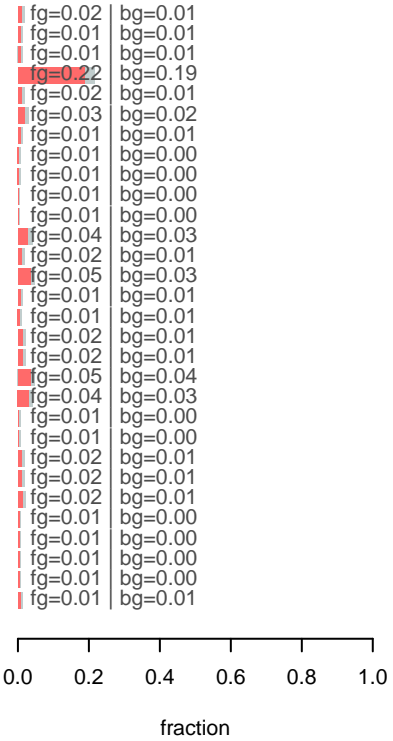
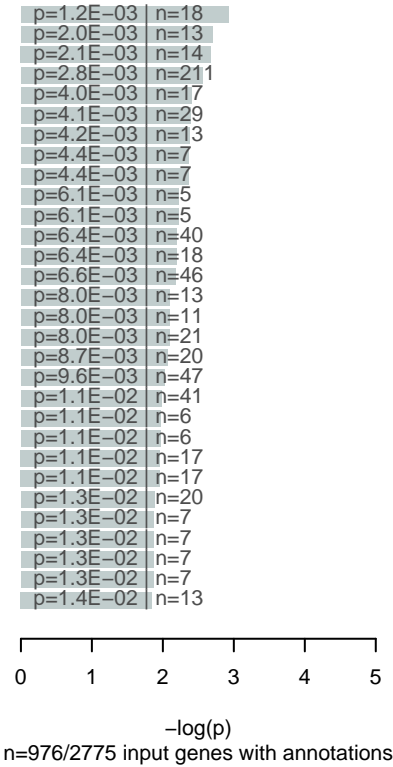


GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001631403.3

fraction genes in fg and expected value

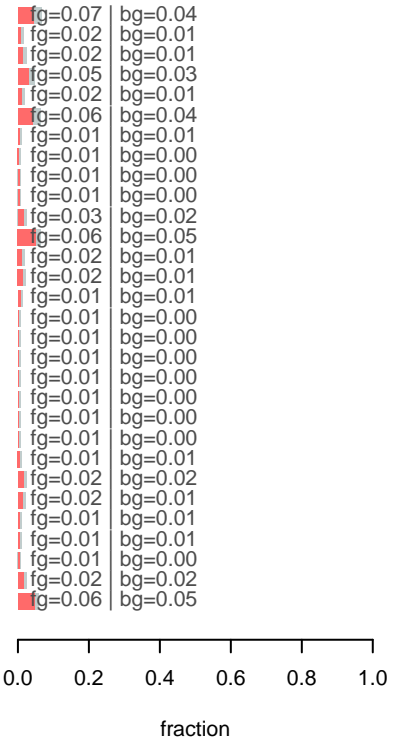
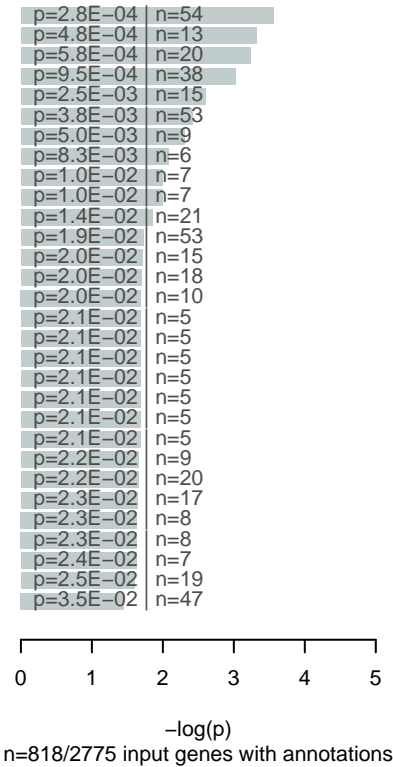
RNA methylation	GO:0001510
mitochondrial translational termination	GO:0070126
mRNA polyadenylation	GO:0006378
intracellular transport	GO:0046907
activation of GTPase activity	GO:0090630
microtubule-based transport	GO:0099111
mitochondrial translational elongation	GO:0070125
snRNA 3'-end processing	GO:0034472
maintenance of protein location in nucle...	GO:0051457
negative regulation of DNA biosynthetic ...	GO:2000279
cytoplasmic pattern recognition receptor...	GO:0039528
rRNA metabolic process	GO:0016072
mitochondrial respiratory chain complex ...	GO:0033108
mRNA splicing, via spliceosome	GO:0000398
maturation of SSU-rRNA	GO:0030490
mitochondrial electron transport, NADH t...	GO:0006120
tRNA processing	GO:0008033
RNA phosphodiester bond hydrolysis	GO:0090501
Golgi vesicle transport	GO:0048193
protein polyubiquitination	GO:0000209
neuromuscular process controlling postur...	GO:0050884
energy coupled proton transmembrane tran...	GO:0015988
histone lysine methylation	GO:0034968
tRNA modification	GO:0006400
negative regulation of chromosome organi...	GO:2001251
extracellular transport	GO:0006858
epithelial cilium movement involved in e...	GO:0003351
pinocytosis	GO:0006907
regulation of locomotion involved in loc...	GO:0090325
NADH dehydrogenase complex assembly	GO:0010257



GO:MF  
Elav\_Nvec\_vc1.1\_XM\_001631403.3

fraction genes in fg and expected value

small GTPase binding	GO:0031267
deubiquitinase activity	GO:0101005
cysteine-type peptidase activity	GO:0008234
ubiquitin protein ligase activity	GO:0061630
RNA methyltransferase activity	GO:0008173
catalytic activity, acting on RNA	GO:0140098
NADH dehydrogenase (ubiquinone) activity	GO:0008137
phosphatase inhibitor activity	GO:0019212
signal sequence binding	GO:0005048
alpha-tubulin binding	GO:0043014
histone binding	GO:0042393
ATP-dependent activity	GO:0140657
ribonuclease activity	GO:0004540
helicase activity	GO:0004386
endoribonuclease activity	GO:0004521
pyrophosphate hydrolysis-driven proton t...	GO:0009678
rDNA binding	GO:0000182
nuclear localization sequence binding	GO:0008139
ATPase activity, coupled to transmembran...	GO:0044769
proton-transporting ATPase activity, rot...	GO:0046961
phosphatidylinositol 3-kinase binding	GO:0043548
tRNA (guanine) methyltransferase activit...	GO:0016423
cysteine-type endopeptidase activity	GO:0004197
nucleotidyltransferase activity	GO:0016779
SNARE binding	GO:0000149
telomeric DNA binding	GO:0042162
cysteine-type deubiquitinase activity	GO:0004843
beta-tubulin binding	GO:0048487
endopeptidase activity	GO:0004175
ATP hydrolysis activity	GO:0016887



GO:CC  
Elav\_Nvec\_vc1.1\_XM\_001631403.3

fraction genes in fg and expected value

nucleoplasm	GO:0005654
intracellular anatomical structure	GO:0005622
mitochondrial ribosome	GO:0005761
ribonucleoprotein complex	GO:1990904
intracellular non-membrane-bounded organ...	GO:0043232
mitochondrial respiratory chain complex ...	GO:0005747
methyltransferase complex	GO:0034708
plasma membrane proton-transporting V-ty...	GO:0033181
catalytic complex	GO:1902494
nuclear protein-containing complex	GO:0140513
nuclear DNA-directed RNA polymerase comp...	GO:0055029
intracellular protein-containing complex	GO:0140535
proton-transporting two-sector ATPase co...	GO:0033178
Prp19 complex	GO:0000974
proteasome regulatory particle, lid subc...	GO:0008541
peptidase complex	GO:1905368
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
axoneme	GO:0005930
organellar large ribosomal subunit	GO:0000315
mitochondrial large ribosomal subunit	GO:0005762
centrosome	GO:0005813
nuclear membrane	GO:0031965
microtubule organizing center	GO:0005815
RNA polymerase I complex	GO:0005736
microtubule cytoskeleton	GO:0015630
spliceosomal complex	GO:0005681
ciliary plasm	GO:0097014

