

Supplemental Table 17. Significant GO terms in common among tissues

No. of significant tissues (p<0.05)	GO Biological Processes	Acg (Down/Up)	Brain (Down/Up)	Fat (Down/Up)	Gut (Down/Up)	MT (Down/Up)	MU (Down/Up)	Testis (Down/Up)
3	GO:0008360 regulation of cell shape	9.91E-04 ^a (1/17) ^b	6.52E-03 (4/9)	3.43E-01 (4/2)	3.05E-02 (6/3)	7.34E-01 (1/4)	7.22E-01 (4/4)	5.05E-01 (0/6)
3	GO:0007610 behavior	1.59E-03 (17/35)	1.06E-01 (12/20)	5.54E-01 (12/8)	5.92E-01 (11/7)	8.62E-03 (21/17)	6.10E-01 (21/17)	2.36E-02 (13/21)
3	GO:0035146 tube fusion	1.55E-02 (0/4)	3.70E-02 (2/1)	4.67E-01 (1/0)	1.05E-01 (0/2)	3.74E-02 (0/3)	7.15E-01 (0/1)	5.28E-01 (1/0)
3	GO:0035147 tracheal branch fusion	1.55E-02 (0/4)	3.70E-02 (2/1)	4.67E-01 (1/0)	1.05E-01 (0/2)	3.74E-02 (0/3)	7.15E-01 (0/1)	5.28E-01 (1/0)
3	GO:0007318 pole plasm protein localization	2.88E-02 (1/3)	5.78E-02 (1/2)	3.20E-02 (2/1)	2.57E-02 (1/2)	2.32E-01 (0/2)	7.73E-01 (1/0)	1.00E+00 (0/0)
3	GO:0051128 regulation of cell organization and biogenesis	3.54E-02 (1/4)	4.71E-02 (3/1)	6.81E-01 (1/0)	2.72E-01 (2/0)	4.16E-01 (0/2)	8.98E-01 (0/1)	3.89E-02 (1/3)
3	GO:0000097 sulfur amino acid biosynthesis	4.75E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.46E-02 (0/2)	2.70E-02 (1/1)	3.66E-01 (0/1)	2.39E-01 (0/1)
3	GO:0009309 amine biosynthesis	8.88E-02 (5/6)	4.19E-01 (3/3)	2.27E-01 (2/4)	3.40E-02 (1/7)	1.75E-03 (7/6)	2.48E-02 (7/7)	8.75E-01 (2/1)
3	GO:0008652 amino acid biosynthesis	1.30E-01 (4/5)	4.41E-01 (2/3)	1.28E-01 (2/4)	3.75E-02 (1/6)	1.06E-02 (5/5)	3.07E-02 (6/6)	7.86E-01 (2/1)
3	GO:0006887 exocytosis	1.80E-01 (4/11)	2.30E-02 (8/7)	3.66E-01 (4/4)	2.14E-02 (6/6)	4.93E-01 (2/7)	6.75E-01 (5/7)	1.39E-02 (3/12)
3	GO:0016079 synaptic vesicle exocytosis	2.52E-01 (1/5)	3.47E-03 (3/6)	7.22E-01 (1/1)	1.74E-03 (5/3)	9.36E-02 (2/4)	8.77E-01 (2/1)	2.65E-02 (2/5)
3	GO:0008105 asymmetric protein localization	2.72E-01 (2/3)	4.19E-02 (4/2)	5.19E-02 (3/2)	3.83E-02 (2/3)	4.26E-02 (0/6)	3.68E-01 (2/3)	7.11E-01 (1/1)
3	GO:0006099 tricarboxylic acid cycle	4.47E-01 (2/3)	1.35E-02 (4/4)	2.51E-01 (2/2)	2.83E-02 (6/0)	8.45E-01 (1/1)	2.23E-04 (14/0)	9.57E-01 (1/0)
3	GO:0009060 aerobic respiration	4.47E-01 (2/3)	1.35E-02 (4/4)	2.51E-01 (2/2)	2.83E-02 (6/0)	8.45E-01 (1/1)	2.23E-04 (14/0)	9.57E-01 (1/0)
3	GO:0045333 cellular respiration	4.47E-01 (2/3)	1.35E-02 (4/4)	2.51E-01 (2/2)	2.83E-02 (6/0)	8.45E-01 (1/1)	2.23E-04 (14/0)	9.57E-01 (1/0)

3	GO:0046356 acetyl-CoA catabolism	4.47E-01 (2/3)	1.35E-02 (4/4)	2.51E-01 (2/2)	2.83E-02 (6/0)	8.45E-01 (1/1)	2.23E-04 (14/0)	9.57E-01 (1/0)
3	GO:0006084 acetyl-CoA metabolism	4.66E-01 (2/3)	1.53E-02 (4/4)	2.63E-01 (2/2)	3.11E-02 (6/0)	8.54E-01 (1/1)	7.29E-05 (15/0)	9.60E-01 (1/0)
3	GO:0009109 coenzyme catabolism	4.66E-01 (2/3)	1.53E-02 (4/4)	2.63E-01 (2/2)	3.11E-02 (6/0)	8.54E-01 (1/1)	2.87E-04 (14/0)	8.26E-01 (2/0)
3	GO:0048489 synaptic vesicle transport	4.80E-01 (1/7)	4.83E-02 (3/7)	9.39E-01 (1/1)	2.08E-03 (7/4)	2.17E-02 (4/7)	4.83E-01 (6/3)	7.44E-02 (3/6)
3	GO:0051187 cofactor catabolism	4.85E-01 (2/3)	1.73E-02 (4/4)	1.26E-01 (3/2)	3.40E-02 (6/0)	8.62E-01 (1/1)	3.65E-04 (14/0)	8.35E-01 (2/0)
3	GO:0016082 synaptic vesicle priming	6.98E-01 (0/1)	7.51E-03 (1/3)	4.96E-01 (1/0)	2.38E-03 (2/2)	4.74E-02 (1/2)	7.46E-01 (0/1)	5.59E-01 (1/0)
3	GO:0006119 oxidative phosphorylation	9.83E-01 (3/4)	3.93E-01 (7/4)	4.66E-02 (7/6)	7.23E-04 (14/3)	8.72E-01 (5/2)	1.78E-03 (25/2)	8.25E-01 (4/3)
2	GO:0008104 protein localization	1.16E-07 (32/57)	1.29E-02 (25/27)	3.28E-01 (16/17)	3.62E-01 (16/14)	6.91E-01 (16/20)	3.45E-01 (23/39)	1.23E-01 (12/31)
2	GO:0051258 protein polymerization	1.21E-06 (0/10)	3.32E-02 (2/2)	7.46E-02 (1/2)	6.11E-01 (1/0)	1.00E+00 (0/0)	8.72E-01 (0/1)	1.00E+00 (0/0)
2	GO:0006886 intracellular protein transport	3.63E-06 (29/48)	3.39E-02 (23/22)	4.61E-01 (13/15)	5.28E-01 (14/11)	8.63E-01 (13/16)	3.30E-01 (20/36)	1.20E-01 (11/28)
2	GO:0016043 cell organization and biogenesis	3.66E-06 (29/87)	4.69E-02 (30/40)	6.36E-01 (25/19)	7.98E-02 (32/19)	7.87E-01 (18/35)	8.07E-01 (49/33)	2.63E-01 (26/33)
2	GO:0009993 oogenesis (sensu Insecta)	5.31E-06 (14/33)	5.25E-01 (8/10)	7.65E-01 (5/7)	6.58E-01 (7/5)	3.40E-01 (8/12)	9.55E-01 (11/9)	4.81E-02 (10/14)
2	GO:0048477 oogenesis	5.31E-06 (14/33)	5.25E-01 (8/10)	7.65E-01 (5/7)	6.58E-01 (7/5)	3.40E-01 (8/12)	9.55E-01 (11/9)	4.81E-02 (10/14)
2	GO:0015031 protein transport	7.87E-06 (29/48)	3.14E-02 (23/23)	5.06E-01 (13/15)	4.87E-01 (15/11)	7.98E-01 (14/17)	2.36E-01 (22/37)	1.10E-01 (11/29)
2	GO:0045184 establishment of protein localization	9.15E-06 (29/48)	3.33E-02 (23/23)	5.15E-01 (13/15)	4.95E-01 (15/11)	8.05E-01 (14/17)	2.46E-01 (22/37)	1.15E-01 (11/29)
2	GO:0046907 intracellular transport	1.32E-05 (33/54)	4.84E-02 (26/26)	6.61E-01 (15/16)	3.17E-01 (20/13)	6.95E-01 (18/21)	5.58E-01 (25/38)	9.80E-02 (17/30)
2	GO:0000902 cellular morphogenesis	2.35E-04 (4/33)	4.63E-02 (8/14)	3.07E-01 (10/4)	8.23E-02 (10/6)	4.47E-01 (3/13)	7.18E-01 (12/9)	2.51E-01 (4/13)

2	GO:0035239 tube morphogenesis	7.56E-04 (2/13)	6.66E-01 (2/2)	6.98E-01 (2/1)	6.42E-01 (0/3)	3.41E-02 (2/7)	3.84E-01 (3/5)	8.04E-01 (1/2)
2	GO:0007317 regulation of pole plasm oskar mRNA localization	8.45E-04 (2/5)	3.63E-01 (0/2)	1.54E-02 (2/2)	6.11E-01 (1/0)	1.29E-01 (1/2)	3.05E-01 (1/2)	1.11E-01 (2/1)
2	GO:0030005 di- tri-valent inorganic cation homeostasis	8.45E-04 (2/5)	3.63E-01 (1/1)	6.43E-01 (0/1)	1.00E+00 (0/0)	3.65E-01 (0/2)	1.79E-03 (4/3)	7.08E-01 (1/0)
2	GO:0035295 tube development	9.50E-04 (3/13)	7.53E-01 (2/2)	7.71E-01 (2/1)	5.05E-01 (0/4)	1.13E-02 (4/7)	3.71E-01 (4/5)	8.63E-01 (1/2)
2	GO:0002009 morphogenesis of an epithelium	9.91E-04 (2/21)	6.31E-01 (4/4)	1.74E-02 (8/5)	4.31E-01 (1/6)	3.56E-01 (3/7)	7.77E-01 (7/4)	2.83E-01 (4/6)
2	GO:0007300 nurse cell to oocyte transport	1.04E-03 (1/8)	6.14E-01 (1/1)	8.10E-01 (0/1)	4.40E-01 (2/0)	6.16E-01 (0/2)	9.64E-01 (0/1)	1.03E-02 (3/3)
2	GO:0007409 axonogenesis	1.29E-03 (5/14)	3.29E-02 (3/9)	1.56E-01 (5/3)	7.22E-01 (2/2)	3.53E-01 (4/4)	8.99E-01 (3/4)	1.73E-01 (3/6)
2	GO:0006873 cell ion homeostasis	1.59E-03 (3/5)	5.32E-01 (1/1)	4.08E-01 (0/2)	1.00E+00 (0/0)	2.56E-01 (0/3)	1.38E-02 (4/3)	4.98E-01 (1/1)
2	GO:0030003 cation homeostasis	1.59E-03 (3/5)	5.32E-01 (1/1)	4.08E-01 (0/2)	1.00E+00 (0/0)	2.56E-01 (0/3)	1.38E-02 (4/3)	4.98E-01 (1/1)
2	GO:0050801 ion homeostasis	1.59E-03 (3/5)	5.32E-01 (1/1)	4.08E-01 (0/2)	1.00E+00 (0/0)	2.56E-01 (0/3)	1.38E-02 (4/3)	4.98E-01 (1/1)
2	GO:0006875 metal ion homeostasis	1.74E-03 (2/5)	4.14E-01 (1/1)	3.06E-01 (0/2)	1.00E+00 (0/0)	1.63E-01 (0/3)	3.60E-03 (4/3)	3.84E-01 (1/1)
2	GO:0006879 iron ion homeostasis	2.23E-03 (0/4)	8.14E-02 (1/1)	3.30E-01 (0/1)	1.00E+00 (0/0)	8.20E-02 (0/2)	3.13E-02 (1/2)	3.80E-01 (1/0)
2	GO:0046916 transition metal ion homeostasis	2.23E-03 (0/4)	8.14E-02 (1/1)	3.30E-01 (0/1)	1.00E+00 (0/0)	8.20E-02 (0/2)	3.13E-02 (1/2)	3.80E-01 (1/0)
2	GO:0016331 morphogenesis of embryonic epithelium	2.32E-03 (1/15)	3.06E-01 (3/4)	2.80E-02 (7/2)	7.68E-01 (1/2)	6.51E-01 (1/4)	8.59E-01 (4/2)	7.66E-01 (2/2)
2	GO:0007391 dorsal closure	2.68E-03 (1/14)	3.93E-01 (2/4)	4.51E-02 (6/2)	7.19E-01 (1/2)	7.56E-01 (1/3)	9.00E-01 (4/1)	7.08E-01 (2/2)
2	GO:0042592 homeostasis	3.08E-03 (6/9)	5.88E-01 (1/4)	3.82E-01 (1/4)	8.94E-01 (1/1)	2.53E-01 (2/5)	2.22E-02 (8/6)	3.50E-01 (4/2)
2	GO:0006826 iron ion transport	3.17E-03 (0/3)	2.68E-02 (1/1)	2.04E-01 (0/1)	1.00E+00 (0/0)	2.53E-01 (0/1)	6.00E-02 (1/1)	1.00E+00 (0/0)

