

Table S5 GO analysis of Yan datasets. DAVID was used to perform GO analysis of Genes assigned to Yan-bound regions at stage 5-7 (A) and stage 11 (B) and of genes assigned to Yan-bound regions in the *D. virilis* datasets (C) {Huang, 2009 #62;Huang, 2009 #63}. Only clusters that contain a GO-term with a p-value <0.0001 (Bonferroni-corrected) are shown.

A. Stg5-7 Top 2000 genes +/- 3kb from Yan bound region			
Cluster 1			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	dna-binding	3.078305244	5.24E-43
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	2.370622284	1.05E-39
GOTERM_BP_FAT	GO:0045449~regulation of transcription	2.189821722	3.88E-35
GOTERM_MF_FAT	GO:0003700~transcription factor activity	2.806327586	3.38E-35
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	2.258051786	3.74E-32
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	2.317119826	3.98E-31
GOTERM_MF_FAT	GO:0003677~DNA binding	2.039477281	1.62E-29
SP_PIR_KEYWORDS	transcription regulation	2.67305822	1.38E-26
SP_PIR_KEYWORDS	nucleus	2.033269269	2.54E-26
SP_PIR_KEYWORDS	Transcription	2.516967229	1.62E-22
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2.823780256	7.62E-20
GOTERM_BP_FAT	GO:0006350~transcription	2.13651513	1.56E-16
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	2.500234278	2.18E-15
Cluster 2			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007444~imaginal disc development	2.50011219	3.11E-25
GOTERM_BP_FAT	GO:0048569~post-embryonic organ development	2.779286195	4.18E-24
GOTERM_BP_FAT	GO:0009791~post-embryonic development	2.389634409	4.34E-23
GOTERM_BP_FAT	GO:0007552~metamorphosis	2.51411418	4.13E-22
GOTERM_BP_FAT	GO:0009886~post-embryonic morphogenesis	2.478282657	1.76E-20
GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	2.480471342	3.91E-20
GOTERM_BP_FAT	GO:0007560~imaginal disc morphogenesis	2.658087637	6.17E-20
GOTERM_BP_FAT	GO:0048563~post-embryonic organ morphogenesis	2.658087637	6.17E-20
GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	2.312321106	9.87E-20
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	2.623801653	7.57E-16
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	2.627217108	1.11E-15
GOTERM_BP_FAT	GO:0048736~appendage development	2.581138211	2.60E-15

GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	2.583970736	3.81E-15
GOTERM_BP_FAT	GO:0035220~wing disc development	2.385179913	1.04E-13
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	2.557092673	1.27E-13
GOTERM_BP_FAT	GO:0007476~imaginal disc-derived wing morphogenesis	2.45958002	4.60E-11
GOTERM_BP_FAT	GO:0007472~wing disc morphogenesis	2.437220202	8.01E-11

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0030182~neuron differentiation	2.535700081	3.46E-26
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	2.346383107	3.62E-22
GOTERM_BP_FAT	GO:0048666~neuron development	2.521134806	3.07E-21
GOTERM_BP_FAT	GO:0006928~cell motion	2.567597814	2.17E-19
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	2.124705277	1.01E-18
GOTERM_BP_FAT	GO:0030030~cell projection organization	2.377475799	1.62E-18
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	2.547679012	1.13E-17
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	2.540826729	2.25E-17
GOTERM_BP_FAT	GO:0031175~neuron projection development	2.531973674	3.02E-17
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	2.468124679	6.98E-17
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	2.403147222	1.92E-16
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	2.344598859	1.05E-15
GOTERM_BP_FAT	GO:0007409~axonogenesis	2.779286195	5.04E-15
GOTERM_BP_FAT	GO:0007411~axon guidance	3.11254902	1.33E-13

Cluster 4

Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2.823780256	7.62E-20
SP_PIR_KEYWORDS	Homeobox	3.920660491	6.63E-18
INTERPRO	IPR017970:Homeobox, conserved site	3.893088965	1.32E-16
INTERPRO	IPR001356:Homeobox	3.773448411	3.45E-16
INTERPRO	IPR012287:Homeodomain-related	3.562543676	1.86E-14
SMART	SM00389:HOX	3.009109526	9.59E-13
UP_SEQ_FEATURE	DNA-binding region:Homeobox	3.67965368	2.06E-10

