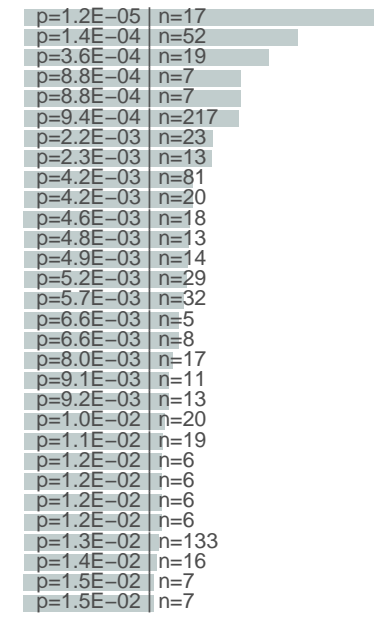


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_048725325.1

fraction genes in fg and expected value

mRNA polyadenylation	GO:0006378
mRNA splicing, via spliceosome	GO:0000398
RNA methylation	GO:0001510
neuromuscular process controlling postur...	GO:0050884
positive regulation of mRNA processing	GO:0050685
intracellular transport	GO:0046907
post-Golgi vesicle-mediated transport	GO:0006892
mitochondrial translational termination	GO:0070126
ncRNA metabolic process	GO:0034660
ncRNA transcription	GO:0098781
histone lysine methylation	GO:0034968
mitochondrial translational elongation	GO:0070125
mitochondrial respiratory chain complex ...	GO:0032981
microtubule-based transport	GO:0099111
rRNA processing	GO:0006364
dolichol-linked oligosaccharide biosynth...	GO:0006488
maintenance of protein localization in o...	GO:0072595
ribosomal small subunit biogenesis	GO:0042274
mitochondrial electron transport, NADH t...	GO:0006120
double-strand break repair via nonhomolo...	GO:0006303
mRNA transport	GO:0051028
mRNA export from nucleus	GO:0006406
peptidyl-lysine dimethylation	GO:0018027
mRNA methylation	GO:0080009
negative regulation of histone methylati...	GO:0031061
energy coupled proton transmembrane tran...	GO:0015988
RNA processing	GO:0006396
activation of GTPase activity	GO:0090630
negative regulation of mRNA processing	GO:0050686
regulation of locomotion involved in loc...	GO:0090325



0 1 2 3 4 5  
-log(p)  
n=990/2790 input genes with annotations

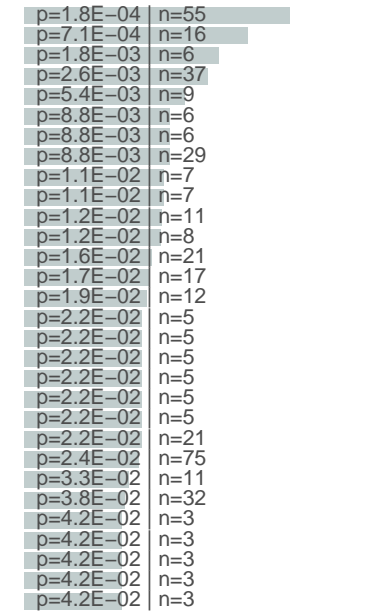
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fraction

GO:MF  
Fox\_Nvec\_vc1.1\_XM\_048725325.1

fraction genes in fg and expected value

small GTPase binding	GO:0031267
RNA methyltransferase activity	GO:0008173
O-methyltransferase activity	GO:0008171
ubiquitin protein ligase activity	GO:0061630
NADH dehydrogenase (ubiquinone) activity	GO:0008137
polynucleotide adenyllyltransferase activ...	GO:0004652
phosphatase inhibitor activity	GO:0019212
structural constituent of ribosome	GO:0003735
signal sequence binding	GO:0005048
alpha-tubulin binding	GO:0043014
deubiquitinase activity	GO:0101005
tRNA methyltransferase activity	GO:0008175
histone binding	GO:0042393
cysteine-type peptidase activity	GO:0008234
ubiquitin-like protein peptidase activit...	GO:0019783
pyrophosphate hydrolysis-driven proton t...	GO:0009678
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
S-adenosylmethionine-dependent methyltra...	GO:0008757
catalytic activity, acting on a nucleic ...	GO:0140640
protein serine/threonine phosphatase act...	GO:0004722
peptidase activity	GO:0008233
RNA 7-methylguanosine cap binding	GO:0000340
PTB domain binding	GO:0051425
Lys48-specific deubiquitinase activity	GO:1990380
annealing activity	GO:0140666
oligosaccharyl transferase activity	GO:0004576



0 1 2 3 4 5  
-log(p)  
n=827/2790 input genes with annotations

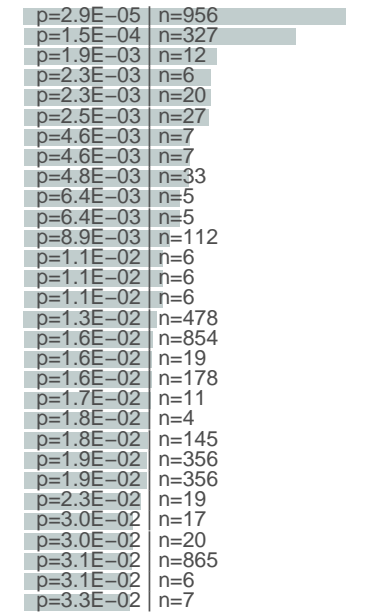
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0.0 0.2 0.4 0.6 0.8 1.0  
fraction

GO:CC  
Fox\_Nvec\_vc1.1\_XM\_048725325.1

fraction genes in fg and expected value

intracellular anatomical structure	GO:0005622
nucleoplasm	GO:0005654
mitochondrial respiratory chain complex ...	GO:0005747
plasma membrane proton-transporting V-ty...	GO:0033181
methyltransferase complex	GO:0034708
nuclear DNA-directed RNA polymerase comp...	GO:0055029
U12-type spliceosomal complex	GO:0005689
mitochondrial small ribosomal subunit	GO:0005763
nuclear membrane	GO:0031965
proton-transporting two-sector ATPase co...	GO:0033178
Prp19 complex	GO:0000974
ribonucleoprotein complex	GO:1990904
AP-type membrane coat adaptor complex	GO:0030119
vacuolar proton-transporting V-type ATPa...	GO:0016471
periribosome, small subunit precursor	GO:0030688
protein-containing complex	GO:0032991
intracellular organelle	GO:0043229
axoneme	GO:0005930
catalytic complex	GO:1902494
cytosolic small ribosomal subunit	GO:0022627
RNA polymerase I complex	GO:0005736
nuclear protein-containing complex	GO:0140513
non-membrane-bounded organelle	GO:0043228
intracellular non-membrane-bounded organ...	GO:0043232
ciliary plasm	GO:0097014
small ribosomal subunit	GO:0015935
RNA polymerase II, holoenzyme	GO:0016591
organelle	GO:0043226
nuclear envelope lumen	GO:0005641
integrator complex	GO:0032039



0 1 2 3 4 5  
-log(p)  
n=985/2790 input genes with annotations

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fraction