2	GO:0006457 protein folding	3.73E-03 (5/16)	2.12E-01 (6/5)	6.56E-02 (9/2)	7.34E-01 (3/2)	7.43E-01 (1/6)	7.65E-03 (6/16)	5.30E-01 (1/7)
2	GO:0051179 localization	4.07E-03 (62/106)	3.32E-01 (48/60)	5.81E-01 (41/40)	1.33E-02 (54/39)	7.78E-01 (41/57)	6.43E-01 (76/80)	5.47E-01 (41/56)
2	GO:0019725 cell homeostasis	4.71E-03 (5/9)	5.37E-01 (1/4)	5.39E-01 (0/4)	8.74E-01 (1/1)	2.11E-01 (2/5)	3.08E-02 (8/5)	3.02E-01 (4/2)
2	GO:0044272 sulfur compound biosynthesis	4.92E-03 (4/2)	3.63E-01 (0/2)	1.00E+00 (0/0)	2.33E-01 (0/2)	6.74E-03 (2/3)	5.92E-01 (1/1)	7.08E-01 (0/1)
2	GO:0001700 embryonic development (sensu Insecta)	5.86E-03 (3/16)	2.25E-01 (4/6)	3.66E-02 (7/4)	8.09E-01 (1/3)	7.82E-01 (2/4)	6.25E-01 (6/5)	5.75E-01 (3/4)
2	GO:0007301 ovarian ring canal formation	6.89E-03 (0/4)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.77E-02 (1/2)
2	GO:0006959 humoral immune response	9.34E-03 (4/9)	3.29E-01 (3/3)	5.15E-01 (0/4)	6.72E-01 (1/2)	5.14E-01 (5/0)	3.78E-06 (2/19)	9.41E-01 (1/1)
2	GO:0007399 neurogenesis	1.01E-02 (19/41)	4.21E-02 (18/25)	8.83E-01 (15/6)	5.36E-01 (10/14)	1.20E-01 (19/21)	9.88E-01 (23/14)	1.94E-01 (18/18)
2	GO:0006963 antibacterial polypeptide induction	1.02E-02 (0/5)	1.75E-02 (1/3)	2.01E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.92E-01 (0/2)	6.41E-01 (1/0)
2	GO:0030725 ring canal formation	1.06E-02 (0/4)	1.00E+00 (0/0)	4.35E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.41E-02 (1/2)
2	GO:0043063 intercellular bridge organization and biogenesis	1.06E-02 (0/4)	1.00E+00 (0/0)	4.35E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.41E-02 (1/2)
2	GO:0046785 microtubule polymerization	1.06E-02 (0/4)	2.84E-02 (2/1)	1.03E-01 (1/1)	4.08E-01 (1/0)	1.00E+00 (0/0)	6.80E-01 (0/1)	1.00E+00 (0/0)
2	GO:0009966 regulation of signal transduction	1.22E-02 (5/11)	3.17E-01 (3/5)	6.83E-02 (9/0)	1.89E-01 (2/5)	1.98E-01 (3/6)	2.85E-01 (8/4)	3.87E-02 (6/5)
2	GO:0006928 cell motility	1.30E-02 (7/26)	3.77E-02 (8/16)	4.26E-01 (9/5)	7.64E-01 (7/3)	1.48E-01 (10/11)	7.13E-01 (11/12)	9.10E-02 (8/13)
2	GO:0001738 morphogenesis of a polarized epithelium	1.32E-02 (1/9)	2.45E-01 (2/3)	1.26E-01 (4/1)	9.62E-02 (0/5)	4.91E-02 (3/4)	2.55E-01 (4/3)	6.22E-01 (1/2)
2	GO:0016998 cell wall catabolism	1.37E-02 (2/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-01 (1/0)	3.25E-04 (3/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
2	GO:0040011 locomotion	1.74E-02 (7/26)	2.79E-02 (8/17)	4.58E-01 (9/5)	6.83E-01 (7/4)	1.71E-01 (10/11)	7.50E-01 (11/12)	1.07E-01 (8/13)

2	GO:0046843 dorsal appendage formation	1.79E-02 (0/5)	1.00E+00 (0/0)	6.22E-01 (0/1)	2.14E-01 (0/2)	3.39E-01 (1/1)	2.94E-02 (4/1)	6.87E-01 (0/1)
2	GO:0006810 transport	1.85E-02 (59/96)	3.27E-01 (46/57)	7.27E-01 (38/36)	1.34E-02 (52/37)	7.80E-01 (39/54)	5.80E-01 (73/77)	6.53E-01 (38/52)
2	GO:0051234 establishment of localization	1.89E-02 (59/96)	3.30E-01 (46/57)	7.29E-01 (38/36)	1.37E-02 (52/37)	7.82E-01 (39/54)	5.84E-01 (73/77)	6.56E-01 (38/52)
2	GO:0000270 peptidoglycan metabolism	2.15E-02 (0/4)	1.00E+00 (0/0)	4.96E-01 (0/1)	1.00E+00 (0/0)	2.05E-01 (1/1)	3.26E-02 (0/4)	1.85E-01 (0/2)
2	GO:0009253 peptidoglycan catabolism	2.15E-02 (0/4)	1.00E+00 (0/0)	4.96E-01 (0/1)	1.00E+00 (0/0)	2.05E-01 (1/1)	3.26E-02 (0/4)	1.85E-01 (0/2)
2	GO:0015674 di- tri-valent inorganic cation transport	2.39E-02 (4/4)	5.04E-01 (1/2)	8.87E-01 (0/1)	4.23E-02 (2/3)	5.07E-01 (2/1)	3.90E-01 (4/1)	1.00E+00 (0/0)
2	GO:0008064 regulation of actin polymerization and or depolymerization	2.88E-02 (0/4)	2.30E-01 (2/0)	5.24E-01 (1/0)	1.40E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.96E-02 (1/2)
2	GO:0030832 regulation of actin filament length	2.88E-02 (0/4)	2.30E-01 (2/0)	5.24E-01 (1/0)	1.40E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.96E-02 (1/2)
2	GO:0031109 microtubule polymerization or depolymerization	2.88E-02 (0/4)	1.03E-02 (2/2)	1.60E-01 (1/1)	4.94E-01 (1/0)	6.13E-01 (0/1)	7.73E-01 (0/1)	1.00E+00 (0/0)
2	GO:0006967 antifungal polypeptide induction	3.32E-02 (0/3)	1.04E-01 (2/0)	3.67E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.61E-02 (1/2)	1.00E+00 (0/0)
2	GO:0030722 oocyte nucleus positioning	3.32E-02 (0/3)	1.00E+00 (0/0)	3.67E-01 (0/1)	5.93E-02 (1/1)	1.00E+00 (0/0)	4.61E-02 (2/1)	4.21E-01 (1/0)
2	GO:0019732 antifungal humoral response	3.73E-02 (1/3)	2.57E-01 (2/0)	5.51E-01 (0/1)	1.58E-01 (0/2)	1.00E+00 (0/0)	1.25E-02 (1/4)	6.16E-01 (1/0)
2	GO:0006790 sulfur metabolism	4.02E-02 (6/4)	7.73E-01 (1/2)	9.62E-01 (1/0)	3.32E-01 (1/3)	4.48E-02 (2/6)	4.17E-01 (4/3)	5.24E-01 (3/1)
2	GO:0000096 sulfur amino acid metabolism	4.64E-02 (2/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	8.80E-03 (0/3)	1.28E-01 (1/1)	2.52E-01 (0/2)	4.59E-01 (0/1)
2	GO:0048070 regulation of pigmentation	4.75E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
2	GO:0048130 oocyte microtubule cytoskeleton organization (sensu	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	3.66E-01 (1/0)	2.39E-01 (1/0)
2	GO:0019730 antimicrobial humoral response	4.94E-02 (3/7)	2.31E-01 (3/3)	4.16E-01 (0/4)	5.86E-01 (1/2)	4.02E-01 (5/0)	1.63E-06 (2/18)	9.82E-01 (1/0)

2	GO:0050830 defense response to Gram-positive bacteria	9.82E-02 (1/2)	4.69E-02 (2/1)	1.00E+00 (0/0)	4.67E-01 (0/1)	1.00E+00 (0/0)	5.93E-03 (0/5)	5.59E-01 (1/0)
2	GO:0007179 transforming growth factor beta receptor signaling pathway	1.89E-01 (0/4)	5.10E-01 (1/1)	9.10E-03 (3/2)	3.15E-02 (1/3)	1.00E+00 (0/0)	4.86E-01 (2/1)	1.00E+00 (0/0)
2	GO:0006936 muscle contraction	2.11E-01 (5/6)	5.89E-01 (1/5)	2.16E-01 (2/5)	4.89E-03 (9/2)	5.93E-01 (4/2)	8.68E-04 (17/3)	3.61E-01 (1/6)
2	GO:0043170 macromolecule metabolism	2.33E-01 (93/147)	1.88E-01 (78/102)	1.68E-02 (85/70)	3.13E-02 (73/68)	7.77E-01 (75/89)	2.19E-01 (117/155)	8.65E-01 (72/78)
2	GO:0019932 second-messenger-mediated signaling	2.73E-01 (6/4)	2.35E-01 (6/2)	4.24E-02 (4/5)	6.28E-01 (2/2)	7.15E-01 (2/3)	2.92E-01 (6/5)	4.85E-02 (4/6)
2	GO:0007224 smoothened signaling pathway	3.76E-01 (1/2)	7.31E-02 (2/2)	7.54E-03 (5/0)	2.74E-02 (1/3)	8.14E-01 (0/1)	2.31E-01 (1/3)	1.91E-01 (1/2)
2	GO:0006950 response to stress	4.11E-01 (8/22)	4.46E-01 (14/8)	1.53E-02 (14/12)	9.07E-01 (5/6)	5.45E-01 (8/13)	1.73E-03 (8/41)	8.46E-01 (8/8)
2	GO:0019226 transmission of nerve impulse	6.32E-01 (14/17)	1.38E-02 (15/20)	4.33E-01 (9/11)	2.13E-01 (14/7)	2.37E-02 (15/19)	6.49E-01 (16/19)	2.45E-01 (9/17)
2	GO:0007269 neurotransmitter secretion	6.66E-01 (1/8)	2.92E-02 (4/9)	8.37E-01 (2/2)	1.66E-02 (7/4)	3.10E-01 (3/6)	4.46E-01 (7/5)	2.46E-01 (3/6)
2	GO:0045055 regulated secretory pathway	6.66E-01 (1/8)	2.92E-02 (4/9)	8.37E-01 (2/2)	1.66E-02 (7/4)	3.10E-01 (3/6)	4.46E-01 (7/5)	2.46E-01 (3/6)
2	GO:0001505 regulation of neurotransmitter levels	6.74E-01 (1/9)	3.16E-02 (5/9)	8.93E-01 (2/2)	1.49E-02 (7/5)	2.99E-01 (4/6)	4.84E-01 (7/6)	2.34E-01 (3/7)
2	GO:0019941 modification-dependent protein catabolism	7.41E-01 (2/4)	1.62E-01 (2/6)	1.41E-05 (12/3)	3.47E-01 (1/4)	6.28E-01 (2/3)	1.42E-02 (2/13)	1.26E-01 (3/5)
2	GO:0009308 amine metabolism	7.44E-01 (18/12)	3.18E-01 (8/19)	2.92E-01 (7/15)	1.87E-02 (13/14)	4.13E-03 (20/18)	2.35E-01 (25/17)	4.40E-01 (13/11)
2	GO:0006120 mitochondrial electron transport NADH to ubiquinone	7.46E-01 (1/2)	9.46E-01 (0/1)	6.86E-02 (4/1)	1.49E-02 (4/2)	9.47E-01 (1/0)	8.32E-03 (10/0)	4.97E-01 (2/1)
2	GO:0006519 amino acid and derivative metabolism	7.67E-01 (15/8)	5.56E-01 (7/12)	2.62E-01 (5/13)	3.98E-02 (7/14)	7.79E-04 (17/17)	1.61E-01 (18/17)	3.50E-01 (9/11)
2	GO:0006511 ubiquitin-dependent protein catabolism	8.45E-01 (2/3)	1.45E-01 (2/6)	1.00E-05 (12/3)	3.26E-01 (1/4)	6.04E-01 (2/3)	2.48E-02 (2/12)	2.14E-01 (3/4)
2	GO:0006510 ATP-dependent proteolysis	8.50E-01 (1/0)	1.00E+00 (0/0)	4.12E-04 (6/0)	6.31E-01 (0/1)	3.91E-01 (0/2)	4.46E-04 (1/7)	7.27E-01 (0/1)

2	GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	9.47E-01 (1/2)	6.54E-01 (3/1)	1.35E-01 (5/1)	1.41E-02 (6/2)	6.57E-01 (4/0)	6.15E-03 (14/0)	7.95E-01 (2/1)
2	GO:0042773 ATP synthesis coupled electron transport	9.54E-01 (1/2)	6.78E-01 (3/1)	1.51E-01 (5/1)	1.69E-02 (6/2)	4.87E-01 (4/1)	8.19E-03 (14/0)	8.12E-01 (2/1)
2	GO:0042810 pheromone metabolism	1.00E+00 (0/0)	1.00E+00 (0/0)	2.75E-02 (0/2)	1.00E+00 (0/0)	4.29E-02 (2/0)	1.00E+00 (0/0)	2.89E-01 (0/1)
1	GO:0007010 cytoskeleton organization and biogenesis	5.18E-09 (15/71)	1.28E-01 (18/23)	6.24E-01 (14/12)	1.66E-01 (17/13)	8.16E-01 (7/23)	6.80E-01 (32/18)	6.21E-01 (16/15)
1	GO:0008154 actin polymerization and or depolymerization	7.60E-07 (0/11)	5.51E-02 (2/2)	3.27E-01 (1/1)	8.88E-02 (2/1)	7.85E-01 (0/1)	1.00E+00 (0/0)	1.57E-01 (1/2)
1	GO:0030029 actin filament-based process	8.31E-07 (2/23)	1.95E-01 (3/6)	7.60E-01 (3/1)	9.66E-02 (6/2)	8.97E-01 (1/3)	9.41E-01 (4/2)	5.72E-01 (2/4)
1	GO:0030036 actin cytoskeleton organization and biogenesis	8.31E-07 (2/23)	1.95E-01 (3/6)	7.60E-01 (3/1)	9.66E-02 (6/2)	8.97E-01 (1/3)	9.41E-01 (4/2)	5.72E-01 (2/4)
1	GO:0006996 organelle organization and biogenesis	1.66E-06 (27/79)	5.23E-02 (26/36)	6.73E-01 (20/18)	9.15E-02 (27/18)	6.99E-01 (17/31)	7.55E-01 (43/30)	2.72E-01 (25/27)
1	GO:0007424 tracheal system development (sensu Insecta)	1.44E-05 (6/18)	2.67E-01 (5/4)	8.14E-01 (3/1)	4.03E-01 (1/5)	2.71E-01 (2/7)	5.19E-01 (6/5)	2.12E-01 (3/6)
1	GO:0030041 actin filament polymerization	1.70E-05 (0/6)	4.41E-01 (0/1)	3.67E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0051223 regulation of protein transport	3.50E-05 (1/6)	5.82E-01 (1/0)	1.00E+00 (0/0)	4.67E-01 (0/1)	5.84E-01 (0/1)	1.31E-01 (1/2)	1.00E+00 (0/0)
1	GO:0007163 establishment and or maintenance of cell polarity	5.22E-05 (3/15)	2.08E-01 (3/4)	5.39E-01 (3/1)	1.39E-01 (1/5)	5.16E-02 (2/7)	3.24E-01 (6/3)	6.76E-01 (2/2)
1	GO:0007292 female gamete generation	5.51E-05 (15/33)	3.56E-01 (11/11)	7.28E-01 (6/8)	4.96E-01 (10/5)	2.10E-01 (11/13)	9.70E-01 (13/9)	5.78E-02 (12/14)
1	GO:0035152 regulation of tracheal tube architecture	6.14E-05 (1/8)	7.83E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.41E-01 (0/2)	6.78E-01 (2/0)	1.00E+00 (0/0)
1	GO:0007015 actin filament organization	6.51E-05 (1/15)	5.88E-01 (2/2)	4.04E-01 (3/1)	7.39E-02 (5/1)	9.23E-01 (1/1)	8.85E-01 (3/1)	5.38E-01 (1/3)
1	GO:0046822 regulation of nucleocytoplasmic transport	6.96E-05 (1/6)	6.12E-01 (1/0)	1.00E+00 (0/0)	4.94E-01 (0/1)	6.13E-01 (0/1)	1.58E-01 (1/2)	1.00E+00 (0/0)
1	GO:0048110 oocyte construction (sensu Insecta)	7.42E-05 (2/12)	4.21E-01 (1/3)	1.18E-01 (3/2)	8.97E-02 (2/3)	4.24E-01 (2/2)	5.82E-01 (3/2)	6.08E-01 (2/1)

1	GO:0048111 oocyte axis determination (sensu Insecta)	7.42E-05 (2/12)	4.21E-01 (1/3)	1.18E-01 (3/2)	8.97E-02 (2/3)	4.24E-01 (2/2)	5.82E-01 (3/2)	6.08E-01 (2/1)
1	GO:0007276 gametogenesis	8.52E-05 (20/43)	4.53E-01 (12/18)	6.19E-01 (12/10)	7.96E-01 (12/6)	4.63E-01 (14/16)	9.54E-01 (19/16)	3.94E-01 (13/16)
1	GO:0007308 oocyte construction	1.16E-04 (3/15)	5.88E-01 (2/3)	2.18E-01 (3/3)	1.68E-01 (2/4)	7.66E-01 (2/2)	9.07E-01 (3/2)	5.32E-01 (3/2)
1	GO:0009653 morphogenesis	1.37E-04 (34/91)	1.08E-01 (32/46)	8.40E-01 (32/16)	3.84E-01 (26/26)	1.43E-01 (35/42)	9.19E-01 (58/35)	6.03E-02 (33/43)
1	GO:0000003 reproduction	1.50E-04 (20/43)	3.46E-01 (14/18)	5.70E-01 (12/11)	8.21E-01 (12/6)	5.07E-01 (14/16)	9.66E-01 (19/16)	4.36E-01 (13/16)
1	GO:0019953 sexual reproduction	1.50E-04 (20/43)	3.46E-01 (14/18)	5.70E-01 (12/11)	8.21E-01 (12/6)	5.07E-01 (14/16)	9.66E-01 (19/16)	4.36E-01 (13/16)
1	GO:0016325 oocyte microtubule cytoskeleton organization	1.86E-04 (2/6)	1.44E-01 (0/3)	8.51E-02 (2/1)	2.53E-01 (2/0)	3.91E-01 (1/1)	6.23E-01 (1/1)	7.27E-01 (1/0)
1	GO:0030951 establishment and or maintenance of microtubule	1.86E-04 (2/6)	1.44E-01 (0/3)	8.51E-02 (2/1)	2.53E-01 (2/0)	3.91E-01 (1/1)	6.23E-01 (1/1)	7.27E-01 (1/0)
1	GO:0030952 establishment and or maintenance of cytoskeleton polarity	1.86E-04 (2/6)	1.44E-01 (0/3)	8.51E-02 (2/1)	2.53E-01 (2/0)	3.91E-01 (1/1)	6.23E-01 (1/1)	7.27E-01 (1/0)
1	GO:0042306 regulation of protein-nucleus import	2.19E-04 (1/5)	5.51E-01 (1/0)	1.00E+00 (0/0)	4.38E-01 (0/1)	5.52E-01 (0/1)	3.36E-01 (1/1)	1.00E+00 (0/0)
1	GO:0007309 oocyte axis determination	2.61E-04 (3/14)	5.63E-01 (2/3)	2.00E-01 (3/3)	1.53E-01 (2/4)	7.47E-01 (2/2)	8.93E-01 (3/2)	5.07E-01 (3/2)
1	GO:0006612 protein-membrane targeting	2.84E-04 (7/1)	4.14E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	7.68E-01 (1/0)	5.64E-02 (1/4)	7.45E-01 (1/0)
1	GO:0045451 pole plasm oskar mRNA localization	2.88E-04 (2/8)	3.52E-01 (0/3)	8.21E-02 (2/2)	4.58E-01 (1/1)	3.55E-01 (1/2)	6.42E-01 (1/2)	3.17E-01 (2/1)
1	GO:0051235 maintenance of localization	3.60E-04 (4/3)	9.71E-02 (1/2)	2.22E-01 (2/0)	5.68E-01 (1/0)	3.12E-01 (1/1)	2.44E-01 (2/1)	6.65E-01 (0/1)
1	GO:0009887 organogenesis	3.88E-04 (32/78)	1.82E-01 (30/37)	9.05E-01 (27/13)	5.78E-01 (19/24)	1.25E-01 (33/36)	7.91E-01 (55/31)	7.45E-02 (31/36)
1	GO:0048513 organ development	3.88E-04 (32/78)	1.82E-01 (30/37)	9.05E-01 (27/13)	5.78E-01 (19/24)	1.25E-01 (33/36)	7.91E-01 (55/31)	7.45E-02 (31/36)
1	GO:0006605 protein targeting	4.92E-04 (12/25)	2.18E-01 (10/9)	4.69E-01 (5/8)	4.68E-01 (6/6)	8.00E-01 (5/8)	1.62E-01 (10/19)	1.49E-01 (9/10)

1	GO:0019094 pole plasm mRNA localization	5.20E-04 (2/8)	3.91E-01 (0/3)	9.89E-02 (2/2)	4.91E-01 (1/1)	3.94E-01 (1/2)	4.58E-01 (2/2)	3.54E-01 (2/1)
1	GO:0006614 SRP-dependent cotranslational protein-membrane	5.62E-04 (7/0)	3.37E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	7.11E-01 (1/0)	1.02E-01 (0/4)	6.87E-01 (1/0)
1	GO:0007316 pole plasm RNA localization	6.83E-04 (2/8)	4.11E-01 (0/3)	1.08E-01 (2/2)	2.36E-01 (1/2)	4.13E-01 (1/2)	4.82E-01 (2/2)	3.72E-01 (2/1)
1	GO:0008103 oocyte microtubule cytoskeleton polarization	6.87E-04 (2/4)	2.30E-01 (0/2)	1.60E-01 (1/1)	1.00E+00 (0/0)	6.13E-01 (1/0)	7.73E-01 (0/1)	1.00E+00 (0/0)
1	GO:0045185 maintenance of protein localization	6.94E-04 (2/3)	1.27E-01 (1/1)	4.02E-01 (1/0)	3.76E-01 (1/0)	1.28E-01 (1/1)	2.52E-01 (1/1)	4.59E-01 (0/1)
1	GO:0048113 pole plasm assembly (sensu Insecta)	7.33E-04 (2/9)	2.91E-01 (1/3)	6.27E-02 (3/2)	1.36E-01 (1/3)	5.25E-01 (1/2)	6.18E-01 (2/2)	4.80E-01 (2/1)
1	GO:0006613 cotranslational protein-membrane targeting	8.45E-04 (7/0)	3.63E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	7.32E-01 (1/0)	1.21E-01 (0/4)	7.08E-01 (1/0)
1	GO:0045047 protein-ER targeting	8.45E-04 (7/0)	3.63E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	7.32E-01 (1/0)	1.21E-01 (0/4)	7.08E-01 (1/0)
1	GO:0016311 dephosphorylation	8.52E-04 (5/15)	7.03E-01 (1/5)	8.08E-01 (3/1)	2.41E-01 (2/5)	1.57E-01 (5/5)	8.51E-01 (4/4)	1.16E-01 (3/7)
1	GO:0050817 coagulation	8.54E-04 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (0/1)
1	GO:0050818 regulation of coagulation	8.54E-04 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (0/1)
1	GO:0050819 negative regulation of coagulation	8.54E-04 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (0/1)
1	GO:0000226 microtubule cytoskeleton organization and biogenesis	9.50E-04 (3/13)	6.32E-02 (3/6)	2.09E-01 (3/3)	5.05E-01 (3/1)	8.91E-01 (1/2)	8.02E-01 (3/3)	9.93E-01 (1/0)
1	GO:0031175 neurite morphogenesis	1.04E-03 (5/17)	1.07E-01 (3/9)	1.88E-01 (6/3)	8.46E-01 (2/2)	2.90E-01 (4/6)	8.85E-01 (4/5)	3.47E-01 (3/6)
1	GO:0042060 wound healing	1.04E-03 (0/4)	1.00E+00 (0/0)	2.90E-01 (0/1)	1.00E+00 (0/0)	6.14E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046823 negative regulation of nucleocytoplasmic transport	1.04E-03 (0/4)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.55E-01 (0/1)	1.30E-01 (1/1)	1.00E+00 (0/0)
1	GO:0051051 negative regulation of transport	1.04E-03 (0/4)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.55E-01 (0/1)	1.30E-01 (1/1)	1.00E+00 (0/0)

1	GO:0051224 negative regulation of protein transport	1.04E-03 (0/4)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.55E-01 (0/1)	1.30E-01 (1/1)	1.00E+00 (0/0)
1	GO:0007315 pole plasm assembly	1.16E-03 (2/9)	3.24E-01 (1/3)	7.47E-02 (3/2)	1.55E-01 (1/3)	5.59E-01 (1/2)	6.58E-01 (2/2)	5.14E-01 (2/1)
1	GO:0007275 development	1.26E-03 (61/116)	6.84E-02 (54/67)	3.70E-01 (50/38)	4.22E-01 (43/37)	9.25E-02 (57/63)	9.89E-01 (80/61)	8.86E-02 (51/62)
1	GO:0000041 transition metal ion transport	1.28E-03 (1/4)	1.52E-01 (1/1)	4.35E-01 (0/1)	8.91E-02 (1/1)	1.53E-01 (1/1)	8.40E-02 (2/1)	1.00E+00 (0/0)
1	GO:0048112 oocyte anterior posterior axis determination (sensu Insecta)	1.44E-03 (2/9)	3.40E-01 (1/3)	8.12E-02 (3/2)	1.65E-01 (1/3)	5.76E-01 (1/2)	6.77E-01 (2/2)	5.30E-01 (2/1)
1	GO:0007349 cellularization	1.59E-03 (0/8)	1.00E+00 (0/0)	4.08E-01 (0/2)	1.00E+00 (0/0)	5.34E-01 (0/2)	1.00E+00 (0/0)	2.26E-01 (2/1)
1	GO:0035151 regulation of tracheal tube size	1.70E-03 (0/6)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	8.19E-01 (1/0)	1.00E+00 (0/0)
1	GO:0009792 embryonic development (sensu Metazoa)	1.95E-03 (6/21)	9.05E-02 (6/10)	1.72E-01 (7/5)	9.15E-01 (1/4)	5.70E-01 (4/7)	7.46E-01 (7/8)	6.09E-01 (4/6)
1	GO:0008298 intracellular mRNA localization	2.16E-03 (2/9)	6.05E-01 (0/3)	9.49E-02 (2/3)	1.85E-01 (2/2)	6.08E-01 (1/2)	5.21E-01 (3/2)	3.30E-01 (2/2)
1	GO:0030707 ovarian follicle cell development (sensu Insecta)	2.18E-03 (5/16)	9.89E-01 (2/1)	7.67E-01 (2/3)	6.99E-01 (1/4)	2.81E-01 (3/7)	7.99E-01 (6/4)	4.81E-01 (3/5)
1	GO:0019991 septate junction assembly	2.23E-03 (0/4)	1.00E+00 (0/0)	3.30E-01 (1/0)	3.07E-01 (0/1)	1.00E+00 (0/0)	5.50E-01 (1/0)	1.00E+00 (0/0)
1	GO:0045478 fusome organization and biogenesis	2.23E-03 (0/4)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	5.50E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006470 protein amino acid dephosphorylation	2.32E-03 (3/13)	4.69E-01 (1/5)	6.36E-01 (3/1)	2.07E-01 (2/4)	1.82E-01 (5/3)	7.50E-01 (4/3)	2.54E-01 (3/4)
1	GO:0043297 apical junction assembly	2.50E-03 (0/6)	6.88E-01 (1/0)	2.22E-01 (2/0)	5.68E-01 (0/1)	3.12E-01 (0/2)	5.27E-01 (1/1)	1.00E+00 (0/0)
1	GO:0006606 protein-nucleus import	2.62E-03 (2/9)	8.34E-01 (1/1)	7.22E-01 (0/2)	6.77E-01 (0/2)	6.23E-01 (2/1)	5.42E-01 (2/3)	5.78E-01 (2/1)
1	GO:0051170 nuclear import	3.16E-03 (2/9)	8.43E-01 (1/1)	7.33E-01 (0/2)	6.89E-01 (0/2)	6.38E-01 (2/1)	5.62E-01 (2/3)	3.60E-01 (3/1)
1	GO:0009306 protein secretion	3.17E-03 (3/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.39E-01 (0/1)

1	GO:0017038 protein import	3.40E-03 (2/10)	8.95E-01 (1/1)	8.02E-01 (0/2)	5.13E-01 (1/2)	3.17E-01 (4/1)	2.06E-01 (4/4)	2.70E-01 (3/2)
1	GO:0007043 intercellular junction assembly	3.56E-03 (0/6)	7.10E-01 (1/0)	2.43E-01 (2/0)	5.90E-01 (0/1)	3.39E-01 (0/2)	5.61E-01 (1/1)	1.00E+00 (0/0)
1	GO:0035150 regulation of tube size	3.56E-03 (0/6)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	8.56E-01 (1/0)	1.00E+00 (0/0)
1	GO:0051301 cell division	3.60E-03 (5/15)	8.98E-01 (4/1)	5.87E-01 (2/4)	6.76E-01 (1/4)	5.26E-01 (2/6)	9.84E-01 (5/1)	4.51E-01 (3/5)
1	GO:0000910 cytokinesis	4.10E-03 (2/11)	9.88E-01 (1/0)	2.49E-01 (2/3)	8.26E-01 (1/1)	6.32E-01 (1/3)	9.07E-01 (3/1)	3.75E-01 (2/3)
1	GO:0009798 axis specification	4.75E-03 (6/19)	8.51E-01 (3/5)	1.42E-01 (7/5)	6.71E-01 (3/4)	2.80E-01 (5/8)	9.10E-01 (6/6)	6.87E-01 (5/4)
1	GO:0007017 microtubule-based process	6.35E-03 (8/20)	2.00E-01 (8/8)	4.23E-01 (4/7)	5.82E-01 (7/2)	7.38E-01 (3/8)	9.62E-01 (8/5)	9.18E-01 (6/2)
1	GO:0007626 locomotory behavior	6.41E-03 (10/30)	6.15E-02 (9/18)	6.13E-01 (9/6)	3.72E-01 (9/7)	6.40E-02 (14/13)	3.39E-01 (18/15)	1.20E-01 (9/15)
1	GO:0007389 pattern specification	6.43E-03 (12/23)	7.18E-01 (6/9)	2.58E-01 (9/7)	9.30E-01 (4/4)	4.26E-01 (8/10)	9.95E-01 (9/6)	4.16E-01 (10/7)
1	GO:0007293 egg chamber formation (sensu Insecta)	6.51E-03 (1/8)	4.86E-01 (1/2)	6.17E-01 (1/1)	2.92E-01 (2/1)	7.46E-01 (1/1)	9.85E-01 (1/0)	9.34E-02 (2/3)
1	GO:0045216 intercellular junction assembly and or maintenance	6.62E-03 (0/6)	7.49E-01 (1/0)	2.85E-01 (2/0)	6.31E-01 (0/1)	3.91E-01 (0/2)	3.36E-01 (1/2)	1.00E+00 (0/0)
1	GO:0015012 heparan sulfate proteoglycan biosynthesis	6.89E-03 (3/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.82E-01 (0/1)	6.42E-01 (1/0)	1.00E+00 (0/0)
1	GO:0030201 heparan sulfate proteoglycan metabolism	6.89E-03 (3/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.82E-01 (0/1)	6.42E-01 (1/0)	1.00E+00 (0/0)
1	GO:0009595 detection of biotic stimulus	7.37E-03 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	9.29E-02 (0/2)	2.89E-01 (0/1)
1	GO:0016045 detection of bacteria	7.37E-03 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	9.29E-02 (0/2)	2.89E-01 (0/1)
1	GO:0030042 actin filament depolymerization	7.37E-03 (0/3)	3.05E-01 (0/1)	1.00E+00 (0/0)	2.31E-01 (0/1)	3.06E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035026 leading edge cell differentiation	7.37E-03 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.06E-01 (0/1)	4.35E-01 (1/0)	1.00E+00 (0/0)

1	GO:0042308 negative regulation of protein-nucleus import	7.37E-03 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.06E-01 (0/1)	4.35E-01 (1/0)	1.00E+00 (0/0)
1	GO:0046663 dorsal closure leading edge cell differentiation	7.37E-03 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.06E-01 (0/1)	4.35E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006081 aldehyde metabolism	9.01E-03 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.04E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007396 suture of dorsal opening	9.01E-03 (0/2)	1.00E+00 (0/0)	1.08E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0015785 UDP-galactose transport	9.01E-03 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035160 maintenance of tracheal epithelial integrity	9.01E-03 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.04E-01 (1/0)	1.00E+00 (0/0)
1	GO:0042994 cytoplasmic sequestering of transcription factor	9.01E-03 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.36E-01 (0/1)	2.04E-01 (1/0)	1.00E+00 (0/0)
1	GO:0051046 regulation of secretion	9.01E-03 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.04E-01 (0/1)	1.00E+00 (0/0)
1	GO:0051220 cytoplasmic sequestering of protein	9.01E-03 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.36E-01 (0/1)	2.04E-01 (1/0)	1.00E+00 (0/0)
1	GO:0007455 eye-antennal disc metamorphosis	9.55E-03 (8/14)	3.66E-01 (4/7)	2.29E-01 (7/3)	9.03E-02 (5/6)	2.57E-01 (6/6)	5.15E-01 (11/4)	2.93E-01 (2/9)
1	GO:0007314 oocyte anterior posterior axis determination	9.80E-03 (2/9)	5.15E-01 (1/3)	1.69E-01 (3/2)	1.32E-01 (1/4)	7.32E-01 (1/2)	8.38E-01 (2/2)	4.66E-01 (2/2)
1	GO:0035214 eye-antennal disc development	1.04E-02 (8/14)	2.60E-01 (5/7)	2.36E-01 (7/3)	9.39E-02 (5/6)	2.65E-01 (6/6)	4.17E-01 (12/4)	3.01E-01 (2/9)
1	GO:0001736 establishment of planar polarity	1.11E-02 (1/8)	3.07E-01 (1/3)	3.85E-01 (2/1)	1.45E-01 (0/4)	5.90E-02 (3/3)	2.57E-01 (4/2)	4.97E-01 (1/2)
1	GO:0007164 establishment of tissue polarity	1.11E-02 (1/8)	3.07E-01 (1/3)	3.85E-01 (2/1)	1.45E-01 (0/4)	5.90E-02 (3/3)	2.57E-01 (4/2)	4.97E-01 (1/2)
1	GO:0051049 regulation of transport	1.29E-02 (1/10)	3.42E-01 (4/1)	5.96E-01 (1/2)	5.38E-01 (0/3)	7.54E-01 (0/3)	3.81E-01 (3/4)	4.95E-01 (0/4)
1	GO:0009611 response to wounding	1.36E-02 (0/7)	8.70E-01 (1/0)	6.68E-02 (1/3)	7.70E-01 (0/1)	5.97E-01 (1/1)	3.56E-01 (1/3)	2.80E-01 (1/2)
1	GO:0007312 oocyte nucleus migration	1.37E-02 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-01 (1/0)	1.00E+00 (0/0)	1.30E-01 (2/0)	3.36E-01 (1/0)

1	GO:0051169 nuclear transport	1.42E-02 (3/9)	6.54E-01 (2/2)	4.66E-01 (2/2)	4.02E-01 (0/4)	6.57E-01 (2/2)	8.24E-01 (2/3)	2.34E-01 (3/3)
1	GO:0001745 compound eye morphogenesis (sensu Endopterygota)	1.49E-02 (6/13)	3.14E-01 (3/7)	3.32E-01 (5/3)	1.48E-01 (4/5)	3.18E-01 (5/5)	5.10E-01 (10/3)	2.50E-01 (2/8)
1	GO:0030855 epithelial cell differentiation	1.55E-02 (1/3)	5.51E-01 (0/1)	4.67E-01 (1/0)	1.00E+00 (0/0)	5.52E-01 (0/1)	3.36E-01 (1/1)	1.00E+00 (0/0)
1	GO:0046328 regulation of JNK cascade	1.55E-02 (1/3)	5.51E-01 (1/0)	4.67E-01 (1/0)	4.38E-01 (0/1)	5.52E-01 (0/1)	3.36E-01 (2/0)	5.28E-01 (1/0)
1	GO:0017145 stem cell division	1.75E-02 (3/5)	9.28E-01 (1/0)	8.73E-01 (0/1)	8.49E-01 (0/1)	2.46E-01 (1/3)	9.84E-01 (1/0)	1.00E+00 (0/0)
1	GO:0007016 cytoskeletal anchoring	1.79E-02 (2/3)	3.37E-01 (1/1)	6.22E-01 (1/0)	1.00E+00 (0/0)	1.13E-01 (1/2)	1.02E-01 (3/1)	1.00E+00 (0/0)
1	GO:0007392 initiation of dorsal closure	2.15E-02 (1/3)	2.04E-01 (1/1)	1.00E+00 (0/0)	4.67E-01 (0/1)	2.05E-01 (1/1)	7.46E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006461 protein complex assembly	2.15E-02 (1/14)	4.46E-01 (3/4)	5.65E-01 (4/1)	8.77E-02 (4/4)	2.99E-01 (2/6)	9.33E-01 (3/3)	9.85E-01 (2/0)
1	GO:0007484 genitalia morphogenesis (sensu Endopterygota)	2.23E-02 (1/2)	3.99E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.80E-01 (0/1)
1	GO:0035112 genitalia morphogenesis	2.23E-02 (1/2)	3.99E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.80E-01 (0/1)
1	GO:0048103 somatic stem cell division	2.23E-02 (2/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007243 protein kinase cascade	2.25E-02 (4/15)	3.61E-01 (2/8)	2.43E-01 (3/6)	4.40E-01 (3/4)	3.66E-01 (5/5)	2.48E-01 (9/7)	6.08E-02 (6/7)
1	GO:0007254 JNK cascade	2.35E-02 (1/8)	9.22E-02 (1/5)	1.02E-01 (3/2)	9.06E-01 (0/1)	3.92E-01 (1/3)	2.06E-01 (5/2)	5.78E-01 (2/1)
1	GO:0031098 stress-activated protein kinase signaling pathway	2.35E-02 (1/8)	9.22E-02 (1/5)	1.02E-01 (3/2)	9.06E-01 (0/1)	3.92E-01 (1/3)	2.06E-01 (5/2)	5.78E-01 (2/1)
1	GO:0006913 nucleocytoplasmic transport	2.50E-02 (3/9)	5.24E-01 (2/3)	5.27E-01 (2/2)	4.60E-01 (0/4)	7.15E-01 (2/2)	8.71E-01 (2/3)	2.91E-01 (3/3)
1	GO:0006621 protein-ER retention	2.53E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.97E-01 (1/0)	2.90E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007395 dorsal closure spreading of leading edge cells	2.53E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.97E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)

1	GO:0007629 flight behavior	2.53E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (1/0)
1	GO:0008054 cyclin catabolism	2.53E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (1/0)
1	GO:0015780 nucleotide-sugar transport	2.53E-02 (1/1)	1.00E+00 (0/0)	1.58E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0015781 pyrimidine nucleotide-sugar transport	2.53E-02 (1/1)	1.00E+00 (0/0)	1.58E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0042992 negative regulation of transcription factor-nucleus import	2.53E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.97E-01 (0/1)	2.90E-01 (1/0)	1.00E+00 (0/0)
1	GO:0048071 sex-specific pigmentation	2.53E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.97E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0042067 establishment of ommatidial polarity (sensu	2.77E-02 (1/6)	3.91E-01 (1/2)	8.40E-01 (1/0)	7.79E-02 (0/4)	7.07E-02 (2/3)	1.23E-01 (4/2)	3.54E-01 (1/2)
1	GO:0007444 imaginal disc development	2.84E-02 (12/22)	3.46E-01 (9/11)	5.70E-01 (10/4)	1.06E-01 (9/9)	9.33E-02 (11/13)	6.66E-01 (16/10)	5.18E-02 (6/18)
1	GO:0008258 head involution	2.87E-02 (2/3)	1.00E+00 (0/0)	6.63E-01 (0/1)	1.00E+00 (0/0)	7.51E-01 (0/1)	3.36E-01 (1/2)	7.27E-01 (0/1)
1	GO:0030166 proteoglycan biosynthesis	2.88E-02 (3/1)	2.30E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.32E-01 (1/1)	7.73E-01 (1/0)	1.00E+00 (0/0)
1	GO:0009795 embryonic morphogenesis	3.03E-02 (2/17)	5.37E-01 (4/5)	9.41E-02 (8/3)	7.84E-01 (2/3)	4.05E-01 (4/6)	9.71E-01 (4/4)	8.52E-01 (3/3)
1	GO:0006403 RNA localization	3.10E-02 (4/10)	5.66E-01 (2/4)	2.00E-01 (4/3)	1.49E-01 (2/5)	7.34E-01 (2/3)	9.62E-01 (3/2)	2.05E-01 (3/5)
1	GO:0046903 secretion	3.12E-02 (13/17)	1.01E-01 (10/11)	8.01E-01 (5/5)	1.66E-01 (8/7)	5.07E-01 (7/9)	1.62E-01 (10/19)	9.78E-02 (5/15)
1	GO:0007452 imaginal disc metamorphosis	3.25E-02 (10/18)	3.72E-01 (6/10)	4.75E-01 (8/4)	1.67E-01 (7/7)	3.79E-01 (8/8)	7.98E-01 (14/5)	5.16E-02 (4/16)
1	GO:0008045 motor axon guidance	3.32E-02 (0/3)	4.41E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.04E-01 (0/2)	5.98E-01 (0/1)	9.32E-02 (2/0)
1	GO:0030204 chondroitin sulfate metabolism	3.32E-02 (2/1)	1.04E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.04E-01 (1/1)	5.98E-01 (1/0)	1.00E+00 (0/0)
1	GO:0030206 chondroitin sulfate biosynthesis	3.32E-02 (2/1)	1.04E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.04E-01 (1/1)	5.98E-01 (1/0)	1.00E+00 (0/0)

1	GO:0050650 chondroitin sulfate proteoglycan biosynthesis	3.32E-02 (2/1)	1.04E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.04E-01 (1/1)	5.98E-01 (1/0)	1.00E+00 (0/0)
1	GO:0050654 chondroitin sulfate proteoglycan metabolism	3.32E-02 (2/1)	1.04E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.04E-01 (1/1)	5.98E-01 (1/0)	1.00E+00 (0/0)
1	GO:0016318 ommatidial rotation	3.54E-02 (1/4)	1.61E-01 (1/2)	6.81E-01 (1/0)	7.90E-02 (0/3)	1.63E-01 (1/2)	3.67E-01 (2/1)	3.84E-01 (0/2)
1	GO:0042078 germ-line stem cell division	3.54E-02 (2/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.16E-01 (0/2)	8.98E-01 (1/0)	1.00E+00 (0/0)
1	GO:0007264 small GTPase mediated signal transduction	3.73E-02 (6/11)	1.67E-01 (4/7)	7.60E-01 (2/3)	6.91E-01 (2/3)	6.92E-01 (3/4)	6.85E-01 (5/6)	8.75E-01 (0/5)
1	GO:0006029 proteoglycan metabolism	3.73E-02 (3/1)	2.57E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.59E-01 (1/1)	7.98E-01 (1/0)	1.00E+00 (0/0)
1	GO:0001501 skeletal development	3.77E-02 (3/3)	8.60E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	8.61E-01 (1/0)	5.68E-01 (3/0)	5.40E-01 (2/0)
1	GO:0009790 embryonic development	3.99E-02 (12/28)	4.77E-01 (11/12)	2.37E-01 (13/8)	9.69E-01 (4/6)	3.97E-01 (10/14)	9.94E-01 (9/13)	7.14E-01 (10/9)
1	GO:0016477 cell migration	4.03E-02 (5/17)	3.07E-01 (4/9)	5.10E-01 (5/4)	9.63E-01 (2/2)	1.39E-01 (8/7)	7.28E-01 (4/11)	1.53E-01 (4/10)
1	GO:0016192 vesicle-mediated transport	4.13E-02 (15/21)	6.15E-02 (12/15)	6.13E-01 (8/7)	1.33E-01 (12/7)	4.34E-01 (10/11)	6.44E-01 (12/17)	1.72E-01 (6/17)
1	GO:0001654 eye morphogenesis	4.34E-02 (8/15)	2.82E-01 (6/8)	4.50E-01 (7/3)	1.45E-01 (5/7)	5.15E-01 (6/6)	7.29E-01 (12/4)	4.22E-01 (3/9)
1	GO:0016052 carbohydrate catabolism	4.51E-02 (3/8)	3.16E-01 (2/4)	7.20E-02 (3/4)	6.62E-01 (2/1)	5.01E-01 (1/4)	9.31E-02 (6/5)	1.42E-01 (2/5)
1	GO:0044275 cellular carbohydrate catabolism	4.51E-02 (3/8)	3.16E-01 (2/4)	7.20E-02 (3/4)	6.62E-01 (2/1)	5.01E-01 (1/4)	9.31E-02 (6/5)	1.42E-01 (2/5)
1	GO:0002165 larval or pupal development (sensu Insecta)	4.60E-02 (15/27)	3.56E-01 (11/15)	1.91E-01 (15/8)	6.68E-02 (11/13)	1.64E-01 (15/14)	8.25E-01 (16/16)	1.83E-01 (7/20)
1	GO:0006022 aminoglycan metabolism	4.64E-02 (2/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (1/1)	6.42E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006023 aminoglycan biosynthesis	4.64E-02 (2/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (1/1)	6.42E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006024 glycosaminoglycan biosynthesis	4.64E-02 (2/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (1/1)	6.42E-01 (1/0)	1.00E+00 (0/0)

1	GO:0006966 antifungal humoral response (sensu Protostomia)	4.64E-02 (1/2)	4.80E-01 (1/0)	1.00E+00 (0/0)	7.37E-02 (0/2)	1.00E+00 (0/0)	6.37E-02 (1/2)	4.59E-01 (1/0)
1	GO:0030203 glycosaminoglycan metabolism	4.64E-02 (2/1)	1.27E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (1/1)	6.42E-01 (1/0)	1.00E+00 (0/0)
1	GO:0007281 germ cell development	4.67E-02 (3/5)	9.57E-01 (0/1)	6.98E-01 (2/0)	6.53E-01 (0/2)	8.17E-01 (0/2)	8.57E-01 (1/2)	9.47E-01 (1/0)
1	GO:0007280 pole cell migration	4.72E-02 (2/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.86E-01 (1/1)	8.19E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007377 germ-band extension	4.75E-02 (0/2)	2.52E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0015014 heparan sulfate proteoglycan biosynthesis	4.75E-02 (2/0)	2.52E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0015749 monosaccharide transport	4.75E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0030239 myofibril assembly	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (0/1)	3.66E-01 (1/0)	2.39E-01 (0/1)
1	GO:0030721 spectrosome organization and biogenesis	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0030833 regulation of actin filament polymerization	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035148 lumen formation	4.75E-02 (0/2)	2.52E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035149 tracheal lumen formation	4.75E-02 (0/2)	2.52E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035158 regulation of tracheal tube diameter	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.66E-01 (1/0)	1.00E+00 (0/0)
1	GO:0042990 regulation of transcription factor-nucleus import	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.89E-01 (0/1)	2.53E-01 (0/1)	3.66E-01 (1/0)	1.00E+00 (0/0)
1	GO:0042991 transcription factor-nucleus import	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.89E-01 (0/1)	2.53E-01 (0/1)	3.66E-01 (1/0)	1.00E+00 (0/0)
1	GO:0043161 proteasomal ubiquitin-dependent protein catabolism	4.75E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.39E-01 (1/0)
1	GO:0046844 micropyle formation	4.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (1/0)	3.66E-01 (1/0)	1.00E+00 (0/0)

1	GO:0007456 eye morphogenesis (sensu Endopterygota)	4.82E-02 (8/14)	3.31E-01 (5/8)	5.34E-01 (6/3)	1.94E-01 (4/7)	4.54E-01 (6/6)	6.63E-01 (12/4)	3.64E-01 (3/9)
1	GO:0000165 MAPKKK cascade	4.95E-02 (3/12)	1.62E-01 (2/8)	1.02E-01 (3/6)	7.59E-01 (2/2)	1.65E-01 (5/5)	2.78E-01 (8/5)	2.12E-01 (4/5)
1	GO:0007018 microtubule-based movement	4.95E-02 (4/11)	7.12E-01 (3/3)	4.83E-01 (2/4)	5.84E-01 (5/0)	8.43E-01 (1/4)	9.66E-01 (4/2)	7.98E-01 (5/0)
1	GO:0007530 sex determination	5.26E-02 (5/3)	3.19E-02 (5/2)	9.49E-02 (4/1)	3.91E-01 (2/1)	8.60E-02 (6/0)	8.67E-01 (1/2)	1.62E-01 (0/5)
1	GO:0016065 humoral defense mechanism (sensu Protostomia)	5.26E-02 (4/4)	6.05E-01 (2/1)	7.10E-01 (0/2)	3.91E-01 (1/2)	1.95E-01 (5/0)	1.31E-04 (2/12)	7.97E-01 (1/1)
1	GO:0009613 response to pest pathogen or parasite	5.67E-02 (4/9)	2.44E-01 (5/3)	3.33E-01 (1/5)	4.39E-01 (2/3)	7.24E-01 (5/0)	6.46E-05 (2/20)	4.93E-01 (2/4)
1	GO:0001763 branching morphogenesis	5.94E-02 (1/5)	3.52E-01 (2/1)	8.20E-01 (1/0)	1.96E-01 (0/3)	1.64E-02 (1/5)	2.16E-01 (2/3)	5.98E-01 (1/1)
1	GO:0051261 protein depolymerization	6.17E-02 (0/3)	1.52E-01 (0/2)	1.00E+00 (0/0)	4.08E-01 (0/1)	2.87E-02 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007411 axon guidance	6.45E-02 (1/10)	2.32E-02 (2/8)	9.22E-02 (4/3)	7.01E-01 (2/1)	1.17E-01 (4/4)	7.80E-01 (3/3)	8.82E-02 (3/5)
1	GO:0009968 negative regulation of signal transduction	6.56E-02 (5/3)	8.43E-01 (0/2)	4.03E-02 (6/0)	2.06E-01 (1/3)	4.08E-01 (1/3)	7.45E-01 (2/2)	1.84E-01 (4/1)
1	GO:0002164 larval development	7.15E-02 (3/4)	7.70E-01 (1/1)	1.69E-01 (3/1)	4.66E-02 (2/3)	7.72E-01 (2/0)	6.18E-01 (1/3)	7.38E-01 (2/0)
1	GO:0006955 immune response	7.51E-02 (4/11)	6.21E-01 (4/3)	2.35E-01 (2/6)	7.98E-01 (1/3)	6.26E-01 (5/2)	1.35E-05 (3/24)	3.99E-01 (2/6)
1	GO:0006874 calcium ion homeostasis	7.90E-02 (2/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.37E-02 (3/1)	1.00E+00 (0/0)
1	GO:0018991 oviposition	7.90E-02 (2/1)	5.51E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.79E-01 (2/0)	7.15E-01 (1/0)	4.24E-03 (3/1)
1	GO:0050832 defense response to fungi	8.44E-02 (1/3)	3.63E-01 (2/0)	6.43E-01 (0/1)	2.33E-01 (0/2)	1.00E+00 (0/0)	1.79E-03 (1/6)	7.08E-01 (1/0)
1	GO:0006960 antimicrobial humoral response (sensu Protostomia)	8.89E-02 (3/4)	5.56E-01 (2/1)	6.73E-01 (0/2)	3.49E-01 (1/2)	1.59E-01 (5/0)	5.47E-05 (2/12)	9.39E-01 (1/0)
1	GO:0002168 larval development (sensu Insecta)	9.42E-02 (2/3)	5.53E-01 (1/1)	1.73E-01 (3/0)	9.12E-03 (2/3)	5.56E-01 (2/0)	5.42E-01 (0/3)	5.19E-01 (2/0)

1	GO:0043207 response to external biotic stimulus	9.63E-02 (4/11)	3.66E-01 (5/4)	4.11E-01 (2/5)	4.94E-01 (2/4)	8.95E-01 (5/0)	7.76E-05 (2/24)	3.00E-01 (3/6)
1	GO:0009620 response to fungi	9.93E-02 (1/3)	3.89E-01 (2/0)	6.63E-01 (0/1)	2.53E-01 (0/2)	1.00E+00 (0/0)	2.58E-03 (1/6)	7.27E-01 (1/0)
1	GO:0006825 copper ion transport	1.04E-01 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.40E-02 (1/1)	3.55E-01 (1/0)	4.95E-01 (1/0)	1.00E+00 (0/0)
1	GO:0035153 tracheal cell type specification	1.04E-01 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.40E-02 (0/2)	3.55E-01 (0/1)	1.00E+00 (0/0)	3.36E-01 (0/1)
1	GO:0008063 Toll signaling pathway	1.21E-01 (0/5)	3.13E-01 (2/1)	4.66E-01 (1/1)	7.70E-01 (0/1)	1.00E+00 (0/0)	2.57E-02 (1/6)	2.80E-01 (2/1)
1	GO:0044260 cellular macromolecule metabolism	1.27E-01 (85/139)	6.46E-02 (74/97)	6.58E-02 (80/57)	2.18E-02 (69/62)	8.97E-01 (63/81)	1.26E-01 (112/141)	7.19E-01 (65/76)
1	GO:0016081 synaptic vesicle docking during exocytosis	1.32E-01 (0/4)	5.51E-02 (1/3)	6.99E-01 (0/1)	8.88E-02 (2/1)	4.41E-01 (0/2)	6.78E-01 (2/0)	4.56E-02 (1/3)
1	GO:0019731 antibacterial humoral response	1.34E-01 (1/5)	2.59E-01 (1/3)	3.38E-01 (0/3)	5.70E-01 (0/2)	7.46E-01 (2/0)	4.09E-07 (0/16)	9.20E-01 (1/0)
1	GO:0006904 vesicle docking during exocytosis	1.35E-01 (0/5)	1.42E-01 (1/3)	4.84E-01 (0/2)	1.82E-01 (2/1)	3.35E-01 (0/3)	8.35E-01 (2/0)	3.89E-02 (1/4)
1	GO:0048278 vesicle docking	1.35E-01 (0/5)	1.42E-01 (1/3)	4.84E-01 (0/2)	1.82E-01 (2/1)	3.35E-01 (0/3)	8.35E-01 (2/0)	3.89E-02 (1/4)
1	GO:0007154 cell communication	1.43E-01 (49/110)	4.59E-03 (56/77)	5.85E-01 (47/38)	5.90E-01 (41/37)	8.81E-02 (51/71)	9.80E-01 (73/73)	8.24E-02 (44/71)
1	GO:0008406 gonad development	1.50E-01 (3/1)	7.99E-01 (0/1)	3.47E-01 (2/0)	6.85E-01 (0/1)	1.64E-02 (4/1)	9.19E-01 (0/1)	1.00E+00 (0/0)
1	GO:0045137 development of primary sexual characteristics	1.50E-01 (3/1)	7.99E-01 (0/1)	3.47E-01 (2/0)	6.85E-01 (0/1)	1.64E-02 (4/1)	9.19E-01 (0/1)	1.00E+00 (0/0)
1	GO:0044262 cellular carbohydrate metabolism	1.50E-01 (12/18)	2.06E-01 (8/14)	4.78E-01 (7/8)	1.75E-01 (15/2)	3.73E-01 (10/10)	1.95E-02 (33/6)	5.52E-01 (10/7)
1	GO:0007165 signal transduction	1.62E-01 (39/89)	3.31E-02 (43/60)	5.83E-01 (38/30)	7.14E-01 (29/31)	4.55E-01 (37/52)	9.17E-01 (60/61)	9.59E-02 (38/55)
1	GO:0008344 adult locomotory behavior	1.65E-01 (2/1)	8.30E-02 (1/2)	5.76E-01 (0/1)	5.81E-03 (2/2)	6.66E-01 (0/1)	4.92E-01 (2/0)	6.41E-01 (1/0)
1	GO:0006518 peptide metabolism	1.72E-01 (2/0)	1.04E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.55E-03 (1/3)	1.00E+00 (0/0)

1	GO:0006890 retrograde transport Golgi to ER	1.72E-01 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.43E-01 (1/0)	4.61E-02 (0/3)	4.21E-01 (0/1)
1	GO:0042069 regulation of catecholamine metabolism	1.81E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.60E-03 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (0/1)
1	GO:0008585 female gonad development	2.08E-01 (1/1)	4.80E-01 (0/1)	8.55E-02 (2/0)	3.76E-01 (0/1)	2.12E-02 (2/1)	6.42E-01 (0/1)	1.00E+00 (0/0)
1	GO:0046545 development of primary female sexual characteristics	2.08E-01 (1/1)	4.80E-01 (0/1)	8.55E-02 (2/0)	3.76E-01 (0/1)	2.12E-02 (2/1)	6.42E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007398 ectoderm development	2.31E-01 (7/18)	2.01E-03 (11/17)	9.38E-01 (6/2)	8.96E-01 (3/5)	1.65E-01 (8/12)	9.35E-01 (12/6)	3.14E-01 (9/8)
1	GO:0008586 wing vein morphogenesis	2.45E-01 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.41E-02 (0/3)
1	GO:0008589 regulation of smoothened signaling pathway	2.45E-01 (1/1)	5.17E-01 (0/1)	1.52E-02 (3/0)	8.91E-02 (0/2)	5.18E-01 (0/1)	2.94E-01 (1/1)	4.95E-01 (1/0)
1	GO:0009894 regulation of catabolism	2.51E-01 (2/2)	8.60E-01 (1/0)	5.97E-02 (2/2)	1.57E-01 (0/3)	5.76E-01 (0/2)	3.31E-01 (2/2)	2.94E-02 (5/0)
1	GO:0006573 valine metabolism	2.59E-01 (1/0)	1.00E+00 (0/0)	8.89E-03 (0/2)	1.00E+00 (0/0)	1.97E-01 (0/1)	2.90E-01 (0/1)	1.00E+00 (0/0)
1	GO:0009612 response to mechanical stimulus	2.59E-01 (1/0)	1.96E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.42E-02 (1/1)	2.90E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007222 frizzled signaling pathway	2.68E-01 (0/3)	3.89E-01 (0/2)	1.00E+00 (0/0)	2.53E-01 (1/1)	4.04E-02 (2/2)	8.86E-01 (0/1)	7.27E-01 (0/1)
1	GO:0009064 glutamine family amino acid metabolism	2.68E-01 (1/2)	3.89E-01 (1/1)	6.63E-01 (0/1)	1.00E+00 (0/0)	1.46E-01 (1/2)	4.62E-02 (3/2)	3.59E-01 (1/1)
1	GO:0006793 phosphorus metabolism	2.68E-01 (21/39)	3.85E-01 (20/23)	4.07E-01 (19/15)	1.32E-02 (28/14)	7.77E-01 (20/17)	1.42E-01 (48/23)	2.36E-01 (22/21)
1	GO:0006796 phosphate metabolism	2.68E-01 (21/39)	3.85E-01 (20/23)	4.07E-01 (19/15)	1.32E-02 (28/14)	7.77E-01 (20/17)	1.42E-01 (48/23)	2.36E-01 (22/21)
1	GO:0007155 cell adhesion	2.81E-01 (9/23)	7.66E-02 (11/17)	6.16E-01 (11/5)	4.76E-01 (10/6)	2.24E-01 (9/16)	9.41E-01 (9/16)	4.09E-02 (9/19)
1	GO:0015980 energy derivation by oxidation of organic compounds	2.85E-01 (6/7)	1.74E-01 (5/6)	1.81E-01 (5/4)	2.26E-01 (7/1)	4.11E-01 (4/5)	1.46E-04 (25/1)	3.37E-01 (5/4)
1	GO:0009617 response to bacteria	2.88E-01 (1/7)	1.78E-01 (3/4)	1.58E-01 (1/5)	6.62E-01 (0/3)	9.52E-01 (2/0)	1.14E-05 (0/20)	4.42E-01 (3/2)

1	GO:0007548 sex differentiation	3.03E-01 (3/3)	8.60E-01 (1/1)	1.26E-01 (4/1)	9.20E-01 (0/1)	4.91E-02 (6/1)	9.96E-01 (0/1)	2.07E-01 (3/2)
1	GO:0044248 cellular catabolism	3.08E-01 (35/56)	9.04E-02 (37/37)	3.54E-03 (40/29)	3.64E-01 (24/25)	4.71E-01 (29/36)	1.16E-01 (49/60)	4.65E-01 (30/31)
1	GO:0016579 protein deubiquitination	3.22E-01 (0/3)	2.52E-03 (2/4)	6.99E-01 (1/0)	2.91E-01 (0/2)	4.41E-01 (1/1)	6.78E-01 (1/1)	7.62E-01 (0/1)
1	GO:0051325 interphase	3.22E-01 (3/0)	7.83E-01 (0/1)	6.99E-01 (0/1)	2.91E-01 (1/1)	7.85E-01 (0/1)	6.78E-01 (1/1)	4.56E-02 (1/3)
1	GO:0051329 interphase of mitotic cell cycle	3.22E-01 (3/0)	7.83E-01 (0/1)	6.99E-01 (0/1)	2.91E-01 (1/1)	7.85E-01 (0/1)	6.78E-01 (1/1)	4.56E-02 (1/3)
1	GO:0009056 catabolism	3.28E-01 (35/57)	9.30E-02 (37/38)	2.24E-03 (42/29)	2.95E-01 (25/26)	4.74E-01 (29/37)	1.09E-01 (51/60)	3.05E-01 (34/31)
1	GO:0006965 anti-Gram-positive bacterial polypeptide induction	3.29E-01 (0/1)	2.68E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.66E-01 (0/1)	2.39E-01 (1/0)
1	GO:0007176 regulation of epidermal growth factor receptor activity	3.29E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-01 (0/1)	6.00E-02 (2/0)	2.38E-02 (1/1)
1	GO:0007405 neuroblast proliferation	3.29E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0008302 ring canal formation actin assembly	3.29E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.38E-02 (1/1)
1	GO:0008333 endosome to lysosome transport	3.29E-01 (0/1)	2.52E-01 (0/1)	2.04E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.38E-02 (1/1)
1	GO:0008335 ovarian ring canal stabilization	3.29E-01 (0/1)	2.68E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.39E-01 (1/0)
1	GO:0030037 actin filament reorganization during cell cycle	3.29E-01 (0/1)	2.68E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0030588 pseudocleavage	3.29E-01 (0/1)	2.68E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0030589 pseudocleavage (sensu Insecta)	3.29E-01 (0/1)	2.68E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046835 carbohydrate phosphorylation	3.29E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046853 inositol and derivative phosphorylation	3.29E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)

1	GO:0006092 main pathways of carbohydrate metabolism	3.51E-01 (5/6)	9.01E-02 (5/6)	1.02E-01 (5/4)	1.37E-01 (7/1)	4.08E-01 (3/5)	7.82E-04 (21/1)	4.92E-01 (3/4)
1	GO:0006952 defense response	3.51E-01 (11/36)	7.81E-01 (14/15)	6.04E-01 (12/13)	9.96E-01 (8/5)	1.44E-01 (22/17)	3.13E-02 (11/52)	6.59E-01 (10/19)
1	GO:0009070 serine family amino acid biosynthesis	3.54E-01 (1/1)	1.00E+00 (0/0)	1.60E-01 (1/1)	2.57E-02 (0/3)	5.84E-02 (1/2)	7.73E-01 (1/0)	5.88E-01 (0/1)
1	GO:0042742 defense response to bacteria	3.59E-01 (1/6)	2.55E-01 (3/3)	1.21E-01 (1/5)	6.09E-01 (0/3)	9.35E-01 (2/0)	4.62E-05 (0/18)	5.78E-01 (3/1)
1	GO:0009057 macromolecule catabolism	3.62E-01 (27/51)	4.21E-01 (26/31)	1.38E-02 (37/21)	4.73E-01 (17/24)	8.11E-01 (22/28)	4.17E-01 (31/56)	2.41E-01 (28/29)
1	GO:0044265 cellular macromolecule catabolism	3.87E-01 (27/50)	4.59E-01 (26/30)	1.22E-02 (37/21)	4.55E-01 (17/24)	7.97E-01 (22/28)	3.92E-01 (31/56)	3.25E-01 (26/29)
1	GO:0042401 biogenic amine biosynthesis	3.90E-01 (1/1)	6.39E-01 (1/0)	1.00E+00 (0/0)	5.20E-01 (0/1)	1.38E-02 (3/1)	4.55E-01 (1/1)	1.00E+00 (0/0)
1	GO:0000272 polysaccharide catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006032 chitin catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006034 cuticle chitin metabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006036 cuticle chitin catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006043 glucosamine catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006046 N-acetylglucosamine catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007096 regulation of exit from mitosis	3.93E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.35E-01 (0/1)	3.80E-02 (1/1)
1	GO:0007500 mesoderm cell fate determination	3.93E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.29E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007628 adult walking behavior	3.93E-01 (1/0)	3.05E-01 (0/1)	2.49E-01 (0/1)	2.34E-02 (1/1)	3.06E-01 (0/1)	4.35E-01 (1/0)	1.00E+00 (0/0)
1	GO:0009593 detection of chemical substance	3.93E-01 (0/1)	1.00E+00 (0/0)	2.49E-01 (1/0)	1.00E+00 (0/0)	3.06E-01 (0/1)	1.00E+00 (0/0)	3.80E-02 (1/1)

1	GO:0043241 protein complex disassembly	3.93E-01 (0/1)	4.26E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0044247 cellular polysaccharide catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046348 amino sugar catabolism	3.93E-01 (0/1)	4.26E-02 (0/2)	2.49E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0048072 eye pigmentation (sensu Endopterygota)	3.93E-01 (0/1)	1.00E+00 (0/0)	2.75E-02 (0/2)	2.31E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.89E-01 (0/1)
1	GO:0009607 response to biotic stimulus	4.20E-01 (11/37)	5.44E-01 (17/17)	5.38E-01 (14/13)	9.91E-01 (9/6)	1.72E-01 (22/18)	2.77E-02 (11/55)	6.16E-01 (11/20)
1	GO:0006979 response to oxidative stress	4.24E-01 (0/2)	2.84E-01 (2/0)	4.70E-02 (2/1)	5.45E-01 (0/1)	6.66E-01 (0/1)	4.92E-01 (0/2)	6.41E-01 (1/0)
1	GO:0050829 defense response to Gram-negative bacteria	4.24E-01 (0/2)	1.00E+00 (0/0)	5.76E-01 (0/1)	5.45E-01 (0/1)	1.00E+00 (0/0)	4.84E-04 (0/7)	1.00E+00 (0/0)
1	GO:0009112 nucleobase metabolism	4.51E-01 (3/5)	2.94E-01 (3/4)	2.60E-02 (2/7)	1.99E-01 (6/0)	9.02E-02 (5/4)	1.21E-01 (4/8)	2.43E-01 (5/2)
1	GO:0015931 nucleobase nucleoside nucleotide and nucleic acid transport	4.51E-01 (2/2)	4.68E-01 (1/2)	3.23E-01 (3/0)	8.99E-03 (1/5)	9.28E-01 (0/1)	9.12E-01 (1/1)	4.27E-01 (1/2)
1	GO:0006020 myo-inositol metabolism	4.51E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-01 (0/1)	5.91E-03 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0006124 ferredoxin metabolism	4.51E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.55E-01 (0/1)	1.00E+00 (0/0)	4.90E-03 (1/2)
1	GO:0007030 Golgi organization and biogenesis	4.51E-01 (1/0)	3.54E-01 (1/0)	1.00E+00 (0/0)	3.40E-02 (2/0)	3.55E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007620 copulation	4.51E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	5.91E-03 (1/2)	1.00E+00 (0/0)	5.45E-02 (1/1)
1	GO:0001710 mesoderm cell fate commitment	4.58E-01 (1/1)	6.88E-01 (0/1)	1.00E+00 (0/0)	5.68E-01 (0/1)	2.24E-02 (2/2)	1.00E+00 (0/0)	6.65E-01 (0/1)
1	GO:0042398 amino acid derivative biosynthesis	4.58E-01 (1/1)	6.88E-01 (1/0)	1.00E+00 (0/0)	5.68E-01 (0/1)	3.86E-03 (3/2)	5.27E-01 (1/1)	2.85E-01 (1/1)
1	GO:0048333 mesoderm cell differentiation	4.58E-01 (1/1)	6.88E-01 (0/1)	1.00E+00 (0/0)	5.68E-01 (0/1)	2.24E-02 (2/2)	1.00E+00 (0/0)	6.65E-01 (0/1)
1	GO:0012502 induction of programmed cell death	4.87E-01 (3/4)	7.23E-01 (2/2)	3.37E-01 (5/0)	2.35E-02 (5/3)	8.74E-01 (1/2)	3.24E-01 (4/5)	3.02E-01 (2/4)

1	GO:0001709 cell fate determination	4.89E-01 (3/8)	8.00E-01 (2/4)	2.74E-01 (5/3)	5.03E-01 (3/3)	4.74E-02 (5/8)	5.41E-01 (9/3)	7.49E-01 (2/4)
1	GO:0006909 phagocytosis	4.90E-01 (1/1)	2.73E-02 (1/3)	6.22E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	8.56E-01 (0/1)	1.00E+00 (0/0)
1	GO:0009069 serine family amino acid metabolism	4.90E-01 (1/1)	1.00E+00 (0/0)	6.47E-02 (1/2)	9.35E-03 (1/3)	1.13E-01 (1/2)	5.61E-01 (2/0)	6.87E-01 (0/1)
1	GO:0045944 positive regulation of transcription from RNA polymerase II	4.90E-01 (0/2)	7.10E-01 (0/1)	2.43E-01 (1/1)	5.90E-01 (0/1)	7.11E-01 (0/1)	5.61E-01 (1/1)	2.23E-02 (1/3)
1	GO:0007370 ventral furrow formation	5.03E-01 (0/1)	3.99E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	9.80E-03 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0009081 branched chain family amino acid metabolism	5.03E-01 (1/0)	1.00E+00 (0/0)	5.03E-03 (0/3)	1.00E+00 (0/0)	4.00E-01 (0/1)	1.69E-01 (0/2)	3.80E-01 (1/0)
1	GO:0046112 nucleobase biosynthesis	5.03E-01 (0/1)	1.00E+00 (0/0)	3.30E-01 (0/1)	4.60E-02 (2/0)	4.00E-01 (1/0)	5.50E-01 (0/1)	1.00E+00 (0/0)
1	GO:0050874 organismal physiological process	5.08E-01 (29/44)	5.55E-02 (25/40)	4.28E-01 (21/23)	5.33E-01 (22/17)	2.93E-01 (28/30)	1.97E-02 (39/61)	1.10E-01 (21/38)
1	GO:0043285 biopolymer catabolism	5.09E-01 (24/43)	3.60E-01 (23/29)	2.62E-02 (34/17)	3.77E-01 (15/23)	8.95E-01 (21/21)	6.08E-01 (25/49)	5.47E-01 (23/23)
1	GO:0048522 positive regulation of cellular process	5.10E-01 (4/11)	5.29E-01 (5/6)	2.42E-01 (10/1)	1.68E-01 (6/5)	2.96E-01 (4/9)	2.27E-01 (10/10)	6.23E-03 (6/13)
1	GO:0050790 regulation of enzyme activity	5.29E-01 (2/1)	4.87E-02 (2/3)	2.16E-01 (3/0)	1.82E-01 (1/2)	6.16E-01 (1/1)	1.00E+00 (0/0)	5.79E-01 (0/2)
1	GO:0043068 positive regulation of programmed cell death	5.33E-01 (3/4)	7.53E-01 (2/2)	3.71E-01 (5/0)	2.95E-02 (5/3)	5.79E-01 (1/4)	3.71E-01 (4/5)	3.38E-01 (2/4)
1	GO:0030163 protein catabolism	5.38E-01 (24/42)	4.59E-01 (23/27)	3.38E-02 (34/16)	3.60E-01 (15/23)	8.85E-01 (21/21)	5.81E-01 (25/49)	5.26E-01 (23/23)
1	GO:0035107 appendage morphogenesis	5.46E-01 (3/7)	4.58E-01 (3/5)	9.37E-01 (2/1)	9.10E-01 (2/1)	2.03E-01 (5/5)	9.45E-01 (5/2)	3.49E-03 (4/11)
1	GO:0007464 R3 R4 cell fate commitment	5.50E-01 (0/1)	4.41E-01 (0/1)	1.00E+00 (0/0)	5.93E-02 (0/2)	4.43E-01 (1/0)	4.61E-02 (2/1)	4.21E-01 (0/1)
1	GO:0007618 mating	5.50E-01 (0/1)	4.41E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.35E-03 (2/2)	1.00E+00 (0/0)	9.32E-02 (1/1)
1	GO:0016476 shape changes of embryonic cells	5.50E-01 (0/1)	1.47E-02 (1/2)	1.00E+00 (0/0)	3.43E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)

1	GO:0030509 BMP signaling pathway	5.50E-01 (0/1)	1.00E+00 (0/0)	3.67E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.61E-02 (2/1)	1.00E+00 (0/0)
1	GO:0048056 R3 R4 cell differentiation (sensu Endopterygota)	5.50E-01 (0/1)	4.41E-01 (0/1)	1.00E+00 (0/0)	5.93E-02 (0/2)	4.43E-01 (1/0)	4.61E-02 (2/1)	4.21E-01 (0/1)
1	GO:0006576 biogenic amine metabolism	5.53E-01 (2/1)	8.88E-01 (1/0)	1.00E+00 (0/0)	1.96E-01 (2/1)	4.03E-03 (5/2)	4.07E-01 (2/2)	5.98E-01 (1/1)
1	GO:0019098 reproductive behavior	5.58E-01 (3/2)	7.17E-01 (1/2)	5.58E-01 (2/1)	9.35E-01 (0/1)	1.57E-01 (3/3)	9.30E-01 (2/1)	1.81E-03 (4/6)
1	GO:0006508 proteolysis and peptidolysis	5.67E-01 (24/41)	4.99E-01 (23/26)	3.02E-02 (34/16)	3.42E-01 (15/23)	8.75E-01 (21/21)	5.54E-01 (25/49)	6.32E-01 (21/23)
1	GO:0044257 cellular protein catabolism	5.67E-01 (24/41)	4.99E-01 (23/26)	3.02E-02 (34/16)	3.42E-01 (15/23)	8.75E-01 (21/21)	5.54E-01 (25/49)	6.32E-01 (21/23)
1	GO:0035220 wing disc development	5.93E-01 (2/6)	4.10E-01 (2/5)	9.58E-01 (1/1)	9.42E-01 (1/1)	2.68E-01 (3/5)	8.42E-01 (5/2)	1.12E-02 (3/9)
1	GO:0016080 synaptic vesicle targeting	5.93E-01 (0/1)	2.09E-02 (1/2)	4.02E-01 (0/1)	3.76E-01 (1/0)	1.28E-01 (0/2)	6.42E-01 (1/0)	1.15E-01 (0/2)
1	GO:0048518 positive regulation of biological process	5.94E-01 (5/11)	3.36E-01 (6/8)	3.73E-01 (10/1)	2.75E-01 (6/5)	4.54E-01 (4/9)	4.14E-01 (10/10)	1.03E-02 (6/14)
1	GO:0048193 Golgi vesicle transport	5.98E-01 (2/1)	6.67E-01 (1/1)	1.00E+00 (0/0)	2.22E-01 (3/0)	7.07E-02 (4/1)	1.40E-03 (3/7)	1.57E-01 (0/4)
1	GO:0006333 chromatin assembly or disassembly	6.06E-01 (4/3)	6.36E-01 (3/2)	4.27E-01 (3/2)	5.59E-01 (4/0)	4.26E-02 (6/4)	7.37E-01 (3/4)	3.98E-01 (2/4)
1	GO:0043067 regulation of programmed cell death	6.30E-01 (3/7)	6.79E-01 (4/3)	2.82E-01 (7/1)	1.14E-02 (6/6)	8.10E-01 (1/5)	3.18E-01 (7/7)	6.43E-02 (5/7)
1	GO:0006903 vesicle targeting	6.32E-01 (0/1)	2.84E-02 (1/2)	4.35E-01 (0/1)	4.08E-01 (1/0)	1.53E-01 (0/2)	6.80E-01 (1/0)	1.37E-01 (0/2)
1	GO:0007549 dosage compensation	6.32E-01 (0/1)	1.52E-01 (2/0)	1.00E+00 (0/0)	1.21E-02 (2/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046667 retinal programmed cell death (sensu Endopterygota)	6.32E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.08E-01 (0/1)	1.00E+00 (0/0)	6.80E-01 (1/0)	2.41E-02 (0/3)
1	GO:0046483 heterocycle metabolism	6.40E-01 (4/8)	6.13E-01 (5/4)	3.64E-02 (4/9)	8.34E-02 (10/1)	1.54E-01 (9/4)	1.35E-01 (9/10)	2.76E-01 (7/4)
1	GO:0035114 appendage morphogenesis (sensu Endopterygota)	6.43E-01 (2/7)	4.25E-01 (3/5)	9.28E-01 (2/1)	9.00E-01 (2/1)	2.90E-01 (4/5)	9.34E-01 (5/2)	6.73E-03 (4/10)

1	GO:0050875 cellular physiological process	6.47E-01 (228/325)	1.72E-01 (189/229)	1.01E-01 (185/149)	3.27E-02 (161/150)	4.24E-01 (177/237)	5.32E-01 (296/334)	4.63E-01 (177/210)
1	GO:0042981 regulation of apoptosis	6.55E-01 (3/6)	5.91E-01 (4/3)	3.47E-01 (6/1)	7.92E-02 (4/5)	7.42E-01 (1/5)	3.15E-01 (7/6)	3.77E-02 (5/7)
1	GO:0007476 wing morphogenesis	6.60E-01 (1/6)	5.06E-01 (2/4)	9.45E-01 (1/1)	9.24E-01 (1/1)	2.09E-01 (3/5)	7.84E-01 (5/2)	6.41E-03 (3/9)
1	GO:0006458 'de novo' protein folding	6.67E-01 (0/1)	5.30E-03 (1/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	5.52E-01 (0/1)	3.36E-01 (0/2)	1.00E+00 (0/0)
1	GO:0007307 chorion gene amplification	6.67E-01 (1/0)	5.51E-01 (1/0)	1.00E+00 (0/0)	1.05E-01 (1/1)	3.74E-02 (1/2)	7.15E-01 (0/1)	1.61E-01 (2/0)
1	GO:0007501 mesoderm cell fate specification	6.67E-01 (0/1)	5.51E-01 (0/1)	1.00E+00 (0/0)	4.38E-01 (0/1)	5.38E-03 (2/2)	1.00E+00 (0/0)	5.28E-01 (0/1)
1	GO:0030307 positive regulation of cell growth	6.67E-01 (0/1)	1.78E-01 (2/0)	4.67E-01 (1/0)	4.38E-01 (1/0)	1.00E+00 (0/0)	7.15E-01 (0/1)	3.16E-02 (1/2)
1	GO:0006512 ubiquitin cycle	6.76E-01 (6/10)	3.10E-02 (5/15)	4.38E-01 (6/5)	4.59E-01 (2/8)	5.29E-01 (2/11)	9.00E-01 (6/9)	5.52E-01 (5/7)
1	GO:0006575 amino acid derivative metabolism	6.81E-01 (2/2)	9.70E-01 (1/0)	9.36E-01 (1/0)	9.62E-02 (3/2)	1.77E-02 (6/2)	4.16E-01 (3/3)	6.22E-01 (1/2)
1	GO:0007472 wing disc metamorphosis	6.86E-01 (1/6)	3.64E-01 (2/5)	9.50E-01 (1/1)	9.31E-01 (1/1)	2.28E-01 (3/5)	8.05E-01 (5/2)	7.79E-03 (3/9)
1	GO:0016265 death	6.89E-01 (8/16)	4.53E-01 (10/10)	4.92E-02 (17/5)	2.30E-01 (7/10)	2.84E-01 (4/18)	7.13E-01 (9/18)	4.38E-01 (8/11)
1	GO:0051242 positive regulation of cellular physiological process	6.90E-01 (4/8)	6.56E-01 (4/5)	2.50E-01 (9/1)	1.01E-01 (6/5)	5.29E-01 (3/7)	4.41E-01 (7/9)	1.03E-02 (6/11)
1	GO:0007617 mating behavior	6.97E-01 (2/2)	6.78E-01 (1/2)	5.17E-01 (2/1)	9.24E-01 (0/1)	1.28E-01 (3/3)	9.10E-01 (2/1)	1.38E-02 (3/5)
1	GO:0045793 positive regulation of cell size	6.98E-01 (0/1)	2.04E-01 (2/0)	4.96E-01 (1/0)	4.67E-01 (1/0)	1.00E+00 (0/0)	7.46E-01 (0/1)	4.01E-02 (1/2)
1	GO:0043119 positive regulation of physiological process	7.09E-01 (4/8)	6.73E-01 (4/5)	2.64E-01 (9/1)	1.09E-01 (6/5)	5.48E-01 (3/7)	4.64E-01 (7/9)	1.18E-02 (6/11)
1	GO:0001708 cell fate specification	7.13E-01 (2/2)	6.91E-01 (0/3)	9.43E-01 (1/0)	4.74E-01 (1/2)	7.38E-03 (5/4)	9.77E-01 (1/1)	4.21E-01 (1/3)
1	GO:0007219 Notch signaling pathway	7.14E-01 (2/1)	2.75E-01 (2/2)	8.87E-01 (1/0)	4.23E-02 (1/4)	2.78E-01 (2/2)	5.97E-01 (3/1)	1.02E-01 (0/5)

1	GO:0040007 growth	7.17E-01 (0/6)	4.19E-01 (3/3)	2.27E-01 (6/0)	3.40E-02 (4/4)	9.71E-01 (0/2)	6.98E-01 (1/6)	2.14E-01 (3/4)
1	GO:0007379 segment specification	7.22E-01 (2/0)	2.74E-01 (1/2)	4.28E-01 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.53E-02 (2/3)
1	GO:0006720 isoprenoid metabolism	7.27E-01 (1/0)	1.03E-02 (1/3)	1.00E+00 (0/0)	4.94E-01 (1/0)	2.32E-01 (1/1)	7.73E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006891 intra-Golgi transport	7.27E-01 (0/1)	6.12E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.13E-01 (0/1)	4.32E-02 (1/3)	5.88E-01 (0/1)
1	GO:0007032 endosome organization and biogenesis	7.27E-01 (0/1)	6.12E-01 (0/1)	1.60E-01 (0/2)	1.40E-01 (1/1)	2.32E-01 (1/1)	4.32E-02 (2/2)	2.10E-01 (1/1)
1	GO:0007469 antennal morphogenesis	7.27E-01 (0/1)	2.30E-01 (1/1)	1.00E+00 (0/0)	4.94E-01 (0/1)	6.13E-01 (0/1)	1.00E+00 (0/0)	4.96E-02 (1/2)
1	GO:0016197 endosome transport	7.27E-01 (0/1)	6.12E-01 (0/1)	1.60E-01 (0/2)	1.40E-01 (1/1)	2.32E-01 (1/1)	4.32E-02 (2/2)	2.10E-01 (1/1)
1	GO:0030097 hemopoiesis	7.27E-01 (1/3)	8.82E-01 (1/1)	7.84E-01 (1/1)	1.00E+00 (0/0)	4.88E-01 (2/2)	1.78E-01 (4/4)	4.84E-02 (5/2)
1	GO:0006732 coenzyme metabolism	7.48E-01 (8/11)	4.18E-01 (9/8)	2.73E-01 (3/12)	1.14E-01 (12/4)	6.34E-01 (8/7)	2.54E-04 (30/12)	6.37E-01 (8/6)
1	GO:0006888 ER to Golgi transport	7.53E-01 (0/1)	2.57E-01 (1/1)	1.00E+00 (0/0)	1.58E-01 (2/0)	7.06E-02 (2/1)	5.55E-02 (1/3)	1.10E-02 (0/4)
1	GO:0009893 positive regulation of metabolism	7.68E-01 (1/3)	7.41E-01 (0/3)	3.52E-01 (3/1)	9.42E-01 (0/1)	1.77E-01 (2/4)	7.05E-01 (2/3)	2.40E-02 (3/5)
1	GO:0031325 positive regulation of cellular metabolism	7.68E-01 (1/3)	7.41E-01 (0/3)	3.52E-01 (3/1)	9.42E-01 (0/1)	1.77E-01 (2/4)	7.05E-01 (2/3)	2.40E-02 (3/5)
1	GO:0006520 amino acid metabolism	7.85E-01 (13/7)	3.44E-01 (7/12)	1.92E-01 (4/13)	1.15E-01 (4/13)	6.38E-03 (13/15)	1.80E-01 (15/16)	3.38E-01 (8/10)
1	GO:0006406 mRNA-nucleus export	7.98E-01 (1/0)	9.71E-02 (1/2)	2.22E-01 (2/0)	4.50E-02 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.65E-01 (0/1)
1	GO:0051028 mRNA transport	7.98E-01 (1/0)	9.71E-02 (1/2)	2.22E-01 (2/0)	4.50E-02 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.65E-01 (0/1)
1	GO:0051186 cofactor metabolism	8.32E-01 (8/11)	5.20E-01 (9/8)	2.58E-01 (4/12)	1.06E-01 (12/5)	7.24E-01 (8/7)	2.50E-04 (32/12)	4.16E-01 (9/8)
1	GO:0001558 regulation of cell growth	8.35E-01 (0/1)	3.63E-01 (2/0)	2.64E-01 (2/0)	2.33E-01 (2/0)	7.32E-01 (0/1)	5.92E-01 (0/2)	2.72E-02 (1/3)

1	GO:0042330 taxis	8.35E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.11E-01 (0/1)	3.37E-02 (2/2)	5.92E-01 (1/1)	3.35E-01 (0/2)
1	GO:0009987 cellular process	8.43E-01 (248/348)	2.78E-02 (206/250)	3.25E-01 (195/160)	1.67E-01 (171/158)	4.36E-01 (192/256)	9.68E-01 (314/356)	6.13E-01 (190/227)
1	GO:0050877 neurophysiological process	8.48E-01 (19/25)	1.62E-02 (20/30)	7.72E-01 (12/14)	6.86E-01 (15/10)	1.72E-01 (19/24)	8.60E-01 (22/28)	3.06E-01 (14/24)
1	GO:0009063 amino acid catabolism	8.57E-01 (2/1)	5.30E-02 (3/4)	2.88E-01 (0/4)	7.22E-01 (1/1)	1.99E-02 (4/4)	2.72E-01 (4/3)	6.36E-01 (2/1)
1	GO:0006629 lipid metabolism	8.64E-01 (15/23)	7.77E-01 (18/11)	5.16E-01 (16/10)	6.79E-01 (9/13)	2.52E-02 (22/22)	8.06E-01 (16/29)	3.53E-01 (17/16)
1	GO:0016071 mRNA metabolism	8.71E-01 (9/5)	7.83E-01 (7/4)	3.58E-01 (8/4)	8.56E-01 (1/6)	9.61E-01 (1/7)	8.20E-01 (4/13)	6.30E-03 (6/16)
1	GO:0006397 mRNA processing	8.71E-01 (9/4)	8.05E-01 (6/4)	3.94E-01 (8/3)	8.07E-01 (1/6)	9.88E-01 (1/5)	8.08E-01 (4/12)	2.36E-02 (4/15)
1	GO:0051239 regulation of organismal physiological process	8.77E-01 (0/1)	7.83E-01 (0/1)	6.99E-01 (1/0)	6.68E-01 (1/0)	1.00E+00 (0/0)	2.01E-02 (5/1)	1.00E+00 (0/0)
1	GO:0009310 amine catabolism	8.84E-01 (2/1)	6.91E-02 (3/4)	3.27E-01 (0/4)	7.52E-01 (1/1)	9.57E-03 (4/5)	3.26E-01 (4/3)	4.51E-01 (3/1)
1	GO:0040029 regulation of gene expression epigenetic	8.85E-01 (3/1)	4.97E-01 (3/2)	8.89E-01 (0/2)	5.00E-02 (4/3)	6.93E-01 (1/3)	9.36E-01 (4/0)	9.38E-01 (1/1)
1	GO:0006961 antibacterial humoral response (sensu Protostomia)	8.89E-01 (1/0)	4.63E-01 (1/1)	3.47E-01 (0/2)	3.11E-01 (0/2)	4.65E-01 (2/0)	4.86E-06 (0/11)	1.00E+00 (0/0)
1	GO:0045935 positive regulation of nucleobase nucleoside nucleotide	8.91E-01 (0/3)	7.29E-01 (0/3)	3.39E-01 (3/1)	9.38E-01 (0/1)	1.67E-01 (2/4)	6.89E-01 (2/3)	2.16E-02 (3/5)
1	GO:0045941 positive regulation of transcription	8.91E-01 (0/3)	7.29E-01 (0/3)	3.39E-01 (3/1)	9.38E-01 (0/1)	1.67E-01 (2/4)	6.89E-01 (2/3)	2.16E-02 (3/5)
1	GO:0016310 phosphorylation	8.94E-01 (13/23)	1.79E-01 (19/18)	1.74E-01 (16/14)	1.38E-02 (25/9)	8.88E-01 (15/11)	8.56E-02 (42/16)	3.61E-01 (18/14)
1	GO:0045893 positive regulation of transcription DNA-dependent	8.97E-01 (0/2)	5.22E-01 (0/3)	6.46E-01 (1/1)	8.71E-01 (0/1)	5.25E-01 (1/2)	8.07E-01 (2/1)	3.36E-03 (3/5)
1	GO:0006082 organic acid metabolism	9.06E-01 (16/12)	4.91E-01 (12/14)	7.38E-02 (10/17)	1.17E-01 (8/16)	2.93E-03 (22/18)	1.05E-01 (24/23)	3.63E-01 (12/14)
1	GO:0019752 carboxylic acid metabolism	9.06E-01 (16/12)	4.91E-01 (12/14)	7.38E-02 (10/17)	1.17E-01 (8/16)	2.93E-03 (22/18)	1.05E-01 (24/23)	3.63E-01 (12/14)

