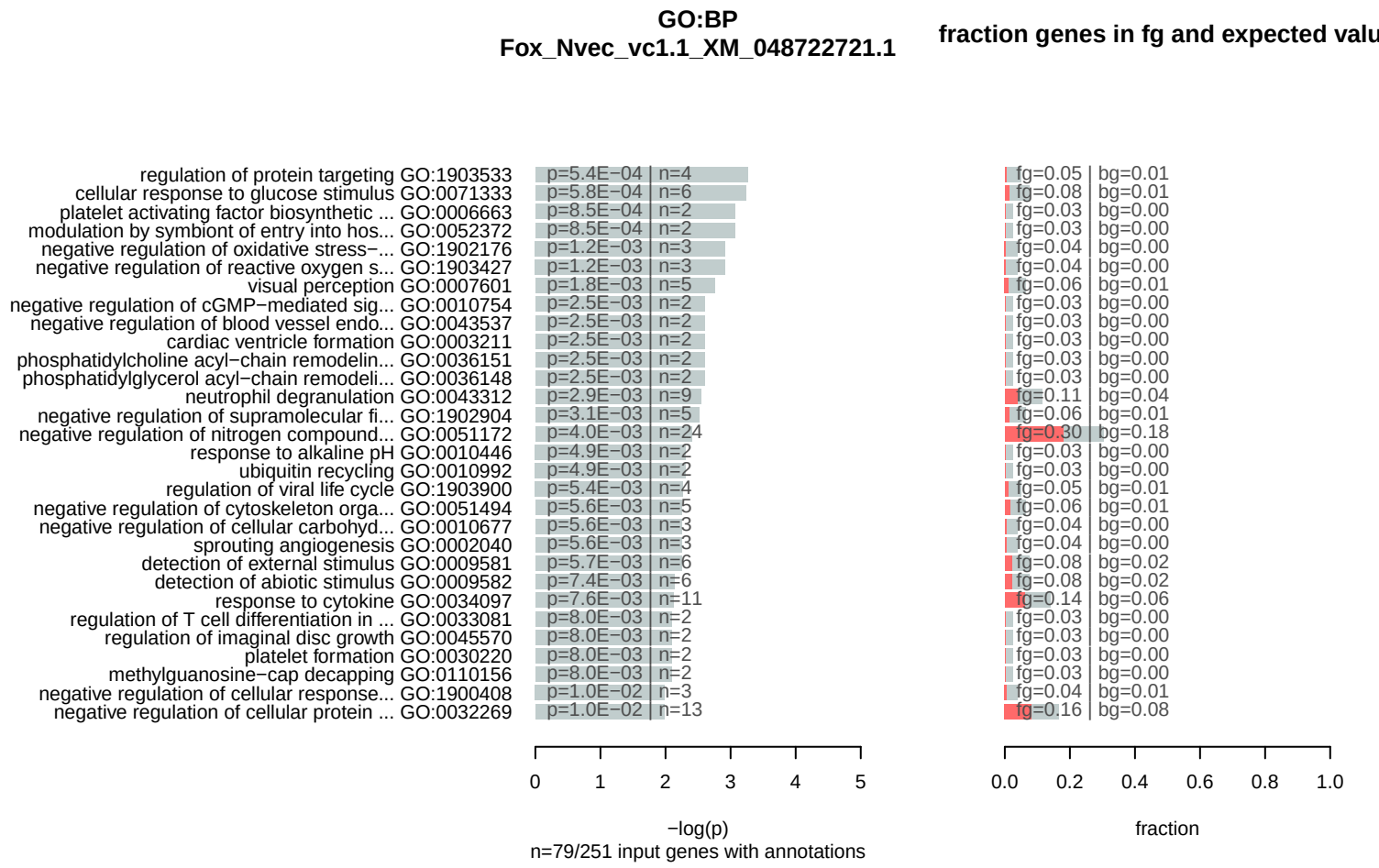
GO:BP
Fox_Nvec_vc1.1_XM_048722721.1
fraction genes in fg and expected valu
regulation of protein targeting GO:1903533 p=5.4E−04 n=4 fg=0.05 bg=0.01
cellular response to glucose stimulus GO:0071333 p=5.8E−04 n=6 fg=0.08 bg=0.01
platelet activating factor biosynthetic ... GO:0006663 p=8.5E−04 n=2 fg=0.03 bg=0.00
modulation by symbiont of entry into hos... GO:0052372 p=8.5E−04 n=2 fg=0.03 bg=0.00
negative regulation of oxidative stress−... GO:1902176 p=1.2E−03 n=3 fg=0.04 bg=0.00
negative regulation of reactive oxygen s... GO:1903427 p=1.2E−03 n=3 fg=0.04 bg=0.00
visual perception GO:0007601 p=1.8E−03 n=5 fg=0.06 bg=0.01
negative regulation of cGMP−mediated sig... GO:0010754 p=2.5E−03 n=2 fg=0.03 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=2.5E−03 n=2 fg=0.03 bg=0.00
cardiac ventricle formation GO:0003211 p=2.5E−03 n=2 fg=0.03 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=2.5E−03 n=2 fg=0.03 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=2.5E−03 n=2 fg=0.03 bg=0.00
neutrophil degranulation GO:0043312 p=2.9E−03 n=9 fg=0.11 bg=0.04
negative regulation of supramolecular fi... GO:1902904 p=3.1E−03 n=5 fg=0.06 bg=0.01
negative regulation of nitrogen compound... GO:0051172 p=4.0E−03 n=24 fg=0.30 bg=0.18
response to alkaline pH GO:0010446 p=4.9E−03 n=2 fg=0.03 bg=0.00
ubiquitin recycling GO:0010992 p=4.9E−03 n=2 fg=0.03 bg=0.00
regulation of viral life cycle GO:1903900 p=5.4E−03 n=4 fg=0.05 bg=0.01
negative regulation of cytoskeleton orga... GO:0051494 p=5.6E−03 n=5 fg=0.06 bg=0.01
negative regulation of cellular carbohyd... GO:0010677 p=5.6E−03 n=3 fg=0.04 bg=0.00
sprouting angiogenesis GO:0002040 p=5.6E−03 n=3 fg=0.04 bg=0.00
detection of external stimulus GO:0009581 p=5.7E−03 n=6 fg=0.08 bg=0.02
detection of abiotic stimulus GO:0009582 p=7.4E−03 n=6 fg=0.08 bg=0.02
response to cytokine GO:0034097 p=7.6E−03 n=11 fg=0.14 bg=0.06
regulation of T cell differentiation in ... GO:0033081 p=8.0E−03 n=2 fg=0.03 bg=0.00
regulation of imaginal disc growth GO:0045570 p=8.0E−03 n=2 fg=0.03 bg=0.00
platelet formation GO:0030220 p=8.0E−03 n=2 fg=0.03 bg=0.00
methylguanosine−cap decapping GO:0110156 p=8.0E−03 n=2 fg=0.03 bg=0.00
negative regulation of cellular response... GO:1900408 p=1.0E−02 n=3 fg=0.04 bg=0.01
negative regulation of cellular protein ... GO:0032269 p=1.0E−02 n=13 fg=0.16 bg=0.08
0 1 2 3 4 5
−log(p)
n=79/251 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_048722721.1
fraction genes in fg and expected valu
transcription corepressor binding GO:0001222 p=7.6E−04 n=2 fg=0.03 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=7.6E−04 n=2 fg=0.03 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=2.2E−03 n=2 fg=0.03 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=2.2E−03 n=2 fg=0.03 bg=0.00
histone deacetylase binding GO:0042826 p=5.2E−03 n=4 fg=0.06 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=5.4E−03 n=8 fg=0.12 bg=0.04
DNA−binding transcription factor activit... GO:0003700 p=5.5E−03 n=11 fg=0.17 bg=0.07
mRNA 3'−UTR binding GO:0003730 p=8.9E−03 n=3 fg=0.05 bg=0.01
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.1E−02 n=2 fg=0.03 bg=0.00
cyclic−nucleotide phosphodiesterase acti... GO:0004112 p=1.1E−02 n=2 fg=0.03 bg=0.00
3',5'−cyclic−nucleotide phosphodiesteras... GO:0004114 p=1.1E−02 n=2 fg=0.03 bg=0.00
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=1.1E−02 n=2 fg=0.03 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=1.5E−02 n=2 fg=0.03 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=1.6E−02 n=6 fg=0.09 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.6E−02 n=6 fg=0.09 bg=0.03
monosaccharide binding GO:0048029 p=2.4E−02 n=2 fg=0.03 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.8E−02 n=1 fg=0.02 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=2.8E−02 n=1 fg=0.02 bg=0.00
ubiquinone binding GO:0048039 p=2.8E−02 n=1 fg=0.02 bg=0.00
protein−membrane adaptor activity GO:0043495 p=2.8E−02 n=1 fg=0.02 bg=0.00
fucose binding GO:0042806 p=2.8E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.8E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on metal... GO:0043783 p=2.8E−02 n=1 fg=0.02 bg=0.00
F−box domain binding GO:1990444 p=2.8E−02 n=1 fg=0.02 bg=0.00
7S RNA binding GO:0008312 p=2.8E−02 n=1 fg=0.02 bg=0.00
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=2.8E−02 n=1 fg=0.02 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=2.8E−02 n=1 fg=0.02 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.8E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=2.8E−02 n=1 fg=0.02 bg=0.00
insulin binding GO:0043559 p=2.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=66/251 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_048722721.1
fraction genes in fg and expected valu
secretory granule membrane GO:0030667 p=3.7E−03 n=6 fg=0.07 bg=0.02
lipid droplet GO:0005811 p=5.1E−03 n=4 fg=0.05 bg=0.01
cytosolic proteasome complex GO:0031597 p=1.7E−02 n=2 fg=0.02 bg=0.00
lysosomal lumen GO:0043202 p=2.1E−02 n=3 fg=0.04 bg=0.01
lysosome GO:0005764 p=2.4E−02 n=8 fg=0.10 bg=0.04
azurophil granule membrane GO:0035577 p=2.8E−02 n=2 fg=0.02 bg=0.00
host intracellular part GO:0033646 p=3.0E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=3.0E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=3.0E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=3.0E−02 n=1 fg=0.01 bg=0.00
acrosomal membrane GO:0002080 p=3.0E−02 n=1 fg=0.01 bg=0.00
outer acrosomal membrane GO:0002081 p=3.0E−02 n=1 fg=0.01 bg=0.00
mitochondrial electron transfer flavopro... GO:0017133 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=3.0E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=3.0E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=3.0E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=3.0E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=3.0E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=3.0E−02 n=1 fg=0.01 bg=0.00
electron transfer flavoprotein complex GO:0045251 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cell nuclear part GO:0044094 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=3.0E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=3.0E−02 n=1 fg=0.01 bg=0.00
lytic vacuole GO:0000323 p=3.0E−02 n=8 fg=0.10 bg=0.05
nuclear speck GO:0016607 p=3.8E−02 n=6 fg=0.07 bg=0.03
vacuole GO:0005773 p=4.4E−02 n=9 fg=0.11 bg=0.06
ruffle membrane GO:0032587 p=4.8E−02 n=2 fg=0.02 bg=0.00
nuclear body GO:0016604 p=5.4E−02 n=9 fg=0.11 bg=0.06
0 1 2 3 4 5
−log(p)
n=81/251 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction