

Table S5. Genes preferentially expressed in TD cells

Overlap of TD genes with other lists

| TD & D(wg) | TD & D(wt) | TD & REG | TD & wing |
|------------|-------------|----------|-----------|
| CG14191 | CG4766 | CG10863 | CG10570 |
| CG15629 | CG6906 | CG12840 | CG1698 |
| CG6906 | CG15611 | CG15611 | CG1794 |
| CG7539 | CG17914 | CG1572 | CG1897 |
| | CG1698 | CG3359 | CG3830 |
| | CG4914 | CG5518 | CG4319 |
| | CG9885, dpp | | CG4746 |
| | CG4746 | | CG4766 |
| | CG12840 | | CG4914 |
| | CG6868 | | CG5518 |
| | CG7722 | | CG6044 |
| | | | CG7539 |
| | | | CG8404 |
| TD & V(wg) | TD & V(wt) | | CG9023 |
| CG6530 | CG1897 | | CG9307 |
| CG2918 | | | |
| CG4027 | | | |
| CG4567 | | | |

Genes enriched in TD cells

confidence level >95%, median >0.85 (log2)

| CG # | Synonym | Median (log2) | p-value | Function |
|---------|--------------|---------------|----------|---|
| CG14059 | CG14059 | -4.74 | 2.01E-04 | JAK-STAT cascade; GO:0007259; blastoderm segmentation; GO:0007350; border cell migration (sensu Insecta); GO:0007298; defense response; GO:0006952; embryonic development (sensu Insecta); GO:0001700; foregut morphogenesis; GO:0007440; germ-line stem cell division; GO:0042078; hindgut morphogenesis; GO:0007442; ovarian follicle cell development (sensu Insecta); GO:0030707; primary sex determination; GO:0007538; sex determination; GO:0007530; sex determination, establishment of X:A ratio; GO:0007540; somatic stem cell division; GO:0048103; stem cell division; GO:0017145 |
| CG5993 | upd, os | -3.62 | 1.36E-04 | microtubule-based movement; GO:0007018; wing margin morphogenesis; GO:0008587; wing morphogenesis; GO:0007476 |
| CG3830 | vg | -3.33 | 4.46E-04 | electron transport; GO:0006118; steroid biosynthesis; GO:0006694 |
| CG6816 | Cyp18a1 | -3.24 | 5.53E-03 | amino acid metabolism; GO:0006520; amino acid transport; GO:0006865; cation transport; GO:0006812; extracellular transport; GO:0006858; neurotransmitter transport; GO:0006836 |
| CG15279 | CG15279 | -2.89 | 5.43E-04 | |
| CG4746 | mab-2 | -2.87 | 1.67E-03 | |
| CG30445 | CG3686 | -2.83 | 2.41E-04 | amino acid metabolism; GO:0006520; transmission of nerve impulse; GO:0019226 |
| CG8394 | CG8394 | -2.59 | 8.17E-05 | amino acid metabolism; GO:0006520; amino acid transport; GO:0006865 |
| CG2198 | Ama | -2.38 | 1.05E-06 | cell adhesion; GO:0007155; cell-cell adhesion; GO:0016337; signal transduction; GO:0007165 |
| CG8404 | Sox15 | -2.36 | 6.67E-07 | ectoderm development; GO:0007398; neurogenesis; GO:0007399; regulation of transcription; GO:0045449; regulation of transcription from Pol II promoter; GO:0006357; tRNA aminoacylation for protein translation; GO:0006418 |
| CG5518 | sda | -2.33 | 8.94E-04 | proteolysis and peptidolysis; GO:0006508 |
| CG11822 | nAcRbeta-21C | -2.23 | 3.37E-04 | ion transport; GO:0006811; transport; GO:0006810 |
| CG4914 | CG4914 | -2.21 | 1.42E-05 | proteolysis and peptidolysis; GO:0006508; regulation of transcription, DNA-dependent; GO:0006355 |
| CG3359 | mfas | -2.11 | 1.83E-03 | axonogenesis; GO:0007409; cell-cell adhesion; GO:0016337; ectoderm development; GO:0007398; signal transduction; GO:0007165 |
| CG9307 | CG9307 | -2.11 | 8.53E-04 | chitin metabolism; GO:0006030; polysaccharide metabolism; GO:0005976 |
| CG6906 | CG6906 | -2.08 | 2.31E-03 | one-carbon compound metabolism; GO:0006730 |
| CG4859 | Mmp1 | -2.06 | 2.90E-05 | anti-apoptosis; GO:0006916; autophagic cell death; GO:0048102; dorsal trunk growth; GO:0035001; larval development (sensu Insecta); GO:0002168; proteolysis and peptidolysis; GO:0006508; salivary gland cell death; GO:0035071; tracheal system development (sensu Insecta); GO:0007424 |
| CG7722 | CG7722 | -2.04 | 2.35E-05 | proteolysis and peptidolysis; GO:0006508 |
| CG1897 | msh, Dr | -1.96 | 1.96E-03 | brain development; GO:0007420; central nervous system development; GO:0007417; dorsal/ventral pattern formation; GO:0009953; dorsal/ventral pattern formation, imaginal disc; GO:0007450; ectoderm development; GO:0007398; muscle development; GO:0007517; neuroblast cell fate determination; GO:0007400; neurogenesis; GO:0007399; pattern specification; GO:0007389; regulation of cell fate specification; GO:0042659; regulation of transcription; GO:0045449; regulation of transcription from Pol II promoter; GO:0006357; ventral cord development; GO:0007419; wing morphogenesis; GO:0007476 |
| CG8805 | wun2 | -1.94 | 4.16E-03 | G-protein coupled receptor protein signaling pathway; GO:0007186; dephosphorylation; GO:0016311; germ cell migration; GO:0008354; germ cell programmed cell death; GO:0035234; germ cell repulsion; GO:0035233; lipid metabolism; GO:0006629 |
| CG10570 | CG10570 | -1.89 | 4.23E-03 | |
| CG7447 | CG7447 | -1.85 | 1.12E-04 | |
| CG7539 | Edg91 | -1.83 | 2.83E-03 | |
| CG17914 | yellow-b | -1.82 | 3.70E-03 | |
| CG10121 | SP1173 | -1.79 | 9.58E-05 | |
| CG15484 | CG15484 | -1.76 | 1.82E-04 | |
| CG9023 | Drip | -1.74 | 1.42E-03 | cell homeostasis; GO:0019725; water homeostasis; GO:0030104; water transport; GO:0006833 |
| CG15629 | CG15629 | -1.71 | 2.91E-04 | metabolism; GO:0008152; visual perception; GO:0007601 |
| CG5840 | CG5840 | -1.71 | 1.20E-04 | amino acid biosynthesis; GO:0008652; proline biosynthesis; GO:0006561 |
| CG12840 | Tsp42E1 | -1.68 | 4.23E-03 | ectoderm development; GO:0007398; neurogenesis; GO:0007399; transmission of nerve impulse; GO:0019226 |
| CG15611 | CG15611 | -1.65 | 7.08E-04 | |
| CG3983 | CG3983 | -1.62 | 7.65E-04 | cell surface receptor linked signal transduction; GO:0007166; intracellular protein transport; GO:0006886; intracellular signaling cascade; GO:0007242; |

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|----------------|-----------------------|--------------|-----------------|--|
| | | | | nucleobase, nucleoside, nucleotide and nucleic acid metabolism; GO:0006139; nucleobase, nucleoside, nucleotide and nucleic acid transport; GO:0015931; protein metabolism; GO:0019538; regulation of translation; GO:0006445; signal transduction; GO:0007165; transport; GO:0006810 |
| CG11073 | CG11073 | -1.60 | 6.09E-03 | / |
| CG10697 | Ddc | -1.57 | 1.10E-03 | catecholamine metabolism; GO:0006584; courtship behavior; GO:0007619; cuticle biosynthesis; GO:0042335; dopamine biosynthesis from tyrosine; GO:0006585; eclosion rhythm; GO:0008062; learning and/or memory; GO:0007611; melanin biosynthesis; GO:0042438; pigmentation; GO:0048066; serotonin biosynthesis from tryptophan; GO:0006587 |
| CG14879 | CG14879 | -1.56 | 2.45E-04 | / |
| CG4766 | CG4766 | -1.54 | 2.14E-03 | / |
| CG13097 | CG13097 | -1.48 | 1.90E-03 | nucleobase, nucleoside, nucleotide and nucleic acid metabolism; GO:0006139; rRNA metabolism; GO:0016072 |
| CG5874 | CG5874 | -1.46 | 3.67E-04 | negative regulation of transcription from Pol II promoter, mitotic; GO:0007070 |
| CG3200 | Reg-2 | -1.46 | 1.03E-03 | metabolism; GO:0008152 |
| CG11259 | MICAL-like | -1.45 | 4.16E-03 | cytoskeleton organization and biogenesis; GO:0007010 |
| CG7367 | CG7367 | -1.43 | 3.50E-03 | lipid metabolism; GO:0006629 |
| CG6044 | CG6044 | -1.41 | 2.61E-04 | / |
| CG6724 | CG6724 | -1.39 | 7.40E-05 | / |
| CG17108 | CG17108 | -1.39 | 1.32E-03 | transport; GO:0006810 |
| CG7182 | CG7182 | -1.33 | 4.57E-04 | defense response; GO:0006952; protein folding; GO:0006457; response to heat; GO:0009408; response to stress; GO:0006950 |
| CG6962 | CG6962 | -1.33 | 5.88E-04 | / |
| CG1698 | CG1698 | -1.33 | 7.62E-03 | amino acid metabolism; GO:0006520; amino acid transport; GO:0006865; cation transport; GO:0006812; extracellular transport; GO:0006858; neurotransmitter transport; GO:0006836 |
| CG33188 | CG16750 | -1.33 | 3.13E-04 | perception of sound; GO:0007605 |
| CG4567 | CG4567 | -1.32 | 3.96E-04 | translational elongation; GO:0006414 |
| CG4357 | CG4357 | -1.29 | 9.90E-04 | amino acid transport; GO:0006865; cation transport; GO:0006812; chloride transport; GO:0006821; sodium ion transport; GO:0006814 |
| CG14479 | CG14479 | -1.29 | 1.14E-03 | / |
| CG4319 | rpr | -1.27 | 1.76E-04 | NOT nurse cell apoptosis; GO:0045476; apoptosis; GO:0006915; apoptotic program; GO:0008632; central nervous system metamorphosis; GO:0035193; ecdysone-mediated induction of salivary gland cell death; GO:0035072; embryonic development (sensu Insecta); GO:0001700; induction of apoptosis; GO:0006917; induction of apoptosis by ionic changes; GO:0008627; larval midgut cell death; GO:0035096; negative regulation of protein biosynthesis; GO:0017148; programmed cell death; GO:0012501; protein ubiquitination; GO:0016567; regulation of proteolysis and peptidolysis; GO:0030162; response to DNA damage stimulus; GO:0006974; salivary gland cell death; GO:0035071 |
| CG5836 | SF1 | -1.26 | 3.67E-04 | nuclear mRNA splicing, via spliceosome; GO:0000398 |
| CG2512 | alphaTub84D | -1.24 | 8.02E-06 | cell motility; GO:0006928; cellular physiological process; GO:0050875; chromosome segregation; GO:0007059; intracellular protein transport; GO:0006886; microtubule polymerization; GO:0046785; microtubule-based movement; GO:0007018; microtubule-based process; GO:0007017; mitosis; GO:0007067 |
| CG10161 | eIF-3p66 | -1.23 | 6.05E-03 | protein biosynthesis; GO:0006412; translational initiation; GO:0006413 |
| CG7108 | DNAPol-alpha50 | -1.23 | 7.18E-05 | DNA replication; GO:0006260; DNA replication, synthesis of RNA primer; GO:0006269 |
| CG7628 | CG7628 | -1.23 | 3.00E-03 | phosphate metabolism; GO:0006796; phosphate transport; GO:0006817 |
| CG12534 | CG12534 | -1.23 | 6.45E-04 | electron transport; GO:0006118; oxidative phosphorylation; GO:0006119 |
| CG1210 | Pk61C | -1.22 | 2.77E-03 | actin cytoskeleton organization and biogenesis; GO:0030036; anti-apoptosis; GO:0006916; glycogen metabolism; GO:0005977; insulin receptor signaling pathway; GO:0008286; intracellular signaling cascade; GO:0007242; oogenesis (sensu Insecta); GO:0009993; positive regulation of cell growth; GO:0030307; positive regulation of cell size; GO:0045793; potassium ion transport; GO:0006813; protein amino acid phosphorylation; GO:0006468; regulation of cell growth; GO:0001558; regulation of organ size; GO:0046620; sex differentiation; GO:0007548; spermatogenesis; GO:0007283 |
| CG1091 | CG1091 | -1.22 | 3.21E-03 | / |
| CG3691 | Pof | -1.21 | 4.87E-03 | protein biosynthesis; GO:0006412 |
| CG6014 | CG6014 | -1.21 | 1.01E-03 | / |
| CG5355 | CG5355 | -1.21 | 1.98E-03 | proteolysis and peptidolysis; GO:0006508 |
| CG17124 | CG17124 | -1.20 | 5.00E-06 | / |
| CG17843 | CG17843 | -1.19 | 3.45E-03 | electron transport; GO:0006118 |
| CG17337 | CG17337 | -1.19 | 4.61E-04 | / |
| CG13849 | Nop56 | -1.18 | 1.02E-03 | rRNA metabolism; GO:0016072 |
| CG4978 | Mcm7 | -1.17 | 5.32E-04 | DNA replication initiation; GO:0006270; pre-replicative complex formation and maintenance; GO:0006267 |
| CG10363 | TepIV | -1.17 | 9.13E-03 | antibacterial humoral response (sensu Protostomia); GO:0006961; phosphoenolpyruvate-dependent sugar phosphotransferase system; GO:0009401 |
| CG1572 | CG1572 | -1.16 | 1.05E-03 | / |
| CG7583 | CtBP | -1.16 | 3.75E-03 | L-serine biosynthesis; GO:0006564; negative regulation of transcription from Pol II promoter; GO:0000122 |
| CG11450 | net | -1.15 | 6.91E-03 | regulation of transcription; GO:0045449 |
| CG18410 | CG18410 | -1.14 | 1.13E-03 | / |
| CG13813 | CG13813 | -1.14 | 1.09E-03 | / |
| CG2863 | Nle | -1.12 | 7.95E-04 | G-protein coupled receptor protein signaling pathway; GO:0007186; Notch signaling pathway; GO:0007219 |
| CG6375 | pit | -1.12 | 4.89E-04 | nucleobase, nucleoside, nucleotide and nucleic acid metabolism; GO:0006139 |
| CG6897 | CG6897 | -1.12 | 1.57E-05 | / |
| CG6868 | tld | -1.12 | 1.73E-03 | amnioserosa formation; GO:0007378; embryonic pattern specification; GO:0009880; positive regulation of BMP signaling pathway; GO:0030513; proteolysis and peptidolysis; GO:0006508; regulation of transforming growth factor beta receptor signaling pathway; GO:0017015; terminal region determination; GO:0007362; torso signaling pathway; GO:0008293; zygotic determination of dorsal/ventral axis; GO:0007352 |
| CG5393 | apt | -1.11 | 2.37E-04 | central nervous system development; GO:0007417; heart development; GO:0007507; negative regulation of oskar mRNA translation; GO:0007319; primary tracheal branching (sensu Insecta); GO:0007428; regulation of transcription from Pol II promoter; GO:0006357; tracheal system development (sensu Insecta); GO:0007424 |
| CG11525 | CycG | -1.10 | 6.53E-04 | DNA repair; GO:0006281 |
| CG3568 | CG3568 | -1.07 | 4.84E-05 | / |
| CG6739 | CG6739 | -1.07 | 4.95E-03 | development; GO:0007275 |
| CG13692 | CG13692 | -1.06 | 1.90E-04 | protein amino acid ADP-ribosylation; GO:0006471 |
| CG6023 | CG6023 | -1.06 | 4.55E-04 | / |
| CG11190 | CG11190 | -1.06 | 9.42E-04 | attachment of GPI anchor to protein; GO:0016255 |

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|----------------|-----------------------|--------------|-----------------|---|
| CG1794 | Mmp2 | -1.05 | 5.54E-04 | anti-apoptosis; GO:0006916; oogenesis (sensu Insecta); GO:0009993; proteolysis and peptidolysis; GO:0006508 |
| CG14984 | CG14984 | -1.05 | 8.72E-03 | / |
| CG12358 | Paip2 | -1.05 | 2.03E-03 | negative regulation of translation; GO:0016478 |
| CG3254 | pgant2 | -1.05 | 1.30E-03 | oligosaccharide biosynthesis; GO:0009312; polysaccharide metabolism; GO:0005976; protein amino acid glycosylation; GO:0006486 |
| CG5913 | CG5913 | -1.04 | 2.11E-04 | / |
| CG7478 | Act79B | -1.03 | 4.75E-03 | cytoskeleton organization and biogenesis; GO:0007010 |
| CG10354 | CG10354 | -1.03 | 1.01E-03 | DNA metabolism; GO:0006259; nucleobase, nucleoside, nucleotide and nucleic acid metabolism; GO:0006139 |
| CG32699 | CG18535 | -1.03 | 7.57E-04 | metabolism; GO:0008152 |
| CG3036 | CG3036 | -1.02 | 6.28E-04 | carbohydrate metabolism; GO:0005975; carbohydrate transport; GO:0008643; cation transport; GO:0006812; extracellular transport; GO:0006858; phosphate metabolism; GO:0006796; phosphate transport; GO:0006817 |
| CG15561 | CG15561 | -1.02 | 2.33E-03 | / |
| CG1874 | CG1874 | -1.01 | 3.24E-03 | / |
| CG5114 | CG5114 | -1.00 | 1.68E-03 | / |
| CG7564 | CG7564 | -1.00 | 7.09E-03 | nuclear mRNA splicing, via spliceosome; GO:0000398 |
| CG11990 | CG11990 | -1.00 | 8.99E-05 | / |
| CG10336 | CG10336 | -0.97 | 1.04E-03 | / |
| CG4027 | Act5C | -0.97 | 3.91E-03 | cytoskeleton organization and biogenesis; GO:0007010; sperm individualization; GO:0007291 |
| CG5014 | Vap-33-1 | -0.97 | 8.06E-03 | intracellular protein transport; GO:0006886; neuromuscular junction development; GO:0007528; neurotransmitter secretion; GO:0007269; synaptic transmission; GO:0007268; synaptic vesicle priming; GO:0016082; transmission of nerve impulse; GO:0019226; vesicle-mediated transport; GO:0016192 |
| CG13586 | itp | -0.97 | 8.36E-04 | neuropeptide signaling pathway; GO:0007218 |
| CG8545 | CG8545 | -0.97 | 2.26E-03 | rRNA metabolism; GO:0016072; rRNA processing; GO:0006364 |
| CG4591 | Tsp86D | -0.96 | 9.46E-07 | cell-cell adhesion; GO:0016337; signal transduction; GO:0007165 |
| CG8171 | dup | -0.96 | 1.22E-03 | DNA replication; GO:0006260; DNA replication checkpoint; GO:0000076; DNA-dependent DNA replication; GO:0006261; chorion gene amplification; GO:0007307; eggshell formation (sensu Insecta); GO:0007304 |
| CG1483 | Map205 | -0.96 | 4.67E-03 | microtubule-based process; GO:0007017 |
| CG13780 | Pvf2 | -0.95 | 7.70E-04 | hemocyte cell migration (sensu Arthropoda); GO:0035099; hemocyte proliferation (sensu Arthropoda); GO:0035172 |
| CG10527 | CG10527 | -0.95 | 2.46E-03 | / |
| CG10337 | CG10337 | -0.95 | 5.78E-03 | / |
| CG7839 | CG7839 | -0.95 | 2.87E-03 | regulation of transcription; GO:0045449; regulation of transcription from Pol II promoter; GO:0006357 |
| CG7059 | CG7059 | -0.95 | 5.91E-04 | glycolysis; GO:0006096; microtubule-based movement; GO:0007018 |
| CG13690 | CG13690 | -0.95 | 3.34E-04 | RNA catabolism; GO:0006401 |
| CG1994 | l(1)G0020 | -0.94 | 2.63E-03 | biological process unknown; GO:0000004 |
| CG10645 | lama | -0.94 | 2.49E-04 | / |
| CG7842 | CG7842 | -0.94 | 1.23E-06 | fatty acid biosynthesis; GO:0006633 |
| CG18290 | Act87E | -0.93 | 3.71E-03 | cytoskeleton organization and biogenesis; GO:0007010 |
| CG1677 | CG1677 | -0.93 | 3.87E-03 | / |
| CG13691 | CG13691 | -0.93 | 8.90E-04 | / |
| CG10722 | CG10722 | -0.93 | 1.01E-03 | / |
| CG6751 | CG6751 | -0.93 | 4.53E-03 | general RNA polymerase II transcription factor activity; GO:0016251; ; GO:0016251 |
| CG8799 | l(2)03659 | -0.93 | 7.08E-04 | defense response; GO:0006952; development; GO:0007275; extracellular transport; GO:0006858; response to toxin; GO:0009636; transport; GO:0006810 |
| CG7804 | CG7804 | -0.92 | 2.95E-03 | nuclear mRNA splicing, via spliceosome; GO:0000398; regulation of transcription from Pol II promoter; GO:0006357 |
| CG2028 | CkIalpha | -0.92 | 9.85E-03 | DNA repair; GO:0006281; Wnt receptor signaling pathway; GO:0016055; intracellular signaling cascade; GO:0007242; negative regulation of smoothened signaling pathway; GO:0045879; protein amino acid phosphorylation; GO:0006468; protein catabolism; GO:0030163; regulation of proteolysis and peptidolysis; GO:0030162; smoothened signaling pathway; GO:0007224 |
| CG7627 | CG7627 | -0.92 | 6.61E-03 | defense response; GO:0006952; extracellular transport; GO:0006858; response to toxin; GO:0009636 |
| CG2918 | CG2918 | -0.91 | 1.07E-03 | defense response; GO:0006952; protein folding; GO:0006457; response to stress; GO:0006950 |
| CG5353 | CG5353 | -0.91 | 7.27E-04 | / |
| CG9373 | CG9373 | -0.91 | 4.95E-03 | / |
| CG5923 | DNAPol-alpha73 | -0.90 | 8.09E-05 | DNA-dependent DNA replication; GO:0006261 |
| CG5371 | RnrL | -0.90 | 2.11E-04 | DNA replication; GO:0006260; purine base metabolism; GO:0006144; pyrimidine base metabolism; GO:0006206 |
| CG6743 | Nup170 | -0.90 | 1.47E-03 | protein targeting; GO:0006605 |
| CG5326 | CG5326 | -0.88 | 3.84E-03 | fatty acid metabolism; GO:0006631; lipid metabolism; GO:0006629 |
| CG9885 | dpp | -0.88 | 3.83E-03 | BMP signaling pathway; GO:0030509; amnioserosa formation; GO:0007378; anterior/posterior axis specification; GO:0009948; anterior/posterior pattern formation, imaginal disc; GO:0007448; branch cell fate determination (sensu Insecta); GO:0046845; cell fate determination; GO:0001709; cell fate specification; GO:0001708; cell-cell signaling; GO:0007267; compound eye morphogenesis (sensu Endopterygota); GO:0001745; dorsal appendage formation; GO:0046843; dorsal closure; GO:0007391; dorsal closure, leading edge cell fate determination; GO:0007393; dorsal/ventral axis specification; GO:0009950; dorsal/ventral pattern formation, imaginal disc; GO:0007450; ectoderm cell fate specification; GO:0001715; ectoderm development; GO:0007398; embryonic morphogenesis; GO:0009795; foregut morphogenesis; GO:0007440; genital disc development; GO:0035215; genital disc sexually dimorphic development; GO:0035263; germ-line stem cell division; GO:0042078; germ-line stem cell maintenance; GO:0030718; heart development; GO:0007507; hindgut morphogenesis; GO:0007442; imaginal disc development; GO:0007444; imaginal disc growth; GO:0007446; imaginal disc pattern formation; GO:0007447; larval development (sensu Insecta); GO:0002168; leg disc proximal/distal pattern formation; GO:0007479; negative regulation of cell proliferation; GO:0008285; negative regulation of salivary gland determination; GO:0045705; nurse cell apoptosis; GO:0045476; oogenesis (sensu Insecta); GO:0009993; ovarian follicle cell development (sensu Insecta); GO:0030707; pigmentation; GO:0048066; progression of morphogenetic furrow (sensu Endopterygota); GO:0007458; regulation of cell proliferation; GO:0042127; regulation of organ size; GO:0046620; regulation of tracheal tube diameter; GO:0035158; sensory organ development; GO:0007423; stem cell division; GO:0017145; stem cell maintenance; GO:0019827; tracheal branch fusion; GO:0035147; tracheal cell fate determination (sensu Insecta); GO:0007425; tracheal cell migration (sensu Insecta); GO:0007427; tracheal system development (sensu Insecta); GO:0007424; transforming growth factor beta receptor signaling pathway; GO:0007179; wing disc anterior/posterior pattern formation; GO:0048100; wing disc proximal/distal pattern formation; GO:0007473; wing morphogenesis; GO:0007476; wing vein morphogenesis; GO:0008586; wing vein specification; GO:0007474; zygotic determination of anterior/posterior axis, embryo; GO:0007354; zygotic determination of dorsal/ventral axis; GO:0007352 |
| CG6530 | imthl3 | -0.88 | 9.78E-03 | G-protein coupled receptor protein signaling pathway; GO:0007186; determination of adult life span; GO:0008340; response to stress; GO:0006950 |

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|-------------------------|-------------------------|--------------|-----------------|--|
| CG14191 | CG14191 | -0.88 | 1.31E-03 | / |
| CG5452 | dnk | -0.88 | 3.23E-03 | TMP biosynthesis; GO:0006230; nucleoside diphosphate phosphorylation; GO:0006165; phosphorylation; GO:0016310; pyrimidine base metabolism; GO:0006206 |
| CG3198 | CG3198 | -0.88 | 5.35E-03 | nuclear mRNA splicing, via spliceosome; GO:0000398 |
| CG17060 | Rab10 | -0.87 | 1.64E-03 | endocytosis; GO:0006897; intracellular protein transport; GO:0006886; regulation of exocytosis; GO:0017157; regulation of transcription, DNA-dependent; GO:0006355; small GTPase mediated signal transduction; GO:0007264; two-component signal transduction system (phosphorelay); GO:0000160 |
| CG5018 | CG5018 | -0.87 | 4.72E-04 | / |
| CG9143 | CG9143 | -0.86 | 2.34E-03 | nucleobase, nucleoside, nucleotide and nucleic acid metabolism; GO:0006139 |
| CG33129 | CG6087 | -0.86 | 5.22E-03 | / |
| CG10863 | CG10863 | -0.86 | 7.11E-03 | / |
| CG5553 | DNAprim | -0.85 | 2.74E-03 | DNA replication; GO:0006260; DNA replication, synthesis of RNA primer; GO:0006269; S phase of mitotic cell cycle; GO:0000084; compound eye morphogenesis (sensu Endopterygota); GO:0001745 |