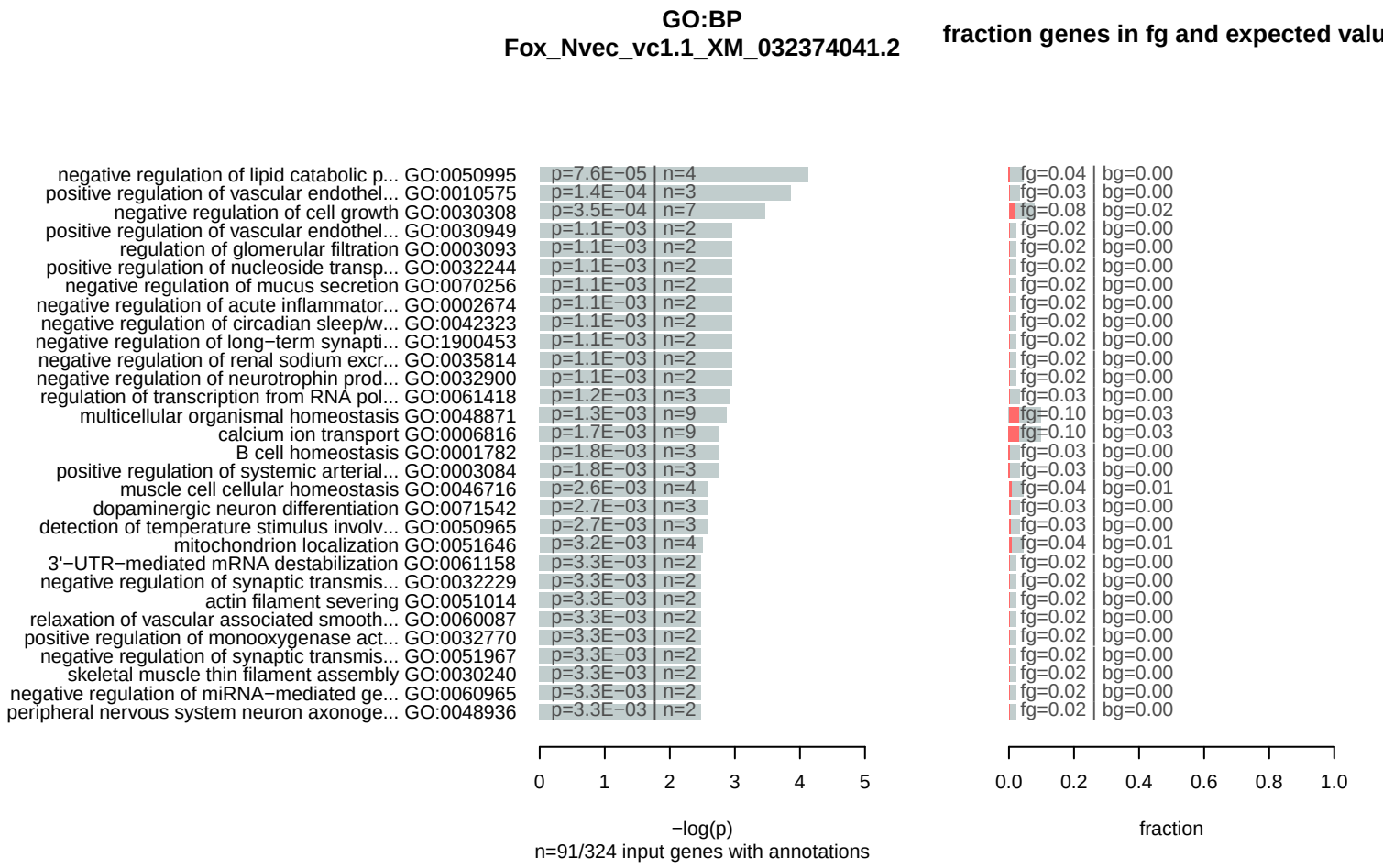
GO:BP
Fox_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
negative regulation of lipid catabolic p... GO:0050995 p=7.6E−05 n=4 fg=0.04 bg=0.00
positive regulation of vascular endothel... GO:0010575 p=1.4E−04 n=3 fg=0.03 bg=0.00
negative regulation of cell growth GO:0030308 p=3.5E−04 n=7 fg=0.08 bg=0.02
positive regulation of vascular endothel... GO:0030949 p=1.1E−03 n=2 fg=0.02 bg=0.00
regulation of glomerular filtration GO:0003093 p=1.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of nucleoside transp... GO:0032244 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of mucus secretion GO:0070256 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of acute inflammator... GO:0002674 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of circadian sleep/w... GO:0042323 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of long−term synapti... GO:1900453 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of renal sodium excr... GO:0035814 p=1.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of neurotrophin prod... GO:0032900 p=1.1E−03 n=2 fg=0.02 bg=0.00
regulation of transcription from RNA pol... GO:0061418 p=1.2E−03 n=3 fg=0.03 bg=0.00
multicellular organismal homeostasis GO:0048871 p=1.3E−03 n=9 fg=0.10 bg=0.03
calcium ion transport GO:0006816 p=1.7E−03 n=9 fg=0.10 bg=0.03
B cell homeostasis GO:0001782 p=1.8E−03 n=3 fg=0.03 bg=0.00
positive regulation of systemic arterial... GO:0003084 p=1.8E−03 n=3 fg=0.03 bg=0.00
muscle cell cellular homeostasis GO:0046716 p=2.6E−03 n=4 fg=0.04 bg=0.01
dopaminergic neuron differentiation GO:0071542 p=2.7E−03 n=3 fg=0.03 bg=0.00
detection of temperature stimulus involv... GO:0050965 p=2.7E−03 n=3 fg=0.03 bg=0.00
mitochondrion localization GO:0051646 p=3.2E−03 n=4 fg=0.04 bg=0.01
3'−UTR−mediated mRNA destabilization GO:0061158 p=3.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of synaptic transmis... GO:0032229 p=3.3E−03 n=2 fg=0.02 bg=0.00
actin filament severing GO:0051014 p=3.3E−03 n=2 fg=0.02 bg=0.00
relaxation of vascular associated smooth... GO:0060087 p=3.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of monooxygenase act... GO:0032770 p=3.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of synaptic transmis... GO:0051967 p=3.3E−03 n=2 fg=0.02 bg=0.00
skeletal muscle thin filament assembly GO:0030240 p=3.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of miRNA−mediated ge... GO:0060965 p=3.3E−03 n=2 fg=0.02 bg=0.00
peripheral nervous system neuron axonoge... GO:0048936 p=3.3E−03 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=91/324 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=4.6E−05 n=3 fg=0.03 bg=0.00
protein−cysteine S−palmitoyltransferase ... GO:0019706 p=1.8E−04 n=3 fg=0.03 bg=0.00
G protein−coupled adenosine receptor act... GO:0001609 p=1.3E−03 n=2 fg=0.02 bg=0.00
heterotrimeric G−protein binding GO:0032795 p=3.8E−03 n=2 fg=0.02 bg=0.00
long−chain fatty acyl−CoA binding GO:0036042 p=3.8E−03 n=2 fg=0.02 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=3.8E−03 n=2 fg=0.02 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=4.6E−03 n=3 fg=0.03 bg=0.00
tau−protein kinase activity GO:0050321 p=7.5E−03 n=2 fg=0.02 bg=0.00
phospholipase C activity GO:0004629 p=7.5E−03 n=2 fg=0.02 bg=0.00
metal ion binding GO:0046872 p=9.1E−03 n=16 fg=0.19 bg=0.10
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=1.2E−02 n=2 fg=0.02 bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683 p=1.2E−02 n=2 fg=0.02 bg=0.00
calcium channel regulator activity GO:0005246 p=1.3E−02 n=3 fg=0.03 bg=0.01
translation initiation factor binding GO:0031369 p=1.3E−02 n=3 fg=0.03 bg=0.01
transition metal ion binding GO:0046914 p=1.3E−02 n=11 fg=0.13 bg=0.06
cytoskeletal protein binding GO:0008092 p=1.7E−02 n=13 fg=0.15 bg=0.08
cis−regulatory region sequence−specific ... GO:0000987 p=1.7E−02 n=7 fg=0.08 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.7E−02 n=7 fg=0.08 bg=0.03
gamma−tubulin binding GO:0043015 p=1.8E−02 n=2 fg=0.02 bg=0.00
mRNA 3'−UTR binding GO:0003730 p=1.8E−02 n=3 fg=0.03 bg=0.01
calcium−release channel activity GO:0015278 p=2.4E−02 n=2 fg=0.02 bg=0.00
nuclear receptor activity GO:0004879 p=2.4E−02 n=2 fg=0.02 bg=0.00
insulin receptor binding GO:0005158 p=2.4E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=2.4E−02 n=2 fg=0.02 bg=0.00
ion binding GO:0043167 p=2.5E−02 n=30 fg=0.35 bg=0.20
translation regulator activity GO:0045182 p=2.5E−02 n=6 fg=0.07 bg=0.01
zinc ion binding GO:0008270 p=2.5E−02 n=8 fg=0.09 bg=0.04
DNA−binding transcription factor activit... GO:0000981 p=2.7E−02 n=10 fg=0.12 bg=0.06
translation repressor activity GO:0030371 p=3.5E−02 n=3 fg=0.03 bg=0.00
steroid hydroxylase activity GO:0008395 p=3.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=86/324 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
manchette GO:0002177 p=6.7E−03 n=2 fg=0.02 bg=0.00
endoplasmic reticulum GO:0005783 p=6.9E−03 n=21 fg=0.23 bg=0.13
presynaptic active zone GO:0048786 p=7.1E−03 n=4 fg=0.04 bg=0.01
dendritic spine GO:0043197 p=8.1E−03 n=6 fg=0.06 bg=0.02
messenger ribonucleoprotein complex GO:1990124 p=1.1E−02 n=2 fg=0.02 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=1.1E−02 n=2 fg=0.02 bg=0.00
dendrite cytoplasm GO:0032839 p=1.1E−02 n=2 fg=0.02 bg=0.00
cytoplasm GO:0005737 p=1.4E−02 n=84 fg=0.90 bg=0.80
supramolecular complex GO:0099080 p=1.4E−02 n=14 fg=0.15 bg=0.08
SNARE complex GO:0031201 p=1.6E−02 n=3 fg=0.03 bg=0.01
integral component of organelle membrane GO:0031301 p=1.8E−02 n=8 fg=0.09 bg=0.04
supramolecular fiber GO:0099512 p=1.9E−02 n=10 fg=0.11 bg=0.05
supramolecular polymer GO:0099081 p=1.9E−02 n=10 fg=0.11 bg=0.05
axolemma GO:0030673 p=2.2E−02 n=2 fg=0.02 bg=0.00
intrinsic component of organelle membran... GO:0031300 p=2.2E−02 n=8 fg=0.09 bg=0.04
intrinsic component of postsynaptic memb... GO:0098936 p=2.9E−02 n=2 fg=0.02 bg=0.00
integral component of postsynaptic membr... GO:0099055 p=2.9E−02 n=2 fg=0.02 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=3.4E−02 n=11 fg=0.12 bg=0.06
SMN−Gemin2 complex GO:0034718 p=3.4E−02 n=1 fg=0.01 bg=0.00
actin rod GO:0031002 p=3.4E−02 n=1 fg=0.01 bg=0.00
SmD−containing SMN−Sm protein complex GO:0034730 p=3.4E−02 n=1 fg=0.01 bg=0.00
plasmodesma GO:0009506 p=3.4E−02 n=1 fg=0.01 bg=0.00
chloroplast GO:0009507 p=3.4E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=3.4E−02 n=1 fg=0.01 bg=0.00
symplast GO:0055044 p=3.4E−02 n=1 fg=0.01 bg=0.00
centralspindlin complex GO:0097149 p=3.4E−02 n=1 fg=0.01 bg=0.00
desmosome GO:0030057 p=3.4E−02 n=1 fg=0.01 bg=0.00
apoplast GO:0048046 p=3.4E−02 n=1 fg=0.01 bg=0.00
Gemini of coiled bodies GO:0097504 p=3.4E−02 n=1 fg=0.01 bg=0.00
cytoplasmic U snRNP body GO:0071254 p=3.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=93/324 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction