Column heading	**Description**
cluster	Cluster id. This is the id that is referenced throughout the paper.
change_int	The interval in which the greatest change is observed. 0: 0-12 hrs, 1: 12-24hrs, 2: 24-48 hrs, 3: 48-96 hrs.
change_mag	The direction and magnitude of change in gene expression at the interval indicated above.
num_genes	the number of genes assigned to the cluster
num_degs	the number of significantly differentially expressed genes (DEGs) assigned to the cluster
% DEGs	the percentage of DEGs in the cluster
odds_rat	the odds ratio from a fisher's exact test, examining enrichment of the cluster for DEGs
p_val	the p-value calculated from fisher's exact test for cluster enrichment of DEGs
q_val	the benjamini-hochberg FDR corrected p-value for DEG enrichment (yellow if <0.05)
# GO terms	the number of significantly enriched gene ontology terms (green if >0)
# TFBS	the number of significantly enriched transcription factor binding sites (green if >0)
GO Term	GO terms ID, class and description
TFBS	TFBS name (*Drosophila melanogaster* ortholog) and the FDR q-value.

Transition from brood care to reproduction

	Cluster information on pattern of expression		Cluster Enrichment for Differentially Expressed Genes									
cluster	change_int	change_mag	num_genes	num_degs	% DEGs	odds_rat	p_val	q_val	# GO terms	# TFBS	GO Term ID, type and definition	Transcription Factor Binding Site and q-value
35	0	-0.57	167	19	11.4%	2.87	0.0001	0.0016	1	1	GO:0020037 [MF] 'heme binding' GO:0016705 [MF] 'oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen' GO:0005506 [MF] 'iron ion binding'	OdsH(0.0099) exex(0.0099) CG11294(0.0144) al(0.0153) Dr(0.0157) ro(0.0157) Rx(0.0157) en(0.0173) Vsx2(0.0174) Pph13(0.0186) otp(0.0189) CG32532(0.0194) unpg(0.0194) inv(0.0217) slou(0.0224) Vsx1(0.0228) repo(0.0237) CG9876(0.0246) ind(0.0258) unc-4(0.0278) Lim1(0.0294) hbn(0.0334) ftz(0.0461) Awh(0.0473)

69	1	-0.52	55	8	14.5%	3.76	0.0025	0.0239	1	1	GO:0043169 [MF] 'cation binding' GO:0004252 [MF] 'serine-type endopeptidase activity' GO:0052689 [MF] 'carboxylic ester hydrolase activity' GO:0016787 [MF] 'hydrolase activity' GO:0003824 [MF] 'catalytic activity' GO:0006508 [BP] 'proteolysis' GO:0007160 [BP] 'cell-matrix adhesion' GO:0009166 [BP] 'nucleotide catabolic process'	
4	3	1.16	156	31	19.9%	5.67	0	0	1	1	GO:0008061 [MF] 'chitin binding' GO:0005319 [MF] 'lipid transporter activity' GO:0016705 [MF] 'oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen' GO:0005506 [MF] 'iron ion binding' GO:0005576 [CL] 'extracellular region' GO:0006030 [BP] 'chitin metabolic process' GO:0006869 [BP] 'lipid transport'	btn(0.0103) CG18599(0.0108) CG9876(0.0148) lbl(0.0148) gt(0.0152) inv(0.0160) pb(0.0160) Rx(0.0163) CG32105(0.0172) fkh(0.0172) repo(0.0173) PHDP(0.0177) zen(0.0192) zen2(0.0194) HGTX(0.0194) br(0.0194) H2.0(0.0202) Vsx2(0.0217) ro(0.0223) exex(0.0226) lms(0.0233) onecut(0.0237) slou(0.0251) slp1(0.0251) otp(0.0251) Vsx1(0.0258) Scr(0.0267) hbn(0.0272) ap(0.0272) eve(0.0272) NK7.1(0.0277) en(0.0278) Pph13(0.0278) Six4(0.0279) Lim1(0.0302) CG11617(0.0308) CG32532(0.0326) unpg(0.0348) C15(0.0359) CG4328-RA(0.0380) Lim3(0.0393) Dbx(0.0411) ems(0.0416) lab(0.0430) Dll(0.0458) Awh(0.0494)
19	3	0.59	245	58	23.7%	7.41	0	0	1	1		fkh(0.0461)
21	3	-0.28	315	25	7.9%	1.93	0.003	0.025	1	1	GO:0005216 [MF] 'ion channel activity' GO:0006811 [BP] 'ion transport'	opa(0.0000) Trl(0.0001) Mad(0.0002) btd(0.0003) usp(0.0013) h(0.0053) gcm2(0.0096) dl(var.2)(0.0096) brk(0.0148) Ets21C(0.0402)
6	3	-0.43	231	28	12.1%	3.12	0	0	1	1		
7	3	-0.31	35	7	20.0%	5.52	0.0007	0.0074	1	1		
36	3	0.28	73	13	17.8%	4.83	0	0.0002	1	1		
44	3	0.27	353	41	11.6%	3.01	0	0	1	1		

3	0	0.19	341	5	1.5%	0.32	0.9993	1	1	1		Mad(0.0073) hkb(0.0173) brk(0.0223) Eip74EF(0.0415)
12	0	-0.08	319	11	3.4%	0.78	0.8292	1	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0007608 [BP] 'sensory perception of smell'	zen(0.0105) pb(0.0117) Dfd(0.0194) lab(0.0219) CG18599(0.0229) Scr(0.0237) vvl(0.0278) Antp(0.0278) E5(0.0348) lbe(0.0367) btn(0.0461) Lim3(0.0461) zen2(0.0475)
17	0	0.04	481	13	2.7%	0.6	0.9796	1	1	1	GO:0015074 [BP] 'DNA integration'	odd(0.0162) Gsc(0.0382) oc(0.0434)
26	0	0.55	194	6	3.1%	0.7	0.8564	1	1	1		h(0.0000) Mad(0.0000) brk(0.0003) opa(0.0068) CTCF(0.0190) btd(0.0194) hkb(0.0308) usp(0.0421)
27	0	-0.14	202	5	2.5%	0.55	0.9441	1	1	1	GO:0006366 [BP] 'transcription from RNA polymerase II promoter'	lab(0.0118) C15(0.0157) cad(0.0173) br(var.3)(0.0212) Dbx(0.0237) Cf2(0.0277) exex(0.0278) Ubx(0.0279) Abd-B(0.0302) abd-A(0.0303) br(0.0341) hb(0.0355) vnd(0.0392) Pph13(0.0475)
29	0	0.49	83	8	9.6%	2.35	0.0283	0.1433	1	1		opa(0.0000) Mad(0.0000) usp(0.0000) Trl(0.0001) brk(0.0002) hkb(0.0003) h(0.0015) btd(0.0042)
42	0	0.64	117	0	0.0%	0	1	1	1	1		Mad(0.0002) opa(0.0017) brk(0.0108) usp(0.0411)

55	0	-0.24	343	25	7.3%	1.75	0.0087	0.059	1	1	GO:0004518 [MF] 'nuclease activity' GO:0008152 [BP] 'metabolic process'	br(var.4)(0.0003) Abd-B(0.0004) cad(0.0031) C15(0.0039) CG4328-RA(0.0041) br(var.3)(0.0047) Dr(0.0138) Dll(0.0151) vnd(0.0153) Pph13(0.0157) fkh(0.0157) H2.0(0.0165) br(0.0173) Ubx(0.0194) CG15696-RA(0.0228) lbe(0.0237) CG9876(0.0237) PHDP(0.0238) D(0.0244) Dbx(0.0250) exd(0.0271) NK7.1(0.0299) tup(0.0303) hbn(0.0303) br(var.2)(0.0328) lms(0.0340) Hmx(0.0359) nub(0.0382) E5(0.0387) Lim3(0.0399) Cf2(0.0412) CG32105(0.0414) Rx(0.0416) B-H2(0.0461) abd-A(0.0461) ap(0.0461) hb(0.0480)
58	0	-0.1	340	7	2.1%	0.45	0.9932	1	1	1		slbo(0.0092) Abd-B(0.0157) H2.0(0.0190) CG4328-RA(0.0206) Dbx(0.0207)

60	0	-0.33	279	9	3.2%	0.73	0.8654	1	1	1		eve(0.0041) CG18599(0.0054) vvl(0.0064) lab(0.0064) Scr(0.0064) pb(0.0064) E5(0.0096) HGTX(0.0096) ap(0.0096) Antp(0.0108) zen(0.0116) slou(0.0138) btn(0.0148) fkh(0.0152) vnd(0.0157) H2.0(0.0171) lms(0.0174) ftz(0.0189) ct(0.0189) ind(0.0194) br(0.0194) abd-A(0.0194) br(var.3)(0.0200) ems(0.0206) Vsx1(0.0207) Abd-B(0.0211) NK7.1(0.0212) br(var.2)(0.0237) lbl(0.0272) C15(0.0279) Awh(0.0299) zen2(0.0340) Dll(0.0380) Pph13(0.0382) nub(0.0402) inv(0.0405) Dfd(0.0415) lbe(0.0415) CG34031(0.0461) otp(0.0461) PHDP(0.0493) Rx(0.0493) Cf2(0.0497)
61	0	0.37	290	9	3.1%	0.7	0.8921	1	1	1		Mad(0.0001) h(0.0001) usp(0.0010) opa(0.0015) btd(0.0048) brk(0.0151)
72	0	0.36	215	5	2.3%	0.52	0.9612	1	1	1		opa(0.0000) Mad(0.0000) h(0.0001) brk(0.0003) CTCF(0.0157) hkb(0.0172) usp(0.0431)
8	0	-0.26	141	3	2.1%	0.47	0.9493	1	1	1	GO:0004812 [MF] 'aminoacyl-tRNA ligase activity' GO:0006418 [BP] 'tRNA aminoacylation for protein translation'	
9	0	-0.18	56	0	0.0%	0	1	1	1	1		
24	0	-0.21	283	4	1.4%	0.31	0.9986	1	1	1		
34	0	-0.24	135	8	5.9%	1.38	0.238	0.8615	1	1		
46	0	-0.25	159	8	5.0%	1.16	0.3932	1	1	1		
48	0	0.11	148	2	1.4%	0.3	0.9898	1	1	1		
51	0	-0.12	115	1	0.9%	0.19	0.9943	1	1	1		
52	0	-0.06	533	6	1.1%	0.24	1	1	1	1		

56	0	0.35	64	0	0.0%	0	1	1	1	1	GO:0008236 [MF] 'serine-type peptidase activity' GO:0008138 [MF] 'protein tyrosine/serine/threonine phosphatase activity' GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0005622 [CL] 'intracellular' GO:0006412 [BP] 'translation'	
59	0	0.2	75	2	2.7%	0.6	0.8456	1	1	1	GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0005622 [CL] 'intracellular' GO:0006412 [BP] 'translation'	
67	0	0	378	0	0.0%	0	1	1	1	1	GO:0004190 [MF] 'aspartic-type endopeptidase activity' GO:0016805 [MF] 'dipeptidase activity' GO:0004222 [MF] 'metalloendopeptidase activity' GO:0003676 [MF] 'nucleic acid binding' GO:0031012 [CL] 'extracellular matrix' GO:0015074 [BP] 'DNA integration' GO:0006508 [BP] 'proteolysis'	
68	0	0.33	56	0	0.0%	0	1	1	1	1		
73	0	0.19	173	1	0.6%	0.13	0.9996	1	1	1		
74	0	0.27	67	0	0.0%	0	1	1	1	1	GO:0017048 [MF] 'Rho GTPase binding' GO:0043565 [MF] 'sequence-specific DNA binding' GO:0030036 [BP] 'actin cytoskeleton organization' GO:0006355 [BP] 'regulation of transcription, DNA-templated' GO:0006812 [BP] 'cation transport' GO:0035556 [BP] 'intracellular signal transduction' GO:0016043 [BP] 'cellular component organization'	
75	0	0.13	131	2	1.5%	0.34	0.9803	1	1	1		
11	1	0.12	261	2	0.8%	0.17	0.9999	1	1	1	GO:0005488 [MF] 'binding'	cnc::maf-S(0.0237) brk(0.0475)
18	1	-0.11	315	2	0.6%	0.14	1	1	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0007608 [BP] 'sensory perception of smell' GO:0006412 [BP] 'translation'	HHEX(0.0355) H2.0(0.0356) CG4328-RA(0.0405)

