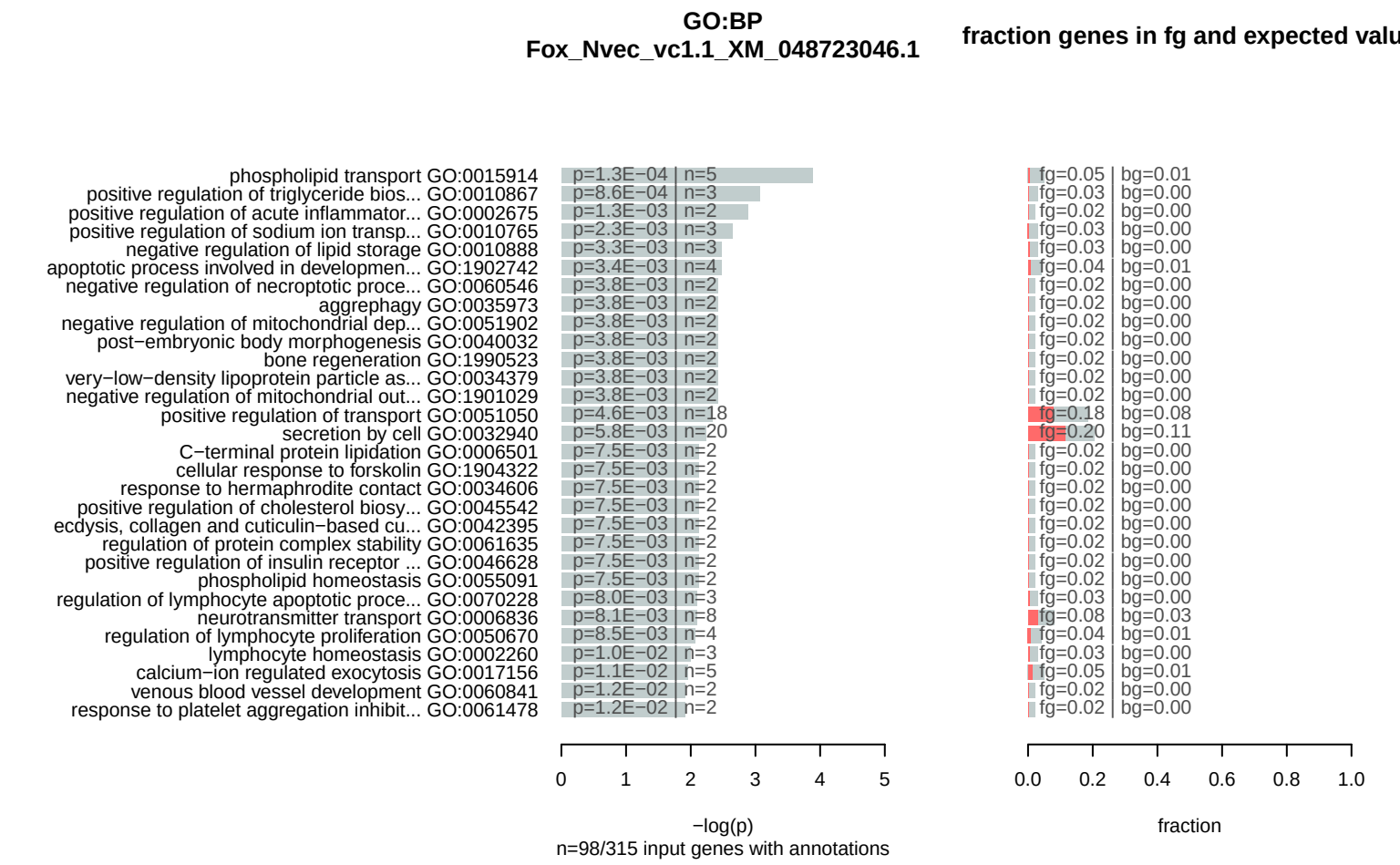
GO:BP
Fox_Nvec_vc1.1_XM_048723046.1
fraction genes in fg and expected valu
phospholipid transport GO:0015914 p=1.3E−04 n=5 fg=0.05 bg=0.01
positive regulation of triglyceride bios... GO:0010867 p=8.6E−04 n=3 fg=0.03 bg=0.00
positive regulation of acute inflammator... GO:0002675 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of sodium ion transp... GO:0010765 p=2.3E−03 n=3 fg=0.03 bg=0.00
negative regulation of lipid storage GO:0010888 p=3.3E−03 n=3 fg=0.03 bg=0.00
apoptotic process involved in developmen... GO:1902742 p=3.4E−03 n=4 fg=0.04 bg=0.01
negative regulation of necroptotic proce... GO:0060546 p=3.8E−03 n=2 fg=0.02 bg=0.00
aggrephagy GO:0035973 p=3.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitochondrial dep... GO:0051902 p=3.8E−03 n=2 fg=0.02 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=3.8E−03 n=2 fg=0.02 bg=0.00
bone regeneration GO:1990523 p=3.8E−03 n=2 fg=0.02 bg=0.00
very−low−density lipoprotein particle as... GO:0034379 p=3.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitochondrial out... GO:1901029 p=3.8E−03 n=2 fg=0.02 bg=0.00
positive regulation of transport GO:0051050 p=4.6E−03 n=18 fg=0.18 bg=0.08
secretion by cell GO:0032940 p=5.8E−03 n=20 fg=0.20 bg=0.11
C−terminal protein lipidation GO:0006501 p=7.5E−03 n=2 fg=0.02 bg=0.00
cellular response to forskolin GO:1904322 p=7.5E−03 n=2 fg=0.02 bg=0.00
response to hermaphrodite contact GO:0034606 p=7.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of cholesterol biosy... GO:0045542 p=7.5E−03 n=2 fg=0.02 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=7.5E−03 n=2 fg=0.02 bg=0.00
regulation of protein complex stability GO:0061635 p=7.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of insulin receptor ... GO:0046628 p=7.5E−03 n=2 fg=0.02 bg=0.00
phospholipid homeostasis GO:0055091 p=7.5E−03 n=2 fg=0.02 bg=0.00
regulation of lymphocyte apoptotic proce... GO:0070228 p=8.0E−03 n=3 fg=0.03 bg=0.00
neurotransmitter transport GO:0006836 p=8.1E−03 n=8 fg=0.08 bg=0.03
regulation of lymphocyte proliferation GO:0050670 p=8.5E−03 n=4 fg=0.04 bg=0.01
lymphocyte homeostasis GO:0002260 p=1.0E−02 n=3 fg=0.03 bg=0.00
calcium−ion regulated exocytosis GO:0017156 p=1.1E−02 n=5 fg=0.05 bg=0.01
venous blood vessel development GO:0060841 p=1.2E−02 n=2 fg=0.02 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=1.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=98/315 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_048723046.1
fraction genes in fg and expected valu
phospholipid transporter activity GO:0005548 p=9.7E−05 n=5 fg=0.06 bg=0.01
oxysterol binding GO:0008142 p=1.4E−03 n=2 fg=0.02 bg=0.00
cholesterol binding GO:0015485 p=1.6E−03 n=3 fg=0.03 bg=0.00
protein heterodimerization activity GO:0046982 p=3.7E−03 n=12 fg=0.14 bg=0.06
sterol transporter activity GO:0015248 p=7.8E−03 n=2 fg=0.02 bg=0.00
FAD binding GO:0071949 p=7.8E−03 n=2 fg=0.02 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=9.9E−03 n=9 fg=0.10 bg=0.04
sequence−specific single stranded DNA bi... GO:0098847 p=1.3E−02 n=2 fg=0.02 bg=0.00
actin filament binding GO:0051015 p=1.4E−02 n=4 fg=0.05 bg=0.01
phospholipid binding GO:0005543 p=1.5E−02 n=8 fg=0.09 bg=0.04
DNA−binding transcription activator acti... GO:0001228 p=1.8E−02 n=7 fg=0.08 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.8E−02 n=7 fg=0.08 bg=0.03
RNA polymerase II general transcription ... GO:0001091 p=1.9E−02 n=2 fg=0.02 bg=0.00
BH domain binding GO:0051400 p=1.9E−02 n=2 fg=0.02 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=1.9E−02 n=7 fg=0.08 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.9E−02 n=7 fg=0.08 bg=0.03
single−stranded DNA binding GO:0003697 p=2.1E−02 n=4 fg=0.05 bg=0.01
phosphatidylinositol binding GO:0035091 p=2.9E−02 n=6 fg=0.07 bg=0.03
DNA−binding transcription factor activit... GO:0000981 p=3.1E−02 n=10 fg=0.11 bg=0.06
Hsp90 protein binding GO:0051879 p=3.6E−02 n=3 fg=0.03 bg=0.01
alkanesulfonate transmembrane transporte... GO:0042959 p=3.7E−02 n=1 fg=0.01 bg=0.00
amino acid:sodium symporter activity GO:0005283 p=3.7E−02 n=1 fg=0.01 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=3.7E−02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=3.7E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=3.7E−02 n=1 fg=0.01 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.7E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=3.7E−02 n=1 fg=0.01 bg=0.00
taurine transmembrane transporter activi... GO:0005368 p=3.7E−02 n=1 fg=0.01 bg=0.00
taurine:sodium symporter activity GO:0005369 p=3.7E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=88/315 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048723046.1
fraction genes in fg and expected valu
protein−DNA complex GO:0032993 p=1.7E−04 n=7 fg=0.07 bg=0.01
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.3E−03 n=2 fg=0.02 bg=0.00
COPI vesicle coat GO:0030126 p=3.9E−03 n=2 fg=0.02 bg=0.00
germline ring canal GO:0045172 p=7.6E−03 n=2 fg=0.02 bg=0.00
microtubule end GO:1990752 p=1.2E−02 n=2 fg=0.02 bg=0.00
TRAPP complex GO:0030008 p=1.2E−02 n=2 fg=0.02 bg=0.00
autophagosome membrane GO:0000421 p=1.8E−02 n=2 fg=0.02 bg=0.00
nucleosome GO:0000786 p=1.8E−02 n=2 fg=0.02 bg=0.00
Golgi apparatus GO:0005794 p=2.0E−02 n=20 fg=0.20 bg=0.11
chromosomal region GO:0098687 p=2.6E−02 n=7 fg=0.07 bg=0.03
early endosome GO:0005769 p=3.2E−02 n=7 fg=0.07 bg=0.03
hemoglobin complex GO:0005833 p=3.7E−02 n=1 fg=0.01 bg=0.00
cortical microtubule GO:0055028 p=3.7E−02 n=1 fg=0.01 bg=0.00
centrosomal corona GO:0031592 p=3.7E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=3.7E−02 n=1 fg=0.01 bg=0.00
cortical microtubule plus−end GO:1903754 p=3.7E−02 n=1 fg=0.01 bg=0.00
ESCRT−0 complex GO:0033565 p=3.7E−02 n=1 fg=0.01 bg=0.00
CCAAT−binding factor complex GO:0016602 p=3.7E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.7E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=3.7E−02 n=1 fg=0.01 bg=0.00
BRISC complex GO:0070552 p=3.7E−02 n=1 fg=0.01 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=3.7E−02 n=1 fg=0.01 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=3.9E−02 n=3 fg=0.03 bg=0.01
mitochondrial outer membrane GO:0005741 p=4.8E−02 n=4 fg=0.04 bg=0.01
potassium channel complex GO:0034705 p=4.9E−02 n=2 fg=0.02 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=4.9E−02 n=2 fg=0.02 bg=0.00
focal adhesion GO:0005925 p=5.0E−02 n=3 fg=0.03 bg=0.01
organelle outer membrane GO:0031968 p=5.2E−02 n=4 fg=0.04 bg=0.01
outer membrane GO:0019867 p=5.2E−02 n=4 fg=0.04 bg=0.01
cytosol GO:0005829 p=5.3E−02 n=48 fg=0.48 bg=0.40
0 1 2 3 4 5
−log(p)
n=99/315 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction