

CLASS I					
Genes ↑ -	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>Ada2b</i>	chromatin remodeling, positive regulation of histone acetylation, SAGA complex, DNA binding	1.01	10 ⁻³	-0.04	NS
<i>arm</i>	transcription activator activity, protein binding, protein binding, cell adhesion, cell morphogenesis, dorsal closure, imaginal disc-derived wing expansion, positive regulation of JNK cascade, wing disc morphogenesis	2.28	10 ⁻¹¹	0.00	NS
<i>Atg6</i>	autophagic cell death, salivary gland cell autophagic cell death	0.68	10 ⁻²	0.38	NS
<i>B4</i>	imaginal disc development, circadian rhythm	0.97	10 ⁻³	0.37	NS
<i>bun</i>	RNA polymerase II transcription factor activity, autophagic cell death, negative regulation of Notch signaling pathway, decapentaplegic receptor signaling pathway	0.78	10 ⁻²	0.40	NS
<i>crq</i>	scavenger receptor activity, apoptosis, autophagic cell death, immune response, phagocytosis, engulfment, membrane	1.39	10 ⁻⁵	-0.30	NS
<i>Cdk7</i>	general RNA polymerase II transcription factor activity, protein serine/threonine kinase activity	0.88	10 ⁻³	0.23	NS
<i>CG16708</i>	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway, autophagic cell death	0.97	10 ⁻³	0.55	NS
<i>dap</i>	cyclin-dependent protein kinase inhibitor activity, negative regulation of cell cycle	0.84	10 ⁻³	0.23	NS
<i>debcl</i>	induction of apoptosis, DNA damage response, signal transduction resulting in induction of apoptosis, negative regulation of neuron apoptosis	1.15	10 ⁻⁴	0.39	NS
<i>dos</i>	antimicrobial humoral response, determination of anterior/posterior axis, embryo, regulation of Ras protein signal transduction, torso signaling pathway	0.66	10 ⁻²	0.30	NS
<i>Dpt</i>	antibacterial humoral response, defense response to bacterium, innate immune response	1.17	10 ⁻⁴	0.00	NS
<i>EcR</i>	transcription factor activity, sequence-specific DNA binding, ecdysteroid hormone receptor activity, steroid binding, autophagy, imaginal disc-derived wing morphogenesis, metamorphosis, epidermis development	1.11	10 ⁻⁴	-0.02	NS
<i>Eip93F</i>	transcription factor activity,	1.95	10 ⁻⁸	0.28	NS

	autophagic cell death, induction of apoptosis by hormones, phagocytosis, engulfment,				
<i>ewg</i>	specific RNA polymerase II transcription factor activity, imaginal disc morphogenesis, DNA binding, central nervous system development, muscle development	0.85	10^{-3}	0.43	NS
<i>Fps85D</i>	protein binding, dorsal closure, dorsal closure, elongation of leading edge cells, adherens junction, membrane	0.62	10^{-2}	0.00	NS
<i>HLHmbeta</i>	transcription factor activity, Notch signaling pathway, negative regulation of transcription from RNA polymerase II promoter, DNA binding	0.77	10^{-2}	-0.38	NS
<i>HLHdelta</i>	transcription factor activity, Notch signaling pathway, negative regulation of transcription from RNA polymerase II promoter, DNA binding	0.62	10^{-2}	0.27	NS
<i>Idgf2</i>	imaginal disc development, imaginal disc growth factor activity	1.93	10^{-8}	-0.03	NS
<i>jumu</i>	chromatin binding, transcription factor activity, sequence-specific DNA binding, dorsal closure, establishment or maintenance of chromatin architecture, imaginal disc-derived wing morphogenesis	1.32	10^{-4}	0.01	NS
<i>malpha</i>	Notch signaling pathway, cell fate specification	0.75	10^{-2}	0.52	NS
<i>Mef2</i>	RNA polymerase II transcription factor activity, sequence-specific DNA binding, muscle fiber development, skeletal muscle development	1.14	10^{-4}	0.00	NS
<i>Mpk2</i>	MAP kinase activity, MAPKKK cascade, immune response, response to stress	0.64	10^{-2}	-0.15	NS
<i>mys</i>	cell adhesion molecule binding, apposition of dorsal and ventral imaginal disc-derived wing surfaces, cell migration, cell-matrix adhesion, dorsal closure, regulation of cell shape, maintenance of epithelial integrity, open tracheal system	0.69	10^{-2}	-0.09	NS
<i>nec</i>	Toll signaling pathway, antifungal humoral response, immune response	0.99	10^{-3}	-0.27	NS
<i>stck</i>	apposition of dorsal and ventral imaginal disc-derived wing surfaces, dorsal closure, embryonic pattern specification, negative regulation of JNK cascade, cell leading edge	0.96	10^{-3}	0.58	NS
<i>PGRP-SA</i>	Toll signaling pathway, detection of bacterium, immune response, pattern recognition receptor activity	1.38	10^{-5}	-0.53	NS

<i>Phk-3</i>	Ras protein signal transduction, response to bacterium, torso signaling pathway	1.89	10 ⁻⁸	-0.40	NS
<i>psq</i>	transcription factor activity, imaginal disc-derived wing morphogenesis, DNA binding, protein binding	0.97	10 ⁻³	0.10	NS
<i>Rel</i>	transcription factor activity, Toll signaling pathway, immune response, positive regulation of transcription from RNA polymerase II promoter, response to bacterium	1.35	10 ⁻⁵	0.10	NS
<i>Smox</i>	transcription factor activity, transforming growth factor beta receptor signaling pathway, imaginal disc-derived wing morphogenesis	0.69	10 ⁻²	0.19	NS
<i>trbl</i>	protein kinase activity, negative regulation of mitosis	1.18	10 ⁻⁴	0.45	NS
<i>unk</i>	imaginal disc-derived wing morphogenesis, DNA binding, bristle morphogenesis	1.34	10 ⁻⁵	0.19	NS
Genes ↓ -	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>asfl</i>	establishment or maintenance of chromatin architecture, nucleosome assembly, regulation of cell cycle, regulation of nuclear mRNA splicing, via spliceosome	-1.05	10 ⁻³	-0.32	NS
<i>blw</i>	growth, ATP synthesis coupled proton transport, phagocytosis, engulfment	-0.84	10 ⁻³	0.14	NS
<i>bonsai</i>	regulation of growth, translation, structural constituent of ribosome	-0.59	10 ⁻²	0.00	NS
<i>cpa</i>	Wing disc development, actin cytoskeleton organization	-0.65	10 ⁻²	-0.29	NS
<i>dom</i>	establishment or maintenance of chromatin architecture, cell proliferation, regulation of alternative nuclear mRNA splicing, via spliceosome, gene silencing, chromatin remodeling complex	-0.60	10 ⁻²	0.04	NS
<i>dve</i>	imaginal disc-derived wing morphogenesis, transcription factor activity	-0.75	10 ⁻²	-0.21	NS
<i>Gli</i>	maintenance of imaginal disc-derived wing hair orientation	-0.60	10 ⁻²	-0.28	NS
<i>path</i>	regulation of growth, amino acid transport	-1.31	10 ⁻⁵	0.00	NS
<i>Rpd3</i>	histone deacetylase activity, chromatin silencing, gene silencing	-0.87	10 ⁻³	-0.43	NS
<i>Samuel</i>	regulation of growth, spermatogenesis	-0.62	10 ⁻²	0.00	NS
<i>Tor</i>	positive regulation of cell growth, positive regulation of cell size, determination of adult life span	-0.69	10 ⁻²	-0.11	NS
<i>tsr</i>	actin binding, establishment of imaginal disc-derived wing hair	-0.91	10 ⁻³	-0.17	NS

	orientation				
CLASS II					
Genes -↑	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>Bap60</i>	Brahma complex, chromatin remodeling, general RNA polymerase II transcription factor activity	0.54	NS	0.79	10 ⁻⁵
<i>CG3328</i>	transcription factor activity, caspase activity	0.55	NS	0.76	10 ⁻⁴
<i>dalao</i>	Brahma complex, chromatin remodeling, general RNA polymerase II transcription factor activity	0.18	NS	0.68	10 ⁻⁴
<i>eIF3-S10</i>	translation initiation factor activity	0.23	NS	0.62	10 ⁻³
<i>eIF-4a</i>	translation initiation factor activity, regulation of alternative nuclear mRNA splicing, via spliceosome, imaginal disc growth, dorsal/ventral axis specification	0.18	NS	0.68	10 ⁻⁴
<i>E(spl)</i>	transcription factor activity, transcription repressor activity, Notch signaling pathway, cell fate commitment, dendrite morphogenesis, epidermal growth factor receptor signaling pathway, imaginal disc-derived wing margin morphogenesis	-0.03	NS	1.04	10 ⁻⁷
<i>feo</i>	cytokinesis, mitotic spindle stabilization	0.48	NS	0.72	10 ⁻⁴
<i>Fs(2)Ket</i>	regulation of cell shape, actin filament organization,	0.32	NS	0.82	10 ⁻⁵
<i>HDAC6</i>	histone deacetylation	0.23	NS	0.79	10 ⁻⁵
<i>Med</i>	RNA polymerase II transcription factor activity, BMP signaling pathway, cell proliferation, imaginal disc-derived wing morphogenesis, transforming growth factor beta receptor signaling pathway	0.11	NS	0.62	10 ⁻³
<i>Nap1</i>	nucleosome assembly, regulation of transcription, DNA-dependent, histone binding	0.57	NS	1.08	10 ⁻⁷
<i>Sox15</i>	transcription factor activity, ATP binding, aminoacyl-tRNA ligase activity	0.48	NS	0.65	10 ⁻⁴
<i>U2af50</i>	spliceosome assembly, nuclear mRNA splicing, via spliceosome, RNA splicing factor activity, transesterification mechanism	0.50	NS	0.91	10 ⁻⁶
Genes -↓	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>14-3-3zeta</i>	protein binding, Ras protein signal transduction, cell proliferation, protein kinase C inhibitor activity	-0.34	NS	-0.62	10 ⁻³
<i>Akap200</i>	negative regulation of Ras protein signal transduction, autophagic cell death, protein kinase A binding	-0.31	NS	-0.71	10 ⁻⁴

<i>AttC</i>	defense response to bacterium, antibacterial humoral response	0.44	NS	-0.70	10 ⁻⁴
<i>bin</i>	transcription factor activity, sequence-specific DNA binding, mesodermal cell fate commitment, salivary gland morphogenesis	0.50	NS	-0.80	10 ⁻⁵
<i>emc</i>	negative regulation of transcription from RNA polymerase II promoter, protein binding, dorsal closure, imaginal disc-derived wing morphogenesis, cell proliferation	-0.24	NS	-0.66	10 ⁻⁴
<i>ena</i>	dorsal closure, cytoskeleton organization and biogenesis, regulation of cell shape	0.15	NS	-0.65	10 ⁻⁴
<i>Ets21C</i>	transcription factor activity, sequence-specific DNA binding, dendrite morphogenesis	0.00	NS	-0.82	10 ⁻⁵
<i>L(1)19Ec</i>	immune response, dorsal closure, central nervous system development, peripheral nervous system development	-0.14	NS	-0.61	10 ⁻³
<i>Mtk</i>	antibacterial humoral response, antifungal humoral response	0.00	NS	-1.16	10 ⁻⁸
<i>stumps</i>	epithelial cell migration, open tracheal system, mesodermal cell migration fibroblast growth factor receptor signaling pathway	0.36	NS	-0.76	10 ⁻⁴
<i>tlk</i>	protein kinase activity, establishment and/or maintenance of chromatin architecture, regulation of cell shape, histone phosphorylation, antimicrobial humoral response	0.11	NS	-0.67	10 ⁻⁴

CLASS III

Genes ↑ ↓	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>cbt</i>	JNK cascade, dorsal closure, transcription activator activity, positive regulation of transcription, autophagic cell death	1.25	10 ⁻⁴	-0.64	10 ⁻⁴
<i>Cg25C</i>	extracellular matrix structural constituent, collagen type IV, dorsal closure	2.02	10 ⁻⁹	-0.68	10 ⁻⁴
<i>chrb</i>	cell death, negative regulation of signal transduction, negative regulation of growth	0.64	10 ⁻²	-0.71	10 ⁻⁴
<i>Drs</i>	antibacterial humoral response, antifungal humoral response, innate immune response	4.43	0	-3.11	0
<i>Gadd45</i>	JNK cascade	1.82	10 ⁻⁷	-1.12	10 ⁻⁸
<i>IM1</i>	defense response, extracellular region	2.16	10 ⁻¹⁰	-0.94	10 ⁻⁶
<i>scyl</i>	cell death, negative regulation of growth, negative regulation of signal transduction	0.79	10 ⁻²	-0.80	10 ⁻⁵
<i>sda</i>	response to mechanical stimulus, mechanosensory behavior	0.79	10 ⁻²	-0.60	10 ⁻³

<i>Tsf1</i>	defense response, cellular iron ion homeostasis	2.41	10 ⁻¹²	-1.41	10 ⁻¹²
CLASS IV					
Genes ↑↑	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>ash2</i>	protein binding, imaginal disc-derived wing morphogenesis, chromatin-mediated maintenance of transcription	1.01	10 ⁻³	0.78	10 ⁻⁵
<i>bigrmax</i>	transcription factor activity, autophagic cell death, dendrite morphogenesis	0.80	10 ⁻²	0.61	10 ⁻³
<i>bip2</i>	regulation of transcription from RNA polymerase II promoter, protein binding, transcription factor TFIID complex	0.60	10 ⁻²	0.90	10 ⁻⁶
<i>crc</i>	transcription factor activity, metamorphosis, pupation, sequence-specific DNA binding	0.78	10 ⁻²	0.63	10 ⁻³
<i>crp</i>	RNA polymerase II transcription factor activity	0.80	10 ⁻²	0.66	10 ⁻⁴
<i>hdc</i>	cell differentiation, open tracheal system development	1.85	10 ⁻⁸	0.75	10 ⁻⁴
<i>HLHm3</i>	transcription factor activity, specific transcriptional repressor activity, Notch signaling pathway	0.98	10 ⁻³	0.70	10 ⁻⁴
<i>HLHm7</i>	transcription factor activity, compound eye development, dendrite morphogenesis	0.64	10 ⁻²	0.69	10 ⁻⁴
<i>Iap2</i>	anti-apoptosis, antimicrobial humoral response	1.30	10 ⁻⁴	0.69	10 ⁻⁴
<i>lok</i>	protein kinase activity, DNA damage response, signal transduction resulting in induction of apoptosis	0.82	10 ⁻²	0.66	10 ⁻⁴
<i>mod(mdg4)</i>	RNA polymerase II transcription factor activity, chromatin binding, establishment or maintenance of chromatin architecture, induction of apoptosis	0.61	10 ⁻²	0.68	10 ⁻⁴
<i>regucalcin</i>	lipid particle	2.04	10 ⁻⁹	0.63	10 ⁻³
<i>thor</i>	regulation of cell growth, negative regulation of cell size, immune response, antibacterial humoral response	3.13	0	1.44	10 ⁻¹²
Genes ↓↓	GO terms	log FC(C0→C24)	P value	log FC(C24→C72)	P value
<i>Act42A</i>	structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, phagocytosis, engulfment	-0.75	10 ⁻²	-0.87	10 ⁻⁵
<i>Act5C</i>	structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, phagocytosis, engulfment	-0.64	10 ⁻²	-0.98	10 ⁻⁶
<i>Act79B</i>	structural constituent of cytoskeleton, cytoskeleton organization and biogenesis	-1.07	10 ⁻³	-0.77	10 ⁻⁵

<i>Hsp26</i>	determination of adult life span, response to heat	-0.89	10 ⁻³	-0.94	10 ⁻⁶
<i>Hsp27</i>	determination of adult life span, response to heat	-1.54	10 ⁻⁶	-1.33	10 ⁻¹¹
<i>tld</i>	metalloendopeptidase activity, imaginal disc-derived wing vein morphogenesis, specific transcriptional repressor activity, regulation of transforming growth factor beta receptor signaling pathway, positive regulation of BMP signaling pathway	-0.74	10 ⁻²	-0.67	10 ⁻⁴
<i>tok</i>	calcium ion binding, imaginal disc-derived wing vein morphogenesis	-1.20	10 ⁻⁴	-0.78	10 ⁻⁵

Additional file 3.

Representatives of each gene class