

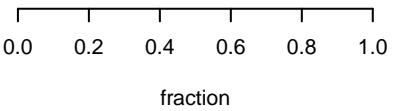
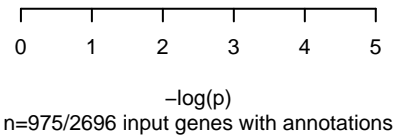
GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_001639766.3

fraction genes in fg and expected value

mRNA splicing, via spliceosome	GO:0000398
mRNA polyadenylation	GO:0006378
post-Golgi vesicle-mediated transport	GO:0006892
positive regulation of mRNA processing	GO:0050685
mitochondrial translational termination	GO:0070126
endoplasmic reticulum to Golgi vesicle-m...	GO:0006888
mitochondrial ATP synthesis coupled elec...	GO:0042775
mitochondrial translational elongation	GO:0070125
rRNA processing	GO:0006364
maintenance of protein localization in o...	GO:0072595
negative regulation of DNA biosynthetic ...	GO:2000279
dolichol-linked oligosaccharide biosynth...	GO:0006488
mitochondrial respiratory chain complex ...	GO:0033108
tRNA methylation	GO:0030488
aerobic electron transport chain	GO:0019646
double-strand break repair via nonhomolo...	GO:0006303
regulation of telomere maintenance via t...	GO:0032210
ribonucleoprotein complex biogenesis	GO:0022613
microtubule-based transport	GO:0099111
negative regulation of telomere maintena...	GO:0032205
neuromuscular process controlling postur...	GO:0050884
negative regulation of chromosome organi...	GO:2001251
extracellular transport	GO:0006858
epithelial cilium movement involved in e...	GO:0003351
regulation of locomotion involved in loc...	GO:0090325
protein ubiquitination	GO:0016567
RNA methylation	GO:0001510
regulation of microtubule-based movement	GO:0060632
negative regulation of mRNA metabolic pr...	GO:1903312
ribonucleoprotein complex subunit organi...	GO:0071826

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p=5.8E-04	n=24
p=7.9E-04	n=7
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p=3.8E-03	n=25
p=4.1E-03	n=16
p=4.1E-03	n=13
p=4.3E-03	n=32
p=5.9E-03	n=8
p=6.1E-03	n=5
p=6.1E-03	n=5
p=6.3E-03	n=18
p=7.0E-03	n=9
p=7.7E-03	n=14
p=7.9E-03	n=13
p=8.0E-03	n=12
p=8.8E-03	n=70
p=8.8E-03	n=28
p=1.1E-02	n=6
p=1.1E-02	n=6
p=1.3E-02	n=20
p=1.3E-02	n=7
p=1.3E-02	n=7
p=1.3E-02	n=7
p=1.5E-02	n=80
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p=1.5E-02	n=11
p=1.6E-02	n=10
p=1.7E-02	n=36

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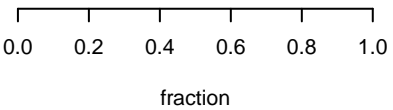
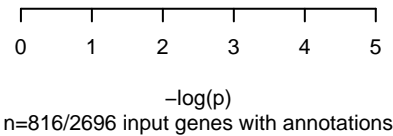
GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_001639766.3

fraction genes in fg and expected value

small GTPase binding	GO:0031267
ubiquitin protein ligase activity	GO:0061630
tRNA (guanine) methyltransferase activit...	GO:0016423
oxidoreduction-driven active transmembra...	GO:0015453
catalytic activity, acting on RNA	GO:0140098
phosphatase inhibitor activity	GO:0019212
alpha-tubulin binding	GO:0043014
NADH dehydrogenase activity	GO:0003954
copper ion binding	GO:0005507
structural constituent of ribosome	GO:0003735
RNA binding	GO:0003723
endoribonuclease activity	GO:0004521
O-methyltransferase activity	GO:0008171
nuclear localization sequence binding	GO:0008139
phosphatidylinositol 3-kinase binding	GO:0043548
oxidoreductase activity, acting on NAD(P...	GO:0016655
unfolded protein binding	GO:0051082
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
pentosyltransferase activity	GO:0016763
telomeric DNA binding	GO:0042162
NADH dehydrogenase (ubiquinone) activity	GO:0008137
NADH dehydrogenase (quinone) activity	GO:0050136
electron transfer activity	GO:0009055
ATP-dependent activity	GO:0140657
histone binding	GO:0042393
RNA methyltransferase activity	GO:0008173
ATP hydrolysis activity	GO:0016887
RNA 7-methylguanosine cap binding	GO:0000340
PTB domain binding	GO:0051425
annealing activity	GO:0140666

p=1.2E-04	n=55
p=3.8E-04	n=39
p=1.6E-03	n=6
p=2.5E-03	n=12
p=7.0E-03	n=50
p=8.2E-03	n=6
p=1.0E-02	n=7
p=1.1E-02	n=9
p=1.1E-02	n=9
p=1.5E-02	n=28
p=1.5E-02	n=100
p=2.0E-02	n=10
p=2.1E-02	n=5
p=2.1E-02	n=5
p=2.1E-02	n=5
p=2.2E-02	n=9
p=2.2E-02	n=20
p=2.3E-02	n=8
p=2.3E-02	n=8
p=2.3E-02	n=8
p=2.3E-02	n=8
p=2.3E-02	n=8
p=2.5E-02	n=16
p=2.8E-02	n=52
p=3.0E-02	n=20
p=3.3E-02	n=16
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p=4.1E-02	n=3

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GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_001639766.3

fraction genes in fg and expected value

catalytic complex	GO:1902494
nucleoplasm	GO:0005654
intracellular protein-containing complex	GO:0140535
intracellular anatomical structure	GO:0005622
nuclear protein-containing complex	GO:0140513
spliceosomal complex	GO:0005681
mitochondrial ribosome	GO:0005761
mitochondrial protein-containing complex	GO:0098798
proton-transporting two-sector ATPase co...	GO:0016469
Prp19 complex	GO:0000974
nuclear telomere cap complex	GO:0000783
small ribosomal subunit	GO:0015935
vesicle tethering complex	GO:0099023
mitochondrial respiratory chain complex ...	GO:0005747
cytoplasm	GO:0005737
AP-type membrane coat adaptor complex	GO:0030119
transferase complex	GO:1990234
intracellular organelle	GO:0043229
RNA polymerase complex	GO:0030880
cytosol	GO:0005829
methyltransferase complex	GO:0034708
nuclear membrane	GO:0031965
RNA polymerase I complex	GO:0005736
catalytic step 2 spliceosome	GO:0071013
nuclear DNA-directed RNA polymerase comp...	GO:0055029
plasma membrane proton-transporting V-ty...	GO:0033181
proton-transporting V-type ATPase comple...	GO:0033176
U12-type spliceosomal complex	GO:0005689
organellar small ribosomal subunit	GO:0000314
mitochondrial small ribosomal subunit	GO:0005763

p=7.1E-06	n=180
p=1.6E-04	n=322
p=4.6E-04	n=106
p=1.5E-03	n=943
p=2.8E-03	n=147
p=3.4E-03	n=25
p=3.9E-03	n=13
p=4.3E-03	n=37
p=5.7E-03	n=8
p=5.9E-03	n=5
p=5.9E-03	n=5
p=6.9E-03	n=15
p=7.5E-03	n=13
p=7.5E-03	n=11
p=8.0E-03	n=798
p=1.0E-02	n=6
p=1.1E-02	n=96
p=1.3E-02	n=842
p=1.4E-02	n=26
p=1.4E-02	n=416
p=1.4E-02	n=18
p=1.5E-02	n=31
p=1.7E-02	n=4
p=2.0E-02	n=14
p=2.3E-02	n=24
p=2.5E-02	n=5
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