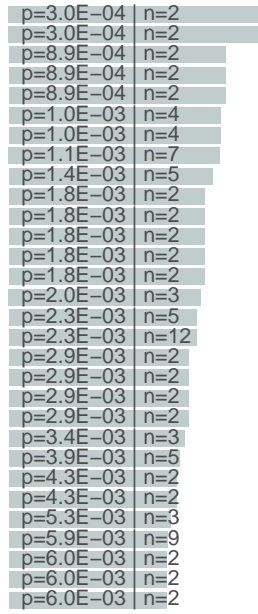


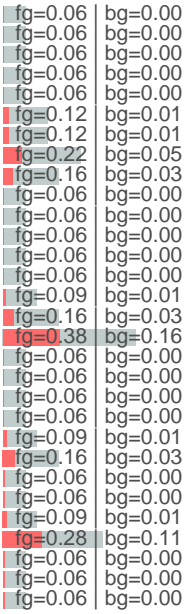
GO:BP
Fox_Nvec_vc1.1_XM_001625998.3

positive regulation of transcription fro...	GO:0061419
positive regulation of transcription fro...	GO:0061408
response to herbicide	GO:0009635
positive regulation of cellular response...	GO:1900409
epithelial cell maturation	GO:0002070
cellular response to antibiotic	GO:0071236
cellular response to toxic substance	GO:0097237
embryonic organ development	GO:0048568
negative regulation of neuron death	GO:1901215
regulation of superoxide metabolic proce...	GO:0090322
molting cycle, collagen and cuticulin-ba...	GO:0018996
negative regulation of long-term synapti...	GO:1900272
regulation of transcription from RNA pol...	GO:0043619
collateral sprouting	GO:0048668
cellular response to hydrogen peroxide	GO:0070301
dorsal/ventral pattern formation	GO:0009953
negative regulation of gene expression	GO:0010629
mRNA transcription	GO:0009299
negative regulation of cardiac muscle ce...	GO:0010667
response to fungicide	GO:0060992
cellular response to angiotensin	GO:1904385
ADP metabolic process	GO:0046031
post-translational protein modification	GO:0043687
positive regulation of cell cycle G2/M p...	GO:1902751
regulation of blood coagulation	GO:0030193
positive regulation of peptidyl-tyrosine...	GO:0050731
negative regulation of RNA metabolic pro...	GO:0051253
lactate metabolic process	GO:0006089
negative regulation of oxidative stress-...	GO:1902176
response to electrical stimulus	GO:0051602



0 1 2 3 4 5
-log(p)
n=32/115 input genes with annotations

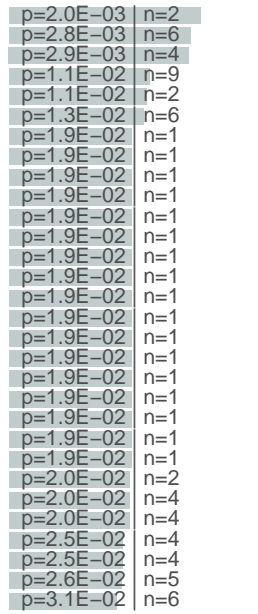
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction

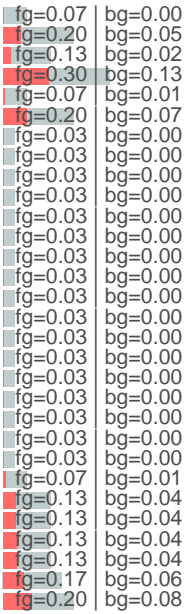
GO:MF
Fox_Nvec_vc1.1_XM_001625998.3

phospholipase C activity	GO:0004629
RNA polymerase II transcription regulato...	GO:0000977
heat shock protein binding	GO:0031072
protein dimerization activity	GO:0046983
transcription coregulator binding	GO:0001221
DNA-binding transcription factor activit...	GO:0000981
cysteine-tRNA ligase activity	GO:0004817
phosphatidylglycerol binding	GO:1901611
cardiolipin binding	GO:1901612
cobalt ion binding	GO:0050897
acetylcholine receptor regulator activit...	GO:0030548
acetylcholine receptor activator activit...	GO:0030549
translation elongation factor binding	GO:0061770
palmitoleyl hydrolase activity	GO:1990699
calcitonin family binding	GO:0097644
neurotransmitter receptor regulator acti...	GO:0099602
amylin binding	GO:0097645
adenosine-phosphate deaminase activity	GO:0047623
heparan sulfate binding	GO:1904399
AMP deaminase activity	GO:0003876
ATPase-coupled intramembrane lipid trans...	GO:0140326
flippase activity	GO:0140327
aminophospholipid flippase activity	GO:0015247
integrin binding	GO:0005178
cis-regulatory region sequence-specific ...	GO:0000987
RNA polymerase II cis-regulatory region ...	GO:0000978
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
protein heterodimerization activity	GO:0046982
DNA-binding transcription factor activit...	GO:0003700



0 1 2 3 4 5
-log(p)
n=30/115 input genes with annotations

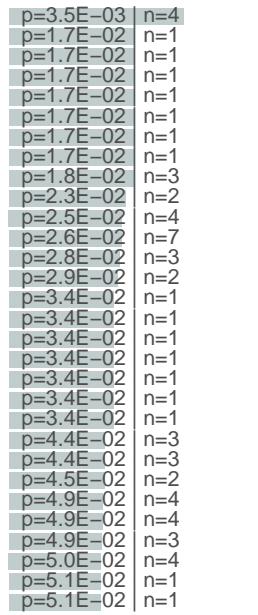
fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction

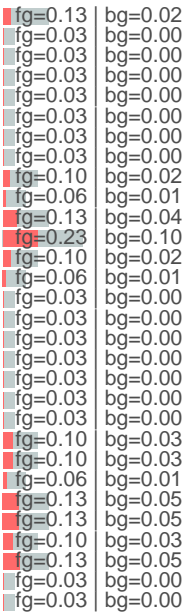
GO:CC
Fox_Nvec_vc1.1_XM_001625998.3

secretory granule membrane	GO:0030667
intermediate-density lipoprotein particl...	GO:0034363
high-density lipoprotein particle	GO:0034364
plasma lipoprotein particle	GO:0034358
triglyceride-rich plasma lipoprotein par...	GO:0034385
amyloid-beta complex	GO:0106003
lipoprotein particle	GO:1990777
endosome to plasma membrane transport ve...	GO:0070381
terminal bouton	GO:0043195
specific granule membrane	GO:0035579
cell projection membrane	GO:0031253
plasma membrane region	GO:0098590
recycling endosome	GO:0055037
main axon	GO:0044304
endosome lumen	GO:0031904
platelet alpha granule membrane	GO:0031092
microtubule minus-end	GO:0036449
protein-lipid complex	GO:0032994
nuclear stress granule	GO:0097165
growth cone filopodium	GO:1990812
ciliary rootlet	GO:0035253
axon terminus	GO:0043679
endocytic vesicle	GO:0030139
specific granule	GO:0042581
cell-cell junction	GO:0005911
anchoring junction	GO:0070161
neuron projection terminus	GO:0044306
distal axon	GO:0150034
zymogen granule membrane	GO:0042589
growth cone lamellipodium	GO:1990761



0 1 2 3 4 5
-log(p)
n=31/115 input genes with annotations

fraction genes in fg and expected value



0.0 0.2 0.4 0.6 0.8 1.0
fraction