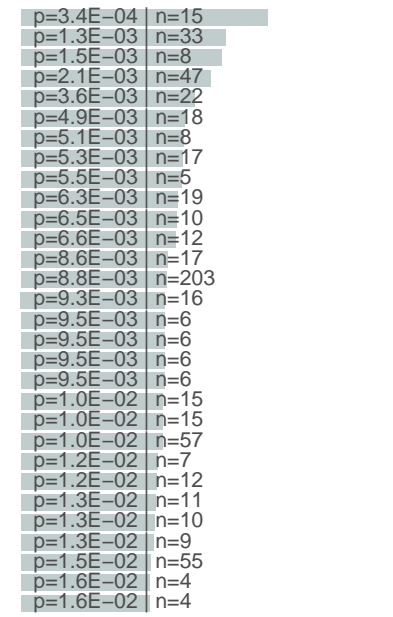


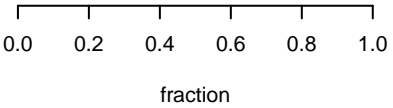
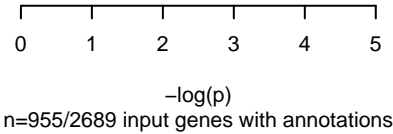
GO:BP
Elav_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

mRNA polyadenylation	GO:0006378
rRNA processing	GO:0006364
epithelial cilium movement involved in e...	GO:0003351
mRNA splicing, via spliceosome	GO:0000398
post-Golgi vesicle-mediated transport	GO:0006892
mitochondrial respiratory chain complex ...	GO:0033108
maintenance of protein localization in o...	GO:0072595
ribosomal small subunit biogenesis	GO:0042274
negative regulation of DNA biosynthetic ...	GO:2000279
RNA methylation	GO:0001510
vesicle-mediated transport between endos...	GO:0098927
mitochondrial translational termination	GO:0070126
tRNA modification	GO:0006400
intracellular transport	GO:0046907
activation of GTPase activity	GO:0090630
peptidyl-lysine dimethylation	GO:0018027
nucleolus organization	GO:0007000
mRNA methylation	GO:0080009
neuromuscular process controlling postur...	GO:0050884
ATP synthesis coupled electron transport	GO:0042773
mitochondrial ATP synthesis coupled elec...	GO:0042775
cilium organization	GO:0044782
regulation of locomotion involved in loc...	GO:0090325
mitochondrial translational elongation	GO:0070125
regulation of vesicle fusion	GO:0031338
negative regulation of mRNA metabolic pr...	GO:1903312
intraciliary transport	GO:0042073
cilium assembly	GO:0060271
proton motive force-driven mitochondrial...	GO:0042776
male sex determination	GO:0030238



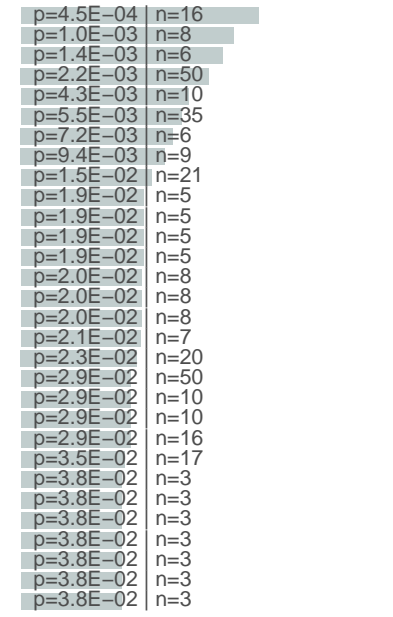
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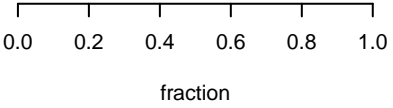
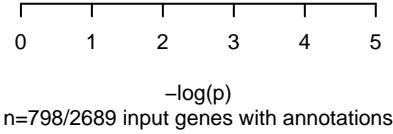
GO:MF
Elav_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

RNA methyltransferase activity	GO:0008173
alpha-tubulin binding	GO:0043014
O-methyltransferase activity	GO:0008171
small GTPase binding	GO:0031267
oxidoreductase activity, acting on NAD(P)...	GO:0016655
ubiquitin protein ligase activity	GO:0061630
phosphatase inhibitor activity	GO:0019212
NADH dehydrogenase activity	GO:0003954
S-adenosylmethionine-dependent methyltra...	GO:0008757
nuclear localization sequence binding	GO:0008139
RNA polymerase II general transcription ...	GO:0001091
phosphatidylinositol 3-kinase binding	GO:0043548
tRNA (guanine) methyltransferase activit...	GO:0016423
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
catalytic activity, acting on RNA	GO:0140098
oxidoreduction-driven active transmembra...	GO:0015453
deubiquitinase activity	GO:0101005
cysteine-type peptidase activity	GO:0008234
helicase activity	GO:0004386
RNA 7-methylguanosine cap binding	GO:0000340
PTB domain binding	GO:0051425
annealing activity	GO:0140666
phosphorylase kinase regulator activity	GO:0008607
oligosaccharyl transferase activity	GO:0004576
dipeptidase activity	GO:0016805
pre-mRNA intronic binding	GO:0097157



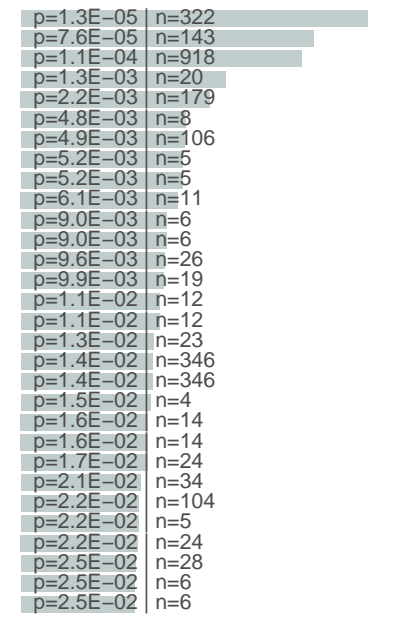
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GO:CC
Elav_Nvec_vc1.1_XM_032361906.2

fraction genes in fg and expected value

nucleoplasm	GO:0005654
nuclear protein-containing complex	GO:0140513
intracellular anatomical structure	GO:0005622
methyltransferase complex	GO:0034708
catalytic complex	GO:1902494
proton-transporting two-sector ATPase co...	GO:0016469
ribonucleoprotein complex	GO:1990904
Prp19 complex	GO:0000974
proteasome regulatory particle, lid subc...	GO:0008541
mitochondrial respiratory chain complex ...	GO:0005747
AP-type membrane coat adaptor complex	GO:0030119
preribosome, small subunit precursor	GO:0030688
RNA polymerase complex	GO:0030880
axoneme	GO:0005930
organellar ribosome	GO:0000313
mitochondrial ribosome	GO:0005761
spliceosomal complex	GO:0005681
non-membrane-bounded organelle	GO:0043228
intracellular non-membrane-bounded organ...	GO:0043232
RNA polymerase I complex	GO:0005736
small ribosomal subunit	GO:0015935
catalytic step 2 spliceosome	GO:0071013
nuclear DNA-directed RNA polymerase comp...	GO:0055029
trans-Golgi network	GO:0005802
intracellular protein-containing complex	GO:0140535
plasma membrane proton-transporting V-ty...	GO:0033181
DNA-directed RNA polymerase complex	GO:0000428
late endosome	GO:0005770
proton-transporting V-type ATPase comple...	GO:0033176
U12-type spliceosomal complex	GO:0005689



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