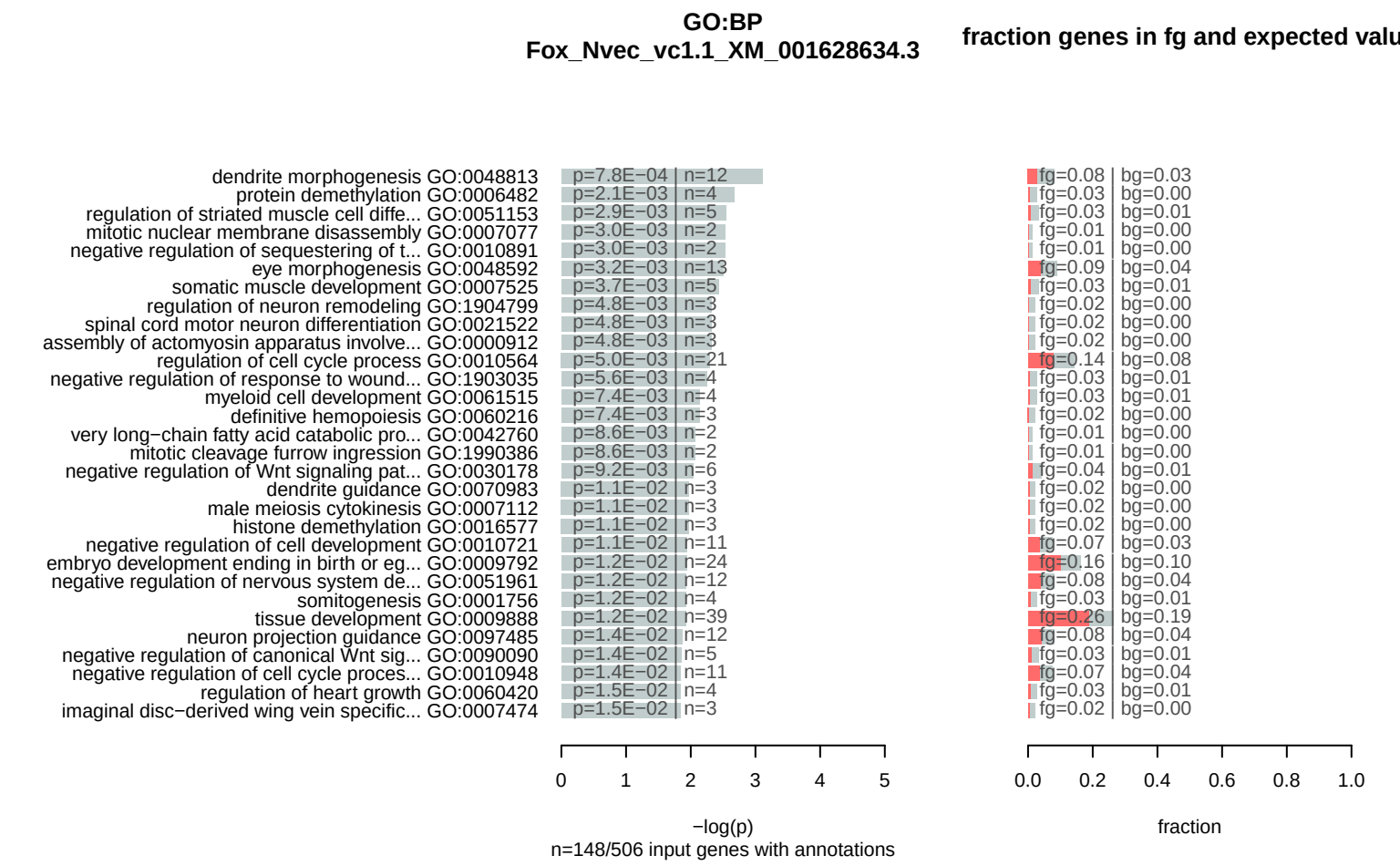
GO:BP
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
dendrite morphogenesis GO:0048813 p=7.8E−04 n=12 fg=0.08 bg=0.03
protein demethylation GO:0006482 p=2.1E−03 n=4 fg=0.03 bg=0.00
regulation of striated muscle cell diffe... GO:0051153 p=2.9E−03 n=5 fg=0.03 bg=0.01
mitotic nuclear membrane disassembly GO:0007077 p=3.0E−03 n=2 fg=0.01 bg=0.00
negative regulation of sequestering of t... GO:0010891 p=3.0E−03 n=2 fg=0.01 bg=0.00
eye morphogenesis GO:0048592 p=3.2E−03 n=13 fg=0.09 bg=0.04
somatic muscle development GO:0007525 p=3.7E−03 n=5 fg=0.03 bg=0.01
regulation of neuron remodeling GO:1904799 p=4.8E−03 n=3 fg=0.02 bg=0.00
spinal cord motor neuron differentiation GO:0021522 p=4.8E−03 n=3 fg=0.02 bg=0.00
assembly of actomyosin apparatus involve... GO:0000912 p=4.8E−03 n=3 fg=0.02 bg=0.00
regulation of cell cycle process GO:0010564 p=5.0E−03 n=21 fg=0.14 bg=0.08
negative regulation of response to wound... GO:1903035 p=5.6E−03 n=4 fg=0.03 bg=0.01
myeloid cell development GO:0061515 p=7.4E−03 n=4 fg=0.03 bg=0.01
definitive hemopoiesis GO:0060216 p=7.4E−03 n=3 fg=0.02 bg=0.00
very long−chain fatty acid catabolic pro... GO:0042760 p=8.6E−03 n=2 fg=0.01 bg=0.00
mitotic cleavage furrow ingression GO:1990386 p=8.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of Wnt signaling pat... GO:0030178 p=9.2E−03 n=6 fg=0.04 bg=0.01
dendrite guidance GO:0070983 p=1.1E−02 n=3 fg=0.02 bg=0.00
male meiosis cytokinesis GO:0007112 p=1.1E−02 n=3 fg=0.02 bg=0.00
histone demethylation GO:0016577 p=1.1E−02 n=3 fg=0.02 bg=0.00
negative regulation of cell development GO:0010721 p=1.1E−02 n=11 fg=0.07 bg=0.03
embryo development ending in birth or eg... GO:0009792 p=1.2E−02 n=24 fg=0.16 bg=0.10
negative regulation of nervous system de... GO:0051961 p=1.2E−02 n=12 fg=0.08 bg=0.04
somitogenesis GO:0001756 p=1.2E−02 n=4 fg=0.03 bg=0.01
tissue development GO:0009888 p=1.2E−02 n=39 fg=0.26 bg=0.19
neuron projection guidance GO:0097485 p=1.4E−02 n=12 fg=0.08 bg=0.04
negative regulation of canonical Wnt sig... GO:0090090 p=1.4E−02 n=5 fg=0.03 bg=0.01
negative regulation of cell cycle proces... GO:0010948 p=1.4E−02 n=11 fg=0.07 bg=0.04
regulation of heart growth GO:0060420 p=1.5E−02 n=4 fg=0.03 bg=0.01
imaginal disc−derived wing vein specific... GO:0007474 p=1.5E−02 n=3 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=148/506 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
ATP−dependent protein binding GO:0043008 p=2.9E−03 n=2 fg=0.02 bg=0.00
2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=7.0E−03 n=4 fg=0.03 bg=0.01
histone demethylase activity GO:0032452 p=7.1E−03 n=3 fg=0.02 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.6E−02 n=2 fg=0.02 bg=0.00
protein−transporting ATPase activity GO:0015450 p=1.6E−02 n=2 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0016616 p=2.0E−02 n=4 fg=0.03 bg=0.01
amide transmembrane transporter activity GO:0042887 p=2.4E−02 n=3 fg=0.02 bg=0.01
nucleobase−containing compound transmemb... GO:0015932 p=2.4E−02 n=3 fg=0.02 bg=0.01
modified amino acid binding GO:0072341 p=2.4E−02 n=4 fg=0.03 bg=0.01
3'−5' DNA helicase activity GO:0043138 p=2.6E−02 n=2 fg=0.02 bg=0.00
satellite DNA binding GO:0003696 p=2.6E−02 n=2 fg=0.02 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=2.6E−02 n=2 fg=0.02 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=2.6E−02 n=2 fg=0.02 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=2.6E−02 n=2 fg=0.02 bg=0.00
protein transporter activity GO:0140318 p=2.6E−02 n=2 fg=0.02 bg=0.00
protein kinase activity GO:0004672 p=3.3E−02 n=12 fg=0.09 bg=0.05
protein serine/threonine kinase activity GO:0004674 p=3.6E−02 n=10 fg=0.08 bg=0.04
oxidoreductase activity, acting on CH−OH... GO:0016614 p=3.7E−02 n=4 fg=0.03 bg=0.01
cytoskeletal anchor activity GO:0008093 p=3.8E−02 n=2 fg=0.02 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.8E−02 n=2 fg=0.02 bg=0.00
non−membrane spanning protein tyrosine k... GO:0004715 p=5.1E−02 n=2 fg=0.02 bg=0.00
phosphotransferase activity, alcohol gro... GO:0016773 p=5.2E−02 n=13 fg=0.10 bg=0.06
polyamine binding GO:0019808 p=5.4E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=5.4E−02 n=1 fg=0.01 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=5.4E−02 n=1 fg=0.01 bg=0.00
ACP phosphopantetheine attachment site b... GO:0044620 p=5.4E−02 n=1 fg=0.01 bg=0.00
acyl binding GO:0000035 p=5.4E−02 n=1 fg=0.01 bg=0.00
acyl carrier activity GO:0000036 p=5.4E−02 n=1 fg=0.01 bg=0.00
prosthetic group binding GO:0051192 p=5.4E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=5.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=128/506 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
elongin complex GO:0070449 p=3.1E−03 n=2 fg=0.01 bg=0.00
protein serine/threonine phosphatase com... GO:0008287 p=1.0E−02 n=4 fg=0.03 bg=0.01
phosphatase complex GO:1903293 p=1.5E−02 n=4 fg=0.03 bg=0.01
eukaryotic translation initiation factor... GO:0071541 p=1.7E−02 n=2 fg=0.01 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=1.7E−02 n=2 fg=0.01 bg=0.00
integral component of peroxisomal membra... GO:0005779 p=1.7E−02 n=2 fg=0.01 bg=0.00
integral component of organelle membrane GO:0031301 p=1.9E−02 n=11 fg=0.07 bg=0.04
cilium GO:0005929 p=2.3E−02 n=16 fg=0.11 bg=0.06
intrinsic component of organelle membran... GO:0031300 p=2.5E−02 n=11 fg=0.07 bg=0.04
extrinsic component of cytoplasmic side ... GO:0031234 p=2.7E−02 n=4 fg=0.03 bg=0.01
protein phosphatase type 1 complex GO:0000164 p=2.8E−02 n=2 fg=0.01 bg=0.00
kinetochore microtubule GO:0005828 p=2.8E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005852 p=4.0E−02 n=2 fg=0.01 bg=0.00
mitotic spindle midzone GO:1990023 p=4.0E−02 n=2 fg=0.01 bg=0.00
AP−type membrane coat adaptor complex GO:0030119 p=5.4E−02 n=2 fg=0.01 bg=0.00
cytoplasmic side of membrane GO:0098562 p=5.5E−02 n=7 fg=0.05 bg=0.02
phagolysosome GO:0032010 p=5.6E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=5.6E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=5.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=5.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061202 p=5.6E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=5.6E−02 n=1 fg=0.01 bg=0.00
USH2 complex GO:1990696 p=5.6E−02 n=1 fg=0.01 bg=0.00
nascent polypeptide−associated complex GO:0005854 p=5.6E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=5.6E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070032 p=5.6E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070033 p=5.6E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=5.6E−02 n=1 fg=0.01 bg=0.00
ribose phosphate diphosphokinase complex GO:0002189 p=5.6E−02 n=1 fg=0.01 bg=0.00
alveolar lamellar body GO:0097208 p=5.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=151/506 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction