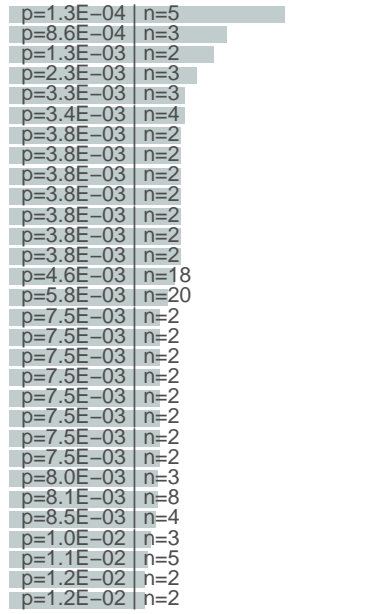


GO:BP
Fox_Nvec_vc1.1_XM_032382493.2

fraction genes in fg and expected value

phospholipid transport	GO:0015914
positive regulation of triglyceride bios...	GO:0010867
positive regulation of acute inflammator...	GO:0002675
positive regulation of sodium ion transp...	GO:0010765
negative regulation of lipid storage	GO:0010888
apoptotic process involved in developmen...	GO:1902742
negative regulation of necroptotic proce...	GO:0060546
aggrephagy	GO:0035973
negative regulation of mitochondrial dep...	GO:0051902
post-embryonic body morphogenesis	GO:0040032
bone regeneration	GO:1990523
very-low-density lipoprotein particle as...	GO:0034379
negative regulation of mitochondrial out...	GO:1901029
positive regulation of transport	GO:0051050
secretion by cell	GO:0032940
C-terminal protein lipidation	GO:0006501
cellular response to forskolin	GO:1904322
response to hermaphrodite contact	GO:0034606
positive regulation of cholesterol biosy...	GO:0045542
ecdysis, collagen and cuticulin-based cu...	GO:0042395
regulation of protein complex stability	GO:0061635
positive regulation of insulin receptor ...	GO:0046628
phospholipid homeostasis	GO:0055091
regulation of lymphocyte apoptotic proce...	GO:0070228
neurotransmitter transport	GO:0006836
regulation of lymphocyte proliferation	GO:0050670
lymphocyte homeostasis	GO:0002260
calcium-ion regulated exocytosis	GO:0017156
venous blood vessel development	GO:0060841
response to platelet aggregation inhibit...	GO:0061478



-log(p)
n=98/315 input genes with annotations

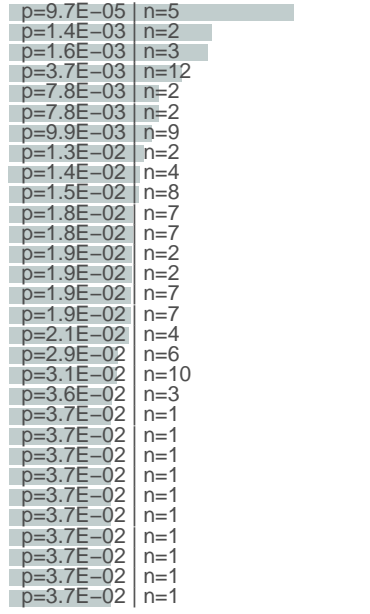
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fraction

GO:MF
Fox_Nvec_vc1.1_XM_032382493.2

fraction genes in fg and expected value

phospholipid transporter activity	GO:0005548
oxysterol binding	GO:0008142
cholesterol binding	GO:0015485
protein heterodimerization activity	GO:0046982
sterol transporter activity	GO:0015248
FAD binding	GO:0071949
RNA polymerase II transcription regulato...	GO:0000977
sequence-specific single stranded DNA bi...	GO:0098847
actin filament binding	GO:0051015
phospholipid binding	GO:0005543
DNA-binding transcription activator acti...	GO:0001228
DNA-binding transcription activator acti...	GO:0001216
RNA polymerase II general transcription ...	GO:0001091
BH domain binding	GO:0051400
cis-regulatory region sequence-specific ...	GO:0000987
RNA polymerase II cis-regulatory region ...	GO:0000978
single-stranded DNA binding	GO:0003697
phosphatidylinositol binding	GO:0035091
DNA-binding transcription factor activit...	GO:0000981
Hsp90 protein binding	GO:0051879
alkanesulfonate transmembrane transporte...	GO:0042959
amino acid:sodium symporter activity	GO:0005283
ATP-dependent DNA/DNA annealing activity	GO:0036310
tRNA 2'-phosphotransferase activity	GO:0000215
testosterone 17-beta-dehydrogenase (NADP...	GO:0047045
TFIIF-class transcription factor complex...	GO:0001096
misfolded RNA binding	GO:0034336
taurine transmembrane transporter activi...	GO:0005368
taurine:sodium symporter activity	GO:0005369
intracellular sodium activated potassium...	GO:0005228



-log(p)
n=88/315 input genes with annotations

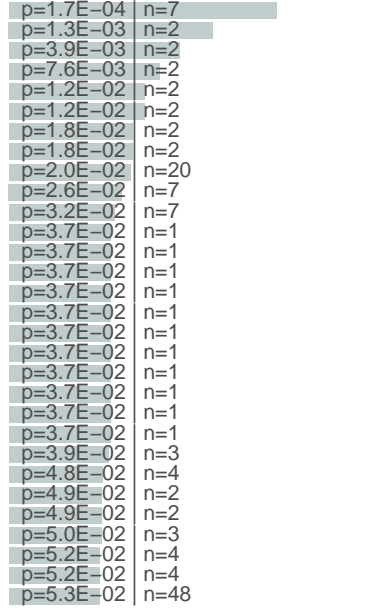
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fraction

GO:CC
Fox_Nvec_vc1.1_XM_032382493.2

fraction genes in fg and expected value

protein-DNA complex	GO:0032993
collagen and cuticulin-based cuticle ext...	GO:0060102
COP1 vesicle coat	GO:0030126
germline ring canal	GO:0045172
microtubule end	GO:1990752
TRAPP complex	GO:0030008
autophagosome membrane	GO:0000421
nucleosome	GO:0000786
Golgi apparatus	GO:0005794
chromosomal region	GO:0098687
early endosome	GO:0005769
hemoglobin complex	GO:0005833
cortical microtubule	GO:0055028
centrosomal corona	GO:0031592
cortical microtubule cytoskeleton	GO:0030981
cortical microtubule plus-end	GO:1903754
ESCRT-0 complex	GO:0033565
CCAAT-binding factor complex	GO:0016602
protein kinase CK2 complex	GO:0005956
neuronal ribonucleoprotein granule	GO:0071598
BRISC complex	GO:0070552
cytoplasmic microtubule plus-end	GO:1904511
extrinsic component of cytoplasmic side ...	GO:0031234
mitochondrial outer membrane	GO:0005741
potassium channel complex	GO:0034705
voltage-gated potassium channel complex	GO:0008076
focal adhesion	GO:0005925
organelle outer membrane	GO:0031968
outer membrane	GO:0019867
cytosol	GO:0005829



-log(p)
n=99/315 input genes with annotations

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fraction