Supplementary Table S1 for *Interaction between Sleep and the Immune Response in Drosophila: A Role for the NFκB Relish*

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Table S1. Changes in gene expression in Deprivation vs Rebound. Genes with significant T-statistic values (Score) and fold change (Δ) as determined by SAM (significance analysis of microarrays) are listed for each condition and for each genotype. Genes in each functional category are listed in descending order according to the SAM score.

Genes Upregulated with Deprivation		***y w***		***rosy***	**Description**
Immune related genes	**Score**	**Δ**	**Score**	**Δ**	
Relish	-1.428	2.734	-2.963	2.912	antibacterial polypeptide induction; antifungal polypeptide induction; immune response; nucleus; specific RNA polymerase II transcription factor activity; transcription factor activity
cactus	-1.282	2.304	-2.933	2.084	Tl signaling pathway; antifungal humoral response (sensu Invertebrata); antifungal polypeptide induction; antimicrobial humoral response (sensu Invertebrata); cytoplasm; defense response; dorsal appendage formation; dorsal/ventral axis specification; female gamete generation; immune response; negative regulation of protein-nucleus import; response to fungi; transcription factor binding, cytoplasmic sequestering
Aldehyde dehydrogenase type III	-0.653	1.375			aldehyde dehydrogenase activity, defense response
kenny	-0.638	1.332			IkappaB kinase activity; IkappaB kinase complex; antibacterial polypeptide induction; antimicrobial humoral response (sensu Invertebrata)
Moca-cyp	-0.615	1.242			cyclophilin-type peptidyl-prolyl cis-trans isomerase activity; nucleus; peptidyl-prolyl cis-trans isomerase activity, defense
Cecropin C			-3.884	6.750	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Cecropin C			-3.232	5.310	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Cecropin B			-2.695	4.571	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Cecropin A2			-2.317	2.765	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity
Cecropin A1			-2.139	2.709	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular

CG9733			-2.039	2.844	defense response; monophenol monooxygenase activator activity; proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
necrotic			-1.990	1.382	Tl signaling pathway; antifungal humoral response (sensu Invertebrata); defense response; serine protease inhibitor activity
malvolio			-1.318	1.443	Natural resistance associated macrophage protein; cation transport (divalent cation (iron) uptake)
pelle			-1.298	1.320	Tl signaling pathway; antifungal humoral response (sensu Invertebrata); cytoplasm; defense response; dorsal/ventral axis specification; plasma membrane; protein amino acid phosphorylation; protein kinase activity; protein serine/threonine kinase activity; protein-nucleus import; response to fungi; zygotic determination of dorsal/ventral axis
CG1102			-1.222	1.297	defense response; monophenol monooxygenase activator activity; proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
Peptidoglycan recognition protein LA			-1.131	1.294	defense response; immune response; integral to membrane; integral to plasma membrane; peptidoglycan recognition activity; perception of bacteria
Chaperone activity/heat shock protein					
Hsp70/Hsp90 organizing protein homolog	-1.019	1.457			Hsp70/Hsp90 organizing protein activity; chaperone activity
CG7409	-0.987	1.556			chaperone activity
CaBP1	-0.951	1.622			protein disulfide isomerase activity
CG4164	-0.911	1.505			heat shock protein activity
Heat shock protein 83	-0.842	1.812			centrosome; centrosome cycle; chaperone activity; chaperonin ATPase activity; cytoplasm; determination of anterior/posterior axis, embryo; heat shock protein activity; protein folding; regulation of sleep; response to heat; spermatogenesis; torso signaling pathway
Hsc70Cb	-0.720	1.551			co-chaperone activity; protein folding
CG7033	-0.710	1.361			chaperone activity; chaperonin-containing T-complex
Glycoprotein 93	-0.679	1.360			chaperone activity
T-complex Chaperonin 5			-1.309	1.304	chaperonin ATPase activity; chaperonin-containing T-complex; protein folding
CG5525			-1.150	1.218	chaperonin ATPase activity; chaperonin-containing T-complex
Redox					
Nmdmc	-1.702	2.382			NAD-dependent methylenetetrahydrofolate dehydrogenase;10-formyltetrahydrofolate metabolism; carbohydrate metabolism; magnesium ion binding; methenyltetrahydrofolate cyclohydrolase activity; methylenetetrahydrofolate dehydrogenase (NAD) activity; methylenetetrahydrofolate dehydrogenase (NADP) activity; mitochondrion
CG17524	-1.667	2.020			glutathione transferase activity
CG17530	-0.921	1.495			glutathione transferase activity
CG6776	-0.860	1.454			glutathione transferase activity
CG9360	-0.852	1.361	-1.956	1.611	oxidoreductase activity, acting on CH-OH group of donors
CG17523	-0.829	1.397			glutathione transferase activity
Glutathione S transferase D3	-0.827	1.530			cellular_component unknown; glutathione conjugation reaction; glutathione transferase activity
Ero1L	-0.777	1.516			oxidoreductase activity
CG6020	-0.726	1.325			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)

Glutathione S transferase E1	-0.709	1.320			glutathione transferase activity; response to oxidative stress
CG12203	-0.701	1.341			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
Photoreceptor dehydrogenase	-0.697	1.392			oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
CG12013	-0.673	1.307			cytoplasm; glutathione peroxidase activity; mitochondrion; response to lipid hydroperoxide
Gst3-1	-0.663	1.324			glutathione transferase activity; response to toxin
CG4169	-0.661	1.318			mitochondrial electron transport, ubiquinol to cytochrome c; ubiquinol-cytochrome-c reductase activity; ubiquinol-cytochrome-c reductase complex (sensu Eukarya)
CG1970	-0.647	1.412			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
CG11455	-0.642	1.330			NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
CG7712	-0.640	1.313			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
CG9027	-0.637	1.278			superoxide dismutase activity
CG9140	-0.634	1.361			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
Glutathione S transferase S1	-0.629	1.478			cellular_component unknown; glutathione conjugation reaction; glutathione peroxidase activity; glutathione transferase activity; response to oxidative stress
NADH:ubiquinone reductase 23kD subunit precursor	-0.625	1.293			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
Superoxide dismutase 2 (Mn)	-0.623	1.271			antioxidant activity; determination of adult life span; manganese superoxide dismutase activity; mitochondrial matrix; removal of superoxide radicals; superoxide dismutase activity; superoxide metabolism
CG5548	-0.616	1.304			NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
CG5590	-0.612	1.318			oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Glutathione S transferase D2			-1.592	1.413	glutathione conjugation reaction; glutathione peroxidase activity; glutathione transferase activity
CG9436			-1.523	1.361	aldehyde reductase activity
CG2254			-1.453	1.294	oxidoreductase activity
CG17531			-1.233	1.275	glutathione transferase activity
CG4670			-1.141	1.316	flavin-linked sulfhydryl oxidase activity
Cytochrome P450					
Cyp6w1	-1.034	1.741	-1.654	1.527	cytochrome P450 activity; membrane; microsome
Cyp6g1	-1.022	1.643	-1.159	1.232	Resistance to DDT; cytochrome P450 activity; membrane; microsome; response to DDT
Cytochrome P450-4p1	-0.931	1.656			cytochrome P450 activity; membrane; microsome
Cytochrome P450-4e2	-0.775	1.413			cytochrome P450 activity; membrane; microsome
Cytochrome c oxidase subunit Va	-0.750	1.361			cytochrome-c oxidase activity; electron transport; mitochondrial electron transport, cytochrome c to oxygen; mitochondrial inner membrane; respiratory chain complex IV (sensu Eukarya)
Cyp6a13	-0.722	1.406			cytochrome P450 activity; membrane; microsome
Cytochrome P450-6a2	-0.644	1.602	-1.129	1.288	cytochrome P450 activity; membrane; microsome; response to insecticide

CG14235	-0.641	1.293			cytochrome-c oxidase activity; respiratory chain complex IV (sensu Eukarya)
Signaling molecules					
GTP binding; GTPase activity					
Rac2	-0.741	1.486			Rho small monomeric GTPase activity; dorsal closure; morphogenesis of an epithelium; myoblast fusion; oocyte microtubule cytoskeleton polarization; pole plasm oskar mRNA localization; protein localization; rhabdomere development; small monomeric GTPase activity; tracheal outgrowth (sensu Insecta); tracheal system development (sensu Insecta)
Rab-protein 7	-0.730	1.321			RAB small monomeric GTPase activity; Rho small monomeric GTPase activity; endosome to lysosome transport; endosome transport; late endosome
CG7197	-0.700	1.338			ARF small monomeric GTPase activity
Rab-protein 14	-0.630	1.300			GTP binding; RAB small monomeric GTPase activity; Rho small monomeric GTPase activity
Septin-2	-0.611	1.328			GTP binding; GTPase activity; cellularization; cytokinesis; ring canal (sensu Drosophila); septin ring
CG7891			-1.217	1.295	ARF small monomeric GTPase activity
Rab-protein 10			-1.137	1.412	RAB small monomeric GTPase activity; Rho small monomeric GTPase activity
G-Protein receptor/signaling					
Drosulfakinin	-0.639	1.356			neuropeptide hormone activity; neuropeptide receptor activity; neuropeptide signaling pathway
CG12290	-0.611	1.265			G-protein coupled receptor activity, unknown ligand; G-protein coupled receptor protein signaling pathway; integral to membrane
CG18314			-1.552	1.442	G-protein coupled receptor protein signaling pathway; amine receptor activity; integral to membrane
kurtz			-1.380	1.340	G-protein coupled receptor signaling; endocytosis; intracellular protein transport; sensory perception
CG12876			-1.379	1.329	signal transducer activity
Trehalose receptor 1			-1.374	1.274	G-protein coupled receptor activity, unknown ligand; G-protein coupled receptor protein signaling pathway; integral to membrane; sweet taste perception; taste; taste receptor activity
mthl2			-1.305	1.336	G-protein coupled receptor activity; G-protein coupled receptor protein signaling pathway; determination of adult life span; integral to membrane; response to stress
Neurotransmitter synthesis/metabolism					
adenosine 3	-0.846	1.574			'de novo' IMP biosynthesis; phosphoribosylamine-glycine ligase activity; phosphoribosylformylglycinamidine cyclo-ligase activity; phosphoribosylglycinamide formyltransferase activity
adenosine 2	-0.799	1.704	-1.316	1.387	'de novo' IMP biosynthesis; phosphoribosylformylglycinamidine synthase activity
CG11089	-0.689	1.480			IMP cyclohydrolase activity; phosphoribosylaminoimidazolecarboxamide formyltransferase activity
black	-0.680	1.444			aspartate 1-decarboxylase activity; glutamate decarboxylase activity
ebony	-0.676	1.542			beta-alanyl-dopamine synthase activity; circadian rhythm; cuticle pigmentation; cuticle tanning; dopamine metabolism; locomotor rhythm; negative regulation of melanin biosynthesis; pigment metabolism

Dopa decarboxylase			-2.223	2.285	aromatic-L-amino-acid decarboxylase activity; catecholamine metabolism; courtship behavior; cuticle biosynthesis; dopamine biosynthesis from tyrosine; eclosion rhythm; learning and/or memory; melanin biosynthesis; serotonin biosynthesis from tryptophan
phosphatase activity					
astray	-1.303	1.861	-2.677	1.643	L-serine biosynthesis; axon guidance; peripheral nervous system development; phosphoserine phosphatase activity
wunen	-0.623	1.317			dephosphorylation; germ-cell migration; integral to membrane; negative regulation of cell migration; phosphatidate phosphatase activity; plasma membrane
puckered			-1.398	1.447	JNK cascade; JUN kinase phosphatase activity; MAP kinase phosphatase activity; actin cytoskeleton organization and biogenesis; dorsal appendage formation; dorsal closure; epidermal differentiation; establishment of planar polarity; micropyle formation; negative regulation of JNK cascade; ommatidial rotation; ovarian follicle cell development (sensu Insecta); peripheral nervous system development; phosphoprotein phosphatase activity; protein amino acid dephosphorylation; protein tyrosine/serine/threonine phosphatase activity; protein-tyrosine-phosphatase activity; suture of dorsal opening; wound healing
CG11425			-1.222	1.408	dephosphorylation; phosphatidate phosphatase activity
retinal degeneration C			-1.158	1.393	calcium-dependent protein serine/threonine phosphatase activity; calcium-mediated signaling; calmodulin binding; deactivation of rhodopsin mediated signaling; photoreceptor maintenance; phototransduction; protein amino acid dephosphorylation; protein serine/threonine phosphatase activity; vision
kinase activity					
CG8286	-1.110	1.834			protein kinase inhibitor activity
Inositol 1,4,5-triphosphate kinase 2	-1.016	1.957	-1.143	1.367	inositol-trisphosphate 3-kinase activity
CG3001	-1.000	1.554			hexokinase-A
CG5288	-0.955	1.590			galactokinase activity
CG8057	-0.708	1.345			SNF1A/AMP-activated protein kinase activity
CG17090	-0.703	1.571			protein amino acid phosphorylation; protein kinase activity; protein serine/threonine kinase activity
Ecdysone-induced protein 63E	-0.686	1.576			cyclin-dependent protein kinase activity; protein amino acid phosphorylation; protein serine/threonine kinase activity
Ady43A			-3.466	2.468	adenosine kinase activity
Slob			-2.585	1.726	protein kinase activity
Glycerol kinase			-1.663	1.544	glycerol kinase activity
fumble			-1.447	1.406	chromosome segregation; cytokinesis; cytoplasm; meiosis; membrane organization and biogenesis; mitosis; pantothenate kinase activity; plasma membrane; spermatogenesis; spindle
Fak-like tyrosine kinase (PR2)			-1.414	1.204	cellular_component unknown; non-membrane spanning protein tyrosine kinase activity; protein amino acid phosphorylation; protein-tyrosine kinase activity
Longevity assurance gene 1			-1.343	1.299	plasma membrane, ser/thr kinase activity
skiff			-1.277	1.247	guanylate kinase activity; plasma membrane
Calcium ion-binding					
TpnC4	-0.801	2.319			calcium ion binding
Putative Achaete Scute Target 1	-0.753	1.414			calcium ion binding; endocytosis
Calreticulin	-0.706	1.408			calcium ion binding; central nervous system development; endoplasmic reticulum lumen; peripheral nervous system development

