

## A

<b>Accession</b>	<b>GO Term Biological Process enriched in up regulated genes</b>	<b>Robin</b>
GO:0001568	blood vessel development	8.58E-10
GO:0001944	vasculature development	2.41E-09
GO:0040011	locomotion	4.53E-08
GO:0048856	anatomical structure development	2.08E-07
GO:0072358	cardiovascular system development	3.26E-07
GO:0072359	circulatory system development	3.26E-07
GO:0009605	response to external stimulus	9.15E-07
GO:0050896	response to stimulus	9.18E-07
GO:0042221	response to chemical stimulus	1.21E-06
GO:0006695	cholesterol biosynthetic process	1.28E-06
GO:0006935	chemotaxis	1.47E-06
GO:0042330	taxis	1.47E-06
GO:0032502	developmental process	2.00E-06
GO:0048646	anatomical structure formation involved in morphogenesis	2.07E-06
GO:0007411	axon guidance	2.74E-06
GO:0007275	multicellular organismal development	3.09E-06
GO:0016126	sterol biosynthetic process	3.19E-06
GO:0048731	system development	3.22E-06
GO:0032501	multicellular organismal process	3.41E-06
GO:0008299	isoprenoid biosynthetic process	8.02E-06
GO:0007155	cell adhesion	8.44E-06
GO:0022610	biological adhesion	8.44E-06
GO:0045636	positive regulation of melanocyte differentiation	8.72E-06
GO:0050942	positive regulation of pigment cell differentiation	8.72E-06
GO:0072089	stem cell proliferation	8.74E-06
GO:0048583	regulation of response to stimulus	9.92E-06
GO:0009653	anatomical structure morphogenesis	1.04E-05
GO:0002576	platelet degranulation	1.16E-05
GO:0006694	steroid biosynthetic process	1.36E-05
GO:0030154	cell differentiation	1.42E-05
GO:0048514	blood vessel morphogenesis	1.70E-05

GO:0032101	regulation of response to external stimulus	1.93E-05
GO:0048087	positive regulation of developmental pigmentation	2.17E-05
GO:0007409	axonogenesis	2.67E-05
GO:0001525	angiogenesis	2.98E-05
GO:0000904	cell morphogenesis involved in differentiation	3.24E-05
GO:0006720	isoprenoid metabolic process	3.53E-05
GO:0023052	signaling	3.59E-05
GO:0048869	cellular developmental process	3.87E-05
GO:0045634	regulation of melanocyte differentiation	4.29E-05
GO:0050932	regulation of pigment cell differentiation	4.29E-05
GO:0043405	regulation of MAP kinase activity	4.31E-05
GO:0035295	tube development	4.76E-05
GO:0060429	epithelium development	4.83E-05
GO:0009888	tissue development	5.51E-05
GO:0048468	cell development	6.71E-05
GO:0008283	cell proliferation	7.14E-05
GO:0048667	cell morphogenesis involved in neuron differentiation	8.01E-05
GO:0008610	lipid biosynthetic process	8.78E-05
GO:0048812	neuron projection morphogenesis	9.05E-05
GO:0007154	cell communication	9.07E-05
GO:0031175	neuron projection development	9.17E-05
GO:0030324	lung development	9.38E-05
GO:0016477	cell migration	9.61E-05
GO:0045137	development of primary sexual characteristics	9.76E-05
GO:0023051	regulation of signaling	1.08E-04
GO:0030323	respiratory tube development	1.10E-04
GO:0051592	response to calcium ion	1.14E-04
GO:0009790	embryo development	1.28E-04
GO:0042127	regulation of cell proliferation	1.29E-04
GO:0006887	exocytosis	1.47E-04
GO:0030168	platelet activation	1.48E-04
GO:0060449	bud elongation involved in lung branching	1.70E-04
GO:0008406	gonad development	1.94E-04
GO:0048666	neuron development	2.09E-04

GO:0031589	cell-substrate adhesion	2.11E-04
GO:0032990	cell part morphogenesis	2.29E-04
GO:0051716	cellular response to stimulus	2.31E-04
GO:0003158	endothelium development	2.34E-04
GO:0030855	epithelial cell differentiation	2.57E-04
GO:0000165	MAPK cascade	2.61E-04
GO:0007165	signal transduction	2.64E-04
GO:0032989	cellular component morphogenesis	2.67E-04
GO:0009611	response to wounding	2.69E-04
GO:0010038	response to metal ion	2.72E-04
GO:0032103	positive regulation of response to external stimulus	2.79E-04
GO:0048870	cell motility	2.86E-04
GO:0051674	localization of cell	2.86E-04
GO:0007548	sex differentiation	2.93E-04
GO:0060541	respiratory system development	2.96E-04
GO:0007243	intracellular protein kinase cascade	2.99E-04
GO:0001936	regulation of endothelial cell proliferation	3.04E-04
GO:0000902	cell morphogenesis	3.05E-04
GO:0048608	reproductive structure development	3.14E-04
GO:0030155	regulation of cell adhesion	3.26E-04
GO:0030198	extracellular matrix organization	3.27E-04
GO:0043062	extracellular structure organization	3.27E-04
GO:0050793	regulation of developmental process	3.31E-04
GO:0007160	cell-matrix adhesion	4.21E-04
GO:0006928	cellular component movement	4.25E-04
GO:0030334	regulation of cell migration	4.37E-04
GO:0043408	regulation of MAPK cascade	4.45E-04
GO:0048070	regulation of developmental pigmentation	4.45E-04
GO:0071900	regulation of protein serine-threonine kinase activity	4.63E-04
GO:0010627	regulation of intracellular protein kinase cascade	4.70E-04
GO:0045765	regulation of angiogenesis	4.87E-04
GO:0048858	cell projection morphogenesis	5.19E-04
GO:0009966	regulation of signal transduction	5.32E-04
GO:0008203	cholesterol metabolic process	5.40E-04

GO:0050673	epithelial cell proliferation	5.42E-04
GO:0071363	cellular response to growth factor stimulus	5.43E-04
GO:0042981	regulation of apoptotic process	5.55E-04
GO:0035556	intracellular signal transduction	5.62E-04
GO:0030030	cell projection organization	5.69E-04
GO:0046546	development of primary male sexual characteristics	5.71E-04
GO:0014032	neural crest cell development	5.76E-04
GO:0034330	cell junction organization	6.11E-04
GO:0043067	regulation of programmed cell death	6.28E-04
GO:0003006	developmental process involved in reproduction	6.29E-04
GO:0030182	neuron differentiation	6.41E-04
GO:0010035	response to inorganic substance	6.44E-04
GO:0048754	branching morphogenesis of a tube	6.44E-04
GO:0001763	morphogenesis of a branching structure	6.61E-04
GO:0050678	regulation of epithelial cell proliferation	6.88E-04
GO:0001935	endothelial cell proliferation	7.14E-04
GO:2000145	regulation of cell motility	7.17E-04
GO:0051234	establishment of localization	7.63E-04
GO:0016125	sterol metabolic process	7.86E-04
GO:0009719	response to endogenous stimulus	8.26E-04
GO:0046661	male sex differentiation	8.28E-04
GO:0006810	transport	8.52E-04
GO:0022008	neurogenesis	8.78E-04
GO:0042692	muscle cell differentiation	8.81E-04
GO:0010941	regulation of cell death	9.38E-04
GO:0048519	negative regulation of biological process	9.41E-04
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	9.50E-04
GO:0010810	regulation of cell-substrate adhesion	9.76E-04
GO:0070848	response to growth factor stimulus	9.82E-04
GO:0060572	morphogenesis of an epithelial bud	1.09E-03
GO:0048584	positive regulation of response to stimulus	1.10E-03
GO:0014033	neural crest cell differentiation	1.11E-03
GO:0050795	regulation of behavior	1.11E-03
GO:0065007	biological regulation	1.16E-03

GO:0022603	regulation of anatomical structure morphogenesis	1.18E-03
GO:0051179	localization	1.21E-03
GO:0050920	regulation of chemotaxis	1.23E-03
GO:0051270	regulation of cellular component movement	1.28E-03
GO:0065008	regulation of biological quality	1.28E-03
GO:0035924	cellular response to vascular endothelial growth factor stimulus	1.31E-03
GO:0034329	cell junction assembly	1.32E-03
GO:0071902	positive regulation of protein serine-threonine kinase activity	1.33E-03
GO:0048041	focal adhesion assembly	1.34E-03
GO:0043066	negative regulation of apoptotic process	1.38E-03
GO:0043406	positive regulation of MAP kinase activity	1.38E-03
GO:0043542	endothelial cell migration	1.46E-03
GO:0040012	regulation of locomotion	1.48E-03
GO:0045446	endothelial cell differentiation	1.48E-03
GO:0043069	negative regulation of programmed cell death	1.51E-03
GO:0008584	male gonad development	1.54E-03
GO:0001885	endothelial cell development	1.56E-03
GO:0034220	ion transmembrane transport	1.56E-03
GO:0010595	positive regulation of endothelial cell migration	1.64E-03
GO:0032940	secretion by cell	1.64E-03
GO:0010839	negative regulation of keratinocyte proliferation	1.66E-03
GO:0048012	hepatocyte growth factor receptor signaling pathway	1.66E-03
GO:0060666	dichotomous subdivision of terminal units involved in salivary gland branching	1.66E-03
GO:0006629	lipid metabolic process	1.76E-03
GO:0007267	cell-cell signaling	1.81E-03
GO:0048699	generation of neurons	1.90E-03
GO:0051094	positive regulation of developmental process	1.91E-03
GO:0010033	response to organic substance	2.02E-03
GO:0035162	embryonic hemopoiesis	2.14E-03
GO:0040036	regulation of fibroblast growth factor receptor signaling pathway	2.14E-03
GO:0051893	regulation of focal adhesion assembly	2.14E-03
GO:0060445	branching involved in salivary gland morphogenesis	2.14E-03
GO:0090109	regulation of cell-substrate junction assembly	2.14E-03
GO:0044255	cellular lipid metabolic process	2.22E-03

