

Table S3: Megachile rotundata GO terms enriched protein clusters

Cluster	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
1	GOTERM_BP_FAT	GO:0007426~tracheal outgrowth, open tracheal system	2	22.22	0.0105434	FBGN0014388, FBGN0015296	5	21	7937	151.1809524	0.694904384	0.694904384	11.321
1	GOTERM_BP_FAT	GO:0008293~torso signaling pathway	2	22.22	0.01653064	FBGN0014388, FBGN0015296	5	33	7937	96.20606061	0.845398606	0.606806162	17.218
1	GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	2	22.22	0.018023195	FBGN0014388, FBGN0015296	5	36	7937	88.18888889	0.869581945	0.492877858	18.631
1	GOTERM_BP_FAT	GO:0051146~striated muscle cell differentiation	2	22.22	0.032363797	FBGN0014388, FBGN0003285	5	65	7937	48.84307692	0.974895233	0.6019487	31.129
1	GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	2	22.22	0.03678222	FBGN0014388, FBGN0003285	5	74	7937	42.9027027	0.984963631	0.568054858	34.611
1	GOTERM_BP_FAT	GO:0035239~tube morphogenesis	2	22.22	0.041673813	FBGN0014388, FBGN0015296	5	84	7937	37.7952381	0.991498494	0.54823147	38.278
1	GOTERM_BP_FAT	GO:0035295~tube development	2	22.22	0.04897624	FBGN0014388, FBGN0015296	5	99	7937	32.06868687	0.996390616	0.552222902	43.404
1	GOTERM_BP_FAT	GO:0007103~transmembrane receptor protein tyrosine kinase signaling pathway	2	22.22	0.053821285	FBGN0014388, FBGN0015296	5	109	7937	29.1266055	0.997962979	0.539081187	46.588
1	GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	2	22.22	0.071110309	FBGN0014388, FBGN0015296	5	145	7937	21.89517241	0.999741783	0.60067035	56.664
1	GOTERM_BP_FAT	GO:0060541~respiratory system development	2	22.22	0.074919912	FBGN0014388, FBGN0015296	5	153	7937	20.7503268	0.999837038	0.581968963	58.637
1	GOTERM_BP_FAT	GO:0007424~open tracheal system development	2	22.22	0.074919912	FBGN0014388, FBGN0015296	5	153	7937	20.7503268	0.999837038	0.581968963	58.637
1	GOTERM_BP_FAT	GO:0007155~cell adhesion	2	22.22	0.084864374	FBGN0002528, FBGN0003285	5	174	7937	18.24597701	0.99995143	0.594629647	63.406
1	GOTERM_BP_FAT	GO:0022610~biological adhesion	2	22.22	0.091449326	FBGN0002528, FBGN0003285	5	188	7937	16.88723404	0.999978368	0.59143724	66.283
1	GOTERM_CC_FAT	GO:0005886~plasma membrane	3	33.33	0.071138741	FBGN0014388, FBGN0003285, FBGN0028399	4	781	4786	4.59603073	0.616856868	0.616856868	38.65
3	GOTERM_BP_FAT	GO:0042039~negative regulation of epidermal growth factor receptor	2	20.00	0.007539549	FBGN0041184, FBGN0020224	5	15	7937	211.6533333	0.527275932	0.527275932	8.0424
3	GOTERM_BP_FAT	GO:0042039~negative regulation of epidermal growth factor receptor signaling pathway	2	20.00	0.011543167	FBGN0041184, FBGN0020224	5	23	7937	138.0347826	0.683179628	0.437132012	12.069
3	GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	2	20.00	0.050431703	FBGN0041184, FBGN0020224	5	102	7937	31.1254902	0.994042083	0.818713769	43.633
3	GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	2	20.00	0.050916485	FBGN0041184, FBGN0020224	5	103	7937	30.82330097	0.9943358	0.72566284	43.951
3	KEGG_PATHWAY	dme04630:Jak-STAT signaling pathway	2	20.00	0.027508093	FBGN0041184, FBGN0020224	4	19	2054	54.05263158	0.177374875	0.177374875	13.394
8	GOTERM_BP_FAT	GO:0007031~peroxisome organization	2	22.22	0.007539549	FBGN0033812, FBGN0035876, FBGN0033812,	5	15	7937	211.6533333	0.288631852	0.288631852	6.8699
8	GOTERM_CC_FAT	GO:0042579~microbody	4	44.44	1.15E-05	FBGN0034145, FBGN0035876, FBGN0032407	7	41	4786	66.70383275	2.75E-04	2.75E-04	0.0092
8	GOTERM_CC_FAT	GO:0005777~peroxisome	4	44.44	1.15E-05	FBGN0033812, FBGN0034145, FBGN0035876, FBGN0032407	7	41	4786	66.70383275	2.75E-04	2.75E-04	0.0092

8	GOTERM_CC_FAT	GO:0044439--peroxisomal part	2	22.22	0.018667796	FBGN0033812, FBGN0035876	7	15	4786	91.16190476	0.363812365	0.202386287	14.029
8	GOTERM_CC_FAT	GO:0044438--microbody part	2	22.22	0.018667796	FBGN0033812, FBGN0035876	7	15	4786	91.16190476	0.363812365	0.202386287	14.029
8	GOTERM_CC_FAT	GO:0031903--microbody membrane	2	22.22	0.018667796	FBGN0033812, FBGN0035876	7	15	4786	91.16190476	0.363812365	0.202386287	14.029
8	GOTERM_CC_FAT	GO:0005778--peroxisomal membrane	2	22.22	0.018667796	FBGN0033812, FBGN0035876	7	15	4786	91.16190476	0.363812365	0.202386287	14.029
8	GOTERM_CC_FAT	GO:0031090--organelle membrane	3	33.33	0.097870107	FBGN0010812, FBGN0035876	7	438	4786	4.68297456	0.915577584	0.561315195	56.23
8	GOTERM_CC_FAT	GO:0005615--extracellular space	2	22.22	0.098545176	FBGN0011556, FBGN0031414	7	82	4786	16.67595819	0.91708078	0.463383772	56.492
9	GOTERM_BP_FAT	GO:0046158--ocellus pigment metabolic process	3	33.33	8.99E-05	FBGN0001087, FBGN0000241, FBGN0003996	7	20	7937	170.0785714	0.011892249	0.011892249	0.1051
9	GOTERM_BP_FAT	GO:0046152--ommochrome metabolic process	3	33.33	8.99E-05	FBGN0001087, FBGN0000241, FBGN0003996	7	20	7937	170.0785714	0.011892249	0.011892249	0.1051
9	GOTERM_BP_FAT	GO:0008055--ocellus pigment biosynthetic process	3	33.33	8.99E-05	FBGN0001087, FBGN0000241, FBGN0003996	7	20	7937	170.0785714	0.011892249	0.011892249	0.1051
9	GOTERM_BP_FAT	GO:0006727--ommochrome biosynthetic process	3	33.33	8.99E-05	FBGN0001087, FBGN0000241, FBGN0003996	7	20	7937	170.0785714	0.011892249	0.011892249	0.1051
9	GOTERM_BP_FAT	GO:0033060--ocellus pigmentation	3	33.33	8.99E-05	FBGN0001087, FBGN0000241, FBGN0003996	7	20	7937	170.0785714	0.011892249	0.011892249	0.1051
9	GOTERM_BP_FAT	GO:0006726--eye pigment biosynthetic process	3	33.33	2.80E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	35	7937	97.1877551	0.036593289	0.018467162	0.3272
9	GOTERM_BP_FAT	GO:0042441--eye pigment metabolic process	3	33.33	2.97E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	36	7937	94.48809524	0.038691183	0.013067066	0.3463
9	GOTERM_BP_FAT	GO:0048069--eye pigmentation	3	33.33	3.85E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	41	7937	82.96515679	0.049983523	0.012737174	0.4498
9	GOTERM_BP_FAT	GO:0006338--chromatin remodeling	3	33.33	4.86E-04	FBGN0000588, FBGN0005624, FBGN0005386	7	46	7937	73.94720497	0.062571305	0.012839774	0.5665
9	GOTERM_BP_FAT	GO:0046148--pigment biosynthetic process	3	33.33	7.20E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	56	7937	60.74234694	0.091380915	0.015844685	0.839
9	GOTERM_BP_FAT	GO:0018130--heterocycle biosynthetic process	3	33.33	8.54E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	61	7937	55.76346604	0.107466254	0.016110382	0.9945
9	GOTERM_BP_FAT	GO:0048066--pigmentation during development	3	33.33	8.54E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	61	7937	55.76346604	0.107466254	0.016110382	0.9945
9	GOTERM_BP_FAT	GO:0043473--pigmentation	3	33.33	9.40E-04	FBGN0001087, FBGN0000241, FBGN0003996	7	64	7937	53.14955357	0.117613562	0.015518968	1.094
9	GOTERM_BP_FAT	GO:0042440--pigment metabolic process	3	33.33	1.00E-03	FBGN0001087, FBGN0000241, FBGN0003996	7	66	7937	51.53896104	0.124575095	0.014674148	1.1629
9	GOTERM_BP_FAT	GO:0019748--secondary metabolic process	3	33.33	0.001189015	FBGN0001087, FBGN0000241, FBGN0003996	7	72	7937	47.24404762	0.146349208	0.015698777	1.3815

9	GOTERM_BP_FAT	GO:0016568~chromatin modification	3	33.33	0.002852798	FBGN0000588, FBGN0005624, FBGN0005386	7	112	7937	30.37117347	0.316114272	0.033952449	3.2853
9	GOTERM_BP_FAT	GO:0006856~eye pigment precursor transport	2	22.22	0.003775005	FBGN0000241, FBGN0003996 FBGN0000588,	7	5	7937	453.5428571	0.395301782	0.041052369	4.326
9	GOTERM_BP_FAT	GO:0040029~regulation of gene expression, epigenetic	3	33.33	0.006390656	FBGN0005624, FBGN0005386 FBGN0000588,	7	169	7937	20.12764159	0.573731051	0.063486309	7.2223
9	GOTERM_BP_FAT	GO:0006325~chromatin organization	3	33.33	0.006464543	FBGN0005624, FBGN0005386	7	170	7937	20.0092437	0.577926305	0.059752861	7.303
9	GOTERM_BP_FAT	GO:0048096~chromatin-mediated maintenance of transcription	2	22.22	0.007538127	FBGN0000588, FBGN0005386	7	10	7937	226.7714286	0.634456066	0.064890135	8.4675
9	GOTERM_BP_FAT	GO:0045815~positive regulation of gene expression, epigenetic	2	22.22	0.008289329	FBGN0000588, FBGN0005386	7	11	7937	206.1558442	0.66947584	0.066852707	9.2743
9	GOTERM_BP_FAT	GO:0048072~compound eye pigmentation	2	22.22	0.009040056	FBGN0001087, FBGN0003996	7	12	7937	188.9761905	0.701144456	0.068581664	10.074
9	GOTERM_BP_FAT	GO:0016571~histone methylation	2	22.22	0.015775316	FBGN0000588, FBGN0005386	7	21	7937	107.9863946	0.879347688	0.1108517	16.967
9	GOTERM_BP_FAT	GO:0051276~chromosome organization	3	33.33	0.017163977	FBGN0000588, FBGN0005624, FBGN0005386	7	282	7937	12.06231003	0.900004195	0.114135166	18.326
9	GOTERM_BP_FAT	GO:0008213~protein amino acid alkylation	2	22.22	0.020987438	FBGN0000588, FBGN0005386	7	28	7937	80.98979592	0.940455842	0.131555722	21.965
9	GOTERM_BP_FAT	GO:0006479~protein amino acid methylation	2	22.22	0.020987438	FBGN0000588, FBGN0005386	7	28	7937	80.98979592	0.940455842	0.131555722	21.965
9	GOTERM_BP_FAT	GO:0043414~biopolymer methylation	2	22.22	0.032078855	FBGN0000588, FBGN0005386	7	43	7937	52.73754153	0.986916708	0.186570613	31.699
9	GOTERM_BP_FAT	GO:0032259~methylation	2	22.22	0.039414799	FBGN0000588, FBGN0005386	7	53	7937	42.78706199	0.995243652	0.21580959	37.512
9	GOTERM_BP_FAT	GO:0016569~covalent chromatin modification	2	22.22	0.040876413	FBGN0000588, FBGN0005386	7	55	7937	41.23116883	0.996115653	0.214424846	38.615
9	GOTERM_BP_FAT	GO:0016570~histone modification	2	22.22	0.040876413	FBGN0000588, FBGN0005386	7	55	7937	41.23116883	0.996115653	0.214424846	38.615
9	GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	2	22.22	0.0561118	FBGN0000588, FBGN0005386	7	76	7937	29.83834586	0.999538221	0.273863803	49.096
9	GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	2	22.22	0.064726808	FBGN0000588, FBGN0005386	7	88	7937	25.76948052	0.999863599	0.299524827	54.271
9	GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	2	22.22	0.066156252	FBGN0000588, FBGN0005386	7	90	7937	25.1968254	0.999888706	0.295402366	55.082
9	GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	3	33.33	0.072306479	FBGN0000588, FBGN0005624, FBGN0005386	7	612	7937	5.558123249	0.999953783	0.309065153	58.422
9	GOTERM_BP_FAT	GO:0045814~negative regulation of gene expression, epigenetic	2	22.22	0.07681916	FBGN0000588, FBGN0005624	7	105	7937	21.59727891	0.999975837	0.315911617	60.726
9	GOTERM_BP_FAT	GO:0006342~chromatin silencing	2	22.22	0.07681916	FBGN0000588, FBGN0005624	7	105	7937	21.59727891	0.999975837	0.315911617	60.726
9	GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	2	22.22	0.084573976	FBGN0000588, FBGN0005386	7	116	7937	19.54926108	0.999992131	0.333198905	64.415
9	GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	2	22.22	0.085276259	FBGN0000588, FBGN0005386	7	117	7937	19.38217338	0.999992895	0.326425793	64.733
9	GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	3	33.33	0.086746389	FBGN0000588, FBGN0005624, FBGN0005386	7	678	7937	5.017067004	0.999994263	0.322476465	65.39
9	GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2	22.22	0.088080904	FBGN0000588, FBGN0005386	7	121	7937	18.74144038	0.999995277	0.318339052	65.977

9	GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	2	22.22	0.088080904	FBGN0000588, FBGN0005386	7	121	7937	18.74144038	0.999995277	0.318339052	65.977
9	GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	2	22.22	0.093668698	FBGN0000588, FBGN0005386	7	129	7937	17.57918051	0.999997915	0.32725019	68.336
9	GOTERM_CC_FAT	GO:0000785~chromatin	4	44.44	4.19E-04	FBGN0000588, FBGN0008654, FBGN0005624, FBGN0005386	8	113	4786	21.17699115	0.019078101	0.019078101	0.395
9	GOTERM_CC_FAT	GO:0000790~nuclear chromatin	3	33.33	0.001128318	FBGN0000588, FBGN0008654, FBGN0005624	8	36	4786	49.85416667	0.050606495	0.025631741	1.0614
9	GOTERM_CC_FAT	GO:0044427~chromosomal part	4	44.44	0.00388574	FBGN0000588, FBGN0008654, FBGN0005624, FBGN0005386	8	243	4786	9.847736626	0.163971203	0.057950452	3.613
9	GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	3	33.33	0.004105774	FBGN0000588, FBGN0008654, FBGN0005624	8	69	4786	26.01086957	0.172424045	0.046211754	3.814
9	GOTERM_CC_FAT	GO:0000228~nuclear chromosome	3	33.33	0.005092229	FBGN0000588, FBGN0008654, FBGN0005624	8	77	4786	23.30844156	0.209303435	0.045882261	4.7108
9	GOTERM_CC_FAT	GO:0005694~chromosome	4	44.44	0.007331005	FBGN0000588, FBGN0008654, FBGN0005624, FBGN0005386	8	304	4786	7.871710526	0.287138705	0.054849781	6.7183
9	GOTERM_CC_FAT	GO:0005725~intercalary heterochromatin	2	22.22	0.010199748	FBGN0008654, FBGN0005624	8	7	4786	170.9285714	0.375995447	0.065151774	9.2354
9	GOTERM_CC_FAT	GO:0005720~nuclear heterochromatin	2	22.22	0.013097531	FBGN0008654, FBGN0005624	8	9	4786	132.9444444	0.454725941	0.073006146	11.716
9	GOTERM_CC_FAT	GO:0031519~PcG protein complex	2	22.22	0.020310193	FBGN0000588, FBGN0005624	8	14	4786	85.46428571	0.610887564	0.099564124	17.63
9	GOTERM_CC_FAT	GO:0000792~heterochromatin	2	22.22	0.028905706	FBGN0008654, FBGN0005624	8	20	4786	59.825	0.740567427	0.126219295	24.213
9	GOTERM_CC_FAT	GO:0043190~ATP-binding cassette (ABC) transporter complex	2	22.22	0.059871938	FBGN0000241, FBGN0003996	8	42	4786	28.48809524	0.941574457	0.227545375	44.208
9	GOTERM_MF_FAT	GO:0005395~eye pigment precursor transporter activity	2	22.22	0.002650175	FBGN0000241, FBGN0003996	8	3	7918	659.8333333	0.095922637	0.095922637	2.3697
9	GOTERM_MF_FAT	GO:0031409~pigment binding	2	22.22	0.003532228	FBGN0000241, FBGN0003996	8	4	7918	494.875	0.125814155	0.065020939	3.1473
9	GOTERM_MF_FAT	GO:0046974~histone methyltransferase activity (H3-K9 specific)	2	22.22	0.007053757	FBGN0000588, FBGN0005386	8	8	7918	247.4375	0.235851076	0.08576186	6.197
9	GOTERM_MF_FAT	GO:0016279~protein-lysine N-methyltransferase activity	2	22.22	0.016683011	FBGN0000588, FBGN0005386	8	19	7918	104.1842105	0.47233945	0.14770752	14.105
9	GOTERM_MF_FAT	GO:0016278~lysine N-methyltransferase activity	2	22.22	0.016683011	FBGN0000588, FBGN0005386	8	19	7918	104.1842105	0.47233945	0.14770752	14.105
9	GOTERM_MF_FAT	GO:0018024~histone-lysine N-methyltransferase activity	2	22.22	0.016683011	FBGN0000588, FBGN0005386	8	19	7918	104.1842105	0.47233945	0.14770752	14.105
9	GOTERM_MF_FAT	GO:0042054~histone methyltransferase activity	2	22.22	0.018425156	FBGN0000588, FBGN0005386	8	21	7918	94.26190476	0.50672405	0.131803585	15.47
9	GOTERM_MF_FAT	GO:0008276~protein methyltransferase activity	2	22.22	0.027959745	FBGN0000588, FBGN0005386	8	32	7918	61.859375	0.659590612	0.164396491	22.608
9	GOTERM_MF_FAT	GO:0003677~DNA binding	4	44.44	0.029076085	FBGN0000588, FBGN0008654, FBGN0005624, FBGN0005386	8	830	7918	4.769879518	0.674135133	0.148011105	23.407
9	GOTERM_MF_FAT	GO:0008170~N-methyltransferase activity	2	22.22	0.030546267	FBGN0000588, FBGN0005386	8	35	7918	56.55714286	0.692369556	0.137014171	24.449