Cluster 5

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048729~tissue	2.856320288	3.54E-21

	morphogenesis		
	GO:0048598~embryonic		
GOTERM_BP_FAT	morphogenesis	2.934426745	1.01E-20
	GO:0002009~morphogenesis of		
GOTERM_BP_FAT	an epithelium	2.727976296	1.77E-16
	GO:0060429~epithelium		
GOTERM_BP_FAT	development	2.671935697	3.11E-16
	GO:0016331~morphogenesis of		
GOTERM_BP_FAT	embryonic epithelium	2.93962963	1.26E-09
GOTERM_BP_FAT	GO:0007391~dorsal closure	3.044837427	5.70E-08
	GO:0001700~embryonic		
GOTERM_BP_FAT	development via the syncytial		
	blastoderm	2.175875389	1.29E-06
	GO:0009792~embryonic		
GOTERM_BP_FAT	development ending in birth or		
	egg hatching	2.110234127	3.88E-06
Cluster 6			
Category	Term	Fold Enrichment	Bonferroni
	GO:0048732~gland		
GOTERM_BP_FAT	development	2.943236537	2.99E-14
	GO:0007431~salivary gland		
GOTERM_BP_FAT	development	2.943859313	1.20E-11
	GO:0035272~exocrine system		
GOTERM_BP_FAT	development	2.943859313	1.20E-11
	GO:0007435~salivary gland		
GOTERM_BP_FAT	morphogenesis	2.475477583	1.18E-04
	GO:0022612~gland		
GOTERM_BP_FAT	morphogenesis	2.475477583	1.18E-04
Cluster 7			
Category	Term	Fold Enrichment	Bonferroni
	GO:0007423~sensory organ		
GOTERM_BP_FAT	development	2.305816802	4.26E-19
GOTERM_BP_FAT	GO:0001654~eye development	2.188784471	4.86E-12
	GO:0048749~compound eye		
GOTERM_BP_FAT	development	2.130277056	7.99E-10
	GO:0046530~photoreceptor		
GOTERM_BP_FAT	cell differentiation	2.755902778	2.19E-08
	GO:0001751~compound eye		
GOTERM_BP_FAT	photoreceptor cell		
	differentiation	2.733061061	1.05E-06
	GO:0001754~eye		
GOTERM_BP_FAT	photoreceptor cell		
	differentiation	2.676076628	1.39E-06
	GO:0048592~eye		
GOTERM_BP_FAT	morphogenesis	2.019492772	1.86E-06
	GO:0001745~compound eye		
GOTERM_BP_FAT	morphogenesis	1.947210667	8.06E-05
Cluster 8			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0006928~cell motion	2.567597814	2.17E-19
GOTERM_BP_FAT	GO:0016477~cell migration	2.53984	2.10E-09
GOTERM_BP_FAT	GO:0048870~cell motility	2.376855615	5.67E-08
GOTERM_BP_FAT	GO:0051674~localization of cell	2.303709751	1.74E-07
Cluster 9			

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007155~cell adhesion	2.635530013	1.19E-10
GOTERM_BP_FAT	GO:0022610~biological adhesion	2.439267139	7.06E-09
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	3.228610169	5.98E-05
Cluster 10			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048645~organ formation	5.291333333	2.86E-13
GOTERM_BP_FAT	GO:0010160~formation of organ boundary	5.198502924	5.72E-12
GOTERM_BP_FAT	GO:0048859~formation of anatomical boundary	4.81030303	1.20E-11
GOTERM_BP_FAT	GO:0008052~sensory organ boundary specification	4.907903382	7.00E-05
GOTERM_BP_FAT	GO:0007432~salivary gland boundary specification	5.644088889	8.93E-04
Cluster 11			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	3.04211213	1.59E-09
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	2.724732567	1.76E-09
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	3.919506173	1.29E-04
Cluster 12			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007389~pattern specification process	2.410496296	9.73E-27
GOTERM_BP_FAT	GO:0003002~regionalization	2.424223201	1.56E-25
GOTERM_BP_FAT	GO:0009880~embryonic pattern specification	2.412786917	4.35E-11
GOTERM_BP_FAT	GO:0035282~segmentation	2.306478632	7.21E-11
GOTERM_BP_FAT	GO:0007350~blastoderm segmentation	2.427217125	1.54E-10
GOTERM_BP_FAT	GO:0007354~zygotic determination of anterior/posterior axis, embryo	4.379034483	8.19E-05
Cluster 13			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0014016~neuroblast differentiation	5.291333333	2.33E-08
GOTERM_BP_FAT	GO:0014017~neuroblast fate commitment	5.22600823	1.20E-07
GOTERM_BP_FAT	GO:0007400~neuroblast fate determination	5.07968	3.00E-06
GOTERM_BP_FAT	GO:0007419~ventral cord development	4.096516129	3.16E-04
Cluster 14			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048565~gut development	3.962459665	8.58E-13

GOTERM_BP_FAT	GO:0035239~tube morphogenesis	3.191597884	6.47E-08
GOTERM_BP_FAT	GO:0048567~ectodermal gut morphogenesis	3.680927536	1.95E-05
GOTERM_BP_FAT	GO:0007439~ectodermal gut development	3.680927536	1.95E-05
GOTERM_BP_FAT	GO:0048547~gut morphogenesis	3.602609929	3.32E-05
GOTERM_BP_FAT	GO:0055123~digestive system development	3.527555556	5.53E-05
GOTERM_BP_FAT	GO:0048546~digestive tract morphogenesis	3.527555556	5.53E-05
GOTERM_BP_FAT	GO:0007442~hindgut morphogenesis	3.527555556	5.28E-04