inactivation no afterpotential D	-0.678	1.471			calmodulin binding; deactivation of rhodopsin mediated signaling; inaD signaling complex; myosin binding; phototransduction; protein localization; receptor signaling complex scaffold activity; rhabdomere; structural molecule activity
CG9297	-0.672	1.449			calcium ion binding; calcium ion transport
CG10126	-0.644	1.402			calcium ion binding
Myosin alkali light chain 1	-0.618	1.403			calcium ion binding; muscle contraction; muscle motor activity; muscle myosin; myosin; myosin ATPase activity
Senescence marker protein-30			-1.326	1.438	calcium ion binding
aralar1			-1.314	1.310	calcium ion binding; carrier activity; integral to membrane; mitochondrial inner membrane; mitochondrial membrane; mitochondrial transport; transport
regucalcin			-1.139	1.285	calcium ion binding
Cell-cell signaling and hormone					
Juvenile hormone epoxide hydrolase 2	-0.865	1.469	-1.124	1.246	epoxide hydrolase activity; juvenile hormone catabolism; juvenile hormone epoxide hydrolase activity; microsome
Juvenile hormone epoxide hydrolase 1	-0.861	1.485	-1.618	1.335	epoxide hydrolase activity; juvenile hormone catabolism; juvenile hormone epoxide hydrolase activity
Tetraspanin 42Ef	-0.780	1.322			integral to membrane
Tetraspanin 42Eg	-0.762	1.373			integral to membrane
Activin Like Protein at 23B	-0.731	1.458			transforming growth factor-beta receptor binding
Neuroglian	-0.685	1.390			EGF receptor signaling pathway; cell adhesion molecule activity; central complex development; lateral plasma membrane; mushroom body development; neuronal cell adhesion; plasma membrane
Keren	-0.612	1.246			EGF receptor signaling pathway; MAPKKK cascade; epidermal growth factor receptor binding; growth factor activity; plasma membrane; positive regulation of EGF receptor activity
Imaginal disc growth factor 1			-1.764	1.469	chitinase activity; extracellular; imaginal disc growth factor activity
Esterase 6			-1.415	1.372	carboxylesterase activity; courtship behavior; pheromone biosynthesis; regulation of female receptivity, post-mating; sexual reproduction
Synaptic vesicle					
Syntaxin 5	-0.741	1.407			Golgi apparatus; cytokinesis; neurotransmitter secretion; plasma membrane; synaptic vesicle docking; synaptic vesicle fusion; t-SNARE activity
gammaSnap	-0.686	1.308			gamma-soluble NSF attachment protein; cytoplasm; neurotransmitter secretion; soluble NSF attachment protein activity; synaptic vesicle priming
Scamp	-0.609	1.306	-1.157	1.206	synaptic vesicle; synaptic vesicle exocytosis
CG11857			-1.182	1.356	vesicle-mediated transport
Transcription factor/ DNA binding					
Clock	-0.870	1.393			
anterior open	-0.825	1.388			JNK cascade; MAPKKK cascade; R7 development; cell fate determination; dorsal closure; induction of apoptosis; negative regulation of RAS protein signal transduction; negative regulation of cell differentiation; negative regulation of eye photoreceptor development (sensu Drosophila); negative regulation of photoreceptor differentiation (sensu Drosophila); nucleus; specific RNA polymerase II transcription factor activity; transcription factor activity; transcriptional repressor activity
Tis11 homolog	-0.747	1.611			DNA binding; nucleus

Elongin C	-0.701	1.331			transcription elongation factor complex; transcriptional elongation regulator activity
Jun-related antigen	-0.695	1.334	-1.893	1.424	JNK cascade; MAPKKK cascade; R3/R4 cell fate commitment; R7 cell fate commitment; RNA polymerase II transcription factor activity; cytoplasm; dorsal appendage formation; dorsal closure; establishment of planar polarity; micropyle formation; nucleus; protein heterodimerization activity; regulation of transcription from Pol II promoter; specific RNA polymerase II transcription factor activity; transcription factor binding
boule	-0.674	1.301			RNA binding; entry into meiosis; male meiosis; meiotic G2/MI transition; nucleus; regulation of translation; spermatogenesis
staufen	-0.654	1.327			RNA binding; RNA localization; apical cortex; basal cortex; bicoid mRNA localization; cell cortex; double-stranded RNA binding; female gamete generation; long-term memory; mRNA 3' UTR binding; mRNA localization, intracellular; microtubule associated complex; microtubule binding; microtubule-based process; neuroblast cell division; pole plasm RNA localization; pole plasm assembly; pole plasm mRNA localization; pole plasm oskar mRNA localization; pole plasm protein localization; positive regulation of oskar mRNA translation; protein localization; regulation of oskar mRNA translation; regulation of pole plasm oskar mRNA localization
CG5735	-0.654	1.349			RNA binding
stripe	-0.629	1.469			RNA polymerase II transcription factor activity; central nervous system development; determination of muscle attachment site; muscle development; nucleus; pigment metabolism; tracheal cell migration (sensu Insecta)
CG17836	-0.610	1.409			protein dimerization activity, transcription factor
vrille			-2.118	1.721	RNA polymerase II transcription factor activity; circadian rhythm; development; locomotor rhythm; nucleus; protein heterodimerization activity; protein homodimerization activity; rhythmic behavior; transcription regulator activity; transcription, DNA-dependent
similar to Deadpan			-1.942	1.411	nucleus; regulation of transcription; transcription factor activity
hairy			-1.781	1.518	bristle morphogenesis; general transcriptional repressor activity; membrane organization and biogenesis; negative regulation of transcription; negative regulation of transcription from Pol II promoter; negative regulation of transcription, DNA-dependent; nucleus; periodic partitioning by pair rule gene; restriction of R8 fate; salivary gland development; salivary gland morphogenesis; specific RNA polymerase II transcription factor activity; specific transcriptional repressor activity
modulator of the activity of Ets			-1.585	1.213	embryonic pattern specification; protein binding; regulation of EGF receptor signaling pathway; regulation of RAS protein signal transduction; regulation of phosphorylation; regulation of transcription, DNA-dependent
nocturnin			-1.550	1.354	nucleic acid binding
Tif-IA			-1.444	1.471	DNA-directed RNA polymerase I complex; RNA polymerase I transcription factor activity; regulation of transcription from Pol I promoter
timeless			-1.417	1.636	circadian rhythm; cytoplasm; eclosion rhythm; entrainment of circadian clock; locomotor rhythm; mating behavior; negative regulation of transcription from Pol II promoter; nucleus; protein binding; protein-nucleus import; regulation of sleep; rhythmic behavior; sleep
CG30420			-1.406	1.397	protein homodimerization activity, transcription factor

fruitless			-1.379	1.215	RNA polymerase II transcription factor activity; central nervous system development; copulation; male courtship behavior; male courtship behavior (sensu Insecta); male courtship behavior (sensu Insecta), orientation; male courtship behavior (sensu Insecta), song production; male courtship behavior (sensu Insecta), wing vibration; male sex differentiation; mating; mating behavior, sex discrimination; nucleus; sex determination; transcription factor activity
Fibrillarin			-1.371	1.323	35S primary transcript processing; small nuclear ribonucleoprotein complex; small nucleolar ribonucleoprotein complex
MTF-1			-1.267	1.427	metal ion homeostasis; nucleoplasm; nucleus; specific RNA polymerase II transcription factor activity; transcription; transcription factor activity
CG11761			-1.264	1.262	DNA binding
drop			-1.194	1.434	dorsal/ventral pattern formation; dorsal/ventral pattern formation, imaginal disc; muscle development; neuroblast cell fate determination; neurogenesis; nucleus; regulation of cell fate; regulation of transcription; specific RNA polymerase II transcription factor activity; ventral cord development; wing morphogenesis
CG5603			-1.158	1.372	nucleus; transcription factor activity
cycle			-1.137	1.265	RNA polymerase II transcription factor activity; behavioral response to cocaine; circadian rhythm; eclosion rhythm; locomotor rhythm; nucleus; positive regulation of transcription from Pol II promoter; positive regulation of transcription, DNA-dependent; regulation of sleep; rhythmic behavior; specific RNA polymerase II transcription factor activity
Cytoskeletal proteins					
Actin 88F	-0.967	2.145			actin filament; cytoskeleton organization and biogenesis; structural constituent of cytoskeleton
Myosin 31DF	-0.916	1.847			actin binding; cytoplasm; motor activity; myosin; myosin ATPase activity
upheld	-0.909	1.546			tropomyosin binding; troponin complex
Protein ejaculatory bulb	-0.847	2.210			extracellular; post-mating behavior; structural molecule activity
flightin	-0.835	2.112			muscle fiber; striated muscle thick filament
Actin 79B	-0.826	1.627			actin filament; cytoskeleton organization and biogenesis; structural constituent of cytoskeleton
BM-40-SPARC	-0.659	1.301			basement membrane; cell adhesion; extracellular matrix
Yolk protein 2	-0.655	1.390			female gamete generation; sex differentiation; structural molecule activity; vitellogenesis
CG8505	-0.654	1.552			structural constituent of cuticle (sensu Insecta) activity
spire	-0.632	1.453			actin binding; actin cytoskeleton organization and biogenesis; eggshell formation (sensu Insecta); female gamete generation; pole plasm RNA localization; pole plasm assembly; pole plasm assembly (sensu Insecta); pole plasm oskar mRNA localization
Tropomyosin 2	-0.628	1.343			actin binding; muscle thin filament tropomyosin; pole plasm assembly
Actin 5C			-1.698	1.478	actin filament; cytoskeleton organization and biogenesis; sperm individualization; structural constituent of cytoskeleton
CG31999			-1.291	1.469	cell adhesion molecule activity; extracellular matrix
CG5869			-1.276	1.275	actin binding; gliogenesis
CG5162			-1.257	1.211	structural molecule activity
Actin 42A			-1.200	1.306	actin filament; cytoskeleton organization and biogenesis; structural constituent of cytoskeleton

Actin-related protein 66B			-1.156	1.384	Arp2/3 protein complex; actin binding; actin cytoskeleton; actin filament; cell cycle dependent actin filament reorganization; cytoskeleton organization and biogenesis; pseudocleavage (sensu Insecta); regulation of actin polymerization and/or depolymerization; structural constituent of cytoskeleton
BM-40-SPARC			-1.122	1.214	basement membrane; cell adhesion; extracellular matrix
Transporters					
CG5002	-1.105	1.801			high affinity sulfate permease activity, extra-cellular transport
CG5853	-1.064	1.857	-1.340	1.481	ATP-binding cassette (ABC) transporter activity
CG3823	-0.947	1.515			tocopherol binding
SRY interacting protein 1	-0.829	1.471	-1.134	1.290	sodium:hydrogen antiporter regulator activity
CG32103	-0.763	1.404			carrier activity; mitochondrial membrane; peroxisomal membrane; transport
ATP synthase-beta	-0.755	1.372			hydrogen-exporting ATPase activity, phosphorylative mechanism; proton transport; proton-transporting ATP synthase complex, catalytic core F(1) (sensu Eukarya)
Nckx30C	-0.731	1.496			calcium ion transport; calcium, potassium:sodium antiporter activity; eye morphogenesis (sensu Drosophila); integral to membrane
CG5802	-0.717	1.341			UDP-galactose transporter activity
CG31793	-0.699	1.329			ATP-binding cassette (ABC) transporter activity; membrane; transport
CG2930	-0.694	1.332			transporter
CG11984	-0.683	1.319			potassium channel regulator activity
porin	-0.675	1.291			mitochondrial outer membrane; mitochondrial transport; voltage-dependent ion-selective channel activity
CG15279	-0.674	1.433			cation:amino acid symporter activity; neurotransmitter:sodium symporter activity
CG9281	-0.665	1.307			ATP-binding cassette (ABC) transporter activity
Na/Ca-exchange protein	-0.643	1.515			calcium:sodium antiporter activity; plasma membrane
CG1746	-0.632	1.289			hydrogen-exporting ATPase activity, phosphorylative mechanism; proton transport; proton-transporting ATP synthase complex, coupling factor F(o) (sensu Eukarya)
CG9090	-0.630	1.346			carrier activity; mitochondrial membrane; phosphate transport; phosphate transporter activity
Multiple drug resistance 65	-0.611	1.508			integral to plasma membrane; multidrug transporter activity; xenobiotic-transporting ATPase activity
CG1718	-0.610	1.346			ATP-binding cassette (ABC) transporter activity
CG7966	-0.609	1.239			selenium binding
Larval serum protein 2			-2.553	1.623	extracellular; larval serum protein complex; nutrient reservoir activity
CG8468			-1.878	1.472	monocarboxylate porter activity
CG8026			-1.839	1.625	carrier activity; folate transport; folate transporter activity; mitochondrial inner membrane; mitochondrial membrane; mitochondrial transport
Transferrin 3			-1.755	2.345	iron ion transporter activity; response to bacteria
Drip			-1.734	1.286	integral to membrane; water channel activity; water homeostasis; water transport; water transporter activity
Larval serum protein 1 beta			-1.670	1.410	extracellular; larval serum protein complex; nutrient reservoir activity
CG13796			-1.533	1.389	glycine transporter activity
CG8062			-1.243	1.396	monocarboxylic acid transporter activity
Na pump alpha subunit			-1.198	1.327	cation transport; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; plasma membrane; sodium/potassium-exchanging ATPase activity; sodium/potassium-exchanging ATPase complex
CG9717			-1.176	1.244	high affinity sulfate permease activity, anion transport

CG5002			-1.173	1.314	high affinity sulfate permease activity
CG3091			-1.122	1.214	tocopherol binding
Metabolism					
Carbohydrate metabolism					
UDP-glycosyltransferase 35b	-1.713	2.252			glucuronosyltransferase activity
Glycerol kinase	-0.959	1.728			glycerol kinase activity
Transaldolase	-0.820	1.436	-1.611	1.323	cytoplasm; pentose-phosphate shunt, non-oxidative branch; transaldolase activity
CG7010	-0.809	1.415			pyruvate dehydrogenase (lipoamide) activity; pyruvate dehydrogenase complex; pyruvate metabolism
CG32444	-0.797	1.486			aldose 1-epimerase activity
Ugt86Da	-0.762	1.487			glucuronosyltransferase activity
Larval visceral protein H	-0.726	1.702			alpha-glucosidase activity; glucose metabolism
glycerol-3-phosphate dehydrogenase	-0.713	1.353			glycerol metabolism; glycerol-3-phosphate dehydrogenase activity; mitochondrion
CG6287	-0.703	1.366			phosphoglycerate dehydrogenase activity
CG1129	-0.699	1.382	-1.251	1.233	mannose-1-phosphate guanylyltransferase activity
Phosphoglycerate kinase	-0.690	1.361			cytoplasm; glycolysis; phosphoglycerate kinase activity
CG5191	-0.681	1.418	-1.951	1.665	glutamyl-tRNA(Gln) amidotransferase activity
fructose-1,6-bisphosphatase	-0.674	1.382			fructose-bisphosphatase activity
Triose phosphate isomerase	-0.659	1.272			triose-phosphate isomerase activity
Glyceraldehyde 3 phosphate dehydrogenase 2	-0.653	1.317			cytoplasm; glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity; glycolysis
Phosphoglyceromutase	-0.644	1.312			phosphoglycerate mutase activity
CG11876	-0.638	1.283			pyruvate dehydrogenase (lipoamide) activity; pyruvate dehydrogenase complex; pyruvate metabolism
CG11909			-3.589	2.014	alpha-glucosidase activity; alpha-glucosidase complex
Glycogen phosphorylase			-1.375	1.388	carbohydrate metabolism; glycogen phosphorylase activity; phosphorylase activity
CG33138			-1.302	1.340	1,4-alpha-glucan branching enzyme activity
CG8036			-1.199	1.229	transketolase activity, pentose-phosphate shunt
Protein					
Endopeptidase					
CG18030	-0.809	2.056			serine-type endopeptidase activity
Serine protease 2	-0.773	2.207			chymotrypsin activity; digestion; proteolysis and peptidolysis; serine-type endopeptidase activity; serine-type peptidase activity
CG5909	-0.741	1.463	-2.804	2.479	proteolysis and peptidolysis; serine-type endopeptidase activity
CG9377	-0.621	1.304			serine-type endopeptidase activity
Neprilysin 4	-0.617	1.346			endothelin-converting enzyme activity; metalloendopeptidase activity
CG8738			-2.122	1.453	serine-type endopeptidase activity
Ser7			-1.848	1.323	proteolysis and peptidolysis; serine-type endopeptidase activity; serine-type peptidase activity; trypsin activity
CG9631			-1.847	1.338	elastase activity; proteolysis and peptidolysis; serine-type endopeptidase activity
CG5896			-1.435	1.346	proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
Protease inhibitors					
CG8066	-0.752	1.438			cysteine protease inhibitor activity
CG7219	-1.360	2.315	-5.101	3.278	serine protease inhibitor activity
Serine protease inhibitor 1			-1.853	1.384	serine protease inhibitor activity

Kaz1-ORFA			-1.385	1.277	serine protease inhibitor activity
Proteolysis					
CG9649	-0.960	1.604			elastase activity; enteropeptidase activity; proteolysis and peptidolysis
Angiotensin converting enzyme	-0.765	1.363			extracellular; peptidyl-dipeptidase A activity; peptidyl-dipeptidase activity; sperm individualization; spermatid nuclear differentiation; zinc ion binding
alphaTrypsin	-0.654	1.841			extracellular; proteolysis and peptidolysis; trypsin activity
CG4847	-0.627	1.348			cathepsin K activity, Proteolysis
CG5798			-3.133	2.033	protein deubiquitination; ubiquitin-specific protease activity
CG3097			-1.946	1.645	carboxypeptidase A activity
Ubiquitin conjugating enzyme 2			-1.595	1.267	ubiquitin conjugating enzyme activity; ubiquitin cycle
omega			-1.276	1.337	dipeptidyl-peptidase IV activity
Peptidyl-alpha-hydroxyglycine-alpha-amidating lyase			-1.148	1.293	peptidylamidoglycolate lyase activity
AA metabolism					
CG6188	-1.723	2.324			glycine N-methyltransferase activity
CG11796	-1.350	1.927			4-hydroxyphenylpyruvate dioxygenase activity
CG5321	-1.180	1.659			gamma-butyrobetaine dioxygenase activity (Vitamin biosynthesis)
CG10621	-0.805	1.475			selenocysteine methyltransferase activity
CG12233	-0.800	1.418			isocitrate dehydrogenase (NAD) activity; mitochondrial matrix; mitochondrion; tricarboxylic acid cycle
CG4233	-0.694	1.394			aspartate metabolism; aspartate transaminase activity; mitochondrial matrix; mitochondrion
CG6415	-0.688	1.285			aminomethyltransferase activity; glycine catabolism; glycine cleavage complex
CG15771	-0.660	1.281			haloacid dehalogenase/epoxide hydrolase
CG5493			-1.885	1.543	cysteine dioxygenase activity
CG1673			-1.683	1.275	branched chain family amino acid biosynthesis; branched-chain-amino-acid transaminase activity; cytoplasm; mitochondrion
Nitrilase and fragile histidine triad fusion protein			-1.573	1.307	nitrilase activity
CG9535			-1.516	1.235	UDP-N-acetylglucosamine diphosphorylase activity
CG32412			-1.294	1.227	glutaminyl-peptide cyclotransferase activity
Lipid metabolism					
CG5966	-1.373	3.186	-2.536	1.655	triacylglycerol lipase activity
CG6675	-0.771	1.396	-3.326	2.031	lipase activity
CG6016	-0.706	1.408			ethanolaminephosphotransferase activity
CG5009	-0.677	1.443			palmitoyl-CoA oxidase activity
CG1444	-0.642	1.264			steroid dehydrogenase activity
CG7529 (JH esterase like)	-0.633	1.375			carboxylesterase activity
CG7529	-0.633	1.375			carboxylesterase activity
Cct1			-1.332	1.276	CTP:phosphocholine cytidylyltransferase 1; choline-phosphate cytidylyltransferase activity; determination of adult life span; female gamete generation
CG6783			-1.283	1.247	fatty acid binding
HMG Coenzyme A synthase			-1.159	1.264	hydroxymethylglutaryl-CoA synthase activity
DNA, RNA and Nucleotide metabolism					
supercoiling factor	-0.913	1.447			DNA supercoiling activity
Deoxyribonuclease II	-0.670	1.298			deoxyribonuclease II activity

Development					
ninjurin A	-0.995	1.527	-2.905	1.394	axon guidance
thread (Inhibitor of apoptosis)	-0.822	1.578	-1.440	1.402	anti-apoptosis; apoptosis; apoptosis inhibitor activity; inhibition of caspase activation; protein monoubiquitination; ubiquitin-protein ligase activity
Buffy	-0.648	1.320			apoptosis; apoptosis activator activity; apoptosis regulator activity; programmed cell death
sticky ch1			-1.242	1.364	peripheral nervous system development
fringe			-1.140	1.229	Golgi apparatus; Golgi stack; N signaling pathway; UDP-glycosyltransferase activity; acetylglucosaminyltransferase activity; dorsal/ventral lineage restriction, imaginal disc; dorsal/ventral pattern formation, imaginal disc; egg chamber formation (sensu Insecta); endoplasmic reticulum; eye morphogenesis (sensu Drosophila); integral to membrane; leg disc metamorphosis; negative regulation of N signaling pathway; positive regulation of N signaling pathway; regulation of N signaling pathway; transferase activity, transferring glycosyl groups; wing margin morphogenesis; wing morphogenesis
prune			-1.128	1.253	eye pigmentation (sensu Drosophila)
Yolk protein 2			-1.124	1.265	female gamete generation; sex differentiation; structural molecule activity; vitellogenesis
Unknown					
CG9989	-1.542	2.076	-3.005	1.860	
CG2004	-1.500	2.228	-1.214	1.362	
CG10553	-1.412	2.031			
CG8317	-1.386	1.974	-1.860	1.481	
CG10560	-1.344	1.748			
CG10513	-1.265	2.135			
CG10420	-1.075	1.691			
CG16926	-1.048	1.493	-1.247	1.252	
CG6429	-0.982	1.834	-2.369	1.942	
CG6908	-0.973	1.673			
CG1416	-0.972	1.563			
CG7079	-0.953	1.490			
CG1441	-0.943	1.603			
CG5156	-0.900	1.593			
CG8206	-0.894	1.481			
CG6921	-0.881	1.492			
CG12560	-0.858	1.479	-2.848	2.059	
CG5295	-0.850	1.473	-1.337	1.357	
CG2217	-0.850	1.483	-1.493	1.507	
CG7832	-0.838	1.565			
CG31676	-0.836	1.411			
CG17352	-0.833	1.552			
CG16772	-0.831	1.506	-3.058	2.006	
CG31764	-0.813	1.571	-1.677	1.447	
CG1774	-0.812	1.419	-1.779	1.443	
CG16978	-0.797	1.553	-3.857	1.968	
CG4618	-0.792	1.383	-1.138	1.288	
CG32647	-0.787	1.404			
CG8128	-0.774	1.348			
CG4710	-0.772	1.563	-1.753	1.822	
CG31436	-0.762	1.445			
CG13328	-0.753	1.401			
CG14542	-0.736	1.314			
CG33091	-0.732	1.325			
CG13360	-0.724	1.327			

CG14645	-0.716	1.729			
CG10639	-0.702	1.368			
yellow-b	-0.690	1.365	-1.200	1.449	
l(3)07882	-0.688	1.285			
CG13631	-0.685	1.287			
CG6910	-0.684	1.349			
CG14259	-0.678	1.346	-1.387	1.432	
CG18021	-0.671	1.292			
CG9312	-0.671	1.304			
CG17059	-0.667	1.333			
CG15203	-0.667	1.346			
CG8229	-0.663	1.340			
CG10103	-0.662	1.277			
CG14536	-0.661	1.364			
CG9821	-0.660	1.475			
CG32706	-0.660	1.321			
CG16817	-0.659	1.330			
CG31352	-0.656	1.406			
CG14687	-0.648	1.311			
CG6218	-0.647	1.303			
CG7778	-0.646	1.320	-2.235	1.940	
CG11791	-0.645	1.300			
CG33091	-0.644	1.334			
Protein ejaculatory bulb II	-0.642	1.954			
CG1124	-0.636	1.316			
CG11309	-0.636	1.305			
jdp	-0.631	1.346			contains a chaperone-j domain; function unknown
CG15304	-0.628	1.300			
CG3556	-0.628	1.251			
CG13565	-0.627	1.413			
CG30084	-0.623	1.415			
CG30492	-0.622	1.396			
CG13551	-0.620	1.366			
CG13315	-0.614	1.399			
CG8309	-0.614	1.339			
CG1882	-0.611	1.253			
Male-specific RNA 57Da	-0.609	1.743			extracellular
CG1021	-0.609	1.344			
CG11594	-0.609	1.377			
CG17278			-3.628	2.135	
CG14567			-3.579	1.901	
CG7299			-3.279	1.707	
CG33085			-2.480	1.605	
CG31324			-2.255	1.524	
CG33056			-2.178	1.685	
CG9914			-2.092	1.393	
CG3165			-2.014	1.414	
CG18779			-1.982	2.115	
CG7192			-1.941	1.480	
CG11819			-1.855	1.780	
CG6891			-1.802	1.405	
CG9400			-1.765	1.400	
CG7816			-1.740	1.726	integral to membrane
CG6830			-1.722	1.430	
CG15046			-1.691	1.378	
CG5059			-1.678	1.514	
CG10680			-1.623	1.394	

CG10824			-1.610	1.310	
CG14186			-1.596	1.423	
CG13795			-1.593	1.506	
CG15678			-1.588	1.340	
CG10167			-1.586	1.426	
CG7296			-1.582	1.439	
CG31052			-1.543	1.326	
CG30269			-1.534	1.297	
CG5172			-1.522	1.615	
CG12065			-1.503	1.320	
CG14495			-1.455	1.302	
CG4269			-1.455	1.906	
polar granule component			-1.446	1.266	Nuclear untranslated RNA gene, encodes an RNA component of polar granules
CG5065			-1.432	1.430	
CG6145			-1.430	1.345	
CG9523			-1.426	1.247	
CG4199			-1.417	1.508	
CG10383			-1.412	1.315	
Olfactory-specific 9			-1.377	1.317	nucleus
CG13335			-1.365	1.521	
CG16718			-1.339	1.813	
CG10512			-1.313	1.367	
CG17734			-1.283	1.269	
CG16887			-1.274	1.310	
Sc2			-1.261	1.211	
CG7530			-1.248	1.363	
CG31006			-1.247	1.314	
CG11825			-1.241	1.216	
CG1648			-1.228	1.320	
CG4962			-1.196	1.274	
CG10514			-1.190	1.233	
CG2121			-1.180	1.423	
CG9304			-1.165	1.332	
CG7135			-1.138	1.426	
CG13117			-1.123	1.257	
CG31006			-1.118	1.272	
Kruppel homolog 2			-1.115	1.390	integral to membrane
		y w		*rosy*	**Description**
Genes Upregulated with Rebound	**Score**	Δ	**Score**	Δ	
Immune related genes					
Diptericin	1.824	2.71807			Gram-negative antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Drosocin	1.344	2.01896			Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; anti-Gram-negative bacterial polypeptide induction; antibacterial humoral response (sensu Invertebrata)
Diptericin B	1.343	1.87401			antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Drosomycin	0.974	1.71847			antifungal humoral response (sensu Invertebrata); antifungal peptide activity

Metchnikowin	0.898	1.47996			Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antifungal humoral response (sensu Invertebrata); antifungal peptide activity
CG4740	0.838	1.61903			Attacin-C
Turandot M			3.532	2.21447	humoral defense mechanism (sensu Protostomia)
Scavenger receptor class C, type I			2.191	1.67428	defense response; integral to plasma membrane; phagocytosis; response to bacteria; scavenger receptor activity
Metabolism					
CG15096	2.104	2.29211			high affinity inorganic phosphate:sodium symporter activity
CG4757	1.111	2.26332	2.549	1.79013	carboxylesterase activity
l(2)08717	1.010	1.59384			high affinity inorganic phosphate:sodium symporter activity
CG5798	0.834	1.50589			protein deubiquitination; ubiquitin-specific protease activity
CG12512	0.823	1.37084			long-chain-fatty-acid-CoA ligase activity
Organic cation transporter	0.782	1.35261			carnitine transporter activity
CG11407			4.003	2.39307	long-chain fatty acid transporter activity
CG11459			2.691	1.72851	NOT cathepsin L activity
CG3239			2.603	1.65053	endothelin-converting enzyme activity
Serine pyruvate aminotransferase			2.283	1.47200	alanine-glyoxylate transaminase activity; mitochondrial matrix; peroxisome; serine-pyruvate transaminase activity
Redox					
Cyp4d21	1.394	1.79932			cytochrome P450 activity; membrane; microsome
Cytochrome P450-18a1	0.873	1.42410			cytochrome P450 activity; membrane; microsome; steroid biosynthesis
Cyp12c1			2.697	1.46903	cytochrome P450 activity; mitochondrion
Cytochrome b5-related			2.477	1.64043	electron transporter activity; mitochondrion
Cyp6d2			2.315	1.54656	cytochrome P450 activity; membrane; microsome
Cell signaling molecules					
CG8147	2.659	3.99306	6.449	3.04393	alkaline phosphatase activity
timeless	1.066	1.97239			circadian rhythm; cytoplasm; eclosion rhythm; entrainment of circadian clock; locomotor rhythm; mating behavior; negative regulation of transcription from Pol II promoter; nucleus; protein binding; protein-nucleus import; regulation of circadian sleep/wake cycle, sleep; rhythmic behavior; sleep
smell impaired 35A	0.836	1.59074			olfaction; protein amino acid phosphorylation; protein kinase activity; protein serine/threonine kinase activity
Unknown					
CG9837	1.500	1.80615			
CG32774	1.368	1.88134			
CG14705	1.349	4.22070			
CG14236	1.249	2.45254			
CG18135	1.105	1.73734			
CG31324	1.049	1.62852			
CG14742	0.841	1.59163			
CG15921	0.789	1.51979			
CG4784			3.762	2.00881	
CG11501			2.636	1.77113	
CG15281			2.419	1.69538	
CG5945			2.311	1.57118	
CG15675			2.288	1.62960	
CG17108			2.249	1.41401	
CG11893			2.244	1.72915	

Supplementary Table S2 for *Interaction between Sleep and the Immune Response in Drosophila: A Role for the NFκB Relish*

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Williams J; Sathyanarayanan S; Hendricks J et al. Interaction
between sleep and the immune response in drosophila: a role for the nfκb
relish. SLEEP 2007;30(4):389-400.

Table S2. Changes in gene expression in Deprivation vs Handled control. Highlighted genes are those that are common to the listed genes that increase in *cyc*^{01} in Table S3. Genes with significant T-statistic values (Score) and fold change (Δ) as determined by SAM (significance analysis of microarrays) are listed for each condition and for each genotype. Genes in each functional category are listed in descending order according to the SAM score.

Genes	***Rosy***		**Description**
Increase with Deprivation	**Score**	Δ	
Immune Response			
CG13422	4.545	10.654	Gram-negative antibacterial peptide activity
Drosomycin	4.186	5.615	antifungal humoral response (sensu Invertebrata); antifungal peptide activity
Attacin-B	3.882	16.456	antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antimicrobial peptide activity; extracellular
Attacin-A	3.704	22.347	Gram-negative antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Metchnikowin	3.524	13.105	Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antifungal humoral response (sensu Invertebrata); antifungal peptide activity
Immune induced protein 1	3.080	4.242	defense response; defense/immunity protein activity; extracellular
Attacin C	2.578	17.456	antibacterial humoral response (sensu Invertebrata); defense response
Diptericin B	2.556	13.409	antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Diptericin	2.181	12.141	Gram-negative antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Drosocin	2.176	12.438	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; anti-Gram-negative bacterial polypeptide induction; antibacterial humoral response (sensu Invertebrata)
Immune induced protein 2	2.155	1.771	defense response; defense/immunity protein activity; extracellular
PGRP-SB1	2.147	5.890	defense response; extracellular; immune response; integral to plasma membrane; peptidoglycan recognition activity
necrotic	2.090	2.042	Tl signaling pathway; antifungal humoral response (sensu Invertebrata); defense response; serine-type endopeptidase inhibitor activity
Relish	1.953	3.854	antibacterial polypeptide induction; antifungal polypeptide induction; immune response; nucleus; specific RNA polymerase II transcription factor activity; transcription factor activity
Peptidoglycan recognition protein LF	1.909	2.659	defense response; integral to plasma membrane; peptidoglycan recognition activity
Thor	1.835	2.110	antibacterial humoral response (sensu Invertebrata); defense response; eukaryotic initiation factor 4E binding; immune response; negative regulation of cell size
Cecropin A2	1.799	17.356	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity
Cecropin A1	1.687	26.928	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Cactus	1.639	1.774	Tl signaling pathway; antifungal humoral response (sensu Invertebrata); antifungal polypeptide induction; antimicrobial humoral response (sensu Invertebrata); cytoplasm; defense response; dorsal appendage formation; dorsal/ventral axis specification; female gamete generation; immune response; negative regulation of protein-nucleus import; response to fungi; transcription factor binding, cytoplasmic sequestering

Cecropin C	1.594	12.494	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Malvolio	1.570	2.396	Natural resistance associated macrophage protein; cation transport (divalent cation (iron) uptake)
Thiolester containing protein IV	1.443	1.995	antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; endopeptidase inhibitor activity
PGRP-SC2	1.415	2.441	defense response; extracellular; immune response; integral to plasma membrane; peptidoglycan recognition activity
Cecropin B	1.363	9.045	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity; antifungal peptide activity; extracellular
Peptidoglycan recognition protein SA	1.326	2.628	anti-Gram-positive bacterial polypeptide induction; defense response; extracellular; immune response; integral to plasma membrane; peptidoglycan recognition activity; perception of bacteria
Defensin	1.319	3.098	Gram-positive antibacterial peptide activity; anti-Gram-positive bacterial polypeptide induction; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Chaperone activity/heat shock protein			
Heat shock protein 68	1.531	1.755	chaperone activity; heat shock protein activity; mitochondrion; response to heat
lethal (2) essential for life	1.425	2.181	heat shock protein activity
CaBP1	1.85117	3.712	protein disulfide isomerase activity
Metabolism			
Carbohydrate			
CG6188	3.023	4.937	glycine N-methyltransferase activity
CG5191	1.954	2.449	glutamyl-tRNA(Gln) amidotransferase activity
CG11307	1.881	1.804	transferase activity, transferring glycosyl groups
CG5802	1.692	2.164	UDP-galactose transporter activity
Protein - Protease inhibitors			
CG16713	3.246	6.611	serine-type endopeptidase inhibitor activity
CG7219	2.909	4.329	serine-type endopeptidase inhibitor activity
CG6687	2.319	3.737	serine-type endopeptidase inhibitor activity
CG16712	1.472	1.535	serine-type endopeptidase inhibitor activity
Serine protease inhibitor 1	1.907	2.034	serine-type endopeptidase inhibitor activity
Serpin-27A	1.840	2.772	serine-type endopeptidase inhibitor activity
CG17278	1.499072	1.889	Kazal type serine protease inhibitor
Protein - Endopeptidase/Proteolysis			
CG3074	1.935	1.992	cathepsin B activity
CG5909	1.756	3.592	proteolysis and peptidolysis; serine-type endopeptidase activity
CG9631	1.689	1.573	elastase activity; proteolysis and peptidolysis; serine-type endopeptidase activity
Ser7	1.585	1.606	proteolysis and peptidolysis; serine-type endopeptidase activity; serine-type peptidase activity; trypsin activity
CG2056	1.585	1.737	proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
CG9645	1.557	1.697	NOT serine-type endopeptidase activity
CG3505	1.547	1.777	NOT serine-type endopeptidase activity
Dipeptidase B	1.486	1.991	cysteine-type endopeptidase activity; dipeptidyl-peptidase and tripeptidyl-peptidase activity; leucyl aminopeptidase activity; lysosome
CG2358	1.422	1.744	signal peptidase activity; signal peptidase complex; signal peptide processing
CG5896	1.402	1.601	proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
shanti	1.370	1.640	signal peptide peptidase activity
Protein - Biosynthesis			
Aspartyl-tRNA synthetase	1.32647	1.645	aspartate-tRNA ligase activity; aspartyl-tRNA aminoacylation

Translocon-associated protein delta	1.548025	1.659	protein-ER retention; signal sequence binding; translocon
CG32701	1.75065	1.869	signal recognition particle receptor complex; signal sequence binding
Sec61alpha	1.311871	1.776	SRP-dependent cotranslational membrane targeting, translocation; cell death; protein transporter activity; translocon
Sec61beta	1.537833	1.768	SRP-dependent cotranslational membrane targeting, translocation; protein transporter activity; translocon
CG11642	1.413558	1.749	SRP-dependent cotranslational membrane targeting; endoplasmic reticulum
Lipid metabolism			
CG5966	2.796	3.563	triacylglycerol lipase activity
CG6675	1.898	1.718	lipase activity
CG33110	1.314	1.875	fatty acid biosynthesis; very-long-chain fatty acid metabolism
Amino acid metabolism			
CG11089	1.808	1.744	IMP cyclohydrolase activity; phosphoribosylaminoimidazolecarboxamide formyltransferase activity
CG10814	1.926532	2.466	gamma-butyrobetaine dioxygenase activity
ade5	1.33477	1.537	phosphoribosylaminoimidazole carboxylase activity; phosphoribosylaminoimidazolesuccinocarboxamide synthase activity
Redox			
CG8913	2.245	2.418	peroxidase activity
Glutathione S transferase D1	2.028	1.668	glutathione conjugation reaction; glutathione transferase activity
Nmdmc	1.972	2.885	NAD-dependent methylenetetrahydrofolate dehydrogenase;10-formyltetrahydrofolate metabolism; carbohydrate metabolism; magnesium ion binding; methenyltetrahydrofolate cyclohydrolase activity; methylenetetrahydrofolate dehydrogenase (NAD+) activity; methylenetetrahydrofolate dehydrogenase (NADP+) activity; mitochondrion
Glutathione S transferase E1	1.790	2.004	glutathione transferase activity; response to oxidative stress
thioredoxin-2	1.696	1.501	cell redox homeostasis; cellular_component unknown; thiol-disulfide exchange intermediate activity
Cyt-b5	1.508	1.598	electron transport; electron transporter activity; membrane; microsome
CG12116	1.46511	1.764	sepiapterin reductase activity
Signaling Molecules			
GTPase/GTP-binding			
gartenzwerg	1.744	1.802	ARF small monomeric GTPase activity; ER to Golgi transport; Golgi vesicle; intra-Golgi transport
Calcium Ion-Binding			
Amylase distal	2.365	3.356	alpha-amylase activity; calcium ion binding
CG10126	1.633	2.087	calcium ion binding
Kinase			
CG8286	1.505	1.965	protein kinase inhibitor activity
Phosphatase			
astray	2.935	3.368	L-serine biosynthesis; axon guidance; peripheral nervous system development; phosphoserine phosphatase activity
Transcription Factor, DNA/RNA binding			
Pabp2	2.036	2.186	RNA binding; mRNA polyadenylation
hairy	1.840	2.335	bristle morphogenesis; general transcriptional repressor activity; membrane organization and biogenesis; negative regulation of transcription; negative regulation of transcription from Pol II promoter; negative regulation of transcription, DNA-dependent; nucleus; periodic partitioning by pair rule gene; restriction of R8 fate; salivary gland development; salivary gland morphogenesis; specific RNA polymerase II transcription factor activity; specific transcriptional repressor activity
CG5064	1.321	1.660	7S RNA binding; RNA binding; SRP-dependent cotranslational membrane targeting; signal recognition particle
Nop56	1.374939	1.528	nucleolus; small nuclear ribonucleoprotein complex
Neurotransmission/ secretion/receptors			

CG13795	1.659	1.967	amino acid metabolism; sodium:neurotransmitter symporter
Cytoskeletal/Structural			
Ccp84Ab	1.923	2.864	structural constituent of larval cuticle (sensu Insecta)
Annexin IX	1.847	2.006	actin binding; calcium ion binding; calcium-dependent phospholipid binding; phospholipid binding
cheerio	1.612	1.880	actin binding; determination of adult life span
CG6891	1.488	1.506	actin binding
Imaginal disc growth factor 1	1.34889	1.934	NOT chitinase activity; extracellular; imaginal disc growth factor activity
ARP-like	1.752543	1.984	extracellular
Transporter			
CG11785	1.399444	1.613	Golgi stack; vesicle-mediated transport
hoepel2	1.694719	1.939	L-tyrosine transporter activity; membrane
Development			
rhea	2.067	2.041	cell adhesion
thread	1.401	1.570	anti-apoptosis; apoptosis; apoptosis inhibitor activity; inhibition of caspase activation; protein monoubiquitination; ubiquitin-protein ligase activity
ninjurin A	1.369	1.542	axon guidance
Unknown/Other			
CG16772	4.541124	6.621	
CG15066	3.569906	5.652	
CG2217	3.429935	8.960	
CG5791	3.312932	5.263	
CG16978	3.010057	3.218	
CG9989	2.896202	3.345	
CG9358	2.737943	4.083	
CG18279	2.472914	2.043	
CG17107	2.427421	2.201	
CG4786	2.425083	2.155	
CG5778	2.379042	2.176	
CG13947	2.281299	1.953	
CG13335	2.244522	5.055	
CG15067	2.168466	2.074	
CG3165	2.105386	2.331	
CG6429	2.041495	3.204	
CG15825	2.020144	1.963	
CG2004	1.98998	2.524	
CG7296	1.950497	2.462	
CG16844	1.894522	1.730	
CG15065	1.888134	1.634	
CG14567	1.872112	1.791	
CG10420	1.850965	2.216	
CG9080	1.790071	2.145	
SCP-containing protein B	1.780085	2.570	
CG7778	1.757517	2.494	
CG4269	1.745457	7.056	
CG16743	1.709699	2.423	
CG14661	1.689963	1.655	
CG31216	1.679231	1.981	
CG6553	1.62495	2.036	
CG18067	1.584681	1.515	
CG3348	1.579373	2.100	
CG17330	1.573292	1.877	
CG4710	1.557204	2.323	

CG6830	1.555506	1.819	
CG12918	1.546504	2.069	
CG31764	1.539969	2.359	
CG1572	1.520898	1.928	
CG14688	1.496259	1.585	
CG13335	1.444032	1.662	
CG13941	1.440502	2.111	
CG4250	1.435128	1.594	
CG5059	1.413791	1.633	
CG15021	1.408572	1.752	
CG10680	1.376553	1.658	
CG14084	1.372333	1.563	
CG9643	1.364892	1.586	
CG13965	1.359651	1.564	
CG31324	1.344769	1.566	
CG11893	1.327103	1.632	
CG8303	1.320132	2.413	
CG10383	1.319035	1.577	
Decrease from Deprivation	***Rosy***		**Description**
Genes	**Score**	Δ	
Immune Response			
CG16756	-1.45325	1.761	antimicrobial humoral response (sensu Invertebrata); lysozyme activity
CG7227	-2.18567	1.708	defense response; integral to plasma membrane; scavenger receptor activity
Metabolism			
Carbohydrate			
CG4347	-1.24385	1.589	UTP-glucose-1-phosphate uridylyltransferase activity
CG30035	-1.74115	1.560	carbohydrate transport; glucose transporter activity; integral to membrane
CG30035	-1.47138	1.663	carbohydrate transport; glucose transporter activity; integral to membrane
CG11909	-1.75746	1.683	alpha-glucosidase activity; alpha-glucosidase complex
lectin-24Db	-1.79553	1.566	fucose binding; galactose binding; mannose binding
lectin-28C	-1.96298	2.787	galactose binding
Sorbitol dehydrogenase 1	-2.55618	2.082	L-iditol 2-dehydrogenase activity
Serine pyruvate aminotransferase	-1.52119	1.583	alanine-glyoxylate transaminase activity; mitochondrial matrix; peroxisome; serine-pyruvate transaminase activity
Protein - Endopeptidase/Proteolysis			
CG4933	-1.23084	1.589	O-sialoglycoprotein endopeptidase activity
CG8539	-3.61641	2.046	metallocarboxypeptidase activity
Ance-4	-1.21505	1.596	NOT peptidyl-dipeptidase A activity
Angiotensin-converting enzyme-related	-1.42284	1.540	peptidyl-dipeptidase A activity
Lipid metabolism			
Lipid storage droplet-1	-1.45523	2.237	lipid storage
sex-specific enzyme 2	-2.00342	2.108	phosphatidylserine-specific phospholipase A1 activity
alpha-Esterase-1	-1.69667	2.099	carboxylesterase activity
alpha-Esterase-7	-1.51657	1.690	carboxylesterase activity
CG7529	-1.71519	1.565	carboxylesterase activity
Retinoid- and fatty-acid binding protein	-1.57729	1.772	fatty acid binding; microtubule binding; retinoid binding; structural molecule activity; transport
midway	-1.83294	1.683	diacylglycerol O-acyltransferase activity; female gamete generation; regulation of nurse cell apoptosis; sterol O-acyltransferase activity; triacylglycerol biosynthesis
CG8112	-2.20879	1.774	sterol O-acyltransferase activity
CG31637	-1.18037	1.599	sulfotransferase activity
Amino acid metabolism			

Pyrroline 5-carboyxlate reductase	-1.61609	1.531	proline biosynthesis; pyrroline-5-carboxylate reductase activity
CG5840	-1.40442	1.586	pyrroline-5-carboxylate reductase activity
Phosphoribosylamidotransferase 2	-2.06107	1.616	'de novo' IMP biosynthesis; amidophosphoribosyltransferase activity
Redox			
Cyp4ac2	-2.05835	1.856	cytochrome P450 activity; hormone metabolism; insecticide catabolism; membrane; microsome
Cytochrome P450-4e3	-1.26095	1.919	cytochrome P450 activity; membrane; microsome
Cyp6g1	-1.52749	1.683	Resistance to DDT; cytochrome P450 activity; membrane; microsome; response to DDT
Cytochrome P450-18a1	-1.37935	1.552	cytochrome P450 activity; membrane; microsome; steroid biosynthesis
Cytochrome b5-related	-3.44837	1.944	electron transporter activity; mitochondrion
CG6673	-3.66494	2.106	glutathione transferase activity
CG31075	-2.975	1.758	aldehyde dehydrogenase (NAD) activity; mitochondrial matrix; mitochondrion; pyruvate metabolism
Signaling Molecules			
Calcium Ion-Binding			
regucalcin	-1.94243	1.538	calcium ion binding
Kinase			
Hexokinase C	-1.48409	1.792	hexokinase activity
Phosphatase			
CG8147	-2.2293	4.087	alkaline phosphatase activity
CG9238	-1.58769	2.227	protein phosphatase 1 binding; protein phosphatase type 1 regulator activity
CG17124	-2.69683	2.148	protein phosphatase inhibitor activity
CG5171	-1.83983	1.707	trehalose-phosphatase activity
Neurotransmission/ secretion/receptors			
Gonadotropin-releasing hormone receptor	-1.99416	2.847	G-protein coupled receptor activity; G-protein coupled receptor protein signaling pathway; gonadotropin-releasing hormone receptor activity; integral to membrane; integral to plasma membrane; neuropeptide receptor activity; peptide receptor activity
Odorant-binding protein 99a	-1.57418	1.900	odorant binding
CG5958	-1.48408	1.500	retinal binding
Esterase 6	-1.33541	1.634	carboxylesterase activity; courtship behavior; pheromone biosynthesis; regulation of female receptivity, post-mating; sexual reproduction
Transporters			
CG4822	-2.58187	2.617	ATP-binding cassette (ABC) transporter activity
Larval serum protein 2	-1.20189	1.683	extracellular; larval serum protein complex; nutrient reservoir activity
CG15096	-1.7691	2.119	high affinity inorganic phosphate:sodium symporter activity
CG7571	-1.18244	1.794	sodium-independent organic anion transporter activity
Development			
Sema-5c	-1.43799	2.129	axon guidance; plasma membrane
Unknown			
CG4716	-3.66413	1.823	
CG9837	-2.71313	1.713	
CG16898	-2.63173	3.530	
CG15092	-2.61478	2.073	
CG6067	-2.26027	2.244	
CG5867	-2.23533	1.605	
CG18302	-2.21142	2.313	
CG2081	-2.09106	1.747	
CG9497	-2.02177	1.848	
CG10553	-1.93129	1.805	
CG17108	-1.8873	1.504	

CG14021	-1.87858	1.694	
CG10799	-1.61258	1.739	
CG31778	-1.61115	2.088	
CG18240	-1.59046	1.874	
CG18135	-1.58017	1.661	
CG6770	-1.56296	1.500	
CG30019	-1.48086	1.580	

Supplementary Table S3 for *Interaction between Sleep and the Immune Response in Drosophila: A Role for the NFκB Relish*

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Williams J; Sathyanarayanan S; Hendricks J et al. Interaction
between sleep and the immune response in drosophila: a role for the nfκb
relish. SLEEP 2007;30(4):389-400.

Table S3. Changes in gene expression in *cyc*^{01} vs *rosy*. Highlighted genes are those that are common to the listed genes that increase with deprivation in Table S2. Genes with significant T-statistic values (Score) and fold change (Δ) as determined by SAM (significance analysis of microarrays) are listed for each condition and for each genotype. Genes in each functional category are listed in descending order according to the SAM score.

Genes upregulated in *cyc*^{01}	**Score**	**Fold Change**	**Description**
Immune Response			
CG13422	1.231	3.136	Gram-negative antibacterial peptide activity
Metchnikowin	1.225	5.246	Gram-positive antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antifungal humoral response (sensu Invertebrata); antifungal peptide activity
Immune induced protein 1	1.148	3.396	defense response; defense/immunity protein activity; extracellular
spatzle	1.120	3.094	Tl signaling pathway; Toll binding; antifungal humoral response (sensu Invertebrata); antifungal polypeptide induction; defense response; dorsal/ventral axis specification; embryonic axis specification; extracellular; innate immune response; maternal determination of dorsal/ventral axis, oocyte, germ-line encoded; morphogen activity; oocyte dorsal/ventral axis determination; response to fungi
BG4	0.947	3.047	death receptor adaptor protein activity; defense response; immune response; protein binding; signal transduction
CG6459	0.886	2.290	mitochondrial matrix; mitochondrion
CG7227	0.856	2.397	defense response; integral to plasma membrane; scavenger receptor activity
Thor	0.852	2.135	antibacterial humoral response (sensu Invertebrata); defense response; eukaryotic initiation factor 4E binding; immune response; negative regulation of cell size
epithelial membrane protein	0.840	2.493	defense response; integral to plasma membrane; plasma membrane; scavenger receptor activity
Drosomycin	0.818	2.278	antifungal humoral response (sensu Invertebrata); antifungal peptide activity
Diptericin	0.816	3.160	Gram-negative antibacterial peptide activity; antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
PGRP-SB1	0.810	2.263	defense response; extracellular; immune response; integral to plasma membrane; peptidoglycan recognition activity
Dorsal-related immunity factor	0.777	2.248	DNA binding; Tl signaling pathway; cytoplasm; defense response; immune response; innate immune response; nucleus; response to fungi; transcription factor activity
CG8193	0.768	2.221	defense response; monophenol monooxygenase activity
CG2736	0.758	2.144	defense response; integral to plasma membrane; scavenger receptor activity
Attacin-C	0.757	2.680	antibacterial humoral response (sensu Invertebrata); defense response

dorsal	0.746	3.366	DNA binding; RNA polymerase II transcription factor activity; Tl signaling pathway; anterior/posterior pattern formation; cytoplasm; defense response; dorsal/ventral axis specification; dorsal/ventral pattern formation; ectoderm cell fate specification; ectoderm development; gastrulation; germ-cell migration; heart development; immune response; maternal determination of anterior/posterior axis, embryo; mesoderm cell fate specification; mesoderm development; morphogen activity; negative regulation of transcription; negative regulation of transcription from Pol II promoter; negative regulation of transcription, DNA-dependent; nucleus; positive regulation of transcription from Pol II promoter; positive regulation of transcription, DNA-dependent; regulation of transcription; specific RNA polymerase II transcription factor activity; transcription factor activity; transcriptional activator activity; transcriptional repressor activity; ventral cord development
Relish	0.745	2.112	antibacterial polypeptide induction; antifungal polypeptide induction; immune response; nucleus; specific RNA polymerase II transcription factor activity; transcription factor activity
Lysozyme D	0.739	2.653	antimicrobial humoral response (sensu Invertebrata); chitinase activity; lysozyme activity
Diptericin B	0.686	2.413	antibacterial humoral response (sensu Invertebrata); antibacterial peptide activity
Drosocin	0.682	2.367	Gram-negative antibacterial peptide activity; Gram-positive antibacterial peptide activity; anti-Gram-negative bacterial polypeptide induction; antibacterial humoral response (sensu Invertebrata)
Chaperone activity/Heat shock			
CG7033	1.921	8.886	chaperone activity; chaperonin-containing T-complex
CG10635	1.311	3.740	'de novo' protein folding; co-chaperonin activity; prefoldin complex
Cctgamma	1.044	2.700	chaperonin ATPase activity; chaperonin-containing T-complex; cytoplasm; protein folding
CG4461	0.986	2.465	heat shock protein activity; response to heat
Hop	0.899	2.515	Hsp70/Hsp90 organizing protein activity; chaperone activity
Roe1	0.874	2.167	chaperone activity; mitochondrial matrix; mitochondrion; protein-mitochondrial targeting
CaBP1	0.874	2.275	protein disulfide isomerase activity
CG7409	0.791	2.119	chaperone activity
l(2)efl	0.759	2.168	heat shock protein activity
Tcp1-like	0.711	2.036	ATP binding; chaperone activity; chaperonin-containing T-complex; protein folding
Metabolism			
Carbohydrate metabolism			
CG9232	1.579	5.194	UDP-glucose-hexose-1-phosphate uridylyltransferase activity; UTP-galactose-1-phosphate uridylyltransferase activity; cellular_component unknown; galactose metabolism
CG1208	1.212	3.054	glucose transporter activity
Phosphomannomutase 45A	1.072	2.912	phosphomannomutase activity
CG32444	1.038	2.872	aldose 1-epimerase activity
CG31414	1.014	2.661	glucosylceramidase activity
Ugt86Da	0.906	2.341	glucuronosyltransferase activity
CG10627	0.860	2.155	phosphoacetylglucosamine mutase activity
Phosphogluconate dehydrogenase	0.829	2.219	pentose-phosphate shunt; phosphogluconate dehydrogenase (decarboxylating) activity
l(2)k05713	0.827	2.066	glycerol metabolism; glycerol-3-phosphate dehydrogenase activity; mitochondrion
CG33138	0.800	2.141	1,4-alpha-glucan branching enzyme activity
CG10178	0.796	2.088	glucuronosyltransferase activity
CG11796	0.789	2.283	4-hydroxyphenylpyruvate dioxygenase activity
Ugt35b	0.760	2.163	glucuronosyltransferase activity
fringe	0.707	2.090	UDP-glycosyltransferase activity

shaggy	0.696	2.277	N signaling pathway; Wnt receptor signaling pathway; blastoderm segmentation; bristle morphogenesis; circadian rhythm; glycogen synthase kinase 3 activity; heart development; locomotor rhythm; negative regulation of Wnt receptor signaling pathway; protein amino acid phosphorylation; protein localization; protein serine/threonine kinase activity; regulation of protein-nucleus import; regulation of proteolysis and peptidolysis; regulation of smoothened receptor signaling pathway; regulation of transcription, DNA-dependent; rhythmic behavior; segment polarity determination; wing morphogenesis
lectin-28C	0.619	2.197	galactose binding
Protein - Synthesis			
mitochondrial ribosomal protein S17	1.389	4.801	mitochondrial small ribosomal subunit; protein biosynthesis; structural constituent of ribosome
mitochondrial ribosomal protein L30	1.285	3.978	mitochondrial large ribosomal subunit; protein biosynthesis; structural constituent of ribosome
alpha-Man-IIb	1.284	6.678	Golgi apparatus; alpha-mannosidase activity; mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity
CG4406	0.943	2.375	GPI-anchor transamidase activity
CG3639	0.888	2.355	integral to peroxisomal membrane; peroxisome organization and biogenesis; protein-peroxisome targeting
Translocon-associated protein delta	0.812	2.033	protein-ER retention; signal sequence binding; translocon
eIF3-S8	0.701	2.043	cytosol; eukaryotic translation initiation factor 3 complex; translation initiation factor activity; translational initiation
Protein - Protease inhibitors			
Thiolester containing protein III	1.133	3.738	endopeptidase inhibitor activity
Serine protease inhibitor 5	1.096	3.292	serine-type endopeptidase inhibitor activity
CG6687	0.929	2.250	serine-type endopeptidase inhibitor activity
CG7219	0.790	2.069	serine-type endopeptidase inhibitor activity
Macroglobulin complement-related	0.626	2.451	endopeptidase inhibitor activity
Protein - Proteolysis, Degradation			
CG11951	1.752	6.971	membrane alanyl aminopeptidase activity
CG6298	1.399	7.678	chymotrypsin activity; proteolysis and peptidolysis
CG2105	1.347	4.751	proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
Proteasome alpha6 subunit	1.334	3.515	endopeptidase activity; proteasome core complex (sensu Eukarya)
CG9649	1.292	3.610	elastase activity; enteropeptidase activity; proteolysis and peptidolysis
Dipeptidase B	1.178	3.214	cysteine-type endopeptidase activity; dipeptidyl-peptidase and tripeptidyl-peptidase activity; leucyl aminopeptidase activity; lysosome
CG9377	1.150	4.222	NOT serine-type endopeptidase activity
CG11459	1.126	2.899	NOT cathepsin L activity
ProsMA5	1.107	2.756	Proteasome alpha subunit; ATP-dependent proteolysis; endopeptidase activity; proteasome complex (sensu Eukarya); proteasome core complex (sensu Eukarya); ubiquitin-dependent protein catabolism
CG3074	1.001	2.482	cathepsin B activity
CG11771	0.943	2.545	oligopeptidase A activity
Serine protease 2	0.929	12.026	chymotrypsin activity; digestion; proteolysis and peptidolysis; serine-type endopeptidase activity; serine-type peptidase activity
CG3775	0.921	2.511	neprilysin activity
CG31217	0.918	2.532	Serine protease like 89E; low-density lipoprotein receptor activity; proteolysis and peptidolysis; scavenger receptor activity; serine-type endopeptidase activity
CG4914	0.834	2.248	proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
Ance-4	0.832	2.770	NOT peptidyl-dipeptidase A activity
Neprilysin 4	0.791	2.117	endothelin-converting enzyme activity; metalloendopeptidase activity
CG10472	0.764	2.069	chymotrypsin activity; proteolysis and peptidolysis; serine-type endopeptidase activity
CG4723	0.736	2.045	endothelin-converting enzyme activity
CG4721	0.721	2.028	metalloendopeptidase activity

CG3513	0.709	2.024	endopeptidase activity
CG9372	0.683	2.008	proteolysis and peptidolysis; serine-type peptidase activity; trypsin activity
Lipid metabolism			
alpha-Esterase-2	1.707	6.701	carboxylesterase activity
bubblegum	1.355	5.607	long-chain-fatty-acid-CoA ligase activity
Cct2	1.121	3.428	choline-phosphate cytidylyltransferase activity
CG4757	0.951	3.091	carboxylesterase activity
CG9743	0.819	2.075	stearoyl-CoA 9-desaturase activity
CG5991	0.807	2.055	phosphatidylserine decarboxylase activity
Sphingosine-1-phosphate lyase	0.804	2.129	sphinganine-1-phosphate aldolase activity; sphingolipid catabolism
Lipid storage droplet-2	0.783	2.372	lipid particle; lipid storage; molecular_function unknown
CG17292	0.776	2.098	triacylglycerol lipase activity
CG5397	0.748	2.210	sterol O-acyltransferase activity
CG3523	0.727	2.176	fatty-acid synthase activity
CG15828	0.657	2.143	extracellular space; lipid binding
Amino Acid metabolism			
CG8734	1.174	3.001	acetylglucosaminyltransferase activity; chondroitin sulfate biosynthesis; galactosyltransferase activity; heparan sulfate proteoglycan biosynthesis; transferase activity, transferring glycosyl groups
Updo	1.080	2.938	uroporphyrinogen decarboxylase activity
CG1827	1.021	2.730	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity
NitFhit	1.007	2.591	nitrilase activity
Fumarylacetoacetase	0.968	2.531	fumarylacetoacetase activity
CG8430	0.963	2.783	aspartate metabolism; aspartate transaminase activity; mitochondrial matrix
CG8745	0.916	2.364	ornithine-oxo-acid transaminase activity
homogentisate 1,2-dioxygenase	0.836	2.096	homogentisate 1,2-dioxygenase activity; phenylalanine catabolism; tyrosine catabolism
CG15093	0.825	2.069	3-hydroxyisobutyrate dehydrogenase activity; amino acid metabolism; mitochondrion
CG5618	0.813	2.102	sulfinoalanine decarboxylase activity
ATP citrate lyase	0.743	2.056	ATP citrate synthase activity; acetyl-CoA biosynthesis
CG11089	0.715	2.069	IMP cyclohydrolase activity; phosphoribosylaminoimidazolecarboxamide formyltransferase activity
CG1461	0.707	2.108	tyrosine transaminase activity
Redox			
CG6910	1.848	9.023	oxidoreductase activity; carbohydrate metabolism
Cyp12c1	1.669	6.450	cytochrome P450 activity; mitochondrion
Cyp4p1	1.641	6.421	cytochrome P450 activity; membrane; microsome
Cyp6a23	1.517	5.540	cytochrome P450 activity; membrane; microsome
Cyp6a20	1.460	5.571	cytochrome P450 activity; membrane; microsome
CG6074	1.367	4.674	carbonate dehydratase activity
Cyp6w1	1.266	4.217	cytochrome P450 activity; membrane; microsome
CG9249	1.188	3.102	hexaprenyldihydroxybenzoate methyltransferase activity; ubiquinone metabolism
CG8888	1.153	3.235	oxidoreductase activity, acting on CH-OH group of donors
CG2254	1.112	3.014	oxidoreductase activity
CG12116	1.047	2.713	sepiapterin reductase activity
CG5590	1.045	2.721	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Cyp4ac1	1.024	3.517	cytochrome P450 activity; hormone metabolism; insecticide catabolism; membrane; microsome
CG3902	0.924	2.473	short-branched-chain-acyl-CoA dehydrogenase activity
Cyt-b5	0.869	2.144	electron transport; electron transporter activity; membrane; microsome
CG10638	0.854	2.183	aldehyde reductase activity
Cyp6a2	0.812	2.194	cytochrome P450 activity; membrane; microsome; response to insecticide

CG8446	0.811	2.203	lipoyltransferase activity
CG7724	0.807	2.088	oxidoreductase activity, acting on CH-OH group of donors
Peroxiredoxin 2540	0.805	2.826	antioxidant activity; non-selenium glutathione peroxidase activity; peroxidase activity
CG9436	0.778	2.101	aldehyde reductase activity
CG9265	0.777	2.012	oxidoreductase activity, acting on CH-OH group of donors
Cyp4d20	0.763	2.180	cytochrome P450 activity; membrane; microsome
l(3)neo18	0.759	2.005	NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone; respiratory chain complex I (sensu Eukarya)
CG4769	0.745	2.057	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity; mitochondrial electron transport, ubiquinol to cytochrome c; oxidative phosphorylation; ubiquinol-cytochrome-c reductase complex (sensu Eukarya)
Signaling Molecules			
Acetylcholine synthesis			
CG12345+CG32848	0.698	2.504	Choline acetyltransferase
Adenosine signaling			
CG4802	0.856	2.224	5'-methylthioadenosine phosphorylase activity; cellular_component unknown; phosphorylation
CG11255	0.742	2.015	adenosine kinase activity
Dopamine synthesis/metabolism			
Dat	0.839	2.116	aralkylamine N-acetyltransferase activity; arylamine N-acetyltransferase activity; behavior; biogenic amine catabolism; catecholamine metabolism; dopamine catabolism; octopamine catabolism; regulation of circadian sleep/wake cycle, sleep; serotonin catabolism; sleep
ebony	0.730	2.120	beta-alanyl-dopamine synthase activity; circadian rhythm; cuticle pigmentation; cuticle tanning; dopamine metabolism; locomotor rhythm; negative regulation of melanin biosynthesis; pigment metabolism
GTP-binding/GTPase			
ran	1.283	3.250	RAN small monomeric GTPase activity; Ras GTPase superfamily
RhoGAP88C	1.090	2.922	Rho GTPase activator activity
CG30115	1.065	2.558	guanyl-nucleotide exchange factor activity
sprint	0.937	2.406	Ras interactor activity; cellular_component unknown; endocytosis
drongo	0.877	2.793	small GTPase regulatory/interacting protein activity
Rab11	0.730	2.173	GTP binding; RAB small monomeric GTPase activity; Rho small monomeric GTPase activity; endocytosis; oocyte microtubule cytoskeleton polarization; regulation of pole plasm oskar mRNA localization
CG8801	0.667	2.043	GTP binding; nucleus
Misexpression suppressor of ras 3	0.621	2.140	
G-protein Receptor/ Other receptors			
kekkon-3	1.888	9.344	G-Protein coupled receptor activity; Immunoglobulin and major histocompatibility complex domain
scab	1.726	6.559	calcium-dependent cell adhesion molecule activity; calcium-dependent cell-matrix adhesion; cell adhesion receptor activity; cell migration; cell-matrix adhesion; dorsal closure; focal adhesion; heterophilic cell adhesion; integral to membrane; integrin complex; laminin receptor activity; learning and/or memory; locomotion; memory; midgut development; olfactory learning; plasma membrane; salivary gland development; short-term memory; structural molecule activity; tracheal system development (sensu Insecta)
CG11155	1.603	6.361	kainate selective glutamate receptor activity
Gonadotropin-releasing hormone receptor	1.450	7.464	
Nmda1	1.343	4.261	N-methyl-D-aspartate selective glutamate receptor activity; N-methyl-D-aspartate selective glutamate receptor complex

cryptochrome	1.178	3.119	
downstream of receptor kinase	1.169	4.076	RAS protein signal transduction; SH3/SH2 adaptor protein activity; determination of anterior/posterior axis, embryo; memory; olfactory learning; plasma membrane; sevenless signaling pathway; torso signaling pathway
Neuroglian	1.127	3.367	EGF receptor signaling pathway; cell adhesion molecule activity; central complex development; lateral plasma membrane; mushroom body development; neuronal cell adhesion; plasma membrane
Kekkon-4	1.028	2.569	Immunoglobulin and major histocompatibility complex domain, Immunoglobulin C-2 type
CG31221	1.022	3.062	lipoprotein receptor activity
inflated	1.013	2.994	cell adhesion receptor activity; cell migration; cell-cell adhesion; cell-matrix adhesion; heterophilic cell adhesion; integrin complex; maintenance of protein localization; midgut development; muscle attachment; muscle fiber; myofibril assembly; protein binding; salivary gland development; tracheal cell migration (sensu Insecta); wing morphogenesis
neuropeptide F receptor	0.988	2.554	
roughoid	0.937	2.550	EGF receptor signaling pathway; cone cell fate commitment (sensu Drosophila); integral to membrane; integral to plasma membrane; leg disc proximal/distal pattern formation; photoreceptor fate commitment (sensu Drosophila); plasma membrane; serine-type peptidase activity
Activin Like Protein at 23B	0.886	2.525	transforming growth factor-beta receptor binding
Keren	0.792	2.063	EGF receptor signaling pathway; MAPKKK cascade; epidermal growth factor receptor binding; growth factor activity; plasma membrane; positive regulation of EGF receptor activity
CG31072	0.743	2.006	receptor activity
CG4684	0.713	2.024	SH3/SH2 adaptor protein activity
strawberry notch	0.706	2.410	EGF receptor signaling pathway; N signaling pathway; cone cell fate commitment (sensu Drosophila); embryonic development; female gamete generation; imaginal disc morphogenesis; nucleus; positive regulation of transcription from Pol II promoter; regulation of proteolysis and peptidolysis; wing margin morphogenesis
decapentaplegic	0.588	2.074	BMP signaling pathway; TGFbeta receptor signaling pathway
Kinases			
CG31640	1.585	5.857	receptor signaling protein tyrosine kinase activity; signal transduction
CG13369	1.425	4.131	ribokinase activity
Selenophosphate synthetase 2	1.399	4.629	purine nucleotide binding; selenide, water dikinase activity; selenocysteine biosynthesis
Fps oncogene analog	1.314	6.512	protein tyrosine kinase activity; photoreceptor cell morphogenesis
Cyclin D	1.267	3.741	
Downstream of raf1	1.188	3.554	EGF receptor signaling pathway; MAP kinase activity; MAP kinase kinase activity; MAPKKK cascade
Cad96Ca	1.104	3.010	calcium-dependent cell adhesion molecule activity; calcium-dependent cell-cell adhesion; cellular_component unknown; integral to plasma membrane; protein amino acid phosphorylation; protein kinase activity; protein-tyrosine kinase activity; transmembrane receptor protein tyrosine kinase activity
center divider	0.959	4.079	protein amino acid phosphorylation; protein kinase activity; protein serine/threonine kinase activity
Adenylate kinase-1	0.943	2.350	
sevenless	0.890	2.365	R7 cell fate commitment; R7 development; boss receptor activity; determination of anterior/posterior axis, embryo; plasma membrane; protein amino acid phosphorylation; protein-tyrosine kinase activity; torso signaling pathway; transmembrane receptor protein tyrosine kinase activity
Phosphofructokinase	0.694	2.076	6-phosphofructokinase activity; glycolysis
CG10967	0.610	2.064	receptor signaling protein serine/threonine kinase activity
Phosphatase			
CG9449	1.312	3.437	acid phosphatase activity
Protein phosphatase 2B at 14D	1.283	5.302	calcineurin complex; calcium-dependent protein serine/threonine phosphatase activity; calmodulin binding; protein amino acid dephosphorylation; protein serine/threonine phosphatase activity

Protein tyrosine phosphatase 61F	1.170	4.687	axon guidance; cytoplasm; nucleus; protein amino acid dephosphorylation; protein-tyrosine-phosphatase activity
CG7042	1.078	3.090	protein tyrosine/serine/threonine phosphatase activity
CG1846	0.994	2.725	inositol-1,3,4-trisphosphate 4-phosphatase activity; phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity; phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity
CG3530	0.990	2.928	protein amino acid dephosphorylation; protein tyrosine/serine/threonine phosphatase activity
Multiple inositol polyphosphate phosphatase 1	0.892	2.520	inositol/phosphatidylinositol phosphatase activity; phosphoprotein phosphatase activity
Ptpmeg	0.642	2.090	cytoskeletal protein binding; protein-tyrosine-phosphatase activity
Protein tyrosine phosphatase-ERK/Enhancer of Ras1	0.609	2.145	R7 cell fate commitment; RAS protein signal transduction; cytoplasm; inactivation of MAPK; protein amino acid dephosphorylation; protein-tyrosine-phosphatase activity
Ion Channel			
inx2	1.672	8.328	gap junction; innexin channel activity; integral to membrane
nAcRalpha-18C	1.364	6.104	nicotinic acetylcholine-activated cation-selective channel activity; nicotinic acetylcholine-gated receptor-channel complex
SK	1.214	3.153	small conductance calcium-activated potassium channel
CG31116	0.831	2.815	chloride channel activity; chloride transport
cacophony	0.731	2.847	apical plasma membrane; basolateral plasma membrane; calcium ion transport; courtship behavior; epithelial fluid transport; male courtship behavior (sensu Insecta), song production; phototransduction; visual behavior; voltage-gated calcium channel activity; voltage-gated calcium channel complex
Calcium Ion Binding			
CG10022	1.232	3.387	calcium ion binding
Amylase distal	1.060	3.501	alpha-amylase activity; calcium ion binding
Troponin C at 73F	0.965	2.505	
CG17272	0.772	2.145	
Glutactin	0.701	2.073	basement membrane; calcium ion binding
CG17271	0.691	2.100	
Calpain-B	0.602	2.057	calpain activity
Nckx30C	0.574	2.031	calcium ion transport; calcium, potassium:sodium antiporter activity; eye morphogenesis (sensu Drosophila); integral to membrane
Cell-cell signaling/neurotransmission			
Pigment-dispersing factor	1.197	2.913	circadian rhythm; eclosion rhythm; gravitactic behavior; locomotor rhythm; neuropeptide hormone activity; neuropeptide signaling pathway
ubisnap	0.921	2.276	neurotransmitter secretion; soluble NSF attachment protein activity; synaptic vesicle fusion; t-SNARE activity; vesicle-mediated transport
Allatostatin 2	0.867	2.251	hormone activity; neuropeptide hormone activity; neuropeptide signaling pathway; regulation of heart rate
Odorant-binding protein 99b	0.761	2.291	
Syntaxin 6	0.712	2.264	neurotransmitter secretion; plasma membrane; synaptic vesicle docking; synaptic vesicle fusion; t-SNARE activity
Accessory gland peptide 63F	0.628	2.060	physiological process; post-mating behavior
CG5958	0.833	2.350	retinal binding
Transcription Factor, DNA/RNA Binding			
CG9104	1.547	4.945	nucleus; transcription factor activity
bicaudal	1.545	4.460	nascent polypeptide-associated complex; transcription factor activity
anterior open	1.485	4.660	JNK cascade; MAPKKK cascade; R7 development; cell fate determination; dorsal closure; induction of apoptosis; negative regulation of RAS protein signal transduction; negative regulation of cell differentiation; negative regulation of eye photoreceptor development (sensu Drosophila); negative regulation of photoreceptor differentiation (sensu Drosophila); nucleus; specific RNA polymerase II transcription factor activity; transcription factor activity; transcriptional repressor activity

Smn	1.334	3.445	survival motor neuron
Sox100B	1.303	13.831	Regulation of transcription from Pol II promoter; sex determination
Heterogeneous nuclear ribonucleoprotein at 87F	1.271	7.200	RNA binding; chromatin; heterogeneous nuclear ribonucleoprotein complex; nuclear speck; nucleoplasm; nucleus; ribonucleoprotein complex
RNA-binding protein 4F	1.181	3.251	RNA binding
Mat1	1.162	4.141	general RNA polymerase II transcription factor activity; transcription factor TFIIH complex; transcription initiation from Pol II promoter
ventral veins lacking	1.125	3.641	DNA binding; RNA polymerase II transcription factor activity; dendrite morphogenesis; nucleus; peripheral nervous system development; protein binding; regulation of transcription, DNA-dependent; tracheal cell fate determination (sensu Insecta)
E(spl) region transcript mbeta	1.125	2.819	DNA binding; N signaling pathway; eye morphogenesis (sensu Drosophila); negative regulation of transcription; neurogenesis; nucleus; specific transcriptional repressor activity; transcription factor activity
CG5728	1.088	2.772	RNA binding; nucleolus; rRNA processing
lola like	1.044	3.442	nucleus; regulation of transcription from Pol II promoter; specific RNA polymerase II transcription factor activity
Jun-related antigen	0.953	2.299	JNK cascade; MAPKKK cascade; R3/R4 cell fate commitment; R7 cell fate commitment; RNA polymerase II transcription factor activity; cytoplasm; dorsal appendage formation; dorsal closure; establishment of planar polarity; micropyle formation; nucleus; protein heterodimerization activity; regulation of transcription from Pol II promoter; specific RNA polymerase II transcription factor activity; transcription factor binding
CG15636	0.945	2.724	DNA binding; nucleus
Optix	0.942	2.533	DNA binding; RNA polymerase II transcription factor activity; eye morphogenesis (sensu Drosophila); nucleus; transcription factor activity
48 related 1	0.909	2.401	nucleus; regulation of transcription; transcription factor activity
glass	0.905	3.215	eye photoreceptor development (sensu Drosophila); nucleus; photoreceptor fate commitment (sensu Drosophila); specific RNA polymerase II transcription factor activity; transcription factor activity
dalao	0.871	2.422	DNA binding; chromatin remodeling; chromatin remodeling complex; general RNA polymerase II transcription factor activity; nucleosome remodeling complex; nucleus
Small ribonucleoprotein particle protein B	0.868	2.194	RNA metabolism; mRNA splicing; nucleus; small nuclear ribonucleoprotein complex; spliceosome complex
Mes4	0.865	2.201	nucleus; transcription factor activity
pipsqueak	0.859	3.191	DNA binding; nucleus; pole plasm assembly
hairy	0.840	2.289	bristle morphogenesis; general transcriptional repressor activity; membrane organization and biogenesis; negative regulation of transcription; negative regulation of transcription from Pol II promoter; negative regulation of transcription, DNA-dependent; nucleus; periodic partitioning by pair rule gene; restriction of R8 fate; salivary gland development; salivary gland morphogenesis; specific RNA polymerase II transcription factor activity; specific transcriptional repressor activity
modulo	0.819	2.473	DNA binding; RNA binding; nucleus; protein binding; spermatid development
Ada2A	0.812	2.176	Ada2/Gcn5/Ada3 transcription activator complex; histone acetyltransferase activity
biniou	0.805	2.122	mesoderm cell fate commitment; nucleus; transcription factor activity
Germ line transcription factor 1	0.798	2.177	DNA binding; DNA replication; DNA replication factor C complex; nucleus
Suppressor of variegation 205	0.797	2.103	centric heterochromatin; chromatin binding; chromosome, telomeric region; establishment of chromatin silencing; nuclear heterochromatin; nucleus
Nonsense-mediated mRNA 3	0.794	2.020	RNA binding; protein binding; ribosomal large subunit-nucleus export
arrest	0.788	2.027	RNA binding; female gamete generation; female germ-line cyst formation (sensu Insecta); germ-line stem cell division; mRNA 3' UTR binding; mRNA polyadenylation; negative regulation of oskar mRNA translation; negative regulation of translation; protein binding; regulation of oskar mRNA translation; spermatid development

Signal recognition particle protein 54k	0.788	3.732	7S RNA binding; SRP-dependent cotranslational membrane targeting; SRP-dependent cotranslational membrane targeting, signal sequence recognition; signal recognition particle; signal sequence binding
combgap	0.775	2.261	nucleus; transcription factor activity; wing morphogenesis
CG5064	0.747	2.009	7S RNA binding; RNA binding; SRP-dependent cotranslational membrane targeting; signal recognition particle
reversed polarity	0.737	2.001	RNA polymerase II transcription factor activity; glial cell differentiation; nucleus; regulation of transcription from Pol II promoter
suppressor of Hairy wing	0.690	2.117	DNA binding; nucleus
CG11386	0.603	2.014	regulation of translation, structural consituent of ribosome, nucleic acid binding
Nucleic Acid Metabolism			
CG8877	1.646	5.734	mRNA splicing; pre-mRNA splicing factor activity; small nuclear ribonucleoprotein complex; snRNP U5; spliceosome complex
Lysyl-tRNA synthetase	1.593	8.342	lysine-tRNA ligase activity; lysyl-tRNA aminoacylation
photorepair	1.511	9.183	DNA repair; deoxyribodipyrimidine photo-lyase activity
CG6418	1.405	3.968	ATP dependent RNA helicase activity; helicase activity
CG33123	1.000	3.171	leucine-tRNA ligase activity
Ski6	0.974	2.535	3'-5' exoribonuclease activity; cytoplasmic exosome (RNase complex); nuclear exosome (RNase complex); polytene chromosome
CG6796	0.880	2.204	asparagine-tRNA ligase activity
Ribonuclease X25	0.873	2.514	endoribonuclease activity
Seryl-tRNA synthetase	0.841	2.094	serine-tRNA ligase activity; seryl-tRNA aminoacylation
ribonuclease H1	0.822	2.096	ribonuclease H1 activity
CG1135	0.742	2.005	nucleolus
Helicase at 25E	0.721	2.069	ATP dependent RNA helicase activity; RNA helicase activity; mRNA splicing; nucleus; spliceosome complex
CG10354	0.667	2.021	5'-3' exoribonuclease activity
Deoxyribonuclease II	0.662	2.066	deoxyribonuclease II activity
Cytoskeletal/Structure			
CG5871	1.868	8.195	hyalurononglucosaminidase activity
CG17052	1.639	5.940	structural constituent of peritrophic membrane (sensu Insecta)
jaguar	1.424	4.432	actin binding; basal protein localization; cytoplasm; dorsal closure; endocytic vesicle; intercellular junction maintenance; membrane organization and biogenesis; microtubule associated complex; microtubule binding; motor activity; myosin; myosin ATPase activity; neuroblast cell division; non-muscle myosin; oogenesis (sensu Insecta); protein binding; pseudocleavage (sensu Insecta); spermatid development; unconventional myosin
CAP	1.365	3.788	focal adhesion; vinculin binding
SCAR	1.232	3.164	actin binding; cytoskeletal regulator activity
CG2555	1.226	3.157	structural constituent of larval cuticle (sensu Insecta)
l(2)06496	1.216	3.241	dynactin complex; microtubule-based movement
CG17052	1.191	3.188	structural constituent of peritrophic membrane (sensu Insecta)
cheerio	1.186	3.071	actin binding; determination of adult life span
spire	1.136	3.204	actin binding; actin cytoskeleton organization and biogenesis; eggshell formation (sensu Insecta); female gamete generation; pole plasm RNA localization; pole plasm assembly; pole plasm assembly (sensu Insecta); pole plasm oskar mRNA localization
CG11142	1.126	2.938	structural constituent of peritrophic membrane (sensu Insecta)
Ank2	1.109	5.469	cytoskeletal anchoring; cytoskeletal protein binding; plasma membrane; structural constituent of cytoskeleton
Actin 42A	1.079	3.134	actin filament; cytoskeleton organization and biogenesis; structural constituent of cytoskeleton
Tropomyosin 1	1.033	2.811	actin binding
Caldesmon-related protein	1.012	2.663	structural molecule activity
Gasp	1.009	3.035	chitin binding; structural constituent of peritrophic membrane (sensu Insecta)

CG33171	0.968	3.384	collagen
CG7970	0.922	2.333	peroxisomal membrane
Ccp84Ab	0.872	3.811	structural constituent of larval cuticle (sensu Insecta)
Actin 88F	0.860	3.983	actin filament; cytoskeleton organization and biogenesis; structural constituent of cytoskeleton
CG8505	0.857	2.390	structural constituent of cuticle (sensu Insecta)
Ecdysone-dependent gene 91	0.852	2.401	structural constituent of pupal cuticle (sensu Insecta)
zormin	0.807	2.259	structural constituent of cytoskeleton
Chd64	0.783	2.193	actin binding
CG13935	0.772	2.103	structural constituent of cuticle (sensu Insecta)
Paramyosin	0.747	2.022	striated muscle thick filament; structural constituent of muscle
Tiggrin	0.746	2.209	binding; extracellular matrix
steamer duck	0.741	2.104	structural constituent of cytoskeleton
upheld	0.729	2.112	tropomyosin binding; troponin complex
CG10323	0.719	2.217	cell adhesion molecule activity; extracellular matrix; structural molecule activity
nuclear fallout	0.698	2.567	centrosome; cytokinesis, actomyosin ring formation; microtubule associated complex; microtubule binding; microtubule-based process
viking	0.645	2.055	collagen; collagen type IV
Transporter Activity			
CG2158	1.583	4.838	nuclear pore
CG13248	1.276	3.689	cationic amino acid transporter activity
CG9887	1.239	4.149	high affinity inorganic phosphate:sodium symporter activity
Tim8	1.199	3.266	mitochondrial inner membrane presequence translocase complex; protein translocase activity; protein transport; protein-mitochondrial targeting
CG3071	1.196	3.466	COPI vesicle coat; retrograde (Golgi to ER) transport
Nhe2	1.158	3.578	regulation of pH; sodium:hydrogen antiporter activity
CG14694	1.147	3.303	reduced folate carrier activity
deltaCOP	1.121	3.263	COPI vesicle coat; retrograde (Golgi to ER) transport
Vha68-1	1.106	3.374	hydrogen-exporting ATPase activity, phosphorylative mechanism; hydrogen-transporting ATPase V1 domain; proton transport
CG17646	1.062	3.618	ATP-binding cassette (ABC) transporter activity
CG4288	0.939	2.593	high affinity inorganic phosphate:sodium symporter activity
CG31085	0.908	2.990	ATP-binding cassette (ABC) transporter activity; transport
CG8860	0.869	2.182	SRP-dependent cotranslational membrane targeting, translocation; protein transporter activity; translocon
CG6070	0.822	2.041	amino acid transporter activity
JhI-21	0.770	2.120	L-amino acid transporter activity; amino acid transporter activity
Zip3	0.764	2.019	Zinc/iron regulated transporter-related protein 3
CG8219	0.752	2.097	nuclear pore; protein carrier activity; protein-nucleus import
no mechanoreceptor potential B	0.741	2.032	hearing; intraflagellar transport
vibrator	0.693	2.018	phosphatidylinositol binding; phospholipid transporter activity
CG11897	0.682	2.020	multidrug transporter activity; xenobiotic-transporting ATPase activity
CG6126	0.673	2.112	organic cation transporter activity
CG3252	0.671	2.025	integral to membrane; neurotransmitter transport; neurotransmitter:sodium symporter activity; potassium:amino acid transporter activity; sodium ion transport
Transportin	0.648	2.042	nuclear pore; protein carrier activity; protein-nucleus import
Eaat1	0.606	2.135	Excitatory amino acid transporter 1
Development			
Nucleolar protein at 60B	1.990	10.416	germ-cell development; nucleolus; nucleus; pseudouridylate synthase activity; rRNA processing
Laminin B1	1.795	10.096	basal lamina; basement membrane; embryonic morphogenesis; histogenesis; organogenesis
modifier of rudimentary	1.637	5.322	

Cad87A	1.391	4.753	calcium-dependent cell adhesion molecule activity; calcium-dependent cell-cell adhesion; integral to membrane; integral to plasma membrane
Brother	1.342	4.611	core-binding factor complex; eye morphogenesis (sensu Drosophila); nucleus; regulation of transcription from Pol II promoter; transcription coactivator activity
lethal (2) 37Cc	1.221	3.548	larval/pupal development (sensu Insecta); mitochondrial membrane; mitochondrion
Ecdysone-inducible gene L2	1.159	3.035	cell adhesion; cell adhesion molecule activity; extracellular
roughex	1.085	2.762	eye morphogenesis (sensu Drosophila); eye-antennal disc metamorphosis; mitotic cell cycle; nucleus; regulation of cell cycle; regulation of meiosis; regulation of mitosis
Yolk protein 2	0.994	2.580	female gamete generation; sex differentiation; structural molecule activity; vitellogenesis
Imaginal disc growth factor 2	0.862	2.371	NOT chitinase activity; extracellular; imaginal disc growth factor activity
Nedd2-like caspase	0.855	2.104	NOT mitochondrion; apoptosis; apoptotic program; caspase activity; cytoplasm; embryonic development (sensu Insecta); metamorphosis (sensu Insecta); regulation of retinal programmed cell death
retina aberrant in pattern	0.770	2.071	cyclin catabolism
dreadlocks	0.750	2.631	SH3/SH2 adaptor protein activity; axon guidance; axonogenesis
Muscle LIM protein at 84B	0.748	2.153	cell differentiation; cytoplasm; myogenesis; nucleus; protein binding
gustavus	0.736	2.574	dorsal appendage formation; oocyte anterior/posterior axis determination
Iris	0.666	2.019	female gamete generation
Other/Unknown			
CG30412	1.855	7.826	
CG33206	1.801	10.610	
CG8155	1.784	7.889	
CG14959	1.770	6.800	
CG10662	1.762	8.162	
CG32954	1.731	12.569	
CG9839	1.727	5.788	
CG10560	1.712	7.710	
CG17906	1.706	7.447	
CG15197	1.706	6.354	
CG8336	1.705	8.382	
CG31052	1.705	5.643	
CG17349	1.691	5.872	
CG31203	1.690	5.719	
CG5739	1.677	8.181	
CG1148	1.644	6.442	
CG13321	1.642	6.495	
CG30387	1.614	6.481	
CG32687	1.613	5.536	
CG13565	1.605	5.480	
CG6115	1.599	5.363	
CG30493	1.598	5.198	
CG31150	1.596	5.890	
CG18779	1.595	6.640	
CG5791	1.593	5.418	
CG12316	1.584	6.390	
CG10082	1.572	5.747	
CG2277	1.563	6.346	
CG14084	1.501	4.860	
CG3625	1.496	6.871	
CG15890	1.470	4.611	
CG1501	1.464	4.972	
CG8204	1.459	3.981	
CG9034	1.454	4.445	

CG5458	1.443	4.776	
CG9318	1.427	5.231	
CG8793	1.420	4.067	
CG5783	1.384	4.792	
CG13601	1.353	4.131	
CG14419	1.340	3.623	
CG13384	1.339	4.316	
CG13999	1.333	3.803	
CG32016	1.325	5.023	
CG18166	1.302	4.438	
CG2614	1.293	3.420	
CG16772	1.292	3.343	
CG7567	1.289	3.844	
CG18162	1.235	3.418	
CG17492	1.232	3.147	
CG10713	1.227	3.241	
CG10618	1.219	3.140	
CG14688	1.210	3.002	
CG30389	1.206	3.147	
CG7275	1.206	3.070	
CG30387	1.203	3.151	
CG11808	1.199	4.105	
CG13213	1.194	5.024	
CG5597	1.190	2.982	
CG7549	1.179	3.345	
CG17111	1.178	3.652	
CG2641	1.172	3.006	
CG31772	1.171	3.190	
CG33129	1.170	2.908	
female-specific independent of transformer	1.165	2.817	
Olfactory-specific 9	1.153	3.432	
CG16743	1.146	3.234	
CG6852	1.146	2.821	
CG3732	1.145	3.292	
CG15383	1.145	2.847	
CG7175	1.137	3.077	
CG1623	1.137	2.801	
CG4042	1.136	3.591	
CG12190	1.133	3.632	
CG10778	1.128	2.878	
CG3698	1.126	3.224	
CG31436	1.124	3.384	
CG9396	1.123	3.074	
CG5053	1.116	5.025	
CG18766	1.109	4.415	
CG31948	1.106	3.249	
CG2330	1.098	2.738	
CG10205	1.097	3.174	
CG15825	1.096	2.942	
CG9511	1.085	3.677	
CG14883	1.074	2.847	
CG3501	1.073	2.876	
Ela	1.071	3.171	Elastin-like
CG10343	1.060	2.590	
CG10562	1.040	2.496	
CG15887	1.032	2.632	

CG1468	1.019	2.646	
CG16826	1.014	8.853	
CG13794	1.001	3.359	
CG7519	0.996	2.560	
CG4930	0.995	2.465	
CG14450	0.992	2.383	
CG12025	0.971	2.491	
CG6665	0.970	2.384	
CG32210	0.950	2.597	
CG1074	0.946	2.435	
CG1785	0.944	2.417	
CG6769	0.933	2.371	
CG13078	0.932	2.331	
CG11753	0.931	2.310	
CG3857	0.928	3.321	
CG11781	0.921	2.227	
CG18081	0.918	2.425	
CG15456	0.917	2.261	
CG12292	0.914	2.407	
CG9572	0.910	2.315	
CG14021	0.905	2.441	
CG12868	0.903	2.235	
CG3002	0.902	2.351	
lcs	0.891	4.607	la costa
CG13908	0.891	2.215	
CG10910	0.889	7.173	
CG11103	0.887	2.231	
CG3735	0.883	2.197	
CG3167	0.883	2.311	
CG10680	0.876	2.354	
CG14984	0.875	2.147	
CG4893	0.872	2.343	
CG5080	0.867	2.160	
CG11737	0.865	2.148	
CG6643	0.863	2.430	
CG3597	0.863	2.150	
CG6630	0.861	2.280	
CG15209	0.856	2.212	
CG6204	0.856	2.460	
CG2813	0.852	2.387	
CG12075	0.852	2.386	
CG6061	0.851	2.318	
CG14481	0.845	2.343	
CG7299	0.844	2.214	
CG17244	0.838	2.222	
CG17734	0.835	2.125	
CG14224	0.833	2.542	
CG15067	0.832	2.155	
CG8928	0.828	2.101	
CG18278	0.827	2.082	
CG30503	0.824	2.131	
CG17189	0.818	2.139	
CG14184	0.817	2.179	
CG7781	0.816	2.615	
CG5346	0.815	2.013	
CG7946	0.815	2.088	
CG5778	0.812	2.256	

CG10420	0.811	2.061	
CG12194	0.807	2.109	
SCP-containing protein B	0.804	4.090	
CG30296	0.801	2.397	
CG9394	0.799	2.134	
CG7888	0.797	2.255	
CG9862	0.795	2.053	
CG6912	0.794	2.215	
CG9338	0.792	2.156	
CG11073	0.791	2.258	
CG14277	0.782	2.156	
CG6294	0.781	2.052	
CG16978	0.777	2.117	
CG6834	0.777	2.451	
CG3672	0.776	2.007	
CG7845	0.776	2.157	
CG13607	0.771	2.251	
CG31751	0.768	2.038	
CG15099	0.766	2.442	
CG17660	0.764	2.021	
CG31126	0.762	2.009	
CG2063	0.760	2.068	
CG6479	0.760	2.128	
CG8198	0.760	2.224	
CG6043	0.759	2.344	
CG6416	0.759	2.214	
CG4710	0.756	2.397	
CG11652	0.755	2.159	
CG10332	0.747	2.054	
CG5727	0.746	2.049	
CG33156	0.742	2.056	
CG1443	0.741	2.145	
CG1540	0.740	2.018	
CG13947	0.738	2.321	
CG10326	0.734	2.030	integral to plasma membrane
CG1358	0.734	2.108	
CG6803	0.731	2.111	
CG13830	0.731	2.128	
CG4269	0.724	2.234	
CG4841	0.714	2.316	
CG7245	0.709	2.244	
CG16884	0.702	2.426	
CG30492	0.701	2.118	
CG10639	0.698	2.083	
CG13604	0.695	2.114	
CG9801	0.690	2.197	
CG9497	0.684	2.141	
CG13335	0.683	2.011	
CG5741	0.681	2.214	
CG33056	0.678	2.042	
CG31778	0.673	2.209	
CG12239	0.668	2.150	
CG2121	0.659	2.089	
CG31058	0.648	2.131	
CG9686	0.646	2.069	
CG16953	0.638	2.033	
CG3825	0.637	2.009	

CG6040	0.607	2.841	
CG12808	0.602	2.157	
CG7053	0.592	2.022	
CG13091	0.587	2.136	
CG8736	0.576	2.001	
CG2247	0.574	2.083	

Genes that are upregulated in *rosy*

Genes	**Score**	Δ	**Description**
Metabolism			
Carbohydrate			
Ugt36Bc	-1.914	12.161	glucuronosyltransferase activity
CG17322	-1.865	8.320	2-hydroxyacylsphingosine 1-beta-galactosyltransferase activity
alpha Mannosidase II	-1.500	4.272	Golgi apparatus; Golgi membrane; Golgi stack; N-linked glycosylation; endoplasmic reticulum; mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity; protein amino acid glycosylation
CG31100	-1.196	2.993	integral to membrane; monosaccharide transport; monosaccharide transporter activity
CG11909	-1.064	2.801	alpha-glucosidase activity; alpha-glucosidase complex
COQ7	-0.976	2.371	mitochondrial inner membrane; ubiquinone metabolism
Protein			
CG10602	-1.114	2.813	leukotriene-A4 hydrolase activity
CG1859	-1.082	2.776	serine-type endopeptidase inhibitor activity
small optic lobes	-1.047	2.675	calpain activity; visual behavior
Tequila	-0.998	3.477	pancreatic elastase activity; proteolysis and peptidolysis; serine-type endopeptidase activity; trypsin activity
mitochondrial ribosomal protein S26	-0.964	2.336	mitochondrial small ribosomal subunit; protein biosynthesis; structural constituent of ribosome
CG8830	-0.956	2.557	protein deubiquitination; ubiquitin-specific protease activity
Lipid			
CG33116	-1.388	5.611	CDP-alcohol phosphotransferase activity
CG6567	-1.056	2.770	lysophospholipase activity
Nucleic Acid/Amino Acid			
CG30104	-1.505	5.095	nucleobase, nucleoside, nucleotide and nucleic acid metabolism; nucleotide phosphatase activity
CG10623	-1.138	2.770	selenocysteine methyltransferase activity
CG6045	-0.966	2.491	xanthine dehydrogenase activity
Adenine phosphoribosyltransferase	-0.950	2.336	adenine phosphoribosyltransferase activity; cytoplasm; purine ribonucleoside salvage
Redox			
Cyp6a17	-1.756	24.201	cytochrome P450 activity; membrane; microsome
Cyp6d2	-1.305	3.770	cytochrome P450 activity; membrane; microsome
Cytochrome P450-4e3	-1.143	5.050	cytochrome P450 activity; membrane; microsome
Cyp4p2	-1.140	3.224	cytochrome P450 activity; membrane; microsome
Chaperone			
CG3492	-1.032	2.772	chaperone activity
Cell-cell signaling			
Neuropeptide-like precursor 3	-1.591	5.987	extracellular; neuropeptide hormone activity; neuropeptide signaling pathway
CG32843	-1.148	3.356	G-protein coupled receptor protein signaling pathway; calcitonin receptor activity; integral to membrane; neuropeptide receptor activity; secretin-like receptor activity
CG16832	-1.023	2.786	transmembrane receptor activity; existence uncertain

CG3814	-0.991	2.639	N-methyl-D-aspartate selective glutamate receptor activity; N-methyl-D-aspartate selective glutamate receptor complex
Intracellular signaling			
CG32465	-1.877	10.049	NOT carboxylesterase activity; neurexin binding
pr-set7	-1.586	8.217	histone methylation; histone lysine N-methyltransferase activity (H4-K20 specific)
CNG channel-like	-1.478	5.476	intracellular cyclic nucleotide activated cation channel activity
carnation	-1.300	3.922	SNARE binding; cytosol; endosome to lysosome transport; eye pigmentation (sensu Drosophila); intracellular transport; lysosome organization and biogenesis; membrane; ommochrome biosynthesis; vesicle-mediated transport
Transcription Factor, DNA/RNA binding			
quaking related 54B	-1.479	5.012	RNA binding
Hormone receptor-like in 96	-1.390	4.488	DNA binding; ligand-dependent nuclear receptor activity; nucleus; transcription factor activity
period	-1.155	3.247	behavioral response to cocaine; circadian rhythm; circadian sleep/wake cycle; courtship behavior; cytoplasm; eclosion rhythm; locomotor rhythm; male courtship behavior (sensu Insecta), song production; mating behavior; negative regulation of transcription from Pol II promoter; nucleus; regulation of circadian sleep/wake cycle, sleep; response to light; response to temperature; rhythmic behavior; transcription cofactor activity; transcription corepressor activity; ultradian rhythm
CG7185	-1.152	3.460	RNA binding; mRNA cleavage; mRNA cleavage factor complex
Cyclin C	-1.095	2.895	G1/S transition of mitotic cell cycle; RNA polymerase II transcription mediator activity; cyclin-dependent protein kinase regulator activity; mediator complex; nuclear cyclin-dependent protein kinase holoenzyme complex; transcription initiation from Pol II promoter
okra	-1.043	2.653	ATP-dependent DNA helicase activity; DNA recombination; DNA repair; chromosome condensation; dorsal appendage formation; double-strand break repair; female gamete generation; meiotic recombination
Trap80	-1.002	2.468	RNA polymerase II transcription mediator activity; cell growth and/or maintenance; mediator complex; nucleus; sex comb development; transcription from Pol II promoter; transcription initiation from Pol II promoter
CG6133	-0.969	2.486	DNA (cytosine-5-)-methyltransferase activity
Transporter			
brown	-1.201	3.352	ATP-binding cassette (ABC) transporter activity; eye pigment biosynthesis; eye pigment precursor transport; eye pigment precursor transporter activity; integral to plasma membrane; ommochrome biosynthesis; pteridine biosynthesis
Monocarboxylate transporter 1	-1.095	2.773	monocarboxylic acid transporter activity
CG1718	-0.972	2.795	ATP-binding cassette (ABC) transporter activity
Development			
CG13185	-1.505	5.451	cell cycle; nucleic acid binding
sticky ch1	-1.278	3.885	peripheral nervous system development
Glued	-0.998	2.454	cell fate determination; cytoplasm; dynactin complex; dynein binding; eye photoreceptor development (sensu Drosophila); female gamete generation; microtubule motor activity; microtubule-based movement; photoreceptor differentiation (sensu Drosophila); retrograde axon cargo transport; rhabdomere development; second mitotic wave (sensu Drosophila)
multiple ankyrin repeats single KH domain	-0.997	2.690	cell growth and/or maintenance; cell proliferation; cytoskeletal anchoring; photoreceptor differentiation (sensu Drosophila); structural constituent of cytoskeleton; transmembrane receptor protein tyrosine kinase signaling pathway
Other/Unknown			
CG31152	-1.765	10.060	

CG14432	-1.738	7.132	
CG15599	-1.694	8.755	
CG9424	-1.617	5.192	
CG12417	-1.545	5.099	
CG4294	-1.545	5.709	
CG11893	-1.439	7.051	
CG10681	-1.414	3.839	
CG33203	-1.374	4.369	
CG16812	-1.356	3.635	
CG11693	-1.329	3.562	
CG33154	-1.319	3.504	
CG30181	-1.290	3.854	
CG12812	-1.275	3.774	
CG32209	-1.274	3.487	
CG5195	-1.259	3.547	
CG31188	-1.236	3.097	
CG7044	-1.226	3.408	
CG18240	-1.198	4.235	
CG32440	-1.188	3.649	
CG8460	-1.183	3.744	
GM130	-1.172	3.296	Golgi cis cisterna; Golgi organization and biogenesis; Golgi stack; endoplasmic reticulum
CG10395	-1.160	3.423	
Andropin	-1.156	3.892	Gram-positive antibacterial peptide activity; anti-Gram-positive bacterial polypeptide induction; extracellular; male-specific antibacterial humoral response; male-specific antibacterial peptide activity
CG18107	-1.153	2.977	
CG31324	-1.134	3.831	
SP2523	-1.109	2.861	
CheA75a	-1.106	3.154	
CG14130	-1.099	2.648	
CheB93a	-1.095	3.019	
CG7357	-1.071	2.840	
CG31764	-1.067	3.020	
CG32951	-1.065	2.654	
CG5746	-1.061	3.033	
CG14812	-1.039	2.736	
CG17085	-1.037	2.550	
CG4699	-1.027	3.424	
CG10550	-1.018	2.605	
CG5733	-1.011	2.497	
CG4281	-0.995	2.564	
CG12268	-0.988	2.343	