

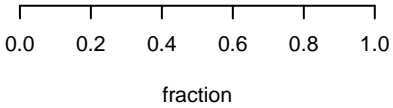
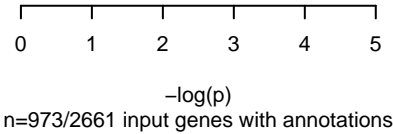
GO:BP
Ncol_Nvec_vc1.1_XM_048731647.1

fraction genes in fg and expected value

mitochondrial translational termination	GO:0070126
mRNA polyadenylation	GO:0006378
neuromuscular process controlling postur...	GO:0050884
positive regulation of mRNA processing	GO:0050685
rRNA processing	GO:0006364
mRNA splicing, via spliceosome	GO:0000398
mitochondrial translational elongation	GO:0070125
positive regulation of transcription of ...	GO:1901838
endoplasmic reticulum to Golgi vesicle-m...	GO:0006888
ribonucleoprotein complex biogenesis	GO:0022613
cytosolic transport	GO:0016482
post-Golgi vesicle-mediated transport	GO:0006892
cilium assembly	GO:0060271
maintenance of protein localization in o...	GO:0072595
negative regulation of DNA biosynthetic ...	GO:2000279
organelle organization	GO:0006996
tRNA methylation	GO:0030488
nuclear-transcribed mRNA catabolic proce...	GO:0000288
microtubule-based movement	GO:0007018
protein polyubiquitination	GO:0000209
dsRNA transport	GO:0033227
negative regulation of telomere maintena...	GO:0032205
activation of GTPase activity	GO:0090630
lipoprotein metabolic process	GO:0042157
ATP synthesis coupled electron transport	GO:0042773
mitochondrial ATP synthesis coupled elec...	GO:0042775
telomere maintenance	GO:0000723
telomere organization	GO:0032200
extracellular transport	GO:0006858
epithelial cilium movement involved in e...	GO:0003351

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p=4.3E-04	n=15
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p=7.8E-04	n=7
p=7.9E-04	n=34
p=8.5E-04	n=49
p=9.1E-04	n=14
p=2.2E-03	n=6
p=3.7E-03	n=25
p=4.2E-03	n=73
p=4.6E-03	n=31
p=4.6E-03	n=22
p=5.0E-03	n=58
p=5.9E-03	n=8
p=6.0E-03	n=5
p=6.5E-03	n=393
p=6.9E-03	n=9
p=7.9E-03	n=12
p=8.8E-03	n=52
p=1.0E-02	n=41
p=1.1E-02	n=6
p=1.1E-02	n=6
p=1.1E-02	n=16
p=1.1E-02	n=16
p=1.2E-02	n=15
p=1.2E-02	n=15
p=1.2E-02	n=15
p=1.3E-02	n=24
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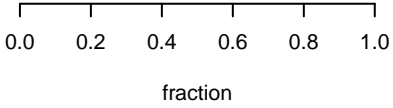
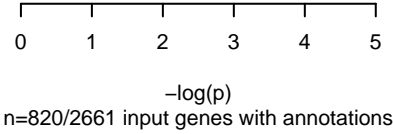
GO:MF
Ncol_Nvec_vc1.1_XM_048731647.1

fraction genes in fg and expected value

small GTPase binding	GO:0031267
ubiquitin protein ligase activity	GO:0061630
tRNA (guanine) methyltransferase activit...	GO:0016423
catalytic activity, acting on RNA	GO:0140098
RNA binding	GO:0003723
ATP-dependent activity	GO:0140657
alpha-tubulin binding	GO:0043014
oxidoreduction-driven active transmembra...	GO:0015453
ATP hydrolysis activity	GO:0016887
palmitoyl hydrolase activity	GO:0098599
palmitoyl-(protein) hydrolase activity	GO:0008474
phosphatidylinositol 3-kinase binding	GO:0043548
oxidoreductase activity, acting on NAD(P...	GO:0016655
SNARE binding	GO:0000149
pentosyltransferase activity	GO:0016763
telomeric DNA binding	GO:0042162
deacetylase activity	GO:0019213
histone deacetylase activity	GO:0004407
primary active transmembrane transporter...	GO:0015399
syntaxin binding	GO:0019905
RNA methyltransferase activity	GO:0008173
hydrolase activity, acting on acid anhyd...	GO:0016817
hydrolase activity, acting on acid anhyd...	GO:0016818
pyrophosphatase activity	GO:0016462
RNA 7-methylguanosine cap binding	GO:0000340
PTB domain binding	GO:0051425
annealing activity	GO:0140666
dipeptidase activity	GO:0016805
pre-mRNA intronic binding	GO:0097157
caspase binding	GO:0089720

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p=1.1E-02	n=11
p=1.4E-02	n=49
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p=1.4E-02	n=4
p=2.1E-02	n=5
p=2.2E-02	n=9
p=2.3E-02	n=17
p=2.4E-02	n=8
p=2.4E-02	n=8
p=2.4E-02	n=8
p=2.4E-02	n=7
p=2.4E-02	n=22
p=2.8E-02	n=12
p=3.4E-02	n=16
p=4.0E-02	n=71
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GO:CC
Ncol_Nvec_vc1.1_XM_048731647.1

fraction genes in fg and expected value

nucleoplasm	GO:0005654
intracellular anatomical structure	GO:0005622
catalytic complex	GO:1902494
nuclear protein-containing complex	GO:0140513
inner mitochondrial membrane protein com...	GO:0098800
intracellular protein-containing complex	GO:0140535
intracellular non-membrane-bounded organ...	GO:0043232
mitochondrial small ribosomal subunit	GO:0005763
trans-Golgi network membrane	GO:0032588
methyltransferase complex	GO:0034708
proton-transporting two-sector ATPase co...	GO:0016469
Prp19 complex	GO:0000974
nuclear telomere cap complex	GO:0000783
ribonucleoprotein complex	GO:1990904
mediator complex	GO:0016592
DNA-directed RNA polymerase complex	GO:0000428
mitochondrial respirasome	GO:0005746
cytosol	GO:0005829
respiratory chain complex	GO:0098803
spliceosomal complex	GO:0005681
AP-type membrane coat adaptor complex	GO:0030119
nuclear DNA-directed RNA polymerase comp...	GO:0055029
axoneme	GO:0005930
nuclear membrane	GO:0031965
RNA polymerase I complex	GO:0005736
ciliary plasm	GO:0097014
catalytic step 2 spliceosome	GO:0071013
centrosome	GO:0005813
vesicle tethering complex	GO:0099023
plasma membrane proton-transporting V-ty...	GO:0033181

p=8.7E-06	n=330
p=2.8E-05	n=946
p=7.8E-05	n=182
p=2.8E-04	n=155
p=1.9E-03	n=20
p=2.0E-03	n=109
p=2.7E-03	n=361
p=4.2E-03	n=7
p=5.5E-03	n=19
p=5.5E-03	n=19
p=5.7E-03	n=8
p=5.9E-03	n=5
p=5.9E-03	n=5
p=6.4E-03	n=114
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p=6.9E-03	n=15
p=7.4E-03	n=419
p=7.5E-03	n=13
p=8.3E-03	n=24
p=1.0E-02	n=6
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p=1.3E-02	n=19
p=1.5E-02	n=31
p=1.7E-02	n=4
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p=2.2E-02	n=62
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