Cluster 15

Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	3.422930977	1.06E-14
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	2.682412037	8.58E-13
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	3.469726776	1.00E-06
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	1.978872629	3.99E-05
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	1.95503079	6.78E-05
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	1.95503079	6.78E-05
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	1.976794418	6.84E-04
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	1.929873443	7.99E-04
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.929873443	7.99E-04

Cluster 16

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035215~genital disc development	5.795269841	7.29E-11
GOTERM_BP_FAT	GO:0035225~determination of genital disc primordium	7.055111111	5.01E-04
GOTERM_BP_FAT	GO:0007445~determination of imaginal disc primordium	7.055111111	5.01E-04

Cluster 17

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	2.615256705	5.11E-06
GOTERM_BP_FAT	GO:0010604~positive	2.434510172	5.21E-06

	regulation of macromolecule metabolic process GO:0010557~positive		
GOTERM_BP_FAT	regulation of macromolecule biosynthetic process GO:0010628~positive	2.515776055	5.37E-06
GOTERM_BP_FAT	regulation of gene expression GO:0045935~positive	2.592904084	6.91E-06
GOTERM_BP_FAT	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process GO:0051173~positive	2.507188246	2.20E-05
GOTERM_BP_FAT	regulation of nitrogen compound metabolic process GO:0009891~positive	2.507188246	2.20E-05
GOTERM_BP_FAT	regulation of biosynthetic process GO:0031328~positive	2.259480029	8.00E-05
GOTERM_BP_FAT	regulation of cellular biosynthetic process GO:0016563~transcription	2.259480029	8.00E-05
GOTERM_MF_FAT	activator activity	2.525962206	2.81E-04
Cluster 18			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035295~tube development	3.420659933	3.43E-12
GOTERM_BP_FAT	GO:0007424~open tracheal system development	2.858933914	6.29E-12
GOTERM_BP_FAT	GO:0060541~respiratory system development	2.858933914	6.29E-12
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	3.191597884	6.47E-08
Cluster 19			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0001667~ameboidal cell migration	4.188972222	7.80E-05
GOTERM_BP_FAT	GO:0007427~epithelial cell migration, open tracheal system	4.135754789	6.69E-04
GOTERM_BP_FAT	GO:0010631~epithelial cell migration	4.135754789	6.69E-04
Cluster 20			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	2.269476301	1.95E-04
GOTERM_BP_FAT	GO:0030029~actin filament- based process	2.253716049	2.46E-04
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	1.608261888	7.66E-04
Cluster 21			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	3.057214815	1.64E-07
GOTERM_BP_FAT	GO:0050767~regulation of	3.369605307	5.89E-07

GOTERM_BP_FAT	neurogenesis GO:0060284~regulation of cell development	2.58507888	7.94E-07
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	3.266255144	1.70E-04
Cluster 22			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	6.3496	6.41E-09
GOTERM_BP_FAT	GO:0010002~cardioblast differentiation	6.512410256	6.72E-05
Cluster 23			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007447~imaginal disc pattern formation	3.01312037	8.46E-08
Cluster 24			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007365~periodic partitioning	3.135604938	8.26E-04
Cluster 25			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007498~mesoderm development	3.023619048	2.44E-07
GOTERM_BP_FAT	GO:0001704~formation of primary germ layer	4.233066667	1.64E-04
GOTERM_BP_FAT	GO:0048332~mesoderm morphogenesis	4.442106996	1.70E-04
GOTERM_BP_FAT	GO:0001707~mesoderm formation	4.341606838	7.25E-04
Cluster 26			
Category	Term	Fold Enrichment	Bonferroni
UP_SEQ_FEATURE	DNA-binding region:Basic motif	3.431028431	2.80E-05
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	3.622159091	3.83E-05
INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHLH	3.200251099	1.04E-04
Cluster 27			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	2.755902778	2.19E-08
GOTERM_BP_FAT	GO:0001751~compound eye photoreceptor cell differentiation	2.733061061	1.05E-06
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	2.676076628	1.39E-06
Cluster 28			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0010941~regulation of cell death	2.453951691	1.55E-04
Cluster 30			

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035218~leg disc development	3.735058824	1.17E-06
Cluster 31			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	2.95551952	5.33E-05
Cluster 32			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0040007~growth	2.437220202	4.28E-04
Cluster 33			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_CC_FAT	GO:0005938~cell cortex	2.529186992	0.004420148
GOTERM_CC_FAT	GO:0045177~apical part of cell	2.887893801	0.012972582
GOTERM_CC_FAT	GO:0045179~apical cortex	3.979490022	0.02123214
GOTERM_CC_FAT	GO:0044448~cell cortex part	2.854851538	0.026635235
Cluster 34			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0001703~gastrulation with mouth forming first	3.527555556	0.005058133
GOTERM_BP_FAT	GO:0010004~gastrulation involving germ band extension	3.527555556	0.005058133
GOTERM_BP_FAT	GO:0007370~ventral furrow formation	4.535428571	0.423844247
GOTERM_BP_FAT	GO:0007377~germ-band extension	5.291333333	0.99636596
Cluster 35			
Category	Term	Fold Enrichment	Bonferroni
INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	4.4689897	3.12E-04
Cluster 36			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc finger	3.405308604	4.85E-05
Cluster 37			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007365~periodic partitioning	3.135604938	8.26E-04
Cluster 38			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007435~salivary gland morphogenesis	2.475477583	1.18E-04
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	2.475477583	1.18E-04
Cluster 39			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035218~leg disc development	3.735058824	1.17E-06
Cluster 40			

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0010941~regulation of cell death	2.453951691	1.55E-04
Cluster 41			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	2.95551952	5.33E-05
Cluster 42			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc-finger	1.779511863	2.45E-04

B. Stg11 Top 2000 genes +/- 3kb from Yan bound region

Cluster1			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	dna-binding	3.210500953	5.65E-47
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	2.408069822	3.54E-41
GOTERM_MF_FAT	GO:0003700~transcription factor activity	2.910388735	1.63E-38
GOTERM_BP_FAT	GO:0045449~regulation of transcription	2.223291648	9.46E-37
GOTERM_MF_FAT	GO:0003677~DNA binding	2.138657366	1.14E-34
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	2.345325656	3.83E-32
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	2.20086198	4.03E-29
SP_PIR_KEYWORDS	transcription regulation	2.783406778	3.22E-29
SP_PIR_KEYWORDS	nucleus	2.036421481	7.25E-26
SP_PIR_KEYWORDS	Transcription	2.62344436	5.92E-25
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2.825795311	1.41E-19
GOTERM_BP_FAT	GO:0006350~transcription	2.182778334	9.20E-18
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	2.637692707	5.42E-18
Cluster 2			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007444~imaginal disc development	2.91469218	6.56E-40
GOTERM_BP_FAT	GO:0048569~post-embryonic organ development	3.301610555	4.61E-39
GOTERM_BP_FAT	GO:0009886~post-embryonic morphogenesis	2.979135229	1.15E-35
GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	2.989692956	2.47E-35
GOTERM_BP_FAT	GO:0007560~imaginal disc morphogenesis	3.22756188	6.33E-35
GOTERM_BP_FAT	GO:0048563~post-embryonic organ morphogenesis	3.22756188	6.33E-35
GOTERM_BP_FAT	GO:0007552~metamorphosis	2.924697171	8.37E-35
GOTERM_BP_FAT	GO:0009791~post-embryonic development	2.701453036	7.62E-34
GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	2.651865686	1.24E-30
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	3.083025666	1.21E-25

GOTERM_BP_FAT	GO:0048736~appendage development	3.061779884	1.29E-25
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	3.091994022	1.71E-25
GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	3.070338318	1.84E-25
GOTERM_BP_FAT	GO:0035220~wing disc development	2.832141253	1.00E-23
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	3.040841618	3.83E-23
GOTERM_BP_FAT	GO:0007476~imaginal disc-derived wing morphogenesis	2.966115825	2.47E-20
GOTERM_BP_FAT	GO:0007472~wing disc morphogenesis	2.939151135	5.34E-20

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0030182~neuron differentiation	2.883951731	2.19E-38
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	2.716862394	3.69E-35
GOTERM_BP_FAT	GO:0048666~neuron development	2.928260909	2.73E-33
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	2.455423898	8.97E-31
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	2.954820639	2.67E-29
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	3.006232353	7.69E-29
GOTERM_BP_FAT	GO:0031175~neuron projection development	2.995757676	1.15E-28
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	2.98535574	1.71E-28
GOTERM_BP_FAT	GO:0030030~cell projection organization	2.647580972	4.42E-26
GOTERM_BP_FAT	GO:0006928~cell motion	2.818958862	1.06E-25
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	2.753435542	2.71E-25
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	2.661931641	1.07E-23
GOTERM_BP_FAT	GO:0007409~axonogenesis	3.15806227	7.65E-22
GOTERM_BP_FAT	GO:0007411~axon guidance	3.605067407	1.63E-20
GOTERM_BP_FAT	GO:0016358~dendrite development	2.915134403	5.71E-09
GOTERM_BP_FAT	GO:0048813~dendrite morphogenesis	2.915134403	5.71E-09

Cluster 4

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	3.221990656	1.04E-29
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	3.081206772	1.11E-23
GOTERM_BP_FAT	GO:0002009~morphogenesis of	3.031739779	1.74E-22

	an epithelium		
GOTERM_BP_FAT	GO:0060429~epithelium development	2.963203109	4.17E-22
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	3.079110713	4.41E-11
GOTERM_BP_FAT	GO:0007391~dorsal closure	3.291033313	3.60E-10
	GO:0001700~embryonic development via the syncytial blastoderm	2.423886579	3.79E-10
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	2.315677356	4.87E-09
Cluster 5			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	Homeobox	4.290958005	7.77E-22
	GO:0043565~sequence-specific DNA binding	2.825795311	1.41E-19
GOTERM_MF_FAT	IPR017970:Homeobox, conserved site	4.100168166	3.81E-19
INTERPRO	IPR001356:Homeobox	3.970073703	1.22E-18
INTERPRO	IPR012287:Homeodomain-related	3.683821758	6.11E-16
SMART	SM00389:HOX	3.171821064	5.63E-15
UP_SEQ_FEATURE	DNA-binding region:Homeobox	3.93258427	1.55E-12
Cluster 6			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0006928~cell motion	2.818958862	1.06E-25
GOTERM_BP_FAT	GO:0016477~cell migration	2.72044507	7.71E-12
GOTERM_BP_FAT	GO:0048870~cell motility	2.545871055	3.15E-10
GOTERM_BP_FAT	GO:0051674~localization of cell	2.501475344	3.44E-10
Cluster 7			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007155~cell adhesion	2.817753836	2.75E-13
	GO:0022610~biological adhesion	2.607921103	3.28E-11
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	3.372168187	9.57E-06
Cluster 8			
Category	Term	Fold Enrichment	Bonferroni
	GO:0007167~enzyme linked receptor protein signaling pathway	2.989269287	1.10E-12
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	2.998710504	5.40E-09
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	4.342335621	1.81E-06
Cluster 9			
Category	Term	Fold Enrichment	Bonferroni
	GO:0007447~imaginal disc pattern formation	3.848888392	2.47E-16
GOTERM_BP_FAT	GO:0035222~wing disc pattern formation	3.552820054	2.36E-08

GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	2.684352929	4.12E-08
GOTERM_BP_FAT	GO:0007450~dorsal/ventral pattern formation, imaginal disc	3.61515023	6.24E-07
GOTERM_BP_FAT	GO:0048190~wing disc dorsal/ventral pattern formation	3.268594449	6.33E-04
Cluster 10			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048859~formation of anatomical boundary	5.16773826	5.09E-14
GOTERM_BP_FAT	GO:0048645~organ formation	5.329230081	2.75E-13
GOTERM_BP_FAT	GO:0010160~formation of organ boundary	5.235734816	4.68E-12
GOTERM_BP_FAT	GO:0008052~sensory organ boundary specification	4.943053988	6.10E-05
GOTERM_BP_FAT	GO:0007432~salivary gland boundary specification	5.684512086	7.98E-04
Cluster 11			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0014016~neuroblast differentiation	5.583002942	1.19E-09
GOTERM_BP_FAT	GO:0014017~neuroblast fate commitment	5.526608972	6.45E-09
GOTERM_BP_FAT	GO:0007400~neuroblast fate determination	5.400286482	1.83E-07
GOTERM_BP_FAT	GO:0007419~ventral cord development	4.58428394	3.67E-06
Cluster 12			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007423~sensory organ development	2.616955259	9.37E-29
GOTERM_BP_FAT	GO:0001654~eye development	2.482693532	5.27E-19
GOTERM_BP_FAT	GO:0048749~compound eye development	2.46851783	4.55E-17
GOTERM_BP_FAT	GO:0048592~eye morphogenesis	2.377351709	1.65E-12
GOTERM_BP_FAT	GO:0001745~compound eye morphogenesis	2.387495076	1.16E-11
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	2.99769192	4.96E-11
GOTERM_BP_FAT	GO:0001751~compound eye photoreceptor cell differentiation	2.816650133	2.04E-07
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	2.756498318	2.78E-07
GOTERM_BP_FAT	GO:0042461~photoreceptor cell development	3.15806227	5.48E-05
Cluster 13			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035218~leg disc development	4.876419682	2.08E-14

GOTERM_BP_FAT	GO:0007449~proximal/distal pattern formation, imaginal disc	6.090548664	2.50E-08
GOTERM_BP_FAT	GO:0009954~proximal/distal pattern formation	5.560935736	3.19E-07
GOTERM_BP_FAT	GO:0007479~leg disc proximal/distal pattern formation	5.773332587	1.48E-04
GOTERM_BP_FAT	GO:0035223~leg disc pattern formation	5.773332587	1.48E-04

Cluster 14

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	2.79367047	9.82E-08
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	2.756498318	2.78E-07
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	2.64395911	3.25E-07
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	2.552025672	3.44E-07
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.642593428	1.37E-06
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	2.642593428	1.37E-06
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	2.368546702	6.69E-06
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	2.368546702	6.69E-06
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	2.826106861	2.12E-05
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	2.763304486	4.16E-05
GOTERM_MF_FAT	GO:0016563~transcription activator activity	2.630090444	6.04E-05

Cluster 15

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007498~mesoderm development	3.66994599	2.75E-13
GOTERM_BP_FAT	GO:0007369~gastrulation	3.848888392	1.87E-11
GOTERM_BP_FAT	GO:0048332~mesoderm morphogenesis	5.000265261	1.34E-06
GOTERM_BP_FAT	GO:0001704~formation of primary germ layer	4.737093405	1.63E-06
GOTERM_BP_FAT	GO:0001707~mesoderm formation	4.919289305	6.48E-06
GOTERM_BP_FAT	GO:0001710~mesodermal cell fate commitment	5.684512086	7.98E-04

GOTERM_BP_FAT	GO:0048333~mesodermal cell differentiation	5.684512086	7.98E-04
Cluster 16			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048732~gland development	3.400244959	1.64E-21
GOTERM_BP_FAT	GO:0007431~salivary gland development	3.322781345	9.27E-17
GOTERM_BP_FAT	GO:0035272~exocrine system development	3.322781345	9.27E-17
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	2.867188114	3.46E-08
GOTERM_BP_FAT	GO:0007435~salivary gland morphogenesis	2.867188114	3.46E-08
Cluster 17			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0051301~cell division	2.114361203	2.12E-05
GOTERM_BP_FAT	GO:0008356~asymmetric cell division	3.307797981	3.19E-05
GOTERM_BP_FAT	GO:0017145~stem cell division	3.483156915	3.56E-05
Cluster 18			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	7.105640107	2.48E-12
GOTERM_BP_FAT	GO:0010002~cardioblast differentiation	7.105640107	1.59E-06
Cluster 19			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007163~establishment or maintenance of cell polarity	2.868331786	1.01E-07
GOTERM_BP_FAT	GO:0001738~morphogenesis of a polarized epithelium	3.248292621	1.84E-06
GOTERM_BP_FAT	GO:0007164~establishment of tissue polarity	3.323605857	7.14E-06
GOTERM_BP_FAT	GO:0001736~establishment of planar polarity	3.261605295	2.35E-05
GOTERM_BP_FAT	GO:0042067~establishment of ommatidial polarity	3.552820054	9.90E-05
Cluster 20			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035218~leg disc development	4.876419682	2.08E-14
GOTERM_BP_FAT	GO:0035110~leg morphogenesis	4.737093405	2.03E-09
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	4.61866607	4.70E-09
GOTERM_BP_FAT	GO:0060173~limb development	4.61866607	4.70E-09
GOTERM_BP_FAT	GO:0007478~leg disc morphogenesis	4.813498137	3.50E-07
GOTERM_BP_FAT	GO:0035127~post-embryonic limb morphogenesis	4.655419381	7.49E-06
GOTERM_BP_FAT	GO:0007480~imaginal disc-	4.655419381	7.49E-06

GOTERM_BP_FAT	derived leg morphogenesis GO:0035109~imaginal disc- derived limb morphogenesis	4.500238735	1.63E-05
Cluster 21			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0060541~respiratory system development	3.018735993	3.81E-14
GOTERM_BP_FAT	GO:0007424~open tracheal system development	3.018735993	3.81E-14
GOTERM_BP_FAT	GO:0035295~tube development	3.373384697	1.46E-11
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	3.129865285	2.46E-07
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	3.891183868	1.13E-05
GOTERM_BP_FAT	GO:0060446~branching involved in open tracheal system development	3.643918004	5.82E-04
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	3.643918004	5.82E-04
Cluster 22			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048565~gut development	3.893501429	4.68E-12
GOTERM_BP_FAT	GO:0048567~ectodermal gut morphogenesis	3.707290491	1.64E-05
GOTERM_BP_FAT	GO:0007439~ectodermal gut development	3.707290491	1.64E-05
GOTERM_BP_FAT	GO:0048547~gut morphogenesis	3.62841197	2.78E-05
GOTERM_BP_FAT	GO:0048546~digestive tract morphogenesis	3.552820054	4.64E-05
GOTERM_BP_FAT	GO:0055123~digestive system development	3.552820054	4.64E-05
GOTERM_BP_FAT	GO:0007442~hindgut morphogenesis	3.552820054	4.51E-04
Cluster 23			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035215~genital disc development	5.583002942	1.19E-09
GOTERM_BP_FAT	GO:0007445~determination of imaginal disc primordium	7.105640107	4.53E-04
GOTERM_BP_FAT	GO:0035225~determination of genital disc primordium	7.105640107	4.53E-04
Cluster 24			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	1.755345876	1.59E-07
GOTERM_BP_FAT	GO:0030707~ovarian follicle cell development	2.159557288	6.36E-06
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	1.676931065	1.15E-05
GOTERM_BP_FAT	GO:0007276~gamete generation	1.480755771	5.51E-04
GOTERM_BP_FAT	GO:0007292~female gamete	1.561679144	5.94E-04

GOTERM_BP_FAT	generation GO:0019953~sexual reproduction	1.469465709	6.66E-04
GOTERM_BP_FAT	GO:0048477~oogenesis	1.55559468	9.67E-04
Cluster 25			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	4.073900328	3.36E-14
GOTERM_BP_FAT	GO:0008356~asymmetric cell division	3.307797981	3.19E-05
Cluster 26			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	3.333975724	2.03E-13
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	2.627606498	8.26E-12
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	3.611063005	1.37E-07
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	1.877506532	8.94E-04
Cluster 27			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0001667~ameboidal cell migration	3.99692256	5.07E-04
GOTERM_BP_FAT	GO:0007427~epithelial cell migration, open tracheal system	4.165375235	5.82E-04
GOTERM_BP_FAT	GO:0010631~epithelial cell migration	4.165375235	5.82E-04
Cluster 28			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	3.372168187	9.57E-06
SP_PIR_KEYWORDS	cell adhesion	3.679802067	2.02E-05
Cluster 29			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_CC_FAT	GO:0005912~adherens junction	3.358703627	1.21E-04
GOTERM_CC_FAT	GO:0070161~anchoring junction	3.288730635	1.87E-04
GOTERM_CC_FAT	GO:0030054~cell junction	2.195461971	4.38E-04
Cluster 30			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0040008~regulation of growth	2.759471886	3.40E-06
Cluster 31			
Category	Term	Fold Enrichment	Bonferroni
INTERPRO	IPR001092:Basic helix-loop- helix dimerisation region bHLH	3.186633009	1.19E-04
UP_SEQ_FEATURE	DNA-binding region:Basic motif	3.162010325	8.88E-04

Cluster 32			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007389~pattern specification process	2.605401373	5.23E-34
GOTERM_BP_FAT	GO:0003002~regionalization	2.629399864	8.19E-33
GOTERM_BP_FAT	GO:0035282~segmentation	2.377656497	4.41E-12
GOTERM_BP_FAT	GO:0009880~embryonic pattern specification	2.430067396	2.78E-11
GOTERM_BP_FAT	GO:0007350~blastoderm segmentation	2.444600954	1.02E-10
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	2.089894149	8.35E-04
Cluster 33			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	2.976687072	4.34E-05
Cluster 34			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0008038~neuron recognition	3.335300459	4.08E-04
GOTERM_BP_FAT	GO:0008037~cell recognition	3.268594449	6.33E-04
Cluster 35			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007365~periodic partitioning	3.289648198	1.42E-04
Cluster 36			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035287~head segmentation	5.07545722	1.20E-04
Cluster 37			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	3.15806227	2.67E-08
GOTERM_BP_FAT	GO:0060284~regulation of cell development	2.657834849	1.64E-07
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	3.393738559	4.71E-07
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	3.289648198	1.42E-04
Cluster 38			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035152~regulation of tube architecture, open tracheal system	4.113791641	7.04E-06
GOTERM_BP_FAT	GO:0048871~multicellular organismal homeostasis	5.433724788	4.38E-04
GOTERM_BP_FAT	GO:0001894~tissue homeostasis	5.433724788	4.38E-04
Cluster 39			
Category	Term	Fold Enrichment	Bonferroni

GOTERM_BP_FAT	GO:0017145~stem cell division	3.483156915	3.56E-05
GOTERM_BP_FAT	GO:0048103~somatic stem cell division	3.920353163	0.004190168
Cluster 40			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042659~regulation of cell fate specification	5.329230081	4.60E-05
GOTERM_BP_FAT	GO:0010453~regulation of cell fate commitment	5.329230081	4.60E-05
Cluster 41			
Category	Term	Fold Enrichment	Bonferroni
UP_SEQ_FEATURE	DNA-binding region:Basic motif	3.162010325	8.88E-04
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	3.307876873	0.001503761
Cluster 42			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007548~sex differentiation	3.079110713	3.56E-04
Cluster 43			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc finger	3.469902484	3.44E-05
Cluster 44			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	2.976687072	4.34E-05
Cluster 45			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc finger	3.469902484	3.44E-05
Cluster 46			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	egf-like domain	3.168171833	8.12E-04
Cluster 47			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_CC_FAT	GO:0030054~cell junction	2.195461971	4.38E-04
GOTERM_CC_FAT	GO:0005911~cell-cell junction	2.947044335	9.20E-04
Cluster 48			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc-finger	1.886777493	1.14E-05
SP_PIR_KEYWORDS	zinc	1.546827149	3.95E-04
Cluster 49			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048634~regulation of muscle development	3.875803695	9.09E-04
Cluster 50			
Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	glycoprotein	1.68032759	9.86E-05

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Cluster 1			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007444~imaginal disc development	2.437469694	2.68E-17
GOTERM_BP_FAT	GO:0048569~post-embryonic organ development	2.669424545	9.52E-16
GOTERM_BP_FAT	GO:0009791~post-embryonic development	2.273316387	1.92E-14
GOTERM_BP_FAT	GO:0007552~metamorphosis	2.409118781	3.22E-14
GOTERM_BP_FAT	GO:0009886~post-embryonic morphogenesis	2.420631153	5.09E-14
GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	2.41171353	2.75E-13
GOTERM_BP_FAT	GO:0007560~imaginal disc morphogenesis	2.574490785	2.75E-13
GOTERM_BP_FAT	GO:0048563~post-embryonic organ morphogenesis	2.574490785	2.75E-13
GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	2.170663643	2.12E-11
GOTERM_BP_FAT	GO:0035220~wing disc development	2.382532655	8.07E-10
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	2.500399847	5.21E-09
GOTERM_BP_FAT	GO:0048736~appendage development	2.435036048	5.76E-09
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	2.438883334	7.91E-09
GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	2.428846777	9.71E-09
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	2.43263877	1.34E-08
GOTERM_BP_FAT	GO:0007476~imaginal disc-derived wing morphogenesis	2.464931931	5.29E-08
GOTERM_BP_FAT	GO:0007472~wing disc morphogenesis	2.442523459	8.00E-08
Cluster 2			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048666~neuron development	2.437099988	4.69E-14
GOTERM_BP_FAT	GO:0006928~cell motion	2.512759957	2.75E-13
GOTERM_BP_FAT	GO:0030182~neuron differentiation	2.239967002	1.65E-12
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	2.052799554	9.75E-10
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	2.294036718	9.16E-09
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	2.279277881	1.83E-08
GOTERM_BP_FAT	GO:0007411~axon guidance	2.979548867	2.16E-08
GOTERM_BP_FAT	GO:0031175~neuron projection development	2.271336146	2.19E-08
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in	2.209543485	4.70E-08

	differentiation		
GOTERM_BP_FAT	GO:0007409~axonogenesis	2.535953318	7.85E-08
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	2.147218368	1.11E-07
GOTERM_BP_FAT	GO:0030030~cell projection organization	2.051434479	1.63E-07
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	2.102474257	2.45E-07
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	1.83664654	3.76E-07

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	1.757531472	7.09E-09
SP_PIR_KEYWORDS	transcription regulation	2.081635007	5.86E-09
GOTERM_BP_FAT	GO:0045449~regulation of transcription	1.67582397	5.43E-08
GOTERM_MF_FAT	GO:0003677~DNA binding	1.623340212	1.67E-07
SP_PIR_KEYWORDS	Transcription	2.003790177	8.10E-08
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	1.702053438	6.48E-07
GOTERM_MF_FAT	GO:0003700~transcription factor activity	1.956755528	4.17E-07
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	1.727274706	1.72E-06
GOTERM_BP_FAT	GO:0006350~transcription	1.861618294	1.83E-06
SP_PIR_KEYWORDS	nucleus	1.604081705	4.57E-07
SP_PIR_KEYWORDS	dna-binding	1.910170608	7.81E-07
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2.09219313	1.04E-04
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	2.008564611	1.52E-04
SP_PIR_KEYWORDS	DNA binding	2.502069372	2.78E-04

Cluster 4

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0006928~cell motion	2.512759957	2.75E-13
GOTERM_BP_FAT	GO:0016477~cell migration	2.46654828	6.42E-06
GOTERM_BP_FAT	GO:0048870~cell motility	2.355374599	2.29E-05
GOTERM_BP_FAT	GO:0051674~localization of cell	2.247219643	1.18E-04

Cluster 5

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	2.567835109	6.39E-11
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	2.42739672	7.15E-08
GOTERM_BP_FAT	GO:0060429~epithelium development	2.361588778	1.71E-07
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	2.33869938	7.90E-07

Cluster 6			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007423~sensory organ development	2.105589995	7.98E-10
GOTERM_BP_FAT	GO:0042461~photoreceptor cell development	3.775329	2.64E-06
GOTERM_BP_FAT	GO:0001654~eye development	2.016541193	4.49E-06
GOTERM_BP_FAT	GO:0048749~compound eye development	2.059270363	4.97E-06
Cluster 7			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007155~cell adhesion	2.430096827	1.62E-05
GOTERM_BP_FAT	GO:0022610~biological adhesion	2.24913217	2.23E-04
Cluster 8			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007292~female gamete generation	1.629522346	0.001014734
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	1.653882599	0.001207502
Cluster 9			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	2.4795988	4.47E-04
Cluster 10			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048645~organ formation	4.184322974	2.01E-04
GOTERM_BP_FAT	GO:0010160~formation of organ boundary	4.172732052	5.14E-04
Cluster 11			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007424~open tracheal system development	2.648487882	1.78E-06
GOTERM_BP_FAT	GO:0060541~respiratory system development	2.648487882	1.78E-06
Cluster 12			
Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048732~gland development	2.377916834	1.52E-04
GOTERM_BP_FAT	GO:0035272~exocrine system development	2.471618266	3.28E-04
GOTERM_BP_FAT	GO:0007431~salivary gland development	2.471618266	3.28E-04
Cluster 13			
Category	Term	Fold Enrichment	Bonferroni

GOTERM_BP_FAT	GO:0007389~pattern specification process	2.20227525	1.53E-14
GOTERM_BP_FAT	GO:0003002~regionalization	2.211976903	8.36E-14
GOTERM_BP_FAT	GO:0009952~anterior/posterior pattern formation	2.331820853	1.96E-04

Cluster 14

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	2.936367	2.20E-04
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	3.155498865	0.001335707
GOTERM_BP_FAT	GO:0060284~regulation of cell development	2.420821649	0.001865557
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	3.0994985	0.035862728
GOTERM_BP_FAT	GO:0046532~regulation of photoreceptor cell differentiation	4.614290999	0.086528316

Cluster 15

Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	2.09219313	1.04E-04

Cluster 16

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	3.05382168	8.21E-04