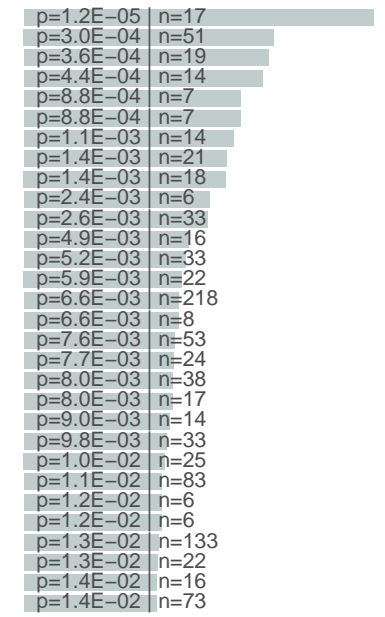


GO:BP
Fox_Nvec_vc1.1_XM_032376930.1

fraction genes in fg and expected value

mRNA polyadenylation	GO:0006378
mRNA splicing, via spliceosome	GO:0000398
RNA methylation	GO:0001510
mitochondrial translational termination	GO:0070126
neuromuscular process controlling postur...	GO:0050884
positive regulation of mRNA processing	GO:0050685
mitochondrial translational elongation	GO:0070125
mRNA export from nucleus	GO:0006406
activation of GTPase activity	GO:0090630
positive regulation of transcription of ...	GO:1901838
rRNA processing	GO:0006364
mitochondrial ATP synthesis coupled elec...	GO:0042775
protein export from nucleus	GO:0006611
post-Golgi vesicle-mediated transport	GO:0006892
intracellular transport	GO:0046907
maintenance of protein localization in o...	GO:0072595
microtubule-based movement	GO:0007018
DNA damage checkpoint signaling	GO:0000077
regulation of mRNA metabolic process	GO:1903311
ribosomal small subunit biogenesis	GO:0042274
aerobic electron transport chain	GO:0019646
purine ribonucleoside monophosphate meta...	GO:0009167
ribonucleoprotein complex localization	GO:0071166
ncRNA metabolic process	GO:0034660
mRNA methylation	GO:0080009
energy coupled proton transmembrane tran...	GO:0015988
RNA processing	GO:0006396
ncRNA transcription	GO:0098781
lipoprotein metabolic process	GO:0042157
mRNA processing	GO:0006397



0 1 2 3 4 5
-log(p)
n=990/2780 input genes with annotations

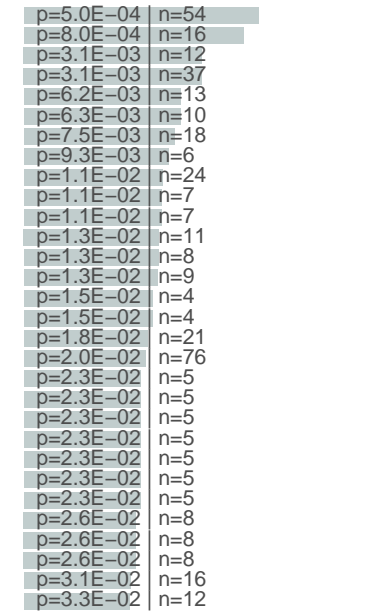
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fraction

GO:MF
Fox_Nvec_vc1.1_XM_032376930.1

fraction genes in fg and expected value

small GTPase binding	GO:0031267
RNA methyltransferase activity	GO:0008173
oxidoreduction-driven active transmembra...	GO:0015453
ubiquitin protein ligase activity	GO:0061630
ubiquitin-like protein peptidase activit...	GO:0019783
oxidoreductase activity, acting on NAD(P...	GO:0016655
cysteine-type peptidase activity	GO:0008234
polynucleotide adenyllyltransferase activ...	GO:0004652
nucleotidyltransferase activity	GO:0016779
signal sequence binding	GO:0005048
alpha-tubulin binding	GO:0043014
deubiquitinase activity	GO:0101005
tRNA methyltransferase activity	GO:0008175
NADH dehydrogenase activity	GO:0003954
palmitoyl hydrolase activity	GO:0098599
palmitoyl-(protein) hydrolase activity	GO:0008474
histone binding	GO:0042393
catalytic activity, acting on a nucleic ...	GO:0140640
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
NAD(P)H dehydrogenase (quinone) activity	GO:0003955
NADH dehydrogenase (ubiquinone) activity	GO:0008137
NADH dehydrogenase (quinone) activity	GO:0050136
electron transfer activity	GO:0009055
proton transmembrane transporter activit...	GO:0015078



0 1 2 3 4 5
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n=835/2780 input genes with annotations

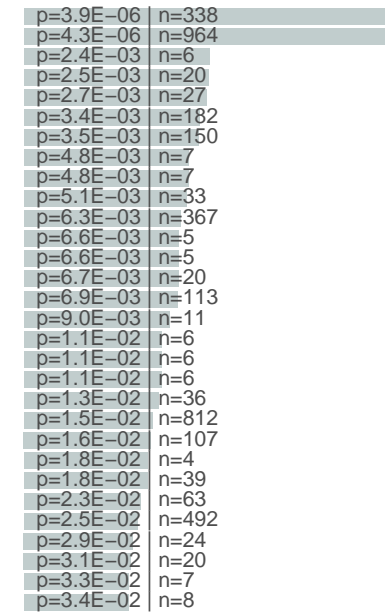
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fraction

GO:CC
Fox_Nvec_vc1.1_XM_032376930.1

fraction genes in fg and expected value

nucleoplasm	GO:0005654
intracellular anatomical structure	GO:0005622
plasma membrane proton-transporting V-ty...	GO:0033181
methyltransferase complex	GO:0034708
nuclear DNA-directed RNA polymerase comp...	GO:0055029
catalytic complex	GO:1902494
nuclear protein-containing complex	GO:0140513
U12-type spliceosomal complex	GO:0005689
mitochondrial small ribosomal subunit	GO:0005763
nuclear membrane	GO:0031965
intracellular non-membrane-bounded organ...	GO:0043232
proton-transporting two-sector ATPase co...	GO:0033178
Prp19 complex	GO:0000974
axoneme	GO:0005930
ribonucleoprotein complex	GO:1990904
mitochondrial respiratory chain complex ...	GO:0005747
AP-type membrane coat adaptor complex	GO:0030119
vacuolar proton-transporting V-type ATPa...	GO:0016471
peribosome, small subunit precursor	GO:0030688
trans-Golgi network	GO:0005802
cytoplasm	GO:0005737
intracellular protein-containing complex	GO:0140535
RNA polymerase I complex	GO:0005736
mitochondrial protein-containing complex	GO:0098798
centrosome	GO:0005813
protein-containing complex	GO:0032991
recycling endosome	GO:0055037
RNA polymerase II, holoenzyme	GO:0016591
integrator complex	GO:0032039
mediator complex	GO:0016592



0 1 2 3 4 5
-log(p)
n=989/2780 input genes with annotations

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fraction