

Figure 5-  
source data 1

Gene ontology enrichment of expression clusters

GO: ID	GO Term	p value
<b>Cluster 1</b>		
GO:0040010	positive regulation of growth rate	2.5e-19
GO:0040035	hemaphrodite genitalia development	1.5e-13
GO:0006364	rRNA processing	6.5e-12
GO:0002119	nematode larval development	2.3e-11
GO:0006898	receptor-mediated endocytosis	1.4e-09
GO:0000398	mRNA splicing, via spliceosome	7.2e-07
GO:0006259	DNA metabolic process	1.5e-06
GO:0009792	embryo development ending in birth or egg hatching	2.6e-06
GO:0042254	ribosome biogenesis	8,00E-06
GO:0000381	regulation of alternative mRNA splicing, via spliceosome	8.4e-06
GO:0006626	protein targeting to mitochondrion	1.6e-05
GO:0030174	regulation of DNA-dependent DNA replication initiation	3.5e-05
GO:0030261	chromosome condensation	4.9e-05
GO:0040020	regulation of meiotic nuclear division	6.5e-05
GO:0051084	de novo' posttranslational protein folding	7.1e-05
GO:0022008	neurogenesis	8.5e-05
GO:0032201	telomere maintenance via semi-conservative replication	9.4e-05
GO:0006271	DNA strand elongation involved in DNA replication	1,00E-04
GO:0006412	translation	0.00016
GO:0006385	transcription elongation from RNA polymerase III promoter	0.00048
GO:0006386	termination of RNA polymerase III transcription	0.00048
GO:0017183	peptidyl-diphthamide biosynthetic process from peptidyl-histidine	0.00048
GO:0030488	tRNA methylation	0.00053
GO:0031167	rRNA methylation	0.00059
GO:0010833	telomere maintenance via telomere lengthening	0.00064
GO:0090305	nucleic acid phosphodiester bond hydrolysis	0.00065
GO:0006997	nucleus organization	0.00068
GO:0000731	DNA synthesis involved in DNA repair	0.00114
GO:0006418	tRNA aminoacylation for protein translation	0.00163
GO:0006369	termination of RNA polymerase II transcription	0.00174
GO:0016973	poly(A)+ mRNA export from nucleus	0.00193
GO:0006376	mRNA splice site selection	0.00193
GO:0006334	nucleosome assembly	0.00216
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00217
GO:0018992	gem-line sex determination	0.00217
GO:0019509	L-methionine salvage from methylthioadenosine	0.00221
GO:0009926	auxin polar transport	0.00221
GO:0007339	binding of sperm to zona pellucida	0.00221
GO:0009304	tRNA transcription	0.00221
GO:0006610	ribosomal protein import into nucleus	0.00221
GO:0043558	regulation of translational initiation in response to stress	0.00236
GO:0034969	histone arginine methylation	0.00236
GO:0009303	rRNA transcription	0.00267
GO:0022618	ribonucleoprotein complex assembly	0.00279
GO:0006406	mRNA export from nucleus	0.00293

GO:0000722	telomere maintenance via recombination	0.00297
GO:0030490	maturation of SSU-rRNA	0.00312
GO:0006595	polyamine metabolic process	0.00321
GO:0009113	purine nucleobase biosynthetic process	0.00321
GO:0032259	methylation	0.00404
GO:0044260	cellular macromolecule metabolic process	0.00408
GO:0048024	regulation of mRNA splicing, via spliceosome	0.00443
GO:0043928	exonucleolytic catabolism of deadenylated mRNA	0.00459
GO:0006268	DNA unwinding involved in DNA replication	0.00472
GO:0044743	protein transmembrane import into intracellular organelle	0.00481
GO:0034660	ncRNA metabolic process	0.00572
GO:0007076	mitotic chromosome condensation	0.00628
GO:0002183	cytoplasmic translational initiation	0.00677
GO:0042246	tissue regeneration	0.00677
GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00677
GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.00677
GO:0006284	base-excision repair	0.00743
GO:0007095	mitotic G2 DNA damage checkpoint	0.00873
GO:0001703	gastrulation with mouth forming first	0.00884
GO:0000469	cleavage involved in rRNA processing	0.009
GO:0007089	traversing start control point of mitotic cell cycle	0.00915
GO:0080034	host response to induction by symbiont of tumor, nodule or growth in host	0.00915
GO:0035247	peptidyl-arginine omega-N-methylation	0.00915
GO:0000470	maturation of LSU-rRNA	0.00915
GO:0009219	pyrimidine deoxyribonucleotide metabolic process	0.00915
GO:0031122	cytoplasmic microtubule organization	0.00965
GO:0040022	feminization of hermaphroditic germ-line	0.00965
GO:0006607	NLS-bearing protein import into nucleus	0.00965
GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rR	0.00965
GO:0000460	maturation of 5.8S rRNA	0.00997
<b>Cluster 2</b>		
GO:1901671	positive regulation of superoxide dismutase activity	0.0018
GO:0048318	axial mesoderm development	0.0018
GO:0034463	90S preribosome assembly	0.0018
GO:0042474	middle ear morphogenesis	0.0073
GO:0006412	translation	0.0075
<b>Cluster 3</b>		
GO:0033120	positive regulation of RNA splicing	0.00044
GO:0000162	tryptophan biosynthetic process	0.00087
GO:0006777	Mo-molybdopterin cofactor biosynthetic process	0.00144
GO:0034508	centromere complex assembly	0.00144
GO:0032324	molybdopterin cofactor biosynthetic process	0.00298
GO:0045144	meiotic sister chromatid segregation	0.00298
GO:0006913	nucleocytoplasmic transport	0.0074
<b>Cluster 4</b>		
GO:0006145	purine nucleobase catabolic process	0.0011
GO:0006573	valine metabolic process	0.0024
GO:0042430	indole-containing compound metabolic process	0.003

GO:0031365	N-terminal protein amino acid modification	0,004
GO:0008593	regulation of Notch signaling pathway	0,0041
GO:0055114	oxidation-reduction process	0,0041
GO:0009083	branched-chain amino acid catabolic process	0,0072
GO:0009072	aromatic amino acid family metabolic process	0,0085

#### Cluster 5

GO:0006891	intra-Golgi vesicle-mediated transport	6.1e-05
GO:0019915	lipid storage	0.00028
GO:0046474	glycerophospholipid biosynthetic process	0.00046
GO:0051208	sequestering of calcium ion	9,00E-04
GO:0006890	retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum	0.00115
GO:0048205	COPI coating of Golgi vesicle	0.00116
GO:0007030	Golgi organization	0.00126
GO:0016185	synaptic vesicle budding from presynaptic endocytic zone membrane	0.00239
GO:0035158	regulation of tube diameter, open tracheal system	0.00241
GO:0044106	cellular amine metabolic process	0.00269
GO:0019884	antigen processing and presentation of exogenous antigen	0.00289
GO:0010883	regulation of lipid storage	0.00321
GO:0006901	vesicle coating	0.0039
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.0042
GO:0030536	larval feeding behavior	0.00472
GO:0046487	glyoxylate metabolic process	0.00472
GO:0035149	lumen formation, open tracheal system	0.00472
GO:0072578	neurotransmitter-gated ion channel clustering	0.00472
GO:0048079	regulation of cuticle pigmentation	0.00472
GO:0032075	positive regulation of nuclease activity	0.00511
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.00511
GO:0015908	fatty acid transport	0.00534
GO:0030258	lipid modification	0.00753
GO:0050690	regulation of defense response to virus by virus	0.00772
GO:0034629	cellular protein-containing complex localization	0.00772
GO:0007286	spermatid development	0.00775
GO:0045807	positive regulation of endocytosis	0.00775
GO:0032101	regulation of response to external stimulus	0.00936
GO:0044070	regulation of anion transport	0.00983

#### Cluster 6

GO:0008360	regulation of cell shape	1.7e-05
GO:0061024	membrane organization	3.4e-05
GO:0019226	transmission of nerve impulse	4.6e-05
GO:0016197	endosomal transport	4.6e-05
GO:0030833	regulation of actin filament polymerization	5.5e-05
GO:0048011	neurotrophin TRK receptor signaling pathway	5.5e-05
GO:0008543	fibroblast growth factor receptor signaling pathway	0.00013
GO:0060341	regulation of cellular localization	0.00013
GO:0019228	neuronal action potential	0.00016
GO:0007015	actin filament organization	2,00E-04
GO:0007173	epidermal growth factor receptor signaling pathway	0.00021
GO:0030163	protein catabolic process	0.00021

GO:0006821	chloride transport	0.00024
GO:0035023	regulation of Rho protein signal transduction	0.00028
GO:0043547	positive regulation of GTPase activity	0.00031
GO:0007110	meiosis I cytokinesis	0.00034
GO:0007111	meiosis II cytokinesis	0.00034
GO:0016080	synaptic vesicle targeting	0.00035
GO:0042552	myelination	0.00052
GO:0007268	chemical synaptic transmission	0.00053
GO:0033121	regulation of purine nucleotide catabolic process	0.00055
GO:0006928	movement of cell or subcellular component	6,00E-04
GO:1901615	organic hydroxy compound metabolic process	6,00E-04
GO:0051650	establishment of vesicle localization	0.00062
GO:0009118	regulation of nucleoside metabolic process	0.00065
GO:0006874	cellular calcium ion homeostasis	0.00074
GO:0007265	Ras protein signal transduction	0.00078
GO:0070588	calcium ion transmembrane transport	0.00083
GO:0032147	activation of protein kinase activity	0.00085
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	0.00095
GO:0048259	regulation of receptor-mediated endocytosis	0.00096
GO:0044089	positive regulation of cellular component biogenesis	0.00098
GO:0007409	axonogenesis	0.00113
GO:0051046	regulation of secretion	0.0012
GO:0030155	regulation of cell adhesion	0.00123
GO:0034314	Arp2/3 complex-mediated actin nucleation	0.00151
GO:0031018	endocrine pancreas development	0.00151
GO:0007031	peroxisome organization	0.00155
GO:0071242	cellular response to ammonium ion	0.00155
GO:0048193	Golgi vesicle transport	0.00164
GO:0048137	spermatocyte division	0.0018
GO:0048814	regulation of dendrite morphogenesis	0.0018
GO:0006487	protein N-linked glycosylation	0.00187
GO:0030031	cell projection assembly	0.0019
GO:0030855	epithelial cell differentiation	0.00194
GO:0000212	meiotic spindle organization	0.00198
GO:0000281	mitotic cytokinesis	0.00206
GO:0006635	fatty acid beta-oxidation	0.00206
GO:0042981	regulation of apoptotic process	0.00207
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	0.00215
GO:0048666	neuron development	0.00219
GO:0046488	phosphatidylinositol metabolic process	0.00224
GO:0010565	regulation of cellular ketone metabolic process	0.00238
GO:0009968	negative regulation of signal transduction	0.00239
GO:0030242	autophagy of peroxisome	0.0025
GO:0051278	fungus-type cell wall polysaccharide biosynthetic process	0.0025
GO:0046325	negative regulation of glucose import	0.0025
GO:0035372	protein localization to microtubule	0.0025
GO:0060049	regulation of protein glycosylation	0.0025
GO:0016137	glycoside metabolic process	0.0025