30	1	0.15	282	13	4.6%	1.06	0.462	1	1	1	GO:0005515 [MF] 'protein binding' GO:0005802 [CL] 'trans-Golgi network' GO:0009113 [BP] 'purine nucleobase biosynthetic process' GO:0010508 [BP] 'positive regulation of autophagy'	kni(0.0157) brk(0.0233) CTCF(0.0237) h(0.0418)
32	1	-0.24	64	1	1.6%	0.35	0.9431	1	1	1	GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0005622 [CL] 'intracellular' GO:0006412 [BP] 'translation'	fkh(0.0151)
41	1	0.08	308	8	2.6%	0.58	0.9623	1	1	1		CTCF(0.0026) h(0.0116) brk(0.0461)
66	1	0.23	107	1	0.9%	0.21	0.9918	1	1	1	GO:0005337 [MF] 'nucleoside transmembrane transporter activity'	Gsc(0.0096) oc(0.0217)
16	1	-0.21	109	1	0.9%	0.2	0.9925	1	1	1		
25	1	-0.19	43	1	2.3%	0.52	0.854	1	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0016020 [CL] 'membrane' GO:0007608 [BP] 'sensory perception of smell'	
33	1	-0.14	172	3	1.7%	0.39	0.9823	1	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0016020 [CL] 'membrane' GO:0007608 [BP] 'sensory perception of smell'	
38	1	0.13	189	2	1.1%	0.23	0.998	1	1	1		
13	2	-0.25	39	1	2.6%	0.58	0.8253	1	1	1		gt(0.0303) CG9876(0.0303) Lim1(0.0338) exex(0.0340) lms(0.0347) inv(0.0359) en(0.0393) OdsH(0.0461) Pph13(0.0461) Awh(0.0461) unpg(0.0461) CG11294(0.0461) Rx(0.0461) repo(0.0473) Vsx2(0.0479)
1	2	-0.14	64	0	0.0%	0	1	1	1	1		
10	2	0.33	17	1	5.9%	1.37	0.5323	1	1	1		
14	2	-0.11	87	0	0.0%	0	1	1	1	1		
40	2	-0.18	40	1	2.5%	0.56	0.833	1	1	1		
43	2	0.12	92	4	4.3%	0.99	0.5755	1	1	1		
49	2	0.14	40	4	10.0%	2.44	0.0958	0.4282	1	1		
53	2	0.12	93	1	1.1%	0.24	0.9845	1	1	1		
20	3	-0.11	204	5	2.5%	0.55	0.9471	1	1	1		Eip74EF(0.0251)

39	3	-0.19	391	14	3.6%	0.81	0.8143	1	1	1		Mad(0.0000) opa(0.0000) btd(0.0000) brk(0.0000) gcm2(0.0021) h(0.0027) Trl(0.0056) usp(0.0092) hkb(0.0162) CTCF(0.0271)
65	3	-0.35	204	17	8.3%	2.02	0.0082	0.059	1	1	GO:0005249 [MF] 'voltage-gated potassium channel activity' GO:0015078 [MF] 'hydrogen ion transmembrane transporter activity' GO:0005216 [MF] 'ion channel activity' GO:0033179 [CL] 'proton-transporting V-type ATPase, V0 domain' GO:0008076 [CL] 'voltage-gated potassium channel complex' GO:0005891 [CL] 'voltage-gated calcium channel complex' GO:0055085 [BP] 'transmembrane transport' GO:0006813 [BP] 'potassium ion transport' GO:0006811 [BP] 'ion transport' GO:0051260 [BP] 'protein homooligomerization'	Mad(0.0000) opa(0.0000) btd(0.0000) brk(0.0000) Trl(0.0000) hkb(0.0000) usp(0.0004) h(0.0006) CTCF(0.0192)
71	3	0.13	314	14	4.5%	1.02	0.5082	1	1	1	GO:0001104 [MF] 'RNA polymerase II transcription cofactor activity' GO:0004812 [MF] 'aminoacyl-tRNA ligase activity' GO:0004817 [MF] 'cysteine-tRNA ligase activity' GO:0051082 [MF] 'unfolded protein binding' GO:0005524 [MF] 'ATP binding' GO:0004828 [MF] 'serine-tRNA ligase activity' GO:0031072 [MF] 'heat shock protein binding' GO:0000166 [MF] 'nucleotide binding' GO:0016592 [CL] 'mediator complex' GO:0006281 [BP] 'DNA repair' GO:0009408 [BP] 'response to heat' GO:0006423 [BP] 'cysteinyl-tRNA aminoacylation' GO:0006418 [BP] 'tRNA aminoacylation for protein translation' GO:0006370 [BP] '7-methylguanosine mRNA capping' GO:0006434 [BP] 'seryl-tRNA aminoacylation'	cad(0.0334) hb(0.0461)
2	3	0.11	178	6	3.4%	0.76	0.7955	1	1	1		
5	3	-0.27	42	6	14.3%	3.67	0.0093	0.059	1	1		

15	3	0.84	78	6	7.7%	1.83	0.1253	0.5014	1	1	GO:0031177 [MF] 'phosphopantetheine binding' GO:0016740 [MF] 'transferase activity' GO:0016491 [MF] 'oxidoreductase activity' GO:0016705 [MF] 'oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen' GO:0020037 [MF] 'heme binding' GO:0016788 [MF] 'hydrolase activity, acting on ester bonds' GO:0005506 [MF] 'iron ion binding' GO:0055114 [BP] 'oxidation-reduction process' GO:0008152 [BP] 'metabolic process' GO:0009058 [BP] 'biosynthetic process' GO:0006629 [BP] 'lipid metabolic process'	
22	3	0.37	72	4	5.6%	1.29	0.3862	1	1	1	GO:0016884 [MF] 'carbon-nitrogen ligase activity, with glutamine as amido-N-donor'	
23	3	-0.12	314	7	2.2%	0.49	0.9857	1	1	1		
28	3	-0.18	183	10	5.5%	1.27	0.2792	0.9644	1	1		
31	3	0.39	141	12	8.5%	2.06	0.0207	0.1122	1	1		
37	3	0.19	94	3	3.2%	0.72	0.7847	1	1	1		
45	3	0.2	134	11	8.2%	1.98	0.0328	0.1558	1	1		
47	3	0.17	29	0	0.0%	0	1	1	1	1		
50	3	0.12	204	13	6.4%	1.5	0.1115	0.4708	1	1		
54	3	-0.13	150	7	4.7%	1.07	0.4844	1	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0007608 [BP] 'sensory perception of smell'	
57	3	-0.12	354	9	2.5%	0.56	0.9747	1	1	1		
62	3	0.26	99	7	7.1%	1.67	0.142	0.5396	1	1		
63	3	-0.2	262	20	7.6%	1.84	0.0111	0.065	1	1	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0016020 [CL] 'membrane' GO:0007608 [BP] 'sensory perception of smell'	
64	3	0.19	117	1	0.9%	0.19	0.9948	1	1	1	GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0015935 [CL] 'small ribosomal subunit' GO:0005622 [CL] 'intracellular' GO:0042254 [BP] 'ribosome biogenesis' GO:0006412 [BP] 'translation'	
70	3	-0.14	72	1	1.4%	0.31	0.9603	1	1	1		

76	3	0.06	334	7	2.1%	0.46	0.9919	1	1	1		

Transition from reproduction to brood care

	Cluster information on pattern of expression		Cluster Enrichment for Differentially Expressed Genes									
cluster	change_int	change_mag	num_genes	num_degs	% DEGs	odds_rat	p_val	q_val	# GO terms	# TFBS	GO Term ID, type and definition	Transcription Factor Binding Site and q-value
93	0	0.25	134	16	11.9%	3.02	0.0002	0.0019	0	6		Mad(0.0000) h(0.0001) opa(0.0015) btd(0.0019) brk(0.0025) usp(0.0076)
56	0	0.21	91	22	24.2%	7.21	0	0	1	0	GO:0005789 [CL] 'endoplasmic reticulum membrane'	
65	0	-1.21	76	17	22.4%	6.46	0	0	3	0	GO:0005576 [CL] 'extracellular region' GO:0005615 [CL] 'extracellular space' GO:0035176 [BP] 'social behavior'	
34	0	0.21	119	17	14.3%	3.73	0	0.0001	0	0		
12	0	0.48	82	13	15.9%	4.19	0.0001	0.0004	0	0		
8	1	-0.35	134	48	35.8%	13.2	0	0	0	1		fkh(0.0252)
47	1	-0.18	206	59	28.6%	9.64	0	0	1	0	GO:0008237 [MF] 'metallopeptidase activity'	
96	1	-0.26	109	17	15.6%	4.13	0	0	0	0		
90	2	0.16	151	30	19.9%	5.66	0	0	5	6	GO:0046933 [MF] 'proton-transporting ATP synthase activity, rotational mechanism' GO:0005834 [CL] 'heterotrimeric G-protein complex' GO:0046034 [BP] 'ATP metabolic process' GO:0015986 [BP] 'ATP synthesis coupled proton transport' GO:0035556 [BP] 'intracellular signal transduction'	opa(0.0000) btd(0.0001) h(0.0026) Mad(0.0029) usp(0.0117) hkb(0.0450)
70	2	0.22	162	45	27.8%	9.02	0	0	1	4	GO:0055114 [BP] 'oxidation-reduction process'	Mad(0.0002) usp(0.0345) opa(0.0398) Trl(0.0475)
58	3	0.25	126	15	11.9%	3.01	0.0004	0.0029	1	0	GO:0043565 [MF] 'sequence-specific DNA binding'	
82	3	0.4	133	14	10.5%	2.61	0.002	0.0137	1	0	GO:0052689 [MF] 'carboxylic ester hydrolase activity'	
73	3	0.66	72	23	31.9%	10.7	0	0	0	0		
91	3	-0.23	169	41	24.3%	7.45	0	0	0	0		

15	0	0.17	187	4	2.1%	0.47	0.966	1	1	8	GO:0005856 [CL] 'cytoskeleton'	opa(0.0013) Mad(0.0073) btd(0.0117) gcm2(0.0162) Trl(0.0162) usp(0.0209) brk(0.0450) schlank(0.0496)
87	0	0.26	180	5	2.8%	0.62	0.8991	1	4	2	GO:0004889 [MF] 'acetylcholine-activated cation-selective channel activity' GO:0004129 [MF] 'cytochrome-c oxidase activity' GO:0045211 [CL] 'postsynaptic membrane' GO:0043044 [BP] 'ATP-dependent chromatin remodeling'	h(0.0073) Mad(0.0142)
5	0	0	385	0	0.0%	0	1	1	10	1	GO:0004190 [MF] 'aspartic-type endopeptidase activity' GO:0003887 [MF] 'DNA-directed DNA polymerase activity' GO:0016805 [MF] 'dipeptidase activity' GO:0008408 [MF] '3'-5' exonuclease activity' GO:0008237 [MF] 'metallopeptidase activity' GO:0004222 [MF] 'metalloendopeptidase activity' GO:0003676 [MF] 'nucleic acid binding' GO:0031012 [CL] 'extracellular matrix' GO:0015074 [BP] 'DNA integration' GO:0006508 [BP] 'proteolysis'	usp(0.0373)
30	0	0.22	545	2	0.4%	0.08	1	1	0	3		h(0.0252) vis(0.0252) brk(0.0252)
25	0	0.08	235	1	0.4%	0.09	1	1	0	1		kni(0.0252)
9	0	-0.29	78	0	0.0%	0	1	1	0	1		nub(0.0249)
68	0	-0.22	206	0	0.0%	0	1	1	7	0	GO:0004984 [MF] 'olfactory receptor activity' GO:0003743 [MF] 'translation initiation factor activity' GO:0005549 [MF] 'odorant binding' GO:0004803 [MF] 'transposase activity' GO:0007608 [BP] 'sensory perception of smell' GO:0006313 [BP] 'transposition, DNA-mediated' GO:0050909 [BP] 'sensory perception of taste'	
33	0	0.12	255	1	0.4%	0.08	1	1	3	0	GO:0008479 [MF] 'queuine tRNA-ribosyltransferase activity' GO:0046873 [MF] 'metal ion transmembrane transporter activity' GO:0008616 [BP] 'queuosine biosynthetic process'	
42	0	-0.36	20	0	0.0%	0	1	1	3	0	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0007608 [BP] 'sensory perception of smell'	

89	0	0.34	51	3	5.9%	1.37	0.3863	1	3	0	GO:0005328 [MF] 'neurotransmitter:sodium symporter activity' GO:0016021 [CL] 'integral component of membrane' GO:0006836 [BP] 'neurotransmitter transport'	
85	0	-1.16	132	12	9.1%	2.21	0.0129	0.0814	7	0	GO:0043169 [MF] 'cation binding' GO:0004252 [MF] 'serine-type endopeptidase activity' GO:0004132 [MF] 'dCMP deaminase activity' GO:0016787 [MF] 'hydrolase activity' GO:0003824 [MF] 'catalytic activity' GO:0006220 [BP] 'pyrimidine nucleotide metabolic process' GO:0006508 [BP] 'proteolysis'	
37	0	-0.53	119	3	2.5%	0.56	0.8975	1	6	0	GO:0016740 [MF] 'transferase activity' GO:0016788 [MF] 'hydrolase activity, acting on ester bonds' GO:0016491 [MF] 'oxidoreductase activity' GO:0055114 [BP] 'oxidation-reduction process' GO:0008152 [BP] 'metabolic process' GO:0019441 [BP] 'tryptophan catabolic process to kynurenine'	
26	0	-0.23	157	4	2.5%	0.57	0.9167	1	5	0	GO:0003735 [MF] 'structural constituent of ribosome' GO:0005840 [CL] 'ribosome' GO:0015935 [CL] 'small ribosomal subunit' GO:0042254 [BP] 'ribosome biogenesis' GO:0006412 [BP] 'translation'	
61	0	-0.52	29	2	6.9%	1.62	0.3637	1	1	0	GO:0005215 [MF] 'transporter activity'	
80	0	-0.19	95	0	0.0%	0	1	1	1	0	GO:0006850 [BP] 'mitochondrial pyruvate transport'	
1	0	0.22	66	1	1.5%	0.34	0.948	1	0	0		
3	0	-0.39	132	0	0.0%	0	1	1	0	0		
4	0	0.25	214	2	0.9%	0.2	0.9993	1	0	0		
17	0	0.17	286	2	0.7%	0.15	1	1	0	0		
40	0	0.44	82	0	0.0%	0	1	1	0	0		
41	0	-0.15	192	3	1.6%	0.34	0.9913	1	0	0		
48	0	0.45	214	2	0.9%	0.2	0.9993	1	0	0		
51	0	0.16	143	0	0.0%	0	1	1	0	0		
52	0	-0.18	246	3	1.2%	0.27	0.9988	1	0	0		
63	0	-0.24	113	6	5.3%	1.23	0.3727	1	0	0		
74	0	-0.19	149	3	2.0%	0.45	0.9611	1	0	0		
78	0	-0.59	183	10	5.5%	1.27	0.2792	1	0	0		
84	0	-0.29	159	0	0.0%	0	1	1	0	0		

88	0	-0.32	309	10	3.2%	0.73	0.8733	1	0	0		
95	0	-0.09	662	3	0.5%	0.1	1	1	0	0		
32	0	-0.1	309	13	4.2%	0.96	0.5962	1	0	0		
21	0	-0.16	130	0	0.0%	0	1	1	0	0		
62	0	-0.33	33	0	0.0%	0	1	1	0	0		
19	1	0.25	47	0	0.0%	0	1	1	2	0	GO:0008146 [MF] 'sulfotransferase activity' GO:0005783 [CL] 'endoplasmic reticulum'	
92	1	-0.18	56	1	1.8%	0.4	0.9185	1	4	0	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0016020 [CL] 'membrane' GO:0007608 [BP] 'sensory perception of smell'	
2	1	-0.25	27	0	0.0%	0	1	1	7	0	GO:0003995 [MF] 'acyl-CoA dehydrogenase activity' GO:0016627 [MF] 'oxidoreductase activity, acting on the CH-CH group of donors' GO:0050660 [MF] 'flavin adenine dinucleotide binding' GO:0006635 [BP] 'fatty acid beta-oxidation' GO:0006631 [BP] 'fatty acid metabolic process' GO:0055114 [BP] 'oxidation-reduction process' GO:0008152 [BP] 'metabolic process'	
53	1	-0.19	17	1	5.9%	1.37	0.5323	1	1	0	GO:0003824 [MF] 'catalytic activity'	
64	1	-0.11	159	8	5.0%	1.16	0.3932	1	0	0		
86	1	-0.33	49	5	10.2%	2.5	0.0616	0.3254	0	0		
13	1	0.3	4	0	0.0%	0	1	1	0	0		
24	1	-0.18	73	0	0.0%	0	1	1	0	0		
29	1	-0.17	130	3	2.3%	0.51	0.9275	1	0	0		
83	1	-0.18	46	0	0.0%	0	1	1	0	0		
69	2	0.36	20	1	5.0%	1.15	0.5911	1	2	0	GO:0004553 [MF] 'hydrolase activity, hydrolyzing O-glycosyl compounds' GO:0005975 [BP] 'carbohydrate metabolic process'	
20	2	0.31	34	1	2.9%	0.66	0.7815	1	1	0	GO:0019752 [BP] 'carboxylic acid metabolic process'	
35	2	0.14	179	1	0.6%	0.12	0.9997	1	1	0	GO:0000166 [MF] 'nucleotide binding'	
44	2	0.24	80	2	2.5%	0.56	0.8702	1	4	0	GO:0003777 [MF] 'microtubule motor activity' GO:0005198 [MF] 'structural molecule activity' GO:0006511 [BP] 'ubiquitin-dependent protein catabolic process' GO:0007018 [BP] 'microtubule-based movement'	

16	2	0.1	209	7	3.3%	0.76	0.8132	1	2	0	GO:0015991 [BP] 'ATP hydrolysis coupled proton transport' GO:0033180 [CL] 'proton-transporting V-type ATPase, V1 domain'	
18	2	-0.09	140	7	5.0%	1.15	0.413	1	1	0	GO:0016972 [MF] 'thiol oxidase activity'	
23	2	0.46	25	0	0.0%	0	1	1	2	0	GO:0008061 [MF] 'chitin binding' GO:0006030 [BP] 'chitin metabolic process'	
46	2	0.12	112	8	7.1%	1.69	0.1169	0.5553	0	0		
28	2	0.1	168	9	5.4%	1.24	0.3136	1	0	0		
31	2	0.17	113	0	0.0%	0	1	1	0	0		
36	2	0.07	231	2	0.9%	0.19	0.9996	1	0	0		
59	2	-0.17	33	2	6.1%	1.41	0.4261	1	0	0		
22	2	0.23	36	0	0.0%	0	1	1	0	0		
27	2	-0.08	117	1	0.9%	0.19	0.9948	1	0	0		
43	2	-0.21	21	0	0.0%	0	1	1	0	0		
49	2	-0.13	120	0	0.0%	0	1	1	0	0		
60	2	0.4	16	0	0.0%	0	1	1	0	0		
77	3	0.36	65	0	0.0%	0	1	1	10	1	GO:0016641 [MF] 'oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor' GO:0004930 [MF] 'G-protein coupled receptor activity' GO:0020037 [MF] 'heme binding' GO:0000062 [MF] 'fatty-acyl-CoA binding' GO:0003824 [MF] 'catalytic activity' GO:0016705 [MF] 'oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen' GO:0005506 [MF] 'iron ion binding' GO:0055114 [BP] 'oxidation-reduction process' GO:0008152 [BP] 'metabolic process' GO:0008299 [BP] 'isoprenoid biosynthetic process'	.
10	3	-0.2	84	8	9.5%	2.32	0.0301	0.1788	0	3		opa(0.0064) btd(0.0099) Mad(0.0290)
50	3	0.13	129	0	0.0%	0	1	1	4	0	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0016020 [CL] 'membrane' GO:0007608 [BP] 'sensory perception of smell'	
45	3	0.09	145	1	0.7%	0.15	0.9985	1	3	0	GO:0004984 [MF] 'olfactory receptor activity' GO:0005549 [MF] 'odorant binding' GO:0007608 [BP] 'sensory perception of smell'	

94	3	0.82	135	10	7.4%	1.76	0.0716	0.3581	8	0	GO:0020037 [MF] 'heme binding' GO:0031177 [MF] 'phosphopantetheine binding' GO:0016491 [MF] 'oxidoreductase activity' GO:0016705 [MF] 'oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen' GO:0005215 [MF] 'transporter activity' GO:0005506 [MF] 'iron ion binding' GO:0055114 [BP] 'oxidation-reduction process' GO:0008152 [BP] 'metabolic process'	
66	3	-0.08	173	2	1.2%	0.25	0.9962	1	3	0	GO:0005248 [MF] 'voltage-gated sodium channel activity' GO:0001518 [CL] 'voltage-gated sodium channel complex' GO:0016012 [CL] 'sarcoglycan complex'	
11	3	0.29	43	0	0.0%	0	1	1	0	0		
14	3	-0.08	175	2	1.1%	0.25	0.9965	1	0	0		
39	3	0.06	291	0	0.0%	0	1	1	0	0		
54	3	0.22	128	5	3.9%	0.89	0.6633	1	0	0		
57	3	0.2	140	2	1.4%	0.31	0.9861	1	0	0		
67	3	0.14	282	1	0.4%	0.08	1	1	0	0		
72	3	-0.03	563	0	0.0%	0	1	1	0	0		
79	3	-0.13	269	11	4.1%	0.93	0.6326	1	0	0		
38	3	0.22	56	1	1.8%	0.4	0.9185	1	0	0		
55	3	-0.22	204	15	7.4%	1.76	0.0342	0.191	0	0		
6	3	-0.47	15	1	6.7%	1.56	0.4886	1	0	0		
7	3	-0.17	118	1	0.8%	0.19	0.995	1	0	0		
71	3	-0.12	185	3	1.6%	0.36	0.9888	1	0	0		
76	3	0.25	47	1	2.1%	0.47	0.878	1	0	0		
81	3	-0.27	71	1	1.4%	0.31	0.9584	1	0	0		