13	GOTERM_BP_FAT	GO:0040001~establishment of mitotic spindle localization	3	37.50	1.43E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	10	7937	793.7	8.43E-05	8.43E-05	0.0014
13	GOTERM_BP_FAT	GO:0045167~asymmetric protein localization involved in cell fate determination	3	37.50	2.89E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	14	7937	566.9285714	1.70E-04	8.52E-05	0.0029
13	GOTERM_BP_FAT	GO:0051653~spindle localization	3	37.50	3.33E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	15	7937	529.1333333	1.97E-04	6.56E-05	0.0033
13	GOTERM_BP_FAT	GO:0051293~establishment of spindle localization	3	37.50	3.33E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	15	7937	529.1333333	1.97E-04	6.56E-05	0.0033
13	GOTERM_BP_FAT	GO:0055057~neuroblast division	3	37.50	7.33E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	22	7937	360.7727273	4.33E-04	1.08E-04	0.0073
13	GOTERM_BP_FAT	GO:0055059~asymmetric neuroblast division	3	37.50	7.33E-06	FBGN0011674, FBGN0001104, FBGN0040080	3	22	7937	360.7727273	4.33E-04	1.08E-04	0.0073
13	GOTERM_BP_FAT	GO:0048103~somatic stem cell division	3	37.50	1.29E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	29	7937	273.6896552	7.60E-04	1.52E-04	0.0129
13	GOTERM_BP_FAT	GO:0007405~neuroblast proliferation	3	37.50	1.78E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	34	7937	233.4411765	0.001050419	1.75E-04	0.0178
13	GOTERM_BP_FAT	GO:0008105~asymmetric protein localization	3	37.50	1.78E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	34	7937	233.4411765	0.001050419	1.75E-04	0.0178
13	GOTERM_BP_FAT	GO:0017145~stem cell division	3	37.50	4.05E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	51	7937	155.627451	0.002385747	3.41E-04	0.0404
13	GOTERM_BP_FAT	GO:0008356~asymmetric cell division	3	37.50	5.25E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	58	7937	136.8448276	0.003091975	3.87E-04	0.0524
13	GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	3	37.50	8.81E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	75	7937	105.8266667	0.005185345	5.77E-04	0.088
13	GOTERM_BP_FAT	GO:0051640~organelle localization	3	37.50	1.05E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	82	7937	96.79268293	0.00620248	6.22E-04	0.1052
13	GOTERM_BP_FAT	GO:0008283~cell proliferation	3	37.50	2.54E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	127	7937	62.49606299	0.01487895	0.001361867	0.2534
13	GOTERM_BP_FAT	GO:0001709~cell fate determination	3	37.50	2.62E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	129	7937	61.52713178	0.015349561	0.001288218	0.2615
13	GOTERM_BP_FAT	GO:0051301~cell division	3	37.50	6.64E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	205	7937	38.71707317	0.038427403	0.003009709	0.661
13	GOTERM_BP_FAT	GO:0045165~cell fate commitment	3	37.50	8.51E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	232	7937	34.2112069	0.048980048	0.003580734	0.8464
13	GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	3	37.50	0.001405124	FBGN0011674, FBGN0001104, FBGN0040080	3	298	7937	26.63422819	0.079612608	0.005515442	1.3943
13	GOTERM_BP_FAT	GO:0045175~basal protein localization	2	25.00	0.00151143	FBGN0011674, FBGN0040080	3	6	7937	881.8888889	0.085375634	0.005562088	1.4991
13	GOTERM_BP_FAT	GO:0051294~establishment of spindle orientation	2	25.00	0.00151143	FBGN0001104, FBGN0040080	3	6	7937	881.8888889	0.085375634	0.005562088	1.4991

13	GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	3	37.50	0.002029052	FBGN0011674, FBGN0001104, FBGN0040080	3	358	7937	22.17039106	0.112933824	0.007024371	2.0078
13	GOTERM_BP_FAT	GO:0008104~protein localization	3	37.50	0.002433351	FBGN0011674, FBGN0001104, FBGN0040080	3	392	7937	20.24744898	0.13388941	0.007953903	2.4035
13	GOTERM_BP_FAT	GO:0007017~microtubule-based process	3	37.50	0.002610496	FBGN0011674, FBGN0001104, FBGN0040080	3	406	7937	19.54926108	0.142917109	0.008084023	2.5764
13	GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	3	37.50	0.003425413	FBGN0011674, FBGN0001104, FBGN0040080	3	465	7937	17.0688172	0.183269639	0.010071256	3.3684
13	GOTERM_BP_FAT	GO:0030010~establishment of cell polarity	2	25.00	0.004530861	FBGN0001104, FBGN0040080	3	18	7937	293.962963	0.235037308	0.012677442	4.4334
13	GOTERM_BP_FAT	GO:0022402~cell cycle process	3	37.50	0.004741567	FBGN0011674, FBGN0001104, FBGN0040080	3	547	7937	14.51005484	0.24453197	0.012665375	4.6352
13	GOTERM_BP_FAT	GO:0007049~cell cycle	3	37.50	0.006014476	FBGN0011674, FBGN0001104, FBGN0040080	3	616	7937	12.88474026	0.299475197	0.015355899	5.8462
13	GOTERM_BP_FAT	GO:0007400~neuroblast fate determination	2	25.00	0.006290084	FBGN0011674, FBGN0040080	3	25	7937	211.6533333	0.310843597	0.015392269	6.1066
13	GOTERM_BP_FAT	GO:0014017~neuroblast fate commitment	2	25.00	0.006792433	FBGN0011674, FBGN0040080	3	27	7937	195.9753086	0.331100062	0.015956162	6.5795
13	GOTERM_BP_FAT	GO:0014016~neuroblast differentiation	2	25.00	0.00704356	FBGN0011674, FBGN0040080	3	28	7937	188.9761905	0.341005777	0.015912064	6.8151
13	GOTERM_BP_FAT	GO:0007163~establishment or maintenance of cell polarity	2	25.00	0.027279404	FBGN0001104, FBGN0040080	3	109	7937	48.54434251	0.804431651	0.058648544	24.133
13	GOTERM_CC_FAT	GO:0045179~apical cortex	3	37.50	2.02E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	22	4786	217.5454545	1.82E-04	1.82E-04	0.0116
13	GOTERM_CC_FAT	GO:0044448~cell cortex part	3	37.50	9.04E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	46	4786	104.0434783	8.13E-04	4.07E-04	0.052
13	GOTERM_CC_FAT	GO:0045177~apical part of cell	3	37.50	9.85E-05	FBGN0011674, FBGN0001104, FBGN0040080	3	48	4786	99.70833333	8.86E-04	2.96E-04	0.0567
13	GOTERM_CC_FAT	GO:0005938~cell cortex	3	37.50	2.42E-04	FBGN0011674, FBGN0001104, FBGN0040080	3	75	4786	63.81333333	0.002179013	5.45E-04	0.1394
17	COG_ONTOLOGY	Amino acid transport and metabolism	2	28.57	0.083888623	FBGN0013307, FBGN0013308	3	53	1237	15.55974843	0.231144315	0.231144315	24.104
17	GOTERM_BP_FAT	GO:0006596~polyamine biosynthetic process	2	28.57	0.003146631	FBGN0013307, FBGN0013308	6	5	7937	529.1333333	0.093078466	0.093078466	2.6712
17	GOTERM_BP_FAT	GO:0006595~polyamine metabolic process	2	28.57	0.003775005	FBGN0013307, FBGN0013308	6	6	7937	440.9444444	0.110634156	0.056938049	3.197
17	GOTERM_BP_FAT	GO:0042401~biogenic amine biosynthetic process	2	28.57	0.011290814	FBGN0013307, FBGN0013308	6	18	7937	146.9814815	0.296724251	0.110713129	9.2943
17	GOTERM_BP_FAT	GO:0042398~cellular amino acid derivative biosynthetic process	2	28.57	0.015654043	FBGN0013307, FBGN0013308	6	25	7937	105.8266667	0.386830398	0.115098046	12.676
17	GOTERM_BP_FAT	GO:0006576~biogenic amine metabolic process	2	28.57	0.021860492	FBGN0013307, FBGN0013308	6	35	7937	75.59047619	0.496006632	0.128063287	17.294
17	GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	2	28.57	0.029266866	FBGN0013307, FBGN0013308	6	47	7937	56.29078014	0.601805307	0.142272677	22.522
17	GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic process	2	28.57	0.037850859	FBGN0013307, FBGN0013308	6	61	7937	43.3715847	0.697646998	0.15707729	28.214
17	GOTERM_MF_FAT	GO:0004586~ornithine decarboxylase activity	2	28.57	7.58E-04	FBGN0013307, FBGN0013308	4	2	7918	1979.5	0.003027243	0.003027243	0.289

17	GOTERM_MF_FAT	GO:0016831~carboxy-lyase activity	2	28.57	0.009443403	FBGN0013307, FBGN0013308	4	25	7918	158.36	0.037241904	0.018797627	3.5579
17	KEGG_PATHWAY	dme00330:Arginine and proline metabolism	2	28.57	0.052849726	FBGN0013307, FBGN0013308	3	55	2054	24.8969697	0.150317511	0.150317511	15.711
17	KEGG_PATHWAY	dme00480:Glutathione metabolism	2	28.57	0.060417438	FBGN0013307, FBGN0013308	3	63	2054	21.73544974	0.170522054	0.089243202	17.813
19	GOTERM_BP_FAT	GO:0048066~pigmentation during development	3	50.00	1.73E-04	FBGN0000422, FBGN0003162, FBGN0005626	4	61	7937	97.58606557	0.02280737	0.02280737	0.2026
19	GOTERM_BP_FAT	GO:0043473~pigmentation	3	50.00	1.91E-04	FBGN0000422, FBGN0003162, FBGN0005626	4	64	7937	93.01171875	0.025090114	0.012624749	0.2231
19	GOTERM_BP_FAT	GO:0042416~dopamine biosynthetic process	2	33.33	0.001133644	FBGN0000422, FBGN0005626	4	3	7937	1322.833333	0.140032061	0.049043276	1.3175
19	GOTERM_BP_FAT	GO:0042423~catecholamine biosynthetic process	2	33.33	0.001511335	FBGN0000422, FBGN0005626	4	4	7937	992.125	0.182218075	0.04904629	1.753
19	GOTERM_BP_FAT	GO:0042417~dopamine metabolic process	2	33.33	0.002266431	FBGN0000422, FBGN0005626	4	6	7937	661.4166667	0.260497342	0.058570186	2.6182
19	GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	3	50.00	0.002524618	FBGN0000422, FBGN0003162, FBGN0005626	4	233	7937	25.54828326	0.28551888	0.054492178	2.9125
19	GOTERM_BP_FAT	GO:0009712~catechol metabolic process	2	33.33	0.004529435	FBGN0000422, FBGN0005626	4	12	7937	330.7083333	0.453260719	0.082639493	5.1698
19	GOTERM_BP_FAT	GO:0006584~catecholamine metabolic process	2	33.33	0.004529435	FBGN0000422, FBGN0005626	4	12	7937	330.7083333	0.453260719	0.082639493	5.1698
19	GOTERM_BP_FAT	GO:0034311~diol metabolic process	2	33.33	0.004529435	FBGN0000422, FBGN0005626	4	12	7937	330.7083333	0.453260719	0.082639493	5.1698
19	GOTERM_BP_FAT	GO:0018958~phenol metabolic process	2	33.33	0.004529435	FBGN0000422, FBGN0005626	4	12	7937	330.7083333	0.453260719	0.082639493	5.1698
19	GOTERM_BP_FAT	GO:0042401~biogenic amine biosynthetic process	2	33.33	0.006789014	FBGN0000422, FBGN0005626	4	18	7937	220.4722222	0.595869651	0.107074587	7.6563
19	GOTERM_BP_FAT	GO:0009072~aromatic amino acid family metabolic process	2	33.33	0.007165278	FBGN0000422, FBGN0005626	4	19	7937	208.8684211	0.61573102	0.100816416	8.0646
19	GOTERM_BP_FAT	GO:0042398~cellular amino acid derivative biosynthetic process	2	33.33	0.009420865	FBGN0000422, FBGN0005626	4	25	7937	158.74	0.716037876	0.118289441	10.477
19	GOTERM_BP_FAT	GO:0006576~biogenic amine metabolic process	2	33.33	0.013172581	FBGN0000422, FBGN0005626	4	35	7937	113.3857143	0.828572438	0.148134621	14.363
19	GOTERM_BP_FAT	GO:0050877~neurological system process	3	50.00	0.013524934	FBGN0000422, FBGN0005626, FBGN0010415	4	546	7937	10.90247253	0.836524387	0.140087198	14.719
19	GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	2	33.33	0.017662121	FBGN0000422, FBGN0005626	4	47	7937	84.43617021	0.906524358	0.166658599	18.809
19	GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic process	2	33.33	0.022882684	FBGN0000422, FBGN0005626	4	61	7937	65.05737705	0.953983624	0.197410001	23.713
19	GOTERM_BP_FAT	GO:0007619~courtship behavior	2	33.33	0.022882684	FBGN0000422, FBGN0005626	4	61	7937	65.05737705	0.953983624	0.197410001	23.713
19	GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	2	33.33	0.022882684	FBGN0000422, FBGN0003162	4	61	7937	65.05737705	0.953983624	0.197410001	23.713
19	GOTERM_BP_FAT	GO:0007617~mating behavior	2	33.33	0.027342703	FBGN0000422, FBGN0005626	4	73	7937	54.3630137	0.974958521	0.217932933	27.687
19	GOTERM_BP_FAT	GO:0051705~behavioral interaction between organisms	2	33.33	0.027713757	FBGN0000422, FBGN0005626	4	74	7937	53.62837838	0.976197601	0.208339828	28.009
19	GOTERM_BP_FAT	GO:0007618~mating	2	33.33	0.032159052	FBGN0000422, FBGN0005626	4	86	7937	46.14534884	0.987060097	0.225650328	31.765
19	GOTERM_BP_FAT	GO:0019098~reproductive behavior	2	33.33	0.03252888	FBGN0000422, FBGN0005626	4	87	7937	45.61494253	0.987701411	0.216785266	32.069
19	KEGG_PATHWAY	dme00350:Tyrosine metabolism	2	33.33	0.050277704	FBGN0000422, FBGN0005626	4	35	2054	29.34285714	0.266196458	0.266196458	21.877
21	GOTERM_BP_FAT	GO:0006379~mRNA cleavage	3	50.00	2.88E-05	FBGN0003559, FBGN0027841, FBGN0037371	6	14	7937	283.4642857	0.002847879	0.002847879	0.0319

21	GOTERM_BP_FAT	GO:0006397~mRNA processing	3	50.00	0.005661801	FBGN0003559, FBGN0027841, FBGN0037371	6	194	7937	20.45618557	0.429995515	0.245013586	6.0964
21	GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	3	50.00	0.007173381	FBGN0003559, FBGN0027841, FBGN0037371	6	219	7937	18.12100457	0.509693247	0.211462004	7.6658
21	GOTERM_BP_FAT	GO:0006396~RNA processing	3	50.00	0.014235971	FBGN0003559, FBGN0027841, FBGN0037371	6	312	7937	12.71955128	0.75816249	0.298737016	14.687
21	GOTERM_CC_FAT	GO:0005848~mRNA cleavage stimulating factor complex	3	50.00	3.14E-06	FBGN0003559, FBGN0027841, FBGN0037371	5	4	4786	717.9	8.80E-05	8.80E-05	0.0026
21	GOTERM_CC_FAT	GO:0005849~mRNA cleavage factor complex	3	50.00	3.45E-05	FBGN0003559, FBGN0027841, FBGN0037371	5	12	4786	239.3	9.65E-04	4.83E-04	0.0288
21	GOTERM_CC_FAT	GO:0044451~nucleoplasm part	3	50.00	0.01404983	FBGN0003559, FBGN0027841, FBGN0037371	5	240	4786	11.965	0.327117778	0.123713035	11.163
21	GOTERM_CC_FAT	GO:0005654~nucleoplasm	3	50.00	0.017013384	FBGN0003559, FBGN0027841, FBGN0037371	5	265	4786	10.83622642	0.381509638	0.113184584	13.372
21	GOTERM_CC_FAT	GO:0031981~nuclear lumen	3	50.00	0.035064543	FBGN0003559, FBGN0027841, FBGN0037371	5	387	4786	7.420155039	0.6319122	0.181176526	25.815
21	GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	3	50.00	0.068905235	FBGN0003559, FBGN0027841, FBGN0037371	5	556	4786	5.164748201	0.864534478	0.283353811	44.968
21	GOTERM_CC_FAT	GO:0043233~organelle lumen	3	50.00	0.068905235	FBGN0003559, FBGN0027841, FBGN0037371	5	556	4786	5.164748201	0.864534478	0.283353811	44.968
21	GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	3	50.00	0.072351605	FBGN0003559, FBGN0027841, FBGN0037371	5	571	4786	5.029071804	0.877894528	0.259485462	46.649
23	GOTERM_BP_FAT	GO:0010553~negative regulation of specific transcription from RNA polymerase II promoter	2	33.33	0.00188893	FBGN0000411, FBGN0025776	6	3	7937	881.8888889	0.159657669	0.159657669	2.0444
23	GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transcription	2	33.33	0.002517939	FBGN0000411, FBGN0025776	6	4	7937	661.4166667	0.207008305	0.109499189	2.7167
23	GOTERM_BP_FAT	GO:0045449~regulation of transcription	4	66.67	0.00869849	FBGN0000411, FBGN0029123, FBGN0036411, FBGN0025776	6	799	7937	6.622444723	0.55235819	0.235031508	9.1032
23	GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymerase II promoter	2	33.33	0.008790602	FBGN0000411, FBGN0025776	6	14	7937	188.9761905	0.556168829	0.183785229	9.1954
23	GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	2	33.33	0.011290814	FBGN0000411, FBGN0025776	6	18	7937	146.9814815	0.648189857	0.188550174	11.667
23	GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	2	33.33	0.037850859	FBGN0000411, FBGN0025776	6	61	7937	43.3715847	0.971272326	0.446586083	34.397
23	GOTERM_CC_FAT	GO:0015934~large ribosomal subunit	2	33.33	0.02131216	FBGN0023170, FBGN0053002	2	102	4786	46.92156863	0.363896135	0.363896135	15.324
23	GOTERM_CC_FAT	GO:0033279~ribosomal subunit	2	33.33	0.034266611	FBGN0023170, FBGN0053002	2	164	4786	29.18292683	0.519158233	0.30657245	23.603
23	GOTERM_CC_FAT	GO:0005840~ribosome	2	33.33	0.038863351	FBGN0023170, FBGN0053002	2	186	4786	25.7311828	0.565001374	0.242302312	26.366
23	GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	2	33.33	0.079189302	FBGN0023170, FBGN0053002	2	379	4786	12.62796834	0.823161232	0.351523309	47.113
23	GOTERM_MF_FAT	GO:0003700~transcription factor activity	4	66.67	0.001092661	FBGN0000411, FBGN0029123, FBGN0036411, FBGN0025776	6	389	7918	13.56983719	0.013033415	0.013033415	0.7009

23	GOTERM_MF_FAT	GO:0030528~transcription regulator activity	4	66.67	0.005573508	FBGN0000411, FBGN0029123, FBGN0036411, FBGN0025776	6	682	7918	7.73998045	0.064869494	0.032978539	3.532
23	GOTERM_MF_FAT	GO:0003677~DNA binding	4	66.67	0.009756761	FBGN0000411, FBGN0029123, FBGN0036411, FBGN0025776	6	830	7918	6.359839357	0.110998218	0.038459583	6.1132
23	GOTERM_MF_FAT	GO:0008134~transcription factor binding	2	33.33	0.054965332	FBGN0000411, FBGN0025776	6	89	7918	29.65543071	0.4925738	0.155998493	30.491
28	GOTERM_BP_FAT	GO:0048806~genitalia development	2	40.00	0.001385914	FBGN0000210, FBGN0000504	2	11	7937	721.5454545	0.193430877	0.193430877	1.6518
28	GOTERM_BP_FAT	GO:0046661~male sex differentiation	2	40.00	0.001511906	FBGN0000210, FBGN0000504	2	12	7937	661.4166667	0.209051803	0.110647316	1.8007
28	GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	2	40.00	0.004535719	FBGN0000210, FBGN0000504	2	36	7937	220.4722222	0.505711358	0.209333126	5.3131
28	GOTERM_BP_FAT	GO:0007548~sex differentiation	2	40.00	0.007559531	FBGN0000210, FBGN0000504	2	60	7937	132.2833333	0.691544797	0.254756795	8.7101
28	GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	2	40.00	0.043719289	FBGN0000210, FBGN0000504	2	347	7937	22.87319885	0.999021105	0.749880666	41.542
28	GOTERM_BP_FAT	GO:0009886~post-embryonic morphogenesis	2	40.00	0.044475243	FBGN0000210, FBGN0000504	2	353	7937	22.48441926	0.999134033	0.691266644	42.095
28	GOTERM_BP_FAT	GO:0007552~metamorphosis	2	40.00	0.045609172	FBGN0000210, FBGN0000504	2	362	7937	21.92541436	0.999279606	0.644302017	42.915
28	GOTERM_BP_FAT	GO:0007423~sensory organ development	2	40.00	0.051656797	FBGN0000210, FBGN0000504	2	410	7937	19.35853659	0.999731058	0.642144864	47.11
28	GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	2	40.00	0.052664735	FBGN0000210, FBGN0000504	2	418	7937	18.98803828	0.999771927	0.606140271	47.782
28	GOTERM_BP_FAT	GO:0009791~post-embryonic development	2	40.00	0.05468061	FBGN0000210, FBGN0000504	2	434	7937	18.28801843	0.999836063	0.581719349	49.1
28	GOTERM_BP_FAT	GO:0003006~reproductive developmental process	2	40.00	0.063752047	FBGN0000210, FBGN0000504	2	506	7937	15.68577075	0.999963222	0.60475034	54.666
28	GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	2	40.00	0.077107219	FBGN0000210, FBGN0000504	2	612	7937	12.96895425	0.999996033	0.645292562	61.851
28	GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	2	40.00	0.085422704	FBGN0000210, FBGN0000504	2	678	7937	11.70648968	0.999999025	0.655151741	65.78
28	GOTERM_BP_FAT	GO:0007276~gamete generation	2	40.00	0.090084415	FBGN0000210, FBGN0000504	2	715	7937	11.1006993	0.999999558	0.648371839	67.817
28	GOTERM_BP_FAT	GO:0019953~sexual reproduction	2	40.00	0.092604259	FBGN0000210, FBGN0000504	2	735	7937	10.79863946	0.999999713	0.633647118	68.871
28	GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	2	40.00	0.098021923	FBGN0000210, FBGN0000504	2	778	7937	10.20179949	0.999999886	0.631904018	71.031
28	GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	2	40.00	0.098021923	FBGN0000210, FBGN0000504	2	778	7937	10.20179949	0.999999886	0.631904018	71.031
28	GOTERM_MF_FAT	GO:0008270~zinc ion binding	3	60.00	0.016776258	FBGN0000210, FBGN0000504, FBGN0085478	3	1026	7918	7.717348928	0.249950248	0.249950248	11.529
28	GOTERM_MF_FAT	GO:0003704~specific RNA polymerase II transcription factor activity	2	40.00	0.019356003	FBGN0000210, FBGN0000504	3	77	7918	68.55411255	0.282712337	0.153071631	13.196
28	GOTERM_MF_FAT	GO:0046914~transition metal ion binding	3	60.00	0.029224044	FBGN0000210, FBGN0000504, FBGN0085478	3	1354	7918	5.847858198	0.396019123	0.15470611	19.326
28	GOTERM_MF_FAT	GO:0046872~metal ion binding	3	60.00	0.04705625	FBGN0000210, FBGN0000504, FBGN0085478	3	1718	7918	4.608847497	0.559299519	0.185228403	29.46

28	GOTERM_MF_FAT	GO:0043169~cation binding	3	60.00	0.049610631	FBGN0000210, FBGN0000504, FBGN0085478	3	1764	7918	4.488662132	0.578956774	0.158865712	30.818
28	GOTERM_MF_FAT	GO:0043167~ion binding	3	60.00	0.050061763	FBGN0000210, FBGN0000504, FBGN0085478	3	1772	7918	4.468397291	0.582341542	0.135423261	31.055
28	GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	2	40.00	0.063865848	FBGN0000210, FBGN0000504	3	257	7918	20.53955901	0.674352669	0.148092379	37.988
28	GOTERM_MF_FAT	GO:0003700~transcription factor activity	2	40.00	0.09584942	FBGN0000210, FBGN0000504	3	389	7918	13.56983719	0.819659608	0.19274336	51.787
39	GOTERM_BP_FAT	GO:0007080~mitotic metaphase plate congression	2	40.00	0.00327332	FBGN00030500, FBGN0031886	3	13	7937	407.025641	0.114242	0.114242	2.9011
39	GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	3	60.00	0.003425413	FBGN00030500, FBGN0012051, FBGN0031886	3	465	7937	17.0688172	0.119229189	0.061506094	3.034
39	GOTERM_BP_FAT	GO:0051310~metaphase plate congression	2	40.00	0.003776432	FBGN00030500, FBGN0031886	3	15	7937	352.7555556	0.130635223	0.045592126	3.3403
39	GOTERM_BP_FAT	GO:0050000~chromosome localization	2	40.00	0.00402794	FBGN00030500, FBGN0031886	3	16	7937	330.7083333	0.13871923	0.036645373	3.5592
39	GOTERM_BP_FAT	GO:0051303~establishment of chromosome localization	2	40.00	0.00402794	FBGN00030500, FBGN0031886	3	16	7937	330.7083333	0.13871923	0.036645373	3.5592
39	GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	2	40.00	0.011558418	FBGN00030500, FBGN0031886	3	46	7937	115.0289855	0.349589919	0.082433704	9.9125
39	GOTERM_BP_FAT	GO:0000819~sister chromatid segregation	2	40.00	0.011808942	FBGN00030500, FBGN0031886	3	47	7937	112.5815603	0.355661572	0.070636371	10.117
39	GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	2	40.00	0.018810716	FBGN00030500, FBGN0031886	3	75	7937	70.55111111	0.504716952	0.095501944	15.677
39	GOTERM_BP_FAT	GO:0051640~organelle localization	2	40.00	0.02055727	FBGN00030500, FBGN0031886	3	82	7937	64.52845528	0.536313199	0.091597979	17.015
39	GOTERM_BP_FAT	GO:0007059~chromosome segregation	2	40.00	0.029266703	FBGN00030500, FBGN0031886	3	117	7937	45.22507123	0.66680591	0.114952936	23.411
39	GOTERM_BP_FAT	GO:0007067~mitosis	2	40.00	0.036453623	FBGN00030500, FBGN0031886	3	146	7937	36.24200913	0.746902978	0.128376956	28.354
39	GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	2	40.00	0.036948289	FBGN00030500, FBGN0031886	3	148	7937	35.75225225	0.75166641	0.118944586	28.684
39	GOTERM_BP_FAT	GO:0000280~nuclear division	2	40.00	0.036948289	FBGN00030500, FBGN0031886	3	148	7937	35.75225225	0.75166641	0.118944586	28.684
39	GOTERM_BP_FAT	GO:0048285~organelle fission	2	40.00	0.038184397	FBGN00030500, FBGN0031886	3	153	7937	34.583878	0.763191506	0.113116777	29.502
39	GOTERM_BP_FAT	GO:0007052~mitotic spindle organization	2	40.00	0.048290539	FBGN00030500, FBGN0031886	3	194	7937	27.27491409	0.839800074	0.131399294	35.881
39	GOTERM_BP_FAT	GO:0007051~spindle organization	2	40.00	0.055896333	FBGN00030500, FBGN0031886	3	225	7937	23.51703704	0.880950294	0.14102486	40.338
39	GOTERM_BP_FAT	GO:0051276~chromosome organization	2	40.00	0.069801546	FBGN00030500, FBGN0031886	3	282	7937	18.76359338	0.931246043	0.163460383	47.78
39	GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	2	40.00	0.07368622	FBGN00030500, FBGN0031886	3	298	7937	17.75615213	0.941108772	0.162223521	49.706
39	GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	2	40.00	0.088181355	FBGN00030500, FBGN0031886	3	358	7937	14.78026071	0.967144102	0.182021364	56.347
39	GOTERM_BP_FAT	GO:0007017~microtubule-based process	2	40.00	0.099695161	FBGN00030500, FBGN0031886	3	406	7937	13.03284072	0.979468786	0.194166613	61.055
39	GOTERM_CC_FAT	GO:0031262~Ndc80 complex	2	40.00	0.002923365	FBGN00030500, FBGN0031886	3	7	4786	455.8095238	0.028852055	0.028852055	1.7426

39	GOTERM_CC_FAT	GO:0000776--kinetochore	2	40.00	0.012083223	FBGN0030500, FBGN0031886	3	29	4786	110.0229885	0.114469325	0.058973606	7.0397
39	GOTERM_CC_FAT	GO:0000775--chromosome, centromeric region	2	40.00	0.020787293	FBGN0030500, FBGN0031886	3	50	4786	63.81333333	0.18946755	0.06762604	11.851
39	GOTERM_CC_FAT	GO:0043228--non-membrane- bounded organelle	3	60.00	0.038788944	FBGN0030500, FBGN0012051, FBGN0031886	3	943	4786	5.075291622	0.326732619	0.094169596	21.145
39	GOTERM_CC_FAT	GO:0043232--intracellular non- membrane-bounded organelle	3	60.00	0.038788944	FBGN0030500, FBGN0012051, FBGN0031886	3	943	4786	5.075291622	0.326732619	0.094169596	21.145
39	GOTERM_CC_FAT	GO:0044427--chromosomal part	2	40.00	0.098978342	FBGN0030500, FBGN0031886	3	243	4786	13.1303155	0.647343167	0.188159972	46.519
54	GOTERM_BP_FAT	GO:0042787--protein ubiquitination during ubiquitin-dependent protein catabolic process	2	40.00	0.00151143	FBGN0260962, FBGN0033260	3	6	7937	881.8888889	0.061552233	0.061552233	1.3901
54	GOTERM_BP_FAT	GO:0016567--protein ubiquitination	2	40.00	0.010556005	FBGN0260962, FBGN0033260	3	42	7937	125.984127	0.359629802	0.19976866	9.3546
54	GOTERM_BP_FAT	GO:0032446--protein modification by small protein conjugation	2	40.00	0.012059434	FBGN0260962, FBGN0033260	3	48	7937	110.2361111	0.399249171	0.156215663	10.621
54	GOTERM_BP_FAT	GO:0070647--protein modification by small protein conjugation or removal	2	40.00	0.016812749	FBGN0260962, FBGN0033260	3	67	7937	78.97512438	0.509406257	0.163086639	14.523
54	GOTERM_BP_FAT	GO:0006511--ubiquitin-dependent protein catabolic process	2	40.00	0.024045711	FBGN0260962, FBGN0033260	3	96	7937	55.11805556	0.640219155	0.184906166	20.169
54	GOTERM_BP_FAT	GO:0019941--modification- dependent protein catabolic process	2	40.00	0.042134607	FBGN0260962, FBGN0033260	3	169	7937	31.30966469	0.836020987	0.260170953	32.861
54	GOTERM_BP_FAT	GO:0043632--modification- dependent macromolecule catabolic process	2	40.00	0.042381226	FBGN0260962, FBGN0033260	3	170	7937	31.1254902	0.837784862	0.228819727	33.021
54	GOTERM_BP_FAT	GO:0051603--proteolysis involved in cellular protein catabolic process	2	40.00	0.045584374	FBGN0260962, FBGN0033260	3	183	7937	28.9143898	0.859078671	0.217251775	35.066
54	GOTERM_BP_FAT	GO:0044257--cellular protein catabolic process	2	40.00	0.045584374	FBGN0260962, FBGN0033260	3	183	7937	28.9143898	0.859078671	0.217251775	35.066
54	GOTERM_BP_FAT	GO:0030163--protein catabolic process	2	40.00	0.049765009	FBGN0260962, FBGN0033260	3	200	7937	26.45666667	0.882806702	0.211966368	37.651
54	GOTERM_BP_FAT	GO:0044265--cellular macromolecule catabolic process	2	40.00	0.055896333	FBGN0260962, FBGN0033260	3	225	7937	23.51703704	0.91070508	0.214614868	41.277
54	GOTERM_BP_FAT	GO:0009057--macromolecule catabolic process	2	40.00	0.068585918	FBGN0260962, FBGN0033260	3	277	7937	19.1022864	0.949417815	0.237602262	48.19
54	KEGG_PATHWAY	dme03420:Nucleotide excision repair	2	40.00	0.017039922	FBGN0260962, FBGN0033260	2	35	2054	58.68571429	0.033789485	0.033789485	3.8057
54	KEGG_PATHWAY	dme04120:Ubiquitin mediated proteolysis	2	40.00	0.047224927	FBGN0260962, FBGN0033260	2	97	2054	21.17525773	0.09221966	0.047224927	10.346
55	GOTERM_BP_FAT	GO:0007428--primary branching, open tracheal system	2	50.00	0.003776432	FBGN0014135, FBGN0259211	3	15	7937	352.7555556	0.244204884	0.244204884	3.8828
55	GOTERM_BP_FAT	GO:0007426--tracheal outgrowth, open tracheal system	2	50.00	0.005285004	FBGN0014135, FBGN0259211	3	21	7937	251.968254	0.32438197	0.178040129	5.3953
55	GOTERM_BP_FAT	GO:0035152--regulation of tube architecture, open tracheal system	2	50.00	0.009553085	FBGN0014135, FBGN0259211	3	38	7937	139.245614	0.508516345	0.210831589	9.5588
55	GOTERM_BP_FAT	GO:0060446--branching involved in open tracheal system development	2	50.00	0.009803862	FBGN0014135, FBGN0259211	3	39	7937	135.6752137	0.517640463	0.166620684	9.7982
55	GOTERM_BP_FAT	GO:0048754--branching morphogenesis of a tube	2	50.00	0.009803862	FBGN0014135, FBGN0259211	3	39	7937	135.6752137	0.517640463	0.166620684	9.7982
55	GOTERM_BP_FAT	GO:0001763--morphogenesis of a branching structure	2	50.00	0.010556005	FBGN0014135, FBGN0259211	3	42	7937	125.984127	0.544015527	0.145346627	10.513

55	GOTERM_BP_FAT	GO:0060562--epithelial tube morphogenesis	2	50.00	0.010556005	FBGN0014135, FBGN0259211	3	42	7937	125.984127	0.544015527	0.145346627	10.513
55	GOTERM_BP_FAT	GO:0035239--tube morphogenesis	2	50.00	0.021056	FBGN0014135, FBGN0259211	3	84	7937	62.99206349	0.792947337	0.230845704	19.968
55	GOTERM_BP_FAT	GO:0035295--tube development	2	50.00	0.024792424	FBGN0014135, FBGN0259211	3	99	7937	53.44781145	0.84397905	0.233097035	23.108
55	GOTERM_BP_FAT	GO:0007424--open tracheal system development	2	50.00	0.038184397	FBGN0014135, FBGN0259211	3	153	7937	34.583878	0.943921737	0.30241149	33.468
55	GOTERM_BP_FAT	GO:0060541--respiratory system development	2	50.00	0.038184397	FBGN0014135, FBGN0259211	3	153	7937	34.583878	0.943921737	0.30241149	33.468
55	GOTERM_BP_FAT	GO:0002009--morphogenesis of an epithelium	2	50.00	0.055896333	FBGN0014135, FBGN0259211	3	225	7937	23.51703704	0.985827167	0.376830348	45.23
55	GOTERM_BP_FAT	GO:0060429--epithelium development	2	50.00	0.058343306	FBGN0014135, FBGN0259211	3	235	7937	22.51631206	0.988303598	0.35907793	46.698
55	GOTERM_BP_FAT	GO:0048729--tissue morphogenesis	2	50.00	0.061275482	FBGN0014135, FBGN0259211	3	247	7937	21.42240216	0.990714101	0.346483253	48.41
56	GOTERM_BP_FAT	GO:0045454--cell redox homeostasis	2	40.00	0.013311418	FBGN0031670, FBGN0025678	3	53	7937	99.83647799	0.101659826	0.101659826	7.0737
56	GOTERM_BP_FAT	GO:0019725--cellular homeostasis	2	40.00	0.027776419	FBGN0031670, FBGN0025678	3	111	7937	47.66966967	0.201767874	0.106561627	14.291
56	GOTERM_BP_FAT	GO:0042592--homeostatic process	2	40.00	0.040654231	FBGN0031670, FBGN0025678	3	163	7937	32.46216769	0.282534014	0.104771763	20.325
57	GOTERM_BP_FAT	GO:0048232--male gamete generation	4	80.00	7.31E-06	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	155	7937	51.20645161	3.36E-04	3.36E-04	0.0069
57	GOTERM_BP_FAT	GO:0007283--spermatogenesis	4	80.00	7.31E-06	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	155	7937	51.20645161	3.36E-04	3.36E-04	0.0069
57	GOTERM_BP_FAT	GO:0007276--gamete generation	4	80.00	7.28E-04	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	715	7937	11.1006993	0.032957028	0.016616569	0.6862
57	GOTERM_BP_FAT	GO:0019953--sexual reproduction	4	80.00	7.91E-04	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	735	7937	10.79863946	0.035754434	0.012063077	0.7453
57	GOTERM_BP_FAT	GO:0032504--multicellular organism reproduction	4	80.00	9.39E-04	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	778	7937	10.20179949	0.042274013	0.010740299	0.8836
57	GOTERM_BP_FAT	GO:0048609--reproductive process in a multicellular organism	4	80.00	9.39E-04	FBGN0034667, FBGN0004372, FBGN0033748, FBGN0033749	4	778	7937	10.20179949	0.042274013	0.010740299	0.8836
57	GOTERM_BP_FAT	GO:0006355--regulation of transcription, DNA-dependent	3	60.00	0.016896928	FBGN0034667, FBGN0033748, FBGN0033749	4	612	7937	9.726715686	0.543378408	0.14510793	14.877
57	GOTERM_BP_FAT	GO:0051252--regulation of RNA metabolic process	3	60.00	0.020619958	FBGN0034667, FBGN0033748, FBGN0033749	4	678	7937	8.779867257	0.616506956	0.147633744	17.875
57	GOTERM_BP_FAT	GO:0045449--regulation of transcription	3	60.00	0.028334321	FBGN0034667, FBGN0033748, FBGN0033749	4	799	7937	7.450250313	0.733451838	0.172118923	23.79
57	GOTERM_CC_FAT	GO:0000785--chromatin	2	40.00	0.023610531	FBGN0034667, FBGN0004372	2	113	4786	42.3539823	0.173991162	0.173991162	12.261
57	GOTERM_CC_FAT	GO:0044427--chromosomal part	2	40.00	0.050773088	FBGN0034667, FBGN0004372	2	243	4786	19.69547325	0.340886298	0.188141821	24.819
57	GOTERM_CC_FAT	GO:0005694--chromosome	2	40.00	0.063518596	FBGN0034667, FBGN0004372	2	304	4786	15.74342105	0.408447542	0.160544354	30.182

57	GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	2	40.00	0.00529767	FBGN0033748, FBGN0033749	3	21	7918	251.3650794	0.05675505	0.05675505	3.2548
57	GOTERM_MF_FAT	GO:0030528~transcription regulator activity	3	60.00	0.007408927	FBGN0034667, FBGN0033748, FBGN0033749	3	682	7918	11.60997067	0.078545251	0.040075655	4.5269
57	GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	2	40.00	0.0158508	FBGN0033748, FBGN0033749	3	63	7918	83.78835979	0.161176897	0.056902064	9.474
57	GOTERM_MF_FAT	GO:0008134~transcription factor binding	2	40.00	0.022355486	FBGN0033748, FBGN0033749	3	89	7918	59.31086142	0.220186688	0.06028175	13.137
57	GOTERM_MF_FAT	GO:0016564~transcription repressor activity	2	40.00	0.027344414	FBGN0033748, FBGN0033749	3	109	7918	48.42813456	0.262860071	0.059172534	15.862
57	GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2	40.00	0.05725527	FBGN0033748, FBGN0033749	3	230	7918	22.95072464	0.477200399	0.102455739	30.739
57	GOTERM_MF_FAT	GO:0003700~transcription factor activity	2	40.00	0.09584942	FBGN0033748, FBGN0033749	3	389	7918	13.56983719	0.669897801	0.146437183	46.617
66	INTERPRO	IPR014775:L27, C-terminal	2	50	0.001176644	FBGN0039269, FBGN0050021	3	6	10196	1132.888889	0.0128672	0.0128672	0.7307
66	INTERPRO	IPR004172:L27	2	50	0.001372683	FBGN0039269, FBGN0050021	3	7	10196	971.047619	0.014996309	0.007526479	0.852
66	SMART	SM00569:L27	2	50	0.001451078	FBGN0039269, FBGN0050021	2	7	4824	689.1428571	0.00579169	0.00579169	0.5529
66	INTERPRO	IPR001478:PDZ/DHR/GLGF	2	50	0.012710078	FBGN0050021, FBGN0039269,	3	65	10196	104.574359	0.131256153	0.045819404	7.6592
66	SMART	SM00228:PDZ	2	50	0.013474295	FBGN0050021	2	65	4824	74.21538462	0.052817593	0.026767034	5.0477
73	GOTERM_BP_FAT	GO:0031053~primary microRNA processing	2	50.00	6.30E-04	FBGN0039861, FBGN0026722	2	5	7937	1587.4	0.010031893	0.010031893	0.4465
73	GOTERM_BP_FAT	GO:0035196~gene silencing by miRNA, production of miRNAs	2	50.00	0.001007938	FBGN0039861, FBGN0026722	2	8	7937	992.125	0.016005659	0.008035111	0.7136
73	GOTERM_BP_FAT	GO:0031050~dsRNA fragmentation	2	50.00	0.001385914	FBGN0039861, FBGN0026722	2	11	7937	721.5454545	0.021945618	0.00736938	0.98
73	GOTERM_BP_FAT	GO:0043331~response to dsRNA	2	50.00	0.001385914	FBGN0039861, FBGN0026722	2	11	7937	721.5454545	0.021945618	0.00736938	0.98
73	GOTERM_BP_FAT	GO:0035195~gene silencing by miRNA	2	50.00	0.002393852	FBGN0039861, FBGN0026722	2	19	7937	417.7368421	0.037621585	0.009541078	1.6876
73	GOTERM_BP_FAT	GO:0016441~posttranscriptional gene silencing	2	50.00	0.005039688	FBGN0039861, FBGN0026722	2	40	7937	198.425	0.077657707	0.016037778	3.5243
73	GOTERM_BP_FAT	GO:0035194~posttranscriptional gene silencing by RNA	2	50.00	0.005039688	FBGN0039861, FBGN0026722	2	40	7937	198.425	0.077657707	0.016037778	3.5243
73	GOTERM_BP_FAT	GO:0031047~gene silencing by RNA	2	50.00	0.005669648	FBGN0039861, FBGN0026722	2	45	7937	176.3777778	0.086957191	0.01504772	3.9572
73	GOTERM_BP_FAT	GO:0034470~ncRNA processing	2	50.00	0.011591281	FBGN0039861, FBGN0026722	2	92	7937	86.27173913	0.170177738	0.026297152	7.946
73	GOTERM_BP_FAT	GO:0010033~response to organic substance	2	50.00	0.015371047	FBGN0039861, FBGN0026722	2	122	7937	65.05737705	0.219520262	0.030505825	10.417
73	GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	2	50.00	0.015875016	FBGN0039861, FBGN0026722	2	126	7937	62.99206349	0.225887429	0.028047811	10.742
73	GOTERM_BP_FAT	GO:0016458~gene silencing	2	50.00	0.019528789	FBGN0039861, FBGN0026722	2	155	7937	51.20645161	0.270613806	0.031062523	13.069
73	GOTERM_BP_FAT	GO:0040029~regulation of gene expression, epigenetic	2	50.00	0.02129268	FBGN0039861, FBGN0026722	2	169	7937	46.96449704	0.291327818	0.030820709	14.173
73	GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	2	50.00	0.032254	FBGN0039861, FBGN0026722	2	256	7937	31.00390625	0.408190194	0.042772472	20.771
73	GOTERM_BP_FAT	GO:0006396~RNA processing	2	50.00	0.039309563	FBGN0039861, FBGN0026722	2	312	7937	25.43910256	0.473576239	0.048159307	24.782

73	GOTERM_BP_FAT	GO:0010605--negative regulation of macromolecule metabolic process	2	50.00	0.039939524	FBGN0039861, FBGN0026722	2	317	7937	25.03785489	0.479072294	0.045513438	25.132
73	GOTERM_MF_FAT	GO:0003725--double-stranded RNA binding	2	50.00	0.004793736	FBGN0039861, FBGN0026722	3	19	7918	277.8245614	0.065060707	0.065060707	3.2115
81	GOTERM_BP_FAT	GO:0006364--rRNA processing	3	75.00	2.48E-05	FBGN0033454, FBGN0038146, FBGN0038597	3	40	7937	198.425	1.98E-04	1.98E-04	0.0136
81	GOTERM_BP_FAT	GO:0016072--rRNA metabolic process	3	75.00	2.60E-05	FBGN0033454, FBGN0038146, FBGN0038597	3	41	7937	193.5853659	2.08E-04	1.04E-04	0.0143
81	GOTERM_BP_FAT	GO:0042254--ribosome biogenesis	3	75.00	6.40E-05	FBGN0033454, FBGN0038146, FBGN0038597	3	64	7937	124.015625	5.12E-04	1.71E-04	0.035
81	GOTERM_BP_FAT	GO:0034470--ncRNA processing	3	75.00	1.33E-04	FBGN0033454, FBGN0038146, FBGN0038597	3	92	7937	86.27173913	0.001062819	2.66E-04	0.0727
81	GOTERM_BP_FAT	GO:0022613--ribonucleoprotein complex biogenesis	3	75.00	1.39E-04	FBGN0033454, FBGN0038146, FBGN0038597	3	94	7937	84.43617021	0.001109767	2.22E-04	0.076
81	GOTERM_BP_FAT	GO:0034660--ncRNA metabolic process	3	75.00	2.79E-04	FBGN0033454, FBGN0038146, FBGN0038597	3	133	7937	59.67669173	0.002227583	3.72E-04	0.1525
81	GOTERM_BP_FAT	GO:0006396--RNA processing	3	75.00	0.001540483	FBGN0033454, FBGN0038146, FBGN0038597	3	312	7937	25.43910256	0.012257623	0.001760358	0.8404
81	GOTERM_CC_FAT	GO:0032040--small-subunit processome	3	75.00	8.73E-07	FBGN0033454, FBGN0038146, FBGN0038597	3	5	4786	957.2	2.62E-06	2.62E-06	#####
81	GOTERM_CC_FAT	GO:0030684--preribosome	3	75.00	1.83E-06	FBGN0033454, FBGN0038146, FBGN0038597	3	7	4786	683.7142857	5.50E-06	2.75E-06	#####
81	GOTERM_CC_FAT	GO:0030529--ribonucleoprotein complex	3	75.00	0.006255707	FBGN0033454, FBGN0038146, FBGN0038597	3	379	4786	12.62796834	0.018649963	0.006255707	1.956
93	GOTERM_BP_FAT	GO:0045451--pole plasm oskar mRNA localization	2	50.00	0.005291672	FBGN0000256, FBGN0004510	2	42	7937	188.9761905	0.2289333	0.2289333	4.9599
93	GOTERM_BP_FAT	GO:0019094--pole plasm mRNA localization	2	50.00	0.006173617	FBGN0000256, FBGN0004510	2	49	7937	161.9795918	0.261729424	0.140773269	5.7648
93	GOTERM_BP_FAT	GO:0007316--pole plasm RNA localization	2	50.00	0.006299609	FBGN0000256, FBGN0004510	2	50	7937	158.74	0.266301611	0.098070646	5.8792
93	GOTERM_BP_FAT	GO:0007315--pole plasm assembly	2	50.00	0.007307547	FBGN0000256, FBGN0004510	2	58	7937	136.8448276	0.301894132	0.085928176	6.7906
93	GOTERM_BP_FAT	GO:0007028--cytoplasm organization	2	50.00	0.008189492	FBGN0000256, FBGN0004510	2	65	7937	122.1076923	0.331646001	0.07742579	7.5816
93	GOTERM_BP_FAT	GO:0008298--intracellular mRNA localization	2	50.00	0.008441477	FBGN0000256, FBGN0004510	2	67	7937	118.4626866	0.339915932	0.066889216	7.8065
93	GOTERM_BP_FAT	GO:0007314--oocyte anterior/posterior axis specification	2	50.00	0.009827391	FBGN0000256, FBGN0004510	2	78	7937	101.7564103	0.383639903	0.066796499	9.0346
93	GOTERM_BP_FAT	GO:0008358--maternal determination of anterior/posterior axis, embryo	2	50.00	0.010205367	FBGN0000256, FBGN0004510	2	81	7937	97.98765432	0.395063723	0.060895971	9.367
93	GOTERM_BP_FAT	GO:0007309--oocyte axis specification	2	50.00	0.014867078	FBGN0000256, FBGN0004510	2	118	7937	67.26271186	0.519993843	0.078314026	13.378
93	GOTERM_BP_FAT	GO:0007308--oocyte construction	2	50.00	0.015245055	FBGN0000256, FBGN0004510	2	121	7937	65.59504132	0.528935529	0.072512565	13.696
93	GOTERM_BP_FAT	GO:0006403--RNA localization	2	50.00	0.015749024	FBGN0000256, FBGN0004510	2	125	7937	63.496	0.540604368	0.068270782	14.119
93	GOTERM_BP_FAT	GO:0048599--oocyte development	2	50.00	0.015875016	FBGN0000256, FBGN0004510	2	126	7937	62.99206349	0.543477047	0.063253919	14.224

93	GOTERM_BP_FAT	GO:0048469~cell maturation	2	50.00	0.016127	FBGN0000256, FBGN0004510	2	128	7937	62.0078125	0.549169714	0.059441913	14.434
93	GOTERM_BP_FAT	GO:0021700~developmental maturation	2	50.00	0.017008945	FBGN0000256, FBGN0004510	2	135	7937	58.79259259	0.568551744	0.058276344	15.167
93	GOTERM_BP_FAT	GO:0009994~oocyte differentiation	2	50.00	0.017386922	FBGN0000256, FBGN0004510	2	138	7937	57.51449275	0.576606232	0.055686285	15.479
93	GOTERM_BP_FAT	GO:0007351~tripartite regional subdivision	2	50.00	0.017638906	FBGN0000256, FBGN0004510	2	140	7937	56.69285714	0.581893863	0.053042673	15.687
93	GOTERM_BP_FAT	GO:0008595~determination of anterior/posterior axis, embryo	2	50.00	0.017638906	FBGN0000256, FBGN0004510	2	140	7937	56.69285714	0.581893863	0.053042673	15.687
93	GOTERM_BP_FAT	GO:0000578~embryonic axis specification	2	50.00	0.018268867	FBGN0000256, FBGN0004510	2	145	7937	54.73793103	0.594831555	0.051756789	16.204
93	GOTERM_BP_FAT	GO:0009948~anterior/posterior axis specification	2	50.00	0.018520852	FBGN0000256, FBGN0004510	2	147	7937	53.99319728	0.599896094	0.049617374	16.41
93	GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	2	50.00	0.021418672	FBGN0000256, FBGN0004510	2	170	7937	46.68823529	0.65386197	0.054307458	18.746
93	GOTERM_BP_FAT	GO:0009798~axis specification	2	50.00	0.02532443	FBGN0000256, FBGN0004510	2	201	7937	39.48756219	0.715459587	0.060910039	21.803
93	GOTERM_BP_FAT	GO:0007350~blastoderm segmentation	2	50.00	0.027466297	FBGN0000256, FBGN0004510	2	218	7937	36.40825688	0.744536787	0.062918117	23.435
93	GOTERM_BP_FAT	GO:0009880~embryonic pattern specification	2	50.00	0.029104196	FBGN0000256, FBGN0004510	2	231	7937	34.35930736	0.764788477	0.063667849	24.662
93	GOTERM_BP_FAT	GO:0007281~germ cell development	2	50.00	0.030616102	FBGN0000256, FBGN0004510	2	243	7937	32.66255144	0.782081409	0.064098408	25.78
93	GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	2	50.00	0.030742094	FBGN0000256, FBGN0004510	2	244	7937	32.52868852	0.783464925	0.061760577	25.872
93	GOTERM_BP_FAT	GO:0035282~segmentation	2	50.00	0.032757969	FBGN0000256, FBGN0004510	2	260	7937	30.52692308	0.804465743	0.063195617	27.337
93	GOTERM_BP_FAT	GO:0003002~regionalization	2	50.00	0.057200454	FBGN0000256, FBGN0004510	2	454	7937	17.48237885	0.944210961	0.105067373	43.15
93	GOTERM_BP_FAT	GO:0007389~pattern specification process	2	50.00	0.06047625	FBGN0000256, FBGN0004510	2	480	7937	16.53541667	0.952958585	0.107038764	45.015
93	GOTERM_BP_FAT	GO:0048610~reproductive cellular process	2	50.00	0.062996094	FBGN0000256, FBGN0004510	2	500	7937	15.874	0.95875905	0.107624883	46.413
93	GOTERM_BP_FAT	GO:0003006~reproductive developmental process	2	50.00	0.063752047	FBGN0000256, FBGN0004510	2	506	7937	15.68577075	0.960358218	0.105334987	46.826
93	GOTERM_BP_FAT	GO:0048477~oogenesis	2	50.00	0.06790979	FBGN0000256, FBGN0004510	2	539	7937	14.72541744	0.968125793	0.108513756	49.048
93	GOTERM_BP_FAT	GO:0007292~female gamete generation	2	50.00	0.068791735	FBGN0000256, FBGN0004510	2	546	7937	14.53663004	0.969570538	0.106542273	49.508
93	GOTERM_BP_FAT	GO:0007276~gamete generation	2	50.00	0.090084415	FBGN0000256, FBGN0004510	2	715	7937	11.1006993	0.99020388	0.134592927	59.551
93	GOTERM_BP_FAT	GO:0019953~sexual reproduction	2	50.00	0.092604259	FBGN0000256, FBGN0004510	2	735	7937	10.79863946	0.991448543	0.134365517	60.613
93	GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	2	50.00	0.098021923	FBGN0000256, FBGN0004510	2	778	7937	10.20179949	0.993623195	0.138154331	62.81
93	GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	2	50.00	0.098021923	FBGN0000256, FBGN0004510	2	778	7937	10.20179949	0.993623195	0.138154331	62.81