<b>GO:0035118</b>	embryonic pectoral fin morphogenesis	0.0025
<b>GO:0010256</b>	endomembrane system organization	0.00252
<b>GO:0032880</b>	regulation of protein localization	0.00261
<b>GO:0009617</b>	response to bacterium	0.00273
<b>GO:0050654</b>	chondroitin sulfate proteoglycan metabolic process	0.00275
<b>GO:0001707</b>	mesoderm formation	0.00275
<b>GO:1900544</b>	positive regulation of purine nucleotide metabolic process	0.00275
<b>GO:0051261</b>	protein depolymerization	0.00291
<b>GO:0007605</b>	sensory perception of sound	0.00291
<b>GO:0032506</b>	cytokinetic process	0.00294
<b>GO:0006023</b>	aminoglycan biosynthetic process	0.00311
<b>GO:0051289</b>	protein homotetramerization	0.00311
<b>GO:0051351</b>	positive regulation of ligase activity	0.00331
<b>GO:0051443</b>	positive regulation of ubiquitin-protein transferase activity	0.00331
<b>GO:0007626</b>	locomotory behavior	0.00351
<b>GO:0030010</b>	establishment of cell polarity	0.00356
<b>GO:0007112</b>	male meiosis cytokinesis	0.00359
<b>GO:0046135</b>	pyrimidine nucleoside catabolic process	0.00359
<b>GO:0030166</b>	proteoglycan biosynthetic process	0.00359
<b>GO:0019932</b>	second-messenger-mediated signaling	0.00391
<b>GO:0002479</b>	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	0.00394
<b>GO:0006893</b>	Golgi to plasma membrane transport	0.00401
<b>GO:0005979</b>	regulation of glycogen biosynthetic process	0.00405
<b>GO:0010677</b>	negative regulation of cellular carbohydrate metabolic process	0.00405
<b>GO:0031340</b>	positive regulation of vesicle fusion	0.00405
<b>GO:0072329</b>	monocarboxylic acid catabolic process	0.00413
<b>GO:0023056</b>	positive regulation of signaling	0.00424
<b>GO:0051130</b>	positive regulation of cellular component organization	0.00433
<b>GO:0007254</b>	JNK cascade	0.00434
<b>GO:0030203</b>	glycosaminoglycan metabolic process	0.00444
<b>GO:0051592</b>	response to calcium ion	0.00453
<b>GO:0007188</b>	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	0.00469
<b>GO:0032940</b>	secretion by cell	0.00501
<b>GO:0050730</b>	regulation of peptidyl-tyrosine phosphorylation	0.00506
<b>GO:0043406</b>	positive regulation of MAP kinase activity	0.00506
<b>GO:0090130</b>	tissue migration	0.00513
<b>GO:0030433</b>	ubiquitin-dependent ERAD pathway	0.00534
<b>GO:0008356</b>	asymmetric cell division	0.00541
<b>GO:0051653</b>	spindle localization	0.00541
<b>GO:0034620</b>	cellular response to unfolded protein	0.00597
<b>GO:0006977</b>	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.00605
<b>GO:0050679</b>	positive regulation of epithelial cell proliferation	0.00616
<b>GO:0120035</b>	regulation of plasma membrane bounded cell projection organization	0.00617
<b>GO:0035020</b>	regulation of Rac protein signal transduction	0.00639
<b>GO:0006895</b>	Golgi to endosome transport	0.00639
<b>GO:0007608</b>	sensory perception of smell	0.00639
<b>GO:0006687</b>	glycosphingolipid metabolic process	0.00639
<b>GO:0051352</b>	negative regulation of ligase activity	0.00642

GO:0051444	negative regulation of ubiquitin-protein transferase activity	0.00642
GO:0006904	vesicle docking involved in exocytosis	0.00679
GO:0050851	antigen receptor-mediated signaling pathway	0.00679
GO:0019933	cAMP-mediated signaling	0.00679
GO:0000916	actomyosin contractile ring contraction	0.00679
GO:0044273	sulfur compound catabolic process	0.00702
GO:0001745	compound eye morphogenesis	0.00713
GO:0007596	blood coagulation	0.00741
GO:0005975	carbohydrate metabolic process	0.0076
GO:0043062	extracellular structure organization	0.00778
GO:0061640	cytoskeleton-dependent cytokinesis	0.00794
GO:0010647	positive regulation of cell communication	0.00805
GO:0001505	regulation of neurotransmitter levels	0.00823
GO:0044262	cellular carbohydrate metabolic process	0.00833
GO:1904062	regulation of cation transmembrane transport	0.00835
GO:0045921	positive regulation of exocytosis	0.00843
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.00868
GO:0070207	protein homotrimerization	0.009
GO:0071377	cellular response to glucagon stimulus	0.009
GO:0019673	GDP-mannose metabolic process	0.009
GO:0075306	regulation of conidium formation	0.009
GO:0007144	female meiosis I	0.009
GO:0002673	regulation of acute inflammatory response	0.009
GO:0044091	membrane biogenesis	0.009
GO:0030866	cortical actin cytoskeleton organization	0.00906
GO:0030258	lipid modification	0.00916
GO:0006984	ER-nucleus signaling pathway	0.00921
GO:0048599	oocyte development	0.00929
GO:0048488	synaptic vesicle endocytosis	0.00931
GO:0090288	negative regulation of cellular response to growth factor stimulus	0.00951
GO:0010863	positive regulation of phospholipase C activity	0.00951
GO:0001667	ameboidal-type cell migration	0.00972
GO:0097164	ammonium ion metabolic process	0.00983
GO:0001933	negative regulation of protein phosphorylation	0.00983
GO:0046879	hormone secretion	0.00997

#### Cluster 7

GO:0008045	motor neuron axon guidance	2.6e-09
GO:0033121	regulation of purine nucleotide catabolic process	3.9e-07
GO:0009118	regulation of nucleoside metabolic process	4.4e-07
GO:0072015	glomerular visceral epithelial cell development	4.2e-05
GO:0003382	epithelial cell morphogenesis	6.6e-05
GO:0007155	cell adhesion	8.4e-05
GO:0031578	mitotic spindle orientation checkpoint	1,00E-04
GO:0001736	establishment of planar polarity	0.00012
GO:0050680	negative regulation of epithelial cell proliferation	0.00012
GO:0043547	positive regulation of GTPase activity	0.00014
GO:0045571	negative regulation of imaginal disc growth	0.00019
GO:0071260	cellular response to mechanical stimulus	0.00019

<b>GO:0042491</b>	inner ear auditory receptor cell differentiation	2,00E-04
<b>GO:0019991</b>	septate junction assembly	0.00026
<b>GO:0043588</b>	skin development	0.00031
<b>GO:0007160</b>	cell-matrix adhesion	0.00037
<b>GO:0016321</b>	female meiosis chromosome segregation	0.00043
<b>GO:0030334</b>	regulation of cell migration	0.00044
<b>GO:0007136</b>	meiotic prophase II	0.00049
<b>GO:0045061</b>	thymic T cell selection	0.00049
<b>GO:2000311</b>	regulation of AMPA receptor activity	0.00049
<b>GO:0033563</b>	dorsal/ventral axon guidance	0.00055
<b>GO:0000916</b>	actomyosin contractile ring contraction	0.00055
<b>GO:0030029</b>	actin filament-based process	0.00063
<b>GO:0019954</b>	asexual reproduction	0.00067
<b>GO:0042048</b>	olfactory behavior	8,00E-04
<b>GO:0090529</b>	cell septum assembly	8,00E-04
<b>GO:0002286</b>	T cell activation involved in immune response	8,00E-04
<b>GO:0035120</b>	post-embryonic appendage morphogenesis	0.00087
<b>GO:0035114</b>	imaginal disc-derived appendage morphogenesis	0.00095
<b>GO:2000146</b>	negative regulation of cell motility	0.00106
<b>GO:0043087</b>	regulation of GTPase activity	0.00121
<b>GO:0043542</b>	endothelial cell migration	0.00134
<b>GO:0061245</b>	establishment or maintenance of bipolar cell polarity	0.00134
<b>GO:0008104</b>	protein localization	0.00139
<b>GO:0070863</b>	positive regulation of protein exit from endoplasmic reticulum	0.00144
<b>GO:0033599</b>	regulation of mammary gland epithelial cell proliferation	0.00144
<b>GO:0032232</b>	negative regulation of actin filament bundle assembly	0.00144
<b>GO:1900006</b>	positive regulation of dendrite development	0.00144
<b>GO:0051764</b>	actin crosslink formation	0.00144
<b>GO:0000281</b>	mitotic cytokinesis	0.00145
<b>GO:0071478</b>	cellular response to radiation	0.00176
<b>GO:0003008</b>	system process	0.00189
<b>GO:0060070</b>	canonical Wnt signaling pathway	0.002
<b>GO:1905330</b>	regulation of morphogenesis of an epithelium	0.00201
<b>GO:0030856</b>	regulation of epithelial cell differentiation	0.00201
<b>GO:0048570</b>	notochord morphogenesis	0.00201
<b>GO:0043113</b>	receptor clustering	0.00201
<b>GO:0001525</b>	angiogenesis	0.00209
<b>GO:0006928</b>	movement of cell or subcellular component	0.00229
<b>GO:0001935</b>	endothelial cell proliferation	0.00233
<b>GO:0007391</b>	dorsal closure	0.00233
<b>GO:0007560</b>	imaginal disc morphogenesis	0.00252
<b>GO:0051493</b>	regulation of cytoskeleton organization	0.00254
<b>GO:0001764</b>	neuron migration	0.00257
<b>GO:0031100</b>	animal organ regeneration	0.00257
<b>GO:0006468</b>	protein phosphorylation	0.00259
<b>GO:2000114</b>	regulation of establishment of cell polarity	0.00284
<b>GO:0032489</b>	regulation of Cdc42 protein signal transduction	0.00284
<b>GO:0030835</b>	negative regulation of actin filament depolymerization	0.00284

<b>GO:0051971</b>	positive regulation of transmission of nerve impulse	0.00284
<b>GO:0010091</b>	trichome branching	0.00284
<b>GO:0003094</b>	glomerular filtration	0.00284
<b>GO:0048646</b>	anatomical structure formation involved in morphogenesis	0.00307
<b>GO:0051056</b>	regulation of small GTPase mediated signal transduction	0.0032
<b>GO:0046847</b>	filopodium assembly	0.00322
<b>GO:0035220</b>	wing disc development	0.00349
<b>GO:0035023</b>	regulation of Rho protein signal transduction	0.00367
<b>GO:0007264</b>	small GTPase mediated signal transduction	0.00391
<b>GO:0034333</b>	adherens junction assembly	0.00399
<b>GO:2000027</b>	regulation of animal organ morphogenesis	0.00399
<b>GO:0060562</b>	epithelial tube morphogenesis	0.00443
<b>GO:0030582</b>	reproductive fruiting body development	0.00462
<b>GO:0030708</b>	gemarium-derived female germ-line cyst encapsulation	0.00466
<b>GO:0048846</b>	axon extension involved in axon guidance	0.00466
<b>GO:0045730</b>	respiratory burst	0.00466
<b>GO:0035204</b>	negative regulation of lamellocyte differentiation	0.00466
<b>GO:0008302</b>	female gemline ring canal formation, actin assembly	0.00466
<b>GO:0050665</b>	hydrogen peroxide biosynthetic process	0.00466
<b>GO:0042554</b>	superoxide anion generation	0.00466
<b>GO:0036360</b>	sorocarp stalk morphogenesis	0.00466
<b>GO:1901069</b>	guanosine-containing compound catabolic process	0.00519
<b>GO:0008360</b>	regulation of cell shape	0.00519
<b>GO:0040039</b>	inductive cell migration	0.00566
<b>GO:0009887</b>	animal organ morphogenesis	0.00571
<b>GO:0007009</b>	plasma membrane organization	0.00573
<b>GO:0001838</b>	embryonic epithelial tube formation	0.00573
<b>GO:0051049</b>	regulation of transport	0.00613
<b>GO:0050764</b>	regulation of phagocytosis	0.00677
<b>GO:0051026</b>	chiasma assembly	0.00689
<b>GO:0000915</b>	actomyosin contractile ring assembly	0.00689
<b>GO:0050806</b>	positive regulation of synaptic transmission	0.00689
<b>GO:0032510</b>	endosome to lysosome transport via multivesicular body sorting pathway	0.00689
<b>GO:0046755</b>	viral budding	0.00689
<b>GO:0003081</b>	regulation of systemic arterial blood pressure by renin-angiotensin	0.00689
<b>GO:0048812</b>	neuron projection morphogenesis	0.0069
<b>GO:0042060</b>	wound healing	0.00693
<b>GO:0007265</b>	Ras protein signal transduction	0.00709
<b>GO:0046039</b>	GTP metabolic process	0.00762
<b>GO:0044766</b>	multi-organism transport	0.00791
<b>GO:0098609</b>	cell-cell adhesion	0.0081
<b>GO:0060538</b>	skeletal muscle organ development	0.0081
<b>GO:0010769</b>	regulation of cell morphogenesis involved in differentiation	0.00854
<b>GO:0021953</b>	central nervous system neuron differentiation	0.00916
<b>GO:0070507</b>	regulation of microtubule cytoskeleton organization	0.00939
<b>GO:0072089</b>	stem cell proliferation	0.00939
<b>GO:0051645</b>	Golgi localization	0.00951
<b>GO:0045887</b>	positive regulation of synaptic growth at neuromuscular junction	0.00951



<b>GO:0044130</b>	negative regulation of growth of symbiont in host	0.00951
<b>GO:0010596</b>	negative regulation of endothelial cell migration	0.00951
<b>GO:0051492</b>	regulation of stress fiber assembly	0.00951
<b>GO:0035090</b>	maintenance of apical/basal cell polarity	0.00951
<b>GO:0031103</b>	axon regeneration	0.00951
<b>GO:0048592</b>	eye morphogenesis	0.00965

#### Cluster 8

<b>GO:0008285</b>	negative regulation of cell population proliferation	0.00016
<b>GO:0007169</b>	transmembrane receptor protein tyrosine kinase signaling pathway	0.00088
<b>GO:0007267</b>	cell-cell signaling	0.00101
<b>GO:0030336</b>	negative regulation of cell migration	0.00105
<b>GO:0034109</b>	homotypic cell-cell adhesion	0.00183
<b>GO:0007596</b>	blood coagulation	0.00194
<b>GO:0032387</b>	negative regulation of intracellular transport	0.00259
<b>GO:0045765</b>	regulation of angiogenesis	0.00302
<b>GO:0051612</b>	negative regulation of serotonin uptake	0.00313
<b>GO:0007263</b>	nitric oxide mediated signal transduction	0.00313
<b>GO:0042738</b>	exogenous drug catabolic process	0.00313
<b>GO:0009725</b>	response to hormone	0.00401
<b>GO:0051224</b>	negative regulation of protein transport	0.0045
<b>GO:0010959</b>	regulation of metal ion transport	0.00594
<b>GO:0031284</b>	positive regulation of guanylate cyclase activity	0.00626
<b>GO:0034332</b>	adherens junction organization	0.00657
<b>GO:0045216</b>	cell-cell junction organization	0.0069
<b>GO:0010038</b>	response to metal ion	0.00858
<b>GO:0006154</b>	adenosine catabolic process	0.00937
<b>GO:0045776</b>	negative regulation of blood pressure	0.00937
<b>GO:0045779</b>	negative regulation of bone resorption	0.00937
<b>GO:0010761</b>	fibroblast migration	0.00937
<b>GO:0009816</b>	defense response to bacterium, incompatible interaction	0.00937

#### Cluster 9

<b>GO:0015991</b>	ATP hydrolysis coupled proton transport	0.0015
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