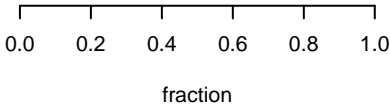
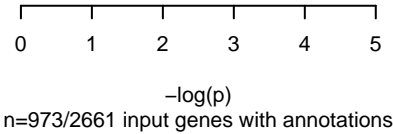
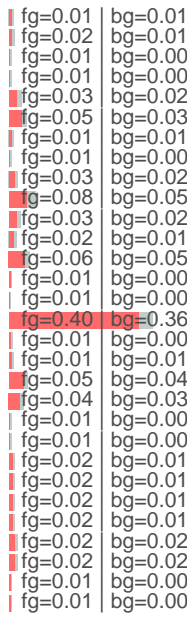
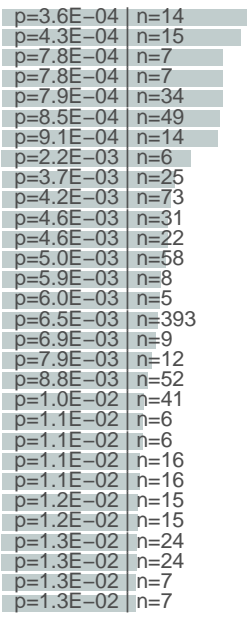


GO:BP
Ncol_Nvec_vc1.1_XM_048730629.1

fraction genes in fg and expected value

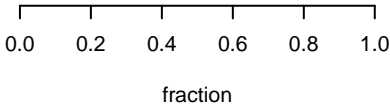
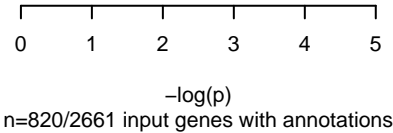
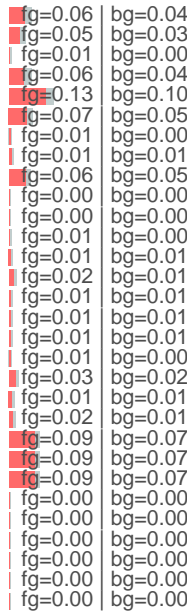
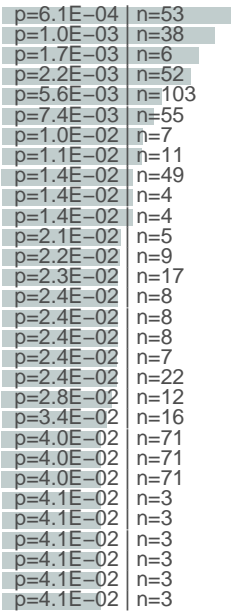
mitochondrial translational termination GO:0070126
mRNA polyadenylation GO:0006378
neuromuscular process controlling postur... GO:0050884
positive regulation of mRNA processing GO:0050685
rRNA processing GO:0006364
mRNA splicing, via spliceosome GO:0000398
mitochondrial translational elongation GO:0070125
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



GO:MF
Ncol_Nvec_vc1.1_XM_048730629.1

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



GO:CC
Ncol_Nvec_vc1.1_XM_048730629.1

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

