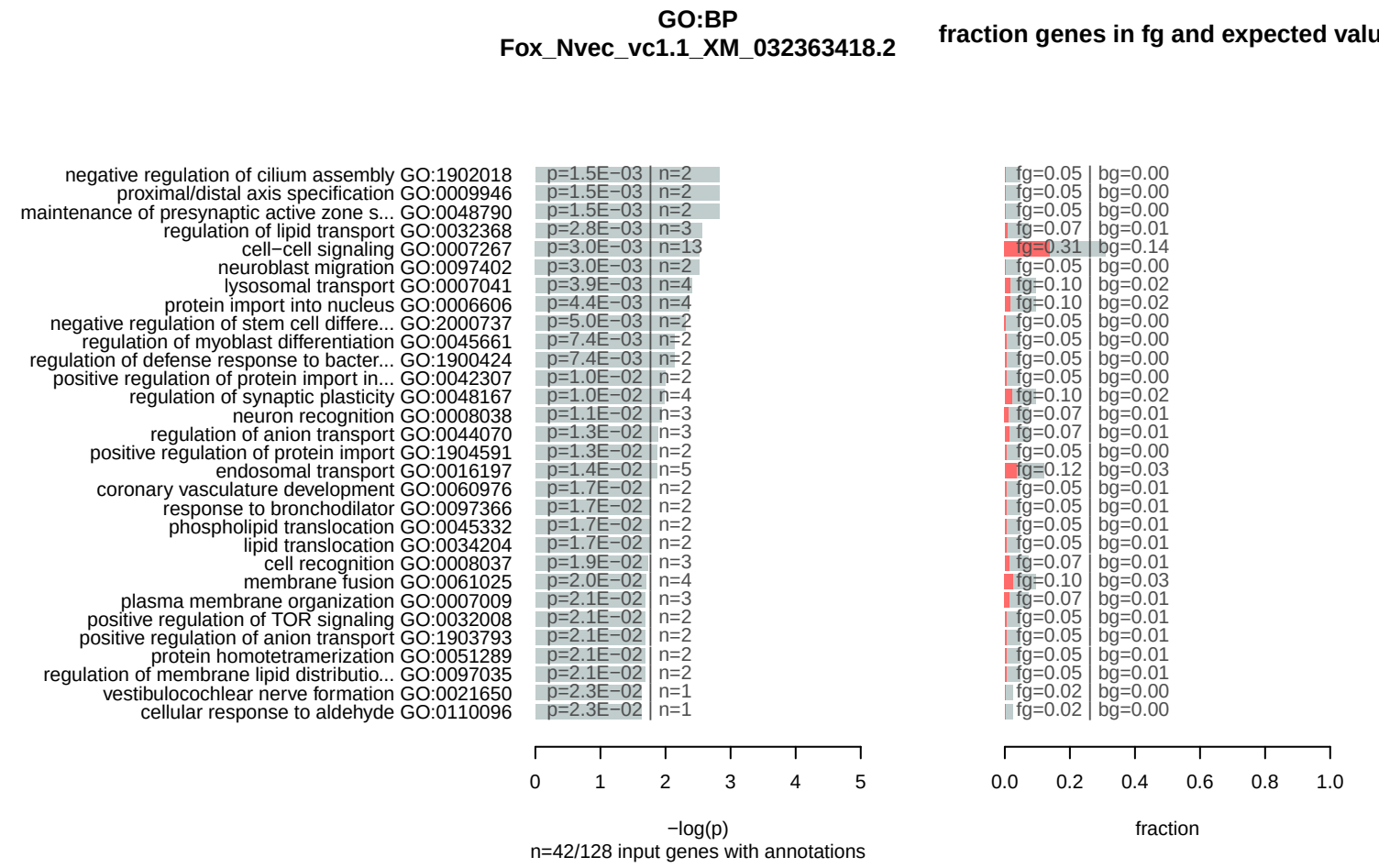
GO:BP
Fox_Nvec_vc1.1_XM_032363418.2
fraction genes in fg and expected valu
negative regulation of cilium assembly GO:1902018 p=1.5E−03 n=2 fg=0.05 bg=0.00
proximal/distal axis specification GO:0009946 p=1.5E−03 n=2 fg=0.05 bg=0.00
maintenance of presynaptic active zone s... GO:0048790 p=1.5E−03 n=2 fg=0.05 bg=0.00
regulation of lipid transport GO:0032368 p=2.8E−03 n=3 fg=0.07 bg=0.01
cell−cell signaling GO:0007267 p=3.0E−03 n=13 fg=0.31 bg=0.14
neuroblast migration GO:0097402 p=3.0E−03 n=2 fg=0.05 bg=0.00
lysosomal transport GO:0007041 p=3.9E−03 n=4 fg=0.10 bg=0.02
protein import into nucleus GO:0006606 p=4.4E−03 n=4 fg=0.10 bg=0.02
negative regulation of stem cell differe... GO:2000737 p=5.0E−03 n=2 fg=0.05 bg=0.00
regulation of myoblast differentiation GO:0045661 p=7.4E−03 n=2 fg=0.05 bg=0.00
regulation of defense response to bacter... GO:1900424 p=7.4E−03 n=2 fg=0.05 bg=0.00
positive regulation of protein import in... GO:0042307 p=1.0E−02 n=2 fg=0.05 bg=0.00
regulation of synaptic plasticity GO:0048167 p=1.0E−02 n=4 fg=0.10 bg=0.02
neuron recognition GO:0008038 p=1.1E−02 n=3 fg=0.07 bg=0.01
regulation of anion transport GO:0044070 p=1.3E−02 n=3 fg=0.07 bg=0.01
positive regulation of protein import GO:1904591 p=1.3E−02 n=2 fg=0.05 bg=0.00
endosomal transport GO:0016197 p=1.4E−02 n=5 fg=0.12 bg=0.03
coronary vasculature development GO:0060976 p=1.7E−02 n=2 fg=0.05 bg=0.01
response to bronchodilator GO:0097366 p=1.7E−02 n=2 fg=0.05 bg=0.01
phospholipid translocation GO:0045332 p=1.7E−02 n=2 fg=0.05 bg=0.01
lipid translocation GO:0034204 p=1.7E−02 n=2 fg=0.05 bg=0.01
cell recognition GO:0008037 p=1.9E−02 n=3 fg=0.07 bg=0.01
membrane fusion GO:0061025 p=2.0E−02 n=4 fg=0.10 bg=0.03
plasma membrane organization GO:0007009 p=2.1E−02 n=3 fg=0.07 bg=0.01
positive regulation of TOR signaling GO:0032008 p=2.1E−02 n=2 fg=0.05 bg=0.01
positive regulation of anion transport GO:1903793 p=2.1E−02 n=2 fg=0.05 bg=0.01
protein homotetramerization GO:0051289 p=2.1E−02 n=2 fg=0.05 bg=0.01
regulation of membrane lipid distributio... GO:0097035 p=2.1E−02 n=2 fg=0.05 bg=0.01
vestibulocochlear nerve formation GO:0021650 p=2.3E−02 n=1 fg=0.02 bg=0.00
cellular response to aldehyde GO:0110096 p=2.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=42/128 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032363418.2
fraction genes in fg and expected valu
lipid binding GO:0008289 p=2.0E−03 n=7 fg=0.19 bg=0.05
anion binding GO:0043168 p=3.2E−03 n=11 fg=0.31 bg=0.13
phospholipid binding GO:0005543 p=1.5E−02 n=5 fg=0.14 bg=0.04
ubiquitin binding GO:0043130 p=1.6E−02 n=2 fg=0.06 bg=0.01
histone acetyltransferase binding GO:0035035 p=2.0E−02 n=2 fg=0.06 bg=0.01
mitogen−activated protein kinase binding GO:0051019 p=2.0E−02 n=2 fg=0.06 bg=0.01
phosphatidylglycerol binding GO:1901611 p=2.3E−02 n=1 fg=0.03 bg=0.00
cardiolipin binding GO:1901612 p=2.3E−02 n=1 fg=0.03 bg=0.00
histamine receptor activity GO:0004969 p=2.3E−02 n=1 fg=0.03 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=2.3E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=2.3E−02 n=1 fg=0.03 bg=0.00
intracellular phosphatidylinositol−3,5−b... GO:0097682 p=2.3E−02 n=1 fg=0.03 bg=0.00
leucine zipper domain binding GO:0043522 p=2.3E−02 n=1 fg=0.03 bg=0.00
insulin−like growth factor II binding GO:0031995 p=2.3E−02 n=1 fg=0.03 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=2.3E−02 n=1 fg=0.03 bg=0.00
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=2.3E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016649 p=2.3E−02 n=1 fg=0.03 bg=0.00
glycogen binding GO:2001069 p=2.3E−02 n=1 fg=0.03 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0050664 p=2.3E−02 n=1 fg=0.03 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=2.3E−02 n=1 fg=0.03 bg=0.00
retinoic acid binding GO:0001972 p=2.3E−02 n=1 fg=0.03 bg=0.00
electron−transferring−flavoprotein dehyd... GO:0004174 p=2.3E−02 n=1 fg=0.03 bg=0.00
AMP deaminase activity GO:0003876 p=2.3E−02 n=1 fg=0.03 bg=0.00
ribosomal large subunit binding GO:0043023 p=2.3E−02 n=1 fg=0.03 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=2.3E−02 n=1 fg=0.03 bg=0.00
flippase activity GO:0140327 p=2.3E−02 n=1 fg=0.03 bg=0.00
mannose binding GO:0005537 p=2.3E−02 n=1 fg=0.03 bg=0.00
kringle domain binding GO:0036143 p=2.3E−02 n=1 fg=0.03 bg=0.00
NAD(P)H oxidase H2O2−forming activity GO:0016174 p=2.3E−02 n=1 fg=0.03 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=2.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=36/128 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032363418.2
fraction genes in fg and expected valu
endolysosome membrane GO:0036020 p=1.6E−03 n=2 fg=0.05 bg=0.00
late endosome GO:0005770 p=3.6E−03 n=5 fg=0.12 bg=0.02
presynaptic active zone membrane GO:0048787 p=5.3E−03 n=2 fg=0.05 bg=0.00
neuromuscular junction GO:0031594 p=6.9E−03 n=4 fg=0.09 bg=0.02
apicolateral plasma membrane GO:0016327 p=1.1E−02 n=2 fg=0.05 bg=0.00
M band GO:0031430 p=2.2E−02 n=2 fg=0.05 bg=0.01
dense core granule membrane GO:0032127 p=2.4E−02 n=1 fg=0.02 bg=0.00
polytene chromosome chromocenter GO:0005701 p=2.4E−02 n=1 fg=0.02 bg=0.00
spectrosome GO:0045170 p=2.4E−02 n=1 fg=0.02 bg=0.00
spectrin GO:0008091 p=2.4E−02 n=1 fg=0.02 bg=0.00
microvesicle GO:1990742 p=2.4E−02 n=1 fg=0.02 bg=0.00
keratin filament GO:0045095 p=2.4E−02 n=1 fg=0.02 bg=0.00
dense core granule GO:0031045 p=2.4E−02 n=1 fg=0.02 bg=0.00
ciliary transition fiber GO:0097539 p=2.4E−02 n=1 fg=0.02 bg=0.00
integral component of lysosomal membrane GO:1905103 p=2.4E−02 n=1 fg=0.02 bg=0.00
desmosome GO:0030057 p=2.4E−02 n=1 fg=0.02 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=2.4E−02 n=1 fg=0.02 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=2.4E−02 n=1 fg=0.02 bg=0.00
synaptic vesicle GO:0008021 p=2.5E−02 n=4 fg=0.09 bg=0.03
lateral plasma membrane GO:0016328 p=2.6E−02 n=2 fg=0.05 bg=0.01
A band GO:0031672 p=3.6E−02 n=2 fg=0.05 bg=0.01
cytoplasmic vesicle membrane GO:0030659 p=3.9E−02 n=9 fg=0.21 bg=0.08
exocytic vesicle GO:0070382 p=3.9E−02 n=4 fg=0.09 bg=0.03
transport vesicle GO:0030133 p=4.0E−02 n=5 fg=0.12 bg=0.04
secretory vesicle GO:0099503 p=4.1E−02 n=7 fg=0.16 bg=0.08
vesicle membrane GO:0012506 p=4.1E−02 n=9 fg=0.21 bg=0.08
IkappaB kinase complex GO:0008385 p=4.7E−02 n=1 fg=0.02 bg=0.00
integral component of vacuolar membrane GO:0031166 p=4.7E−02 n=1 fg=0.02 bg=0.00
HOPS complex GO:0030897 p=4.7E−02 n=1 fg=0.02 bg=0.00
activating signal cointegrator 1 complex GO:0099053 p=4.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=43/128 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction