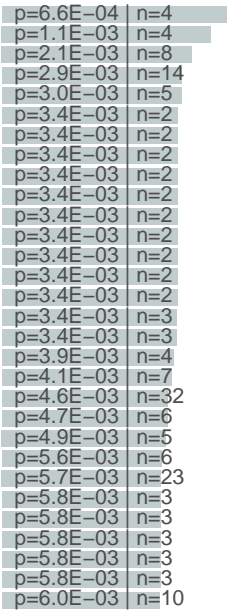


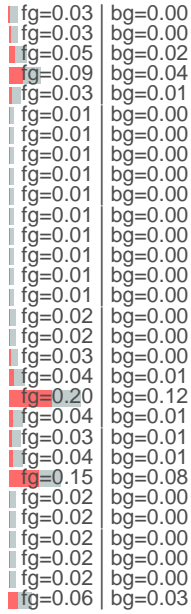
GO:BP
Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

regulation of Rac protein signal transdu... GO:0035020
negative regulation of peptidyl-serine p... GO:0033137
insulin receptor signaling pathway GO:0008286
positive regulation of neuron differenti... GO:0045666
negative regulation of Ras protein signa... GO:0046580
positive regulation of cholesterol efflu... GO:0010875
right ventricular cardiac muscle tissue ... GO:0003221
ventricular trabecula myocardium morphog... GO:0003222
positive regulation of cellular extravas... GO:0002693
regulation of relaxation of muscle GO:1901077
negative regulation of protein targeting... GO:0090315
positive regulation of megakaryocyte dif... GO:0045654
regulation of cell communication by elec... GO:1901844
regulation of primitive erythrocyte diff... GO:0010725
regulation of cardioblast differentiatio... GO:0051890
response to amphetamine GO:0001975
negative regulation of calcium ion-depen... GO:0045955
regulation of cardiac conduction GO:1903779
regulation of neural precursor cell prol... GO:2000177
cell-cell signaling GO:0007267
single fertilization GO:0007338
negative regulation of MAP kinase activi... GO:0043407
chromosome organization involved in meio... GO:0070192
positive regulation of transcription by ... GO:0045944
regulation of release of sequestered cal... GO:0010880
maintenance of organelle location GO:0051657
negative regulation of mitotic metaphase... GO:0045841
response to mitochondrial depolarisation GO:0098780
positive regulation of steroid biosynthe... GO:0010893
positive regulation of GTPase activity GO:0043547



0 1 2 3 4 5
-log(p)
n=158/528 input genes with annotations

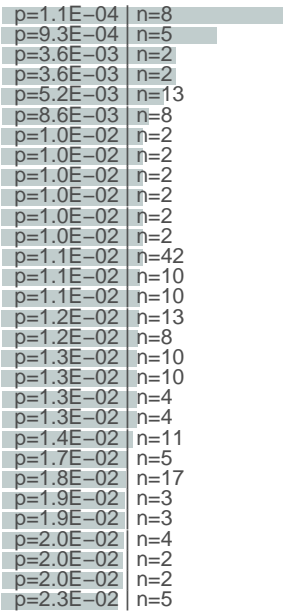


0.0 0.2 0.4 0.6 0.8 1.0
fraction

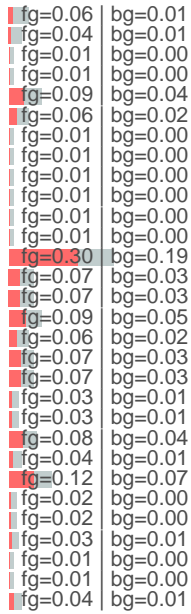
GO:MF
Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

ATPase-coupled transmembrane transporter... GO:0042626
cysteine-type endopeptidase activity GO:0004197
armadillo repeat domain binding GO:0070016
fibronectin binding GO:0001968
RNA polymerase II transcription regulato... GO:0000977
active ion transmembrane transporter act... GO:0022853
protein antigen binding GO:1990405
annealing activity GO:0140666
dipeptidase activity GO:0016805
S100 protein binding GO:0044548
ATPase-coupled lipid transmembrane trans... GO:0034040
organic hydroxy compound transmembrane t... GO:1901618
hydrolase activity GO:0016787
DNA-binding transcription activator acti... GO:0001228
DNA-binding transcription activator acti... GO:0001216
ATP hydrolysis activity GO:0016887
GTPase activator activity GO:0005096
cis-regulatory region sequence-specific ... GO:0000987
RNA polymerase II cis-regulatory region ... GO:0000978
ATPase-coupled ion transmembrane transpo... GO:0042625
translation initiation factor activity GO:0003743
phospholipid binding GO:0005543
histone deacetylase binding GO:0042826
nucleoside-triphosphatase activity GO:0017111
P-type transmembrane transporter activit... GO:0140358
P-type ion transporter activity GO:0015662
transmembrane transporter binding GO:0044325
calcium-dependent cysteine-type endopept... GO:0004198
phosphatidylinositol phosphate 4-phospha... GO:0034596
translation factor activity, RNA binding GO:0008135



0 1 2 3 4 5
-log(p)
n=142/528 input genes with annotations

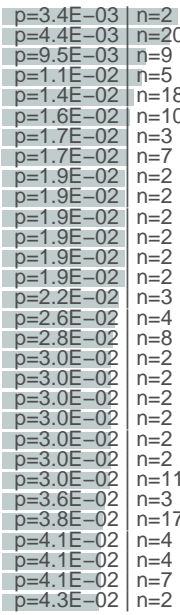


0.0 0.2 0.4 0.6 0.8 1.0
fraction

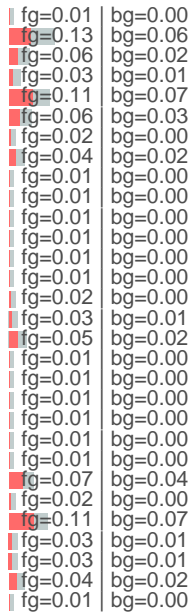
GO:CC
Fox_Nvec_vc1.1_XM_032365977.2

fraction genes in fg and expected value

CA3 pyramidal cell dendrite GO:0097442
dendrite GO:0030425
exocytic vesicle GO:0070382
exocytic vesicle membrane GO:0099501
axon GO:0030424
chromosomal region GO:0098687
sarcoplasmic reticulum GO:0016529
chromosome, centromeric region GO:0000775
integrin complex GO:0008305
intrinsic component of mitochondrial out... GO:0031306
integral component of mitochondrial oute... GO:0031307
protein complex involved in cell adhesio... GO:0098636
intrinsic component of peroxisomal membr... GO:0031231
integral component of peroxisomal membra... GO:0005779
sarcoplasm GO:0016528
spindle microtubule GO:0005876
condensed chromosome GO:0000793
eukaryotic translation initiation factor... GO:0005851
intercellular canalculus GO:0046581
kinetochore microtubule GO:0005828
phagocytic cup GO:0001891
zymogen granule GO:0042588
intrinsic component of the cytoplasmic s... GO:0031235
distal axon GO:0150034
integral component of synaptic vesicle m... GO:0030285
intrinsic component of plasma membrane GO:0031226
synaptic vesicle membrane GO:0030672
focal adhesion GO:0005925
synaptic vesicle GO:0008021
sarcoplasmic reticulum membrane GO:0033017



0 1 2 3 4 5
-log(p)
n=157/528 input genes with annotations



0.0 0.2 0.4 0.6 0.8 1.0
fraction