719025)
FBgn0036698	CG7724	1.67282	1.6	23.6	Not Changed (1.09218)

FBgn0034431	CG7417	1.67144	8.4	5.2	Not Changed (1.36717)
FBgn0038987	CG6926	1.6713	8.8	24.	Not Changed (0.910419)
FBgn0026439	Excitatory amino acid transporter 1	1.66755	18.8	6.	Not Changed (0.998365)
FBgn0000711	flap wing	1.66573	0.8	23.6	Not Changed (1.06101)
FBgn0030258	CG1552	1.66379	23.2	0.8	Not Changed (0.870164)
FBgn0029534	CG5273	1.66197	0.8	23.2	Not Changed (0.701181)
FBgn0004210	puckered	1.65739	12.4	10.4	Not Changed (0.923931)
FBgn0033853	CG6145	1.65468	16.8	18.8	Not Changed (0.641126)
FBgn0038257	Senescence marker protein-3	1.65443	10.	13.6	Not Changed (0.577934)
FBgn0013770	Cysteine proteinase-1	1.65436	17.6	19.2	Not Changed (0.807631)
FBgn0025879	tissue inhibitor of metalloproteases	1.65058	19.2	19.6	Not Changed (0.744938)
FBgn0034870	CG13559	1.646	9.6	9.2	Not Changed (0.823678)
FBgn0014269	proliferation disrupter	1.64505	15.6	12.8	Not Changed (0.638971)
FBgn0027601	BcDNA:GH02901	1.64319	20.8	19.6	Not Changed (0.877353)
FBgn0034259	CG6459	1.64219	17.2	18.	Not Changed (0.856405)
FBgn0039678	CG18111	1.64094	14.8	15.6	Down (0.0912869)
FBgn0035881	CG7176	1.63744	1.6	2.4	Not Changed (0.658178)
FBgn0036876	CG9451	1.6358	3.6	5.2	Not Changed (0.7904)
FBgn0038525	CG14329	1.62397	2.	1.2	Down (0.320034)
FBgn0038738	CG4572	1.62377	17.2	22.4	Not Changed (0.546444)
FBgn0035484	CG11594	1.62141	9.2	11.6	Not Changed (1.26861)
FBgn0036533	CG6151	1.62038	8.4	6.8	Not Changed (1.15278)
FBgn0038556	CG7321	1.61756	7.6	4.4	Not Changed (1.93357)
FBgn0035445	CG12014	1.61732	18.4	6.4	Not Changed (0.801971)
FBgn0032494	CG5945	1.60659	1.2	22.8	Not Changed (0.783012)
FBgn0038749	CG4468	1.60639	17.6	14.8	Not Changed (1.16876)
FBgn0032844	CG10746	1.60335	19.2	20.4	Not Changed (0.928295)
FBgn0038409	CG6815	1.60221	18.4	20.4	Not Changed (1.23986)
FBgn0034632	CG15668	1.60144	18.4	21.6	Not Changed (1.0891)
FBgn0036106	CG6409	1.59712	19.6	19.2	Not Changed (0.676547)
FBgn0037146	CG7470	1.59466	16.8	20.4	Not Changed (1.12553)
FBgn0003738	Triose phosphate isomerase	1.59436	10.	8.	Not Changed (1.30312)
FBgn0036619	CG4784	1.59404	2.8	3.6	Down (0.422368)
FBgn0039338	CG4548	1.59401	9.6	12.8	Not Changed (1.19963)

FBgn0034429	CG18607	1.58708	8.4	17.2	Not Changed (0.647681)
FBgn0028647	CG11902	1.58344	10.8	8.	Not Changed (1.01319)
FBgn0032213	CG5390	1.58308	18.4	19.6	Not Changed (0.839385)
FBgn0026878	EG:22E5.12	1.58016	12.4	16.	Not Changed (0.780674)
FBgn0036572	CG5165	1.57853	9.6	10.4	Not Changed (1.59601)
FBgn0032836	CG10680	1.56876	6.4	1.6	Not Changed (0.51212)
FBgn0010288	Ubiquitin carboxy-terminal hydrolase	1.56719	14.8	0.4	Not Changed (1.14789)
FBgn0035726	CG9953	1.56286	19.2	21.2	Not Changed (1.3658)
FBgn0032729	CG10639	1.56115	11.2	9.6	Not Changed (0.857882)
FBgn0031845	CG9232	1.55565	4.	7.2	Not Changed (0.916696)
FBgn0015622	Calnexin 99A	1.554	17.6	16.	Not Changed (0.981196)
FBgn0033565	CG18003	1.55225	6.4	8.4	Not Changed (1.08237)
FBgn0010621	T-complex Chaperonin 5	1.55122	9.6	16.4	Not Changed (0.735536)

Table 2: Drosophila Genes Rhythmically Expressed in Light-Dark Condition.

Accession #	Gene Name	Correlation(LD)	Phase(LD)	mRNA Levels in *Clk* (*Clk*/*wt*)
FBgn0030106	CG12120	0.9888	1.2	Not Changed (0.741749)
FBgn0036289	CG10657	0.984897	18.8	Not Changed (0.598144)
FBgn0035921	CG13305	0.983021	3.2	Down (0.103586)
FBgn0005614	trp-like	0.975107	7.6	Not Changed (1.20046)
FBgn0001263	inactivation no afterpotential D	0.97196	1.6	Not Changed (0.921595)
FBgn0025814	Microsomal glutathione S-transferase-like	0.961461	8.8	Not Changed (0.647979)
FBgn0027604	BcDNA:GH02712	0.960888	20.	Not Changed (0.646978)
FBgn0037977	CG3132	0.960819	20.	Not Changed (0.526222)
FBgn0036094	CG14153	0.960559	19.6	Not Changed (0.611659)
FBgn0001624	discs large 1	0.960522	21.2	Not Changed (1.28049)
FBgn0031629	CG3244	0.955695	19.2	Not Changed (1.46115)
FBgn0037468	CG1943	0.954076	17.6	Not Changed (0.87738)
FBgn0035499	Chd64	0.949662	2.8	Not Changed (1.14926)
FBgn0039464	CG6330	0.947241	20.4	Not Changed (1.38855)
FBgn0031436	CG3214	0.946706	20.	Not Changed (1.15067)
FBgn0010218	Calphotin	0.94464	22.4	Up (2.51686)
FBgn0016122	Angiotensin-converting enzyme-related	0.943545	8.8	Not Changed (0.914123)
FBgn0033411	CG8805	0.943186	22.	Not Changed (0.751144)
FBgn0037777	CG11722	0.942222	20.	Not Changed (0.879737)
FBgn0011746	anachronism	0.94159	17.6	Not Changed (0.551526)
FBgn0032694	CG15162	0.939453	17.2	Not Changed (1.06215)
FBgn0026619	tafazzin	0.935343	19.6	Not Changed (1.0347)
LD44686.3prime-hit	CG15761	0.933106	15.6	Not Changed (0.973325)
FBgn0026616	alpha-Man-IIb	0.93277	22.4	Not Changed (1.79242)
FBgn0005619	Histidine decarboxylase	0.930556	22.4	Not Changed (1.15452)
FBgn0002936	neither inactivation nor afterpotential A	0.930496	24.	Not Changed (0.907259)
FBgn0031767	CG9131	0.929797	19.6	Not Changed (0.69664)
FBgn0033523	CG12895	0.929786	21.2	Not Changed (0.715952)

FBgn0003888	betaTubulin6D	0.928946	8.8	Not Changed (1.24992)
FBgn0035961	CG4948	0.928059	13.6	Not Changed (0.596847)
FBgn0000489	cAMP-dependent protein kinase	0.927351	16.	Not Changed (0.862854)
FBgn0025725	alpha-coatomer protein	0.924793	8.4	Not Changed (0.847149)
FBgn0038519	CG5826	0.923895	22.4	Not Changed (0.720366)
FBgn0040594	CG11957	0.923862	8.4	Not Changed (1.58088)
LD37921.3prime-hit	EST mapped to FBgn0032812(CG10263) and FBgn0032811(CG10268)	0.923399	6.8	Down (0.297359)
LP11484.3prime-hit	Epidermal growth factor receptor	0.922569	8.	Not Changed (0.967832)
LD8195.3prime-hit	CG3981	0.922121	20.	Not Changed (1.41938)
FBgn0034579	CG9353	0.921983	20.	Not Changed (0.720687)
FBgn0030769	CG13012	0.919985	8.	Not Changed (0.858997)
FBgn0031925	Cyp4d21	0.919672	17.2	Not Changed (0.705324)
FBgn0032159	CG5885	0.919279	8.8	Not Changed (1.16854)
FBgn0032451	CG12292	0.918993	10.	Not Changed (1.32118)
FBgn0004784	inactivation no afterpotential C	0.917874	3.6	Not Changed (1.84412)
FBgn0003091	Protein C kinase 53E	0.917581	22.4	Not Changed (1.49291)
FBgn0032514	CG9302	0.914038	10.8	Not Changed (0.997264)
FBgn0031215	CG11450	0.91391	11.2	Not Changed (1.39138)
FBgn0033189	CG2140	0.9132	6.8	Not Changed (0.761967)
FBgn0033311	CG8643	0.912517	13.6	Not Changed (1.03754)
FBgn0033218	CG1383	0.912291	10.4	Not Changed (1.03467)
FBgn0031684	CG8680	0.911988	20.4	Not Changed (0.937254)
FBgn0040588	CG13841	0.911142	3.2	Up (3.37187)
FBgn0038305	CG6572	0.910951	21.6	Not Changed (0.804201)
FBgn0036462	CG17166	0.910045	20.	Not Changed (0.581676)
FBgn0013272	Metallothionein A promoter construct of Fashena	0.909927	18.4	Not Changed (0.791062)
FBgn0034443	CG10460	0.908479	20.	Not Changed (0.966422)
FBgn0033198	CG2080	0.908124	3.6	Not Changed (1.41531)
FBgn0036157	CG7560	0.908122	8.8	Not Changed (1.28688)

FBgn0036834	CG6836	0.907185	1.2	Not Changed (0.746597)
FBgn0004511	dusky	0.906651	14.4	Not Changed (0.506098)
FBgn0003031	polyA-binding protein	0.90578	6.4	Not Changed (0.872431)
FBgn0030572	CG14413	0.905711	20.8	Not Changed (0.957716)
FBgn0036928	CG7654	0.905641	21.2	Not Changed (0.906804)
FBgn0039208	CG6643	0.905591	8.4	Not Changed (1.51549)
FBgn0025839	EG:152A3.7	0.904707	21.2	Not Changed (1.30516)
FBgn0031999	CG8419	0.904439	20.	Not Changed (1.24126)
FBgn0014002	Protein disulfide isomerase	0.904222	6.8	Not Changed (0.976589)
FBgn0036661	CG9705	0.904179	12.8	Not Changed (0.83109)
FBgn0000579	Enolase	0.903988	9.2	Not Changed (1.28223)
GH28833.3prime-hit	CG2640	0.903512	19.6	Not Changed (0.707981)
FBgn0030967	CG7282	0.903193	9.6	Not Changed (1.13245)
FBgn0030245	CG1637	0.901396	21.2	Not Changed (0.761693)
FBgn0037892	CG5242	0.901039	21.6	Not Changed (0.77375)
FBgn0033944	CG10127	0.900895	22.8	Not Changed (1.19234)
FBgn0022344	CG10340	0.900446	20.8	Not Changed (1.08002)
FBgn0032349	CG4779	0.900267	6.	Not Changed (1.30951)
FBgn0025885	myo-inositol-1-phosphate-synthase	0.899938	11.6	Not Changed (0.982148)
FBgn0000527	ebony	0.899251	23.2	Not Changed (0.953041)
FBgn0004919	goliath	0.898116	14.4	Not Changed (1.28279)
FBgn0037697	CG9363	0.89795	2.	Not Changed (1.61043)
FBgn0033899	CG13016	0.897744	11.2	Not Changed (0.845761)
FBgn0032775	CG17544	0.896862	19.2	Not Changed (0.923974)
FBgn0033356	CG8229	0.896284	0.4	Not Changed (1.16418)
GH188.3prime-hit	CG10732	0.895403	9.6	Up (2.01194)
FBgn0000153	black	0.89512	16.4	Not Changed (0.649156)
FBgn0011674	inscuteable	0.894469	18.8	Down (0.385713)
FBgn0036681	CG13027	0.893135	6.8	Not Changed (1.53048)
FBgn0034343	CG17534	0.891727	6.8	Not Changed (0.608243)
FBgn0014868	Oligosaccharyltransferase 48kD subunit	0.890837	10.	Not Changed (1.11327)

SD7726.3prime-hit	CG3229	0.890694	18.	Down (0.393495)
FBgn0032266	CG18302	0.890397	16.4	Not Changed (0.736976)
FBgn0037159	CG11471	0.890215	18.4	Not Changed (0.722335)
FBgn0037344	CG2926	0.88962	7.6	Not Changed (1.44363)
FBgn0040751	CG13018	0.88863	19.6	Not Changed (0.747751)
FBgn0037127	CG14566	0.888257	9.6	Not Changed (0.601657)
FBgn0004655	wings apart-like	0.887844	8.4	Not Changed (1.82101)
FBgn0039414	CG14557	0.887103	13.6	Not Changed (0.688497)
FBgn0010638	Sec61beta	0.88709	8.4	Not Changed (0.953869)
FBgn0035467	CG1079	0.887063	20.4	Not Changed (0.85724)
FBgn0020412	JIL-1	0.886928	15.2	Not Changed (1.16865)
GH2872.3prime-hit	CG4144	0.88666	0.4	Not Changed (1.15616)
FBgn0015011	Adenosylhomocysteinase 89E	0.886309	10.4	Not Changed (1.08343)
FBgn0038220	CG12207	0.885986	14.	Not Changed (1.00828)
FBgn0019940	Rhodopsin 6	0.885602	10.8	Not Changed (0.60671)
FBgn0031038	CG14208	0.885507	16.4	Not Changed (1.08093)
FBgn0027610	BcDNA:GH02431	0.884726	22.	Not Changed (0.987823)
FBgn0033249	CG11191	0.884	7.2	Not Changed (0.805721)
FBgn0033232	CG12159	0.883912	8.	Not Changed (0.801779)
FBgn0011016	Signal sequence receptor beta	0.883896	8.	Not Changed (0.90539)
FBgn0033039	CG7897	0.882986	17.6	Not Changed (1.10957)
FBgn0003074	Phosphoglucose isomerase	0.882903	9.6	Not Changed (0.981852)
FBgn0038996	CG6949	0.882643	18.	Not Changed (0.945061)
FBgn0000241	brown	0.882362	15.6	Not Changed (0.839488)
FBgn0037648	CG11975	0.881781	21.2	Not Changed (1.25997)
FBgn0032512	CG9305	0.881549	20.	Not Changed (1.20646)
FBgn0032205	CG4957	0.880829	19.6	Not Changed (0.910368)
FBgn0030743	CG9921	0.880802	19.6	Not Changed (0.554965)
FBgn0011336	Oligosaccharyl transferase 3	0.880394	9.2	Not Changed (1.13719)
FBgn0036816	CG3979	0.880284	22.8	Not Changed (1.08762)
FBgn0035046	CG3683	0.880121	20.	Not Changed (1.12581)
FBgn0020386	Protein kinase 61C	0.879943	10.4	Not Changed (0.945787)

FBgn0036824	CG3902	0.879356	3.6	Not Changed (0.656566)
FBgn0038474	CG5184	0.879232	20.8	Not Changed (0.922567)
FBgn0033981	Cyp6a21	0.878532	22.4	Not Changed (0.773527)
FBgn0037117	CG11248	0.878061	12.	Not Changed (1.02485)
FBgn0034179	CG6805	0.877542	23.6	Not Changed (1.07319)
FBgn0012044	BTB-protein-II	0.877529	24.	Not Changed (1.1759)
FBgn0039745	CG7950	0.877124	16.	Not Changed (0.575186)
FBgn0038160	CG9759	0.877072	9.6	Down (0.341763)
FBgn0038617	CG12333	0.877001	19.6	Not Changed (1.58132)
FBgn0035744	CG8628	0.876736	10.	Not Changed (0.730261)
FBgn0037672	CG12952	0.876153	10.	Not Changed (1.06704)
FBgn0031801	CG9498	0.874937	8.4	Not Changed (0.909373)
FBgn0039653	CG1458	0.874911	22.	Not Changed (0.705733)
FBgn0037845	CG14694	0.873926	9.2	Not Changed (0.906723)
FBgn0030817	CG4991	0.873643	19.6	Not Changed (1.05815)
LD1981.3prime-hit	amphiphysin	0.873414	20.8	Not Changed (1.20236)
FBgn0027528	BcDNA:LD21405	0.873319	19.2	Not Changed (0.989338)
FBgn0030013	CG1583	0.873164	8.8	Not Changed (1.4524)
FBgn0031819	CG9539	0.872091	8.4	Not Changed (1.07493)
FBgn0029820	CG16721	0.872021	18.4	Not Changed (1.1983)
FBgn0034576	CG9350	0.871891	21.2	Not Changed (1.33783)
FBgn0032666	CG5758	0.871724	2.4	Up (3.2)
FBgn0036372	CG10083	0.871333	18.4	Not Changed (0.988226)
FBgn0039178	CG6356	0.871265	5.2	Not Changed (1.11908)
FBgn0038149	CG9796	0.870853	18.8	Not Changed (0.688749)
FBgn0037241	CG14646	0.870498	14.8	Not Changed (0.89259)
FBgn0000675	flipper	0.870133	20.	Not Changed (0.599036)
FBgn0035133	Ptpmeg	0.869949	2.	Not Changed (1.74558)
FBgn0030480	CG1660	0.869836	20.4	Not Changed (0.792351)
FBgn0013743	Serotonin receptor 2	0.86982	13.2	Not Changed (0.866807)
FBgn0038141	CG9829	0.869581	18.8	Not Changed (0.946535)
FBgn0027359	Tim8	0.869427	20.	Not Changed (0.757241)

FBgn0029721	CG7010	0.869184	20.	Not Changed (1.04556)
FBgn0035504	CG15003	0.869152	9.2	Not Changed (0.880692)
FBgn0039644	CG11897	0.868551	13.6	Not Changed (0.898246)
FBgn0032222	CG5037	0.868443	17.6	Not Changed (0.811767)
FBgn0036371	CG10745	0.86807	8.4	Not Changed (0.894917)
FBgn0002354	lethal (3) 87Df	0.867929	20.4	Not Changed (1.08643)
FBgn0036182	CG6084	0.867835	7.2	Not Changed (1.28709)
FBgn0014906	CG3488	0.867818	15.2	Not Changed (0.930836)
FBgn0033533	CG18379	0.867593	9.2	Not Changed (1.11166)
FBgn0028507	BG:DS09217.4	0.867335	20.4	Not Changed (1.2061)
FBgn0033663	CG8983	0.866596	10.4	Not Changed (0.910163)
FBgn0033065	Cyp6w1	0.866576	8.8	Down (0.312898)
FBgn0035318	CG9018	0.866033	10.8	Not Changed (0.873648)
FBgn0034909	CG4797	0.866033	7.6	Not Changed (0.610629)
FBgn0035909	CG6822	0.865611	9.2	Not Changed (0.889946)
FBgn0032342	CG4713	0.864725	10.	Not Changed (1.28074)
FBgn0037929	CG14714	0.864662	10.4	Not Changed (1.50447)
FBgn0004597	Cyclin C	0.863679	15.6	Not Changed (0.8358)
FBgn0036288	CG10660	0.863151	16.4	Not Changed (0.72088)
FBgn0032906	CG9273	0.862869	11.2	Down (0.479725)
FBgn0030558	CG1461	0.861678	7.6	Not Changed (0.661567)
FBgn0036312	CG17667	0.861134	19.2	Not Changed (0.894136)
FBgn0035656	CG10479	0.860884	15.2	Not Changed (0.809121)
FBgn0015805	Rpd3	0.860766	10.	Not Changed (0.814574)
FBgn0031539	CG8844	0.860677	21.6	Not Changed (0.832176)
FBgn0035427	CG14959	0.860114	19.2	Not Changed (0.73742)
FBgn0038818	CG4058	0.859927	1.6	Not Changed (1.24036)
FBgn0032713	CG17323	0.859685	21.2	Not Changed (1.32501)
FBgn0023537	EG:171D11.1	0.859634	3.2	Not Changed (1.05569)
FBgn0031590	CG3702	0.858785	9.6	Not Changed (0.958037)
FBgn0036951	CG7017	0.858046	18.8	Not Changed (0.731972)
FBgn0037054	CG10523	0.857663	14.8	Not Changed (0.86489)

GH1453.3prime-hit	CG11142	0.857631	3.2	Not Changed (0.944324)
FBgn0037379	CG10979	0.856797	11.2	Not Changed (0.865291)
FBgn0030921	CG6290	0.856514	22.8	Down (0.447372)
FBgn0000250	cactus	0.856477	20.8	Not Changed (0.845922)
FBgn0032985	CG12628	0.856098	6.8	Not Changed (0.804096)
FBgn0030974	CG7358	0.854878	8.8	Not Changed (1.26818)
FBgn0038682	CG5835	0.854854	10.	Not Changed (1.02493)
FBgn0037757	CG8516	0.854576	5.2	Not Changed (0.781576)
FBgn0036556	CG5830	0.854542	9.6	Not Changed (1.214)
FBgn0027606	BcDNA:GH02636	0.853875	8.	Not Changed (1.17229)
FBgn0034976	CG4049	0.853103	6.8	Not Changed (0.906307)
FBgn0023489	PvuII-PstI homology 13	0.8531	17.6	Not Changed (1.25839)
FBgn0032783	CG10237	0.852585	17.6	Not Changed (0.735589)
FBgn0002783	moira	0.852498	9.2	Not Changed (0.84733)
FBgn0039024	CG4721	0.85246	10.8	Not Changed (1.04974)
FBgn0039502	CG5965	0.851015	8.8	Not Changed (1.43251)
FBgn0036319	CG11010	0.850989	8.4	Not Changed (0.837816)
FBgn0004055	unzipped	0.850356	17.2	Not Changed (0.803668)
FBgn0030610	CG9065	0.849489	19.6	Not Changed (0.760141)
FBgn0003249	Rhodopsin 3	0.849318	4.4	Not Changed (1.25852)
FBgn0037978	CG3571	0.848928	1.6	Not Changed (1.12545)
FBgn0040693	CG13799	0.848924	20.8	Down (0.240425)
FBgn0029648	CG3603	0.848226	16.4	Not Changed (0.817772)
FBgn0022349	CG1910	0.848095	8.8	Not Changed (0.972999)
FBgn0037111	CG14576	0.848001	9.6	Down (0.270514)
FBgn0011673	Myosin 31DF	0.847852	8.8	Not Changed (1.15813)
FBgn0001128	Glycerol 3 phosphate dehydrogenase	0.847422	8.	Not Changed (0.79992)
FBgn0028479	BcDNA:GH12558	0.84733	7.6	Not Changed (0.566172)
FBgn0032164	CG4588	0.847055	20.4	Down (0.494961)
FBgn0014184	gut feeling	0.846375	4.8	Not Changed (1.21304)
FBgn0029545	CG11642	0.846225	6.4	Not Changed (0.789411)

FBgn0004456	multiple edematous wings	0.845501	9.6	Not Changed (1.26838)
FBgn0029762	CG3252	0.845331	7.6	Not Changed (0.888971)
FBgn0034643	CG10321	0.845059	21.6	Not Changed (1.34611)
FBgn0028698	Rho-kinase	0.844632	10.8	Not Changed (0.946048)
FBgn0034605	CG15661	0.844562	4.	Not Changed (0.551974)
FBgn0034436	CG11961	0.84449	11.2	Not Changed (0.686442)
FBgn0038000	CG10014	0.844249	14.8	Not Changed (0.805754)
FBgn0037906	CG14704	0.843776	8.8	Not Changed (0.677468)
FBgn0029896	CG3168	0.843337	12.	Not Changed (1.43122)
FBgn0028582	liquid facets	0.842441	2.4	Not Changed (1.75644)
FBgn0037114	CG7160	0.841945	3.6	Not Changed (0.607901)
FBgn0033208	CG1577	0.841389	18.8	Not Changed (1.08562)
FBgn0035840	CG7528	0.839941	18.8	Not Changed (0.947682)
FBgn0030143	CG12141	0.839873	22.4	Not Changed (0.920032)
FBgn0031049	CG14214	0.839565	8.4	Not Changed (0.801914)
FBgn0033100	CG3420	0.839065	20.	Not Changed (0.695677)
FBgn0011296	lethal (2) essential for life	0.838814	9.6	Not Changed (1.47595)
FBgn0032134	CG3864	0.838536	3.6	Not Changed (1.14483)
FBgn0003471	beta Spectrin	0.838503	6.8	Not Changed (1.2449)
FBgn0037044	CG10585	0.8385	16.4	Not Changed (0.837197)
FBgn0030968	CG7322	0.838064	9.6	Not Changed (0.850436)
FBgn0033717	CG8839	0.837941	8.4	Not Changed (1.10646)
FBgn0031380	CG4233	0.837755	7.6	Not Changed (1.33519)
FBgn0030115	CG15797	0.837333	13.2	Not Changed (1.22346)
FBgn0033638	CG9005	0.83726	18.8	Not Changed (0.633449)
FBgn0038437	CG14898	0.837126	18.4	Not Changed (1.22529)
FBgn0040850	CG15210	0.836736	18.	Not Changed (0.537483)
FBgn0036435	CG5031	0.836481	10.8	Not Changed (1.60861)
FBgn0032032	CG17294	0.836396	1.6	Up (3.26507)
FBgn0040734	CG15065	0.836385	4.8	Not Changed (1.23541)
FBgn0001168	hairy	0.836271	10.8	Not Changed (0.890057)
FBgn0030734	CG9911	0.836024	9.2	Not Changed (0.95587)

FBgn0038038	CG5167	0.83568	8.4	Not Changed (0.840469)
FBgn0038795	CG4335	0.835205	6.4	Not Changed (1.30877)
FBgn0034634	CG10494	0.834925	20.8	Not Changed (0.819302)
FBgn0032336	CG14919	0.834912	22.4	Not Changed (1.22836)
FBgn0035723	CG9943	0.834904	10.8	Not Changed (0.884346)
FBgn0038172	CG9621	0.834804	20.	Not Changed (1.70577)
FBgn0036020	CG8336	0.834732	19.6	Not Changed (1.04314)
FBgn0035055	CG3872	0.834675	18.	Not Changed (0.967525)
FBgn0013725	phyllopod	0.834019	20.8	Not Changed (0.806751)
FBgn0033548	CG7637	0.833637	20.4	Not Changed (0.63177)
FBgn0033085	CG15908	0.833562	20.4	Not Changed (0.900138)
FBgn0023167	Small ribonucleoprotein Sm D3	0.833526	15.2	Not Changed (0.918318)
FBgn0033259	CG11210	0.833421	9.2	Not Changed (1.05957)
FBgn0035483	CG1134	0.832929	12.8	Not Changed (0.791833)
FBgn0038236	Cyp313a1	0.832548	16.	Not Changed (1.18576)
FBgn0029876	CG3960	0.832459	9.2	Not Changed (1.40607)
FBgn0000114	arrest	0.832408	10.4	Not Changed (0.974543)
FBgn0027095	ARP-like	0.832332	7.6	Not Changed (1.14234)
FBgn0030060	CG2004	0.832155	11.2	Not Changed (1.06033)
FBgn0036901	CG8756	0.831885	21.6	Not Changed (0.924105)
FBgn0030704	CG15916	0.831601	20.4	Not Changed (0.746553)
FBgn0034727	CG3633	0.831333	18.4	Not Changed (1.04298)
FBgn0025352	Thiolase	0.831293	9.2	Not Changed (0.87403)
FBgn0038201	CG9918	0.831104	20.4	Not Changed (1.54021)
FBgn0039022	CG4725	0.831069	6.8	Not Changed (0.839101)
FBgn0030767	CG4524	0.830526	15.6	Not Changed (1.02451)
FBgn0036146	CG14141	0.829921	19.6	Not Changed (1.17445)
FBgn0037277	CG17735	0.829908	10.4	Not Changed (1.47714)
FBgn0034245	CG14482	0.829592	20.8	Not Changed (1.10584)
FBgn0024978	EG:95B7.3	0.829466	24.	Not Changed (0.944852)
FBgn0036762	CG7430	0.829159	22.	Not Changed (1.29082)
FBgn0031408	CG10882	0.828549	8.4	Not Changed (1.02928)

FBgn0039064	CG4467	0.82846	6.4	Not Changed (0.676126)
FBgn0027785	NP15.6	0.828424	20.	Not Changed (1.12289)
FBgn0031260	CG11840	0.827925	7.6	Not Changed (1.93671)
FBgn0037528	CG10409	0.827854	16.8	Not Changed (0.913988)
FBgn0011361	mitochondrial acyl carrier protein 1	0.826931	20.8	Not Changed (1.15404)
FBgn0035940	CG5012	0.82673	22.	Not Changed (0.867359)
FBgn0031417	CG3597	0.826537	8.8	Not Changed (1.25577)
FBgn0034474	CG13873	0.82638	20.4	Not Changed (0.921361)
FBgn0033784	CG13322	0.826019	11.6	Not Changed (0.652718)
FBgn0039756	CG9743	0.825978	5.2	Not Changed (0.710164)
FBgn0040551	CG11686	0.825751	3.6	Not Changed (1.18429)
FBgn0010235	Kinesin light chain	0.825314	17.2	Not Changed (0.973826)
FBgn0032900	CG14401	0.824836	15.2	Not Changed (0.987616)
FBgn0023395	Chd3	0.824747	12.	Not Changed (1.31257)
FBgn0032322	CG16743	0.824375	4.4	Not Changed (0.586805)
FBgn0033502	CG12910	0.824149	12.8	Not Changed (1.19988)
FBgn0032606	CG17932	0.824047	20.4	Down (0.284543)
FBgn0013467	igloo	0.823002	18.8	Not Changed (1.22575)
FBgn0024832	AP-50	0.822931	20.	Not Changed (1.32818)
FBgn0035181	CG9205	0.822873	3.2	Not Changed (1.19769)
FBgn0000715	FMRFamide-related	0.822247	3.2	Not Changed (1.45619)
FBgn0014141	cheerio	0.822238	11.6	Not Changed (1.75625)
FBgn0032877	CG2617	0.82217	9.2	Not Changed (0.858738)
FBgn0034949	CG17263	0.822097	9.2	Not Changed (0.800954)
FBgn0035806	CG7496	0.822002	11.6	Down (0.39001)
FBgn0005648	Pabp2	0.821969	7.2	Not Changed (0.840513)
FBgn0038875	CG6056	0.821445	22.4	Not Changed (1.20882)
FBgn0030183	CG15309	0.821437	21.6	Not Changed (1.39141)
FBgn0036891	CG9372	0.82129	4.4	Not Changed (0.766233)
FBgn0033797	CG13328	0.821078	20.	Not Changed (0.943512)
FBgn0011604	Imitation SWI	0.821071	8.	Down (0.44077)

FBgn0030796	CG4829	0.820718	18.8	Not Changed (1.10845)
FBgn0034091	CG8448	0.820696	16.8	Not Changed (1.15893)
FBgn0038678	CG14283	0.820638	20.4	Not Changed (1.14491)
FBgn0039586	CG18436	0.82063	9.6	Not Changed (1.0355)
FBgn0039350	CG17383	0.820545	22.8	Not Changed (1.02919)
FBgn0004580	Calbindin 53E	0.820079	23.2	Not Changed (0.601)
FBgn0033519	CG11825	0.819808	13.6	Not Changed (0.557463)
FBgn0033131	CG12842	0.819797	24.	Not Changed (0.749488)
FBgn0033324	CG14744	0.819709	17.6	Not Changed (0.987532)
FBgn0029615	CG14047	0.819393	7.6	Not Changed (1.27029)
FBgn0026630	nessy	0.819015	23.2	Not Changed (0.913815)
LD224.3prime-hit	Neurotactin	0.819013	7.6	Not Changed (1.05565)
FBgn0036547	CG17032	0.818807	9.6	Not Changed (0.825397)
FBgn0000054	Adh transcription factor 1	0.818707	10.	Not Changed (0.850464)
FBgn0023407	Saccharomyces cerevisiae UAS construct a of Sotillos	0.81858	22.4	Not Changed (0.886797)
FBgn0034698	CG6698	0.818245	8.4	Not Changed (0.864327)
LD22520.3prime-hit	EST mapped to FBgn0002638(Bj1) and FBgn0000079(Amy-p)	0.818185	18.8	Not Changed (1.2406)
FBgn0005776	Protein phosphatase 2A at 29B	0.817884	22.4	Not Changed (1.08512)
FBgn0031024	CG12233	0.817561	20.4	Not Changed (0.800908)
FBgn0036511	CG6498	0.817549	4.8	Not Changed (1.3591)
FBgn0031069	CG12703	0.817473	11.2	Not Changed (0.80104)
FBgn0004777	Ccp84Ag	0.817418	21.6	Not Changed (1.76315)
FBgn0040799	CG13051	0.816937	21.6	Not Changed (1.16694)
FBgn0032720	CG10603	0.816358	19.2	Not Changed (0.91928)
FBgn0029620	CG7981	0.816307	19.6	Up (2.16575)
FBgn0027499	BcDNA:LD26050	0.816038	18.4	Not Changed (1.20622)
FBgn0015621	Clipper	0.815885	5.2	Not Changed (0.578973)
FBgn0037315	CG16708	0.815505	10.8	Not Changed (1.13453)
HL1868.3prime-hit	CG10077	0.815287	12.	Not Changed (1.97693)
FBgn0017429	CG5989	0.815013	19.2	Not Changed (0.957181)

FBgn0027565	BcDNA:GH08385	0.814908	20.4	Not Changed (1.29825)
FBgn0032160	CG4598	0.814753	10.8	Not Changed (0.506154)
FBgn0033588	CG13228	0.814019	4.4	Not Changed (1.06178)
FBgn0039623	CG1951	0.813733	15.6	Not Changed (1.13021)
FBgn0030184	CG2968	0.813712	20.4	Not Changed (1.09383)
FBgn0032263	CG7400	0.8137	12.	Not Changed (0.836588)
FBgn0036857	CG9629	0.813515	9.2	Not Changed (1.05962)
FBgn0033245	CG8723	0.813402	9.6	Not Changed (0.868462)
FBgn0028741	EG:52C10.5	0.813101	16.	Not Changed (1.52548)
FBgn0038347	CG18522	0.812881	1.2	Not Changed (0.564992)
FBgn0037186	CG11241	0.812561	15.6	Not Changed (0.7515)
FBgn0031064	CG12531	0.812165	3.2	Not Changed (1.05979)
FBgn0037933	CG14716	0.811733	21.2	Not Changed (1.09946)
FBgn0039703	CG7829	0.811669	8.8	Up (2.57052)
FBgn0033359	CG8213	0.811668	10.8	Down (0.416378)
FBgn0040878	CG15911	0.811533	18.4	Not Changed (1.47819)
FBgn0032469	CG9932	0.810865	7.2	Not Changed (1.74075)
FBgn0033934	CG17385	0.810844	4.8	Not Changed (1.06727)
FBgn0005649	Rox8	0.810225	13.2	Not Changed (1.16235)
FBgn0035480	CG14984	0.810072	3.2	Not Changed (1.22135)
FBgn0036546	CG17033	0.809829	17.6	Not Changed (1.07427)
FBgn0029843	CG5894	0.80938	11.6	Not Changed (0.671637)
FBgn0028694	Rpn11	0.808808	13.2	Not Changed (0.664207)
FBgn0033095	CG3409	0.808675	8.8	Not Changed (1.57499)
FBgn0036581	CG5057	0.808025	20.	Not Changed (0.848952)
FBgn0030731	CG3415	0.807769	9.2	Not Changed (0.940837)
FBgn0036585	CG13071	0.807599	20.8	Up (2.08237)
FBgn0038612	CG7676	0.807515	20.	Not Changed (1.79033)
FBgn0040962	CG15868	0.807416	7.6	Not Changed (1.04786)
FBgn0036237	CG18593	0.80702	8.	Not Changed (0.667453)
FBgn0031937	CG13795	0.8069	8.4	Not Changed (1.07253)
GH13437.3prime-hit	CG5889	0.806859	20.	Not Changed (0.867643)

FBgn0033329	CG8575	0.806851	8.4	Not Changed (1.45942)
FBgn0004057	Zwischenferment	0.80682	10.	Not Changed (0.716608)
FBgn0031088	CG15322	0.806627	2.4	Not Changed (0.761035)
FBgn0034709	CG3074	0.805989	6.	Not Changed (1.32531)
GH18645.3prime-hit	temperature-induced paralytic E	0.805653	12.	Not Changed (1.90233)
FBgn0031806	CG9506	0.805636	16.8	Not Changed (1.23759)
FBgn0037269	CG1055	0.80561	19.6	Not Changed (1.1074)
FBgn0035111	CG16940	0.804873	8.	Not Changed (1.032)
FBgn0031773	CG9144	0.804871	14.8	Not Changed (0.879661)
FBgn0039753	CG1359	0.804698	20.	Not Changed (0.831683)
FBgn0033949	CG10131	0.80454	10.	Not Changed (0.940996)
FBgn0036645	CG18218	0.804428	18.8	Not Changed (0.745428)
FBgn0030093	CG7055	0.804185	12.	Not Changed (0.967508)
FBgn0027919	BcDNA:GM04682	0.804162	7.6	Not Changed (0.785005)
FBgn0031813	CG9527	0.803989	5.6	Not Changed (1.14009)
FBgn0035423	CG17737	0.803902	20.4	Not Changed (0.990222)
FBgn0035473	maggie	0.803886	20.8	Not Changed (0.592809)
FBgn0030311	CG11699	0.803776	20.	Not Changed (0.904797)
FBgn0035646	CG10487	0.803706	4.4	Not Changed (0.903134)
FBgn0035334	CG8993	0.803612	20.8	Not Changed (1.0418)
FBgn0031515	CG9664	0.803533	11.6	Not Changed (0.850805)
FBgn0025676	CKII-alpha subunit interactor-3	0.803506	19.2	Down (0.315254)
FBgn0032238	CG5251	0.80337	8.4	Not Changed (0.776432)
FBgn0027912	BcDNA:GM12291	0.803183	7.2	Not Changed (1.0067)
FBgn0033466	CG12130	0.802908	9.6	Not Changed (1.83062)
FBgn0036926	CG7646	0.802822	21.2	Not Changed (1.13482)
FBgn0038405	CG8927	0.802746	23.6	Not Changed (0.762008)
FBgn0035471	CG10849	0.802554	12.8	Not Changed (0.757519)
FBgn0035966	CG4684	0.802526	7.2	Not Changed (1.27439)
FBgn0037550	CG9667	0.802412	12.	Down (0.453762)
FBgn0037108	CG11306	0.801726	14.4	Not Changed (0.946048)

FBgn0001942	Eukaryotic initiation factor 4a (middle region of transcript)	0.801441	4.8	Not Changed (0.920225)
FBgn0033721	CG13159	0.80143	17.6	Not Changed (1.04204)
FBgn0038789	CG15685	0.801253	13.2	Not Changed (0.773353)
FBgn0015276	Protein-L-isoaspartate (D-aspartate) O-methyltransferase	0.801076	6.	Not Changed (0.708699)
FBgn0030380	CG18256	0.801028	9.6	Down (0.440395)
FBgn0039625	CG14517	0.800748	10.4	Not Changed (0.996068)
FBgn0030828	CG5162	0.800738	11.6	Not Changed (1.20534)
FBgn0037371	CG2097	0.800699	4.4	Not Changed (1.17734)
FBgn0040846	CG17496	0.800681	7.2	Not Changed (0.753265)
FBgn0020513	ade5	0.800376	10.	Not Changed (1.4366)
FBgn0003250	Rhodopsin 4	0.800204	4.4	Not Changed (0.904268)
FBgn0032864	CG2493	0.800049	9.6	Not Changed (0.716315)
FBgn0031936	CG13794	0.799825	10.4	Not Changed (0.555661)
FBgn0025630	EG:22E5.3	0.799803	12.4	Not Changed (0.9865)
FBgn0031228	CG11455	0.799678	21.6	Not Changed (1.62593)
FBgn0035278	CG12023	0.799633	3.6	Not Changed (0.513892)
FBgn0038665	CG12269	0.799512	22.	Not Changed (0.744644)
FBgn0010220	DEAD box protein 45A	0.799399	22.4	Not Changed (1.22953)
FBgn0036101	CG6449	0.79921	10.	Not Changed (1.3714)
FBgn0030292	CG11752	0.798808	21.6	Not Changed (0.946495)
FBgn0032340	CG6181	0.798529	9.2	Not Changed (1.20068)
FBgn0038925	CG6022	0.798295	20.4	Not Changed (0.973265)
FBgn0037793	CG3953	0.798007	22.8	Not Changed (1.35561)
FBgn0035673	CG6602	0.797795	12.4	Not Changed (0.639905)
FBgn0039293	CG11851	0.797785	16.	Not Changed (0.635268)
FBgn0026415	Imaginal Disc Growth Factor 4	0.797535	4.4	Not Changed (1.24075)
FBgn0034356	CG10924	0.79723	21.6	Down (0.00170775)
FBgn0032513	CG6565	0.796972	20.	Not Changed (0.984242)
FBgn0033071	CG8324	0.796826	6.4	Not Changed (0.693478)
FBgn0026872	EG:80H7.10	0.796591	22.4	Not Changed (0.954048)
FBgn0003691	thread	0.796579	20.4	Not Changed (1.05349)

FBgn0037217	CG14636	0.796065	20.8	Not Changed (0.640948)
FBgn0039635	CG11876	0.795704	20.	Not Changed (1.15085)
FBgn0016672	Inositol polyphosphate 1-phosphatase	0.795362	7.6	Not Changed (0.955502)
FBgn0030782	CG18358	0.795096	4.8	Not Changed (1.33727)
FBgn0033000	CG14464	0.794586	19.2	Not Changed (0.840349)
FBgn0033918	CG8531	0.794537	14.8	Not Changed (0.955616)
FBgn0030576	CG15890	0.794395	8.	Not Changed (0.898768)
FBgn0035076	CG10142	0.794376	21.2	Down (0.456167)
FBgn0000473	Cytochrome P45-6a2	0.79408	9.2	Not Changed (0.837222)
FBgn0035795	CG16998	0.793954	22.	Not Changed (0.617987)
FBgn0027547	BcDNA:GH11112	0.793529	21.2	Not Changed (0.784249)
FBgn0036043	CG8177	0.793502	6.8	Not Changed (0.762211)
FBgn0036303	CG10753	0.793358	8.8	Not Changed (0.733876)
FBgn0034142	CG8306	0.793237	16.4	Not Changed (0.717751)
FBgn0004363	porin	0.79316	4.8	Not Changed (1.02087)
FBgn0029639	CG14419	0.792975	12.	Down (0.423226)
FBgn0027657	globin 1	0.792757	21.6	Not Changed (0.912639)
FBgn0033875	CG6357	0.792711	20.	Up (2.00526)
FBgn0029972	CG1422	0.792507	8.4	Not Changed (1.44212)
FBgn0030672	CG9281	0.792217	8.	Not Changed (0.772432)
FBgn0029888	CG3192	0.792145	19.6	Not Changed (1.10954)
FBgn0004611	Phospholipase C at 21C	0.791669	5.2	Not Changed (1.76061)
FBgn0034428	CG18606	0.791421	10.4	Not Changed (1.17024)
FBgn0038799	CG4288	0.791328	24.	Not Changed (1.67824)
FBgn0032135	CG3881	0.790946	22.	Not Changed (1.24012)
FBgn0030001	CG15335	0.790451	14.4	Not Changed (0.831689)
FBgn0015509	lin-19-like	0.790297	16.4	Not Changed (1.28135)
FBgn0034051	Myelodysplasia/myeloid leukemia factor	0.790296	20.8	Not Changed (0.957546)
FBgn0030510	CG12177	0.790223	21.6	Not Changed (0.723716)
FBgn0039216	CG13621	0.789985	18.4	Not Changed (0.870577)
FBgn0030213	CG15298	0.789848	6.8	Not Changed (0.90723)

FBgn0022268	KDEL receptor	0.789614	9.6	Not Changed (0.700072)
FBgn0004512	Multi drug resistance 49	0.789344	1.2	Up (2.43509)
FBgn0003886	alphaTubulin85E	0.789304	11.6	Not Changed (1.21663)
FBgn0037638	CG8379	0.789273	18.	Down (0.332462)
FBgn0033654	CG8991	0.788444	11.6	Not Changed (1.11896)
FBgn0033881	CG13345	0.78841	17.6	Not Changed (0.982622)
FBgn0034588	CG9394	0.788049	21.6	Not Changed (0.579216)
FBgn0030451	CG15717	0.787743	8.4	Not Changed (0.517254)
FBgn0028469	BcDNA:LD28120	0.787693	10.4	Not Changed (0.600034)
FBgn0002174	lethal (2) tumorous imaginal discs	0.787348	20.4	Not Changed (0.984768)
LD27203.3prime-hit	EST mapped to FBgn0034212(CG6564) and FBgn0034211(CG15901)	0.787179	18.4	Not Changed (0.617882)
FBgn0039737	CG7920	0.787073	3.2	Not Changed (0.962605)
FBgn0035528	CG15012	0.787036	11.6	Not Changed (0.878078)
FBgn0036870	CG14095	0.786219	15.2	Down (0.205065)
FBgn0031800	CG9497	0.786197	23.6	Not Changed (1.41485)
FBgn0038010	CG18158	0.78606	9.2	Not Changed (0.808324)
FBgn0030766	CG4521	0.785915	15.6	Not Changed (1.76502)
FBgn0014340	males absent on the first	0.785611	22.8	Not Changed (0.907364)
FBgn0020383	RasGap	0.785431	9.6	Not Changed (1.06498)
FBgn0024986	EG:132E8.3	0.784411	20.	Not Changed (1.02705)
FBgn0032899	CG9338	0.784352	20.4	Not Changed (1.14229)
FBgn0034855	CG9889	0.783991	17.6	Not Changed (0.773748)
FBgn0003887	betaTubulin56D	0.783695	11.2	Not Changed (0.732308)
FBgn0023479	Tequila	0.78353	6.	Not Changed (1.00887)
FBgn0030201	CG2883	0.783003	18.	Not Changed (1.15252)
FBgn0026753	Vacuolar H+ ATPase G-subunit	0.782865	19.6	Not Changed (0.715765)
FBgn0035070	CG3650	0.782723	6.8	Down (0.146379)
FBgn0040534	CG11985	0.782649	19.6	Not Changed (0.878596)
LD12453.3prime-hit	EST mapped to FBgn0033804(CG4037) and FBgn0033803(CG4055)	0.782362	24.	Not Changed (1.20602)

FBgn0032482	CG5547	0.781749	15.2	Not Changed (0.86173)
FBgn0032084	CG13101	0.781664	23.2	Not Changed (0.983803)
FBgn0020907	Sarcoplasmic calcium-binding protein 2	0.781448	22.4	Not Changed (0.889177)
FBgn0029626	CG17437	0.781147	11.6	Not Changed (1.05266)
FBgn0039056	centaurin beta 1A	0.781028	10.4	Not Changed (1.03411)
FBgn0032926	CG9243	0.780995	18.4	Not Changed (0.788269)
FBgn0000083	Annexin IX	0.78075	6.4	Not Changed (1.1602)
FBgn0035808	SP2523	0.780746	3.2	Up (3.6458)
FBgn0001098	Glutamate dehydrogenase	0.780725	23.2	Not Changed (1.01269)
FBgn0037010	CG4825	0.779946	19.2	Not Changed (0.784968)
FBgn0039176	CG13610	0.779877	7.6	Not Changed (0.787843)
FBgn0031172	CG1704	0.77924	21.2	Not Changed (1.00049)
FBgn0035271	CG2021	0.779178	18.8	Not Changed (1.03098)
FBgn0037288	CG14661	0.778949	23.2	Not Changed (1.1597)
FBgn0034438	CG9416	0.778836	10.	Not Changed (1.50704)
FBgn0031491	CG17223	0.778817	3.2	Not Changed (1.12902)
FBgn0036920	CG8004	0.778684	20.8	Not Changed (0.689589)
FBgn0031362	CG17646	0.778288	24.	Not Changed (0.787003)
FBgn0035314	CG5707	0.778149	9.2	Not Changed (0.821907)
FBgn0035595	CG10668	0.778105	2.8	Down (0.0074996)
FBgn0038413	CG6725	0.777631	12.8	Not Changed (1.72009)
FBgn0002069	Aspartyl-tRNA synthetase	0.777442	8.	Not Changed (0.968428)
FBgn0033073	bicoid-interacting protein 3	0.777015	2.4	Not Changed (1.63818)
FBgn0036826	CG3893	0.776943	18.8	Not Changed (0.581938)
FBgn0030977	CG12527	0.776724	12.4	Not Changed (0.802018)
FBgn0036927	CG7433	0.776369	22.4	Not Changed (1.24305)
FBgn0040575	CG15922	0.776313	19.6	Not Changed (0.88587)
FBgn0034848	CG9872	0.776279	9.2	Not Changed (1.02878)
FBgn0004889	twins	0.776274	12.	Not Changed (1.09173)
FBgn0024980	EG:95B7.1	0.776238	2.	Not Changed (1.39642)
FBgn0037066	CG7752	0.776125	10.	Not Changed (0.664124)

FBgn0038707	CG7237	0.77609	3.2	Not Changed (1.52123)
FBgn0040736	CG16844	0.775905	3.6	Not Changed (1.31632)
FBgn0032726	CG10621	0.775685	10.8	Up (2.65155)
FBgn0036257	CG6811	0.775636	18.8	Not Changed (0.867936)
FBgn0002306	stranded at second	0.775551	2.4	Not Changed (1.11072)
FBgn0035680	CG10733	0.77472	8.	Not Changed (1.08872)
FBgn0035292	CG12361	0.774656	5.6	Not Changed (0.794424)
FBgn0037533	CG2791	0.774577	5.2	Not Changed (1.12075)
FBgn0020261	pacman	0.774248	10.4	Not Changed (1.05039)
FBgn0030160	CG9691	0.774124	4.4	Not Changed (1.07527)
FBgn0035395	CG14954	0.773716	6.4	Not Changed (0.97113)
FBgn0034033	CG8204	0.773629	19.6	Not Changed (0.896595)
FBgn0000206	bride of sevenless	0.773543	0.8	Not Changed (1.32707)
FBgn0037718	CG8286	0.773432	7.6	Not Changed (0.934125)
FBgn0025628	EG:22E5.5	0.773317	11.2	Not Changed (0.81582)
FBgn0030612	CG5599	0.773026	8.	Not Changed (1.16215)
FBgn0038297	CG4196	0.77302	19.2	Not Changed (1.06374)
FBgn0030512	CG9940	0.77265	14.8	Not Changed (0.963185)
FBgn0032601	yellow-b	0.772408	21.2	Not Changed (0.94786)
FBgn0001233	Heat shock protein 83	0.772116	7.2	Not Changed (0.961246)
FBgn0031933	CG7068	0.772071	10.8	Not Changed (1.71364)
FBgn0032076	CG9510	0.771837	10.4	Not Changed (1.56131)
FBgn0024947	NTPase	0.771648	17.6	Not Changed (1.12592)
FBgn0033162	CG1707	0.77163	10.	Not Changed (0.597547)
FBgn0030552	CG15871	0.771574	20.	Not Changed (0.79077)
FBgn0040602	CG14545	0.771509	8.	Down (0.334151)
FBgn0031651	CG8849	0.771063	20.	Not Changed (0.997517)
FBgn0023143	Ubiquitin activating enzyme 1	0.770945	10.4	Not Changed (0.627095)
FBgn0032633	CG6860	0.77067	5.6	Not Changed (0.875732)
FBgn0030087	CG7766	0.770208	6.4	Not Changed (1.08462)
FBgn0030306	CG1751	0.770023	9.6	Not Changed (0.997467)
FBgn0032854	CG10076	0.770006	4.4	Not Changed (1.10643)

FBgn0034602	CG15658	0.769817	19.2	Not Changed (0.528744)
FBgn0034337	CG17524	0.769402	4.	Not Changed (0.527102)
FBgn0038096	CG7340	0.769067	12.4	Not Changed (1.00023)
FBgn0034951	CG3860	0.769	20.	Not Changed (0.901201)
FBgn0034812	CG3037	0.768977	17.6	Not Changed (1.35507)
FBgn0034887	CG5428	0.768958	23.6	Not Changed (1.1499)
FBgn0037900	CG5276	0.768822	12.4	Not Changed (0.930868)
FBgn0001941	infertile crescent	0.768672	16.8	Not Changed (0.810241)
FBgn0040786	CG14104	0.76866	21.2	Down (0.29409)
FBgn0033253	CG8715	0.768449	11.2	Not Changed (1.1336)
FBgn0027556	BcDNA:GH10120	0.768144	3.6	Not Changed (1.56678)
FBgn0005585	Calreticulin	0.767943	6.8	Not Changed (0.96947)
FBgn0033321	CG8738	0.767881	10.8	Not Changed (0.801418)
FBgn0036116	CG7888	0.76769	22.8	Not Changed (1.51516)
FBgn0039484	CG6124	0.767681	6.8	Not Changed (0.717314)
FBgn0037089	CG7193	0.76766	8.8	Not Changed (1.09264)
FBgn0031429	CG15393	0.767269	20.4	Not Changed (1.05597)
FBgn0033932	CG8422	0.767032	0.4	Not Changed (1.04199)
FBgn0036726	CG7603	0.766994	21.2	Not Changed (0.935374)
FBgn0016917	Signal-transducer and activator of transcription protein at 92E	0.766921	10.4	Not Changed (1.09934)
FBgn0013432	bcn92	0.766896	23.2	Not Changed (0.893153)
FBgn0039220	CG13633	0.766563	0.8	Not Changed (0.916845)
FBgn0030315	CG15191	0.766545	15.2	Not Changed (0.779932)
FBgn0034184	CG9646	0.766482	10.8	Not Changed (1.39882)
FBgn0026749	Yippee	0.766375	17.2	Not Changed (1.26961)
FBgn0032426	CG15493	0.76616	21.6	Not Changed (1.92281)
FBgn0004698	mutagen-sensitive 21	0.766154	20.	Not Changed (0.88085)
FBgn0033961	CG12859	0.765534	20.8	Not Changed (1.21079)
FBgn0037896	CG6728	0.765328	23.6	Not Changed (1.64175)
FBgn0030271	CG15202	0.764877	18.4	Not Changed (1.01383)
FBgn0030550	CG1405	0.764857	21.6	Not Changed (0.854241)

FBgn0032262	CG7384	0.764785	10.	Not Changed (1.1749)
FBgn0019925	Surfeit 4	0.764685	12.	Not Changed (0.846268)
FBgn0022787	Helicase 89B	0.764562	6.8	Not Changed (1.06596)
FBgn0039938	CG11153	0.764503	10.	Not Changed (0.900232)
LD28427.3prime-hit	EST mapped to FBgn0024326(Mkk4) and FBgn0000447(Dhod)	0.764	15.6	Down (0.153062)
FBgn0038164	CG9412	0.763534	10.	Not Changed (0.972507)
FBgn0029537	CG14633	0.763266	6.8	Not Changed (0.930736)
FBgn0039496	CG6001	0.76304	4.	Not Changed (1.0727)
FBgn0038823	CG17837	0.762969	20.8	Not Changed (0.726122)

Table 3: Drosophila Genes Rhythmically Expressed in Constant Dark Condition.

Accession #	Gene Name	Correlation(DD)	Phase(DD)	mRNA Levels in *Clk* (*Clk*/*wt*)
FBgn0034997	CG3376	0.973078	21.6	Not Changed (0.635211)
FBgn0014019	Rhodopsin 5	0.959384	20.	Not Changed (1.72489)
FBgn0004780	Ccp84Ad	0.952131	4.4	Not Changed (1.10431)
FBgn0030041	CG12116	0.946845	4.8	Not Changed (0.978994)
FBgn0013981	Histone H4 replacement	0.942907	18.	Not Changed (1.08651)
FBgn0033593	CG9080	0.938923	20.	Not Changed (0.578511)
FBgn0040972	CG16978	0.928852	8.	Not Changed (1.49522)
FBgn0034010	CG8157	0.928276	20.8	Down (0.431862)
FBgn0032197	CG5694	0.924608	24.	Not Changed (1.22068)
FBgn0034405	CG15102	0.923839	23.2	Not Changed (0.946224)
FBgn0003495	spatzle	0.919219	8.	Not Changed (0.671232)
FBgn0035401	CG1291	0.919023	1.6	Not Changed (0.90538)
FBgn0031105	CG11738	0.91897	0.4	Not Changed (0.50426)
FBgn0039218	CG13628	0.916848	4.	Not Changed (0.86316)
FBgn0031189	CG14618	0.916194	18.4	Not Changed (0.984301)
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(3 prime region of transcript)	0.914812	9.2	Not Changed (1.22912)
LD22726.complete-hit	BG:DS04929.3	0.914308	4.4	Not Changed (1.00564)
FBgn0032773	CG15825	0.910682	24.	Not Changed (0.607017)
FBgn0037476	CG14611	0.909874	7.2	Not Changed (0.742651)
FBgn0030425	CG3775	0.909269	20.8	Down (0.416503)
FBgn0039696	CG7837	0.905011	6.8	Not Changed (1.06966)
FBgn0014469	Cytochrome P45-4e2	0.904851	21.2	Down (0.464658)
FBgn0038771	CG4390	0.902746	7.2	Not Changed (0.875122)
FBgn0034341	CG17531	0.901785	23.2	Down (0.469624)
FBgn0040902	CG2766	0.901042	23.2	Not Changed (1.06437)
FBgn0033227	CG1548	0.89908	18.	Not Changed (0.971402)
FBgn0036032	CG16711	0.896703	5.6	Not Changed (1.37986)
FBgn0030963	CG7101	0.895603	8.4	Not Changed (1.36695)

FBgn0032809	CG13078	0.894235	3.6	Not Changed (1.13172)
FBgn0034404	CG15101	0.892912	22.8	Down (0.454531)
FBgn0015287	Replication-factor-C 4kD subunit	0.889101	13.2	Not Changed (1.00016)
FBgn0037909	CG12593	0.888692	12.	Not Changed (1.02374)
FBgn0038407	CG6126	0.887028	22.	Not Changed (0.689865)
FBgn0027348	bubblegum	0.886657	5.2	Not Changed (0.80244)
FBgn0033903	CG8323	0.885093	4.	Not Changed (0.931351)
FBgn0031456	CG2848	0.884793	2.8	Not Changed (0.904029)
FBgn0011695	Ejaculatory bulb protein III	0.884515	19.6	Not Changed (1.11683)
FBgn0037387	CG1213	0.88119	22.4	Not Changed (0.892942)
FBgn0036277	CG10418	0.880041	17.2	Not Changed (1.05616)
FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	0.879763	10.4	Not Changed (1.01442)
FBgn0037926	CG10535	0.879466	19.6	Not Changed (0.938111)
FBgn0036657	CG9697	0.879309	12.8	Not Changed (1.37291)
FBgn0038147	CG14375	0.878836	15.2	Not Changed (0.866729)
FBgn0030222	CG9806	0.878556	8.4	Not Changed (1.00358)
FBgn0040590	CG13826	0.87805	13.6	Not Changed (1.57264)
FBgn0034888	CG5431	0.877301	18.	Not Changed (0.706629)
FBgn0037925	CG17309	0.877203	24.	Not Changed (1.11504)
FBgn0000667	alpha actinin	0.876117	7.2	Not Changed (1.62771)
FBgn0027583	BcDNA:GH06026	0.872941	22.4	Not Changed (0.968589)
FBgn0033269	CG8709	0.8726	21.2	Not Changed (1.14307)
FBgn0034818	CG13537	0.86782	4.4	Not Changed (1.20259)
FBgn0033968	CG10200	0.867775	6.	Not Changed (0.724024)
FBgn0035880	CG17352	0.866924	20.4	Down (0.27546)
FBgn0032099	CG9585	0.866466	6.4	Up (2.4756)
FBgn0032591	CG13261	0.866226	6.4	Not Changed (1.32506)
FBgn0038590	CG12320	0.865567	16.8	Not Changed (1.0043)
GH15485.3prime-hit	CG17762	0.863796	4.	Not Changed (1.55314)
FBgn0015623	Cytochrome P45 reductase	0.863676	23.2	Not Changed (0.761998)
FBgn0030717	CG8931	0.863363	1.2	Not Changed (1.26266)

FBgn0011603	inebriated	0.863179	5.6	Not Changed (0.652296)
FBgn0029794	CG3138	0.861405	2.	Not Changed (0.899659)
FBgn0004855	RNA polymerase II 15kD subunit	0.860417	15.2	Not Changed (0.999371)
FBgn0039118	CG10208	0.860161	21.6	Not Changed (0.708013)
FBgn0030079	CG7267	0.859601	0.4	Not Changed (1.37309)
FBgn0026438	Excitatory amino acid transporter 2	0.858422	23.2	Not Changed (1.11518)
FBgn0013576	heat shock promoter construct of Stowers	0.858236	2.	Not Changed (1.22444)
FBgn0027844	Carbonic anhydrase 1	0.858232	21.2	Not Changed (0.669501)
FBgn0032085	CG9555	0.857142	13.2	Not Changed (0.786192)
FBgn0032961	CG1416	0.856018	0.8	Not Changed (0.538937)
FBgn0031589	CG3714	0.852443	4.4	Up (2.94007)
FBgn0038419	CG14879	0.852141	21.6	Not Changed (0.764843)
FBgn0032402	CG14945	0.852006	12.	Up (2.13695)
FBgn0005278	Minute (2) 21AB	0.849638	20.4	Not Changed (0.928402)
FBgn0026387	Odorant receptor 46b	0.849151	3.2	Not Changed (0.885795)
FBgn0036347	CG11281	0.848662	8.4	Not Changed (0.777881)
FBgn0039526	CG5692	0.847966	8.4	Not Changed (1.12721)
FBgn0037189	CG14449	0.846881	10.4	Not Changed (1.06437)
FBgn0031453	CG9894	0.84648	15.6	Not Changed (1.38597)
FBgn0033962	CG10153	0.846296	3.6	Not Changed (0.952619)
FBgn0033489	CG3459	0.845733	0.8	Not Changed (1.49877)
FBgn0033544	CG7220	0.845684	21.2	Not Changed (0.941674)
FBgn0038171	RPE55	0.845647	4.4	Not Changed (1.56378)
FBgn0038304	CG12241	0.844585	22.8	Not Changed (0.842936)
FBgn0037684	CG8129	0.844574	22.8	Not Changed (1.7099)
FBgn0005198	gigas	0.843921	4.	Not Changed (1.38498)
FBgn0031942	CG7203	0.842866	3.6	Not Changed (0.973846)
FBgn0035083	CG2803	0.840848	0.8	Not Changed (1.13965)
FBgn0024897	b6	0.84084	1.2	Not Changed (1.28906)
FBgn0031948	CG7149	0.840406	0.4	Not Changed (1.37249)

FBgn0003134	Protein phosphatase 1alpha at 96A	0.840354	19.2	Not Changed (0.877062)
FBgn0034564	CG9344	0.840268	12.4	Not Changed (0.819967)
FBgn0033612	CG13210	0.839469	14.8	Not Changed (0.790936)
FBgn0038321	CG6218	0.839333	0.4	Not Changed (1.16807)
FBgn0024939	Ribosomal protein L8	0.838699	17.6	Not Changed (1.09293)
FBgn0013726	peanut	0.838247	4.8	Not Changed (0.946407)
FBgn0030737	CG9914	0.837857	10.8	Up (3.51872)
FBgn0036863	CG9670	0.83768	18.	Not Changed (0.974338)
FBgn0033746	CG13153	0.837451	4.	Not Changed (1.17334)
FBgn0037764	CG9459	0.837291	16.4	Not Changed (0.772493)
FBgn0031145	CG1740	0.836876	14.8	Not Changed (0.934764)
FBgn0031896	CG4502	0.836204	12.	Not Changed (1.35767)
FBgn0029522	CG13373	0.835847	12.4	Not Changed (1.34459)
FBgn0037467	CG1104	0.835123	17.2	Not Changed (0.726636)
FBgn0037537	CG2767	0.834981	0.8	Not Changed (1.4381)
FBgn0033814	CG4670	0.834406	14.4	Not Changed (1.44492)
FBgn0038194	Cyp6d5	0.83421	19.6	Not Changed (1.15827)
FBgn0004885	tolkin	0.834147	20.4	Not Changed (0.908193)
FBgn0030701	CG16952	0.8334	5.2	Not Changed (1.06025)
FBgn0038111	CG12360	0.833242	16.	Not Changed (1.11352)
FBgn0038022	CG4381	0.832626	1.6	Not Changed (0.600297)
FBgn0030423	CG18453	0.832109	21.6	Not Changed (0.718705)
FBgn0031897	CG13784	0.832053	23.6	Not Changed (1.43047)
FBgn0035270	CG13933	0.831879	11.2	Not Changed (1.52169)
FBgn0032403	CG12317	0.831619	17.6	Not Changed (0.970787)
FBgn0039672	CG1906	0.831427	4.4	Not Changed (1.27405)
FBgn0031645	CG3036	0.830976	23.6	Not Changed (0.88862)
FBgn0033398	CG2049	0.830899	17.6	Not Changed (1.52959)
FBgn0038357	CG5623	0.830824	12.8	Up (4.08674)
FBgn0032323	CG6093	0.830606	10.8	Not Changed (1.92119)
FBgn0038878	CG3301	0.830361	8.8	Not Changed (1.06366)

FBgn0031263	CG2789	0.829538	1.6	Not Changed (0.926468)
FBgn0031418	CG3609	0.828503	12.4	Not Changed (0.688517)
FBgn0038462	CG17556	0.82784	8.4	Not Changed (1.32437)
FBgn0038805	CG4217	0.827778	15.6	Not Changed (0.945294)
FBgn0035296	CG11814	0.827756	3.2	Not Changed (0.81649)
FBgn0033805	CG4062	0.827662	23.6	Not Changed (1.83595)
FBgn0027567	BcDNA:GH07921	0.826927	24.	Not Changed (1.08063)
FBgn0032681	CG10283	0.826131	22.4	Not Changed (0.939026)
FBgn0029588	CG14798	0.826035	22.8	Not Changed (1.14374)
FBgn0033562	CG6751	0.825989	21.2	Not Changed (0.832886)
FBgn0034851	CG11079	0.82573	10.8	Up (2.88794)
GH15539.3prime-hit	Protein tyrosine phosphatase 4E	0.825545	22.8	Not Changed (0.705514)
FBgn0015788	Rab-related protein 1	0.824886	20.8	Not Changed (0.999635)
FBgn0037653	CG11982	0.824551	6.	Not Changed (0.839259)
FBgn0035197	CG9130	0.823958	15.2	Not Changed (1.01938)
FBgn0034394	CG15096	0.823874	23.2	Not Changed (0.77221)
FBgn0039115	CG10214	0.822851	20.4	Not Changed (0.955817)
FBgn0031389	CG4259	0.822636	20.4	Down (0.354375)
FBgn0032400	CG6770	0.822075	22.	Not Changed (1.02709)
FBgn0011327	Ubiquitin C-terminal hydrolase	0.822011	10.8	Not Changed (0.821561)
FBgn0039931	CG11091	0.821227	8.	Not Changed (0.926711)
FBgn0039656	CG11951	0.820884	4.8	Down (0.288498)
FBgn0030834	CG8675	0.820729	17.2	Not Changed (0.853952)
FBgn0040993	CG17325	0.820724	5.6	Not Changed (1.82619)
FBgn0030026	CG10964	0.820341	24.	Not Changed (0.847895)
FBgn0040827	CG13315	0.820091	16.	Not Changed (1.08916)
FBgn0040931	CG9034	0.82006	16.	Not Changed (0.856957)
FBgn0035013	CG13580	0.819697	10.	Not Changed (1.11615)
FBgn0038037	Cyp9f2	0.818758	23.2	Not Changed (1.06086)
FBgn0032162	CG4592	0.818649	13.6	Not Changed (0.627709)
FBgn0032904	CG9342	0.818526	14.8	Not Changed (0.839055)

FBgn0013263	Trithorax-like	0.818112	3.2	Not Changed (0.689646)
SD02875.3prime-hit	Vacuolar H+ ATPase 16kD subunit	0.817878	19.2	Not Changed (0.726146)
FBgn0033657	CG8271	0.817662	4.8	Down (0.481255)
FBgn0033835	CG18279	0.817465	22.8	Up (2.00779)
FBgn0031657	CG3756	0.816953	4.	Not Changed (1.19915)
FBgn0003447	singed	0.816204	21.6	Not Changed (0.919273)
FBgn0038573	CG7913	0.815706	4.	Not Changed (0.943133)
FBgn0030542	CG12481	0.815686	19.6	Down (0.332016)
FBgn0031399	CG7074	0.815125	23.2	Not Changed (1.10187)
FBgn0038981	CG5346	0.814991	3.6	Not Changed (0.818062)
FBgn0037106	CG11307	0.814891	13.2	Not Changed (1.09022)
FBgn0038535	CG18212	0.813996	12.8	Not Changed (1.26899)
FBgn0037234	CG9795	0.813738	15.2	Not Changed (0.847769)
FBgn0030446	CG2190	0.813702	14.4	Not Changed (0.660296)
FBgn0035943	CG5653	0.813525	15.6	Up (3.45413)
FBgn0031871	CG10158	0.813512	13.6	Not Changed (0.584122)
FBgn0026429	gamma-tubulin ring protein 91	0.813259	6.	Not Changed (1.0888)
FBgn0032299	CG17127	0.812942	23.2	Not Changed (0.735391)
FBgn0038339	CG6118	0.812643	8.	Not Changed (0.529198)
FBgn0039253	CG6238	0.812618	7.2	Not Changed (0.875152)
FBgn0040871	CG12479	0.8123	6.8	Not Changed (1.39714)
FBgn0037292	CG2022	0.81229	5.2	Not Changed (1.9927)
FBgn0001142	Glutamine synthetase 1	0.812115	15.6	Not Changed (1.54112)
FBgn0038306	CG6563	0.811942	15.2	Not Changed (0.66844)
FBgn0036022	CG8329	0.811017	19.2	Not Changed (0.957881)
FBgn0037788	CG3940	0.810837	9.6	Not Changed (1.29858)
LD32106.3prime-hit	EST mapped to FBgn0036008(CG3408) and FBgn0010408(RpS9)	0.810642	19.2	Up (2.99359)
FBgn0030447	CG2200	0.810405	10.8	Not Changed (0.835245)
FBgn0037548	CG7900	0.81012	19.6	Up (4.1138)
FBgn0038872	CG5874	0.809946	22.4	Not Changed (0.99537)

FBgn0035851	CG7999	0.809723	14.8	Not Changed (1.11792)
FBgn0035392	CG1271	0.809164	19.2	Not Changed (0.73087)
FBgn0039494	CG5896	0.808557	9.6	Not Changed (0.504433)
FBgn0031221	CG3164	0.80853	19.2	Not Changed (0.702182)
FBgn0000416	Saposin-related	0.808184	22.8	Not Changed (0.989542)
FBgn0040532	CG8369	0.808161	18.4	Not Changed (1.08628)
FBgn0033854	CG6152	0.807825	2.	Not Changed (0.767081)
FBgn0032699	CG10383	0.80777	2.4	Not Changed (0.740033)
FBgn0036270	CG18638	0.807752	3.2	Not Changed (1.16758)
FBgn0038299	CG6687	0.80773	22.	Not Changed (0.977344)
FBgn0035039	CG3608	0.807569	14.8	Not Changed (0.839651)
FBgn0013307	Ornithine decarboxylase 1	0.807448	7.2	Not Changed (0.906127)
FBgn0038343	CG14871	0.80724	3.2	Not Changed (1.08186)
FBgn0030593	CG9512	0.806896	22.8	Not Changed (1.32485)
FBgn0032467	CG9934	0.806868	3.2	Not Changed (0.861557)
FBgn0037913	CG6783	0.806378	11.2	Not Changed (1.03096)
GM686.3prime-hit	CG7369	0.806253	6.4	Not Changed (1.45529)
FBgn0015568	alpha-Esterase-1	0.805595	0.4	Down (0.395918)
FBgn0040614	CG12882	0.803861	7.6	Not Changed (0.545733)
FBgn0028918	BG:DS01068.1	0.803393	8.4	Not Changed (0.841634)
FBgn0015513	myoblast city	0.803154	16.8	Not Changed (0.942626)
FBgn0034500	CG11200	0.802848	10.4	Not Changed (0.626345)
FBgn0038109	CG11656	0.802765	15.2	Down (0.408715)
FBgn0020236	ATP citrate lyase	0.802639	12.	Not Changed (0.687114)
FBgn0038166	CG9588	0.802592	3.6	Not Changed (0.914578)
FBgn0036302	CG10632	0.802144	22.8	Not Changed (0.742021)
LD29477.3prime-hit	CG17138	0.800031	10.4	Not Changed (1.0997)
FBgn0000606	even skipped	0.799931	12.8	Not Changed (0.849444)
FBgn0033557	CG12325	0.799785	22.	Not Changed (0.895876)
FBgn0036314	CG10754	0.799626	3.2	Not Changed (1.10149)
FBgn0040732	CG16926	0.799258	10.4	Down (0.448041)
FBgn0031865	CG10806	0.798442	7.6	Not Changed (0.529693)

FBgn0034897	CG11299	0.798066	14.8	Not Changed (0.791813)
FBgn0029544	CG16994	0.798018	5.6	Not Changed (1.01412)
FBgn0028691	Rpn4	0.797923	24.	Not Changed (0.80274)
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(5 prime region of transcript)	0.797495	8.	Up (2.49185)
FBgn0023000	methuselah	0.79637	18.	Not Changed (1.2607)
FBgn0033125	CG12846	0.795898	22.	Not Changed (0.571452)
FBgn0036663	CG9674	0.79588	23.2	Not Changed (1.32933)
FBgn0035229	CG7852	0.795704	2.8	Up (3.1151)
FBgn0036837	CG18135	0.795509	16.	Down (0.489702)
FBgn0010770	peter pan	0.795152	15.2	Not Changed (0.82451)
FBgn0015766	Msr-110	0.793851	12.8	Not Changed (1.10527)
FBgn0039565	CG4884	0.793826	17.6	Not Changed (0.67232)
FBgn0035995	CG3529	0.793236	1.2	Not Changed (0.785187)
FBgn0013756	Bx34	0.793197	6.4	Not Changed (0.97967)
FBgn0034483	CG16894	0.793089	11.6	Not Changed (0.715747)
FBgn0028399	TMS1d	0.792762	20.	Not Changed (1.02325)
FBgn0030317	CG1561	0.792416	11.2	Not Changed (0.708132)
FBgn0032398	CG6766	0.791743	23.6	Not Changed (0.86334)
FBgn0037095	CG7184	0.79116	7.2	Not Changed (1.05634)
FBgn0027571	BcDNA:GH07626	0.79095	7.2	Not Changed (0.831247)
FBgn0014073	Tie-like receptor tyrosine kinase	0.790161	0.4	Not Changed (1.00968)
FBgn0030749	Annexin B11	0.790141	17.6	Not Changed (1.1903)
FBgn0011760	cut up	0.789501	22.8	Not Changed (1.30312)
FBgn0035027	CG3511	0.789319	14.8	Not Changed (1.88666)
FBgn0004876	center divider	0.788803	11.2	Up (3.34025)
FBgn0036283	CG4392	0.788291	20.4	Up (2.27925)
FBgn0033485	CG1381	0.788285	0.4	Not Changed (1.15141)
FBgn0037699	CG8147	0.788235	4.4	Not Changed (0.631967)
FBgn0033900	CG8257	0.787632	23.6	Not Changed (0.926932)
FBgn0038914	CG17820	0.787332	13.2	Not Changed (1.1534)

FBgn0030883	CG7772	0.786593	22.4	Not Changed (0.766523)
FBgn0038588	CG7156	0.786102	18.4	Not Changed (0.82633)
FBgn0000150	abnormal wing discs	0.78588	16.4	Not Changed (1.04858)
FBgn0031368	CG12704	0.785588	3.2	Not Changed (1.63252)
FBgn0035389	CG1274	0.785293	11.2	Down (0.448034)
FBgn0038725	CG6184	0.785269	7.2	Not Changed (1.48077)
FBgn0029709	CG3564	0.784965	17.6	Not Changed (0.827657)
FBgn0030173	CG15313	0.78492	13.6	Not Changed (0.633513)
FBgn0039114	CG10374	0.784771	10.4	Not Changed (0.781277)
FBgn0034048	CG8256	0.784685	9.2	Not Changed (1.13122)
FBgn0033989	CG7639	0.784564	3.6	Not Changed (1.65778)
FBgn0040609	CG3348	0.783903	10.4	Down (0.0518378)
FBgn0033988	CG7761	0.783749	3.2	Down (0.440083)
FBgn0037714	CG9396	0.783711	6.8	Not Changed (1.52259)
FBgn0036433	CG9628	0.783401	7.2	Not Changed (0.984248)
FBgn0040890	CG14199	0.78303	14.8	Not Changed (0.95058)
FBgn0034328	CG15066	0.782785	21.6	Down (0.128703)
FBgn0032214	CG4968	0.782766	5.6	Not Changed (0.696025)
FBgn0027378	MRG15	0.782307	6.4	Not Changed (1.10884)
FBgn0037761	CG8534	0.782127	8.8	Not Changed (1.13706)
FBgn0011638	La autoantigen-like	0.782029	22.	Down (0.34108)
FBgn0001108	Glued	0.782002	2.4	Not Changed (1.17585)
FBgn0039743	CG7946	0.781782	20.	Not Changed (0.914369)
FBgn0028946	Odorant receptor 35a	0.781742	9.6	Not Changed (0.915059)
FBgn0030681	CG8231	0.781571	12.8	Not Changed (0.900145)
FBgn0038421	CG17931	0.781456	14.4	Not Changed (1.12683)
FBgn0035500	CG14998	0.78142	13.6	Not Changed (0.748155)
FBgn0003231	refractory to sigma P	0.781217	1.6	Not Changed (0.817752)
FBgn0033571	CG11979	0.781194	6.	Not Changed (1.03726)
FBgn0004629	Cystatin-like	0.780822	19.2	Not Changed (1.5299)
FBgn0034953	CG18020	0.780373	9.2	Not Changed (0.852751)
FBgn0036123	CG6302	0.780158	1.6	Not Changed (0.989942)

FBgn0039846	CG11337	0.779853	6.	Not Changed (1.06935)
FBgn0039835	CG12220	0.779696	18.4	Not Changed (0.885124)
FBgn0031143	CG1532	0.779497	10.	Not Changed (0.815783)
FBgn0037073	CG7338	0.779196	22.	Not Changed (0.942615)
FBgn0029906	CG4542	0.779003	3.2	Not Changed (1.1248)
FBgn0036290	CG10638	0.778849	15.6	Down (0.398665)
FBgn0037309	CG2676	0.778825	12.8	Not Changed (1.81424)
FBgn0032285	CG17108	0.778558	11.2	Not Changed (1.41312)
FBgn0023507	EG:87B1.3	0.77822	6.	Not Changed (1.84299)
FBgn0034584	CG9364	0.778093	24.	Not Changed (0.969752)
FBgn0032476	CG5439	0.778086	10.4	Not Changed (1.0676)
FBgn0033338	CG8269	0.777909	22.8	Not Changed (0.968697)
FBgn0011704	Ribonucleoside diphosphate reductase small subunit	0.777769	9.6	N.D.
FBgn0030363	CG15736	0.777686	17.6	Not Changed (0.893939)
FBgn0036517	CG16980	0.776453	1.2	Not Changed (0.760008)
FBgn0036697	CG7725	0.775914	6.	Not Changed (0.529161)
FBgn0010416	heat shock construct of Banga	0.775313	11.2	Not Changed (1.07891)
GH4717.3prime-hit	CG3811	0.774991	4.	Not Changed (1.43596)
FBgn0034762	CG13515	0.774981	12.	Not Changed (0.677972)
GH04205.3prime-hit	EST mapped to FBgn0038749(CG4468) and FBgn0038748(CG12378)	0.774851	21.6	Not Changed (0.883047)
FBgn0039917	CG9905	0.77466	16.4	Not Changed (1.57343)
FBgn0037936	CG6908	0.774654	22.	Not Changed (0.894006)
FBgn0039875	CG1937	0.774515	0.4	Not Changed (0.716815)
FBgn0000242	Beadex	0.77383	12.8	Not Changed (0.871129)
FBgn0032246	CG5168	0.773319	10.4	Not Changed (1.0135)
FBgn0033837	CG17034	0.773174	2.4	Not Changed (1.4434)
FBgn0030897	CG5744	0.77305	2.4	Not Changed (1.60894)
FBgn0037676	CG8861	0.772473	6.4	Not Changed (1.38139)
FBgn0038563	CG7780	0.772038	21.6	Not Changed (0.505361)
FBgn0027580	BcDNA:GH06348	0.771959	4.4	Not Changed (0.735164)

FBgn0038074	CG6188	0.771942	21.6	Not Changed (1.05572)
FBgn0033800	CG4016	0.771931	21.2	Not Changed (1.27662)
FBgn0031605	CG15438	0.77193	19.2	Not Changed (0.97493)
FBgn0034046	CG8253	0.771526	20.4	Down (0.464903)
FBgn0032155	CG4539	0.771425	14.8	Not Changed (0.650997)
FBgn0003317	saxophone	0.771398	7.2	Not Changed (0.92914)
LD45776.3prime-hit	CG9126	0.771366	22.4	Not Changed (1.04174)
FBgn0039538	CG12883	0.771124	23.6	Not Changed (1.06137)
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(middle region of transcript)	0.771018	8.4	Not Changed (1.46543)
FBgn0031493	CG3605	0.770599	16.8	Not Changed (1.50126)
FBgn0026414	Kaz1	0.769979	0.4	Not Changed (1.5539)
FBgn0019650	twin of eyeless	0.7699	9.6	Not Changed (0.933142)
FBgn0037874	CG4800	0.769684	10.8	Not Changed (1.09885)
FBgn0040823	CG14162	0.769678	5.2	Not Changed (0.922601)
FBgn0030540	CG11581	0.769053	12.8	Not Changed (1.37033)
FBgn0028536	BG:DS00810.3	0.768907	17.2	Not Changed (0.939787)
FBgn0015298	Signal recognition particle protein 19	0.768395	14.8	Not Changed (1.20012)
FBgn0035060	CG16932	0.768293	23.2	Not Changed (0.862682)
FBgn0031290	CG4276	0.767879	10.4	Not Changed (1.49703)
FBgn0032114	CG3752	0.767696	5.2	Not Changed (1.47385)
FBgn0030729	CG12507	0.767561	13.2	Not Changed (1.14423)
FBgn0038420	CG10311	0.76693	8.4	Not Changed (1.04736)
FBgn0011661	Moesin-like	0.766816	18.	Not Changed (0.846695)
FBgn0031124	CG1379	0.766549	10.8	Not Changed (0.756784)
FBgn0025864	Calmodulin-binding protein related to a Rab3 GDP/GTP exchange protein	0.766454	18.	Not Changed (0.94504)
FBgn0030456	CG4332	0.766229	2.	Not Changed (0.978823)
FBgn0038338	CG5166	0.765934	4.	Not Changed (1.50107)
FBgn0012034	Acetyl Coenzyme A synthase	0.765871	9.2	Not Changed (0.721255)
FBgn0023178	Pigment-dispersing factor	0.765658	22.8	Not Changed (0.778467)

FBgn0030234	CG15211	0.765387	0.4	Not Changed (0.989739)
FBgn0036864	CG14090	0.76528	16.4	Not Changed (0.940102)
FBgn0033387	CG8008	0.765092	17.6	Not Changed (0.560978)
FBgn0000139	absent, small, or homeotic discs 2	0.76497	22.4	Not Changed (1.04421)
FBgn0039643	CG11886	0.764948	4.4	Not Changed (0.938265)
FBgn0030996	CG14194	0.764461	3.6	Not Changed (1.36787)
FBgn0029800	CG15929	0.763595	7.2	Not Changed (0.737703)

Table 4: Rhythmic Biological Processes in Light-Dark Condition.
Categories are defined in the Gene Ontology database and downloaded on March 21, 2001.

Accession #	Gene Name	Class	Phase (LD)
lipid metabolism Genes in Categories = **79**; Cycling Genes = **16**; P-value = **5.58025**			
FBgn0011693	Photoreceptor dehydrogenase	I	2.8
FBgn0004611	Phospholipase C at 21C	II	5.2
FBgn0039756	CG9743	II	5.2
FBgn0036182	CG6084	II	7.2
FBgn0028479	BcDNA:GH12558	II	7.6
FBgn0030731	CG3415	II	9.2
FBgn0025352	Thiolase	II	9.2
FBgn0033245	CG8723	II	9.6
FBgn0030968	CG7322	II	9.6
FBgn0035744	CG8628	II	10.
FBgn0032160	CG4598	II	10.8
FBgn0032482	CG5547	II	15.2
FBgn0029648	CG3603	II	16.4
FBgn0034812	CG3037	II	17.6
FBgn0032513	CG6565	II	20.
FBgn0011361	mitochondrial acyl carrier protein 1	II	20.8
circadian rhythm Genes in Categories = **7**; Cycling Genes = **4**; P-value = **3.63911**			
FBgn0023076	Clock	I	2.
FBgn0025680	cryptochrome	I	5.2
FBgn0003068	period	I	13.6
FBgn0014396	timeless	I	14.8

phototransduction

Genes in Categories = **20**; Cycling Genes = **6**; P-value = **3.38197**

FBgn0001263	inactivation no afterpotential D	II	1.6
FBgn0004784	inactivation no afterpotential C	II	3.6
FBgn0003249	Rhodopsin 3	II	4.4
FBgn0003250	Rhodopsin 4	II	4.4
FBgn0019940	Rhodopsin 6	II	10.8
FBgn0002936	neither inactivation nor afterpotential A	II	24.

cytoplasm organization and biogenesis

Genes in Categories = **21**; Cycling Genes = **5**; P-value = **2.4075**

FBgn0030734	CG9911	II	9.2
FBgn0025352	Thiolase	II	9.2
FBgn0032514	CG9302	II	10.8
FBgn0024986	EG:132E8.3	II	20.
FBgn0035334	CG8993	II	20.8

protein folding

Genes in Categories = **72**; Cycling Genes = **10**; P-value = **2.38612**

FBgn0014002	Protein disulfide isomerase	II	6.8
FBgn0030734	CG9911	II	9.2
FBgn0010621	T-complex Chaperonin 5	I	9.6
FBgn0033663	CG8983	II	10.4
FBgn0032514	CG9302	II	10.8
FBgn0033918	CG8531	II	14.8
FBgn0028741	EG:52C10.5	II	16.
FBgn0034091	CG8448	II	16.8
FBgn0024986	EG:132E8.3	II	20.
FBgn0002174	lethal (2) tumorous imaginal discs	II	20.4

metabolism
Genes in Categories = **156**; Cycling Genes = **16**; P-value = **2.11378**

FBgn0023537	EG:171D11.1	II	3.2
LD224.3prime-hit	Neurotactin	II	7.6
FBgn0031380	CG4233	II	7.6
FBgn0033065	Cyp6w1	II	8.8
FBgn0036857	CG9629	II	9.2
FBgn0000473	Cytochrome P45-6a2	II	9.2
FBgn0032340	CG6181	II	9.2
FBgn0031515	CG9664	II	11.6
FBgn0000241	brown	II	15.6
FBgn0032167	CG5853	I	16.
FBgn0038236	Cyp313a1	II	16.
FBgn0031925	Cyp4d21	II	17.2
FBgn0039084	CG10175	I	17.6
FBgn0010383	Cytochrome P45-18a1	I	17.6
FBgn0033981	Cyp6a21	II	22.4
FBgn0015714	Cyp6a17	I	23.6

amino acid and derivative metabolism
Genes in Categories = **79**; Cycling Genes = **10**; P-value = **2.09867**

FBgn0035881	CG7176	I	1.6
LD224.3prime-hit	Neurotactin	II	7.6
FBgn0031380	CG4233	II	7.6
FBgn0036157	CG7560	II	8.8
FBgn0032076	CG9510	II	10.4
FBgn0000153	black	II	16.4
FBgn0036762	CG7430	II	22.
FBgn0036975	CG5618	I	22.

FBgn0005619	Histidine decarboxylase	II	22.4
FBgn0036927	CG7433	II	22.4
transport Genes in Categories = **156**; Cycling Genes = **15**; P-value = **1.77491**			
FBgn0039178	CG6356	II	5.2
FBgn0036043	CG8177	II	6.8
FBgn0034909	CG4797	II	7.6
FBgn0029762	CG3252	II	7.6
FBgn0039176	CG13610	II	7.6
FBgn0031937	CG13795	II	8.4
FBgn0033095	CG3409	II	8.8
FBgn0037845	CG14694	II	9.2
FBgn0028469	BcDNA:LD28120	II	10.4
FBgn0029896	CG3168	II	12.
SD1469.3prime-hit	CG8468	I	13.2
FBgn0034812	CG3037	II	17.6
FBgn0026439	Excitatory amino acid transporter 1	I	18.8
FBgn0000527	ebony	II	23.2
FBgn0038799	CG4288	II	24.

Table 5: Rhythmic Biological Processes in Constant Dark Condition.
Categories are defined in the Gene Ontology database and downloaded on March 21, 2001.

Accession #	Gene Name	Class	Phase (DD)
circadian rhythm Genes in Categories = **7**; Cycling Genes = **4**; P-value = **4.39497**			
FBgn0023076	Clock	I	2.
FBgn0025680	cryptochrome	I	5.2
FBgn0003068	period	I	13.6
FBgn0014396	timeless	I	15.2
main pathways of carbohydrate metabolism Genes in Categories = **52**; Cycling Genes = **6**; P-value = **2.1199**			
FBgn0035881	CG7176	I	2.4
FBgn0027580	BcDNA:GH06348	III	4.4
FBgn0003738	Triose phosphate isomerase	I	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(5 prime region of transcript)	III	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(middle prime region of transcript)	III	8.4
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(3 prime region of transcript)	III	9.2
FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	III	10.4
FBgn0020236	ATP citrate lyase	III	12.
deubiquitylation Genes in Categories = **8**; Cycling Genes = **2**; P-value = **1.56121**			
FBgn0010288	Ubiquitin carboxy-terminal hydrolase	I	0.4
FBgn0011327	Ubiquitin C-terminal hydrolase	III	10.8

Table 6: Candidate Molecules Rhythmically Metabolized in Light-Dark Condition.
Information of Enzymes are downloaded on March 21, 2001 from LIGAND metabolic database.

Accession #	Gene Name	Class	Phase (LD)
NAD+ All Related Enzymes= **62**; Cycling Enzymes = **16**; P-value = **7.11518**			
FBgn0034390	CG15093	I	3.2
FBgn0023537	EG:171D11.1	II	3.2
FBgn0036182	CG6084	II	7.2
FBgn0028479	BcDNA:GH12558	II	7.6
FBgn0001128	Glycerol 3 phosphate dehydrogenase	II	8.
FBgn0030731	CG3415	II	9.2
FBgn0011768	Formaldehyde dehydrogenase	I	9.6
FBgn0004057	Zwischenferment	II	10.
FBgn0024289	Sorbitol dehydrogenase 1	I	10.4
FBgn0030512	CG9940	II	14.8
FBgn0038617	CG12333	II	19.6
FBgn0029888	CG3192	II	19.6
FBgn0035046	CG3683	II	20.
FBgn0031024	CG12233	II	20.4
FBgn0036762	CG7430	II	22.
FBgn0001098	Glutamate dehydrogenase	II	23.2
NADH All Related Enzymes= **60**; Cycling Enzymes = **15**; P-value = **6.51177**			
FBgn0034390	CG15093	I	3.2
FBgn0023537	EG:171D11.1	II	3.2
FBgn0036182	CG6084	II	7.2
FBgn0028479	BcDNA:GH12558	II	7.6
FBgn0001128	Glycerol 3 phosphate dehydrogenase	II	8.

FBgn0030731	CG3415	II	9.2
FBgn0011768	Formaldehyde dehydrogenase	I	9.6
FBgn0004057	Zwischenferment	II	10.
FBgn0024289	Sorbitol dehydrogenase 1	I	10.4
FBgn0038617	CG12333	II	19.6
FBgn0029888	CG3192	II	19.6
FBgn0035046	CG3683	II	20.
FBgn0031024	CG12233	II	20.4
FBgn0036762	CG7430	II	22.
FBgn0001098	Glutamate dehydrogenase	II	23.2

CO2
All Related Enzymes= **57**; Cycling Enzymes = **14**; P-value = **6.01616**

FBgn0035881	CG7176	I	1.6
FBgn0023537	EG:171D11.1	II	3.2
FBgn0036992	CG11796	I	4.
FBgn0037607	CG8036	I	8.8
FBgn0033245	CG8723	II	9.6
FBgn0000153	black	II	16.4
FBgn0038617	CG12333	II	19.6
FBgn0039635	CG11876	II	20.
GH13437.3prime-hit	CG5889	II	20.
FBgn0029721	CG7010	II	20.
FBgn0031024	CG12233	II	20.4
FBgn0034356	CG10924	II	21.6
FBgn0036975	CG5618	I	22.
FBgn0005619	Histidine decarboxylase	II	22.4

2-Oxoglutarate
All Related Enzymes= **20**; Cycling Enzymes = **7**; P-value = **4.35145**

FBgn0035881	CG7176	I	1.6
FBgn0030558	CG1461	II	7.6
FBgn0031380	CG4233	II	7.6
FBgn0038617	CG12333	II	19.6
FBgn0031024	CG12233	II	20.4
FBgn0036927	CG7433	II	22.4
FBgn0001098	Glutamate dehydrogenase	II	23.2

NADP+
All Related Enzymes= **28**; Cycling Enzymes = **8**; P-value = **4.17958**

FBgn0035881	CG7176	I	1.6
FBgn0036182	CG6084	II	7.2
FBgn0030731	CG3415	II	9.2
FBgn0030968	CG7322	II	9.6
FBgn0004057	Zwischenferment	II	10.
FBgn0037146	CG7470	I	16.8
GH13437.3prime-hit	CG5889	II	20.
FBgn0001098	Glutamate dehydrogenase	II	23.2

NADPH
All Related Enzymes= **28**; Cycling Enzymes = **8**; P-value = **4.17958**

FBgn0035881	CG7176	I	1.6
FBgn0036182	CG6084	II	7.2
FBgn0030731	CG3415	II	9.2
FBgn0030968	CG7322	II	9.6
FBgn0004057	Zwischenferment	II	10.
FBgn0037146	CG7470	I	16.8
GH13437.3prime-hit	CG5889	II	20.
FBgn0001098	Glutamate dehydrogenase	II	23.2

L-Glutamate

All Related Enzymes= **30**; Cycling Enzymes = **8**; P-value = **3.94514**

FBgn0030558	CG1461	II	7.6
FBgn0031380	CG4233	II	7.6
FBgn0030512	CG9940	II	14.8
FBgn0000153	black	II	16.4
FBgn0037146	CG7470	I	16.8
FBgn0036975	CG5618	I	22.
FBgn0036927	CG7433	II	22.4
FBgn0001098	Glutamate dehydrogenase	II	23.2

Protein Cys-Cys

All Related Enzymes= **4**; Cycling Enzymes = **3**; P-value = **3.26027**

FBgn0014002	Protein disulfide isomerase	II	6.8
FBgn0033663	CG8983	II	10.4
FBgn0032514	CG9302	II	10.8

3-(4-Hydroxyphenyl)pyruvate

All Related Enzymes= **4**; Cycling Enzymes = **3**; P-value = **3.26027**

FBgn0036992	CG11796	I	4.
FBgn0030558	CG1461	II	7.6
FBgn0031380	CG4233	II	7.6

4-Aminobutanoate

All Related Enzymes= **4**; Cycling Enzymes = **3**; P-value = **3.26027**

FBgn0000153	black	II	16.4
FBgn0036975	CG5618	I	22.
FBgn0036927	CG7433	II	22.4

beta-Alanine

All Related Enzymes= **4**; Cycling Enzymes = **3**; P-value = **3.26027**

FBgn0000153	black	II	16.4

FBgn0036975	CG5618	I	22.
FBgn0036927	CG7433	II	22.4

S-Acetyldihydrolipoamide
All Related Enzymes= **6**; Cycling Enzymes = **3**; P-value = **2.59581**

FBgn0030612	CG5599	II	8.
FBgn0039635	CG11876	II	20.
FBgn0029721	CG7010	II	20.

(1R,2S)-1-Hydroxypropane-1,2,3-tricarboxylate
All Related Enzymes= **6**; Cycling Enzymes = **3**; P-value = **2.59581**

FBgn0035881	CG7176	I	1.6
FBgn0038617	CG12333	II	19.6
FBgn0031024	CG12233	II	20.4

alpha-D-Glucose 6-phosphate
All Related Enzymes= **2**; Cycling Enzymes = **2**; P-value = **2.56276**

FBgn0036572	CG5165	I	9.6
FBgn0003074	Phosphoglucose isomerase	II	9.6

Homogentisate
All Related Enzymes= **2**; Cycling Enzymes = **2**; P-value = **2.56276**

FBgn0036992	CG11796	I	4.
FBgn0032349	CG4779	II	6.

2-Methyl-3-oxopropanoate
All Related Enzymes= **2**; Cycling Enzymes = **2**; P-value = **2.56276**

FBgn0034390	CG15093	I	3.2
FBgn0023537	EG:171D11.1	II	3.2

(2R)-2-Hydroxy-3-(phosphonooxy)-propanal
All Related Enzymes= **7**; Cycling Enzymes = **3**; P-value = **2.36995**

FBgn0037607	CG8036	I	8.8
FBgn0034934	CG2827	I	9.6

FBgn0003738	Triose phosphate isomerase	I	10.
L-Aspartate All Related Enzymes= **15**; Cycling Enzymes = **4**; P-value = **2.1941**			
FBgn0031380	CG4233	II	7.6
FBgn0002069	Aspartyl-tRNA synthetase	II	8.
FBgn0000153	black	II	16.4
FBgn0036975	CG5618	I	22.
3-Sulfino-L-alanine All Related Enzymes= **3**; Cycling Enzymes = **2**; P-value = **2.10102**			
FBgn0000153	black	II	16.4
FBgn0036975	CG5618	I	22.
Hypotaurine All Related Enzymes= **3**; Cycling Enzymes = **2**; P-value = **2.10102**			
FBgn0000153	black	II	16.4
FBgn0036975	CG5618	I	22.

Table 7: Candidate Molecules Rhythmically Metabolized in Contact Dark Condition.
Information of Enzymes are downloaded on March 21, 2001 from LIGAND metabolic database.

Accession #	Gene Name	Class	Phase (DD)
(2R)-2-Hydroxy-3-(phosphonooxy)-propanal All Related Enzymes = **7**; Cycling Enzymes = **5**; P-value = **6.08439**			
FBgn0003738	Triose phosphate isomerase	I	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(5 prime region of transcript)	III	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(middle prime region of transcript)	III	8.4
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(3 prime region of transcript)	III	9.2
FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	III	10.4
FBgn0034934	CG2827	I	10.8
FBgn0037607	CG8036	I	12.
D-Glyceraldehyde All Related Enzymes = **2**; Cycling Enzymes = **2**; P-value = **2.95013**			
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(5 prime region of transcript)	III	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(middle prime region of transcript)	III	8.4
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(3 prime region of transcript)	III	9.2
FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	III	10.4
Thiol All Related Enzymes = **8**; Cycling Enzymes = **3**; P-value = **2.73316**			
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(5 prime region of transcript)	III	8.
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(middle prime region of transcript)	III	8.4
FBgn0001092	Glyceraldehyde 3 phosphate dehydrogenase 2(3 prime region of transcript)	III	9.2
FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	III	10.4

FBgn0011327	Ubiquitin C-terminal hydrolase	III	10.8

CO2
All Related Enzymes = **57**; Cycling Enzymes = **7**; P-value = **2.54911**

FBgn0036992	CG11796	I	1.2
FBgn0035881	CG7176	I	2.4
FBgn0013307	Ornithine decarboxylase 1	III	7.2
FBgn0037788	CG3940	III	9.6
FBgn0037607	CG8036	I	12.
FBgn0033800	CG4016	III	21.2
FBgn0036975	CG5618	I	24.

Arene oxide
All Related Enzymes = **3**; Cycling Enzymes = **2**; P-value = **2.48279**

FBgn0034404	CG15101	III	22.8
FBgn0034405	CG15102	III	23.2

Arene diol
All Related Enzymes = **3**; Cycling Enzymes = **2**; P-value = **2.48279**

FBgn0034404	CG15101	III	22.8
FBgn0034405	CG15102	III	23.2

Glycol
All Related Enzymes = **3**; Cycling Enzymes = **2**; P-value = **2.48279**

FBgn0034404	CG15101	III	22.8
FBgn0034405	CG15102	III	23.2

Epoxide
All Related Enzymes = **3**; Cycling Enzymes = **2**; P-value = **2.48279**

FBgn0034404	CG15101	III	22.8
FBgn0034405	CG15102	III	23.2

D-Erythrose 4-phosphate
All Related Enzymes = **4**; Cycling Enzymes = **2**; P-value = **2.1915**

FBgn0034934	CG2827	I	10.8
FBgn0037607	CG8036	I	12.

Sedoheptulose 7-phosphate
All Related Enzymes = **5**; Cycling Enzymes = **2**; P-value = **1.97938**

FBgn0034934	CG2827	I	10.8
FBgn0037607	CG8036	I	12.

CDP
All Related Enzymes = **5**; Cycling Enzymes = **2**; P-value = **1.97938**

FBgn0039846	CG11337	III	6.
FBgn0000150	abnormal wing discs	III	16.4

Table 8: Drosophila Genes Rhythmically Expressed in *Clk* Mutants under Light-Dark Condition.

Accession #	Gene Name	Correlation(*Clk*)	Phase(*Clk*)	Class
SD1469.3prime-hit	CG8468	0.853454	20.4	I
FBgn0033821	CG10799	0.845298	8.	I
FBgn0039309	CG11891	0.824478	14.	I
FBgn0010288	Ubiquitin carboxy-terminal hydrolase	0.821589	19.6	I
FBgn0039678	CG18111	0.797167	8.4	I
FBgn0034934	CG2827	0.785692	9.6	I
LD29569.3prime-hit	CG12790	0.767905	22.	I
FBgn0011296	lethal (2) essential for life	0.894915	1.2	II
FBgn0031590	CG3702	0.882282	7.6	II
FBgn0033245	CG8723	0.872222	10.	II
FBgn0037533	CG2791	0.871614	22.4	II
FBgn0033329	CG8575	0.840156	7.2	II
FBgn0024980	EG:95B7.1	0.824781	18.4	II
FBgn0001098	Glutamate dehydrogenase	0.82167	0.4	II
FBgn0038795	CG4335	0.791893	9.6	II
FBgn0029648	CG3603	0.791122	13.2	II
FBgn0035314	CG5707	0.785339	9.2	II
FBgn0039024	CG4721	0.780064	20.	II
FBgn0032263	CG7400	0.776932	6.8	II
FBgn0036901	CG8756	0.774376	14.	II
FBgn0032775	CG17544	0.772725	23.2	II
FBgn0039623	CG1951	0.772627	4.	II
FBgn0025814	Microsomal glutathione S-transferase-like	0.771772	10.4	II
FBgn0039672	CG1906	0.931337	22.4	III
FBgn0039114	CG10374	0.913198	9.2	III
FBgn0038914	CG17820	0.880089	10.	III
FBgn0037095	CG7184	0.852037	19.6	III
FBgn0030540	CG11581	0.828543	6.4	III
FBgn0038299	CG6687	0.827149	8.4	III
FBgn0039253	CG6238	0.821042	22.	III

FBgn0026414	Kaz1	0.815857	10.	III
LD29477.3prime-hit	CG17138	0.805106	7.6	III
FBgn0032961	CG1416	0.802808	14.8	III
FBgn0032162	CG4592	0.799051	14.4	III
FBgn0037309	CG2676	0.797918	20.8	III
LD22726.complete-hit	BG:DS04929.3	0.796376	18.4	III
FBgn0038981	CG5346	0.786236	14.4	III
FBgn0025864	Calmodulin-binding protein related to a Rab3 GDP/GTP exchange protein	0.784721	4.8	III
FBgn0035027	CG3511	0.777969	23.2	III
FBgn0032681	CG10283	0.777751	22.8	III
FBgn0030447	CG2200	0.77364	7.2	III
FBgn0012034	Acetyl Coenzyme A synthase	0.77052	10.	III
FBgn0031290	CG4276	0.767908	20.	III
FBgn0037653	CG11982	0.76414	22.8	III

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J. Biol. Chem. 2002, 277:14048-14052.
doi: 10.1074/jbc.C100765200 originally published online February 19, 2002
