

Table 2 The overrepresented GO terms of the 5% lowest codon biased genes

GO ACCESSION	CHI-SQUARED	P-VALUE	GO TERM
GO:0000187	8.4261	0.003699	activation of MAPK activity
GO:0009952	17.0015	3.74E-005	anterior/posterior pattern specification
GO:0019882	0.009208	0.0009208	antigen processing and presentation
GO:0045177	8.6621	0.003249	apical part of cell
GO:0016324	18.6789	1.55E-005	apical plasma membrane
GO:0006915	37.8925	7.48E-010	apoptotic process
GO:0008026	20.1178	7.28E-006	ATP-dependent helicase activity
GO:0030424	7.4806	2.90E-005	axon
GO:0007411	15.8045	7.02E-005	axon guidance
GO:0001568	8.8982	0.00002854	blood vessel development
GO:0030054	25.8794	3.63E-007	cell junction
GO:0016477	16.0439	6.19E-005	cell migration
GO:0000902	10.556	0.001158	cell morphogenesis
GO:0007166	22.7576	1.84E-006	cell surface receptor signaling pathway
GO:0005911	14.1308	0.0001705	cell-cell junction
GO:0008234	12.9371	0.0003221	cysteine-type peptidase activity
GO:0019221	10.3192	0.0001317	cytokine-mediated signaling pathway
GO:0006952	9.608	0.0001937	defense response
GO:0042742	5.6186	0.0001777	defense response to bacterium
GO:0050830	4.4694	0.00003451	defense response to Gram-positive bacterium
GO:0051607	4.927	0.00000264	defense response to virus
GO:0050911	210.002	2.20E-016	detection of chemical stimulus involved in sensory perception of smell
GO:0003677	250.5647	2.20E-016	DNA binding
GO:0006310	9.608	0.001937	DNA recombination
GO:0009953	5.8503	0.01557	dorsal/ventral pattern formation
GO:0009790	11.7456	0.0006099	embryo development
GO:0031012	40.535	1.93E-010	extracellular matrix
GO:0030198	13.8919	0.0001936	extracellular matrix organization
GO:0007156	22.5175	2.08E-006	homophilic cell adhesion
GO:0006955	38.6133	5.17E-010	immune
GO:0001822	13.4144	0.0002497	kidney development
GO:0030027	13.1757	0.0002836	lamellipodium
GO:0016874	14.8478	0.0001165	ligate activity
GO:0006629	24.6785	6.77E-007	lipid metabolic process
GO:0005764	0.8375	5.00E-006	lysosome
GO:0008237	20.1178	7.28E-006	metallopeptidase activity
GO:0015630	16.5226	4.81E-005	microtubule cytoskeleton
GO:0007399	14.1308	0.0001705	nervous system development
GO:0001764	13.8919	0.0001936	neuron migration
GO:0005654	19.8779	8.26E-006	nucleoplasm
GO:0017111	31.4052	2.09E-008	nucleoside-triphosphatase activity
GO:0006334	18.6789	1.55E-005	nucleosome assembly
GO:0004984	210.002	2.20E-016	olfactory receptor activity
GO:0009887	11.7456	0.0006099	organ morphogenesis
GO:0008233	59.0155	1.56E-014	peptidase activity

Continuing table 2

GO ACCESSION	CHI-SQUARED	P-VALUE	GO TERM
GO:0005543	4.5283	9.52E-016	phospholipid binding
GO:0016773	15.8045	7.02E-005	phosphotransferase activity, alcohol group as acceptor
GO:0005886	267.1531	2.20E-016	plasma membrane
GO:0010628	22.9977	1.62E-006	positive regulation of gene expression
GO:0051712	988.1238	2.20E-016	positive regulation of killing of cells of other organism
GO:0006813	22.7576	1.84E-006	potassium ion transport
GO:0046777	25.399	4.66E-007	protein autophosphorylation
GO:0046983	6.5226	4.81E-005	protein dimerization activity
GO:0019904	19.6381	9.36E-006	protein domain specific binding
GO:0006468	144.374	2.20E-016	protein phosphorylation
GO:0004713	95.6153	2.20E-016	protein tyrosine kinase activity
GO:0004725	18.9187	1.36E-005	protein tyrosine phosphatase activity
GO:0042127	20.5976	5.67E-006	regulation of cell proliferation
GO:0009411	4.4694	0.00003451	response to UV
GO:0009615	13.6531	0.0002199	response to virus
GO:0008236	19.3982	1.06E-005	serine-type peptidase activity
GO:0007165	377.3029	2.20E-016	signal transduction
GO:0001501	12.4602	0.0004157	skeletal system development
GO:0043588	5.3875	0.02028	skin development
GO:0046332	4.0154	0.00004509	SMAD binding
GO:0048538	0.02644	0.02644	thymus development
GO:0016055	12.9371	0.0003221	Wnt receptor signaling pathway