GO:0060548	negative regulation of cell death	2.24E-03
GO:0061061	muscle structure development	2.27E-03
GO:0048010	vascular endothelial growth factor receptor signaling pathway	2.36E-03
GO:0048513	organ development	2.41E-03
GO:0010463	mesenchymal cell proliferation	2.57E-03
GO:0007399	nervous system development	2.70E-03
GO:0046903	secretion	2.76E-03
GO:0060485	mesenchyme development	2.76E-03
GO:0010811	positive regulation of cell-substrate adhesion	2.79E-03
GO:0008202	steroid metabolic process	2.83E-03
GO:0045766	positive regulation of angiogenesis	2.83E-03
GO:0010646	regulation of cell communication	2.86E-03
GO:0042060	wound healing	2.99E-03
GO:0016310	phosphorylation	3.01E-03
GO:0010453	regulation of cell fate commitment	3.22E-03
GO:0021846	cell proliferation in forebrain	3.22E-03
GO:0050789	regulation of biological process	3.22E-03
GO:0060571	morphogenesis of an epithelial fold	3.22E-03
GO:0007215	glutamate receptor signaling pathway	3.27E-03
GO:0048523	negative regulation of cellular process	3.28E-03
GO:0006950	response to stress	3.38E-03
GO:0038084	vascular endothelial growth factor signaling pathway	3.43E-03
GO:0060592	mammary gland formation	3.43E-03
GO:0072091	regulation of stem cell proliferation	3.43E-03
GO:2000310	regulation of N-methyl-D-aspartate selective glutamate receptor activity	3.43E-03
GO:0000188	inactivation of MAPK activity	3.65E-03
GO:0042445	hormone metabolic process	3.88E-03
GO:0042493	response to drug	3.91E-03
GO:0008285	negative regulation of cell proliferation	3.95E-03
GO:0071495	cellular response to endogenous stimulus	4.06E-03
GO:0006468	protein phosphorylation	4.09E-03
GO:0050794	regulation of cellular process	4.10E-03
GO:0061138	morphogenesis of a branching epithelium	4.16E-03
GO:0009791	post-embryonic development	4.18E-03

GO:0035107	appendage morphogenesis	4.20E-03
GO:0035108	limb morphogenesis	4.20E-03
GO:0051403	stress-activated MAPK cascade	4.31E-03
GO:0008343	adult feeding behavior	4.53E-03
GO:0035767	endothelial cell chemotaxis	4.53E-03
GO:0060484	lung-associated mesenchyme development	4.53E-03
GO:0061028	establishment of endothelial barrier	4.53E-03
GO:0050878	regulation of body fluid levels	4.59E-03
GO:0001952	regulation of cell-matrix adhesion	4.72E-03
GO:0031098	stress-activated protein kinase signaling cascade	4.72E-03
GO:0003007	heart morphogenesis	4.79E-03
GO:0001101	response to acid	4.89E-03
GO:0043410	positive regulation of MAPK cascade	4.96E-03
GO:0007044	cell-substrate junction assembly	5.05E-03
GO:0010740	positive regulation of intracellular protein kinase cascade	5.11E-03
GO:0018108	peptidyl-tyrosine phosphorylation	5.13E-03
GO:0030879	mammary gland development	5.37E-03
GO:0002688	regulation of leukocyte chemotaxis	5.40E-03
GO:0070887	cellular response to chemical stimulus	5.42E-03
GO:0018212	peptidyl-tyrosine modification	5.48E-03
GO:0048762	mesenchymal cell differentiation	5.58E-03
GO:0006200	ATP catabolic process	5.67E-03
GO:0018149	peptide cross-linking	5.68E-03
GO:0035115	embryonic forelimb morphogenesis	5.68E-03
GO:0043009	chordate embryonic development	5.72E-03
GO:0042574	retinal metabolic process	5.78E-03
GO:0043288	apocarotenoid metabolic process	5.78E-03
GO:0060536	cartilage morphogenesis	5.78E-03
GO:0060841	venous blood vessel development	5.78E-03
GO:0071392	cellular response to estradiol stimulus	5.78E-03
GO:0007596	blood coagulation	6.16E-03
GO:0000910	cytokinesis	6.24E-03
GO:0007435	salivary gland morphogenesis	6.28E-03
GO:0048008	platelet-derived growth factor receptor signaling pathway	6.28E-03

GO:0060428	lung epithelium development	6.28E-03
GO:0048729	tissue morphogenesis	6.36E-03
GO:0009792	embryo development ending in birth or egg hatching	6.49E-03
GO:0045859	regulation of protein kinase activity	6.58E-03
GO:0007599	hemostasis	6.59E-03
GO:0050817	coagulation	6.59E-03
GO:0048732	gland development	6.65E-03
GO:0007610	behavior	6.73E-03
GO:0048736	appendage development	6.75E-03
GO:0060173	limb development	6.75E-03
GO:0002009	morphogenesis of an epithelium	6.81E-03
GO:0060711	labyrinthine layer development	6.91E-03
GO:0060326	cell chemotaxis	7.01E-03
GO:0015936	coenzyme A metabolic process	7.16E-03
GO:0060174	limb bud formation	7.16E-03
GO:0046034	ATP metabolic process	7.27E-03
GO:2000026	regulation of multicellular organismal development	7.29E-03
GO:0051781	positive regulation of cell division	7.39E-03
GO:0001657	ureteric bud development	7.49E-03
GO:0007163	establishment or maintenance of cell polarity	7.49E-03
GO:0006915	apoptotic process	7.53E-03
GO:0002053	positive regulation of mesenchymal cell proliferation	7.58E-03
GO:0031399	regulation of protein modification process	7.78E-03
GO:0008360	regulation of cell shape	7.83E-03
GO:0001570	vasculogenesis	7.84E-03
GO:0043407	negative regulation of MAP kinase activity	7.84E-03
GO:0001701	in utero embryonic development	8.06E-03
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	8.18E-03
GO:0006916	anti-apoptosis	8.25E-03
GO:0030318	melanocyte differentiation	8.28E-03
GO:0010594	regulation of endothelial cell migration	8.31E-03
GO:0012501	programmed cell death	8.40E-03
GO:0008354	germ cell migration	8.67E-03
GO:0009214	cyclic nucleotide catabolic process	8.67E-03



GO:0010837	regulation of keratinocyte proliferation	8.67E-03
GO:0032793	positive regulation of CREB transcription factor activity	8.67E-03
GO:0060736	prostate gland growth	8.67E-03
GO:0071622	regulation of granulocyte chemotaxis	8.67E-03
GO:0080134	regulation of response to stress	8.70E-03
GO:0003281	ventricular septum development	9.03E-03
GO:0007431	salivary gland development	9.03E-03
GO:0050931	pigment cell differentiation	9.03E-03
GO:0060603	mammary gland duct morphogenesis	9.03E-03
GO:0061180	mammary gland epithelium development	9.29E-03
GO:0022612	gland morphogenesis	9.68E-03
GO:0046545	development of primary female sexual characteristics	9.68E-03
GO:0035136	forelimb morphogenesis	9.81E-03
GO:0043200	response to amino acid stimulus	9.81E-03
GO:0008219	cell death	9.96E-03
GO:0045860	positive regulation of protein kinase activity	9.96E-03

**B**

<b>Accession</b>	<b>GO Term Biological Process enriched in up regulated genes</b>	<b>Canary</b>
GO:0023052	signaling	2.63E-18
GO:0007154	cell communication	9.71E-18
GO:0032501	multicellular organismal process	3.57E-15
GO:0051179	localization	7.31E-14
GO:0007275	multicellular organismal development	7.14E-13
GO:0044281	small molecule metabolic process	2.44E-12
GO:0048731	system development	4.76E-12
GO:0040011	locomotion	1.09E-11

GO:0006928	cellular component movement	1.82E-11
GO:0007165	signal transduction	1.93E-11
GO:0032502	developmental process	1.84E-10
GO:0048856	anatomical structure development	2.02E-10
GO:0048666	neuron development	2.20E-10
GO:0050896	response to stimulus	3.36E-10
GO:0048667	cell morphogenesis involved in neuron differentiation	4.03E-10
GO:0016477	cell migration	4.49E-10
GO:0051716	cellular response to stimulus	5.24E-10
GO:0048812	neuron projection morphogenesis	5.90E-10
GO:0031175	neuron projection development	7.50E-10
GO:0023051	regulation of signaling	7.62E-10
GO:0042221	response to chemical stimulus	8.69E-10
GO:0048870	cell motility	1.18E-09
GO:0051674	localization of cell	1.18E-09
GO:0048468	cell development	1.69E-09
GO:0007399	nervous system development	3.31E-09
GO:0051234	establishment of localization	4.47E-09
GO:0007409	axonogenesis	5.66E-09
GO:0009987	cellular process	7.74E-09
GO:0007267	cell-cell signaling	1.08E-08
GO:0000904	cell morphogenesis involved in differentiation	1.20E-08
GO:0035556	intracellular signal transduction	2.03E-08
GO:0035637	multicellular organismal signaling	2.41E-08
GO:0022008	neurogenesis	2.65E-08
GO:0030182	neuron differentiation	2.88E-08
GO:0006810	transport	2.93E-08
GO:0048699	generation of neurons	2.96E-08
GO:0030154	cell differentiation	3.71E-08
GO:0040012	regulation of locomotion	3.84E-08
GO:0019226	transmission of nerve impulse	4.56E-08
GO:0003008	system process	5.69E-08
GO:0030030	cell projection organization	1.09E-07
GO:0007268	synaptic transmission	1.19E-07

GO:0048858	cell projection morphogenesis	1.20E-07
GO:0030334	regulation of cell migration	1.32E-07
GO:0032879	regulation of localization	1.36E-07
GO:0010035	response to inorganic substance	1.51E-07
GO:0051270	regulation of cellular component movement	1.74E-07
GO:0032990	cell part morphogenesis	2.01E-07
GO:2000145	regulation of cell motility	2.07E-07
GO:0048869	cellular developmental process	2.25E-07
GO:0055086	nucleobase-containing small molecule metabolic process	2.74E-07
GO:0046483	heterocycle metabolic process	3.38E-07
GO:0000902	cell morphogenesis	4.78E-07
GO:0032989	cellular component morphogenesis	4.85E-07
GO:0006753	nucleoside phosphate metabolic process	4.85E-07
GO:0009117	nucleotide metabolic process	4.85E-07
GO:0009605	response to external stimulus	7.48E-07
GO:0009966	regulation of signal transduction	8.01E-07
GO:0072521	purine-containing compound metabolic process	8.21E-07
GO:0007411	axon guidance	8.52E-07
GO:0009653	anatomical structure morphogenesis	1.00E-06
GO:0001666	response to hypoxia	1.81E-06
GO:0065007	biological regulation	1.85E-06
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	2.08E-06
GO:0006163	purine nucleotide metabolic process	2.23E-06
GO:0050877	neurological system process	3.99E-06
GO:0007166	cell surface receptor signaling pathway	4.43E-06
GO:0030155	regulation of cell adhesion	5.00E-06
GO:0007167	enzyme linked receptor protein signaling pathway	5.07E-06
GO:0008283	cell proliferation	5.54E-06
GO:0050793	regulation of developmental process	6.00E-06
GO:0050794	regulation of cellular process	6.82E-06
GO:0070482	response to oxygen levels	7.27E-06
GO:0000165	MAPK cascade	7.37E-06
GO:0006732	coenzyme metabolic process	7.94E-06
GO:0010038	response to metal ion	9.21E-06

GO:0006811	ion transport	1.16E-05
GO:0015980	energy derivation by oxidation of organic compounds	1.21E-05
GO:0006935	chemotaxis	1.37E-05
GO:0042330	taxis	1.37E-05
GO:0009060	aerobic respiration	1.42E-05
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	1.68E-05
GO:0042325	regulation of phosphorylation	1.99E-05
GO:0016043	cellular component organization	2.04E-05
GO:0071842	cellular component organization at cellular level	2.05E-05
GO:0010646	regulation of cell communication	2.14E-05
GO:0010033	response to organic substance	2.21E-05
GO:0006084	acetyl-CoA metabolic process	2.23E-05
GO:0034329	cell junction assembly	2.49E-05
GO:0050789	regulation of biological process	2.91E-05
GO:0030705	cytoskeleton-dependent intracellular transport	2.94E-05
GO:0007610	behavior	2.97E-05
GO:0007264	small GTPase mediated signal transduction	2.99E-05
GO:0006099	tricarboxylic acid cycle	3.00E-05
GO:0046356	acetyl-CoA catabolic process	3.00E-05
GO:0051239	regulation of multicellular organismal process	3.22E-05
GO:0046460	neutral lipid biosynthetic process	3.35E-05
GO:0046463	acylglycerol biosynthetic process	3.35E-05
GO:0048583	regulation of response to stimulus	3.41E-05
GO:0071841	cellular component organization or biogenesis at cellular level	3.65E-05
GO:0035336	long-chain fatty-acyl-CoA metabolic process	3.74E-05
GO:0046949	fatty-acyl-CoA biosynthetic process	3.74E-05
GO:0051338	regulation of transferase activity	3.75E-05
GO:0031589	cell-substrate adhesion	3.98E-05
GO:0009108	coenzyme biosynthetic process	4.26E-05
GO:0071840	cellular component organization or biogenesis	4.31E-05
GO:0034330	cell junction organization	4.39E-05
GO:0034220	ion transmembrane transport	4.44E-05
GO:0035384	thioester biosynthetic process	5.36E-05
GO:0071616	acyl-CoA biosynthetic process	5.36E-05

GO:0009259	ribonucleotide metabolic process	5.63E-05
GO:0065008	regulation of biological quality	5.88E-05
GO:0010970	microtubule-based transport	5.97E-05
GO:0001935	endothelial cell proliferation	6.12E-05
GO:0043549	regulation of kinase activity	6.62E-05
GO:0040013	negative regulation of locomotion	6.99E-05
GO:0048522	positive regulation of cellular process	7.12E-05
GO:0019220	regulation of phosphate metabolic process	7.15E-05
GO:0051174	regulation of phosphorus metabolic process	7.15E-05
GO:2000026	regulation of multicellular organismal development	7.19E-05
GO:0044283	small molecule biosynthetic process	7.31E-05
GO:0035337	fatty-acyl-CoA metabolic process	7.52E-05
GO:0043542	endothelial cell migration	7.58E-05
GO:0016310	phosphorylation	7.94E-05
GO:0051128	regulation of cellular component organization	8.40E-05
GO:0019432	triglyceride biosynthetic process	8.48E-05
GO:0046504	glycerol ether biosynthetic process	8.51E-05
GO:0001932	regulation of protein phosphorylation	9.34E-05
GO:0009719	response to endogenous stimulus	9.42E-05
GO:0006091	generation of precursor metabolites and energy	9.90E-05
GO:0051271	negative regulation of cellular component movement	1.10E-04
GO:0006793	phosphorus metabolic process	1.12E-04
GO:0006796	phosphate-containing compound metabolic process	1.12E-04
GO:0010810	regulation of cell-substrate adhesion	1.19E-04
GO:0008354	germ cell migration	1.21E-04
GO:0009109	coenzyme catabolic process	1.21E-04
GO:0055085	transmembrane transport	1.22E-04
GO:0060749	mammary gland alveolus development	1.30E-04
GO:0061377	mammary gland lobule development	1.30E-04
GO:0001944	vasculature development	1.37E-04
GO:0009150	purine ribonucleotide metabolic process	1.37E-04
GO:0030336	negative regulation of cell migration	1.39E-04
GO:0007266	Rho protein signal transduction	1.40E-04
GO:0042493	response to drug	1.42E-04

GO:0016126	sterol biosynthetic process	1.49E-04
GO:0014070	response to organic cyclic compound	1.55E-04
GO:0042127	regulation of cell proliferation	1.58E-04
GO:0009141	nucleoside triphosphate metabolic process	1.63E-04
GO:0070887	cellular response to chemical stimulus	1.67E-04
GO:0043410	positive regulation of MAPK cascade	1.69E-04
GO:0051347	positive regulation of transferase activity	1.71E-04
GO:2000146	negative regulation of cell motility	1.74E-04
GO:0009199	ribonucleoside triphosphate metabolic process	1.77E-04
GO:0051188	cofactor biosynthetic process	1.85E-04
GO:0001936	regulation of endothelial cell proliferation	1.95E-04
GO:0034599	cellular response to oxidative stress	1.95E-04
GO:0072358	cardiovascular system development	1.99E-04
GO:0072359	circulatory system development	1.99E-04
GO:0051186	cofactor metabolic process	2.00E-04
GO:0009144	purine nucleoside triphosphate metabolic process	2.03E-04
GO:0038084	vascular endothelial growth factor signaling pathway	2.06E-04
GO:0008610	lipid biosynthetic process	2.20E-04
GO:0006464	cellular protein modification process	2.25E-04
GO:0036211	protein modification process	2.25E-04
GO:0006629	lipid metabolic process	2.27E-04
GO:0034655	nucleobase-containing compound catabolic process	2.52E-04
GO:0050673	epithelial cell proliferation	2.56E-04
GO:0006695	cholesterol biosynthetic process	2.60E-04
GO:0006195	purine nucleotide catabolic process	2.75E-04
GO:0045785	positive regulation of cell adhesion	3.00E-04
GO:0006468	protein phosphorylation	3.04E-04
GO:0009205	purine ribonucleoside triphosphate metabolic process	3.26E-04
GO:0042180	cellular ketone metabolic process	3.27E-04
GO:0044271	cellular nitrogen compound biosynthetic process	3.39E-04
GO:0072523	purine-containing compound catabolic process	3.41E-04
GO:0006066	alcohol metabolic process	3.50E-04
GO:0001525	angiogenesis	3.64E-04
GO:0001568	blood vessel development	3.66E-04

GO:0009725	response to hormone stimulus	3.79E-04
GO:0043085	positive regulation of catalytic activity	3.84E-04
GO:0007010	cytoskeleton organization	3.87E-04
GO:0043408	regulation of MAPK cascade	4.09E-04
GO:0033555	multicellular organismal response to stress	4.43E-04
GO:0043648	dicarboxylic acid metabolic process	4.43E-04
GO:0045445	myoblast differentiation	4.51E-04
GO:0051187	cofactor catabolic process	4.51E-04
GO:0048646	anatomical structure formation involved in morphogenesis	4.56E-04
GO:0033674	positive regulation of kinase activity	4.57E-04
GO:0007243	intracellular protein kinase cascade	4.62E-04
GO:0045859	regulation of protein kinase activity	4.64E-04
GO:0009165	nucleotide biosynthetic process	4.87E-04
GO:0019227	neuronal action potential propagation	5.00E-04
GO:0048518	positive regulation of biological process	5.00E-04
GO:0043412	macromolecule modification	5.02E-04
GO:0045595	regulation of cell differentiation	5.10E-04
GO:0007215	glutamate receptor signaling pathway	5.23E-04
GO:0071407	cellular response to organic cyclic compound	5.23E-04
GO:0006639	acylglycerol metabolic process	5.27E-04
GO:0009636	response to toxin	5.27E-04
GO:0007265	Ras protein signal transduction	5.30E-04
GO:0044267	cellular protein metabolic process	5.45E-04
GO:0006637	acyl-CoA metabolic process	5.46E-04
GO:0034637	cellular carbohydrate biosynthetic process	5.46E-04
GO:0035383	thioester metabolic process	5.46E-04
GO:0006638	neutral lipid metabolic process	5.84E-04
GO:0034654	nucleobase-containing compound biosynthetic process	5.97E-04
GO:0009166	nucleotide catabolic process	6.08E-04
GO:0065009	regulation of molecular function	6.10E-04
GO:0019752	carboxylic acid metabolic process	6.23E-04
GO:0043436	oxoacid metabolic process	6.23E-04
GO:0048513	organ development	6.28E-04
GO:0051349	positive regulation of lyase activity	6.29E-04



GO:0006082	organic acid metabolic process	6.40E-04
GO:0006112	energy reserve metabolic process	6.40E-04
GO:0006694	steroid biosynthetic process	6.46E-04
GO:0035295	tube development	6.55E-04
GO:0007155	cell adhesion	6.58E-04
GO:0022610	biological adhesion	6.58E-04
GO:0050905	neuromuscular process	6.78E-04
GO:0006641	triglyceride metabolic process	6.79E-04
GO:0046700	heterocycle catabolic process	6.82E-04
GO:0016125	sterol metabolic process	7.26E-04
GO:1900542	regulation of purine nucleotide metabolic process	7.26E-04
GO:0044270	cellular nitrogen compound catabolic process	7.36E-04
GO:0006821	chloride transport	8.24E-04
GO:0009146	purine nucleoside triphosphate catabolic process	8.37E-04
GO:0048523	negative regulation of cellular process	8.64E-04
GO:0006140	regulation of nucleotide metabolic process	8.87E-04
GO:0006836	neurotransmitter transport	9.31E-04
GO:0010469	regulation of receptor activity	9.42E-04
GO:0042981	regulation of apoptotic process	9.45E-04
GO:0009143	nucleoside triphosphate catabolic process	9.88E-04
GO:0006820	anion transport	9.90E-04
GO:0050678	regulation of epithelial cell proliferation	1.06E-03
GO:0015936	coenzyme A metabolic process	1.10E-03
GO:0007565	female pregnancy	1.10E-03
GO:0006915	apoptotic process	1.13E-03
GO:0051339	regulation of lyase activity	1.13E-03
GO:0030001	metal ion transport	1.15E-03
GO:0043067	regulation of programmed cell death	1.19E-03
GO:0008219	cell death	1.19E-03
GO:0010839	negative regulation of keratinocyte proliferation	1.22E-03
GO:0034063	stress granule assembly	1.22E-03
GO:0034614	cellular response to reactive oxygen species	1.22E-03
GO:0070120	ciliary neurotrophic factor-mediated signaling pathway	1.22E-03
GO:0008202	steroid metabolic process	1.24E-03

GO:0016265	death	1.24E-03
GO:0035924	cellular response to vascular endothelial growth factor stimulus	1.25E-03
GO:0008285	negative regulation of cell proliferation	1.25E-03
GO:0008088	axon cargo transport	1.25E-03
GO:0031399	regulation of protein modification process	1.27E-03
GO:0048010	vascular endothelial growth factor receptor signaling pathway	1.29E-03
GO:0050790	regulation of catalytic activity	1.31E-03
GO:0071363	cellular response to growth factor stimulus	1.32E-03
GO:0051056	regulation of small GTPase mediated signal transduction	1.32E-03
GO:0006662	glycerol ether metabolic process	1.34E-03
GO:0045860	positive regulation of protein kinase activity	1.39E-03
GO:0048732	gland development	1.40E-03
GO:0030073	insulin secretion	1.42E-03
GO:0042692	muscle cell differentiation	1.47E-03
GO:0012501	programmed cell death	1.47E-03
GO:0050900	leukocyte migration	1.47E-03
GO:0009203	ribonucleoside triphosphate catabolic process	1.49E-03
GO:0009207	purine ribonucleoside triphosphate catabolic process	1.49E-03
GO:0051649	establishment of localization in cell	1.50E-03
GO:0007160	cell-matrix adhesion	1.51E-03
GO:0016051	carbohydrate biosynthetic process	1.52E-03
GO:0046903	secretion	1.53E-03
GO:0051146	striated muscle cell differentiation	1.53E-03
GO:0010941	regulation of cell death	1.63E-03
GO:0007611	learning or memory	1.63E-03
GO:0034765	regulation of ion transmembrane transport	1.63E-03
GO:0007190	activation of adenylate cyclase activity	1.64E-03
GO:0015807	L-amino acid transport	1.64E-03
GO:0060736	prostate gland growth	1.65E-03
GO:0050890	cognition	1.65E-03
GO:0071780	mitotic cell cycle G2-M transition checkpoint	1.65E-03
GO:0070848	response to growth factor stimulus	1.71E-03
GO:0010975	regulation of neuron projection development	1.72E-03
GO:0018130	heterocycle biosynthetic process	1.72E-03

GO:0032412	regulation of ion transmembrane transporter activity	1.72E-03
GO:0043434	response to peptide hormone stimulus	1.74E-03
GO:0001894	tissue homeostasis	1.81E-03
GO:0051641	cellular localization	1.83E-03
GO:0048519	negative regulation of biological process	1.87E-03
GO:0006184	GTP catabolic process	1.89E-03
GO:0009154	purine ribonucleotide catabolic process	1.89E-03
GO:0044057	regulation of system process	1.89E-03
GO:0003001	generation of a signal involved in cell-cell signaling	1.99E-03
GO:0023061	signal release	1.99E-03
GO:0045762	positive regulation of adenylate cyclase activity	2.02E-03
GO:0009261	ribonucleotide catabolic process	2.04E-03
GO:0044093	positive regulation of molecular function	2.11E-03
GO:0030072	peptide hormone secretion	2.15E-03
GO:0007214	gamma-aminobutyric acid signaling pathway	2.16E-03
GO:1900449	regulation of glutamate receptor signaling pathway	2.16E-03
GO:0018904	organic ether metabolic process	2.17E-03
GO:0055002	striated muscle cell development	2.17E-03
GO:0045666	positive regulation of neuron differentiation	2.19E-03
GO:0015810	aspartate transport	2.34E-03
GO:0045761	regulation of adenylate cyclase activity	2.35E-03
GO:0046364	monosaccharide biosynthetic process	2.35E-03
GO:0043129	surfactant homeostasis	2.38E-03
GO:0048875	chemical homeostasis within a tissue	2.38E-03
GO:0043066	negative regulation of apoptotic process	2.40E-03
GO:0031281	positive regulation of cyclase activity	2.46E-03
GO:0046165	alcohol biosynthetic process	2.58E-03
GO:0006423	cysteinyl-tRNA aminoacylation	2.59E-03
GO:0010868	negative regulation of triglyceride biosynthetic process	2.59E-03
GO:0035617	stress granule disassembly	2.59E-03
GO:0042231	interleukin-13 biosynthetic process	2.59E-03
GO:0015837	amine transport	2.62E-03
GO:0045664	regulation of neuron differentiation	2.68E-03
GO:0007018	microtubule-based movement	2.73E-03

GO:0010039	response to iron ion	2.76E-03
GO:0050926	regulation of positive chemotaxis	2.76E-03
GO:0072384	organelle transport along microtubule	2.76E-03
GO:0043069	negative regulation of programmed cell death	2.84E-03
GO:0022898	regulation of transmembrane transporter activity	2.86E-03
GO:0001569	patterning of blood vessels	2.97E-03
GO:0002790	peptide secretion	2.97E-03
GO:0008038	neuron recognition	2.97E-03
GO:0046039	GTP metabolic process	3.01E-03
GO:0006950	response to stress	3.03E-03
GO:0031344	regulation of cell projection organization	3.07E-03
GO:0032268	regulation of cellular protein metabolic process	3.07E-03
GO:0031279	regulation of cyclase activity	3.08E-03
GO:0044255	cellular lipid metabolic process	3.10E-03
GO:0033002	muscle cell proliferation	3.14E-03
GO:0048638	regulation of developmental growth	3.14E-03
GO:0009991	response to extracellular stimulus	3.15E-03
GO:0008203	cholesterol metabolic process	3.31E-03
GO:0055001	muscle cell development	3.39E-03
GO:0015698	inorganic anion transport	3.42E-03
GO:0044262	cellular carbohydrate metabolic process	3.42E-03
GO:0060548	negative regulation of cell death	3.44E-03
GO:0051592	response to calcium ion	3.46E-03
GO:0042596	fear response	3.48E-03
GO:0035023	regulation of Rho protein signal transduction	3.49E-03
GO:0010594	regulation of endothelial cell migration	3.53E-03
GO:0000302	response to reactive oxygen species	3.58E-03
GO:0055114	oxidation-reduction process	3.67E-03
GO:0008015	blood circulation	3.72E-03
GO:0006006	glucose metabolic process	3.84E-03
GO:0003013	circulatory system process	3.89E-03
GO:0006897	endocytosis	3.92E-03
GO:0009743	response to carbohydrate stimulus	3.93E-03
GO:0006101	citrate metabolic process	3.94E-03

GO:0006108	malate metabolic process	3.94E-03
GO:0006208	pyrimidine base catabolic process	3.94E-03
GO:0006538	glutamate catabolic process	3.94E-03
GO:0048268	clathrin coat assembly	3.94E-03
GO:0051775	response to redox state	3.94E-03
GO:0051938	L-glutamate import	3.94E-03
GO:0072350	tricarboxylic acid metabolic process	3.94E-03
GO:0071844	cellular component assembly at cellular level	3.95E-03
GO:0009914	hormone transport	4.06E-03
GO:0019318	hexose metabolic process	4.08E-03
GO:0040017	positive regulation of locomotion	4.29E-03
GO:0072522	purine-containing compound biosynthetic process	4.29E-03
GO:0008299	isoprenoid biosynthetic process	4.32E-03
GO:0001937	negative regulation of endothelial cell proliferation	4.32E-03
GO:0006835	dicarboxylic acid transport	4.43E-03
GO:0006979	response to oxidative stress	4.47E-03
GO:0009123	nucleoside monophosphate metabolic process	4.49E-03
GO:0030816	positive regulation of cAMP metabolic process	4.49E-03
GO:0030819	positive regulation of cAMP biosynthetic process	4.49E-03
GO:0045333	cellular respiration	4.49E-03
GO:0046620	regulation of organ growth	4.49E-03
GO:0051272	positive regulation of cellular component movement	4.53E-03
GO:0009056	catabolic process	4.54E-03
GO:0008016	regulation of heart contraction	4.55E-03
GO:0006164	purine nucleotide biosynthetic process	4.56E-03
GO:0008284	positive regulation of cell proliferation	4.56E-03
GO:0070507	regulation of microtubule cytoskeleton organization	4.57E-03
GO:0050796	regulation of insulin secretion	4.88E-03
GO:0022603	regulation of anatomical structure morphogenesis	4.90E-03
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	4.90E-03
GO:0070301	cellular response to hydrogen peroxide	4.90E-03
GO:0032886	regulation of microtubule-based process	4.97E-03
GO:0048167	regulation of synaptic plasticity	5.03E-03
GO:0007044	cell-substrate junction assembly	5.06E-03

GO:0048871	multicellular organismal homeostasis	5.13E-03
GO:0006812	cation transport	5.15E-03
GO:0009110	vitamin biosynthetic process	5.29E-03
GO:0005975	carbohydrate metabolic process	5.30E-03
GO:0030335	positive regulation of cell migration	5.38E-03
GO:0050767	regulation of neurogenesis	5.45E-03
GO:0071310	cellular response to organic substance	5.47E-03
GO:0030817	regulation of cAMP biosynthetic process	5.52E-03
GO:0071702	organic substance transport	5.57E-03
GO:0046847	filopodium assembly	5.61E-03
GO:0001964	startle response	5.80E-03
GO:0007413	axonal fasciculation	5.80E-03
GO:0071312	cellular response to alkaloid	5.80E-03
GO:0042364	water-soluble vitamin biosynthetic process	6.08E-03
GO:0042415	norepinephrine metabolic process	6.08E-03
GO:0046113	nucleobase catabolic process	6.08E-03
GO:0048514	blood vessel morphogenesis	6.27E-03
GO:0046879	hormone secretion	6.32E-03
GO:2000147	positive regulation of cell motility	6.32E-03
GO:0031532	actin cytoskeleton reorganization	6.38E-03
GO:0015833	peptide transport	6.39E-03
GO:0031111	negative regulation of microtubule polymerization or depolymerization	6.40E-03
GO:0009611	response to wounding	6.52E-03
GO:0048771	tissue remodeling	6.56E-03
GO:0010647	positive regulation of cell communication	6.60E-03
GO:0030814	regulation of cAMP metabolic process	6.63E-03
GO:0043269	regulation of ion transport	6.66E-03
GO:0044248	cellular catabolic process	6.70E-03
GO:0007618	mating	6.77E-03
GO:0034103	regulation of tissue remodeling	6.77E-03
GO:0030804	positive regulation of cyclic nucleotide biosynthetic process	7.09E-03
GO:0010811	positive regulation of cell-substrate adhesion	7.23E-03
GO:0019319	hexose biosynthetic process	7.32E-03
GO:0060284	regulation of cell development	7.37E-03

GO:0006106	fumarate metabolic process	7.38E-03
GO:0009448	gamma-aminobutyric acid metabolic process	7.38E-03
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	7.38E-03
GO:0019896	axon transport of mitochondrion	7.38E-03
GO:0042816	vitamin B6 metabolic process	7.38E-03
GO:0042819	vitamin B6 biosynthetic process	7.38E-03
GO:0043490	malate-aspartate shuttle	7.38E-03
GO:0048014	Tie receptor signaling pathway	7.38E-03
GO:0060312	regulation of blood vessel remodeling	7.38E-03
GO:0070777	D-aspartate transport	7.38E-03
GO:0070779	D-aspartate import	7.38E-03
GO:0019538	protein metabolic process	7.42E-03
GO:0030260	entry into host cell	7.43E-03
GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	7.43E-03
GO:0044409	entry into host	7.43E-03
GO:0051806	entry into cell of other organism involved in symbiotic interaction	7.43E-03
GO:0051828	entry into other organism involved in symbiotic interaction	7.43E-03
GO:0052126	movement in host environment	7.43E-03
GO:0052192	movement in environment of other organism involved in symbiotic interaction	7.43E-03
GO:0048585	negative regulation of response to stimulus	7.56E-03
GO:0033865	nucleoside bisphosphate metabolic process	7.67E-03
GO:0023056	positive regulation of signaling	7.77E-03
GO:0009066	aspartate family amino acid metabolic process	7.83E-03
GO:0071495	cellular response to endogenous stimulus	7.86E-03
GO:0007017	microtubule-based process	7.86E-03
GO:0031667	response to nutrient levels	7.86E-03
GO:0030810	positive regulation of nucleotide biosynthetic process	7.89E-03
GO:0044264	cellular polysaccharide metabolic process	7.89E-03
GO:1900373	positive regulation of purine nucleotide biosynthetic process	7.89E-03
GO:0008286	insulin receptor signaling pathway	8.06E-03
GO:0050804	regulation of synaptic transmission	8.06E-03
GO:0001505	regulation of neurotransmitter levels	8.07E-03
GO:0001655	urogenital system development	8.10E-03
GO:0006936	muscle contraction	8.10E-03

GO:0032409	regulation of transporter activity	8.15E-03
GO:0070588	calcium ion transmembrane transport	8.16E-03
GO:0010740	positive regulation of intracellular protein kinase cascade	8.17E-03
GO:0009888	tissue development	8.47E-03
GO:0010648	negative regulation of cell communication	8.72E-03
GO:0023057	negative regulation of signaling	8.72E-03
GO:0030801	positive regulation of cyclic nucleotide metabolic process	8.76E-03
GO:0035335	peptidyl-tyrosine dephosphorylation	8.76E-03
GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	8.77E-03
GO:0032331	negative regulation of chondrocyte differentiation	8.77E-03
GO:0045749	negative regulation of S phase of mitotic cell cycle	8.77E-03
GO:0060292	long term synaptic depression	8.77E-03
GO:0060384	innervation	8.77E-03
GO:0008584	male gonad development	8.81E-03
GO:0010906	regulation of glucose metabolic process	8.84E-03
GO:0035265	organ growth	8.84E-03
GO:0090276	regulation of peptide hormone secretion	8.90E-03
GO:0051130	positive regulation of cellular component organization	8.94E-03
GO:0090287	regulation of cellular response to growth factor stimulus	9.11E-03
GO:0060443	mammary gland morphogenesis	9.18E-03
GO:0030879	mammary gland development	9.23E-03
GO:0032940	secretion by cell	9.29E-03
GO:0015813	L-glutamate transport	9.33E-03
GO:0031113	regulation of microtubule polymerization	9.33E-03
GO:0043279	response to alkaloid	9.33E-03
GO:0046546	development of primary male sexual characteristics	9.45E-03
GO:0050680	negative regulation of epithelial cell proliferation	9.68E-03
GO:0014065	phosphatidylinositol 3-kinase cascade	9.70E-03
GO:0044237	cellular metabolic process	9.81E-03



**C**

<b>Accession</b>	<b>GO Term Biological Processes enriched in down regulated genes</b>	<b>Robin</b>
GO:0030030	cell projection organization	1.20E-07
GO:0016043	cellular component organization	1.08E-06
GO:0071840	cellular component organization or biogenesis	2.18E-06
GO:0071842	cellular component organization at cellular level	2.63E-06
GO:0071841	cellular component organization or biogenesis at cellular level	4.78E-06
GO:0009653	anatomical structure morphogenesis	5.18E-06
GO:0048858	cell projection morphogenesis	6.27E-06
GO:0032990	cell part morphogenesis	8.10E-06
GO:0048869	cellular developmental process	1.15E-05
GO:0048667	cell morphogenesis involved in neuron differentiation	1.50E-05
GO:0000904	cell morphogenesis involved in differentiation	2.92E-05
GO:0000902	cell morphogenesis	3.21E-05
GO:0030154	cell differentiation	4.89E-05
GO:0032502	developmental process	5.12E-05
GO:0048812	neuron projection morphogenesis	5.21E-05
GO:0023052	signaling	5.49E-05
GO:0048856	anatomical structure development	7.29E-05
GO:0007399	nervous system development	8.05E-05
GO:0032989	cellular component morphogenesis	8.25E-05
GO:0007154	cell communication	8.67E-05
GO:0007165	signal transduction	9.39E-05
GO:0016568	chromatin modification	1.33E-04
GO:0040011	locomotion	1.95E-04
GO:0016570	histone modification	1.98E-04

GO:0007275	multicellular organismal development	1.98E-04
GO:0042522	regulation of tyrosine phosphorylation of Stat5 protein	1.99E-04
GO:0006928	cellular component movement	2.00E-04
GO:0031175	neuron projection development	2.03E-04
GO:0043954	cellular component maintenance	2.12E-04
GO:0048666	neuron development	2.22E-04
GO:0016569	covalent chromatin modification	2.49E-04
GO:0007409	axonogenesis	3.46E-04
GO:0042506	tyrosine phosphorylation of Stat5 protein	3.61E-04
GO:0007411	axon guidance	3.91E-04
GO:0050794	regulation of cellular process	4.05E-04
GO:0009790	embryo development	4.22E-04
GO:0048731	system development	4.66E-04
GO:0007167	enzyme linked receptor protein signaling pathway	5.18E-04
GO:0032501	multicellular organismal process	5.98E-04
GO:0045494	photoreceptor cell maintenance	6.02E-04
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	6.18E-04
GO:0048699	generation of neurons	7.18E-04
GO:0035234	germ cell programmed cell death	7.41E-04
GO:0051716	cellular response to stimulus	7.82E-04
GO:0022008	neurogenesis	8.44E-04
GO:0030182	neuron differentiation	9.80E-04
GO:0034204	lipid translocation	1.00E-03
GO:0045332	phospholipid translocation	1.00E-03
GO:0007018	microtubule-based movement	1.16E-03
GO:0002028	regulation of sodium ion transport	1.39E-03
GO:0022029	telencephalon cell migration	1.39E-03
GO:0022610	biological adhesion	1.40E-03
GO:0007155	cell adhesion	1.40E-03
GO:0065007	biological regulation	1.42E-03
GO:0033152	immunoglobulin V(D)J recombination	1.47E-03
GO:0048496	maintenance of organ identity	1.47E-03
GO:0006325	chromatin organization	1.51E-03
GO:0018205	peptidyl-lysine modification	1.54E-03

GO:0007166	cell surface receptor signaling pathway	1.55E-03
GO:0007420	brain development	1.57E-03
GO:0060113	inner ear receptor cell differentiation	1.57E-03
GO:0021885	forebrain cell migration	1.76E-03
GO:0042523	positive regulation of tyrosine phosphorylation of Stat5 protein	1.90E-03
GO:0006357	regulation of transcription from RNA polymerase II promoter	2.06E-03
GO:0050793	regulation of developmental process	2.18E-03
GO:0010390	histone monoubiquitination	2.28E-03
GO:0090286	cytoskeletal anchoring at nuclear membrane	2.43E-03
GO:0002024	diet induced thermogenesis	2.43E-03
GO:0048468	cell development	2.44E-03
GO:0042490	mechanoreceptor differentiation	2.44E-03
GO:0009987	cellular process	2.53E-03
GO:0051270	regulation of cellular component movement	2.59E-03
GO:0097035	regulation of membrane lipid distribution	2.70E-03
GO:0007517	muscle organ development	2.85E-03
GO:0048513	organ development	2.87E-03
GO:0046209	nitric oxide metabolic process	2.99E-03
GO:0009628	response to abiotic stimulus	3.13E-03
GO:0050789	regulation of biological process	3.14E-03
GO:0048839	inner ear development	3.47E-03
GO:0060425	lung morphogenesis	3.61E-03
GO:0060501	positive regulation of epithelial cell proliferation involved in lung morphogenesis	3.61E-03
GO:0060013	righting reflex	3.61E-03
GO:0060429	epithelium development	3.65E-03
GO:0008045	motor axon guidance	3.68E-03
GO:0044253	positive regulation of multicellular organismal metabolic process	3.68E-03
GO:0007417	central nervous system development	3.78E-03
GO:0007266	Rho protein signal transduction	3.85E-03
GO:0048870	cell motility	3.86E-03
GO:0051674	localization of cell	3.86E-03
GO:0051173	positive regulation of nitrogen compound metabolic process	3.86E-03
GO:0001539	ciliary or flagellar motility	4.25E-03
GO:0035272	exocrine system development	4.31E-03

GO:0060541	respiratory system development	4.52E-03
GO:0061061	muscle structure development	4.60E-03
GO:0016925	protein sumoylation	4.86E-03
GO:0018193	peptidyl-amino acid modification	4.95E-03
GO:0050957	equilibrioception	4.99E-03
GO:0035518	histone H2A monoubiquitination	4.99E-03
GO:0055091	phospholipid homeostasis	4.99E-03
GO:0033235	positive regulation of protein sumoylation	4.99E-03
GO:2000794	regulation of epithelial cell proliferation involved in lung morphogenesis	4.99E-03
GO:0055098	response to low-density lipoprotein particle stimulus	4.99E-03
GO:0022028	tangential migration from the subventricular zone to the olfactory bulb	4.99E-03
GO:0043967	histone H4 acetylation	5.10E-03
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	5.36E-03
GO:0051276	chromosome organization	5.41E-03
GO:0021772	olfactory bulb development	5.53E-03
GO:0021988	olfactory lobe development	5.53E-03
GO:0051050	positive regulation of transport	5.82E-03
GO:0032879	regulation of localization	5.97E-03
GO:0009888	tissue development	6.14E-03
GO:0002790	peptide secretion	6.21E-03
GO:0009268	response to pH	6.24E-03
GO:0051897	positive regulation of protein kinase B signaling cascade	6.46E-03
GO:0060502	epithelial cell proliferation involved in lung morphogenesis	6.59E-03
GO:0021537	telencephalon development	6.74E-03
GO:0030324	lung development	7.00E-03
GO:0044246	regulation of multicellular organismal metabolic process	7.01E-03
GO:0016573	histone acetylation	7.15E-03
GO:0032388	positive regulation of intracellular transport	7.15E-03
GO:0031344	regulation of cell projection organization	7.24E-03
GO:0010975	regulation of neuron projection development	7.34E-03
GO:0031328	positive regulation of cellular biosynthetic process	7.52E-03
GO:0006897	endocytosis	7.53E-03
GO:0040012	regulation of locomotion	7.63E-03
GO:0051179	localization	7.80E-03

GO:0018393	internal peptidyl-lysine acetylation	7.81E-03
GO:0030323	respiratory tube development	7.83E-03
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	8.04E-03
GO:0048266	behavioral response to pain	8.39E-03
GO:0031958	corticosteroid receptor signaling pathway	8.39E-03
GO:0042921	glucocorticoid receptor signaling pathway	8.39E-03
GO:0043949	regulation of cAMP-mediated signaling	8.39E-03
GO:0033233	regulation of protein sumoylation	8.39E-03
GO:0009887	organ morphogenesis	8.46E-03
GO:0010927	cellular component assembly involved in morphogenesis	8.51E-03
GO:0018394	peptidyl-lysine acetylation	8.51E-03
GO:0050954	sensory perception of mechanical stimulus	8.51E-03
GO:0006513	protein monoubiquitination	8.71E-03
GO:0072332	signal transduction by p53 class mediator resulting in induction of apoptosis	8.71E-03
GO:0006935	chemotaxis	9.10E-03
GO:0042330	taxis	9.10E-03
GO:0009891	positive regulation of biosynthetic process	9.36E-03
GO:0043583	ear development	9.38E-03
GO:0015833	peptide transport	9.46E-03
GO:0006475	internal protein amino acid acetylation	9.64E-03
GO:0048646	anatomical structure formation involved in morphogenesis	9.65E-03
GO:0060038	cardiac muscle cell proliferation	9.65E-03
GO:0016574	histone ubiquitination	9.65E-03
GO:0009605	response to external stimulus	9.76E-03

