

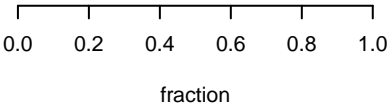
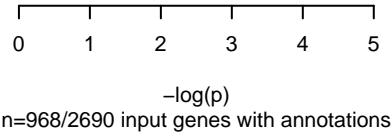
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_048730629.1

fraction genes in fg and expected value

RNA methylation	GO:0001510
mRNA polyadenylation	GO:0006378
ncRNA processing	GO:0034470
activation of GTPase activity	GO:0090630
mitochondrial translational termination	GO:0070126
maturation of SSU-rRNA	GO:0030490
positive regulation of transcription of ...	GO:1901838
Golgi vesicle transport	GO:0048193
mRNA splicing, via spliceosome	GO:0000398
protein export from nucleus	GO:0006611
mitochondrial translational elongation	GO:0070125
protein polyubiquitination	GO:0000209
maintenance of protein localization in o...	GO:0072595
negative regulation of DNA biosynthetic ...	GO:2000279
cytoplasmic pattern recognition receptor...	GO:0039528
ribosome biogenesis	GO:0042254
microtubule-based movement	GO:0007018
cilium organization	GO:0044782
mRNA export from nucleus	GO:0006406
positive regulation of mRNA metabolic pr...	GO:1903313
mRNA methylation	GO:0080009
neuromuscular process controlling postur...	GO:0050884
energy coupled proton transmembrane tran...	GO:0015988
lipoprotein metabolic process	GO:0042157
post-Golgi vesicle-mediated transport	GO:0006892
ATP synthesis coupled electron transport	GO:0042773
mitochondrial ATP synthesis coupled elec...	GO:0042775
cilium assembly	GO:0060271
extracellular transport	GO:0006858
epithelial cilium movement involved in e...	GO:0003351

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p=4.0E-04	n=15
p=9.3E-04	n=62
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p=1.9E-03	n=14
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p=2.4E-03	n=49
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p=3.5E-03	n=33
p=3.8E-03	n=13
p=4.8E-03	n=42
p=5.6E-03	n=8
p=5.9E-03	n=5
p=5.9E-03	n=5
p=7.7E-03	n=50
p=7.9E-03	n=52
p=8.4E-03	n=58
p=8.5E-03	n=19
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p=1.0E-02	n=6
p=1.0E-02	n=6
p=1.0E-02	n=6
p=1.1E-02	n=16
p=1.1E-02	n=21
p=1.2E-02	n=15
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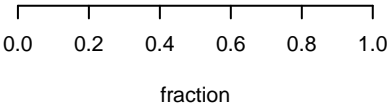
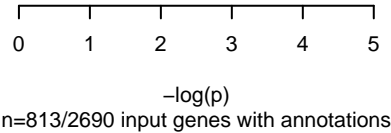
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_048730629.1

fraction genes in fg and expected value

RNA methyltransferase activity	GO:0008173
ubiquitin protein ligase activity	GO:0061630
alpha-tubulin binding	GO:0043014
small GTPase binding	GO:0031267
oxidoreductase activity, acting on NAD(P)...	GO:0016655
cysteine-type peptidase activity	GO:0008234
deubiquitinase activity	GO:0101005
NADH dehydrogenase activity	GO:0003954
catalytic activity, acting on RNA	GO:0140098
palmitoyl hydrolase activity	GO:0098599
palmitoyl-(protein) hydrolase activity	GO:0008474
ATP-dependent activity	GO:0140657
RNA binding	GO:0003723
pyrophosphate hydrolysis-driven proton t...	GO:0009678
O-methyltransferase activity	GO:0008171
ATPase activity, coupled to transmembran...	GO:0044769
proton-transporting ATPase activity, rot...	GO:0046961
phosphatidylinositol 3-kinase binding	GO:0043548
oxidoreductase activity, acting on the a...	GO:0016903
tRNA (guanine) methyltransferase activit...	GO:0016423
nucleotidyltransferase activity	GO:0016779
SNARE binding	GO:0000149
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
NADH dehydrogenase (ubiquinone) activity	GO:0008137
NADH dehydrogenase (quinone) activity	GO:0050136
beta-tubulin binding	GO:0048487
histone binding	GO:0042393
ATP hydrolysis activity	GO:0016887
oxidoreduction-driven active transmembra...	GO:0015453
RNA 7-methylguanosine cap binding	GO:0000340

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p=5.5E-03	n=18
p=1.0E-02	n=11
p=1.1E-02	n=9
p=1.2E-02	n=52
p=1.4E-02	n=4
p=1.4E-02	n=4
p=1.7E-02	n=53
p=1.9E-02	n=99
p=2.0E-02	n=5
p=2.0E-02	n=5
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p=2.0E-02	n=5
p=2.1E-02	n=20
p=2.1E-02	n=17
p=2.2E-02	n=8
p=2.2E-02	n=8
p=2.2E-02	n=8
p=2.3E-02	n=7
p=2.8E-02	n=20
p=3.2E-02	n=47
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_048730629.1

fraction genes in fg and expected value

nucleoplasm	GO:0005654
intracellular anatomical structure	GO:0005622
nuclear protein-containing complex	GO:0140513
ribonucleoprotein complex	GO:1990904
methyltransferase complex	GO:0034708
plasma membrane proton-transporting V-ty...	GO:0033181
intracellular protein-containing complex	GO:0140535
intracellular non-membrane-bounded organ...	GO:0043232
endopeptidase complex	GO:1905369
mitochondrial ribosome	GO:0005761
trans-Golgi network	GO:0005802
catalytic complex	GO:1902494
axoneme	GO:0005930
RNA polymerase complex	GO:0030880
proton-transporting two-sector ATPase co...	GO:0033178
Prp19 complex	GO:0000974
mediator complex	GO:0016592
mitochondrial respiratory chain complex ...	GO:0005747
mitochondrial protein-containing complex	GO:0098798
AP-type membrane coat adaptor complex	GO:0030119
vacuolar proton-transporting V-type ATPa...	GO:0016471
preribosome, small subunit precursor	GO:0030688
proteasome complex	GO:0000502
trans-Golgi network membrane	GO:0032588
DNA-directed RNA polymerase complex	GO:0000428
RNA polymerase I complex	GO:0005736
spliceosomal complex	GO:0005681
centrosome	GO:0005813
small ribosomal subunit	GO:0015935
catalytic step 2 spliceosome	GO:0071013

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p=2.8E-03	n=108
p=3.3E-03	n=362
p=3.5E-03	n=16
p=3.6E-03	n=13
p=4.0E-03	n=37
p=4.3E-03	n=183
p=4.6E-03	n=20
p=5.6E-03	n=27
p=5.7E-03	n=5
p=5.7E-03	n=5
p=6.3E-03	n=9
p=7.1E-03	n=11
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