1	GO:0006367 transcription initiation from RNA polymerase II promoter	9.12E-01 (2/3)	8.50E-01 (1/3)	5.03E-01 (3/2)	2.67E-02 (4/5)	5.47E-01 (3/3)	6.97E-01 (2/6)	6.58E-01 (3/2)
1	GO:0006352 transcription initiation	9.22E-01 (2/3)	8.63E-01 (1/3)	5.24E-01 (3/2)	3.05E-02 (4/5)	4.03E-01 (3/4)	5.89E-01 (2/7)	5.05E-01 (4/2)
1	GO:0008202 steroid metabolism	9.29E-01 (4/4)	5.47E-01 (5/4)	9.76E-01 (2/1)	9.63E-01 (1/2)	8.06E-03 (10/7)	8.96E-01 (3/7)	7.49E-01 (2/5)
1	GO:0006396 RNA processing	9.32E-01 (11/5)	7.49E-01 (8/6)	7.39E-01 (8/3)	7.45E-01 (2/8)	9.93E-01 (2/6)	8.75E-01 (5/15)	2.32E-03 (6/21)
1	GO:0016125 sterol metabolism	9.39E-01 (1/0)	5.94E-01 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.15E-01 (2/1)	8.20E-01 (1/1)	3.40E-02 (1/4)
1	GO:0007582 physiological process	9.39E-01 (260/348)	5.69E-01 (207/248)	8.88E-02 (197/170)	2.42E-01 (175/160)	4.82E-01 (201/257)	1.37E-02 (324/389)	6.31E-01 (197/230)
1	GO:0006400 tRNA modification	9.43E-01 (3/0)	6.41E-01 (1/3)	6.77E-01 (2/1)	3.75E-02 (1/6)	6.77E-02 (2/6)	9.70E-01 (2/1)	1.12E-01 (2/5)
1	GO:0007591 molting cycle (sensu Insecta)	9.45E-01 (1/0)	8.79E-01 (0/1)	1.00E+00 (0/0)	4.40E-01 (1/1)	1.00E+00 (0/0)	8.35E-01 (0/2)	2.26E-03 (3/4)
1	GO:0018988 molting cycle (sensu Protostomia and Nematoda)	9.59E-01 (1/0)	9.03E-01 (0/1)	1.00E+00 (0/0)	4.91E-01 (1/1)	9.04E-01 (1/0)	8.74E-01 (0/2)	4.11E-03 (3/4)
1	GO:0042303 molting cycle	9.59E-01 (1/0)	9.03E-01 (0/1)	1.00E+00 (0/0)	4.91E-01 (1/1)	9.04E-01 (1/0)	8.74E-01 (0/2)	4.11E-03 (3/4)
1	GO:0007568 aging	9.63E-01 (0/1)	6.84E-01 (1/1)	3.38E-02 (4/1)	5.08E-01 (1/1)	7.87E-02 (1/4)	2.79E-01 (0/5)	6.50E-01 (1/1)
1	GO:0008340 determination of adult life span	9.63E-01 (0/1)	6.84E-01 (1/1)	3.38E-02 (4/1)	5.08E-01 (1/1)	7.87E-02 (1/4)	2.79E-01 (0/5)	6.50E-01 (1/1)
1	GO:0006418 tRNA aminoacylation for protein translation	9.75E-01 (2/0)	5.60E-01 (1/3)	6.09E-01 (2/1)	6.44E-02 (1/5)	4.09E-02 (2/6)	9.87E-01 (2/0)	7.34E-02 (2/5)
1	GO:0043039 tRNA aminoacylation	9.75E-01 (2/0)	5.60E-01 (1/3)	6.09E-01 (2/1)	6.44E-02 (1/5)	4.09E-02 (2/6)	9.87E-01 (2/0)	7.34E-02 (2/5)
1	GO:0044255 cellular lipid metabolism	9.75E-01 (8/13)	7.24E-01 (12/8)	4.97E-01 (12/6)	8.32E-01 (6/7)	8.52E-03 (18/16)	8.94E-01 (10/18)	6.17E-01 (12/8)
1	GO:0043038 amino acid activation	9.77E-01 (2/0)	5.74E-01 (1/3)	6.21E-01 (2/1)	6.90E-02 (1/5)	4.48E-02 (2/6)	9.88E-01 (2/0)	7.92E-02 (2/5)
1	GO:0006399 tRNA metabolism	9.85E-01 (3/0)	8.22E-01 (1/3)	8.29E-01 (2/1)	5.04E-02 (2/6)	1.08E-01 (2/7)	8.75E-01 (3/3)	3.65E-02 (3/7)

1	GO:0006091 generation of precursor metabolites and energy	9.90E-01 (17/17)	6.82E-01 (21/12)	1.29E-01 (15/19)	5.28E-02 (24/10)	5.52E-01 (15/20)	4.13E-04 (56/22)	6.09E-01 (16/16)
1	GO:0016070 RNA metabolism	9.91E-01 (15/6)	8.27E-01 (10/10)	8.58E-01 (10/5)	4.72E-01 (4/14)	7.69E-01 (4/17)	9.69E-01 (9/18)	4.26E-04 (11/28)
1	GO:0009058 biosynthesis	9.96E-01 (31/29)	4.72E-01 (28/32)	4.49E-01 (20/28)	1.45E-02 (29/28)	2.73E-01 (29/35)	2.13E-01 (43/55)	7.72E-01 (23/28)
1	GO:0006413 translational initiation	9.97E-01 (1/0)	5.68E-03 (7/3)	3.91E-01 (1/3)	5.63E-01 (2/1)	5.77E-01 (1/3)	5.88E-01 (1/5)	8.98E-01 (2/0)
1	GO:0043037 translation	9.97E-01 (6/2)	1.32E-01 (9/8)	2.05E-01 (6/7)	4.30E-02 (5/10)	5.11E-02 (4/15)	9.33E-01 (6/8)	3.06E-01 (4/10)
1	GO:0044238 primary metabolism	9.97E-01 (163/213)	4.95E-01 (135/167)	2.55E-02 (134/123)	2.10E-01 (116/111)	5.04E-01 (136/167)	5.76E-01 (199/262)	4.94E-01 (133/151)
1	GO:0008152 metabolism	9.99E-01 (181/239)	7.47E-01 (150/179)	1.34E-02 (150/135)	1.03E-01 (135/120)	4.17E-01 (157/182)	4.05E-01 (235/283)	3.57E-01 (152/167)
1	GO:0044249 cellular biosynthesis	9.99E-01 (29/23)	6.19E-01 (25/28)	4.11E-01 (18/27)	2.42E-02 (26/26)	1.99E-01 (27/34)	1.21E-01 (43/51)	8.88E-01 (18/26)
1	GO:0044237 cellular metabolism	9.99E-01 (164/218)	5.20E-01 (140/169)	3.19E-02 (142/120)	1.64E-01 (123/111)	4.92E-01 (141/170)	4.41E-01 (217/260)	3.45E-01 (140/155)
1	GO:0000394 RNA splicing via endonucleolytic cleavage and ligation	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.24E-02 (1/1)
1	GO:0001775 cell activation	1.00E+00 (0/0)	4.80E-01 (1/0)	1.11E-02 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.42E-01 (0/1)	1.15E-01 (1/1)
1	GO:0006106 fumarate metabolism	1.00E+00 (0/0)	4.26E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.06E-01 (0/1)	9.29E-02 (2/0)	1.00E+00 (0/0)
1	GO:0006388 tRNA splicing	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.24E-02 (1/1)
1	GO:0006430 lysyl-tRNA aminoacylation	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.24E-02 (1/1)
1	GO:0006595 polyamine metabolism	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	5.91E-03 (2/1)	4.95E-01 (1/0)	3.36E-01 (1/0)
1	GO:0006596 polyamine biosynthesis	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.29E-02 (2/0)	4.35E-01 (1/0)	1.00E+00 (0/0)
1	GO:0006637 acyl-CoA metabolism	1.00E+00 (0/0)	3.89E-01 (1/1)	2.85E-01 (0/2)	1.00E+00 (0/0)	4.04E-02 (2/2)	3.36E-01 (1/2)	1.26E-01 (2/1)

1	GO:0006855 multidrug transport	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.34E-03 (1/1)
1	GO:0006954 inflammatory response	1.00E+00 (0/0)	4.80E-01 (1/0)	1.11E-02 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.42E-01 (0/1)	1.15E-01 (1/1)
1	GO:0007375 anterior midgut invagination	1.00E+00 (0/0)	2.52E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007460 R8 cell fate commitment	1.00E+00 (0/0)	5.17E-01 (0/1)	1.00E+00 (0/0)	8.91E-02 (0/2)	5.18E-01 (0/1)	1.00E+00 (0/0)	2.41E-02 (0/3)
1	GO:0007461 restriction of R8 fate	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.40E-02 (0/2)	3.55E-01 (0/1)	1.00E+00 (0/0)	5.45E-02 (0/2)
1	GO:0007499 ectoderm and mesoderm interaction	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.42E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0007594 puparial adhesion	1.00E+00 (0/0)	5.51E-01 (0/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.24E-03 (1/3)
1	GO:0008216 spermidine metabolism	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	3.66E-01 (1/0)	2.39E-01 (1/0)
1	GO:0008299 isoprenoid biosynthesis	1.00E+00 (0/0)	2.09E-02 (0/3)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.28E-01 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0008363 larval cuticle biosynthesis (sensu Insecta)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.24E-02 (2/0)
1	GO:0015904 tetracycline transport	1.00E+00 (0/0)	1.00E+00 (0/0)	2.75E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0016204 determination of muscle attachment site	1.00E+00 (0/0)	1.40E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (1/0)
1	GO:0019216 regulation of lipid metabolism	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0030728 ovulation	1.00E+00 (0/0)	2.52E-01 (1/0)	1.00E+00 (0/0)	1.89E-01 (1/0)	2.70E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0035156 fusion cell fate specification	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	7.53E-03 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.85E-01 (0/1)
1	GO:0042116 macrophage activation	1.00E+00 (0/0)	4.80E-01 (1/0)	1.11E-02 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.42E-01 (0/1)	1.15E-01 (1/1)
1	GO:0042127 regulation of cell proliferation	1.00E+00 (0/0)	1.00E+00 (0/0)	4.69E-02 (4/0)	1.33E-01 (1/2)	5.34E-01 (0/2)	7.68E-01 (0/2)	4.98E-01 (1/1)

1	GO:0042336 cuticle biosynthesis during molting (sensu Protostomia and	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.89E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.38E-02 (2/0)
1	GO:0042337 cuticle biosynthesis during molting (sensu Insecta)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.89E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.38E-02 (2/0)
1	GO:0045168 cell-cell signaling involved in cell fate commitment	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.46E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.39E-01 (0/1)
1	GO:0045321 immune cell activation	1.00E+00 (0/0)	4.80E-01 (1/0)	1.11E-02 (1/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	6.42E-01 (0/1)	1.15E-01 (1/1)
1	GO:0045463 R8 development	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.34E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.89E-01 (0/1)
1	GO:0045465 R8 cell differentiation	1.00E+00 (0/0)	6.12E-01 (0/1)	1.00E+00 (0/0)	1.40E-01 (0/2)	6.13E-01 (0/1)	1.00E+00 (0/0)	4.96E-02 (0/3)
1	GO:0045468 regulation of R8 spacing	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.34E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.89E-01 (0/1)
1	GO:0045477 regulation of nurse cell apoptosis	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.42E-02 (0/2)	1.00E+00 (0/0)	1.85E-01 (1/0)
1	GO:0045742 positive regulation of epidermal growth factor receptor	1.00E+00 (0/0)	1.00E+00 (0/0)	1.58E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.23E-02 (2/0)	1.85E-01 (0/1)
1	GO:0045747 positive regulation of Notch signaling pathway	1.00E+00 (0/0)	1.40E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0045815 positive regulation of gene expression epigenetic	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.80E-02 (1/1)
1	GO:0045850 positive regulation of nurse cell apoptosis	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.95E-03 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046008 regulation of female receptivity post-mating	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.70E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046331 lateral inhibition	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.46E-02 (0/2)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.39E-01 (0/1)
1	GO:0046662 regulation of oviposition	1.00E+00 (0/0)	1.96E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.42E-02 (2/0)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046669 regulation of retinal programmed cell death (sensu	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	4.35E-01 (1/0)	3.80E-02 (0/2)
1	GO:0046671 negative regulation of retinal programmed cell death	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.90E-01 (1/0)	1.24E-02 (0/2)

1	GO:0046673 negative regulation of retinal programmed cell death (sensu	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	2.90E-01 (1/0)	1.24E-02 (0/2)
1	GO:0046693 sperm storage	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.89E-01 (1/0)	2.70E-02 (1/1)	3.66E-01 (1/0)	1.00E+00 (0/0)
1	GO:0046890 regulation of lipid biosynthesis	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.42E-02 (1/1)	1.00E+00 (0/0)	1.00E+00 (0/0)
1	GO:0046953 phototactic behavior	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.45E-01 (0/1)	1.97E-01 (1/0)	3.23E-02 (1/1)	1.00E+00 (0/0)
1	GO:0048096 chromatin-mediated maintenance of transcription	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.80E-02 (1/1)
1	GO:0050795 regulation of behavior	1.00E+00 (0/0)	5.51E-01 (1/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	3.74E-02 (3/0)	7.15E-01 (0/1)	1.00E+00 (0/0)
1	GO:0007510 cardioblast cell fate determination	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/0)	1.00E+00 (0/1)	1.89E-01 (2/0)	2.70E-02 (1/0)	3.66E-01 (/)

^a*p* values of an age-related GO term in a tissue.

^bNumbers of downregulated and upregulated genes with age (formatted as (down/up)) in a GO term.