

Table S2 Gene ontology enrichment of expression clusters

GO: ID	GO Term	p value
Cluster 1		
GO:0040010	positive regulation of growth rate	2.5e-19
GO:0040035	hermaphrodite 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	germ-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 rF	0.00965
GO:0000460	maturation of 5.8S rRNA	0.00997
Cluster 2		
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
Cluster 3		
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
Cluster 4		
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

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

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

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

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

Cluster 8

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

Cluster 9

GO:0015991	ATP hydrolysis coupled proton transport	0.0015
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