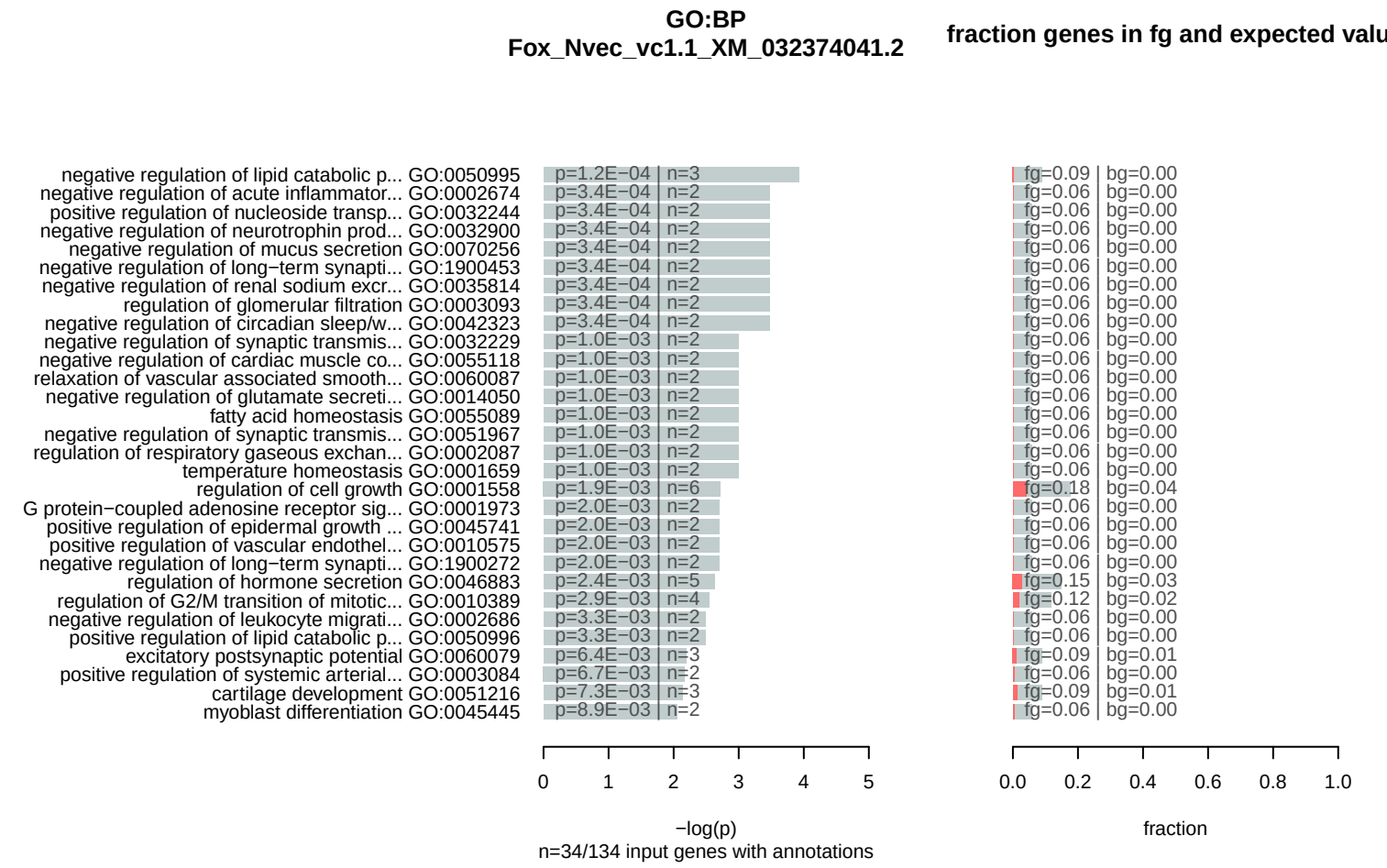
GO:BP
Fox_Nvec_vc1.1_XM_032374041.2
fraction genes in fg and expected valu
negative regulation of lipid catabolic p... GO:0050995 p=1.2E−04 n=3 fg=0.09 bg=0.00
negative regulation of acute inflammator... GO:0002674 p=3.4E−04 n=2 fg=0.06 bg=0.00
positive regulation of nucleoside transp... GO:0032244 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of neurotrophin prod... GO:0032900 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of mucus secretion GO:0070256 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of long−term synapti... GO:1900453 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of renal sodium excr... GO:0035814 p=3.4E−04 n=2 fg=0.06 bg=0.00
regulation of glomerular filtration GO:0003093 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of circadian sleep/w... GO:0042323 p=3.4E−04 n=2 fg=0.06 bg=0.00
negative regulation of synaptic transmis... GO:0032229 p=1.0E−03 n=2 fg=0.06 bg=0.00
negative regulation of cardiac muscle co... GO:0055118 p=1.0E−03 n=2 fg=0.06 bg=0.00
relaxation of vascular associated smooth... GO:0060087 p=1.0E−03 n=2 fg=0.06 bg=0.00
negative regulation of glutamate secreti... GO:0014050 p=1.0E−03 n=2 fg=0.06 bg=0.00
fatty acid homeostasis GO:0055089 p=1.0E−03 n=2 fg=0.06 bg=0.00
negative regulation of synaptic transmis... GO:0051967 p=1.0E−03 n=2 fg=0.06 bg=0.00
regulation of respiratory gaseous exchan... GO:0002087 p=1.0E−03 n=2 fg=0.06 bg=0.00
temperature homeostasis GO:0001659 p=1.0E−03 n=2 fg=0.06 bg=0.00
regulation of cell growth GO:0001558 p=1.9E−03 n=6 fg=0.18 bg=0.04
G protein−coupled adenosine receptor sig... GO:0001973 p=2.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of epidermal growth ... GO:0045741 p=2.0E−03 n=2 fg=0.06 bg=0.00
positive regulation of vascular endothel... GO:0010575 p=2.0E−03 n=2 fg=0.06 bg=0.00
negative regulation of long−term synapti... GO:1900272 p=2.0E−03 n=2 fg=0.06 bg=0.00
regulation of hormone secretion GO:0046883 p=2.4E−03 n=5 fg=0.15 bg=0.03
regulation of G2/M transition of mitotic... GO:0010389 p=2.9E−03 n=4 fg=0.12 bg=0.02
negative regulation of leukocyte migrati... GO:0002686 p=3.3E−03 n=2 fg=0.06 bg=0.00
positive regulation of lipid catabolic p... GO:0050996 p=3.3E−03 n=2 fg=0.06 bg=0.00
excitatory postsynaptic potential GO:0060079 p=6.4E−03 n=3 fg=0.09 bg=0.01
positive regulation of systemic arterial... GO:0003084 p=6.7E−03 n=2 fg=0.06 bg=0.00
cartilage development GO:0051216 p=7.3E−03 n=3 fg=0.09 bg=0.01
myoblast differentiation GO:0045445 p=8.9E−03 n=2 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=34/134 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
G protein−coupled adenosine receptor act... GO:0001609 p=3.4E−04 n=2 fg=0.07 bg=0.00
heterotrimeric G−protein binding GO:0032795 p=1.0E−03 n=2 fg=0.07 bg=0.00
phospholipase C activity GO:0004629 p=2.0E−03 n=2 fg=0.07 bg=0.00
translation repressor activity GO:0030371 p=2.0E−03 n=2 fg=0.07 bg=0.00
heat shock protein binding GO:0031072 p=2.9E−03 n=4 fg=0.13 bg=0.02
G−protein beta/gamma−subunit complex bin... GO:0031683 p=3.3E−03 n=2 fg=0.07 bg=0.00
calcium−release channel activity GO:0015278 p=3.3E−03 n=2 fg=0.07 bg=0.00
carbohydrate derivative binding GO:0097367 p=7.5E−03 n=7 fg=0.23 bg=0.08
translation initiation factor binding GO:0031369 p=1.1E−02 n=2 fg=0.07 bg=0.01
adenyl ribonucleotide binding GO:0032559 p=1.6E−02 n=5 fg=0.17 bg=0.05
adenyl nucleotide binding GO:0030554 p=1.7E−02 n=5 fg=0.17 bg=0.05
leptin receptor binding GO:1990460 p=1.9E−02 n=1 fg=0.03 bg=0.00
cobalt ion binding GO:0050897 p=1.9E−02 n=1 fg=0.03 bg=0.00
transferrin receptor binding GO:1990459 p=1.9E−02 n=1 fg=0.03 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=1.9E−02 n=1 fg=0.03 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=1.9E−02 n=1 fg=0.03 bg=0.00
histone methyltransferase activity (H3−K... GO:0046976 p=1.9E−02 n=1 fg=0.03 bg=0.00
UFM1 activating enzyme activity GO:0071566 p=1.9E−02 n=1 fg=0.03 bg=0.00
nickel cation binding GO:0016151 p=1.9E−02 n=1 fg=0.03 bg=0.00
DNA/DNA annealing activity GO:1990814 p=1.9E−02 n=1 fg=0.03 bg=0.00
CoA carboxylase activity GO:0016421 p=1.9E−02 n=1 fg=0.03 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=1.9E−02 n=1 fg=0.03 bg=0.00
elongation factor−2 kinase activity GO:0004686 p=1.9E−02 n=1 fg=0.03 bg=0.00
small molecule binding GO:0036094 p=2.4E−02 n=7 fg=0.23 bg=0.10
G protein−coupled receptor binding GO:0001664 p=2.4E−02 n=3 fg=0.10 bg=0.02
signaling receptor binding GO:0005102 p=2.9E−02 n=7 fg=0.23 bg=0.10
protein serine/threonine kinase activity GO:0004674 p=3.1E−02 n=4 fg=0.13 bg=0.04
Hsp90 protein binding GO:0051879 p=3.5E−02 n=2 fg=0.07 bg=0.01
translation factor activity, RNA binding GO:0008135 p=3.5E−02 n=2 fg=0.07 bg=0.01
ATP binding GO:0005524 p=3.6E−02 n=4 fg=0.13 bg=0.04
0 1 2 3 4 5
−log(p)
n=30/134 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
axolemma GO:0030673 p=3.5E−03 n=2 fg=0.06 bg=0.00
messenger ribonucleoprotein complex GO:1990124 p=3.5E−03 n=2 fg=0.06 bg=0.00
presynaptic active zone GO:0048786 p=4.4E−03 n=3 fg=0.09 bg=0.01
integral component of postsynaptic membr... GO:0099055 p=7.2E−03 n=2 fg=0.06 bg=0.00
integral component of presynaptic membra... GO:0099056 p=7.2E−03 n=2 fg=0.06 bg=0.00
autosome GO:0030849 p=1.9E−02 n=1 fg=0.03 bg=0.00
SMN−Gemin2 complex GO:0034718 p=1.9E−02 n=1 fg=0.03 bg=0.00
SMN−Sm protein complex GO:0034719 p=1.9E−02 n=1 fg=0.03 bg=0.00
SMN complex GO:0032797 p=1.9E−02 n=1 fg=0.03 bg=0.00
desmosome GO:0030057 p=1.9E−02 n=1 fg=0.03 bg=0.00
SmD−containing SMN−Sm protein complex GO:0034730 p=1.9E−02 n=1 fg=0.03 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=1.9E−02 n=1 fg=0.03 bg=0.00
cytoplasmic U snRNP body GO:0071254 p=1.9E−02 n=1 fg=0.03 bg=0.00
ciliary transition fiber GO:0097539 p=1.9E−02 n=1 fg=0.03 bg=0.00
Gemini of coiled bodies GO:0097504 p=1.9E−02 n=1 fg=0.03 bg=0.00
molybdopterin synthase complex GO:0019008 p=1.9E−02 n=1 fg=0.03 bg=0.00
keratin filament GO:0045095 p=1.9E−02 n=1 fg=0.03 bg=0.00
terminal bouton GO:0043195 p=2.4E−02 n=3 fg=0.09 bg=0.02
U2AF complex GO:0089701 p=3.8E−02 n=1 fg=0.03 bg=0.00
neuron spine GO:0044309 p=4.0E−02 n=3 fg=0.09 bg=0.02
dendritic spine GO:0043197 p=4.0E−02 n=3 fg=0.09 bg=0.02
cytoplasmic ribonucleoprotein granule GO:0036464 p=5.1E−02 n=3 fg=0.09 bg=0.02
manchette GO:0002177 p=5.7E−02 n=1 fg=0.03 bg=0.00
intermediate filament GO:0005882 p=5.7E−02 n=1 fg=0.03 bg=0.00
nuclear lamina GO:0005652 p=5.7E−02 n=1 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=5.7E−02 n=1 fg=0.03 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=5.7E−02 n=1 fg=0.03 bg=0.00
U2−type prespliceosome GO:0071004 p=5.7E−02 n=1 fg=0.03 bg=0.00
commitment complex GO:0000243 p=5.7E−02 n=1 fg=0.03 bg=0.00
muscle tendon junction GO:0005927 p=5.7E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/134 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction