Supplemental Materials

Figure Legends

Supplemental Figure 1: Validation of transcript profiling experiments.
Graphs representing the Q-PCR validation of selected up (**A**) and down (**B**) -regulated genes identified by transcript profiling. Solid black bars represent Q-PCR results plotted next to Affymetrix chip-derived data (dashed outlines). Trends of expression are consistent for each locus successfully tested.

Supplemental Figure 2: Effects of *baz* modulation on tumour development.
Graphs representing tumour index (**A**) and tumour size (**B**) in flies with the Hop^{Tuml} mutation and expressing indicated genotype. *UAS-GFP* and *RNAi-white* flies are used as negative controls. Significant changes were assessed using Students t-test (** = $p<0.01$). $n>100$ for each genotype.

Supplemental Table 1: Genes differentially regulated by Upd
Table showing the 1168 genes differentially regulated in Kc_{167} cells at one or more time points following stimulation by UPD. Data presented represents significant changes in log2 expression at each time point with a score 0.0 indicating that any change measured was not classified as statistically significant by differential fold change analysis. GO terms and potential human homologues identified. Reciprocal best-hit alignments are indicated by '*' for human homologues. The top three alignments are shown for each gene where available at E-values $<10^{-10}$. Six CG numbers (*CG34375, CG42340, CG34139, CG34373, CG6214, CG42276*) appear twice on this table due to differences in previous genome annotations used to develop the Affymetrix GeneChips.

Supplemental Table 2: Proliferation of human cell lines following knock down of *Drosophila* gene putative homologues. Cell lines include the cancer-derived HeLa and HepG2 as well as the human embryonic kidney-derived Hek293T cells. Numbers given represent the number of cells as a percentage of controls as well as the z-score for each result indicating the statistical significance of this deviation from 100%. z-scores >1.8 and <-1.8 are highlighted (T. Horn and M. Boutros, unpublished data).

Supplemental Table 3: JAK/STAT regulated genes identified in both *Drosophila* and vertebrate transcriptomes. Putative homologues of the genes identified in this study (Supplemental Table 1) that appear in the lists reported in (Li *et al*., 2007) and (Dauer *et al*., 2005) are shown with their corresponding alignment E-values.

Supplemental Table 4: Oligonucleotides used for Q-PCR assays

Supplemental Table 5: Transformant IDs (VDRC) of *UAS-RNAi* stocks
Identifier numbers of individual stocks used for *in vivo* TI assays shown in Fig 3F are given. Details of these stocks and their generation are available at http://www.vdrc.at/

Supplemental Materials & Methods

Upd conditioned media & Transcript profiling

Conditioned media was prepared as described in (Harrison *et al.*, 1998) and assayed for activity using the *6x2xDrafluc* reporter (Müller *et al.*, 2005). For each transcript profiling condition and time point biological duplicates were treated with conditioned media (Upd or Mock) for 30min, washed and total RNA extracted after 2, 4, or 10h according to the Affymetrix protocols. 12 samples were hybridized to GeneChip® *Drosophila* Genome 2.0 arrays. The raw probe set data were analyzed using the PUMA package (Liu *et al.*, 2005; Pearson *et al.*, 2009) and used to generate intensity-dependent Z-scores for each Log2 ratio (Yang *et al.*, 2002). Genes >= two standard deviations from the mean were flagged as differentially expressed. Raw data has been deposited in the GEO database under accession number: GSE15584.

Transfection of HeLa cells with JAK2 V617F and Q-PCR

HeLa cells grown in DMEM supplemented with 10% FCS at 37 C were transfected with pMX-IRES-JAK2 V617F or empty vector (kind gifts of Stefan Constantinescu) using Lipofectamine transfection reagent (Invitrogen) according to the manufacturers protocol. Cells were harvested after 24hrs and total RNA extracted. Q-PCR was then performed in triplicate as described below and normalised to a *β–actin* control.

Q-PCR of Kc_{167} cells

Q-PCR used total RNA and primers shown in Supplemental Table 4, SYBR® Green JumpStart^{TM} TaqReadyMix^{TM} (Sigma-Aldrich) and standard Verso^{TM} RT-PCR (Thermo Scientific) protocol. PCR was undertaken in a Biorad MyIQ^{TM} detection system and performed in triplicate. The data were analyzed by $\Delta\Delta C_T$ and normalised to the ribosomal protein-encoding control gene *Rpl32* as previously described in Livak and Schmittgen, 2001.

In vivo analysis

A recombinant between P[G5] *dome-Gal4* (Bourbon *et al.*, 2002) and *hop*^{Tuml} (Luo *et al.*, 1995) was generated and verified on the basis of Gal4 expression and phenotype. Virgin recombinant females balanced over FM7 were crossed to males carrying the appropriate *UAS-RNAi* constructs described in (Dietzl *et al*., 2007); Table S5), *UAS-Baz* (Kuchinke *et al*., 1998), *UAS-SOCS36E-GFP* (Karsten & Zeidler unpublished) and *UAS-SOCS36E* (Almudi *et al*., 2009). Crosses were set up between 40-50 recombinant virgins and >15 males in yeasted bottles, aged at 19°C for 24h before transfer to new bottles. Original bottles were kept for a further 24h at 19°C before transfer to 29°C (Fig 3F) or 25°C (Fig 3D & E, Fig S2A & B) for 12 days. Adults were then collected and either scored immediately or frozen at –20°C for later analysis. All scoring was done 'blind' with coded vials decrypted only after all data had been gathered. The average tumour index (TI) for each cross was calculated as previously described (Shi *et al*., 2006).

For blood cell pictures wandering third instar larvae of the appropriate genotype were washed in water, dried and bled by tearing the larva with two pairs of forceps in a 15 l drop of serum-free Schneider's medium placed on a hemocytometer for immediate counting.

For adult fly photographs individuals were first frozen at –20°C before selected individuals were arranged on a white ceramic tile and photographed using a Zess STEMI 2000-C stereomicroscope and QIMAGING Micropublisher camera system.

Bioinformatics

The 1168 genes regulated by UPD in at least one time point were clustered using the average linkage method (Eisen *et al*., 1998) and examined for association to gene ontology (GO) categories using GoMiner (Zeeberg *et al*., 2005). Statistical analysis (via 'Fisher's exact test') calculates the level of significance of enriched GO categories. Differential expression are shown as MA plots where $M = \log2(Upd) - \log2(Mock)$ and $A = (\log2(Upd) + \log2(Mock)) / 2$. For promoter analysis, 3kb upstream region of 1168 UPD-regulated genes and a similar sized group of random *Drosophila* genes were retrieved and searched for TTC(3n or 4n)GAA binding sites. Enrichment of STAT92E binding sites was tested using unpaired t-tests.

Putative human homologues of the 1168 *Drosophila* genes were identified using a local installation of BLASTp, aligning protein sequences against the human proteome obtained from the Integr8 FTP site (ftp://ftp.ebi.ac.uk/pub/databases/integr8/fasta/proteomes/). An E-value cut-off of 10^{-10} was used, and where possible reciprocal best-hit or top three scoring alignments were taken. In-house Perl scripts were designed to parse BLAST files giving a total of 1818 putative homologues.

Overlap between homologues identified here and the 100 genes identified as being differentially regulated from human lung cells following STAT3 stimulation (Dauer et al., 2005), was identified using in-house Perl scripts – 8 proteins were found to overlap. Significance was assessed by constructing a list of 100 randomly selected genes from the human genome and counting overlap to our putative homologues. The test was repeated 1000 times to give a distribution (mean = 3.66; S.D = 1.86), significance was assessed by z-score analysis (2.34). A similar comparative analysis was carried out for a study on mouse lung tissue (Li et al., 2007) resulting in an overlap of 12, which was found to be significant (mean = 4.94, S.D. = 2.17, z-score = 3.25).

Proliferation data of HeLa, Hek293T and HepG2 cells was measured following treatment with genome wide siRNA library (Dharmacon) and was kindly made available by Michael Boutros and Thomas Horn (DKFZ, Heidelberg). As data is unpublished and available on a gene by gene basis, only human homologues of the short listed *Drosophila* genes are shown. Full genome data is available at www.GenomeRNAi.org (Horn *et al.*, 2007).

References

Almudi, I., Stocker, H., Hafen, E., Corominas, M. and Serras, F. (2009) SOCS36E specifically interferes with Sevenless signaling during Drosophila eye development *Dev Biol* **326:** 212-223.

Bourbon, H.M., Gonzy-Treboul, G., Peronnet, F., Alin, M.F., Ardourel, C., Benassayag, C., Cribbs, D., Deutsch, J., Ferrer, P., Haenlin, M., Lepesant, J.A., Noselli, S. and Vincent, A. (2002) A P-insertion screen identifying novel X-linked essential genes in Drosophila *Mech Dev* **110:** 71-83.

Dauer, D.J., Ferraro, B., Song, L., Yu, B., Mora, L., Buettner, R., Enkemann, S., Jove, R. and Haura, E.B. (2005) Stat3 regulates genes common to both wound healing and cancer *Oncogene* **24:** 3397-3408.

Dietzl, G., Chen, D., Schnorrer, F., Su, K.C., Barinova, Y., Fellner, M., Gasser, B., Kinsey, K., Oppel, S., Scheiblauer, S., Couto, A., Marra, V., Keleman, K. and Dickson, B.J. (2007) A genome-wide transgenic RNAi library for conditional gene inactivation in Drosophila *Nature* **448:** 151-156.

Eisen, M.B., Spellman, P.T., Brown, P.O. and Botstein, D. (1998) Cluster analysis and display of genome-wide expression patterns *Proc Natl Acad Sci U S A* **95:** 14863-14868.

Harrison, D.A., McCoon, P.E., Binari, R., Gilman, M. and Perrimon, N. (1998) Drosophila unpaired encodes a secreted protein that activates the JAK signaling pathway *Genes Dev* **12:** 3252-3263.

Horn, T., Arziman, Z., Berger, J. and Boutros, M. (2007) GenomeRNAi: a database for cell-based RNAi phenotypes *Nucleic Acids Res* **35:** D492-497.

Kuchinke, U., Grawe, F. and Knust, E. (1998) Control of spindle orientation in Drosophila by the Par-3-related PDZ-domain protein Bazooka *Curr Biol* **8:** 1357-1365.

Li, Y., Du, H., Qin, Y., Roberts, J., Cummings, O.W. and Yan, C. (2007) Activation of the signal transducers and activators of the transcription 3 pathway in alveolar epithelial cells induces inflammation and adenocarcinomas in mouse lung *Cancer Res* **67:** 8494-8503.

Liu, X., Milo, M., Lawrence, N.D. and Rattray, M. (2005) A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips *Bioinformatics* **21:** 3637-3644.

Livak, K.J. and Schmittgen, T.D. (2001) Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method *Methods* **25:** 402-408.

Luo, H., Hanratty, W.P. and Dearolf, C.R. (1995) An amino acid substitution in the Drosophila hopTum-l Jak kinase causes leukemia-like hematopoietic defects *Embo J* **14:** 1412-1420.

Müller, P., Kuttenkeuler, D., Gesellchen, V., Zeidler, M.P. and Boutros, M. (2005) Identification of JAK/STAT signalling components by genome-wide RNA interference *Nature* **436:** 871-875.

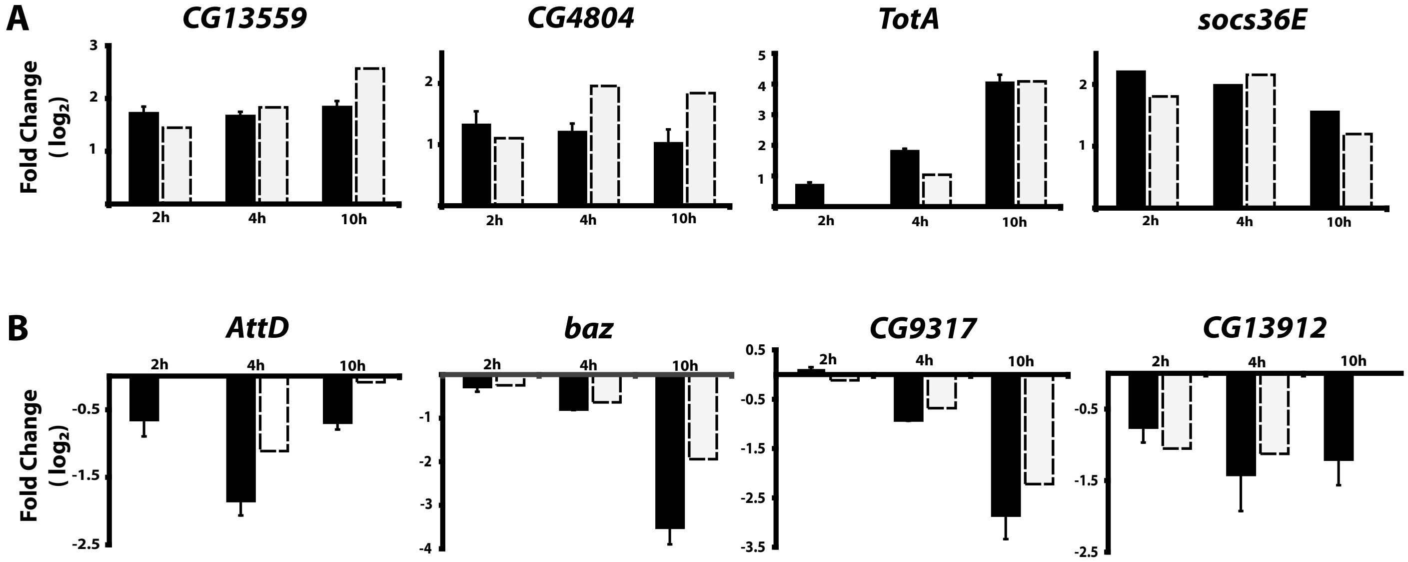
Pearson, R.D., Liu, X., Sanguinetti, G., Milo, M., Lawrence, N.D. and Rattray, M. (2009) puma: a Bioconductor package for propagating uncertainty in microarray analysis *BMC Bioinformatics* **10:** 211.

Shi, S., Calhoun, H.C., Xia, F., Li, J., Le, L. and Li, W.X. (2006) JAK signaling globally counteracts heterochromatic gene silencing *Nat Genet* **38:** 1071-1076.

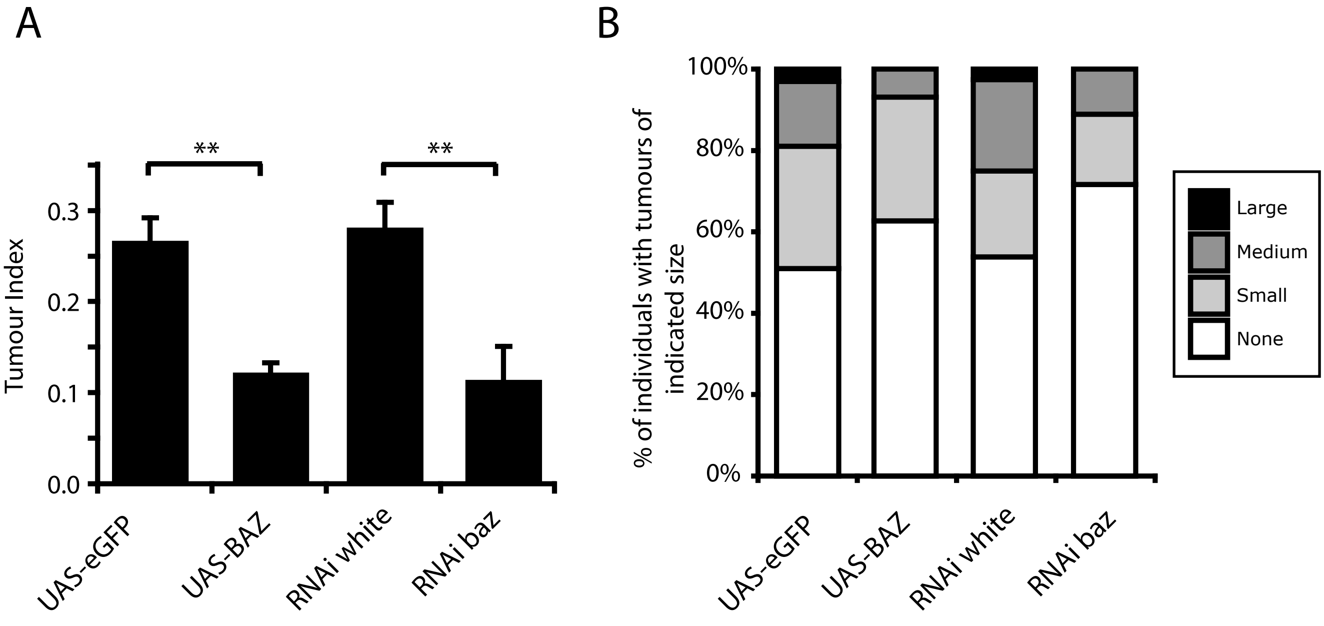
Yang, I.V., Chen, E., Hasseman, J.P., Liang, W., Frank, B.C., Wang, S., Sharov, V., Saeed, A.I., White, J., Li, J., Lee, N.H., Yeatman, T.J. and Quackenbush, J. (2002) Within the fold: assessing differential expression measures and reproducibility in microarray assays *Genome Biol* **3:** research0062.

Zeeberg, B.R., Qin, H., Narasimhan, S., Sunshine, M., Cao, H., Kane, D.W., Reimers, M., Stephens, R.M., Bryant, D., Burt, S.K., Elnekave, E., Hari, D.M., Wynn, T.A., Cunningham-Rundles, C., Stewart, D.M., Nelson, D. and Weinstein, J.N. (2005) High-Throughput GoMiner, an 'industrial-strength' integrative gene ontology tool for interpretation of multiple-microarray experiments, with application to studies of Common Variable Immune Deficiency (CVID) *BMC Bioinformatics* **6:** 168.

Supplemental Figure 1



Supplemental Figure 2



Supplemental Table 1

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
Aats-glupro	CG5394	0.0	0.0	-1.1	glutamyl-tRNA aminoacylation	glutamate-tRNA ligase activity	EPRS QARS EARS2
Acon	CG9244	0.0	0.3	-0.4	tricarboxylic acid cycle	aconitate hydratase activity	-
Adh	CG3481	0.4	0.5	-2.0	ethanol oxidation	alcohol dehydrogenase activity	HPGD
Alas	CG3017	0.0	0.0	-1.1	heme biosynthetic process	5-aminolevulinate synthase activity	ALAS2 ALAS1 GCAT
alpha-Est3	CG1257	0.0	0.0	-2.0	-	carboxylesterase activity	CES8 ACHE CES7
alpha-Man-II	CG18802	0.0	0.0	-1.5	protein amino acid glycosylation	mannosyl-oligosaccharide 1,3-1,6-alpha-m	MAN2A2* MAN2A1 MAN2B1
alphaCop	CG7961	0.0	0.1	-1.1	retrograde vesicle-mediated transport, Golgi to	protein binding	COPA* COPB2 PAFAH1B1
amon	CG6438	-0.4	-0.3	-1.5	peptide hormone processing	peptidase activity	PCSK2 FURIN PCSK6
amos	CG10393	0.0	-2.3	0.6	regulation of transcription, DNA-dependent	transcription factor activity	-
Ance-2	CG16869	-0.8	-0.6	-0.2	proteolysis	peptidyl-dipeptidase activity	ACE ACE2
AP-1sigma	CG5864	0.0	0.1	-2.0	neurotransmitter secretion	protein transporter activity	AP1S1* AP1S3 DKFZp779P0659
Art2	CG3675	0.0	0.0	-2.8	-	protein-arginine N-methyltransferase activi	PRMT8 PRMT1 PRMT3
aru	CG4276	0.0	0.0	-2.1	epidermal growth factor receptor signaling pathw	-	RPS27A UBC UBB
ash1	CG8887	-1.7	-0.1	0.0	embryonic development via the syncytial blastod	histone methyltransferase activity	ASH1L SETD2 NSD1
Ast-C	CG14919	0.0	1.6	0.0	neuropeptide signaling pathway	neuropeptide hormone activity	-
Atg18	CG7986	0.0	0.0	-1.0	autophagy	-	WIPI2* WIPI1 WDR45L
Atg2	CG1241	0.0	0.0	-1.9	autophagy	-	ATG2B ATG2A
Atg4	CG4428	0.0	0.0	-1.0	-	cysteine-type endopeptidase activity	ATG4B ATG4A ATG4D
AttA	CG10146	0.0	-1.3	-0.1	defense response to Gram-negative bacterium	-	-
AttB	CG18372	0.0	-1.4	0.0	defense response to bacterium	-	-
AttC	CG4740	0.0	-3.2	0.0	antibacterial humoral response	-	-
AttD	CG7629	0.0	-1.1	-0.1	antibacterial humoral response	-	-
Awh	CG1072	0.0	-0.5	2.2	imaginal disc development	transcription factor activity	LHX8 LHX6 LHX9
b	CG7811	0.0	0.0	-2.2	visual behavior	glutamate decarboxylase activity	CSAD* GADL1 GAD2
bab1	CG9097	-2.0	0.3	1.1	sex differentiation	transcription factor activity	-
baz	CG5055	-0.2	-0.6	-1.9	establishment or maintenance of polarity of emb	protein kinase C binding	PARD3 PARD3B MPDZ
bcd	CG1034	0.0	-2.4	0.0	anterior region determination	specific RNA polymerase II transcription fac	-
beat-IIb	CG4135	0.9	0.0	1.5	-	-	-
Best3	CG12327	2.3	0.0	0.0	-	-	BEST3 BEST2 BEST1
beta-Spec	CG5870	0.0	0.0	-2.3	maintenance of presynaptic active zone structur	cytoskeletal protein binding	SPTBN1* SPTBN2* SPTB* SPTBN4*
bib	CG4722	-1.1	0.0	0.0	ectoderm development	water channel activity	AQP1 AQP4 AQP2
blot	CG3897	0.0	0.0	-2.3	morphogenesis of an epithelium	neurotransmitter transporter activity	-
blue	CG6451	0.0	-0.1	-2.0	regulation of pole plasm oskar mRNA localizatior	-	NEURL4*
Brd	CG3096	2.0	0.0	0.3	Notch signaling pathway	calmodulin inhibitor activity	-
bru-2	CG31761	0.0	-2.1	-2.2	negative regulation of translation	mRNA binding	CUGBP1 CUGBP2 BRUNOL4
BRWD3	CG31132	0.0	0.0	-1.6	phagocytosis, engulfment	-	PHIP BRWD3 BRWD1
Buffy	CG8238	0.0	0.0	-2.2	apoptosis	-	BOK
c(2)M	CG4249	0.0	-0.6	0.0	meiosis	-	-
c11.1	CG12132	0.0	0.0	-2.2	-	binding	HEATR7A HEATR7B1
c12.2	CG12149	0.0	0.0	-1.8	-	ATP binding	KIAA0564
cactin	CG1676	0.0	0.0	-0.9	dorsal/ventral axis specification	-	C19orf29*
Cad88C	CG3389	0.1	0.0	1.3	calcium-dependent cell-cell adhesion	calcium ion binding	CDH23 FAT4 FAT1
Cad96Cb	CG13664	0.7	2.0	-0.2	calcium-dependent cell-cell adhesion	phosphopantetheine binding	FAT1 PCDHB1 PCDHB7
Caf1-180	CG12109	0.0	0.0	-1.5	nucleosome assembly	-	-
Caki	CG6703	0.0	0.0	-1.6	adult walking behavior	guanylate kinase activity	CASK* MPP1 MPP2
CanA-14F	CG9819	0.0	-1.0	-1.3	protein amino acid dephosphorylation	protein serine/threonine phosphatase activi	-
CanA1	CG1455	-0.1	2.1	0.2	protein amino acid dephosphorylation	protein serine/threonine phosphatase activi	PPP3CA* PPP3CB* PPP3CC
capaR	CG14575	0.0	0.7	0.3	G-protein coupled receptor protein signaling pat	neuropeptide receptor activity	NMUR2 GHSR NMUR1
caps	CG11282	-0.1	-0.1	-3.8	axon guidance	protein binding	LRRN2 LGR5 LRRN1
capt	CG33979	-0.1	0.1	-0.6	actin polymerization or depolymerization	actin binding	CAP1* CAP2
CcapR	CG33344	0.8	-0.4	0.8	G-protein coupled receptor protein signaling pat	vasopressin receptor activity	NPSR1* AVPR1B AVPR1A
Cdk5	CG8203	0.0	-2.4	0.0	protein amino acid phosphorylation	cyclin-dependent protein kinase activity	CDK5 CDK3 CDK2
CecB	CG1878	-0.1	-1.7	0.0	defense response to bacterium	-	-
CecC	CG1373	-0.1	-1.3	0.0	defense response to Gram-negative bacterium	-	-
cenB1A	CG6742	0.0	0.0	-0.9	phagocytosis, engulfment	ARF GTPase activator activity	ACAP3* ACAP2 ACAP1
CG10017	CG34340	0.1	0.0	1.3	dendrite morphogenesis	transcription factor activity	DRGX ARX PHOX2B
CG10019	CG10019	-0.1	0.0	2.1	-	monocarboxylic acid transmembrane trans	SLC16A12 SLC16A14 SLC16A7
CG10029	CG10029	-1.6	-0.4	0.0	cell redox homeostasis	protein disulfide isomerase activity	ERP44 PDIA4 PDIA3
CG10035	CG10035	2.7	0.0	-0.6	-	-	-
CG10062	CG10062	0.0	0.0	-1.0	proteolysis	peptidase activity	ERMP1
CG10077	CG10077	0.0	0.0	-1.0	-	RNA helicase activity	-
CG10083	CG10083	0.0	0.0	-1.1	cell migration	actin binding	DBNL* DBN1 CTTN
CG10089	CG10089	3.1	0.0	0.0	protein amino acid dephosphorylation	protein tyrosine/serine/threonine phosphat	DUSP22* DUSP15 DUSP6
CG10102	CG10102	0.0	0.2	-0.4	-	zinc ion binding	-
CG10140	CG10140	0.0	0.0	-3.0	chitin metabolic process	chitin binding	-
CG10170	CG10170	-2.6	0.0	0.0	metabolic process	2-hydroxyacylsphingosine 1-beta-galactosy	UGT8 UGT1A10 UGT1A9
CG10182	CG10182	0.0	-1.7	0.0	-	transferase activity, transferring groups oth	-
CG10184	CG10184	-0.5	0.1	0.0	amino acid metabolic process	threonine aldolase activity	-
CG10188	CG10188	0.0	0.0	-2.0	regulation of Rho protein signal transduction	Rho guanyl-nucleotide exchange factor acti	AKAP13* ARHGEF18 RGNEF
CG10237	CG10237	0.0	-1.0	-0.1	transport	retinal binding	TTPAL RLBP1L2 RLBP1L1
CG10252	CG10252	-2.3	-0.1	0.0	-	-	ODF3L2* ODF3 ODF3B
CG10260	CG10260	0.0	0.0	-2.3	phosphorylation	1-phosphatidylinositol 4-kinase activity	PI4KA* PI4KAP2 PI4KB
CG10262	CG10262	-1.3	-0.1	-0.1	DNA replication	DNA binding	PCNA
CG10274	CG10274	0.0	0.0	-2.0	-	zinc ion binding	ZNF136 ZFP90 ZNF91
CG10339	CG10339	0.0	-0.2	-2.9	transport	carboxylesterase activity	NLGN4Y NLGN3 NLGN4X
CG10361	CG10361	0.0	0.0	-2.0	amino acid metabolic process	glycine C-acetyltransferase activity	GCAT ALAS2 ALAS1
CG10426	CG10426	-0.2	0.0	-2.9	dephosphorylation	inositol trisphosphate phosphatase activity	INPP5E* INPP5B SYNJ1
CG10465	CG10465	0.0	0.0	0.6	potassium ion transport	protein binding	KCTD10* TNFAIP1 KCTD13
CG10494	CG10494	0.0	-2.2	-3.2	-	DNA binding	-
CG10505	CG10505	-0.6	0.0	0.0	response to zinc ion	ATPase activity, coupled to transmembrane	ABCC4* ABCC1* ABCC3*
CG10514	CG10514	-1.4	0.0	0.0	-	-	-
CG10542	CG10542	-0.1	0.0	-2.0	peripheral nervous system development	protein binding	RNF40* RNF20
CG10543	CG10543	0.0	-0.2	-2.4	-	zinc ion binding	ZNF567 ZNF133 ZFP112
CG10621	CG10621	0.0	0.0	-3.5	-	selenocysteine methyltransferase activity	-
CG10662	CG34343	0.0	0.2	-1.6	defense response to Gram-negative bacterium	nucleoside-triphosphatase activity	-
CG10677	CG10677	-2.0	0.0	0.0	-	-	-
CG10702	CG10702	0.0	0.0	-2.1	transmembrane receptor protein tyrosine kinase	insulin-like growth factor receptor activity	INSRR INSR IGF1R
CG10732	CG10732	0.0	0.0	-2.5	-	-	-
CG10737	CG10737	0.0	-0.1	-2.2	intracellular signaling cascade	diacylglycerol binding	-
CG10738	CG10738	0.0	-0.1	-2.5	signal transduction	guanylate cyclase activity	NPR2 NPR1 GUCY2F
CG10764	CG10764	0.5	1.3	2.5	proteolysis	serine-type endopeptidase activity	F9 PRSS8 F10
CG10824	CG10824	0.3	3.4	5.4	proteolysis	protein binding	LRRC70 LGR6 LRRC26
CG10845	CG10845	0.0	0.7	0.0	microtubule-based movement	motor activity	KIF5C KIF5B
CG10881	CG10881	0.0	-0.6	0.0	translational initiation	mRNA binding	EIF3G
CG10882	CG10882	0.0	0.0	-0.9	intracellular protein transport	serine-type endopeptidase activity	SEC24D* SEC24C SEC24B
CG10887	CG10887	0.0	0.0	3.0	-	-	LEO1
CG1090	CG1090	0.1	-0.3	-1.7	sodium ion transport	calcium, potassium:sodium antiporter activ	SLC24A2 SLC24A5 SLC24A4
CG10924	CG10924	0.0	-1.1	-0.1	gluconeogenesis	phosphoenolpyruvate carboxykinase (GTP)	PCK2 PCK1
CG10987	CG10987	0.0	1.1	0.0	-	-	-
CG10990	CG10990	-0.1	0.1	-0.9	-	-	PDCD4
CG11008	CG11008	0.0	-0.9	-1.7	-	-	-
CG11029	CG11029	0.0	1.4	0.0	lipid metabolic process	lysophospholipase activity	PLB1
CG11033	CG11033	0.0	0.0	-1.7	-	DNA binding	KDM2A* KDM2B FBXL10
CG11043	CG11043	0.0	0.0	-2.3	mitochondrial electron transport, cytochrome c t	cytochrome-c oxidase activity	-
CG11093	CG11093	0.0	-0.8	-0.4	-	protein binding	CORL2* LBXCOR1 SKI
CG11112	CG11112	0.0	0.0	2.1	-	-	-
CG11141	CG11141	0.0	0.0	-1.6	-	-	KIAA0329
CG11198	CG11198	0.0	0.0	-2.4	fatty acid biosynthetic process	acetyl-CoA carboxylase activity	ACACA* ACACB* MCCC1
CG11241	CG11241	-0.6	0.0	0.0	-	alanine-glyoxylate transaminase activity	AGXT2 AGXT2L1 AGXT2L2
CG11263	CG11263	0.0	-0.8	-0.1	-	nucleic acid binding	-
CG11265	CG11265	0.0	0.0	-2.1	sister chromatid cohesion	DNA-directed DNA polymerase activity	PAPD5* POLS
CG11403	CG11403	0.0	0.0	-1.8	nucleotide-excision repair	helicase activity	DDX11* DDX12 RTEL1
CG11407	CG11407	0.0	0.0	-2.3	metabolic process	long-chain fatty acid transporter activity	ACSF2 ACSM2B ACSM3
CG11414	CG11414	0.0	0.0	-1.0	-	protein binding	ZNF598*

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG1142	CG1142	0.0	0.0	0.5	-	-	DNTTIP2
CG11426	CG11426	0.0	0.8	3.0	dephosphorylation	phosphatidate phosphatase activity	PPAP2B PPAP2A PPAP2C
CG11438	CG11438	2.0	-0.3	-0.1	dephosphorylation	phosphatidate phosphatase activity	PPAP2A PPAP2B PPAP2C
CG11458	CG11458	-1.2	-0.6	0.2	-	-	-
CG11504	CG11504	0.0	0.0	-1.6	-	-	-
CG11505	CG11505	0.0	0.0	-3.1	-	nucleic acid binding	LARP4* LARP5 LARP1
CG11509	CG11509	0.0	1.0	-1.3	proteolysis	aspartic-type endopeptidase activity	-
CG11526	CG11526	0.0	0.0	-1.1	-	-	FAM40A* FAM40B*
CG11538	CG11538	0.0	0.0	-2.0	-	-	-
CG11552	CG11552	-2.0	0.0	0.1	proteolysis	-	PSMD8
CG11555	CG11555	0.0	0.1	1.0	-	-	-
CG11581	CG11581	0.1	1.8	-0.1	-	-	-
CG11583	CG11583	0.0	0.3	0.6	ribosomal large subunit biogenesis	-	BXDC2
CG11588	CG11588	0.1	-2.1	0.1	-	-	-
CG11594	CG11594	0.0	0.0	-2.7	carbohydrate metabolic process	phosphotransferase activity, alcohol group	FGGY*
CG11619	CG11619	-0.1	-0.7	0.0	carbohydrate metabolic process	carbohydrate binding	GDE5 RP5-1022P6.2
CG11630	CG11630	0.0	-1.5	0.0	-	-	-
CG11656	CG11656	0.0	-3.0	-0.3	-	-	-
CG11666	CG11666	0.0	0.0	-2.8	-	-	-
CG11674	CG11674	0.2	0.0	1.5	nuclear mRNA splicing, via spliceosome	ATP-dependent RNA helicase activity	-
CG11775	CG11775	0.0	-0.6	-2.0	-	extracellular-glutamate-gated ion channel	-
CG11786	CG11786	-0.6	0.0	0.0	-	-	-
CG11897	CG11897	0.0	0.0	-1.9	transport	multidrug transporter activity	ABCC4* ABCC1* ABCC3* ABCC2
CG11905	CG11905	0.5	0.0	0.5	-	-	-
CG11915	CG11915	-3.5	-0.1	0.0	-	-	-
CG11928	CG34351	-2.0	0.1	0.6	-	-	-
CG11940	CG11940	0.0	0.0	-2.1	signal transduction	-	RAPH1* APBB1IP GRB14
CG11943	CG11943	0.0	0.0	-2.0	-	-	NUP205
CG11984	CG11984	0.0	0.0	-1.3	-	potassium channel regulator activity	KCMF1
CG12017	CG12017	1.3	0.0	0.1	-	-	-
CG12061	CG12061	0.3	-1.7	0.0	-	calcium, potassium:sodium antiporter activ	SLC24A4 SLC24A3 SLC24A2
CG12065	CG12065	0.0	0.0	-3.5	oxidation reduction	oxidoreductase activity	-
CG12147	CG12147	-1.1	0.0	0.0	protein amino acid phosphorylation	protein serine/threonine kinase activity	CSNK1A1 CSNK1A1L CSNK1E
CG12207	CG12207	0.0	0.0	-1.8	cell wall catabolic process	-	LYSMD1 LYSMD2
CG12439	CG12439	2.7	-1.9	-0.2	-	-	-
CG12488	CG12488	0.0	0.0	-3.2	-	-	-
CG12523	CG12523	-0.5	1.5	-0.1	-	-	-
CG12531	CG12531	-1.8	2.7	-0.1	amino acid transport	cationic amino acid transmembrane transp	SLC7A14 SLC7A3 SLC7A1
CG12539	CG12539	0.0	-2.3	-0.2	cellular alcohol metabolic process	glucose dehydrogenase activity	CHDH
CG12543	CG42340	-0.7	0.0	0.0	potassium ion transport	potassium channel activity	KCNK10
CG12551	CG12551	-2.3	1.7	0.1	-	-	-
CG12584	CG34425	-0.1	0.0	-1.5	-	-	-
CG12602	CG12602	0.0	1.1	0.2	ATP synthesis coupled proton transport	hydrogen-exporting ATPase activity, phosp	ATP6V0A4 ATP6V0A1 ATP6V0A2
CG12609	CG12609	-2.5	0.0	0.2	-	-	-
CG12655	CG12655	0.0	0.0	2.9	-	-	-
CG12656	CG12656	0.0	0.0	1.5	-	-	-
CG12674	CG12674	-0.5	-2.5	0.0	-	-	-
CG12703	CG12703	0.0	0.0	-1.8	peroxisome organization	ATPase activity, coupled to transmembrane	ABCD3* ABCD2 ABCD1
CG12716	CG12716	-1.7	0.0	0.7	-	-	-
CG12789	CG12789	0.0	-1.4	-0.7	defense response	scavenger receptor activity	SCARB1 SCARB2 CD36
CG12798	CG12798	-0.2	-1.1	0.0	protein amino acid phosphorylation	ATP binding	MAP2K4
CG12802	CG34360	-2.2	0.0	0.5	-	zinc ion binding	ZNF704 ZNF395 SLC2A4RG
CG12816	CG34108	0.0	0.0	2.8	-	-	-
CG12817	CG12817	0.0	1.4	-0.1	-	calcium ion binding	-
CG12831	CG12831	2.0	-0.4	1.1	-	-	-
CG12861	CG12861	0.0	2.1	-0.4	-	-	-
CG12902	CG12902	0.0	1.8	-0.8	-	-	-
CG12909	CG12909	0.0	0.4	0.6	-	-	LYAR
CG1294	CG1294	-0.9	0.0	0.1	-	-	-
CG12959	CG34365	-0.4	-1.1	0.0	intracellular signaling cascade	diacylglycerol binding	-
CG12991	CG12991	0.0	-1.1	0.0	-	-	-
CG13002	CG13002	-0.8	-0.8	0.1	-	-	-
CG13008	CG13008	-0.7	2.0	-0.1	-	-	-
CG13038	CG13038	1.1	0.0	0.8	-	-	-
CG13042	CG13042	0.0	0.0	-1.5	-	-	-
CG13062	CG13062	0.0	-0.7	0.0	-	-	-
CG13116	CG13116	0.0	1.0	0.0	-	-	-
CG13121	CG13121	0.0	2.0	-0.2	sodium ion transport	sodium channel activity	-
CG13130	CG13130	-2.7	0.0	0.0	-	-	-
CG13133	CG13133	-0.2	0.0	-1.9	-	-	-
CG1315	CG1315	1.1	-2.3	1.2	argininosuccinate metabolic process	argininosuccinate synthase activity	ASS1 LOC402295
CG13168	CG13168	0.8	0.0	-1.2	-	-	-
CG13278	CG13278	1.1	0.0	-0.1	sodium ion transport	sodium channel activity	-
CG13333	CG13333	0.0	-0.1	2.8	-	-	-
CG13386	CG13386	0.0	-0.1	2.2	-	-	-
CG13404	CG13404	0.6	-2.2	-0.1	-	-	C9orf46
CG13437	CG13437	0.0	1.6	0.1	-	-	-
CG13449	CG13449	0.8	0.0	-0.1	-	-	-
CG13506	CG13506	0.3	0.8	1.9	-	-	-
CG13527	CG13527	-0.4	0.0	2.0	proteolysis	serine-type endopeptidase activity	TMPRSS11D TPSAB1 TMPRSS11B
CG13540	CG13540	-0.6	0.7	0.0	-	-	-
CG13548	CG34371	1.3	-0.1	0.0	-	-	HMCN1 TTN KIRREL2
CG13550	CG13550	0.0	0.0	-1.8	mitotic spindle organization	calcium ion binding	-
CG13559	CG13559	1.5	1.8	2.6	-	-	LITAF
CG13565	CG13565	0.0	-0.1	-1.7	-	-	-
CG13576	CG13576	-2.5	0.0	0.9	-	-	-
CG13597	CG13597	0.0	1.3	2.0	-	-	BRD2 BRD3 BRD4
CG13627	CG13627	0.0	1.9	-0.2	-	-	-
CG13673	CG13673	-0.7	-2.0	-3.2	-	-	-
CG13676	CG13676	-0.1	0.0	-1.4	chitin metabolic process	chitin binding	-
CG13680	CG34373	-1.1	0.0	0.0	signal transduction	binding	SARM1*
CG13707	CG13707	-1.8	0.4	0.0	-	-	-
CG13708	CG13708	0.2	-1.7	-0.7	-	protein binding	-
CG13737	CG13737	-1.4	0.0	0.0	-	-	-
CG13829	CG13829	0.0	-2.3	0.0	-	-	-
CG13834	CG34375	-1.3	0.0	0.0	multicellular organismal development	protein binding	-
CG13835	CG34375	1.0	-1.9	-0.5	multicellular organismal development	protein binding	-
CG13872	CG13872	0.4	0.0	-2.3	-	-	-
CG13907	CG13907	0.0	-0.4	-1.6	-	secondary active monocarboxylate transme	SLC16A14 SLC16A12 SLC16A7
CG13912	CG13912	-1.0	-1.1	0.0	-	-	-
CG13928	CG13928	0.0	0.0	-1.0	-	protein binding	-
CG13937	CG13937	0.0	-0.8	-1.2	carbohydrate biosynthetic process	HNK-1 sulfotransferase activity	CHST11 CHST9 CHST8
CG13949	CG13949	0.0	0.0	-2.6	-	-	-
CG13964	CG13964	0.0	0.0	-1.7	-	-	-
CG1397	CG1397	0.9	-0.5	0.0	-	-	-
CG13978	CG13978	0.0	0.8	1.4	GPI anchor biosynthetic process	transferase activity	PIGN
CG1399	CG1399	0.1	1.0	0.0	cilium biogenesis	myosin I binding	-
CG13999	CG13999	0.0	-2.3	0.0	-	-	TMEM138*
CG14013	CG14013	0.0	2.0	0.0	proteolysis	serine-type peptidase activity	C4orf22
CG14015	CG14015	0.0	-3.0	0.0	-	mannan endo-1,6-alpha-mannosidase activ	MANEAL* MANEA
CG14022	CG14022	-1.3	-0.6	-0.1	-	acylphosphatase activity	ACYP2 ACYP1
CG14033	CG14033	0.0	3.3	0.0	-	-	-
CG14098	CG14098	0.6	0.5	2.7	-	-	-
CG14101	CG14101	0.0	-0.6	-0.7	-	-	-
CG14116	CG34429	0.0	0.0	-2.3	-	-	-
CG14118	CG14118	0.0	-1.0	0.0	-	endonuclease activity	-

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG14120	CG14120	0.0	-1.5	0.0	metabolic process	endonuclease activity	-
CG14129	CG34420	0.0	0.0	3.2	proteolysis	dipeptidase activity	DPEP1 DPEP2 DPEP3
CG14160	CG14160	-1.5	0.0	0.0	-	-	-
CG1421	CG1421	-2.1	-1.3	-0.2	-	-	-
CG14215	CG14215	0.0	0.0	-1.8	-	-	AHCTF1
CG14219	CG14219	0.0	-1.5	0.0	-	transferase activity, transferring groups oth	-
CG14253	CG14253	0.1	0.7	1.4	-	-	-
CG14306	CG14306	-0.9	0.0	-0.4	-	protein binding	-
CG14340	CG14340	0.0	0.8	3.0	-	-	-
CG14351	CG14351	-0.2	-1.5	-2.4	-	protein binding	CPN2 LGR5 LRIG3
CG14362	CG14362	2.0	0.1	0.4	-	calcium ion binding	-
CG14372	CG14372	-0.4	-1.2	0.0	-	-	HMCN1 KIRREL3 IGSF9
CG14394	CG14394	-0.4	0.0	3.3	tissue regeneration	-	-
CG1440	CG1440	0.0	0.0	-0.9	proteolysis	cysteine-type endopeptidase activity	BLMH
CG14431	CG14431	0.0	0.0	-2.6	-	phosphopantetheine binding	-
CG14435	CG14435	0.0	0.0	-3.8	-	protein binding	ZNRF2 ZNRF1
CG14442	CG14442	0.0	0.0	-1.6	transport	transporter activity	-
CG14476	CG14476	0.0	0.0	-1.2	carbohydrate metabolic process	alpha-glucosidase activity	GANAB* GANC GAA
CG14487	CG14487	-1.6	-0.2	-0.4	-	-	-
CG14502	CG14502	0.0	0.0	-2.3	-	-	-
CG14516	CG14516	0.0	-0.2	-3.2	proteolysis	aminopeptidase activity	ANPEP TRHDE ENPEP
CG14526	CG14526	-0.4	1.0	2.4	proteolysis	metalloendopeptidase activity	ECEL1 ECE2 ECE1
CG14556	CG14556	2.5	0.0	0.2	-	-	-
CG14565	CG14565	0.0	-0.3	-3.1	-	-	-
CG14584	CG14584	0.0	1.6	0.0	-	-	-
CG14624	CG14624	-0.7	0.0	0.0	-	-	-
CG14632	CG14632	1.1	2.8	0.0	-	-	-
CG14635	CG14635	1.6	0.0	0.0	-	-	-
CG14638	CR14638	0.0	0.0	-2.5	-	-	-
CG14642	CG14642	0.0	0.0	-1.4	proteolysis	serine-type endopeptidase activity	GZMH
CG14656	CG14656	-1.1	0.0	2.5	-	-	TRIP12 HECTD1 WWP2
CG14659	CG14659	-2.0	0.0	0.0	-	-	-
CG14668	CG14668	0.0	2.3	-0.1	-	-	-
CG14669	CG14669	-1.6	-0.1	0.8	small GTPase mediated signal transduction	GTP binding	-
CG14687	CG14687	0.0	0.0	2.7	-	myosin light chain binding	-
CG14714	CG42327	-0.6	0.0	-1.9	protein amino acid dephosphorylation	protein tyrosine phosphatase activity	PTPN6 PTPN9 PTPRR
CG14755	CG14755	-0.7	0.2	0.0	-	-	-
CG14780	CG14780	0.0	-0.4	-2.0	proteolysis	serine-type endopeptidase activity	PRSS33 serase-1B TMPRSS9
CG14785	CG14785	0.0	0.6	-0.1	-	-	-
CG14801	CG14801	-0.1	0.0	-2.1	-	exonuclease activity	REXO1 REXO1L1 REXO1L2P
CG14841	CG14841	0.0	0.0	3.0	-	-	-
CG14843	CG34388	0.0	-1.0	0.0	-	-	-
CG14846	CG34389	0.4	0.0	2.4	Malpighian tubule morphogenesis	GTPase activator activity	STARD13 DLC1 STARD8
CG14869	CG14869	0.5	0.2	0.0	proteolysis	metalloendopeptidase activity	ADAMTS9* ADAMTS20 ADAMTS15
CG14871	CG14871	-1.6	-0.3	-2.8	-	-	-
CG14872	CG14872	0.0	0.2	1.1	transport	transporter activity	-
CG14921	CG14921	0.4	-0.8	0.0	-	-	-
CG14947	CG14947	0.0	-0.1	-1.4	-	-	-
CG14955	CG14955	-1.2	1.6	0.1	-	-	-
CG14959	CG14959	0.0	0.8	0.4	chitin metabolic process	chitin binding	-
CG14973	CG42324	-0.6	0.0	0.5	-	-	TJAP1 BEGAIN
CG14982	CG14982	0.0	0.0	-2.2	-	-	-
CG14989	CG14989	-2.4	0.0	0.2	-	-	-
CG15004	CG15004	0.0	1.7	0.0	-	sodium channel auxiliary protein activity	-
CG15032	CG15032	-0.4	-1.0	-0.9	-	-	-
CG15040	CG15040	0.0	0.2	2.8	-	-	-
CG15080	CG15080	2.0	0.0	0.0	-	-	-
CG15088	CG15088	-1.3	0.3	-0.1	neurotransmitter transport	potassium:amino acid symporter activity	SLC6A7 SLC6A5 SLC6A9
CG15142	CG15142	0.0	-0.6	-2.0	-	-	-
CG1516	CG1516	0.0	-0.1	-1.6	pyruvate metabolic process	pyruvate carboxylase activity	PC PCCA MCCC1
CG15170	CG15170	-0.9	0.5	-0.1	-	-	-
CG15198	CG15198	1.1	0.0	-1.2	-	-	-
CG15211	CG15211	0.0	0.6	0.0	-	-	-
CG15233	CG15233	0.0	0.0	-2.2	-	-	-
CG15240	CG42541	0.0	-0.9	0.4	small GTPase mediated signal transduction	GTP binding	-
CG15260	CG15260	0.0	-2.7	0.3	-	-	-
CG15325	CG15325	1.1	0.0	2.0	-	-	-
CG15332	CG15332	0.0	0.0	-1.7	-	-	-
CG15390	CG15390	0.0	0.0	0.7	-	-	-
CG15393	CG15393	-0.1	0.0	-2.5	-	-	-
CG15418	CG15418	1.2	0.7	0.0	-	endopeptidase inhibitor activity	-
CG15434	CG15434	0.0	0.0	-2.9	mitochondrial electron transport, NADH to ubiqu	NADH dehydrogenase activity	NDUFA2
CG15439	CG15439	0.0	0.0	-1.9	-	protein binding	PHF14
CG15485	CG15485	0.1	-0.1	2.2	proteolysis	metalloendopeptidase activity	ECE2 ECE1 ECEL1
CG15488	CG34395	-2.2	0.0	0.0	pattern specification process	transcription factor activity	POU2F1 POU2F2 POU3F2
CG15497	CG15497	0.4	-1.5	0.0	-	-	-
CG15510	CG15510	1.3	0.0	2.7	-	-	-
CG15522	CG15522	0.0	-0.6	0.0	-	-	-
CG15594	CG15594	0.0	-0.1	2.8	-	-	-
CG15617	CG15617	1.8	1.0	-0.2	-	protein binding	-
CG15618	CG15618	0.0	0.0	-1.7	-	-	THADA*
CG15627	CG15627	0.4	0.0	1.9	ion transport	extracellular-glutamate-gated ion channel a	GRIA4 GRIK2 GRIK3
CG15628	CG15628	0.0	-0.2	-2.3	metabolic process	N-acetyltransferase activity	-
CG15678	CG15678	0.8	0.1	0.7	negative regulation of innate immune response	-	-
CG15684	CG15684	0.0	1.9	0.0	microtubule-based process	GTP binding	-
CG15708	CG15708	0.1	0.0	-2.3	-	-	-
CG1571	CG1571	0.0	-2.3	0.0	microtubule-based movement	motor activity	DNAI2 WDR63
CG15715	CG15715	0.0	0.0	0.6	-	zinc ion binding	ZNF706
CG1572	CG1572	0.0	0.6	0.6	-	-	-
CG15743	CG15743	0.0	0.0	-2.1	-	3'(2'),5'-bisphosphate nucleotidase activity	IMPAD1 BPNT1
CG15747	CG15747	0.0	-0.8	0.1	-	-	-
CG15757	CG15757	1.7	0.1	0.0	-	structural constituent of chitin-based cuticle	-
CG1582	CG1582	0.0	0.0	-1.5	-	helicase activity	DHX57* DHX36 DHX29
CG15859	CG15859	0.4	-0.1	0.0	-	-	-
CG15876	CG15876	-2.8	-3.0	-0.3	regulation of localization	-	-
CG15909	CG15909	0.0	-0.9	0.0	-	-	-
CG1600	CG1600	-0.2	0.0	-0.6	metabolic process	zinc ion binding	-
CG1620	CG1620	0.0	0.0	-1.0	-	DNA binding	MIER1 MIER3 MIER2
CG1628	CG1628	0.2	0.7	0.0	mitochondrial ornithine transport	L-ornithine transmembrane transporter acti	SLC25A15 SLC25A2 SLC25A20
CG1648	CG1648	0.1	1.1	1.5	-	-	-
CG1657	CG1657	0.0	0.0	-1.9	phosphoenolpyruvate-dependent sugar phospho	Rab guanyl-nucleotide exchange factor acti	GAPVD1* RABGEF1
CG16710	CG16710	0.0	0.1	1.5	proteolysis	serine-type endopeptidase activity	TMPRSS4 CELA2A CELA2B
CG1677	CG1677	0.0	0.0	-1.2	-	zinc ion binding	ZC3H18*
CG16772	CG16772	0.0	2.0	0.0	-	-	-
CG16777	CG16777	0.0	0.0	-2.9	-	-	-
CG16800	CG16800	2.1	-0.8	-1.6	-	-	-
CG16848	CG16848	0.0	-0.8	-2.3	metabolic process	FMN adenylyltransferase activity	FLAD1*
CG16850	CG16850	0.0	1.6	-0.7	-	-	-
CG16863	CG16863	0.0	0.0	-2.0	-	-	ZBED1
CG16903	CG16903	0.0	0.0	-1.1	-	cyclin-dependent protein kinase regulator a	CCNL2* CCNL1 CCNK
CG16905	CG16905	0.0	0.0	2.3	courtship behavior	fatty acid elongase activity	ELOVL1 ELOVL7 ELOVL4
CG16918	CG34437	0.5	0.0	2.2	-	-	TMPRSS3 CTRL F9
CG1695	CG1695	-0.7	0.0	0.0	regulation of Rab GTPase activity	Rab GTPase activator activity	SGSM1 SGSM2 TBC1D15
CG16956	CG16956	0.0	-2.8	0.1	-	-	-
CG16971	CG16971	0.0	0.0	-4.3	-	-	-
CG16975	CG16975	0.0	0.0	-1.2	chromatin silencing	methylated histone residue binding	MBTD1* L3MBTL2 SFMBT2

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG16989	CG16989	0.0	0.0	-2.2	-	binding	HEATR6
CG17019	CG17019	0.0	0.0	-1.2	negative regulation of apoptosis	protein binding	RFFL* RNF34
CG17027	CG17027	0.0	2.3	0.0	dephosphorylation	inositol-1(or 4)-monophosphatase activity	IMPA1 IMPA2
CG1718	CG1718	0.0	0.0	-1.6	-	ATPase activity, coupled to transmembrane	ABCA3 ABCA2 ABCA1
CG17239	CG17239	0.0	-1.5	0.0	proteolysis	serine-type endopeptidase activity	KLK14 PRSS1 KLK13
CG17242	CG17242	0.0	-3.1	0.0	proteolysis	serine-type endopeptidase activity	TMPRSS4 TMPRSS11D TMPRSS9
CG17255	CG17255	0.0	0.0	-2.0	-	-	-
CG17258	CG17258	-0.1	-0.7	-0.1	-	-	KIAA1407
CG17273	CG17273	0.0	0.1	-0.5	purine nucleotide biosynthetic process	adenylosuccinate synthase activity	ADSSL1* ADSS
CG17286	CG17286	0.0	0.0	-1.1	mitotic spindle organization	-	-
CG17319	CG17319	0.0	2.2	0.3	-	protein binding	-
CG17323	CG17323	0.0	2.1	0.0	metabolic process	glucuronosyltransferase activity	UGT8 UGT2B15 UGT2B17
CG17344	CG17344	0.0	0.8	0.6	-	-	-
CG17374	CG17374	-0.6	-0.1	-1.4	fatty acid biosynthetic process	fatty-acid synthase activity	FASN TP53I3 OXSM
CG17646	CG17646	2.5	0.6	0.0	-	ATPase activity, coupled to transmembrane	ABCG1 ABCG4 ABCG2
CG17660	CG17660	0.4	1.1	0.5	-	-	TMEM87B* TMEM87A
CG17681	CG17681	-1.1	0.4	0.0	metabolic process	N-acetyltransferase activity	-
CG17724	CG17724	0.0	-0.8	-2.1	-	-	-
CG1773	CG1773	0.0	-0.1	2.8	proteolysis	serine-type endopeptidase activity	CTRL ACR F11
CG17734	CG17734	-0.5	0.0	0.0	-	-	HIGD1C HIGD1A
CG17738	CG17738	-0.1	0.1	2.1	-	-	-
CG17760	CG17760	0.1	0.2	0.7	G-protein coupled receptor protein signaling pat	GTPase activity	GNAQ GNA11 GNA14
CG17778	CG17778	-1.7	-0.3	0.0	-	-	-
CG17781	CG17781	0.0	0.0	2.0	-	-	-
CG17786	CG17786	0.0	0.0	-2.1	-	-	-
CG17816	CG17816	-0.1	0.0	-3.9	-	-	-
CG17834	CG17834	-1.0	1.0	0.0	-	-	-
CG17999	CG17999	0.0	-2.1	-0.6	metabolic process	catalytic activity	ACSF2 ACSM5 ACSF3
CG1806	CG1806	0.0	-1.1	-0.5	-	-	-
CG18130	CG18130	0.0	0.0	-2.0	cell redox homeostasis	-	TXNDC6* TXNDC3
CG18173	CG18173	-2.1	0.0	-1.0	GPI anchor biosynthetic process	transferase activity, transferring acyl group	PIGW
CG18178	CG18178	0.0	0.3	1.2	-	-	-
CG18258	CG18258	-2.9	0.0	0.0	lipid metabolic process	catalytic activity	PNLIPRP1 PNLIP PNLIPRP2
CG18327	CG18327	0.0	0.0	-1.8	transport	transmembrane transporter activity	SLC25A35 SLC25A34 SLC25A27
CG18331	CG18331	0.3	0.2	-2.2	blood coagulation	-	-
CG18336	CG18336	0.0	-1.2	0.0	-	-	-
CG18416	CG18416	0.0	0.0	2.8	-	-	-
CG18418	CG18418	-2.3	0.0	0.0	alpha-ketoglutarate transport	oxoglutarate:malate antiporter activity	SLC25A11 SLC25A14 UCP3
CG18446	CG18446	-0.7	-0.8	0.0	-	zinc ion binding	-
CG1845	CG1845	0.0	0.0	-2.2	-	protein binding	BRPF1 DKFZp547C058 BRD1
CG18469	CG18469	0.0	-1.5	0.0	-	-	-
CG18490	CG18490	0.0	0.0	-2.1	-	-	-
CG18522	CG18522	0.0	0.0	-2.2	-	iron-sulfur cluster binding	XDH AOX1
CG18539	CG18539	-2.0	0.0	0.0	-	-	-
CG18557	CG18557	0.2	0.8	2.3	proteolysis	serine-type endopeptidase activity	PRSS22 UNQ9391/PRO34284 PRSS8
CG18558	CG18558	0.2	-1.9	0.0	-	-	C1GALT1 C1GALT1C1
CG18581	CG18581	0.0	-1.3	0.6	-	-	-
CG18598	CG18598	0.0	-1.8	-0.1	-	-	-
CG18682	CG18682	1.3	0.3	0.0	-	-	-
CG18778	CG18778	1.8	0.0	0.0	-	structural constituent of chitin-based cuticle	-
CG18806	CG18806	-0.8	0.0	0.0	-	-	-
CG1894	CG1894	-0.1	-0.9	-0.5	regulation of transcription	histone acetyltransferase activity	MYST1 MYST2 MYST3
CG1958	CG1958	0.0	0.0	-2.4	-	-	-
CG1973	CG1973	0.0	0.0	-1.9	protein amino acid phosphorylation	protein kinase activity	SCYL1* SCYL3 SCYL2
CG2017	CG2017	0.0	0.0	-1.0	-	GTP binding	GTPBP2* GTPBP1
CG2051	CG2051	-0.7	-0.2	0.3	histone acetylation	histone acetyltransferase activity	HAT1
CG2112	CG42233	-0.9	0.0	-2.6	-	-	WDR22* WDR5 WDR5B
CG2120	CG2120	0.0	-1.5	0.1	-	zinc ion binding	ZNF227 ZNF234 ZNF71
CG2121	CG2121	0.0	-2.9	2.0	-	-	UNC93A
CG2162	CG2162	0.0	0.0	-1.0	-	-	GIDRP88* R3HCC1
CG2186	CG2186	0.0	0.0	-2.4	-	-	-
CG2196	CG2196	0.5	1.3	0.1	transport	sodium:iodide symporter activity	SLC5A12 SLC5A8 SLC5A5
CG2218	CG2218	0.0	0.0	-1.4	protein ubiquitination	protein binding	UBOX5
CG2225	CG2225	-0.6	0.0	0.0	-	-	-
CG2444	CG2444	0.0	-0.8	-1.1	-	-	-
CG2446	CG2446	0.0	0.0	-1.0	-	-	-
CG2469	CG2469	0.0	0.0	-0.9	-	binding	CTR9
Cg25C	CG4145	0.0	0.0	-2.2	dorsal closure	extracellular matrix structural constituent	COL4A6* COL4A2 COL4A1
CG2658	CG2658	0.0	0.0	-1.8	proteolysis	metallopeptidase activity	SPG7* AFG3L2 YME1L1
CG2812	CG2812	0.0	0.0	-1.6	-	GTPase activity	WDR47* KATNB1 WDR51A
CG2930	CG2930	0.0	-0.1	-2.0	oligopeptide transport	proton-dependent oligopeptide secondary a	SLC15A1 SLC15A2 hPEPT1-RF
CG2938	CG2938	0.0	0.0	-1.6	-	-	CASD1
CG2967	CG34408	0.0	0.0	-2.0	regulation of small GTPase mediated signal trans	GTPase activator activity	KIAA1219* RP5-1100H13.1
CG30002	CG30002	0.0	3.2	0.0	proteolysis	serine-type endopeptidase activity	MASP2 ST14 CTRL
CG30027	CG30027	1.6	0.2	0.1	-	-	-
CG30035	CG30035	0.0	-0.6	-0.8	carbohydrate transport	glucose transmembrane transporter activity	SLC2A8 SLC2A6 SLC2A7
CG30036	CG30036	-0.6	1.0	0.0	protein amino acid glycosylation	UDP-galactose:beta-N-acetylglucosamine b	B3GALT1 B3GNT4 B3GNT5
CG30090	CG30090	0.0	0.0	-2.6	proteolysis	serine-type endopeptidase activity	PROC CTRL CTRB2
CG30122	CG30122	0.0	0.0	-1.0	-	mRNA binding	HNRNPUL1* HNRNPU HNRNPUL2
CG3016	CG3016	0.0	0.0	-1.1	ubiquitin-dependent protein catabolic process	ubiquitin thiolesterase activity	USP30 USP27X USP22
CG30163	CG30163	-0.8	0.0	-1.5	-	structural constituent of chitin-based cuticle	-
CG30197	CG30197	-1.3	0.0	0.0	-	protease inhibitor activity	-
CG30282	CG30282	0.0	1.4	0.4	-	-	-
CG3033	CG3033	0.0	0.0	-1.1	attachment of GPI anchor to protein	-	GPAA1*
CG30339	CG30339	0.0	0.0	-2.0	transport	transporter activity	TTPAL TTPA RLBP1L2
CG30359	CG30359	0.0	0.0	-1.6	carbohydrate metabolic process	cation binding	SLC3A1
CG30377	CG30377	-2.1	-0.9	-0.1	-	-	-
CG30389	CG30389	0.0	0.0	-1.6	-	-	TMEM57
CG30429	CG30429	-1.4	-0.2	-0.1	-	-	MORN3* RSPH10B2 RSPH10B
CG30456	CG30456	0.0	-0.9	0.0	regulation of Rho protein signal transduction	Rho guanyl-nucleotide exchange factor acti	-
CG30460	CG30460	-0.1	0.3	-1.7	-	-	-
CG30495	CG30495	-0.1	0.1	-2.1	metabolic process	oxidoreductase activity	RDH13 RDH12 RDH11
CG3088	CG3088	2.4	0.0	0.0	translation	serine-type endopeptidase activity	CTRB2 KLKB1 F11
CG3099	CG3099	0.0	0.0	-1.9	protein modification process	ubiquitin-protein ligase activity	HECW2* HECW1 NEDL1
CG31012	CG31012	0.0	1.5	0.0	-	SH3/SH2 adaptor activity	SH3KBP1* CD2AP ITSN1
CG31052	GA15967	0.0	-0.7	-0.2	cation transport	solute:hydrogen antiporter activity	NHEDC2 NHEDC1
CG31064	CG31064	0.0	0.0	-2.8	phagocytosis, engulfment	zinc ion binding	RUFY3 RUFY2 RUFY1
CG31077	CG31077	-1.8	0.0	0.4	chitin metabolic process	chitin binding	-
CG31079	CG31079	-0.3	0.0	-1.4	-	-	-
CG31116	CG31116	-0.2	-0.3	-1.5	chloride transport	chloride channel activity	CLCN2* CLCN1 CLCNKA
CG31121	CG31121	0.0	1.7	0.0	transport	ATPase activity, coupled to transmembrane	ABCG8 ABCG5 ABCG1
CG31150	CG31150	0.0	0.0	-1.3	lipid transport	lipid transporter activity	-
CG31151	CG31151	0.0	0.1	-2.0	-	DNA binding	BAHCC1 TNRC18 TNRC18C
CG31158	CG31158	0.7	0.7	0.0	regulation of ARF protein signal transduction	ARF guanyl-nucleotide exchange factor acti	PSD3 PSD PSD2
CG31163	CG31163	-2.0	-2.1	0.1	-	SH3/SH2 adaptor activity	SASH3 SASH1 SAMD5
CG31169	CG31169	0.0	0.0	-2.4	glycerol-3-phosphate metabolic process	glycerol-3-phosphate dehydrogenase (NAD	GPD1 GPD1L
CG31209	CG34139	2.7	-1.1	0.1	-	carboxylesterase activity	-
CG31217	CG31217	0.6	0.1	0.0	proteolysis	serine-type endopeptidase activity	VLDLR LRP2 LRP1B
CG31272	CG31272	-0.4	-0.7	0.0	transport	transporter activity	SV2B SV2C SV2A
CG31285	CG42250	0.0	0.0	-3.1	neurotransmitter secretion	-	CLINT1 EPN2 EPN3
CG31288	CG31288	0.0	0.0	2.2	-	-	-
CG31303	CG42542	-0.6	0.0	-0.7	-	-	-
CG31347	CG31347	-2.2	0.8	0.1	-	-	-
CG31355	CG31355	0.0	-1.2	-3.2	-	-	-
CG31418	CG31418	0.1	0.0	2.9	-	-	-
CG31446	CG31446	0.6	-1.2	-2.7	-	binding	-

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG31459	CG31459	0.0	0.0	3.0	-	-	-
CG31469	CG31469	0.0	-0.7	0.0	protein amino acid dephosphorylation	protein tyrosine phosphatase activity	ACP1
CG31475	CG31475	0.0	-0.5	2.8	-	calcium ion binding	SDF4* CALU RCN2
CG31533	CG31533	0.0	-2.4	0.0	-	-	-
CG31555	CG31555	0.7	-0.4	-0.1	-	-	-
CG31606	CG31606	0.2	-1.7	0.0	-	-	-
CG31661	CG31661	-2.0	0.0	0.7	proteolysis	aspartic-type endopeptidase activity	PGA3 PGA5 CTSD
CG3168	CG3168	0.0	-0.6	-1.4	DNA topological change	transporter activity	SV2C SV2B SV2A
CG31681	CG31681	-1.7	0.0	0.0	proteolysis	serine-type endopeptidase activity	TMPRSS4 TMPRSS9 serase-1B
CG31688	CG31688	0.0	0.0	-1.8	-	-	-
CG31703	CG31703	0.1	0.7	-2.1	transcription initiation	DNA binding	RTF1
CG3173	CG3173	0.0	0.0	-1.8	-	binding	INTS1 DKFZP586J0619 INT1
CG31769	CG31769	-1.0	0.0	-2.0	-	-	-
CG31772	CG31772	0.0	-2.0	0.0	-	protein binding	-
CG31792	CG31792	0.1	0.1	-2.7	transport	ATPase activity, coupled to transmembrane	ABCC4* ABCC3* ABCC1* ABCC2
CG31801	CG31801	-1.6	-0.1	1.4	-	-	-
CG31820	CG31820	0.0	-1.5	0.0	-	-	-
CG31859	CG31859	-1.6	0.0	-0.5	-	-	-
CG31860	CG31860	0.0	0.1	1.9	zinc ion transport	zinc ion transmembrane transporter activity	SLC30A2 SLC30A3 SLC30A8
CG31867	CG31867	0.0	-0.2	1.4	-	-	-
CG31871	CG31871	0.4	0.0	1.3	lipid metabolic process	triacylglycerol lipase activity	LIPA LIPM LIPK
CG31918	CG31918	0.2	0.7	0.1	proteolysis	metalloendopeptidase activity	-
CG31988	CG31988	0.0	0.0	2.3	-	zinc ion binding	TGFB1I1 PXN LPXN
CG31989	CG31989	0.0	-1.1	-1.1	chromosome organization	binding	-
CG31992	CG31992	0.0	0.0	-1.0	nuclear-transcribed mRNA catabolic process, nor	nucleic acid binding	-
CG31997	CG31997	-1.3	0.0	0.0	-	-	-
CG32021	CG32021	-0.7	0.0	-0.7	-	-	-
CG32023	CG32023	-0.6	0.0	3.9	-	-	-
CG32046	CG42268	0.7	-1.3	-0.1	-	-	-
CG32048	CG32048	-0.5	-0.9	-0.4	-	-	NOS1AP
CG32052	CG32052	0.0	-3.1	0.0	-	sphingomyelin phosphodiesterase activity	SMPDL3B* SMPDL3A SMPD1
CG32066	CG32066	0.0	0.0	-0.9	-	-	FAM49B FAM49A BM009
CG32107	CG32107	-0.9	0.0	-0.1	-	-	-
CG32110	CG32110	-0.8	-1.2	0.0	proteolysis	peptidase activity	SENP1 SENP3 SENP5
CG32117	CG32117	0.0	0.0	-2.3	-	-	-
CG32143	CG42280	0.0	0.0	-2.1	proteolysis	dipeptidyl-peptidase activity	FAP* DPP4 DPP10
CG3216	CG3216	0.0	0.0	-2.6	G-protein coupled receptor protein signaling pat	guanylate cyclase activity	NPR2* NPR1 GUCY2F
CG32185	CG32185	0.0	-0.7	0.0	-	-	-
CG32187	CG32187	-0.5	0.0	-2.2	-	-	-
CG32203	CG32203	0.0	-2.4	0.0	-	serine-type endopeptidase inhibitor activity	SERPINB1 SERPINB9 SERPINI1
CG32204	CG32204	-1.4	0.0	0.1	-	-	-
CG32219	CG32219	0.0	2.9	0.0	-	-	-
CG32226	CG32226	0.0	0.1	-2.2	-	sugar binding	TECPR1*
CG32232	CG32232	0.3	0.0	1.8	microtubule cytoskeleton organization	-	-
CG32263	CG32263	0.0	2.4	0.3	-	-	MPV17L2
CG32284	CG32284	-0.4	0.0	-0.1	chitin metabolic process	chitin binding	-
CG32306	CG32306	-0.1	-0.1	-1.6	-	-	-
CG32319	CG32319	0.0	-0.1	-2.1	protein amino acid acetylation	N-acetyltransferase activity	NAT12
CG32374	CG32374	2.5	0.2	1.0	proteolysis	serine-type endopeptidase activity	TMPRSS2 PRSS1 KLK7
CG32387	CG42256	0.0	-0.1	-3.1	homophilic cell adhesion	-	DSCAM* DSCAML1* HMCN1
CG32431	CG32431	0.0	2.4	0.0	-	-	-
CG32437	CG32437	-1.2	0.0	-0.1	-	-	-
CG32463	CG32463	0.0	2.2	0.0	-	endodeoxyribonuclease activity	ENDOG ENDOGL1
CG32506	CG32506	-2.1	-2.1	-1.7	regulation of Rab GTPase activity	Rab GTPase activator activity	SGSM1* SGSM2 TBC1D15
CG3251	CG3251	0.0	-0.1	2.3	-	-	ALG13 OTUD4 HIN1L
CG32533	CG32533	0.0	0.0	-2.0	nuclear mRNA splicing, via spliceosome	helicase activity	DHX8 DHX33 DHX16
CG32542	CG34401	0.0	0.0	-1.8	-	zinc ion binding	KIAA0913* ZSWIM4 ZSWIM6
CG32544	CG32544	0.0	0.0	-2.1	-	-	-
CG32564	CG32564	1.1	0.1	0.2	-	-	-
CG32570	CG32570	0.0	-1.6	0.0	-	-	-
CG3259	CG3259	-2.2	0.0	-1.9	cilium biogenesis	-	TRAF3IP1*
CG32603	CG32603	-0.1	2.5	0.1	-	-	-
CG32613	CG32613	-0.6	0.0	0.0	-	-	-
CG32647	CG32647	0.7	-0.1	0.0	methylation	methyltransferase activity	-
CG32651	CG32651	0.0	0.0	-2.2	-	-	-
CG32663	CG32663	0.0	0.0	-2.1	-	-	BCAS3* MAAB2
CG32670	CG32670	1.9	0.5	0.0	small GTPase mediated signal transduction	GTPase activity	RAB1A RAB1B RAB8B
CG32675	CG32675	0.0	0.0	-1.7	Golgi organization	-	TMEM49
CG3270	CG3270	-2.0	0.9	0.3	-	oxidoreductase activity	FOXRED1*
CG32702	CG32702	0.0	0.0	-2.1	-	calcium ion binding	CUBN TLL1 BMP1
CG32705	CG34450	0.0	0.0	-1.6	-	-	-
CG32792	CG32792	0.0	-2.0	0.3	sodium ion transport	sodium channel activity	-
CG32816	CG32816	2.5	0.0	0.1	-	-	-
CG32833	CG32833	-0.1	0.0	1.5	proteolysis	serine-type endopeptidase activity	KLK5 KLK8 KLKB1
CG32834	CG32834	0.0	2.5	0.0	proteolysis	serine-type peptidase activity	KLK6 PRSS1 PRSS3
CG32835	CG32835	0.0	1.6	0.7	-	-	-
CG32850	CG32850	-0.8	0.0	0.0	-	protein binding	RNF11
CG32972	CG32972	0.0	-1.9	0.0	-	-	TGFBI
CG32973	CG32973	1.1	0.0	0.1	-	-	-
CG32982	CG32982	0.0	1.8	-0.7	-	-	-
CG33087	CG33087	0.0	0.0	-2.3	-	low-density lipoprotein receptor activity	LRP1 LRP1B LRP2
CG33099	CG33099	0.0	0.2	1.1	-	gibberellin 20-oxidase activity	-
CG33137	CG33137	0.0	0.0	-1.7	-	-	-
CG33143	CG33143	0.2	1.3	0.0	-	-	-
CG33144	CG33144	-0.2	0.1	-3.1	-	protein binding	RNF144A RNF144B RNF14
CG33171	CG42543	0.0	0.0	-2.9	cell adhesion	binding	COL15A1 COL18A1
CG33203	CG33203	0.3	0.7	2.6	-	-	PAQR4* ADIPOR1 ADIPOR2
CG33217	CG33217	0.0	0.0	0.8	-	-	-
CG33218	CG33218	0.0	-0.9	0.0	-	-	-
CG33249	CG42271	0.0	0.0	-2.2	phosphoinositide dephosphorylation	phosphatidylinositol-3,4-bisphosphate 4-ph	-
CG33253	CG33253	0.0	2.3	0.0	phagocytosis, engulfment	-	STOM STOML3 NPHS2
CG33268	CG33268	-1.5	0.1	-2.1	-	-	-
CG33281	CG33281	-0.1	2.4	0.0	monosaccharide transport	monosaccharide transmembrane transporte	SLC2A8 SLC2A6 SLC2A2
CG33300	CG33300	0.0	-1.0	-0.4	-	-	-
CG33309	CG33309	0.0	0.0	2.2	-	-	-
CG33324	CG33324	0.0	0.4	-2.2	-	-	-
CG33337	CG33337	1.9	0.1	0.0	-	acyltransferase activity	-
CG3339	CG3339	0.2	0.2	2.3	microtubule-based movement	motor activity	DNAH9* DNAH17* DNAH10*
CG3345	CG3345	0.0	0.0	-2.4	-	-	-
CG33459	CG33459	0.5	1.8	3.4	proteolysis	serine-type endopeptidase activity	ESSPL CTRL F2
CG33470	CG33470	-1.3	-2.1	0.0	-	-	-
CG33474	CG33474	-0.9	0.0	0.0	peroxisome fission	-	-
CG33493	CG33493	0.0	0.5	-2.6	-	-	-
CG33528	CG33528	0.0	-0.5	2.4	dopamine transport	monoamine transmembrane transporter ac	SLC18A2 SLC18A1 SLC18A3
CG33557	CG33557	-2.6	0.2	-1.4	regulation of transcription	transcription factor activity	TCF15 SCXA
CG33631	CG33631	1.8	-1.9	1.2	-	-	-
CG33639	CG33639	1.6	0.0	0.0	G-protein coupled receptor protein signaling pat	neuropeptide receptor activity	-
CG3367	CG42340	-1.0	0.0	0.1	potassium ion transport	potassium channel activity	KCNK10
CG3368	CG3368	0.0	0.0	-1.2	-	binding	-
CG33690	CG33690	0.0	-0.9	0.0	-	-	-
CG33703	CG33703	0.0	0.0	-2.7	-	-	-
CG33966	CG33966	0.0	0.9	-2.2	-	vitamin E binding	TTPAL TTPA RLBP1L2
CG33967	CG33967	0.0	0.0	-2.3	-	protein binding	WWC1* WWC2 WWC3
CG33970	CG33970	0.0	-0.9	-0.1	transport	ATPase activity, coupled to transmembrane	ABCA3 ABCA5 ABCA12
CG33978	CG33978	0.0	-2.2	-0.1	-	-	-
CG33980	CG33980	0.0	0.0	1.7	regulation of transcription, DNA-dependent	sequence-specific DNA binding	VSX2 VSX1 ALX4

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG34006	CG34006	-2.6	-1.4	-0.3	-	-	-
CG34007	CG34007	0.0	-1.5	2.8	-	-	-
CG34010	CG34010	0.4	-0.1	0.2	-	-	-
CG34012	CG34012	-2.0	0.0	0.0	-	-	-
CG34017	CG34017	0.0	0.6	0.1	-	-	-
CG34051	CG34051	-0.1	0.2	2.0	-	-	-
CG3409	CG3409	0.0	-0.6	0.0	-	monocarboxylic acid transmembrane trans	SLC16A14 SLC16A9 SLC16A12
CG3523	CG3523	0.0	0.2	-1.5	oxidation reduction	fatty-acid synthase activity	FASN TP53I3 CRYZ
CG3573	CG3573	0.0	0.0	-1.7	dephosphorylation	inositol-polyphosphate 5-phosphatase activ	INPP5B* OCRL SYNJ1
CG3585	CG3585	0.0	-0.2	-2.7	open tracheal system development	GTP binding	DMXL2 DMXL1
CG3744	CG3744	0.0	0.0	-1.5	proteolysis	dipeptidyl-peptidase activity	DPP9* DPP8 DPP4
CG3754	CG42276	0.0	0.0	-2.5	microtubule-based process	3',5'-cyclic-GMP phosphodiesterase activity	PDE9A* PDE4D PDE4C
CG3764	CG3764	0.0	-0.3	-2.2	-	-	FNIP2* FNIP1
CG3770	CG3770	-0.2	-0.1	-1.1	establishment or maintenance of cell polarity	-	-
CG3805	CG34126	-0.3	-0.2	-1.5	-	nucleotide binding	UHRF1BP1L* UHRF1BP1 DKFZp686F10110
CG3810	CG3810	0.0	-0.1	-2.2	ER-associated protein catabolic process	mannosyl-oligosaccharide 1,2-alpha-mann	EDEM2* EDEM1 EDEM3
CG3829	CG3829	0.7	1.4	0.1	defense response	scavenger receptor activity	SCARB1 SCARB2 CD36
CG3842	CG3842	-0.2	0.0	2.8	metabolic process	oxidoreductase activity, acting on CH-OH g	RDH12 RDH14 RDH11
CG3875	CG3875	0.1	0.0	-2.9	ubiquinone biosynthetic process	RNA binding	KHDRBS3 KHDRBS2 KHDRBS1
CG3884	CG3884	0.1	1.1	3.9	-	-	-
CG3994	CG3994	2.8	1.6	0.0	response to zinc ion	metal ion transmembrane transporter activ	SLC30A3 SLC30A2 SLC30A8
CG40050	CG40050	0.0	-1.0	0.0	metamorphosis	2 iron, 2 sulfur cluster binding	-
CG40067	CG41520	-0.1	-1.0	0.0	signal transduction	receptor binding	ANGPT4 ANGPT2 FGL1
CG40169	CG40169	0.0	-1.7	0.0	-	-	-
CG40172	CG40172	0.0	0.0	2.5	-	-	-
CG40176	CG40176	0.0	2.3	0.0	-	-	-
CG40204	CG40204	2.5	0.0	0.0	signal transduction	-	-
CG40290	CG40290	-0.8	0.0	0.0	-	-	-
CG40339	CG40339	1.3	-0.3	0.0	-	-	-
CG40380	CG40380	0.1	0.5	0.0	-	heat shock protein binding	-
CG40484	CG40484	0.0	0.0	2.3	-	-	-
CG40498	CG40498	-1.2	-0.1	0.0	-	-	-
CG4066	CG4066	1.8	0.0	-3.7	-	-	-
CG4080	CG4080	0.7	1.1	0.0	-	protein binding	MARCH8 MARCH2 MARCH1
CG4096	CG4096	0.0	0.0	-2.7	proteolysis	metalloendopeptidase activity	ADAMTS12* ADAMTS7 ADAMTS6
CG4199	CG4199	0.0	0.0	-1.0	oxidation reduction	2 iron, 2 sulfur cluster binding	AIFM3*
CG4301	CG4301	0.0	0.0	-1.9	phospholipid transport	calcium-transporting ATPase activity	ATP10D ATP10A ATP11B
CG4318	CG4318	0.0	-0.5	2.3	-	zinc ion binding	ZNF600 ZNF658B ZNF708
CG4372	CG4372	0.0	-0.8	2.7	-	N4-(beta-N-acetylglucosaminyl)-L-asparagi	AGA ASRGL1
CG4389	CG4389	0.0	0.3	-0.5	fatty acid beta-oxidation	long-chain-3-hydroxyacyl-CoA dehydrogen	HADHA EHHADH HADH
CG4538	CG4538	0.0	0.0	-1.3	ATP-dependent proteolysis	serine-type endopeptidase activity	CLPX
CG4562	CG4562	0.0	-0.7	-2.6	transport	ATPase activity, coupled to transmembrane	ABCC4* ABCC1 ABCC3
CG4631	CG4631	0.0	0.2	-2.1	-	-	-
CG4660	CG4660	0.0	-2.6	-0.4	-	-	C8orf55
CG4751	CG4751	0.0	0.0	-1.3	-	-	MPND MYSM1
CG4781	CG4781	0.0	-2.4	0.0	-	protein binding	CHADL LRRC4 LRRN2
CG4793	CG4793	0.7	1.6	3.7	carbohydrate metabolic process	serine-type endopeptidase activity	TMPRSS13 KLKB1 CTRB2
CG4797	CG4797	0.0	0.0	-2.8	transport	glucose transmembrane transporter activit	SLC2A6 SLC2A8 SLC2A7
CG4804	CG4804	1.1	2.0	1.8	-	serine-type endopeptidase inhibitor activity	PAI-2 SERPINI1 SERPINB8
CG4814	CG34391	0.4	-0.5	-1.7	-	-	HNT NTM OPCML
CG4822	CG4822	0.9	1.3	0.5	-	ATPase activity, coupled to transmembrane	ABCG4 ABCG1 ABCG2
CG4827	CG4827	0.0	-1.3	-0.8	nucleotide catabolic process	5'-nucleotidase activity	NT5E
CG4842	CG4842	0.0	-0.8	0.0	metabolic process	alcohol dehydrogenase activity	HPGD CBR4 DHRS11
CG4983	CG4983	-3.1	-0.1	0.0	-	-	-
CG5011	CG5011	0.0	-0.3	2.1	-	-	-
CG5022	CG5022	0.0	-2.3	0.0	-	cytoskeletal protein binding	FRMD5 FRMD3 EPB41
CG5030	CG34139	2.2	-0.4	0.0	-	carboxylesterase activity	-
CG5065	CG5065	1.5	-1.6	0.0	metabolic process	catalytic activity	FAR1 FAR2
CG5115	CG5115	0.0	-1.4	0.5	-	-	-
CG5191	CG5191	0.0	0.0	-2.3	-	glutaminyl-tRNA synthase (glutamine-hydr	FAAH2
CG5197	CG34458	0.0	-1.4	0.0	-	-	serase-1B TMPRSS9 TMPRSS11E
CG5205	CG5205	0.0	0.0	-1.2	nuclear mRNA splicing, via spliceosome	helicase activity	SNRNP200* ASCC3 HFM1
CG5246	CG5246	0.3	1.2	1.2	proteolysis	serine-type endopeptidase activity	-
CG5270	CG5270	0.0	0.0	-2.3	-	zinc ion binding	ZFYVE26*
CG5388	CG5388	0.0	0.0	-3.1	-	-	-
CG5392	CG5392	0.1	0.5	0.2	-	serine-type endopeptidase inhibitor activity	RECK
CG5418	CG5418	0.0	-2.9	-0.5	-	-	-
CG5431	CG5431	-1.0	0.0	0.0	-	tyrosine-ester sulfotransferase activity	SULT1A3 ST1A5 SULT1C3
CG5480	CG5480	1.9	0.0	0.0	-	-	-
CG5508	CG5508	0.0	0.0	-1.1	phospholipid biosynthetic process	glycerol-3-phosphate O-acyltransferase act	GPAM RP11-426E5.2 GNPAT
CG5550	CG5550	-1.7	2.4	0.0	signal transduction	receptor binding	TNC TNR ANGPTL6
CG5561	CG5561	0.0	-1.6	0.0	methylation	methyltransferase activity	HDHD1A
CG5566	CG34353	0.0	0.0	2.4	-	-	NEGR1 NTM DKFZp686H1949
CG5577	CG5577	0.7	0.0	0.0	metabolic process	4-nitrophenylphosphatase activity	PGP PDXP HDHD2
CG5591	CG5591	0.0	0.0	-2.1	phagocytosis, engulfment	transcription regulator activity	MLL2 MLL3
CG5794	CG5794	0.0	0.0	-2.3	ubiquitin-dependent protein catabolic process	ubiquitin thiolesterase activity	USP34* USP24 USP9Y
CG5850	CG5850	0.0	0.0	-0.9	-	-	TMEM184C TMEM184A TMEM184B
CG5866	CG5866	2.2	0.0	1.3	-	-	-
CG5928	CG5928	0.0	-1.0	-2.2	-	-	-
CG5932	CG5932	1.0	-0.1	0.0	lipid metabolic process	triacylglycerol lipase activity	LIPA LIPN LIPM
CG5945	CG5945	1.0	0.0	0.0	-	-	-
CG5953	CG5953	0.0	0.2	-1.1	-	-	-
CG6006	CG6006	-0.6	-1.2	0.0	transport	carnitine transporter activity	SLC22A5 OCTN2VT SLC22A13
CG6014	CG6014	0.0	1.0	0.0	-	binding	REG1A
CG6045	CG6045	0.0	0.0	-1.0	-	xanthine dehydrogenase activity	XDH AOX1
CG6083	CG6083	-0.4	-1.3	-2.2	mushroom body development	aldehyde reductase activity	AKR1A1 AKR1B1 AKR1B10
CG6126	CG6126	0.0	-0.1	-0.9	transport	organic cation transmembrane transporter	SLC22A16 SLC22A13 SLC22A8
CG6142	CG6142	0.1	-1.1	-0.4	cellular alcohol metabolic process	FAD binding	CHDH
CG6199	CG6199	0.0	0.0	-0.9	protein metabolic process	procollagen-lysine 5-dioxygenase activity	PLOD3 PLOD2
CG6201	CG6201	-0.9	0.0	0.0	carbohydrate metabolic process	L-iduronidase activity	IDUA
CG6214	CG6214	0.0	0.0	-1.0	transport	ATPase activity, coupled to transmembrane	ABCC1* ABCC3* ABCC4* ABCC12*
CG6225	CG6225	-1.2	-0.1	0.0	cellular process	aminopeptidase activity	XPNPEP2 XPNPEP1
CG6231	CG6231	0.7	0.4	0.0	-	secondary active organic cation transmem	SLC22A13 SLC22A3 SLC22A5
CG6232	CG6232	0.0	-0.2	-2.6	-	metalloendopeptidase activity	ADAMTS18 PAPLN ADAMTS16
CG6262	CG6262	0.0	-2.0	1.1	trehalose metabolic process	trehalase activity	TREH
CG6294	CG6294	0.0	-0.7	-1.5	proteolysis	metallopeptidase activity	-
CG6299	CG6299	0.0	0.0	-1.0	glycolipid transport	glycolipid transporter activity	GLTP PLEKHA8 PLEKHA9
CG6327	CG6327	0.6	1.4	1.1	-	-	SLC36A4 SLC36A2 SLC36A1
CG6330	CG6330	0.0	0.0	-0.9	nucleoside metabolic process	uridine phosphorylase activity	UPP2 UPP1
CG6340	CG6340	-0.1	0.0	-1.0	-	-	RSRC2* FLJ11021
CG6357	CG6357	0.0	0.2	2.7	-	cysteine-type endopeptidase activity	-
CG6406	CG6406	0.0	0.0	-1.2	-	-	FAM126A* FAM126B MGC39518
CG6414	CG6414	-1.0	0.0	0.2	-	carboxylesterase activity	ACHE CES7 CES8
CG6420	CG6420	0.0	0.0	-2.2	-	-	WDR20* DMWD
CG6461	CG6461	0.0	-0.8	0.0	-	gamma-glutamyltransferase activity	GGT1* GGT3P GGT2
CG6498	CG6498	0.0	-0.2	-1.8	protein amino acid phosphorylation	protein serine/threonine kinase activity	MAST2 MAST1 MAST3
CG6511	CG6511	-0.7	0.0	-0.6	-	-	EDRF1*
CG6512	CG6512	0.0	0.0	-1.1	ATP-dependent proteolysis	ATPase activity	AFG3L2 SPG7 YME1L1
CG6525	CG6525	0.0	0.0	-2.5	regulation of transcription	transcription factor activity	PHF3* DIDO1 SPOCD1
CG6659	CG6659	0.0	0.0	-1.7	-	-	DPY19L2 DPY19L1 DPY19L3
CG6687	CG6687	0.6	0.0	0.0	ATP synthesis coupled proton transport	serine-type endopeptidase inhibitor activity	SERPINB9 SERPINC1 SERPINB8
CG6695	CG6695	0.0	0.0	-1.6	-	mRNA binding	SFRS16*
CG6718	CG6718	0.0	0.0	-0.9	lipid metabolic process	calcium-independent phospholipase A2 acti	PLA2G6 PNPLA8 DAPK1
CG6752	CG6752	-0.9	0.0	0.0	-	protein binding	RNF123*
CG6763	CG6763	-0.1	-2.0	-0.7	proteolysis	metalloendopeptidase activity	MEP1B ASTL BMP1
CG6791	CG6791	0.0	0.0	-2.9	-	zinc ion binding	-

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
CG6834	CG6834	-0.1	-0.7	0.0	-	protein binding	-
CG6885	CG6885	0.0	-1.4	0.0	-	-	-
CG6933	CG6933	0.0	0.0	-2.0	chitin metabolic process	structural constituent of peritrophic membr	-
CG6954	CG6954	-0.2	0.0	-2.3	signal transduction	-	-
CG7017	CG7017	0.7	0.0	0.1	chitin metabolic process	structural constituent of peritrophic membr	-
CG7029	CG7029	0.0	-0.1	-2.5	-	-	-
CG7072	CG34461	0.0	1.7	2.0	-	structural constituent of chitin-based cuticle	-
CG7134	CG7134	0.0	0.0	-2.5	protein amino acid dephosphorylation	protein tyrosine/serine/threonine phosphata	CDC14A* CDC14B CDC14C
CG7142	CG7142	-2.1	0.0	0.0	proteolysis	serine-type endopeptidase activity	ACR PRSS8 TMPRSS9
CG7158	CG7158	0.0	0.0	-1.6	-	-	ALS2* ALS2CL FLJ00189
CG7207	CG7207	0.0	-0.1	-1.1	-	protein serine/threonine kinase activity	COL4A3BP* OSBP OSBP2
CG7235	CG7235	0.0	-3.2	0.0	open tracheal system development	ATPase activity, coupled	HSPD1
CG7280	CG7280	0.0	0.0	-1.6	protein catabolic process	sulfite oxidase activity	SUOX
CG7282	CG34422	0.0	0.0	-1.8	phagocytosis, engulfment	ATP binding	ARID4B* ARID4A ARID5B
CG7306	CG7306	0.9	0.0	0.0	chitin metabolic process	structural constituent of peritrophic membr	-
CG7358	CG7358	0.0	0.0	-2.0	-	-	-
CG7414	CG7414	0.0	0.1	-1.1	regulation of translation	tRNA binding	EIF2A* EIF3B
CG7497	CG7497	0.0	0.0	-1.9	protein amino acid phosphorylation	protein serine/threonine kinase activity	-
CG7518	CG7518	0.0	0.0	-1.6	-	DNA binding	C4orf8*
CG7532	CG7532	0.0	-1.1	0.0	-	serine-type endopeptidase activity	FRRS1
CG7543	CG7543	0.1	0.8	0.4	-	-	-
CG7556	CG7556	0.0	0.0	-1.7	protein folding	unfolded protein binding	DNAJC1 DNAJC2 DNAJC10
CG7600	CG7600	0.0	0.0	-1.3	-	oxygen binding	FAM91A1 FAM91A2
CG7611	CG7611	0.0	0.0	-0.9	-	-	WDR26* WDR5 WDR5B
CG7637	CG7637	0.0	0.0	0.5	-	-	NOP10
CG7669	CG7669	1.9	0.0	0.0	-	-	-
CG7724	CG7724	0.0	-0.8	0.0	steroid biosynthetic process	oxidoreductase activity, acting on CH-OH gr	HSD3B2* HSD3B1 HSD3B7
CG7766	CG7766	0.0	0.0	-1.6	glycogen metabolic process	phosphorylase kinase regulator activity	PHKA1* PHKA2 PHKB
CG7816	CG7816	-0.1	-0.6	-0.8	metal ion transport	metal ion transmembrane transporter activ	SLC39A13* SLC39A7 SLC39A14
CG7852	CG7852	0.0	0.0	-1.9	-	-	DENND5B* DENND5A SBF2
CG7906	CG7906	0.0	0.0	1.9	-	-	-
CG7971	CG7971	0.0	0.0	-1.0	RNA splicing	-	SRRM2*
CG8029	CG8029	0.0	0.0	-1.0	ATP synthesis coupled proton transport	hydrogen:potassium-exchanging ATPase ac	-
CG8108	CG8108	0.0	0.0	-1.1	-	zinc ion binding	-
CG8134	CG8134	0.0	-0.1	-1.1	-	-	-
CG8184	CG8184	-0.1	0.0	-2.4	protein modification process	ubiquitin-protein ligase activity	HUWE1* ITCH WWP1
CG8192	CG8192	0.1	-2.4	0.0	chitin metabolic process	chitin binding	-
CG8271	CG8271	-0.1	-0.3	-2.1	-	secondary active monocarboxylate transme	SLC16A12 SLC16A14 SLC16A7
CG8277	CG8277	-1.8	0.0	0.0	autophagic cell death	RNA cap binding	EIF4E1B EIF4E EIF4E2
CG8291	CG8291	0.0	0.0	-1.5	neurotransmitter transport	neurotransmitter transporter activity	SLC6A1 SLC6A12 SLC6A7
CG8399	CG8399	0.0	0.0	-1.6	histidine catabolic process	dopamine beta-monooxygenase activity	FRRS1*
CG8405	CG8405	0.0	0.0	-2.3	wing disc dorsal/ventral pattern formation	-	C19orf6*
CG8441	CG8441	0.0	0.1	0.8	-	-	PRKRIP1
CG8444	CG8444	0.0	0.1	-0.5	-	receptor activity	ATP6AP2
CG8446	CG8446	0.0	0.0	-0.9	protein modification process	lipoyltransferase activity	LIPT1
CG8468	CG8468	0.0	0.0	-0.9	-	secondary active monocarboxylate transme	SLC16A14 SLC16A12 SLC16A6
CG8516	CG8516	0.0	0.0	-2.4	-	-	-
CG8539	CG8539	0.6	-3.1	0.4	proteolysis	metallocarboxypeptidase activity	CPA2 CPA4 CPO
CG8679	CG8679	0.0	0.0	-2.0	-	-	LEM3 ANKLE1
CG8693	CG8693	0.0	0.0	1.4	carbohydrate metabolic process	alpha-glucosidase activity	SLC3A1 SLC3A2
CG8768	CG8768	-0.1	-0.6	-0.3	cellular metabolic process	coenzyme binding	SDR39U1*
CG8773	CG8773	1.0	2.5	0.0	proteolysis	aminopeptidase activity	ENPEP ANPEP ERAP1
CG8776	CG8776	0.0	1.0	0.1	-	carbon-monoxide oxygenase activity	CYBRD1 CYBASC3 CYB561
CG8785	CG8785	0.5	0.0	0.0	amino acid transport	amino acid transmembrane transporter acti	SLC36A4 SLC36A1 SLC36A2
CG8816	CG8816	0.0	0.1	0.7	protein amino acid phosphorylation	adenylate kinase activity	AK6 TAF9
CG8829	CG34393	0.6	2.1	0.0	regulation of small GTPase mediated signal trans	guanyl-nucleotide exchange factor activity	RASGEF1B RASGEF1A RASGEF1C
CG8863	CG8863	0.0	0.3	-0.5	protein folding	unfolded protein binding	DKFZp686G2074 DNAJA4 DNAJA1
CG8915	CG8915	0.0	0.1	-1.3	-	helicase activity	DHX36 YTHDC2 DHX29
CG8932	CG42235	-0.1	0.0	-1.9	vitamin transport	sodium-dependent multivitamin transmemb	SLC5A8 SLC5A12 SLC5A6
CG8963	CG8963	0.0	0.0	-1.0	olfactory behavior	protein binding	PAIP1*
CG8965	CG8965	0.0	-0.1	-1.4	signal transduction	-	-
CG9005	CG9005	0.0	0.0	-2.2	-	-	-
CG9030	CG9030	0.0	1.0	0.4	amino acid metabolic process	pyridoxal phosphate binding	-
CG9056	CG9056	0.0	-0.1	-2.5	-	-	-
CG9063	CG9063	0.0	0.0	-1.9	-	-	KIAA1432*
CG9164	CG9164	0.2	1.3	0.0	-	-	WSCD2* WSCD1
CG9171	CG9171	0.5	0.6	0.0	-	N-acetyllactosaminide beta-1,6-N-acetylglu	B3GNT1
CG9236	CG9236	0.0	2.7	0.0	-	calcium-dependent protein serine/threonine	CIB3 CIB2 CIB1
CG9270	CG9270	2.0	0.0	0.0	transport	ATPase activity, coupled to transmembrane	ABCC4* ABCC1* ABCC3*
CG9281	CG9281	0.0	0.0	-0.9	-	ATPase activity, coupled to transmembrane	ABCF2 ABCF3 ABCF1
CG9290	CG9290	-2.4	1.2	0.1	-	structural constituent of adult chitin-based	-
CG9312	CG9312	-0.3	-0.1	2.4	-	-	-
CG9317	CG9317	-0.1	-0.7	-2.2	-	secondary active organic cation transmemb	SLC22A3 SLC22A5 SLC22A4
CG9380	CG9380	0.1	1.9	0.2	-	-	-
CG9411	CG9411	0.0	0.1	-2.5	-	-	-
CG9425	CG9425	0.0	0.0	-1.7	tRNA aminoacylation for protein translation	ATP binding	HELZ PRIC285 MOV10L1
CG9430	CG9430	-0.9	0.0	0.0	metal ion transport	metal ion transmembrane transporter activ	SLC39A1 SLC39A3 SLC39A2
CG9444	CG9444	0.0	-0.1	-2.4	oligopeptide transport	proton-dependent oligopeptide secondary a	SLC15A1 SLC15A2 hPEPT1-RF
CG9485	CG9485	-0.1	0.0	-2.2	glycogen biosynthetic process	4-alpha-glucanotransferase activity	AGL*
CG9536	CG9536	0.0	0.0	-0.9	-	-	TMEM115
CG9573	CG9573	-0.7	-0.4	0.0	-	-	RQCD1
CG9616	CG9616	0.0	0.0	2.0	-	-	-
CG9649	CG9649	0.0	2.4	0.1	proteolysis	endopeptidase activity	PRSS7 TMPRSS9 ESSPL
CG9650	CG9650	-0.1	1.6	1.0	-	zinc ion binding	BCL11A BCL11B ZNF296
CG9673	CG9673	-1.7	0.0	0.0	proteolysis	serine-type endopeptidase activity	TMPRSS4 TPSAB1 CELA2A
CG9674	CG9674	0.0	0.0	-1.8	glutamate biosynthetic process	glutamate synthase (NADPH) activity	DPYD
CG9676	CG9676	0.6	0.0	0.2	proteolysis	serine-type endopeptidase activity	TMPRSS6 TMPRSS11D KLKB1
CG9782	CG9782	-1.0	0.0	0.2	-	-	-
CG9813	CG9813	0.0	-1.2	0.0	ATP synthesis coupled proton transport	hydrolase activity, acting on acid anhydride	-
CG9867	CG9867	0.0	0.0	-1.8	-	transferase activity, transferring glycosyl gr	AER61*
CG9941	CG9941	0.0	-0.3	-2.4	-	protein binding	RNF157* MGRN1
CG9977	CG9977	0.0	0.0	-2.0	one-carbon compound metabolic process	adenosylhomocysteinase activity	AHCYL1* AHCYL2 AHCY
CG9989	CG9989	0.3	0.3	2.9	-	endonuclease activity	-
Chc	CG9012	0.0	0.0	-0.9	sperm individualization	protein binding	CLTC* CLTCL1*
Chd1	CG3733	0.0	0.0	-1.6	fertilization, exchange of chromosomal proteins	chromatin binding	CHD2* CHD1 CHD4
Cht2	CG2054	0.0	0.0	-0.9	cuticle chitin catabolic process	chitinase activity	CHIA CHIT1 CHI3L1
ci	CG2125	-0.1	0.0	2.0	smoothened signaling pathway	transcription factor activity	GLI2* GLI3 GLI1
Cka	CG7392	0.0	0.0	-1.5	JNK cascade	protein binding	STRN3* STRN4 STRN
comm2	CG7554	-0.4	-0.8	0.0	-	-	-
Cpr	CG11567	0.0	0.0	-1.2	-	NADPH-hemoprotein reductase activity	POR DKFZp686G04235 NDOR1
Crag	CG12737	0.0	0.0	-1.7	-	calmodulin binding	DENND4A DENND4B DENND4C
CSN1a	CG4697	1.2	-1.5	-2.6	regulation of G-protein coupled receptor protein	regulator of G-protein signaling activity	GPS1
CtBP	CG7583	0.0	0.0	-1.0	embryonic development via the syncytial blastoc	protein binding	CTBP2* CTBP1 PHGDH
Cyp12c1	CG4120	0.0	1.5	-0.4	-	electron carrier activity	CYP24A1 CYP27C1 CYP11A1
Cyp311a1	CG1488	0.0	0.0	-2.5	-	electron carrier activity	CYP4V2 CYP4A11 CYP4A22
Cyp4ac1	CG14032	-2.0	0.0	1.2	hormone metabolic process	electron carrier activity	CYP4V2 CYP4F8 CYP4F12
Cyp4e1	CG2062	-1.3	-2.0	-2.4	-	electron carrier activity	CYP4V2 CYP4F11 CYP4F2
Cyp4p3	CG10843	0.0	0.6	1.3	-	electron carrier activity	CYP4V2 CYP4F3 CYP4F8
Cyp6a18	CG13977	0.0	-2.4	0.0	-	electron carrier activity	CYP3A5 CYP3A4 CYP3A7
Cyp6a21	CG10247	0.1	0.5	0.8	-	electron carrier activity	CYP3A5 CYP3A7 CYP3A4
Cyp6v1	CG1829	0.0	-0.1	-2.0	-	electron carrier activity	CYP3A5 CYP3A7 CYP3A4
Cyp9h1	CG17577	0.0	-1.1	0.1	-	electron carrier activity	CYP3A5 CYP3A4 CYP3A7
d	CG10595	-1.8	0.0	0.0	leg disc development	ATPase activity, coupled	MYO6 MYO1B MYO1A
da	CG5102	0.0	0.1	-1.0	regulation of transcription, DNA-dependent	specific RNA polymerase II transcription fac	TCF4* TCF12 TCF3
DAAM	CG14622	0.0	0.0	-2.7	actin cytoskeleton organization	actin binding	DAAM1* DAAM2 FMNL3
Dab	CG9695	0.0	0.0	-3.0	compound eye photoreceptor development	SH2 domain binding	DAB1* DAB2

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
dalao	CG7055	0.0	0.0	-1.0	positive regulation of transcription, DNA-depend	transcription coactivator activity	-
Dbp80	CG17023	0.0	0.3	0.5	-	ATP-dependent RNA helicase activity	DDX19B* DDX19A TDBP
dco	CG2048	0.0	0.0	-1.1	imaginal disc growth	protein serine/threonine kinase activity	CSNK1E CSNK1D CSNK1A1
Dhc64C	CG7507	0.0	0.0	-1.9	cellularization	ATPase activity, coupled	DNAH6* DNAH2* DNAH1*
dhd	CG4193	0.0	-2.0	0.0	embryonic development	disulfide oxidoreductase activity	TXN TXNDC2 TXN2
dimm	CG8667	-1.3	-0.9	-2.7	regulation of transcription	transcription factor activity	BHLHA15 NEUROD6 NEUROD1
disco	CG9908	0.0	0.0	2.2	positive regulation of transcription from RNA pol	DNA binding	BNC2* BNC1
dl	CG6667	0.4	0.6	0.0	immune response	transcription factor activity	REL RELA RELB
Dl	CG3619	-1.5	0.0	0.4	germ-line stem cell maintenance	Notch binding	DLL1 JAG1 DLL4
Dll	CG3629	0.4	0.0	-2.7	proboscis development	specific RNA polymerase II transcription fac	DLX1 DLX2 DLX6
DnaJ-1	CG10578	-0.8	0.0	-0.1	response to heat	unfolded protein binding	DNAJB4 DNAJB5 DNAJB1
DNApol-delta	CG5949	0.0	0.0	-2.7	lagging strand elongation	DNA-directed DNA polymerase activity	POLD1 REV3L POLA1
Dnr1	CG12489	0.0	-0.3	-2.1	immune response	protein binding	MYLIP*
dom	CG9696	0.0	0.0	-1.7	cell proliferation	helicase activity	SRCAP EP400 INO80
dome	CG14226	0.3	0.8	-0.8	JAK-STAT cascade	transmembrane receptor activity	DSCAML1 SDK2 PTPRQ
dpr17	CG31361	0.0	0.0	-1.5	-	-	-
Dro	CG10816	0.0	-0.7	0.0	defense response to Gram-negative bacterium	-	-
drongo	CG3365	0.2	0.7	0.0	regulation of ARF GTPase activity	ARF GTPase activator activity	AGFG1 AGFG2
Dys	CG34157	0.0	-0.1	-4.0	imaginal disc-derived wing vein morphogenesis	structural molecule activity	DMD* UTRN dystrophin
e	CG3331	-0.6	0.2	-2.0	cuticle pigmentation	beta-alanyl-dopamine synthase activity	AASDH ACSS1 ACSF3
e(y)3	CG12238	0.0	0.2	-2.0	gene silencing	chromatin binding	PHF10* DPF2 MYST3
Eaat2	CG3159	-1.2	0.0	-2.8	taurine transport	glutamate:sodium symporter activity	SLC1A2 SLC1A1 SLC1A7
east	CG4399	0.0	0.0	-2.3	achiasmate meiosis I	metallocarboxypeptidase activity	-
Ect4	CG34373	0.2	0.4	-2.1	signal transduction	binding	SARM1*
eEF1delta	CG4912	0.0	0.4	0.5	translational elongation	translation elongation factor activity	EEF1D EEF1B2
Egfr	CG10079	-1.5	0.0	-1.0	dorsal appendage formation	epidermal growth factor receptor activity	EGFR* ERBB3 ERBB4
eIF-4B	CG10837	0.0	0.0	0.7	translational initiation	translation initiation factor activity	-
eIF-5C	CG2922	0.0	0.4	0.4			BZW1* BZW2 BZW1L1
Eig71Ec	CG7608	-0.7	0.0	2.3	-	-	-
Eig71Ee	CG7604	0.0	-1.2	0.0	puparial adhesion	structural molecule activity	-
Eig71Eh	CG7594	0.0	1.1	-0.1	-	-	-
Eig71Ek	CG7325	1.2	2.0	0.0	-	-	-
Eip75B	CG8127	0.0	-0.2	-3.1	ecdysone-mediated induction of salivary gland c	ligand-dependent nuclear receptor activity	PPARG NR1C3 PPARD
en	CG9015	0.0	0.0	2.1	neuroblast fate determination	specific RNA polymerase II transcription fac	EN2 EN1 HOXC5
eve	CG2328	-1.7	0.9	-0.1	negative regulation of cardioblast cell fate specif	transcription factor activity	EVX1 EVX2 HOXA2
faf	CG1945	-0.1	0.0	-1.9	cellularization	ubiquitin-specific protease activity	USP9X* USP9Y* USP24
fan	CG7919	-0.8	-0.3	0.0	-	structural molecule activity	VAPA VAPB
fat-spondin	CG6953	0.0	0.0	-1.9	-	serine-type endopeptidase inhibitor activity	SPON1 SPON2 SPINT1
fau	CG6544	-0.5	0.0	-1.8	-	-	-
fdl	CG8824	0.0	0.0	-0.9	brain development	beta-N-acetylhexosaminidase activity	HEXB
feo	CG11207	0.0	0.0	-1.3	cytokinesis	-	-
fig	CG7615	-2.8	0.0	0.0	-	phosphoprotein phosphatase activity	PPTC7
form3	CG33556	0.0	0.0	-2.6	branch fusion, open tracheal system	actin binding	FHDC1 INF2 DAAM1
fos28F	CG18103	-1.2	0.0	0.0	-	-	-
fru	CG14307	0.8	0.0	0.0	male courtship behavior, veined wing vibration	transcription factor activity	-
fry	CG32045	0.0	0.8	-1.0	rhabdomere development	transcription activator activity	FRYL* FRY WUGSC:H_2G3A.1
fs(1)M3	CG4790	0.0	0.0	-2.0	vitelline membrane formation in chorion-contain	-	-
fs(1)Ya	CG2707	0.0	0.0	-2.1	nuclear division	protein binding	-
fs(1)Yb	CG2706	0.0	0.0	-1.8	germ-line stem cell division	-	-
fs(2)ltoPP43	CG10528	0.0	0.0	-0.9	chorion-containing eggshell formation	-	-
Fur2	CG18734	0.0	0.0	-1.6	proteolysis	serine-type endopeptidase activity	PCSK6* PCSK5 FURIN
Galpha49B	CG17759	0.0	1.3	-0.1	activation of phospholipase C activity	GTPase activity	GNAQ GNA11 GNA14
Galpha73B	CG12232	1.2	2.6	2.9	G-protein coupled receptor protein signaling pat	GTPase activity	GNAS GNAL GSA
garz	CG8487	0.0	-0.1	-1.5	ER to Golgi vesicle-mediated transport	guanyl-nucleotide exchange factor activity	GBF1
Gbeta13F	CG10545	0.0	0.2	-0.6	actin filament organization	GTPase activity	GNB4 GNB2 GNB1
Gbeta76C	CG8770	-1.7	0.0	0.0	deactivation of rhodopsin mediated signaling	GTPase activity	GNB4 GNB2 GNB3
gce	CG6211	0.0	0.0	-1.7	regulation of transcription	transcription factor activity	ARNTL ARNTL2 NPAS2
Gdh	CG5320	0.0	0.0	-0.6	sperm storage	glutamate dehydrogenase [NAD(P)+] activi	GLUD1 GLUD2
Gef26	CG9491	-0.6	-0.5	-0.4	axon target recognition	guanyl-nucleotide exchange factor activity	RAPGEF2 RAPGEF6 RAPGEF4
GlcT-1	CG6437	-0.2	0.0	-2.3	negative regulation of apoptosis	ceramide glucosyltransferase activity	UGCG
Gli	CG3903	-0.2	-0.5	-2.1	establishment of blood-nerve barrier	carboxylesterase activity	NLGN3 NLGN4Y NLGN4X
Gp93	CG5520	0.0	0.0	-0.9	protein folding	unfolded protein binding	HSP90B1 GRP94c HSP90B2P
Gr22a	CG31662	0.1	0.3	3.8	sensory perception of taste	taste receptor activity	-
Gr47b	CG30030	0.0	-0.9	-0.1	sensory perception of taste	taste receptor activity	-
Gr59f	CG33150	0.0	-2.1	0.0	sensory perception of taste	taste receptor activity	-
Gr66a	CG7189	0.0	0.0	-1.7	sensory perception of taste	taste receptor activity	-
Gr85a	CG31405	0.0	0.0	-2.5	sensory perception of taste	taste receptor activity	-
Gr89a	CG14901	0.0	-2.5	0.0	sensory perception of taste	-	-
Gr98d	CG31061	0.0	0.1	-2.2	sensory perception of taste	taste receptor activity	-
Grip	CG14447	0.1	-0.1	-2.5	determination of muscle attachment site	protein binding	GRIP1 GRIP2 DLG1
grp	CG17161	0.0	0.0	-0.9	protein amino acid phosphorylation	protein serine/threonine kinase activity	CHEK1 PRKAA1 MARK3
gry	CG17569	0.0	0.0	-1.2	learning or memory	-	C4orf41
GstE8	CG17533	0.0	-1.0	0.0	-	-	GSTT1 GSTT2
hbs	CG7449	1.9	-2.3	-2.6	regulation of striated muscle development	-	NPHS1 HMCN1 KIRREL
Hdac3	CG2128	0.0	0.0	-0.9	histone deacetylation	histone deacetylase activity	HDAC3* HDAC2 HDAC1
HDAC6	CG6170	0.0	0.0	-2.7	histone deacetylation	histone deacetylase activity	HDAC10 HDAC9 HDAC4
He	CG31770	0.0	-2.9	0.0	innate immune response	-	-
Hel89B	CG4261	0.0	0.3	-1.0	antimicrobial humoral response	helicase activity	BTAF1 ERCC6 SMARCA1
HERC2	CG11734	0.0	0.0	-6.0	regulation of mitotic metaphase/anaphase transi	guanyl-nucleotide exchange factor activity	HERC2 DKFZp547P028 HERC1
Hex-t1	CG33102	-1.4	0.1	0.0	glycolysis	hexokinase activity	HK1 HKDC1 HK2
Hexo2	CG1787	-0.1	0.0	-1.1	carbohydrate metabolic process	beta-N-acetylhexosaminidase activity	HEXB
His2A:CG3382	CG33820	0.0	-0.6	0.4	chromatin assembly or disassembly	DNA binding	HIST1H2AA HIST2H2AB H2AFJ
HLH106	CG8522	0.0	0.0	-1.3	fatty acid biosynthetic process	transcription factor activity	SREBF2 SREBF1
HLHm3	CG8346	-0.1	0.0	-2.0	Notch signaling pathway	transcription factor activity	HES1 HES4
Hmu	CG3373	0.0	0.0	-1.0	biosynthetic process	mRNA binding	APMAP* C20orf3
Hnf4	CG9310	0.0	0.0	-1.6	lipid biosynthetic process	ligand-dependent nuclear receptor activity	HNF4A* HNF4G NR2A3
Hrb27C	CG10377	0.0	0.0	-0.9	negative regulation of oskar mRNA translation	mRNA 3'-UTR binding	DAZAP1* MSI2 MSI1
Hsc70-3	CG4147	0.0	0.0	-0.9	sleep	ATPase activity	HSPA8* HSPA5 HSPA2
Hsp27	CG4466	0.5	1.4	1.3	determination of adult life span	-	HSPB1 CRYAB HSPB2
Hsp67Bb	CG4456	-0.8	0.0	0.0	response to heat	-	KAT*
Hsp68	CG5436	-1.1	0.0	-0.9	determination of adult life span	unfolded protein binding	HSPA8* HSPA1A HSPA1L
Hsp70Aa	CG31366	-2.1	-0.2	0.0	heat shock-mediated polytene chromosome puff	ATP binding	HSPA8* HSPA1A HSPA1L
Hsp70Bb	CG31359	-1.5	0.0	-0.1	heat shock-mediated polytene chromosome puff	ATP binding	HSPA8* HSPA1A HSPA1L
Hsp70Bc	CG6489	-1.8	0.0	-0.1	heat shock-mediated polytene chromosome puff	ATP binding	HSPA8* HSPA1A HSPA1L
htt	CG9995	0.0	0.0	-2.1	axon cargo transport	microtubule binding	HTT
Idgf1	CG4472	0.0	0.9	2.9	imaginal disc development	imaginal disc growth factor activity	CHIT1 CHI3L2 CHIA
Ih	CG8585	0.0	-0.8	1.4	potassium ion transport	intracellular cyclic nucleotide activated cati	-
iHog	CG9211	0.0	0.0	-1.7	smoothened signaling pathway	heparin binding	NEO1 BOC HMCN1
Ilp5	CG33273	0.1	0.3	-2.2	insulin receptor signaling pathway	insulin receptor binding	-
Imp	CG1691	-1.1	0.0	0.0	spermatogenesis	mRNA binding	IGF2BP2 IGF2BP1 IGF2BP3
Ipk1	CG30295	-0.4	-0.4	-3.4	inositol and derivative phosphorylation	inositol pentakisphosphate 2-kinase activity	IPPK
Ipod	CG2961	0.0	2.2	0.0	DNA methylation	-	-
Irk2	CG4370	0.7	-0.5	1.8	potassium ion transport	inward rectifier potassium channel activity	KCNJ12 KCNJ9 KCNJ5
jing	CG9397	0.0	0.0	-2.2	specification of segmental identity, maxillary seg	transcription repressor activity	-
Jon65Aii	CG6580	-1.8	0.0	0.3	proteolysis	serine-type endopeptidase activity	TMPRSS11D TMPRSS11B KLK7
Jon74E	CG6298	-0.1	0.6	0.0	proteolysis	serine-type endopeptidase activity	CELA3B CTRC CELA3A
Jupiter	CG31363	-0.8	-0.1	1.3	-	microtubule binding	-
Karybeta3	CG1059	0.0	0.1	-1.1	protein import into nucleus	protein transmembrane transporter activity	IPO5* RANBP6
kdn	CG3861	0.0	-0.3	-1.0	tricarboxylic acid cycle	citrate (Si)-synthase activity	CS
kek5	CG12199	0.9	0.0	0.0	-	protein binding	LRFN1 LRFN4 PXDNL
kl-2	CG17866	0.0	1.7	-0.3	microtubule-based movement	motor activity	DNAH2 DNAH1 DNAH3
kl-3	CG17629	0.0	0.0	-2.2	microtubule-based movement	microtubule binding	DNAH8* DNAH10* DNAH2*
Klp3A	CG8590	0.0	0.0	-1.2	cytokinesis	microtubule motor activity	KIF4A* KIF4B KIF21B
ko	CG10573	-2.0	0.0	2.5	motor axon guidance	-	STOX1* STOX2
KP78b	CG17216	0.0	0.0	-2.3	protein amino acid phosphorylation	protein serine/threonine kinase activity	MARK3 MARK4 MARK2
KrT95D	CG5405	-0.1	-0.1	-1.9	protein targeting to Golgi	-	PACS2* PACS1

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
kto	CG8491	0.0	0.0	-1.9	transcription initiation from RNA polymerase II p	RNA polymerase II transcription mediator a	MED12L* MED12
kuk	CG5175	0.0	0.0	-0.5	nucleus organization	-	-
L	CG10109	0.0	0.0	-0.9	negative regulation of programmed cell death	-	-
l(1)G0222	CG8465	0.0	0.0	-1.7	-	-	ANKLE2*
l(1)G0289	CG2221	0.0	0.0	-1.0	-	-	PLXDC2* PLXDC1
l(2)35Df	CG4152	0.0	0.0	-0.9	-	ATP-dependent RNA helicase activity	SKIV2L2 SKIV2L SKI2W
l(2)gl	CG2671	0.0	1.3	2.4	neurotransmitter secretion	myosin II binding	LLGL1 LLGL2 STXBP5
l(2)k05819	CG3054	0.3	2.0	-0.7	-	-	KIAA0195*
l(2)k16918	CG3920	-0.2	-1.0	0.0	-	-	-
l(3)02640	CG9165	0.0	0.0	-1.6	tetrapyrrole biosynthetic process	hydroxymethylbilane synthase activity	HMBS*
l(3)05822	CG7129	-0.1	0.0	-1.1	-	-	SH3D19
l(3)82Fd	CG32464	-0.1	0.0	-1.9	cell wall catabolic process	-	NCOA7* OXR1 C20orf118
LamC	CG10119	0.0	0.0	-1.1	mitotic nuclear envelope reassembly	structural molecule activity	LMNA LMNB2 LMNB1
LanB1	CG7123	0.0	0.0	-1.1	embryonic morphogenesis	-	LAMB4* LAMB1 LAMB2
lig	CG8715	0.0	0.0	-1.3	copulation	-	UBAP2
lilli	CG8817	0.0	-0.7	1.0	periodic partitioning	DNA binding	-
lin19	CG1877	0.0	0.0	-0.9	ubiquitin-dependent protein catabolic process	ubiquitin protein ligase binding	CUL1 CUL2 CUL3
Lk6	CG17342	0.0	0.0	-1.2	microtubule-based process	protein kinase activity	MKNK1* MKNK2 DKFZp686E14208
LpR1	CG31094	0.0	0.7	-0.1	cholesterol metabolic process	lipoprotein binding	VLDLR LDLR LRP8
Lsp1beta	CG4178	0.0	0.0	-1.9	transport	nutrient reservoir activity	-
lva	CG6450	0.0	0.1	-2.2	cellularization	actin binding	-
mal	CG1692	0.0	-0.1	-1.0	ommochrome biosynthetic process	Mo-molybdopterin cofactor sulfurase activit	MOCOS MOSC1 MOSC2
mam	CG8118	0.0	0.1	-1.7	ectoderm development	-	-
Map60	CG1825	0.0	0.0	-0.9	microtubule-based process	microtubule binding	-
Marf	CG3869	0.0	0.0	-1.0	mitochondrion organization	GTP binding	MFN2* MFN1* hfzo2
mars	CG17064	0.0	0.0	-1.5	cell-cell signaling	-	DLGAP5
Mcm2	CG7538	0.0	0.0	-0.6	pre-replicative complex assembly	chromatin binding	MCM2 MCM5 MCM6
Mef2	CG1429	0.2	0.0	-2.2	mesoderm development	RNA polymerase II transcription factor activ	MEF2A* MEF2D MEF2C
Mekk1	CG7717	0.0	0.1	-1.6	protein amino acid phosphorylation	MAP kinase kinase kinase activity	MAP3K4* MAP3K3 YSK4
MESR4	CG4903	-0.5	0.0	-1.7	-	protein binding	-
mew	CG1771	0.0	0.0	-1.9	cell adhesion	cell adhesion molecule binding	ITGA7* ITGA6 ITGA3
mfas	CG3359	0.0	0.8	1.0	axonogenesis	-	TGFBI POSTN
Mgat2	CG7921	0.0	-0.2	-2.3	protein amino acid terminal N-glycosylation	alpha-1,6-mannosylglycoprotein 2-beta-N-a	-
Mhcl	CG31045	-0.1	-0.9	0.0	-	ATPase activity, coupled	MYO18A
Mi-2	CG8103	0.0	0.0	-1.7	nucleosome mobilization	ATPase activity	CHD4* CHD3* CHD5
mib1	CG5841	0.0	0.0	-1.6	positive regulation of endocytosis	protein binding	MIB1 MIB2 ANK3
mib2	CG17492	0.0	0.0	-1.5	myoblast fusion	protein binding	MIB2* MIB1 DKFZp686I225
Mical	CG33208	-0.1	0.0	-3.7	axon guidance	actin binding	MICAL3* MICAL2* MICAL2PV1
milt	CG13777	0.0	0.0	-2.1	axon transport of mitochondrion	protein binding	TRAK1* DKFZp686M03244 TRAK2
mip120	CG6061	0.0	0.0	-1.0	eggshell chorion gene amplification	DNA binding	LIN54* MTL5
mira	CG12249	0.0	-1.2	0.0	asymmetric protein localization	actin binding	-
Mlp60A	CG42309	1.3	-0.3	0.0	regulation of striated muscle development	protein binding	CSRP3 CSRP2
Mmp1	CG4859	-0.6	0.0	-0.5	autophagic cell death	metalloendopeptidase activity	MMP14 MMP24 MMP16
mod(mdg4)	CG32491	-0.5	0.0	-0.6	regulation of chromatin assembly or disassembly	protein binding	-
Moe	CG10701	0.0	0.5	-0.6	establishment or maintenance of epithelial cell a	protein binding	MSN RDX EZR
mor	CG18740	0.0	0.0	-0.9	chromatin remodeling	general RNA polymerase II transcription fac	-
MRP	CG6214	0.0	0.1	-1.0	transport	ATPase activity, coupled to transmembrane	ABCC1* ABCC3* ABCC4* ABCC12*
Mrtf	CG32296	0.0	-0.1	-2.2	positive regulation of transcription, DNA-depend	transcription activator activity	MKL2 MKL1 MYOCD
Msp-300	CG33715	-0.8	0.7	0.2	cytoskeleton organization	cytoskeletal protein binding	-
Mst84Dc	CG17945	0.0	-1.0	0.0	-	iron-sulfur cluster binding	-
mthl3	CG6530	0.1	0.8	0.2	G-protein coupled receptor protein signaling patl	G-protein coupled receptor activity	GPR112
mthl4	CG6536	0.0	0.7	0.0	G-protein coupled receptor protein signaling patl	G-protein coupled receptor activity	-
Mtk	CG8175	0.0	-1.8	0.0	defense response to Gram-positive bacterium	-	-
mud	CG12047	0.0	-1.0	0.0	spindle assembly involved in female meiosis II	steroid hormone receptor activity	-
mus101	CG11156	0.0	0.0	-2.9	mitosis	-	TOPBP1 ECT2 ANKRD32
mXr	CG30361	0.0	0.0	-3.0	G-protein signaling, coupled to IP3 second mess	G-protein coupled receptor activity	GRM8* GRM7* GRM2
Myo28B1	CG6976	-0.8	-0.7	-0.6	-	actin binding	MYO7A* MYO7B* MYO10
MYPT-75D	CG6896	-0.1	-0.1	-1.9	imaginal disc-derived wing morphogenesis	myosin phosphatase regulator activity	PPP1R16B PPP1R16A KIAA0823
NaPi-T	CG10207	0.0	-1.9	-1.1	phosphate transport	high affinity inorganic phosphate:sodium sy	SLC17A6 SLC17A7 SLC17A5
net	CG11450	2.3	1.2	2.2	regulation of transcription	RNA polymerase II transcription factor activ	ATOH8*
NFAT	CG11172	-0.3	-0.6	-1.4	transcription	transcription factor activity	NFAT5 NFATC3 NFATC2
nito	CG2910	0.0	0.0	-3.0	regulation of transcription	mRNA binding	RBM15B RBM15 SPEN
noc	CG4491	-0.1	0.0	-2.6	regulation of transcription from RNA polymerase	RNA polymerase II transcription factor activ	ZNF503*
nompA	CG13207	0.0	0.0	-2.0	dendrite morphogenesis	-	-
nos	CG5637	0.4	0.0	0.0	spermatogenesis	protein binding	NANOS1 NANOS3 NANOS2
Nrk	CG4007	0.0	0.2	-3.0	protein amino acid phosphorylation	protein tyrosine kinase activity	MUSK* ROR1 ROR2
Ntf-2r	CG10174	-0.5	-0.1	0.0	protein import into nucleus	-	NUTF2
nullo	CG14426	-0.9	0.0	0.7	cell-cell junction assembly	actin binding	-
Nup358	CG11856	0.0	0.2	-1.5	intracellular transport	Ran GTPase binding	RANBP2 RGPD1 RGPD8
Nup98	CG10198	0.0	0.1	-1.7	phagocytosis, engulfment	-	NUP98
Oatp58Db	CG3382	0.0	-0.7	-2.0	organic anion transport	organic anion transmembrane transporter a	SLCO1C1 SLCO5A1 SLCO1B3
Oatp58Dc	CG3380	-0.1	0.0	-0.9	organic anion transport	organic anion transmembrane transporter a	SLCO5A1 SLCO4A1 SLCO3A1
Obp50b	CG30073	0.9	-1.4	0.0	sensory perception of chemical stimulus	odorant binding	-
Obp57c	CG13421	0.0	0.0	-2.3	sensory perception of chemical stimulus	odorant binding	-
Obp57d	CG30150	-0.1	2.0	-0.6	sensory perception of chemical stimulus	odorant binding	-
ocn	CG7929	-1.0	0.0	0.0	-	-	-
Oli	CG5545	0.8	0.1	0.3	regulation of transcription	transcription factor activity	BHLHE23 OLIG2 OLIG3
Or43a	CG1854	0.0	-1.4	0.0	sensory perception of smell	protein binding	-
Or46a	CG33478	-0.4	0.0	-1.4	sensory perception of smell	olfactory receptor activity	-
Or98a	CG5540	0.0	-2.7	-1.8	sensory perception of smell	olfactory receptor activity	-
orb	CG10868	0.8	0.0	0.1	oocyte dorsal/ventral axis determination	uridine-rich cytoplasmic polyadenylylation e	CPEB1* CPEB4 CPEB2
Orct	CG6331	0.0	-0.1	-1.0	apoptosis	organic cation transmembrane transporter	SLC22A5* SLC22A13 SLC22A4
Osbp	CG6708	0.0	0.0	-1.7	steroid metabolic process	oxysterol binding	OSBP* OSBP2 OSBPL7
Oseg1	CG7161	0.0	0.0	-1.5	sensory cilium biogenesis	-	IFT122* WDR10 APAF1
Oseg3	CG11838	0.0	-0.3	-3.6	sensory cilium biogenesis	binding	IFT140
Osi10	CG15593	-1.9	0.0	0.0	-	-	-
Osi7	CG1153	-1.9	0.0	0.2	-	-	-
osm-1	CG13809	0.2	-0.7	0.0	microtubule-based movement	microtubule motor activity	IFT172*
ovo	CG6824	0.0	0.0	2.0	cuticle pattern formation	sequence-specific DNA binding	OVOL1 OVOL2 MYNN
oxt	CG32300	0.0	0.0	-1.7	D-xylose metabolic process	protein xylosyltransferase activity	XYLT1 XYLT2 GCNT2
p130CAS	CG1212	-0.1	0.0	-2.2	cytoskeletal anchoring at plasma membrane	-	BCAR1 NEDD9 EFS
p53	CG33336	-0.6	0.0	0.0	DNA damage response, signal transduction by p	transcription factor activity	-
Pbprp1	CG10436	0.1	-0.1	2.4	sensory perception of chemical stimulus	phenylalkylamine binding	-
pcm	CG3291	0.0	0.0	-1.8	RNA catabolic process	5'-3' exoribonuclease activity	XRN1* XRN2
Pde6	CG8279	0.0	0.0	-2.3	signal transduction	3',5'-cyclic-GMP phosphodiesterase activity	PDE11A* PDE5A PDE6C
Pde9	CG42276	-0.1	2.2	0.0	microtubule-based process	3',5'-cyclic-GMP phosphodiesterase activity	PDE9A* PDE4D PDE4C
Pepck	CG17725	-0.3	-0.4	-1.5	gluconeogenesis	phosphoenolpyruvate carboxykinase (GTP)	PCK2 PCK1
per	CG2647	0.0	0.0	-2.2	mating behavior	transcription cofactor activity	PER3 PER1 PER2
Peritrophin-15l	CG31893	-2.1	0.9	-1.2	chitin metabolic process	chitin binding	-
PGRP-LB	CG14704	0.0	-0.7	-0.6	detection of bacterium	peptidoglycan binding	PGLYRP3 PGLYRP4 PGLYRP2
PGRP-SB1	CG9681	-1.8	-0.9	0.0	immune response	peptidoglycan binding	PGLYRP3 PGLYRP4 PGLYRP1
pHCl	CG33989	-0.1	-0.1	2.8	ion transport	chloride channel activity	GLRA3 GLRA1 GLRA4
PIP5K59B	CG3682	-2.1	-0.1	0.0	phosphorylation	1-phosphatidylinositol-4-phosphate 5-kinas	PIP5K1A PIP5K1C PIP5K1B
pk	CG11084	-0.1	-1.7	0.0	establishment of ommatidial polarity	protein binding	-
Pkc53E	CG6622	0.2	0.0	2.2	protein amino acid phosphorylation	protein kinase C activity	PRKCB* PRKCA PRKCE
Pmm45A	CG8073	0.0	0.0	-1.1	carbohydrate metabolic process	phosphomannomutase activity	PGM2L1 PGM2
PNUTS	CG33526	0.0	0.0	-1.9	protein targeting	protein phosphatase regulator activity	PPP1R10
polybromo	CG11375	0.0	0.0	-1.6	-	DNA binding	PBRM1* ASH1L SMARCA2
Pp2C1	CG2984	-0.1	0.0	-2.4	protein amino acid dephosphorylation	protein serine/threonine phosphatase activi	PPM1D PPM1K PPM1E
ppa	CG9952	-0.1	-0.5	-2.1	ubiquitin-dependent protein catabolic process	protein binding	FBXL14 FBXL2 FBXL7
ppk12	CG10972	-0.3	0.0	-2.6	sodium ion transport	sodium channel activity	ACCN1* ACCN3 ACCN4
ppk28	CG4805	0.0	-0.7	-1.1	sodium ion transport	sodium channel activity	ACCN2 ACCN1 ACCN3
Ppn	CG33103	0.0	0.0	-2.1	extracellular matrix organization	extracellular matrix structural constituent	PAPLN* ADAMTS6 ADAMTS18
Prosap	CG30483	-0.2	0.0	-2.0	-	protein binding	-
Psa	CG1009	0.0	0.0	-1.0	proteolysis	aminopeptidase activity	NPEPPS ENPEP ERAP2
Pten	CG5671	0.0	0.0	1.0	sequestering of lipid	non-membrane spanning protein tyrosine p	-

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG number**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
Ptp99A	CG11516	-0.2	-1.0	0.0	protein amino acid dephosphorylation	transmembrane receptor protein tyrosine p	PTPRG* PTPRZ1 PTPRD
ptr	CG2841	-1.3	-0.1	0.0	-	-	-
Pvf1	CG7103	0.0	0.0	-1.5	border follicle cell migration	receptor binding	PDGFA*
Pvr	CG8222	0.0	0.4	-1.2	border follicle cell migration	protein tyrosine kinase activity	PDGFRB FLT1 FGFR3
pxb	CG33207	-0.7	-0.8	0.0	smoothened signaling pathway	-	-
Pxn	CG12002	0.0	0.0	-1.8	response to oxidative stress	peroxidase activity	PXDN* PXDNL* TPO
Rab27	CG14791	0.0	0.0	-2.2	regulation of transcription, DNA-dependent	GTP binding	RAB27A* RAB27B RAB8B
rad	CG15720	0.1	-1.5	0.0	olfactory learning	phospholipase A2 activity	PLA2G3
Ranbp21	CG12234	0.0	0.0	-1.8	protein import into nucleus, docking	Ran GTPase binding	XPO5*
Rbp1	CG17136	-0.1	-3.2	0.0	nuclear mRNA splicing, via spliceosome	mRNA binding	SFRS7 SFRS3 RBM4B
rdgA	CG34344	0.0	-1.9	0.0	deactivation of rhodopsin mediated signaling	diacylglycerol kinase activity	DGKZ* DGKI DGKB
Rfx	CG6312	0.0	-0.1	-3.5	nervous system development	RNA polymerase II transcription factor acti	RFX3* RFX2 RFX1
Rgk1	CG9811	0.0	-0.6	-0.1	small GTPase mediated signal transduction	GTPase activity	RRAD GEM REM1
Rgk2	CG34390	0.0	0.0	-2.7	small GTPase mediated signal transduction	GTP binding	RRAD GEM REM1
Rgl	CG8865	0.0	-0.3	-1.6	regulation of small GTPase mediated signal tran	Ral guanyl-nucleotide exchange factor acti	RGL1* RALGDS RGL2
rho	CG1004	-0.1	-0.7	-1.5	imaginal disc-derived wing vein specification	serine-type peptidase activity	RHBDL3 RHBDL1 RHBDL2
RhoBTB	CG5701	0.0	0.0	-1.1	small GTPase mediated signal transduction	GTPase activity	RHOBTB1 RHOBTB2 RHOBTB3
RhoGAP71E	CG32149	0.0	0.0	-2.1	signal transduction	magnesium ion binding	ARHGAP20* TAGAP
rictor	CG8002	0.0	0.0	-2.1	-	binding	RICTOR*
Rip11	CG6606	0.0	-0.2	-1.6	rhabdomere development	-	-
Rm62	CG10279	0.0	0.2	-0.5	RNA interference	ATP-dependent helicase activity	DDX17* DDX5 DDX42
RN-tre	CG8085	0.0	-0.5	0.0	regulation of Rab GTPase activity	Rab GTPase activator activity	USP6NL RABGAP1L RABGAP1
robl22E	CG10838	0.0	-0.9	0.0	microtubule-based movement	ATPase activity, coupled	DYNLRB1 DYNLRB2
robl62A	CG1014	0.0	0.0	2.4	microtubule-based movement	ATPase activity, coupled	-
Rpb4	CG33520	-0.2	-0.2	-2.0	transcription from RNA polymerase II promoter	histone acetyltransferase activity	TADA2L TADA2B
RpII215	CG1554	0.0	0.0	-1.2	transcription from RNA polymerase II promoter	DNA-directed RNA polymerase activity	POLR2A POLR3A POLR1A
Rpn2	CG11888	0.0	0.1	-1.0	proteolysis	endopeptidase activity	PSMD1*
rut	CG9533	0.0	0.0	-2.2	neuromuscular synaptic transmission	adenylate cyclase activity	ADCY1 ADCY5 ADCY6
ry	CG7642	0.0	0.0	-2.5	determination of adult life span	xanthine dehydrogenase activity	XDH AOX1
S6kII	CG17596	0.0	0.0	-1.7	associative learning	ribosomal protein S6 kinase activity	RPS6KA2* RPS6KA3 RPS6KA1
Sac1	CG9128	0.0	0.0	-1.1	dorsal closure	polyphosphoinositide phosphatase activity	SACM1L INPP5F SYNJ1
salr	CG4881	2.6	0.0	0.0	antennal joint development	specific RNA polymerase II transcription fa	SALL1 SALL3 SALL4
Samuel	CG31868	-0.5	0.0	-2.9	spermatogenesis	-	SAMD11* SAMD7 PHC3
sav	CG33193	0.0	0.0	-1.3	regulation of multicellular organism growth	protein binding	SAV1
sbb	CG5580	0.0	0.0	-2.3	axon target recognition	transcription factor activity	ZNF608 ZNF609
sca	CG17579	-0.1	0.0	1.4	bristle morphogenesis	signal transducer activity	MFAP4 TNXB ANGPTL1
scarface	CG11066	-1.3	0.0	-0.8	proteolysis	serine-type endopeptidase activity	KLKB1 TMPRSS9 F11
scat	CG3766	0.0	0.0	-1.9	spermatid development	protein binding	VPS54*
Scp1	CG15848	0.0	-2.2	0.1	-	calcium ion binding	-
scro	CG17594	-1.2	0.8	0.0	regulation of transcription, DNA-dependent	DNA binding	NKX2-1 TITF1 NKX2-4
scrt	CG1130	0.0	0.0	-2.5	regulation of transcription	transcription factor activity	SCRT1 SCRT2 SNAI2
scyl	CG7590	-0.5	0.0	0.0	negative regulation of growth	-	DDIT4L
sdt	CG32717	0.3	-1.7	0.0	establishment or maintenance of neuroblast pol	guanylate kinase activity	MPP5 MPP7 MPP2
sec31	CG8266	0.0	0.0	-1.2	-	-	SEC31A SEC31B
shd	CG13478	-0.7	0.0	0.0	dorsal closure	electron carrier activity	CYP24A1 CYP27A1 CYP24
shn	CG7734	-0.6	0.0	0.0	ectoderm development	transcription factor activity	HIVEP2 HIVEP1 HIVEP3
shot	CG18076	0.0	0.0	-0.9	muscle attachment	cytoskeletal protein binding	PLEC1* MACF1 DST
shtd	CG9198	0.0	0.0	-2.2	-	-	ANAPC1
simj	CG32067	0.0	0.0	-4.1	negative regulation of transcription, DNA-depen	transcription repressor activity	GATAD2B GATAD2A
SIP2	CG13164	-0.1	-2.2	0.0	-	-	-
slp2	CG2939	0.0	1.5	0.0	regulation of transcription	RNA polymerase II transcription factor acti	FOXG1 FOXL2 FOXC2
sls	CG1915	-1.6	-2.2	0.0	myoblast fusion	myosin light chain kinase activity	TTN HMCN1 DKFZp451F042
Smg1	CG32743	0.0	0.0	-2.0	phosphorylation	protein kinase activity	SMG1* FRAP1 ATR
SNF1A	CG3051	0.0	0.0	-1.1	establishment or maintenance of epithelial cell a	G-protein coupled receptor kinase activity	PRKAA2 PRKAA1 SIK2
sob	CG3242	2.0	-2.4	0.2	regulation of transcription	RNA polymerase II transcription factor acti	OSR2 OSR1 ZNF226
Socs36E	CG15154	1.8	2.2	1.2	regulation of JAK-STAT cascade	protein binding	SOCS5 SOCS4 SOCS6
sol	CG1391	0.0	0.0	-2.8	visual behavior	calcium-dependent cysteine-type endopept	SOLH* CAPN5 CAPN8
Sop2	CG8978	0.0	0.0	-0.7	actin filament polymerization	actin binding	ARPC1A ARPC1B
Sox21b	CG32139	0.0	0.0	-3.2	regulation of transcription	DNA bending activity	SOX21 SOX14 SOX2
SP1070	CG9138	-1.9	0.4	0.0	cell adhesion	Notch binding	NOTCH2 NOTCH1 NOTCH3
SP1173	CG10121	-0.3	-0.1	2.8	-	-	-
spas	CG5977	-0.2	-0.2	-1.8	positive regulation of microtubule depolymerizat	ATPase activity	SPAST* FIGNL1 KATNA1
spin	CG8428	0.0	0.0	-0.9	regulation of synaptic growth at neuromuscular	tetracycline:hydrogen antiporter activity	SPNS1* SPNS2 SPNS3
spir	CG10076	0.0	-1.0	0.0	pole plasm RNA localization	microtubule binding	SPIRE1* SPIRE2 DKFZp434O034
sPLA2	CG11124	-0.2	0.0	-2.3	phospholipid metabolic process	phospholipase A2 activity	-
Sply	CG8946	0.0	0.0	-0.9	sphingolipid catabolic process	sphinganine-1-phosphate aldolase activity	SGPL1
Spn	CG16757	-0.1	0.0	-2.1	olfactory behavior	protein phosphatase 1 binding	-
Spp	CG11840	-0.1	0.1	-0.4	open tracheal system development	aspartic endopeptidase activity, intramemb	HM13* SPPL3 SPPL2A
spri	CG34414	0.0	0.0	-1.9	border follicle cell migration	Ras GTPase binding	RIN2* RIN3 RIN1
sprt	CG30023	-0.5	0.0	-1.9	larval heart development	protein binding	-
Spt6	CG12225	0.0	0.0	-2.0	RNA elongation	chromatin binding	SUPT6H*
SRm160	CG11274	0.0	0.0	-1.5	translation	structural constituent of ribosome	SRRM1*
Sry-beta	CG7938	0.0	-0.1	-4.3	-	DNA binding	ZNF764 ZNF57 ZNF250
stc	CG3647	0.0	0.0	-1.2	regulation of transcription	RNA polymerase II transcription factor acti	NFX1* NFXL1
stg	CG1395	0.0	0.0	-1.1	G2/M transition of mitotic cell cycle	protein tyrosine phosphatase activity	CDC25B* CDC25C* CDC25A
Strn-Mlck	CG18255	-0.4	0.0	-2.0	protein amino acid phosphorylation	myosin light chain kinase activity	MYLK* MYLK2 MYLK3
sty	CG1921	0.0	0.0	-1.5	muscle fiber development	-	SPRY3 SPRY4 SPRY1
Su(Tpl)	CG32217	0.0	0.0	-1.8	wing disc dorsal/ventral pattern formation	transcription elongation regulator activity	ELL ELL2 DKFZp779C185
Su(z)12	CG8013	0.0	0.0	-1.2	chromatin silencing	DNA binding	SUZ12
sut4	CG1380	0.0	2.1	0.0	transmembrane transport	sugar:hydrogen symporter activity	SLC2A8 SLC2A6 SLC2A1
syd	CG8110	-1.2	-0.1	-0.2	axon cargo transport	kinesin binding	MAPK8IP3* SPAG9 ARHGEF17
Syn2	CG4905	0.1	-1.5	0.0	-	structural constituent of muscle	SNTG1 SNTG2 SNTB1
synj	CG6562	0.0	0.0	-1.0	dephosphorylation	inositol trisphosphate phosphatase activity	SYNJ1* SYNJ2* INPP5B
Syt7	CG2381	0.1	-1.3	0.0	neurotransmitter secretion	calcium-dependent phospholipid binding	SYT7 SYT2 SYT1
Taf12L	CG15632	2.6	0.0	0.0	transcription initiation from RNA polymerase II	general RNA polymerase II transcription fa	-
tai	CG13109	0.0	-0.3	-2.0	border follicle cell migration	transcription coactivator activity	-
Takr99D	CG7887	2.4	0.0	0.0	G-protein coupled receptor protein signaling pat	neuropeptide receptor activity	TACR3 TACR1 TACR2
tam	CG8987	0.0	0.0	-2.0	DNA-dependent DNA replication	DNA-directed DNA polymerase activity	POLG
tamo	CG4057	0.0	-0.2	-1.9	negative regulation of protein import into nucleu	nuclear localization sequence binding	-
TepIV	CG10363	0.0	0.0	-1.2	antibacterial humoral response	protease inhibitor activity	CD109 A2ML1 PZP
Thor	CG8846	-0.6	0.0	0.0	immune response	eukaryotic initiation factor 4E binding	EIF4EBP2 EIF4EBP1 EIF4EBP3
Tim17b2	CG15257	0.0	0.1	2.1	protein transport	P-P-bond-hydrolysis-driven protein transm	TIMM17A TIMM17B
tio	CG12630	0.0	0.0	-2.2	epidermis morphogenesis	transcription factor activity	-
Tk	CG14734	0.0	0.1	2.2	neuropeptide signaling pathway	receptor binding	-
Tm1	CG4898	-0.8	0.0	-0.1	pole plasm oskar mRNA localization	actin binding	TPM1 TPM3 TPM2
tna	CG7958	0.0	0.0	-1.7	chromatin-mediated maintenance of transcriptio	zinc ion binding	ZMIZ1* ZMIZ2 PIAS2
toe	CG10704	0.0	0.0	1.4	regulation of transcription	transcription factor activity	PAX2 PAX8 PAX5
tomboy40	CG8330	0.0	0.1	-2.1	protein targeting to mitochondrion	P-P-bond-hydrolysis-driven protein transm	TOMM40 TOMM40L
Top3alpha	CG10123	0.0	0.0	-2.4	double-strand break repair via homologous reco	DNA topoisomerase type I activity	TOP3A* TOP3B
topi	CG8484	0.0	0.0	-3.1	male meiosis	DNA binding	ZNF629 ZFP2 ZNF311
tor	CG1389	0.0	0.0	-2.2	terminal region determination	transmembrane receptor protein tyrosine k	RET/PTC2 FGFR1 RET
TotA	CG31509	0.0	1.1	4.1	response to stress	-	-
TotM	CG14027	0.0	0.1	3.0	response to stress	-	-
TppII	CG3991	0.0	0.0	-1.2	proteolysis	exopeptidase activity	TPP2
tral	CG10686	0.0	0.0	-1.2	ER to Golgi vesicle-mediated transport	-	LSM14B* LSM14A
Trax	CG5063	0.0	-0.7	0.0	-	sequence-specific DNA binding	TSNAX
Trc8	CG2304	0.0	0.0	-2.1	negative regulation of growth	protein binding	RNF139 RNF145 SYVN1
trn	CG11280	0.1	1.3	-0.1	cell adhesion	protein binding	LRRN2 LRRN3 LRIG3
trr	CG3848	0.0	0.0	-2.3	histone methylation	histone lysine N-methyltransferase activity	MLL3* MLL2 MLL
Tsp29Fb	CG9496	0.0	-0.4	1.9	-	-	TSPAN6 CD63 TSPAN33
Uba1	CG1782	0.0	0.0	-1.0	neuron remodeling	ubiquitin activating enzyme activity	UBA6* UBA1 UBA7
Ubp64E	CG5486	0.0	0.0	-1.3	proteolysis	ubiquitin thiolesterase activity	USP47* USP7 USP40
Ucp4A	CG6492	0.0	-0.5	-2.9	proton transport	oxidative phosphorylation uncoupler activit	SLC25A27 SLC25A30 SLC25A14
unc	CG1501	0.0	-0.1	-2.2	locomotory behavior	-	-
unc-5	CG8166	-0.2	-0.6	-1.7	axon guidance	netrin receptor activity	UNC5C* UNC5B UNC5D
Unc-76	CG3981	0.0	0.0	-1.1	axon cargo transport	kinesin binding	-

D. melanogaster		**Fold Change (log2)**			**Gene Ontologies**		***H. sapiens***
Gene Name	**CG numbe**	**2h**	**4h**	**10h**	**Biological Process**	**Molecular Function**	**Gene Name**
Upf1	CG1559	0.0	0.0	-1.9	nuclear-transcribed mRNA catabolic process, nor	helicase activity	UPF1* IGHMBP2 SETX
Usp36	CG5505	0.0	0.0	-1.7	molting cycle, chitin-based cuticle	ubiquitin thiolesterase activity	USP36* USP42 USP17A
ventrally-expre	CG33200	0.0	-0.9	1.5	multicellular organismal development	-	-
Vha100-2	CG18617	0.0	0.0	-1.2	ATP synthesis coupled proton transport	hydrogen-exporting ATPase activity, phosph	ATP6V0A1* ATP6V0A4 ATP6V0A2
Vha55	CG17369	0.0	0.0	-0.9	proton transport	hydrogen-exporting ATPase activity, phosph	ATP6V1B2 ATP6V1B1 ATP5B
VhaPPA1-1	CG7007	0.0	0.1	-0.8	mitotic spindle organization	hydrogen-exporting ATPase activity, phosph	ATP6V0B
vkg	CG16858	0.0	0.0	-2.4	-	extracellular matrix structural constituent	COL4A6 COL4A2 COL4A1
w	CG2759	0.0	-1.1	0.2	eye pigment precursor transport	ATPase activity, coupled to transmembrane	ABCG1 ABCG4 ABCG2
wb	CG15288	-1.7	0.0	0.0	cell-cell signaling	binding	LAMA1 LAMA2 LAMA3
wdn	CG1454	0.0	0.0	-1.6	regulation of transcription, DNA-dependent	RNA polymerase II transcription factor activ	ZNF836 ZNF668 ZNF184
Wnt4	CG4698	2.2	-1.5	0.0	Wnt receptor signaling pathway	signal transducer activity	WNT9B WNT9A WNT16
woc	CG5965	0.0	0.0	-1.1	telomere capping	zinc ion binding	ZMYM3* ZMYM4 QRICH1
xmas-1	CG32561	0.0	0.0	-4.3	embryonic development	-	-
XNP	CG4548	0.0	0.0	-1.3	transcription	DNA helicase activity	RAD54L2 ATRX RAD54L
yemalpha	CG14513	0.0	0.0	-2.5	oogenesis	DNA binding	UBN1* UBN2
yin	CG2913	0.0	-0.6	-1.0	oligopeptide transport	proton-dependent oligopeptide secondary a	SLC15A2 SLC15A1 hPEPT1-RF

Supplemental Table 2

Gene name		Cellular Proliferation					
		HeLa		Hek293T		HepG2	
D. melanogaster	***Homo sapiens***	**% of ctrl**	**Z-score**	**% of ctrl**	**Z-score**	**% of ctrl**	**Z-score**
baz	PARD3	86.8%	0.56	107.0%	-1.26	102.0%	-0.18
	PARD3B	112.5%	-0.55	110.5%	-1.85	106.5%	-0.58
	MPDZ	119.0%	-0.81	99.7%	0.06	96.3%	0.39
CG13559	LITAF	99.8%	0.01	100.2%	0.00	96.0%	0.35
CG31158	PSD3	109.5%	-0.42	104.0%	-0.67	102.5%	-0.37
	PSD	82.0%	0.77	97.8%	0.38	95.3%	0.46
	PSD2	131.5%	-1.33	102.0%	-0.36	93.0%	0.55
CG3829	SCARB1	142.5%	-1.83	102.0%	-0.39	95.6%	0.47
	SCARB2	86.8%	0.56	94.2%	1.01	104.5%	-0.38
	CD36	108.0%	-0.34	105.5%	-0.92	105.0%	-0.48
CG4793	TMPRSS13	127.0%	-1.15	102.5%	-0.43	114.5%	-1.16
	KLKB1	86.7%	0.57	98.7%	0.23	92.0%	0.79
	CTRB2	59.6%	1.72	98.0%	0.33	96.0%	0.35
CG4080	MARCH8	125.0%	-1.08	97.4%	0.45	102.0%	-0.19
	MARCH2	49.4%	2.15	83.0%	2.99	102.2%	-0.29
	MARCH1	89.0%	0.47	98.9%	0.16	93.4%	0.66
CG4804	PAI-2	95.2%	0.2	107.0%	-1.20	111.5%	-1.17
	SERPINI1	56.2%	1.86	84.5%	2.71	68.4%	3.18
	SERPINB8	71.4%	1.22	94.1%	1.03	90.1%	1.19
CG6014	REG1A	125.0%	-1.07	109.0%	-1.54	108.0%	-0.93
Ga73B	GNAL	124.5%	-1.03	104.0%	-0.66	117.5%	-1.81
	GNAS	108.4%	-0.34	101.5%	-0.27	111.0%	-1.06
idgf1	CHIT1	48.6%	2.19	92.1%	1.39	89.4%	1.10
	CHI3L2	95.6%	0.19	94.0%	1.06	87.1%	1.10
	CHIA	81.8%	0.78	102.0%	-0.31	91.1%	0.96
l(2)gl	LLGL1	56.6%	1.85	88.4%	2.02	87.5%	1.32
	LLGL2	100.4%	-0.02	99.3%	0.16	96.6%	0.47
	STXBP5	101.4%	-0.06	97.9%	0.41	99.0%	0.07
mfas	TGFBI	110.5%	-0.43	101.6%	-1.21	99.9%	1.40
	POSTN	121.0%	-0.89	103.0%	-0.51	90.9%	0.90
mthl3	GPR112	22.6%	3.29	92.6%	0.15	75.4%	0.13
net	ATOH8	95.6%	0.19	94.6%	0.94	104.0%	-0.45
socs36e	SOCS5	104.0%	-0.17	101.0%	-0.15	98.4%	0.13
	SOCS4	121.0%	-0.89	98.4%	0.29	102.2%	-0.20
	SOCS6	124.5%	-1.04	105.5%	-0.88	103.5%	-0.36
Wnt4	WNT9A	124.0%	-1.02	101.0%	-0.15	114.5%	-1.45
	WNT9B	80.4%	0.83	104.5%	-0.73	109.0%	-0.92
	WNT16	75.6%	1.04	88.9%	1.94	98.9%	0.10

Supplemental Table 3

	Gene Name		
Comparison Screen	***Drosophila melanogaster***	**Homo sapiens**	**Alignment e-value**
Li *et al.* , 2007 (lung tissue from transgenic mice)	*CG10924*	PCK1	0.0
	Egfr	ERBB4	1.0×10^{-119}
	shot	DST	1.0×10^{-110}
	bru-2	CUGBP2	1.0×10^{-69}
	Rab27	RAB27A	4.0×10^{-64}
	Cht2	CHI3L1	1.0×10^{-60}
	Tm1	TPM2	2.0×10^{-47}
	CG40067	FGL1	2.0×10^{-46}
	CG33281	SLC2A2	1.0×10^{-20}
	iHog	BOC	5.0×10^{-19}
	mus101	ECT2	2.0×10^{-18}
	Jon65Aii	KLK7	3.0×10^{-11}
Dauer *et al* ., 2005 (human A549 lung cells)	*Hsp70Bb*	HSPA1A	0.0
	LpR1	LDLR	1.0×10^{-134}
	CG1718	ABCA1	1.0×10^{-130}
	GlcT-1	UGCG	1.0×10^{-121}
	DnaJ-1	DNAJB4	1.0×10^{-94}
	CG11426	PPAP2B	2.0×10^{-36}
	CG11940	GRB14	1.0×10^{-33}
	CG4842	HPGD	3.0×10^{-30}

Supplemental Table 4: Q-PCR primers

Target	Species	Forward/Reverse	Sequence (5′->3′)
ATOH8	*H. sapiens*	F	TCAGCTTCTCCGAGTGTGTG
ATOH8	*H. sapiens*	R	ACAGTGGTGGCCTTGGTCTT
β actin	*H. sapiens*	F	CTGGAACGGTGAAGGTGACA
β actin	*H. sapiens*	R	AAGGGACTTCCTGTAACAATGCA
GNAL	*H. sapiens*	F	AAGAGCATAGCCCCTATCACTG
GNAL	*H. sapiens*	R	TCGTTGGATCTCTCAAAGCA
GNAS	*H. sapiens*	F	AGGGAACTTTTGTGGCCTTT
GNAS	*H. sapiens*	R	CCACCCATAGGGCATGATTA
LITAF	*H. sapiens*	F	GCAGGACGTGGACCATTACT
LITAF	*H. sapiens*	R	CCCCCAAAAGAAGACATGAA
LLGL1	*H. sapiens*	F	GAGCTTTTCGCCTTCAACAA
LLGL1	*H. sapiens*	R	ATGGCCATGATGCGAAGT
March2	*H. sapiens*	F	AGTTTGCAGTGGAGAAACGG
March2	*H. sapiens*	R	TCTTCAGGCGAACTTTCTGG
March8	*H. sapiens*	F	CCAAAGAAAAGGAGAGGGAA
March8	*H. sapiens*	R	GGAGGACTCCCAGCCTTAGA
PARD3	*H. sapiens*	F	GGAACATGGAGATGGAGGAA
PARD3	*H. sapiens*	R	TGGATCCTGCTCATCAAACA
PSD3	*H. sapiens*	F	GCAAATCTGCAAGGGGTAAA
PSD3	*H. sapiens*	R	ACTGCCCATTCAAGCTTCTC
REG1A	*H. sapiens*	F	TCAATGTCTGGATTGGCCTC
REG1A	*H. sapiens*	R	CAATGCCCCAGGACTTGTAG
SOCS3	*H. sapiens*	F	GGCTCAGCCCCAAGGAC
SOCS3	*H. sapiens*	R	GAGCCAGCGTGGATCTG
TGFβI	*H. sapiens*	F	CCCTGGACACCAACTATTGC
TGFβI	*H. sapiens*	R	CTTCCAGCCGAGGTCCTT
TMPRSS13	*H. sapiens*	F	ATCGGGTGCGTGCTCCTCCT
TMPRSS13	*H. sapiens*	R	CCCGTCACAGCGAACAGCGT
Wnt9A	*H. sapiens*	F	CTTCGGCCGCCTACTTC
Wnt9A	*H. sapiens*	R	GTCGCAGGCCTTGTAGTGC
Wnt9B	*H. sapiens*	F	GCCGCCTCCTACTTCGG
Wnt9B	*H. sapiens*	R	GTCACACTGCTTCAGGTGGG
AttD	*D. melanogaster*	F	GGAGTAAGGGTCGGTGATGA
AttD	*D. melanogaster*	R	CGATCGGCTATGACTGTGAA
Baz	*D. melanogaster*	F	GGCACCTATCAGCGGAATAA
Baz	*D. melanogaster*	R	AAACTGGGCATTAGCACTGG
CG13559	*D. melanogaster*	F	ATCTGTCCAATGTGCCATGA
CG13559	*D. melanogaster*	R	TGAAACAGTCGAGGATGCAG
CG13912	*D. melanogaster*	F	AAGCCGGAATACGATCACAG
CG13912	*D. melanogaster*	R	GATACCGGAAACGCTGACTC
CG4804	*D. melanogaster*	F	TTCTTCAAAAGCTGCGCATA
CG4804	*D. melanogaster*	R	CAGCTCGGAAGAATTTCTGG
CG9317	*D. melanogaster*	F	CCCCAATATGCGCTTAAAGA
CG9317	*D. melanogaster*	R	CACAACAGCCGACAGAAAGA
socs36E	*D. melanogaster*	F	AAGTGCACACTGTCGAATGG
socs36E	*D. melanogaster*	R	TTCCCCGTTTTCACGTTATC
TotA	*D. melanogaster*	F	TGAGGAACGGGAGAGTATCG
TotA	*D. melanogaster*	R	GCCCTTCACACCTGGAGATA

Supplemental Table 5

Gene Name	**VDRC Transformant ID**
Rh4	46919
white	30033
baz	2914
CG10764	15516
CG13559	6643
CG15211	35704
CG15678	23784
CG1572	23220
CG31158	42321
CG3829	3829
CG4080	9026
CG4793	13203
CG4804	38018
CG6014	31067
Galpha73B	17054
Idgf1	12414
lgl	51247
mfas	37888
mthl3	49623
net	41069
pxb	24932
socs36E	51821
stat92e	43866
totA	14415
wnt4	38010