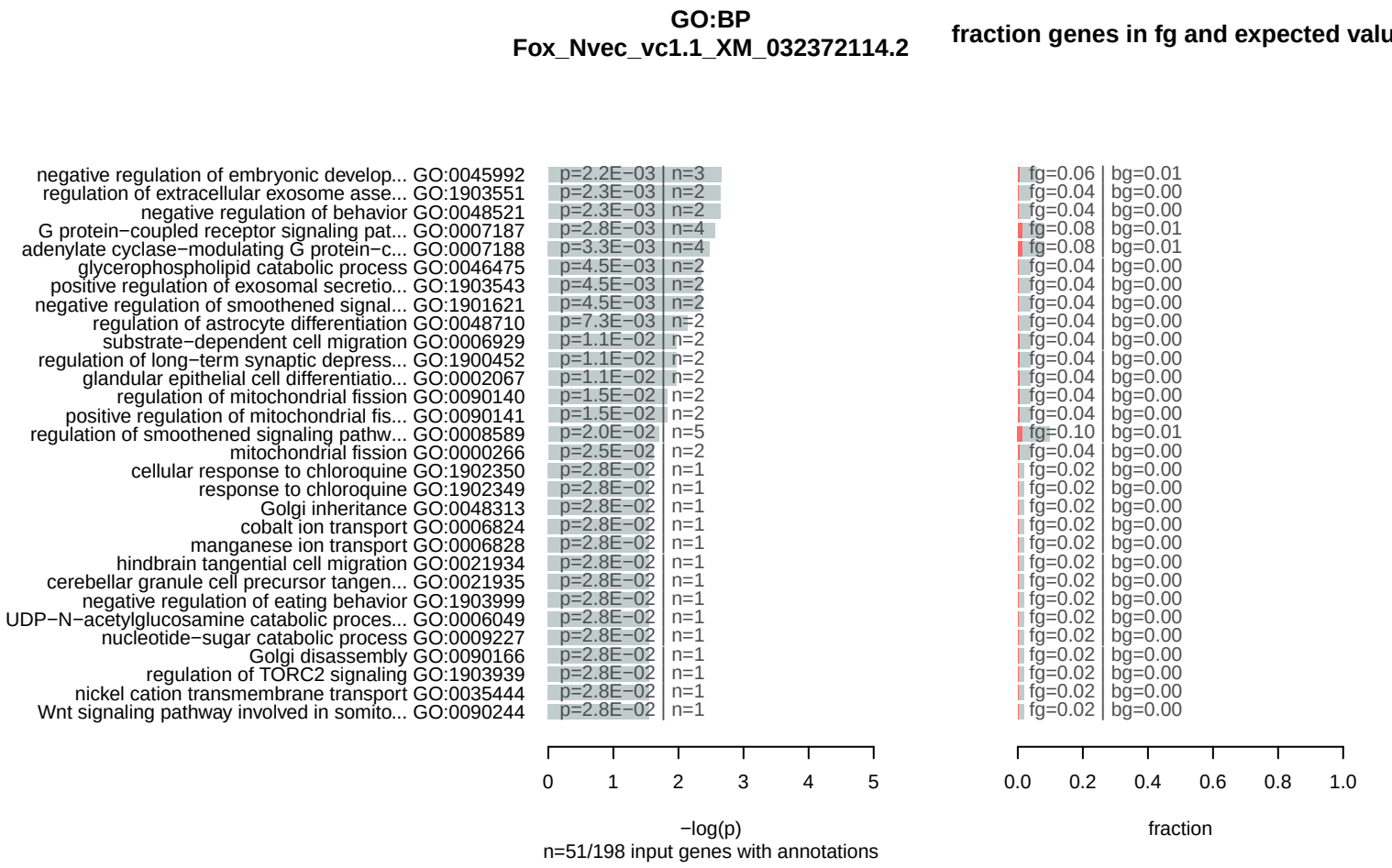
GO:BP
Fox_Nvec_vc1.1_XM_032372114.2
fraction genes in fg and expected valu
negative regulation of embryonic develop... GO:0045992 p=2.2E−03 n=3 fg=0.06 bg=0.01
regulation of extracellular exosome asse... GO:1903551 p=2.3E−03 n=2 fg=0.04 bg=0.00
negative regulation of behavior GO:0048521 p=2.3E−03 n=2 fg=0.04 bg=0.00
G protein−coupled receptor signaling pat... GO:0007187 p=2.8E−03 n=4 fg=0.08 bg=0.01
adenylate cyclase−modulating G protein−c... GO:0007188 p=3.3E−03 n=4 fg=0.08 bg=0.01
glycerophospholipid catabolic process GO:0046475 p=4.5E−03 n=2 fg=0.04 bg=0.00
positive regulation of exosomal secretio... GO:1903543 p=4.5E−03 n=2 fg=0.04 bg=0.00
negative regulation of smoothened signal... GO:1901621 p=4.5E−03 n=2 fg=0.04 bg=0.00
regulation of astrocyte differentiation GO:0048710 p=7.3E−03 n=2 fg=0.04 bg=0.00
substrate−dependent cell migration GO:0006929 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of long−term synaptic depress... GO:1900452 p=1.1E−02 n=2 fg=0.04 bg=0.00
glandular epithelial cell differentiatio... GO:0002067 p=1.1E−02 n=2 fg=0.04 bg=0.00
regulation of mitochondrial fission GO:0090140 p=1.5E−02 n=2 fg=0.04 bg=0.00
positive regulation of mitochondrial fis... GO:0090141 p=1.5E−02 n=2 fg=0.04 bg=0.00
regulation of smoothened signaling pathw... GO:0008589 p=2.0E−02 n=5 fg=0.10 bg=0.01
mitochondrial fission GO:0000266 p=2.5E−02 n=2 fg=0.04 bg=0.00
cellular response to chloroquine GO:1902350 p=2.8E−02 n=1 fg=0.02 bg=0.00
response to chloroquine GO:1902349 p=2.8E−02 n=1 fg=0.02 bg=0.00
Golgi inheritance GO:0048313 p=2.8E−02 n=1 fg=0.02 bg=0.00
cobalt ion transport GO:0006824 p=2.8E−02 n=1 fg=0.02 bg=0.00
manganese ion transport GO:0006828 p=2.8E−02 n=1 fg=0.02 bg=0.00
hindbrain tangential cell migration GO:0021934 p=2.8E−02 n=1 fg=0.02 bg=0.00
cerebellar granule cell precursor tangen... GO:0021935 p=2.8E−02 n=1 fg=0.02 bg=0.00
negative regulation of eating behavior GO:1903999 p=2.8E−02 n=1 fg=0.02 bg=0.00
UDP−N−acetylglucosamine catabolic proces... GO:0006049 p=2.8E−02 n=1 fg=0.02 bg=0.00
nucleotide−sugar catabolic process GO:0009227 p=2.8E−02 n=1 fg=0.02 bg=0.00
Golgi disassembly GO:0090166 p=2.8E−02 n=1 fg=0.02 bg=0.00
regulation of TORC2 signaling GO:1903939 p=2.8E−02 n=1 fg=0.02 bg=0.00
nickel cation transmembrane transport GO:0035444 p=2.8E−02 n=1 fg=0.02 bg=0.00
Wnt signaling pathway involved in somito... GO:0090244 p=2.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=51/198 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032372114.2
fraction genes in fg and expected valu
phospholipase activity GO:0004620 p=6.6E−04 n=4 fg=0.09 bg=0.01
protein N−terminus binding GO:0047485 p=6.7E−03 n=3 fg=0.07 bg=0.01
G−protein beta/gamma−subunit complex bin... GO:0031683 p=6.8E−03 n=2 fg=0.05 bg=0.00
G protein−coupled receptor activity GO:0004930 p=1.6E−02 n=4 fg=0.09 bg=0.02
transmembrane signaling receptor activit... GO:0004888 p=2.3E−02 n=5 fg=0.12 bg=0.04
aspartate−tRNA ligase activity GO:0004815 p=2.7E−02 n=1 fg=0.02 bg=0.00
ribokinase activity GO:0004747 p=2.7E−02 n=1 fg=0.02 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=2.7E−02 n=1 fg=0.02 bg=0.00
cobalt ion transmembrane transporter act... GO:0015087 p=2.7E−02 n=1 fg=0.02 bg=0.00
D5 dopamine receptor binding GO:0031752 p=2.7E−02 n=1 fg=0.02 bg=0.00
phospholipase A1 activity GO:0008970 p=2.7E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor binding GO:0005137 p=2.7E−02 n=1 fg=0.02 bg=0.00
aminoacylase activity GO:0004046 p=2.7E−02 n=1 fg=0.02 bg=0.00
glycogen (starch) synthase activity GO:0004373 p=2.7E−02 n=1 fg=0.02 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=2.7E−02 n=1 fg=0.02 bg=0.00
glycogen synthase activity, transferring... GO:0061547 p=2.7E−02 n=1 fg=0.02 bg=0.00
alpha−1,3−mannosylglycoprotein 2−beta−N−... GO:0003827 p=2.7E−02 n=1 fg=0.02 bg=0.00
nickel cation transmembrane transporter ... GO:0015099 p=2.7E−02 n=1 fg=0.02 bg=0.00
sphingomyelin phosphodiesterase D activi... GO:0050290 p=2.7E−02 n=1 fg=0.02 bg=0.00
manganese ion transmembrane transporter ... GO:0005384 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein−macromolecule adaptor activity GO:0030674 p=4.0E−02 n=4 fg=0.09 bg=0.03
molecular adaptor activity GO:0060090 p=4.0E−02 n=4 fg=0.09 bg=0.03
signaling receptor activity GO:0038023 p=5.1E−02 n=5 fg=0.12 bg=0.05
molecular transducer activity GO:0060089 p=5.3E−02 n=5 fg=0.12 bg=0.05
copper ion transmembrane transporter act... GO:0005375 p=5.3E−02 n=1 fg=0.02 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=5.3E−02 n=1 fg=0.02 bg=0.00
ISG15 transferase activity GO:0042296 p=5.3E−02 n=1 fg=0.02 bg=0.00
sphingomyelin phosphodiesterase activity GO:0004767 p=5.3E−02 n=1 fg=0.02 bg=0.00
ATPase inhibitor activity GO:0042030 p=5.3E−02 n=1 fg=0.02 bg=0.00
beta−glucosidase activity GO:0008422 p=5.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/198 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032372114.2
fraction genes in fg and expected valu
Golgi medial cisterna GO:0005797 p=5.2E−03 n=3 fg=0.06 bg=0.01
COPII−coated ER to Golgi transport vesic... GO:0030134 p=5.2E−03 n=3 fg=0.06 bg=0.01
cis−Golgi network GO:0005801 p=9.6E−03 n=3 fg=0.06 bg=0.01
piP−body GO:0071547 p=2.9E−02 n=1 fg=0.02 bg=0.00
RNA polymerase III transcription regulat... GO:0090576 p=2.9E−02 n=1 fg=0.02 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=2.9E−02 n=1 fg=0.02 bg=0.00
PeBoW complex GO:0070545 p=2.9E−02 n=1 fg=0.02 bg=0.00
TSC1−TSC2 complex GO:0033596 p=2.9E−02 n=1 fg=0.02 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=2.9E−02 n=1 fg=0.02 bg=0.00
ESCRT−0 complex GO:0033565 p=2.9E−02 n=1 fg=0.02 bg=0.00
ectoplasm GO:0043265 p=2.9E−02 n=1 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=2.9E−02 n=1 fg=0.02 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=2.9E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor complex GO:0005895 p=2.9E−02 n=1 fg=0.02 bg=0.00
Golgi trans cisterna GO:0000138 p=3.8E−02 n=2 fg=0.04 bg=0.01
cytoplasmic region GO:0099568 p=5.2E−02 n=6 fg=0.12 bg=0.05
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=5.7E−02 n=1 fg=0.02 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=5.7E−02 n=1 fg=0.02 bg=0.00
activating signal cointegrator 1 complex GO:0099053 p=5.7E−02 n=1 fg=0.02 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=5.7E−02 n=1 fg=0.02 bg=0.00
aminoacyl−tRNA synthetase multienzyme co... GO:0017101 p=5.7E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=5.7E−02 n=1 fg=0.02 bg=0.00
transport vesicle membrane GO:0030658 p=5.7E−02 n=3 fg=0.06 bg=0.02
cell cortex GO:0005938 p=5.8E−02 n=5 fg=0.10 bg=0.04
azurophil granule lumen GO:0035578 p=5.9E−02 n=2 fg=0.04 bg=0.01
ciliary membrane GO:0060170 p=7.5E−02 n=2 fg=0.04 bg=0.01
perinuclear region of cytoplasm GO:0048471 p=8.0E−02 n=7 fg=0.13 bg=0.07
Golgi−associated vesicle GO:0005798 p=8.2E−02 n=3 fg=0.06 bg=0.02
skeletal muscle myofibril GO:0098723 p=8.4E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=8.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=52/198 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction