Table S7 GO analysis implicates Yan HDRs in multiple aspects of development. DAVID was used to perform GO analysis of genes assigned as single-peak (A), multiple-peak (B), or high-density genes (C; see Materials and Methods for details on assigning genes) at stage 11 of embryogenesis. Only clusters that contain a GO-term with a p-value <0.0001 (Bonferroni-corrected) are shown.

A. Stg11 single peak genes +/- 3kb from Yan bound region

Cluster 1

Category	Term	Fold Enrichment	Bonferroni
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	1.334179681	**0.019328277**

Cluster 2

Category	Term	Fold Enrichment	Bonferroni
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	1.42692377	**0.057959603**

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_CC_FAT	GO:0022626~cytosolic ribosome	2.494825855	**0.005017369**

B. Stg11 multiple peaks +/- 3kb from Yan bound region

Cluster 1

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	dna-binding	3.823803027	8.88E-16
SP_PIR_KEYWORDS	nucleus	2.607485814	4.40E-13
GOTERM_MF_FAT	GO:0003700~transcription factor activity	3.321992784	1.59E-12
GOTERM_BP_FAT	GO:0045449~regulation of transcription	2.499234712	1.25E-11
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	2.549370415	1.66E-11
GOTERM_MF_FAT	GO:0003677~DNA binding	2.292939116	2.44E-10

SP_PIR_KEYWORDS	transcription regulation	3.397375924	1.23E-10
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	3.881873307	5.95E-10
SP_PIR_KEYWORDS	Homeobox	6.455570292	3.24E-10
INTERPRO	IPR017970:Homeobox, conserved site	6.136061542	7.21E-09
SP_PIR_KEYWORDS	Transcription	3.203145565	3.15E-09
INTERPRO	IPR001356:Homeobox	5.835274211	2.09E-08
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	2.478144124	8.30E-08
INTERPRO	IPR012287:Homeodomain-related	5.615075184	4.67E-08
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	2.311472484	6.36E-07
GOTERM_BP_FAT	GO:0006350~transcription	2.533213993	1.34E-05
SMART	SM00389:HOX	4.216142271	1.80E-06
SP_PIR_KEYWORDS	DNA binding	4.77607233	2.90E-06
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	2.651248715	0.001801188

Cluster 2

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048569~post-embryonic organ development	3.829859101	1.63E-11
GOTERM_BP_FAT	GO:0048563~post-embryonic organ morphogenesis	3.827162017	7.53E-11
GOTERM_BP_FAT	GO:0007560~imaginal disc morphogenesis	3.827162017	7.53E-11
GOTERM_BP_FAT	GO:0007444~imaginal disc development	3.128957702	6.67E-10
GOTERM_BP_FAT	GO:0007552~metamorphosis	3.142177218	1.92E-08
GOTERM_BP_FAT	GO:0009886~post-embryonic	3.150682954	3.15E-08

	morphogenesis		
GOTERM_BP_FAT	GO:0009791~post-embryonic development	2.853862749	6.22E-08
GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	3.13231704	6.82E-08
GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	2.842158596	2.01E-07
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	3.490139381	1.33E-06
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	3.446873191	1.83E-06
GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	3.432688527	2.04E-06
GOTERM_BP_FAT	GO:0048736~appendage development	3.390826472	2.79E-06
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	3.311406559	3.11E-05
GOTERM_BP_FAT	GO:0035220~wing disc development	2.878527552	2.52E-04
GOTERM_BP_FAT	GO:0007476~imaginal disc-derived wing morphogenesis	3.130646292	5.78E-04
GOTERM_BP_FAT	GO:0007472~wing disc morphogenesis	3.102185871	6.92E-04

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007423~sensory organ development	3.452477862	5.00E-13
GOTERM_BP_FAT	GO:0001654~eye development	3.426108894	9.42E-10
GOTERM_BP_FAT	GO:0048749~compound eye development	3.5289416	1.27E-09

GOTERM_BP_FAT	GO:0048592~eye morphogenesis	3.382804916	4.53E-07
GOTERM_BP_FAT	GO:0001745~compound eye morphogenesis	3.437681529	1.04E-06
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	4.344496417	3.34E-05
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	4.358115528	1.64E-04
GOTERM_BP_FAT	GO:0001751~compound eye photoreceptor cell differentiation	4.326705687	4.16E-04

Cluster 4

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	3.490139381	1.33E-06
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	3.446873191	1.83E-06
GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	3.432688527	2.04E-06
GOTERM_BP_FAT	GO:0048736~appendage development	3.390826472	2.79E-06
GOTERM_BP_FAT	GO:0035110~leg morphogenesis	8.425690021	2.58E-05
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	3.311406559	3.11E-05
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	8.215047771	3.56E-05
GOTERM_BP_FAT	GO:0060173~limb development	8.215047771	3.56E-05

Cluster 5

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0003002~regionalization	2.616789192	3.10E-06
GOTERM_BP_FAT	GO:0007389~pattern specification process	2.475046444	1.84E-05

Cluster 6

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007498~mesoderm development	4.999860013	1.07E-04
GOTERM_BP_FAT	GO:0001704~formation of primary germ layer	9.268259023	1.76E-04
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	3.131672397	3.30E-04
GOTERM_BP_FAT	GO:0001707~mesoderm formation	9.721950024	5.33E-04
GOTERM_BP_FAT	GO:0048332~mesoderm morphogenesis	9.361877801	7.72E-04

Cluster 7

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0030182~neuron differentiation	3.090106365	1.94E-09
GOTERM_BP_FAT	GO:0006928~cell motion	3.066398663	3.80E-06
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	2.516269418	3.76E-05
GOTERM_BP_FAT	GO:0048666~neuron development	2.695249546	1.16E-04
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	2.195884465	0.001274019
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in	2.669525551	0.001330054

differentiation

Cluster 8

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	3.581771062	1.77E-07

C. Stg 11 high-density genes +/- 3kb from Yan bound region

Cluster 1

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007389~pattern specification process	4.152904186	3.68E-37
GOTERM_BP_FAT	GO:0007444~imaginal disc development	4.438839426	2.92E-36
GOTERM_BP_FAT	GO:0003002~regionalization	4.108761851	6.33E-34
GOTERM_BP_FAT	GO:0048569~post-embryonic organ development	4.987641391	2.90E-32
GOTERM_BP_FAT	GO:0009791~post-embryonic development	3.918861093	1.06E-28
GOTERM_BP_FAT	GO:0048563~post-embryonic organ morphogenesis	4.700793471	8.08E-27
GOTERM_BP_FAT	GO:0007560~imaginal disc morphogenesis	4.700793471	8.08E-27
GOTERM_BP_FAT	GO:0009886~post-embryonic morphogenesis	4.19640083	1.55E-26
GOTERM_BP_FAT	GO:0048707~instar larval or pupal morphogenesis	4.216257852	2.66E-26
GOTERM_BP_FAT	GO:0007552~metamorphosis	4.041551035	5.66E-25
GOTERM_BP_FAT	GO:0048736~appendage development	4.832199993	3.60E-24
GOTERM_BP_FAT	GO:0002165~instar larval or pupal development	3.718855423	4.16E-24
GOTERM_BP_FAT	GO:0035220~wing disc	4.490652213	7.74E-24

	development		
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	4.836500743	9.22E-24
GOTERM_BP_FAT	GO:0048737~imaginal disc-derived appendage development	4.816597447	1.18E-23
GOTERM_BP_FAT	GO:0035114~imaginal disc-derived appendage morphogenesis	4.820691051	3.03E-23
GOTERM_BP_FAT	GO:0035120~post-embryonic appendage morphogenesis	4.871480893	1.19E-22
GOTERM_BP_FAT	GO:0007476~imaginal disc-derived wing morphogenesis	4.78172959	1.71E-20
GOTERM_BP_FAT	GO:0007472~wing disc morphogenesis	4.738259321	2.79E-20

Cluster 2

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	developmental protein	4.994181682	1.37E-50
SP_PIR_KEYWORDS	dna-binding	4.627001102	3.15E-32
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	3.194881365	7.20E-28
GOTERM_BP_FAT	GO:0045449~regulation of transcription	2.838190595	1.33E-25
GOTERM_MF_FAT	GO:0003677~DNA binding	2.812705367	6.12E-25
GOTERM_MF_FAT	GO:0003700~transcription factor activity	3.950923113	1.77E-24
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	3.107767838	8.59E-24
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	2.886162201	6.87E-22
SP_PIR_KEYWORDS	nucleus	2.699709203	2.60E-19
SP_PIR_KEYWORDS	transcription regulation	3.739262518	3.52E-18

GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	4.087725504	2.02E-16
SP_PIR_KEYWORDS	Transcription	3.459012448	3.00E-15
GOTERM_BP_FAT	GO:0006350~transcription	2.629649709	7.04E-10

Cluster 3

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	3.84793148	4.80E-28
GOTERM_BP_FAT	GO:0030182~neuron differentiation	3.979544353	8.89E-28
GOTERM_BP_FAT	GO:0048666~neuron development	4.163554629	1.59E-25
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	3.424590324	3.18E-25
GOTERM_BP_FAT	GO:0006928~cell motion	4.257210848	3.91E-23
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	4.348200187	1.47E-22
GOTERM_BP_FAT	GO:0031175~neuron projection development	4.333049664	1.83E-22
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	4.164598257	8.93E-22
GOTERM_BP_FAT	GO:0030030~cell projection organization	3.807916167	8.93E-22
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	4.254504288	1.36E-21
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	4.000504032	4.66E-21
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	3.867556768	3.72E-20
GOTERM_BP_FAT	GO:0007409~axonogenesis	4.895277661	2.54E-19

GOTERM_BP_FAT	GO:0007411~axon guidance	5.109887503	1.99E-13

Cluster 4

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	4.738595869	3.18E-23
GOTERM_BP_FAT	GO:0002009~morphogenesis of an epithelium	4.795524834	2.09E-21
GOTERM_BP_FAT	GO:0060429~epithelium development	4.591459947	2.30E-20
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	4.612464826	1.17E-19
GOTERM_BP_FAT	GO:0001700~embryonic development via the syncytial blastoderm	4.101985443	7.66E-14
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	3.918861093	7.95E-13
GOTERM_BP_FAT	GO:0016331~morphogenesis of embryonic epithelium	5.181605223	5.17E-12
GOTERM_BP_FAT	GO:0007391~dorsal closure	5.582658259	1.02E-10

Cluster 5

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048732~gland development	5.497625173	5.39E-20
GOTERM_BP_FAT	GO:0007431~salivary gland development	5.262739117	5.37E-15
GOTERM_BP_FAT	GO:0035272~exocrine system development	5.262739117	5.37E-15
GOTERM_BP_FAT	GO:0007435~salivary gland morphogenesis	4.170951572	2.58E-06
GOTERM_BP_FAT	GO:0022612~gland	4.170951572	2.58E-06

morphogenesis

Cluster 6

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007447~imaginal disc pattern formation	7.62000768	1.18E-21
GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	4.876804916	5.17E-12
GOTERM_BP_FAT	GO:0035222~wing disc pattern formation	6.992477636	7.15E-12
GOTERM_BP_FAT	GO:0007450~dorsal/ventral pattern formation, imaginal disc	7.05853343	1.14E-09
GOTERM_BP_FAT	GO:0048190~wing disc dorsal/ventral pattern formation	6.583686636	8.18E-07

Cluster 7

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	4.918846337	1.99E-13
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	2.446168071	1.23E-11
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	5.36895954	1.31E-11
GOTERM_BP_FAT	GO:0007173~epidermal growth factor receptor signaling pathway	8.636008705	2.24E-08

Cluster 8

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0006928~cell motion	4.257210848	3.91E-23
GOTERM_BP_FAT	GO:0016477~cell migration	4.389124424	9.94E-13
GOTERM_BP_FAT	GO:0048870~cell motility	4.107469381	1.11E-11
GOTERM_BP_FAT	GO:0051674~localization of cell	4.012167309	1.21E-11

Cluster 9

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007449~proximal/distal pattern formation, imaginal disc	14.80458635	1.99E-13
GOTERM_BP_FAT	GO:0009954~proximal/distal pattern formation	13.51723102	1.39E-12
GOTERM_BP_FAT	GO:0035218~leg disc development	8.247537725	6.16E-12
GOTERM_BP_FAT	GO:0035223~leg disc pattern formation	14.85901498	1.60E-09
GOTERM_BP_FAT	GO:0007479~leg disc proximal/distal pattern formation	14.85901498	1.60E-09
GOTERM_BP_FAT	GO:0007474~imaginal disc-derived wing vein specification	8.001008065	7.62E-06

Cluster 10

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007423~sensory organ development	3.523788918	1.62E-20
GOTERM_BP_FAT	GO:0001654~eye development	3.470316751	2.86E-15
GOTERM_BP_FAT	GO:0048749~compound eye development	3.384470944	7.95E-13
GOTERM_BP_FAT	GO:0048592~eye morphogenesis	3.127319137	1.43E-08

GOTERM_BP_FAT	GO:0001745~compound eye morphogenesis	3.072387097	2.46E-07
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	4.143379176	2.76E-07
GOTERM_BP_FAT	GO:0001751~compound eye photoreceptor cell differentiation	3.954166148	3.74E-05
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	3.783727952	8.95E-05

Cluster 11

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	Homeobox	6.113890333	2.26E-12
INTERPRO	IPR001356:Homeobox	5.575501914	1.99E-10
INTERPRO	IPR017970:Homeobox, conserved site	5.653509673	4.02E-10
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	3.55256917	5.60E-10
INTERPRO	IPR012287:Homeodomain-related	5.1734947	3.76E-09
UP_SEQ_FEATURE	DNA-binding region:Homeobox	5.542986425	6.95E-08
SMART	SM00389:HOX	4.138235294	3.22E-08

Cluster 12

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048645~organ formation	10.05841014	1.99E-13
GOTERM_BP_FAT	GO:0010160~formation of organ boundary	10.1065365	7.95E-13
GOTERM_BP_FAT	GO:0048859~formation of anatomical boundary	9.144009217	2.19E-12
GOTERM_BP_FAT	GO:0008052~sensory organ	9.541574835	1.50E-05

	boundary specification		
GOTERM_BP_FAT	GO:0016360~sensory organ precursor cell fate determination	9.62527286	4.00E-04
GOTERM_BP_FAT	GO:0007432~salivary gland boundary specification	10.97281106	6.04E-04

Cluster 13

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0060541~respiratory system development	5.020240354	4.43E-15
GOTERM_BP_FAT	GO:0007424~open tracheal system development	5.020240354	4.43E-15
GOTERM_BP_FAT	GO:0035295~tube development	5.541823768	4.25E-11
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	5.442862629	1.41E-08
GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	7.402293175	3.76E-07
GOTERM_BP_FAT	GO:0048754~branching morphogenesis of a tube	6.564929694	1.25E-04
GOTERM_BP_FAT	GO:0060446~branching involved in open tracheal system development	6.564929694	1.25E-04
GOTERM_BP_FAT	GO:0060562~epithelial tube morphogenesis	6.096006144	3.39E-04

Cluster 14

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0014016~neuroblast differentiation	10.45029625	3.10E-09
GOTERM_BP_FAT	GO:0014017~neuroblast fate commitment	10.16001024	3.15E-08

GOTERM_BP_FAT	GO:0007400~neuroblast fate determination	9.509769585	2.91E-06

Cluster 15

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007155~cell adhesion	3.783727952	1.68E-08
GOTERM_BP_FAT	GO:0022610~biological adhesion	3.501960977	1.66E-07
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	6.199328282	2.23E-07

Cluster 16

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035215~genital disc development	12.40972679	1.99E-13
GOTERM_BP_FAT	GO:0035225~determination of genital disc primordium	18.28801843	6.74E-08
GOTERM_BP_FAT	GO:0007445~determination of imaginal disc primordium	18.28801843	6.74E-08

Cluster 17

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0030707~ovarian follicle cell development	3.585885967	5.54E-09
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	2.421536038	2.11E-08
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	2.304290323	8.21E-07
GOTERM_BP_FAT	GO:0007292~female gamete generation	2.210639591	1.66E-06
GOTERM_BP_FAT	GO:0007276~gamete generation	2.020634205	1.78E-06
GOTERM_BP_FAT	GO:0048477~oogenesis	2.205419663	2.54E-06

GOTERM_BP_FAT	GO:0019953~sexual reproduction	1.990532619	2.75E-06
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	1.880516034	3.75E-05
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	1.880516034	3.75E-05

Cluster 18

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0048565~gut development	6.513540812	4.89E-11
GOTERM_BP_FAT	GO:0035239~tube morphogenesis	5.442862629	1.41E-08
GOTERM_BP_FAT	GO:0007439~ectodermal gut development	7.156181126	1.78E-07
GOTERM_BP_FAT	GO:0048567~ectodermal gut morphogenesis	7.156181126	1.78E-07
GOTERM_BP_FAT	GO:0048547~gut morphogenesis	7.003921953	2.65E-07
GOTERM_BP_FAT	GO:0048546~digestive tract morphogenesis	6.858006912	3.90E-07
GOTERM_BP_FAT	GO:0055123~digestive system development	6.858006912	3.90E-07
GOTERM_BP_FAT	GO:0007442~hindgut morphogenesis	6.531435155	3.89E-05

Cluster 19

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	4.191004224	9.94E-13
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	5.53294412	4.83E-12

GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	3.048003072	5.47E-07
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	3.011280144	7.97E-07
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	3.011280144	7.97E-07
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	5.696268037	3.44E-06
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	2.653781855	3.84E-06
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	3.003829115	3.49E-05
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	2.788307743	2.21E-04
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.788307743	2.21E-04
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	2.571752592	6.62E-04

Cluster 20

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	4.532927646	2.82E-08
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	4.414349277	1.31E-07
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen	4.23193815	3.67E-07

	compound metabolic process		
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	4.23193815	3.67E-07
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	3.969492373	1.70E-06
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	3.734877004	3.47E-06
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	3.466356435	1.99E-05
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	3.466356435	1.99E-05
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	3.948549434	0.001607775

Cluster 21

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	neurogenesis	8.831174925	3.51E-17
SP_PIR_KEYWORDS	differentiation	5.0703125	1.76E-13
GOTERM_MF_FAT	GO:0016566~specific transcriptional repressor activity	9.186868687	2.32E-09
UP_SEQ_FEATURE	DNA-binding region:Basic motif	5.093555094	6.84E-04
UP_SEQ_FEATURE	domain:Helix-loop-helix motif	5.46875	8.10E-04

Cluster 22

Category	Term	Fold Enrichment	Bonferroni

GOTERM_BP_FAT	GO:0007163~establishment or maintenance of cell polarity	4.362279626	9.42E-07
GOTERM_BP_FAT	GO:0001736~establishment of planar polarity	5.096660875	1.75E-04
GOTERM_BP_FAT	GO:0007164~establishment of tissue polarity	5.014456667	2.24E-04
GOTERM_BP_FAT	GO:0001738~morphogenesis of a polarized epithelium	4.702633311	2.37E-04

Cluster 23

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0001667~ameboidal cell migration	6.858006912	9.14E-04

Cluster 24

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0009880~embryonic pattern specification	3.562600993	2.34E-10
GOTERM_BP_FAT	GO:0035282~segmentation	3.305911024	1.04E-09
GOTERM_BP_FAT	GO:0007350~blastoderm segmentation	3.439489705	1.13E-08

Cluster 25

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	10.97281106	2.16E-06

Cluster 26

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	4.143379176	2.76E-07
GOTERM_BP_FAT	GO:0001751~compound eye	3.954166148	3.74E-05

	photoreceptor cell differentiation		
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	3.783727952	8.95E-05
GOTERM_BP_FAT	GO:0042461~photoreceptor cell development	4.64457611	0.001722476

Cluster 27

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007365~periodic partitioning	5.757339136	2.59E-05

Cluster 28

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035152~regulation of tube architecture, open tracheal system	6.737691002	8.78E-05
GOTERM_BP_FAT	GO:0048871~multicellular organismal homeostasis	10.7576579	1.16E-04
GOTERM_BP_FAT	GO:0001894~tissue homeostasis	10.7576579	1.16E-04

Cluster 29

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035218~leg disc development	8.247537725	6.16E-12
GOTERM_BP_FAT	GO:0007478~leg disc morphogenesis	7.079232942	6.30E-04
GOTERM_BP_FAT	GO:0035110~leg morphogenesis	6.096006144	0.001085789

Cluster 30

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0010453~regulation of cell fate commitment	10.05841014	4.26E-05
GOTERM_BP_FAT	GO:0042659~regulation of cell fate specification	10.05841014	4.26E-05

Cluster 31

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0046530~photoreceptor cell differentiation	4.143379176	2.76E-07
GOTERM_BP_FAT	GO:0001751~compound eye photoreceptor cell differentiation	3.954166148	3.74E-05
GOTERM_BP_FAT	GO:0001754~eye photoreceptor cell differentiation	3.783727952	8.95E-05

Cluster 32

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	4.448436916	5.64E-04

Cluster 33

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007369~gastrulation	4.826004864	6.21E-05

Cluster 34

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035287~head segmentation	8.708580206	0.001152031

Cluster 35

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007498~mesoderm development	4.823213653	5.95E-07
GOTERM_BP_FAT	GO:0007369~gastrulation	4.826004864	6.21E-05

Cluster 36

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	glycoprotein	2.520192606	8.66E-07
SP_PIR_KEYWORDS	disulfide bond	2.73036716	1.01E-04

Cluster 37

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0008356~asymmetric cell division	5.675591928	1.09E-05
GOTERM_BP_FAT	GO:0051301~cell division	2.943924919	9.64E-05

Cluster 38

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0042692~muscle cell differentiation	4.448436916	5.64E-04

Cluster 39

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0035051~cardiac cell differentiation	10.97281106	2.16E-06

Cluster 40

Category	Term	Fold Enrichment	Bonferroni

GOTERM_BP_FAT	GO:0010941~regulation of cell death	3.975656181	1.58E-05
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	3.624652302	7.91E-04

Cluster 41

Category	Term	Fold Enrichment	Bonferroni
SP_PIR_KEYWORDS	zinc finger	6.44872814	8.66E-06
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	4.67032967	1.18E-04
UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	4.576923077	1.62E-04
SP_PIR_KEYWORDS	zinc-finger	2.443944741	5.53E-04

Cluster 42

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0007548~sex differentiation	5.181605223	1.36E-04

Cluster 43

Category	Term	Fold Enrichment	Bonferroni
GOTERM_BP_FAT	GO:0022612~gland morphogenesis	4.170951572	2.58E-06
GOTERM_BP_FAT	GO:0007435~salivary gland morphogenesis	4.170951572	2.58E-06