

## Additional file 3

GO term	number of samples	number of control	P-value for high conservation	P-value for low conservation
P:development	649	4136	0	1.000000
P:regulation of transcription	602	4183	1.67E-15	1.000000
F:transcription factor activity	263	4760	3.44E-15	1.000000
P:transcription	640	4145	4.11E-14	1.000000
P:nervous system development	154	4631	1.99E-10	1.000000
P:organ development	213	4572	2.30E-10	1.000000
P:signal transduction	994	3791	5.19E-10	1.000000
F:DNA binding	628	4395	3.19E-08	1.000000
P:morphogenesis	212	4573	9.78E-08	1.000000
P:cell surface receptor linked signal transduction	363	4422	2.23E-06	0.999998
P:negative regulation of metabolism	107	4678	1.02E-05	0.999990
F:receptor binding	221	4802	1.90E-05	0.999981
P:cell-cell signaling	176	4609	2.27E-05	0.999977
F:cytoskeletal protein binding	137	4886	4.97E-05	0.999950
P:negative regulation of biological process	327	4458	6.87E-05	0.999931
F:ion channel activity	98	4925	9.87E-05	0.999901
C:extracellular matrix	111	4401	0.000119	0.999881
C:actin cytoskeleton	85	4427	0.000164	0.999837
P:cell differentiation	173	4612	0.000179	0.999821
P:cell adhesion	242	4543	0.000182	0.999818
P:cellular morphogenesis	111	4674	0.000607	0.999393
F:ion transporter activity	237	4786	0.001493	0.998508
P:protein amino acid phosphorylation	213	4572	0.001593	0.998407
P:ion transport	239	4546	0.001825	0.998176
F:protein kinase activity	220	4803	0.002033	0.997967
P:intracellular signaling cascade	431	4354	0.006872	0.993129
P:chromosome organization and biogenesis	105	4680	0.007832	0.992170
C:plasma membrane	608	3904	0.008026	0.991975
F:GTPase activity	88	4935	0.011437	0.988566
P:cytoskeleton organization and biogenesis	155	4630	0.011868	0.988133
P:small GTPase mediated signal transduction	126	4659	0.012373	0.987629
P:cell proliferation	258	4527	0.016427	0.983575
F:GTP binding	160	4863	0.026124	0.973879
F:calcium ion binding	280	4743	0.058031	0.941974
P:cell motility	105	4680	0.061020	0.938989
F:receptor activity	391	4632	0.078737	0.921269
F:structural molecule activity	307	4716	0.079056	0.920950
P:G-protein coupled receptor protein signaling pathway	153	4632	0.108505	0.891506
F:phosphoric ester hydrolase activity	113	4910	0.138352	0.861663
F:enzyme regulator activity	238	4785	0.148055	0.851956
P:protein complex assembly	122	4663	0.154119	0.845897
P:vesicle-mediated transport	190	4595	0.166697	0.833317
P:protein kinase cascade	118	4667	0.173566	0.826451
C:nucleoplasm	107	4405	0.198841	0.801180
C:Golgi apparatus	216	4296	0.202850	0.797165
F:zinc ion binding	600	4423	0.232496	0.767514
F:carrier activity	149	4874	0.239577	0.760441
P:intracellular transport	350	4435	0.240786	0.759226
P:sensory perception	111	4674	0.293922	0.706102
P:cell cycle	340	4445	0.297867	0.702148
F:RNA binding	290	4733	0.320681	0.679334
P:positive regulation of biological process	275	4510	0.345462	0.654555
F:ATP binding	520	4503	0.376693	0.623319
F:ubiquitin-protein ligase activity	144	4879	0.426143	0.573880
P:DNA metabolism	266	4519	0.454829	0.545189
P:apoptosis	244	4541	0.532993	0.467026
C:microtubule cytoskeleton	115	4397	0.540403	0.459626
P:protein folding	121	4664	0.586660	0.413366
C:endoplasmic reticulum	268	4244	0.591106	0.408913
C:extracellular space	179	4333	0.608820	0.391202
P:response to chemical stimulus	129	4656	0.645196	0.354828

F:ATPase activity	130	4893	0.647215	0.352808
P:ubiquitin cycle	235	4550	0.654462	0.345556
C:endomembrane system	163	4349	0.667170	0.332852
C:chromosome	108	4404	0.692915	0.307111
C:organelle envelope	148	4364	0.696927	0.303096
P:response to abiotic stimulus	148	4637	0.720140	0.279881
C:vesicle	86	4426	0.734101	0.265927
P:secretory pathway	102	4683	0.777510	0.222512
C:endosome	33	4479	0.801091	0.198946
C:ubiquitin ligase complex	122	4390	0.815112	0.184907
C:organelle membrane	242	4270	0.832397	0.167616
P:cofactor metabolism	100	4685	0.901092	0.098920
C:cytosol	171	4341	0.924121	0.075887
C:spliceosome complex	37	4475	0.931290	0.068727
F:magnesium ion binding	135	4888	0.946019	0.053988
P:alcohol metabolism	133	4652	0.977205	0.022798
P:lipid biosynthesis	101	4684	0.978371	0.021633
P:RNA processing	198	4587	0.979718	0.020285
P:response to stress	446	4339	0.984169	0.015833
P:proteolysis	259	4526	0.993157	0.006844
F:peptidase activity	227	4796	0.994409	0.005592
F:iron ion binding	111	4912	0.994501	0.005500
P:immune response	270	4515	0.994563	0.005437
C:nucleolus	63	4449	0.995546	0.004455
P:response to biotic stimulus	318	4467	0.999107	0.000893
F:nuclease activity	60	4963	0.999228	0.000772
P:protein biosynthesis	283	4502	0.999370	0.000630
C:peroxisome	49	4463	0.999377	0.000623
P:carbohydrate metabolism	220	4565	0.999722	0.000278
P:catabolism	260	4525	0.999749	0.000251
P:electron transport	151	4634	0.999764	0.000236
P:amino acid metabolism	112	4673	0.999898	0.000102
F:structural constituent of ribosome	130	4893	0.999994	5.76E-06
P:carboxylic acid metabolism	225	4560	0.999996	4.43E-06
P:lipid metabolism	260	4525	0.999999	1.04E-06
C:ribosome	114	4398	0.999999	7.54E-07
C:lysosome	77	4435	1.000000	9.94E-08
F:oxidoreductase activity	309	4714	1.000000	2.07E-08
C:mitochondrion	398	4114	1.000000	5.31E-09