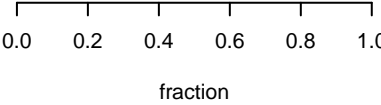
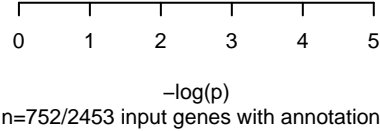


GO:BP
Ncol_Nvec_vc1.1_XM_001627792.3

fraction genes in fg and expected value

macropinocytosis	GO:0044351	p=1.7E-03	n=5
response to platelet aggregation inhibit...	GO:0061478	p=1.7E-03	n=5
regulation of reactive oxygen species bi...	GO:1903426	p=2.5E-03	n=12
regulation of nitric-oxide synthase acti...	GO:0050999	p=2.6E-03	n=7
negative regulation of macromolecule met...	GO:0010605	p=3.4E-03	n=182
cellular response to catecholamine stimu...	GO:0071870	p=3.5E-03	n=13
regulation of vasoconstriction	GO:0019229	p=4.4E-03	n=14
modulation by symbiont of host cellular ...	GO:0044068	p=6.0E-03	n=4
cellular response to forskolin	GO:1904322	p=6.0E-03	n=4
SCF complex assembly	GO:0010265	p=6.0E-03	n=4
mushroom body development	GO:0016319	p=7.3E-03	n=12
retina homeostasis	GO:0001895	p=7.3E-03	n=12
regulation of cell maturation	GO:1903429	p=7.3E-03	n=12
glutamate metabolic process	GO:0006536	p=7.5E-03	n=6
positive regulation of amine transport	GO:0051954	p=7.5E-03	n=6
regulation of embryonic pattern specific...	GO:1902875	p=7.5E-03	n=6
regulation of pole plasm oskar mRNA loca...	GO:0007317	p=7.5E-03	n=6
protein nitrosylation	GO:0017014	p=7.5E-03	n=6
B cell homeostasis	GO:0001782	p=7.5E-03	n=6
regulation of signal transduction by p53...	GO:1901796	p=7.7E-03	n=18
negative regulation of nitrogen compound...	GO:0051172	p=8.4E-03	n=156
G2/M transition of mitotic cell cycle	GO:0000086	p=8.8E-03	n=27
regulation of nitric oxide biosynthetic ...	GO:0045428	p=8.9E-03	n=9
sensory perception of light stimulus	GO:0050953	p=9.0E-03	n=16
response to gamma radiation	GO:0010332	p=9.3E-03	n=11
mRNA polyadenylation	GO:0006378	p=9.3E-03	n=11
regulation of gene expression, epigeneti...	GO:0040029	p=1.1E-02	n=31
photoreceptor cell maintenance	GO:0045494	p=1.2E-02	n=10
negative regulation of G2/M transition o...	GO:0010972	p=1.2E-02	n=10
cellular response to unfolded protein	GO:0034620	p=1.3E-02	n=21

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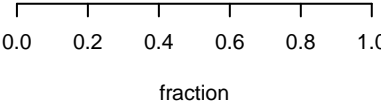
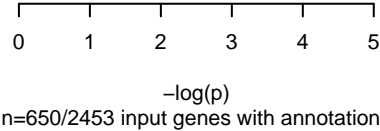


GO:MF
Ncol_Nvec_vc1.1_XM_001627792.3

fraction genes in fg and expected value

regulatory RNA binding	GO:0061980	p=5.6E-03	n=4
carboxy-lyase activity	GO:0016831	p=6.9E-03	n=6
outward rectifier potassium channel acti...	GO:0015271	p=6.9E-03	n=6
ATPase binding	GO:0051117	p=8.9E-03	n=14
mRNA binding	GO:0003729	p=1.1E-02	n=30
transcription corepressor activity	GO:0003714	p=1.2E-02	n=17
hydrolase activity, acting on carbon-nit...	GO:0016810	p=1.8E-02	n=14
potassium channel inhibitor activity	GO:0019870	p=1.9E-02	n=5
miRNA binding	GO:0035198	p=2.1E-02	n=3
Wnt-activated receptor activity	GO:0042813	p=2.1E-02	n=3
pre-mRNA intronic binding	GO:0097157	p=2.1E-02	n=3
tRNA (cytosine) methyltransferase activi...	GO:0016427	p=2.1E-02	n=3
protein serine/threonine/tyrosine kinase...	GO:0004712	p=2.4E-02	n=7
deacetylase activity	GO:0019213	p=2.4E-02	n=7
structural constituent of cytoskeleton	GO:0005200	p=2.4E-02	n=7
peptidyl-prolyl cis-trans isomerase acti...	GO:0003755	p=3.1E-02	n=6
frizzled binding	GO:0005109	p=3.1E-02	n=6
cis-trans isomerase activity	GO:0016859	p=3.1E-02	n=6
histone deacetylase activity	GO:0004407	p=3.1E-02	n=6
cytoskeletal protein binding	GO:0008092	p=3.7E-02	n=63
hydrolase activity, acting on carbon-nit...	GO:0016811	p=3.8E-02	n=10
potassium channel regulator activity	GO:0015459	p=3.9E-02	n=7
structural constituent of ribosome	GO:0003735	p=4.2E-02	n=22
protein kinase binding	GO:0019901	p=4.4E-02	n=55
mRNA 3'-UTR binding	GO:0003730	p=4.5E-02	n=8
phospholipase A2 activity	GO:0004623	p=5.2E-02	n=4
voltage-gated potassium channel activity...	GO:0086090	p=5.2E-02	n=4
voltage-gated potassium channel activity...	GO:0086087	p=5.2E-02	n=4
voltage-gated potassium channel activity...	GO:0086089	p=5.2E-02	n=4
voltage-gated potassium channel activity...	GO:0086008	p=5.2E-02	n=4

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GO:CC
Ncol_Nvec_vc1.1_XM_001627792.3

fraction genes in fg and expected value

protein-containing complex	GO:0032991	p=2.0E-03	n=357
filamentous actin	GO:0031941	p=6.0E-03	n=4
voltage-gated potassium channel complex	GO:0008076	p=6.7E-03	n=7
motile cilium	GO:0031514	p=8.1E-03	n=24
intracellular non-membrane-bounded organ...	GO:0043232	p=9.2E-03	n=279
cell body membrane	GO:0044298	p=1.2E-02	n=10
axoneme	GO:0005930	p=1.3E-02	n=16
ribonucleoprotein complex	GO:1990904	p=1.5E-02	n=82
ciliary plasm	GO:0097014	p=1.8E-02	n=16
ribosome	GO:0005840	p=1.8E-02	n=28
large ribosomal subunit	GO:0015934	p=1.8E-02	n=17
Bcl-2 family protein complex	GO:0097136	p=2.1E-02	n=3
centrosome	GO:0005813	p=2.3E-02	n=50
sensory dendrite	GO:0071683	p=2.3E-02	n=4
polytene chromosome chromocenter	GO:0005701	p=2.3E-02	n=4
neuronal cell body membrane	GO:0032809	p=2.5E-02	n=9
plasma membrane bounded cell projection ...	GO:0032838	p=2.6E-02	n=19
extracellular space	GO:0005615	p=3.0E-02	n=31
intercalated disc	GO:0014704	p=3.2E-02	n=8
ribosomal subunit	GO:0044391	p=3.3E-02	n=24
90S preribosome	GO:0030686	p=3.3E-02	n=6
dendrite	GO:0030425	p=4.1E-02	n=56
nuclear speck	GO:0016607	p=4.2E-02	n=31
photoreceptor inner segment	GO:0001917	p=4.3E-02	n=7
paranode region of axon	GO:0033270	p=4.3E-02	n=5
dendritic tree	GO:0097447	p=4.5E-02	n=56
cytosolic large ribosomal subunit	GO:0022625	p=4.7E-02	n=12
sarcolemma	GO:0042383	p=4.7E-02	n=12
mitochondrial protein-containing complex	GO:0098798	p=4.8E-02	n=24
SCF ubiquitin ligase complex	GO:0019005	p=4.9E-02	n=8

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