**D**

<b>Accession</b>	<b>GO Term Biological Processes enriched in down regulated genes</b>	<b>Canary</b>
GO:0071842	cellular component organization at cellular level	1.18E-14
GO:0016043	cellular component organization	1.46E-14
GO:0071841	cellular component organization or biogenesis at cellular level	5.97E-14
GO:0006996	organelle organization	8.99E-14
GO:0071840	cellular component organization or biogenesis	2.71E-13
GO:0051276	chromosome organization	3.27E-10
GO:0016568	chromatin modification	9.74E-10
GO:0009987	cellular process	1.55E-09
GO:0022402	cell cycle process	2.94E-09
GO:0055085	transmembrane transport	1.51E-08
GO:0006281	DNA repair	6.32E-08
GO:0007010	cytoskeleton organization	9.71E-08
GO:0007049	cell cycle	1.48E-07
GO:0022403	cell cycle phase	4.48E-07
GO:0016570	histone modification	9.72E-07
GO:0000278	mitotic cell cycle	1.24E-06
GO:0030030	cell projection organization	1.56E-06
GO:0042384	cilium assembly	1.93E-06
GO:0016569	covalent chromatin modification	2.10E-06
GO:0030031	cell projection assembly	2.64E-06
GO:0006325	chromatin organization	2.65E-06
GO:0051179	localization	2.68E-06
GO:0071897	DNA biosynthetic process	2.99E-06
GO:0007017	microtubule-based process	4.03E-06
GO:0051297	centrosome organization	4.80E-06
GO:0006260	DNA replication	4.94E-06
GO:0006811	ion transport	5.08E-06
GO:0007163	establishment or maintenance of cell polarity	7.90E-06
GO:0010927	cellular component assembly involved in morphogenesis	1.04E-05
GO:0006261	DNA-dependent DNA replication	1.07E-05

GO:0032502	developmental process	1.08E-05
GO:0006302	double-strand break repair	1.08E-05
GO:0060271	cilium morphogenesis	1.58E-05
GO:0018205	peptidyl-lysine modification	1.70E-05
GO:0032989	cellular component morphogenesis	1.73E-05
GO:0031023	microtubule organizing center organization	1.86E-05
GO:0032508	DNA duplex unwinding	2.19E-05
GO:0051298	centrosome duplication	2.19E-05
GO:0048869	cellular developmental process	2.66E-05
GO:0000902	cell morphogenesis	2.72E-05
GO:0006259	DNA metabolic process	3.07E-05
GO:0032392	DNA geometric change	3.35E-05
GO:0032501	multicellular organismal process	3.73E-05
GO:0000279	M phase	5.18E-05
GO:0048858	cell projection morphogenesis	5.27E-05
GO:0048856	anatomical structure development	5.29E-05
GO:0030010	establishment of cell polarity	5.62E-05
GO:0000226	microtubule cytoskeleton organization	5.67E-05
GO:0018394	peptidyl-lysine acetylation	8.04E-05
GO:0032990	cell part morphogenesis	9.36E-05
GO:0007098	centrosome cycle	9.39E-05
GO:0000724	double-strand break repair via homologous recombination	9.68E-05
GO:0051056	regulation of small GTPase mediated signal transduction	1.01E-04
GO:0016573	histone acetylation	1.10E-04
GO:0009653	anatomical structure morphogenesis	1.21E-04
GO:0000725	recombinational repair	1.25E-04
GO:0034968	histone lysine methylation	1.26E-04
GO:0006475	internal protein amino acid acetylation	1.30E-04
GO:0051647	nucleus localization	1.44E-04
GO:0018393	internal peptidyl-lysine acetylation	1.52E-04
GO:0000086	G2-M transition of mitotic cell cycle	1.58E-04
GO:0006464	cellular protein modification process	1.70E-04
GO:0036211	protein modification process	1.70E-04
GO:0061061	muscle structure development	1.72E-04

GO:0006310	DNA recombination	1.78E-04
GO:0050793	regulation of developmental process	1.93E-04
GO:0071702	organic substance transport	1.93E-04
GO:0006473	protein acetylation	2.03E-04
GO:0000132	establishment of mitotic spindle orientation	2.12E-04
GO:0010824	regulation of centrosome duplication	2.12E-04
GO:0031060	regulation of histone methylation	2.12E-04
GO:0051294	establishment of spindle orientation	2.12E-04
GO:0035023	regulation of Rho protein signal transduction	2.13E-04
GO:0043967	histone H4 acetylation	2.21E-04
GO:0051293	establishment of spindle localization	2.44E-04
GO:0051653	spindle localization	2.44E-04
GO:0022610	biological adhesion	2.76E-04
GO:0007155	cell adhesion	2.76E-04
GO:0000731	DNA synthesis involved in DNA repair	2.86E-04
GO:0031061	negative regulation of histone methylation	3.13E-04
GO:0051325	interphase	3.17E-04
GO:0016571	histone methylation	3.25E-04
GO:0046578	regulation of Ras protein signal transduction	3.54E-04
GO:0034661	ncRNA catabolic process	3.83E-04
GO:0046605	regulation of centrosome cycle	3.96E-04
GO:0048468	cell development	4.22E-04
GO:0030029	actin filament-based process	4.45E-04
GO:0007517	muscle organ development	4.63E-04
GO:0007266	Rho protein signal transduction	4.64E-04
GO:0006974	response to DNA damage stimulus	4.82E-04
GO:0043412	macromolecule modification	5.04E-04
GO:0051329	interphase of mitotic cell cycle	5.05E-04
GO:0043543	protein acylation	5.09E-04
GO:0000768	syncytium formation by plasma membrane fusion	5.70E-04
GO:0006301	postreplication repair	5.70E-04
GO:0051234	establishment of localization	5.95E-04
GO:0060537	muscle tissue development	5.96E-04
GO:0040001	establishment of mitotic spindle localization	6.48E-04



GO:0090286	cytoskeletal anchoring at nuclear membrane	7.16E-04
GO:0016075	rRNA catabolic process	7.56E-04
GO:0043966	histone H3 acetylation	8.17E-04
GO:0018193	peptidyl-amino acid modification	8.28E-04
GO:0043984	histone H4-K16 acetylation	9.29E-04
GO:0021955	central nervous system neuron axonogenesis	1.04E-03
GO:0006869	lipid transport	1.10E-03
GO:0007275	multicellular organismal development	1.12E-03
GO:0046777	protein autophosphorylation	1.12E-03
GO:0051960	regulation of nervous system development	1.14E-03
GO:0015695	organic cation transport	1.16E-03
GO:0051052	regulation of DNA metabolic process	1.16E-03
GO:0006479	protein methylation	1.18E-03
GO:0008213	protein alkylation	1.18E-03
GO:0000723	telomere maintenance	1.34E-03
GO:0030198	extracellular matrix organization	1.34E-03
GO:0043062	extracellular structure organization	1.34E-03
GO:0006928	cellular component movement	1.35E-03
GO:0006200	ATP catabolic process	1.38E-03
GO:0021834	chemorepulsion involved in embryonic olfactory bulb interneuron precursor migration	1.43E-03
GO:0030951	establishment or maintenance of microtubule cytoskeleton polarity	1.43E-03
GO:0034653	retinoic acid catabolic process	1.43E-03
GO:0050955	thermoception	1.43E-03
GO:0071321	cellular response to cGMP	1.43E-03
GO:0014706	striated muscle tissue development	1.52E-03
GO:0022029	telencephalon cell migration	1.54E-03
GO:0006622	protein targeting to lysosome	1.55E-03
GO:0006623	protein targeting to vacuole	1.55E-03
GO:0031062	positive regulation of histone methylation	1.55E-03
GO:0040023	establishment of nucleus localization	1.55E-03
GO:0051569	regulation of histone H3-K4 methylation	1.55E-03
GO:0072665	protein localization to vacuole	1.55E-03
GO:0072666	establishment of protein localization to vacuole	1.55E-03
GO:0032200	telomere organization	1.60E-03

GO:0006814	sodium ion transport	1.72E-03
GO:0033554	cellular response to stress	1.72E-03
GO:0060249	anatomical structure homeostasis	1.72E-03
GO:0034204	lipid translocation	1.73E-03
GO:0045332	phospholipid translocation	1.73E-03
GO:0021952	central nervous system projection neuron axonogenesis	1.73E-03
GO:0007044	cell-substrate junction assembly	1.75E-03
GO:0010876	lipid localization	1.81E-03
GO:0001843	neural tube closure	1.85E-03
GO:0022607	cellular component assembly	1.87E-03
GO:0007140	male meiosis	1.92E-03
GO:0051568	histone H3-K4 methylation	1.92E-03
GO:0033043	regulation of organelle organization	1.96E-03
GO:0030859	polarized epithelial cell differentiation	2.00E-03
GO:0051571	positive regulation of histone H3-K4 methylation	2.00E-03
GO:0070486	leukocyte aggregation	2.00E-03
GO:0007059	chromosome segregation	2.12E-03
GO:0065007	biological regulation	2.20E-03
GO:0060606	tube closure	2.21E-03
GO:0007127	meiosis I	2.26E-03
GO:0051716	cellular response to stimulus	2.35E-03
GO:0097035	regulation of membrane lipid distribution	2.36E-03
GO:0051726	regulation of cell cycle	2.40E-03
GO:0030154	cell differentiation	2.43E-03
GO:0007126	meiosis	2.46E-03
GO:0051327	M phase of meiotic cell cycle	2.46E-03
GO:0051640	organelle localization	2.46E-03
GO:0021885	forebrain cell migration	2.61E-03
GO:0001556	oocyte maturation	2.74E-03
GO:0006949	syncytium formation	2.74E-03
GO:0007099	centriole replication	2.74E-03
GO:0050919	negative chemotaxis	2.74E-03
GO:0000280	nuclear division	2.78E-03
GO:0007067	mitosis	2.78E-03

GO:0007520	myoblast fusion	2.80E-03
GO:0048666	neuron development	2.81E-03
GO:0007265	Ras protein signal transduction	2.93E-03
GO:0022604	regulation of cell morphogenesis	3.03E-03
GO:0051321	meiotic cell cycle	3.03E-03
GO:0014020	primary neural tube formation	3.11E-03
GO:0006468	protein phosphorylation	3.21E-03
GO:0065008	regulation of biological quality	3.22E-03
GO:0006810	transport	3.26E-03
GO:0015914	phospholipid transport	3.33E-03
GO:0000087	M phase of mitotic cell cycle	3.50E-03
GO:0055088	lipid homeostasis	3.57E-03
GO:0017158	regulation of calcium ion-dependent exocytosis	3.59E-03
GO:0061180	mammary gland epithelium development	3.67E-03
GO:0008015	blood circulation	4.09E-03
GO:0043981	histone H4-K5 acetylation	4.13E-03
GO:0043982	histone H4-K8 acetylation	4.13E-03
GO:0022028	tangential migration from the subventricular zone to the olfactory bulb	4.25E-03
GO:0009111	vitamin catabolic process	4.25E-03
GO:0042363	fat-soluble vitamin catabolic process	4.25E-03
GO:0043983	histone H4-K12 acetylation	4.25E-03
GO:0048096	chromatin-mediated maintenance of transcription	4.25E-03
GO:0051570	regulation of histone H3-K9 methylation	4.25E-03
GO:0060177	regulation of angiotensin metabolic process	4.25E-03
GO:0003013	circulatory system process	4.38E-03
GO:0006820	anion transport	4.57E-03
GO:0007143	female meiosis	4.66E-03
GO:0048841	regulation of axon extension involved in axon guidance	4.66E-03
GO:0050667	homocysteine metabolic process	4.66E-03
GO:0007160	cell-matrix adhesion	4.79E-03
GO:0008037	cell recognition	4.91E-03
GO:0031175	neuron projection development	4.93E-03
GO:0007399	nervous system development	5.07E-03
GO:0033152	immunoglobulin V(D)J recombination	5.08E-03

GO:0000019	regulation of mitotic recombination	5.08E-03
GO:0001778	plasma membrane repair	5.08E-03
GO:0010633	negative regulation of epithelial cell migration	5.08E-03
GO:0017014	protein nitrosylation	5.08E-03
GO:0018076	N-terminal peptidyl-lysine acetylation	5.08E-03
GO:0018119	peptidyl-cysteine S-nitrosylation	5.08E-03
GO:0019985	translesion synthesis	5.08E-03
GO:0021831	embryonic olfactory bulb interneuron precursor migration	5.08E-03
GO:0030301	cholesterol transport	5.08E-03
GO:0030952	establishment or maintenance of cytoskeleton polarity	5.08E-03
GO:0034983	peptidyl-lysine deacetylation	5.08E-03
GO:0044268	multicellular organismal protein metabolic process	5.08E-03
GO:0051573	negative regulation of histone H3-K9 methylation	5.08E-03
GO:0070305	response to cGMP	5.08E-03
GO:0070932	histone H3 deacetylation	5.08E-03
GO:0071670	smooth muscle cell chemotaxis	5.08E-03
GO:0006312	mitotic recombination	5.23E-03
GO:0031929	TOR signaling cascade	5.23E-03
GO:0022603	regulation of anatomical structure morphogenesis	5.25E-03
GO:0006812	cation transport	5.38E-03
GO:0060284	regulation of cell development	5.62E-03
GO:0006282	regulation of DNA repair	5.66E-03
GO:0048513	organ development	5.75E-03
GO:0001738	morphogenesis of a polarized epithelium	5.79E-03
GO:0017156	calcium ion-dependent exocytosis	5.90E-03
GO:0015918	sterol transport	5.96E-03
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	6.00E-03
GO:0070207	protein homotrimerization	6.00E-03
GO:0030036	actin cytoskeleton organization	6.17E-03
GO:0010564	regulation of cell cycle process	6.20E-03
GO:0006865	amino acid transport	6.25E-03
GO:0046942	carboxylic acid transport	6.54E-03
GO:0048285	organelle fission	6.56E-03
GO:0051656	establishment of organelle localization	6.70E-03

GO:0006801	superoxide metabolic process	6.86E-03
GO:0060415	muscle tissue morphogenesis	7.03E-03
GO:0030048	actin filament-based movement	7.05E-03
GO:0042632	cholesterol homeostasis	7.05E-03
GO:0055092	sterol homeostasis	7.05E-03
GO:0009314	response to radiation	7.09E-03
GO:0007141	male meiosis I	7.26E-03
GO:0015838	betaine transport	7.26E-03
GO:0015879	carnitine transport	7.26E-03
GO:0032371	regulation of sterol transport	7.26E-03
GO:0032374	regulation of cholesterol transport	7.26E-03
GO:0060601	lateral sprouting from an epithelium	7.26E-03
GO:0060041	retina development in camera-type eye	7.61E-03
GO:0006793	phosphorus metabolic process	7.69E-03
GO:0006796	phosphate-containing compound metabolic process	7.69E-03
GO:0015849	organic acid transport	7.71E-03
GO:0021826	substrate-independent telencephalic tangential migration	7.76E-03
GO:0021843	substrate-independent telencephalic tangential interneuron migration	7.76E-03
GO:0043116	negative regulation of vascular permeability	7.76E-03
GO:0046599	regulation of centriole replication	7.76E-03
GO:0048793	pronephros development	7.76E-03
GO:0050951	sensory perception of temperature stimulus	7.76E-03
GO:0043414	macromolecule methylation	8.04E-03
GO:0055008	cardiac muscle tissue morphogenesis	8.23E-03
GO:0031589	cell-substrate adhesion	8.26E-03
GO:0015697	quaternary ammonium group transport	8.40E-03
GO:0031057	negative regulation of histone modification	8.40E-03
GO:0051898	negative regulation of protein kinase B signaling cascade	8.40E-03
GO:0051493	regulation of cytoskeleton organization	8.42E-03
GO:0032886	regulation of microtubule-based process	8.59E-03
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	8.69E-03
GO:0051128	regulation of cellular component organization	8.94E-03
GO:0051347	positive regulation of transferase activity	9.11E-03
GO:0048812	neuron projection morphogenesis	9.38E-03

GO:0021987 cerebral cortex development 9.62E-03  
 GO:0044085 cellular component biogenesis 9.63E-03  
 GO:0048731 system development 9.77E-03

**E**

Neuronal Process	Accession	GO TERM	Robin	Canary
Development and Differentiation	GO:0048667	cell morphogenesis involved in neuron differentiation	1.50E-05	
	GO:0007399	nervous system development	8.05E-05	5.07E-03
	GO:0048666	neuron development	2.22E-04	2.81E-03
	GO:0030182	neuron differentiation	9.80E-04	
	GO:0007420	brain development	1.57E-03	
	GO:0007417	central nervous system development	3.78E-03	
	GO:0021772	olfactory bulb development	5.53E-03	
	GO:0021988	olfactory lobe development	5.53E-03	
	GO:0021537	telencephalon development	6.74E-03	
	GO:0021987	cerebral cortex development		9.62E-03
Projection Development	GO:0051960	regulation of nervous system development		1.14E-03
	GO:0048812	neuron projection morphogenesis	5.21E-05	9.38E-03
	GO:0031175	neuron projection development	2.03E-04	4.93E-03
	GO:0007409	axonogenesis	3.46E-04	
	GO:0007411	axon guidance	3.91E-04	
	GO:0008045	motor axon guidance	3.68E-03	
	GO:0010975	regulation of neuron projection development	7.34E-03	
	GO:0021952	central nervous system projection neuron axonogenesis		1.73E-03
Neurogenesis	GO:0021955	central nervous system neuron axonogenesis		1.04E-03
	GO:0048841	regulation of axon extension involved in axon guidance		4.66E-03
	GO:0048699	generation of neurons	7.18E-04	
	GO:0022008	neurogenesis	8.44E-04	
	GO:0022029	telencephalon cell migration	1.39E-03	1.54E-03
	GO:0021885	forebrain cell migration	1.76E-03	2.61E-03
	GO:0022028	tangential migration from the subventricular zone to the olfactory bulb	4.99E-03	4.25E-03
	GO:0021826	substrate-independent telencephalic tangential migration		7.76E-03
	GO:0021831	embryonic olfactory bulb interneuron precursor migration		5.08E-03
GO:0021834	chemorepulsion involved in embryonic olfactory bulb interneuron precursor migration		1.43E-03	
GO:0021843	substrate-independent telencephalic tangential interneuron migration		7.76E-03	