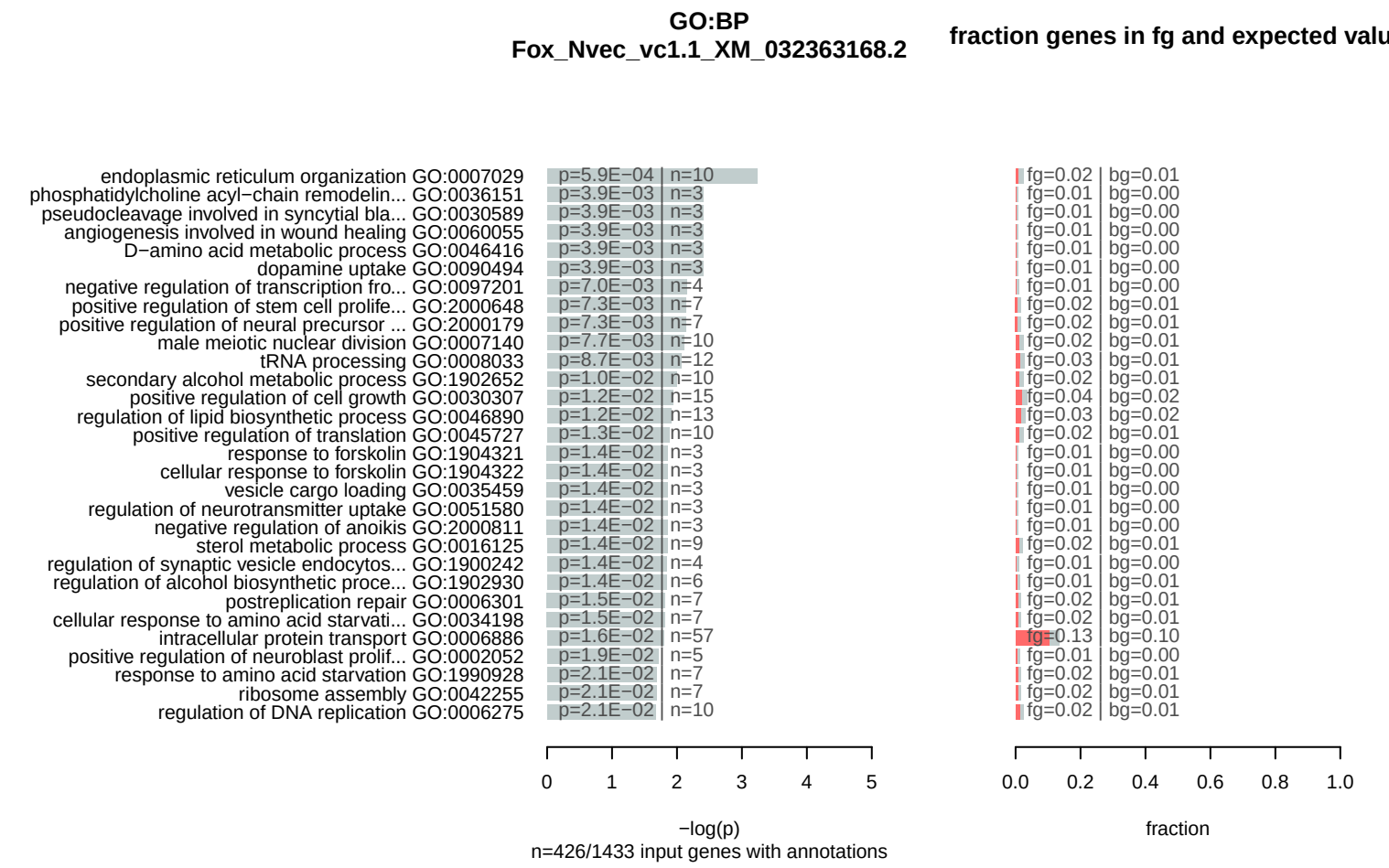
GO:BP
Fox_Nvec_vc1.1_XM_032363168.2
fraction genes in fg and expected valu
endoplasmic reticulum organization GO:0007029 p=5.9E−04 n=10 fg=0.02 bg=0.01
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=3.9E−03 n=3 fg=0.01 bg=0.00
pseudocleavage involved in syncytial bla... GO:0030589 p=3.9E−03 n=3 fg=0.01 bg=0.00
angiogenesis involved in wound healing GO:0060055 p=3.9E−03 n=3 fg=0.01 bg=0.00
D−amino acid metabolic process GO:0046416 p=3.9E−03 n=3 fg=0.01 bg=0.00
dopamine uptake GO:0090494 p=3.9E−03 n=3 fg=0.01 bg=0.00
negative regulation of transcription fro... GO:0097201 p=7.0E−03 n=4 fg=0.01 bg=0.00
positive regulation of stem cell prolife... GO:2000648 p=7.3E−03 n=7 fg=0.02 bg=0.01
positive regulation of neural precursor ... GO:2000179 p=7.3E−03 n=7 fg=0.02 bg=0.01
male meiotic nuclear division GO:0007140 p=7.7E−03 n=10 fg=0.02 bg=0.01
tRNA processing GO:0008033 p=8.7E−03 n=12 fg=0.03 bg=0.01
secondary alcohol metabolic process GO:1902652 p=1.0E−02 n=10 fg=0.02 bg=0.01
positive regulation of cell growth GO:0030307 p=1.2E−02 n=15 fg=0.04 bg=0.02
regulation of lipid biosynthetic process GO:0046890 p=1.2E−02 n=13 fg=0.03 bg=0.02
positive regulation of translation GO:0045727 p=1.3E−02 n=10 fg=0.02 bg=0.01
response to forskolin GO:1904321 p=1.4E−02 n=3 fg=0.01 bg=0.00
cellular response to forskolin GO:1904322 p=1.4E−02 n=3 fg=0.01 bg=0.00
vesicle cargo loading GO:0035459 p=1.4E−02 n=3 fg=0.01 bg=0.00
regulation of neurotransmitter uptake GO:0051580 p=1.4E−02 n=3 fg=0.01 bg=0.00
negative regulation of anoikis GO:2000811 p=1.4E−02 n=3 fg=0.01 bg=0.00
sterol metabolic process GO:0016125 p=1.4E−02 n=9 fg=0.02 bg=0.01
regulation of synaptic vesicle endocytos... GO:1900242 p=1.4E−02 n=4 fg=0.01 bg=0.00
regulation of alcohol biosynthetic proce... GO:1902930 p=1.4E−02 n=6 fg=0.01 bg=0.01
postreplication repair GO:0006301 p=1.5E−02 n=7 fg=0.02 bg=0.01
cellular response to amino acid starvati... GO:0034198 p=1.5E−02 n=7 fg=0.02 bg=0.01
intracellular protein transport GO:0006886 p=1.6E−02 n=57 fg=0.13 bg=0.10
positive regulation of neuroblast prolif... GO:0002052 p=1.9E−02 n=5 fg=0.01 bg=0.00
response to amino acid starvation GO:1990928 p=2.1E−02 n=7 fg=0.02 bg=0.01
ribosome assembly GO:0042255 p=2.1E−02 n=7 fg=0.02 bg=0.01
regulation of DNA replication GO:0006275 p=2.1E−02 n=10 fg=0.02 bg=0.01
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=426/1433 input genes with annotations
GO:MF
Fox_Nvec_vc1.1_XM_032363168.2
fraction genes in fg and expected valu
satellite DNA binding GO:0003696 p=2.6E−03 n=4 fg=0.01 bg=0.00
iron ion binding GO:0005506 p=9.0E−03 n=6 fg=0.02 bg=0.01
calmodulin−dependent protein kinase acti... GO:0004683 p=1.2E−02 n=5 fg=0.01 bg=0.00
syntaxin−1 binding GO:0017075 p=1.3E−02 n=3 fg=0.01 bg=0.00
methyl−CpG binding GO:0008327 p=1.3E−02 n=3 fg=0.01 bg=0.00
RNA binding GO:0003723 p=1.9E−02 n=50 fg=0.14 bg=0.10
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=2.4E−02 n=2 fg=0.01 bg=0.00
D−amino−acid oxidase activity GO:0003884 p=2.4E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0016641 p=2.4E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0016638 p=2.4E−02 n=2 fg=0.01 bg=0.00
aspartate oxidase activity GO:0015922 p=2.4E−02 n=2 fg=0.01 bg=0.00
histone−arginine N−methyltransferase act... GO:0008469 p=2.4E−02 n=2 fg=0.01 bg=0.00
tRNA (cytosine−5−)−methyltransferase act... GO:0016428 p=2.4E−02 n=2 fg=0.01 bg=0.00
O−acetyltransferase activity GO:0016413 p=2.4E−02 n=2 fg=0.01 bg=0.00
D−aspartate oxidase activity GO:0008445 p=2.4E−02 n=2 fg=0.01 bg=0.00
carbon−nitrogen ligase activity, with gl... GO:0016884 p=2.4E−02 n=2 fg=0.01 bg=0.00
protein−arginine omega−N monomethyltrans... GO:0035241 p=2.4E−02 n=2 fg=0.01 bg=0.00
histone methyltransferase activity (H4−R... GO:0044020 p=2.4E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol 3−kinase regulator ... GO:0035014 p=2.4E−02 n=2 fg=0.01 bg=0.00
transcription corepressor binding GO:0001222 p=2.4E−02 n=2 fg=0.01 bg=0.00
protein phosphatase binding GO:0019903 p=2.6E−02 n=11 fg=0.03 bg=0.02
mRNA 3'−UTR binding GO:0003730 p=2.8E−02 n=6 fg=0.02 bg=0.01
glucosyltransferase activity GO:0046527 p=3.0E−02 n=3 fg=0.01 bg=0.00
myosin light chain binding GO:0032027 p=3.0E−02 n=3 fg=0.01 bg=0.00
TFIID−class transcription factor complex... GO:0001094 p=3.0E−02 n=3 fg=0.01 bg=0.00
phosphatase binding GO:0019902 p=3.3E−02 n=14 fg=0.04 bg=0.02
CoA hydrolase activity GO:0016289 p=3.8E−02 n=4 fg=0.01 bg=0.00
transcription coregulator binding GO:0001221 p=3.8E−02 n=4 fg=0.01 bg=0.00
histone deacetylase binding GO:0042826 p=3.9E−02 n=8 fg=0.02 bg=0.01
nucleic acid binding GO:0003676 p=4.6E−02 n=91 fg=0.25 bg=0.21
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=370/1433 input genes with annotations
GO:CC
Fox_Nvec_vc1.1_XM_032363168.2
fraction genes in fg and expected valu
inclusion body GO:0016234 p=8.2E−04 n=8 fg=0.02 bg=0.01
extrinsic component of endoplasmic retic... GO:0042406 p=3.9E−03 n=3 fg=0.01 bg=0.00
excitatory synapse GO:0060076 p=1.4E−02 n=4 fg=0.01 bg=0.00
replication fork GO:0005657 p=2.1E−02 n=7 fg=0.02 bg=0.01
cytosolic ribosome GO:0022626 p=2.1E−02 n=13 fg=0.03 bg=0.02
secretory granule membrane GO:0030667 p=2.2E−02 n=14 fg=0.03 bg=0.02
female pronucleus GO:0001939 p=2.5E−02 n=2 fg=0.00 bg=0.00
delta DNA polymerase complex GO:0043625 p=2.5E−02 n=2 fg=0.00 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=2.5E−02 n=2 fg=0.00 bg=0.00
Elg1 RFC−like complex GO:0031391 p=2.5E−02 n=2 fg=0.00 bg=0.00
aggresome GO:0016235 p=2.5E−02 n=4 fg=0.01 bg=0.00
phagocytic cup GO:0001891 p=3.0E−02 n=3 fg=0.01 bg=0.00
nuclear chromosome GO:0000228 p=3.1E−02 n=28 fg=0.07 bg=0.05
cell cortex region GO:0099738 p=3.6E−02 n=7 fg=0.02 bg=0.01
cytosolic small ribosomal subunit GO:0022627 p=3.9E−02 n=6 fg=0.01 bg=0.01
replisome GO:0030894 p=4.0E−02 n=4 fg=0.01 bg=0.00
nuclear replisome GO:0043601 p=4.0E−02 n=4 fg=0.01 bg=0.00
nuclear replication fork GO:0043596 p=4.1E−02 n=5 fg=0.01 bg=0.00
intracellular organelle GO:0043229 p=4.3E−02 n=367 fg=0.86 bg=0.83
9+2 motile cilium GO:0097729 p=4.6E−02 n=10 fg=0.02 bg=0.01
cytosolic large ribosomal subunit GO:0022625 p=5.0E−02 n=8 fg=0.02 bg=0.01
filopodium membrane GO:0031527 p=5.3E−02 n=3 fg=0.01 bg=0.00
Derlin−1 retrotranslocation complex GO:0036513 p=5.3E−02 n=3 fg=0.01 bg=0.00
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=5.8E−02 n=4 fg=0.01 bg=0.00
nuclear speck GO:0016607 p=5.9E−02 n=19 fg=0.04 bg=0.03
organelle GO:0043226 p=6.1E−02 n=372 fg=0.88 bg=0.85
cell division site GO:0032153 p=6.5E−02 n=6 fg=0.01 bg=0.01
multimeric ribonuclease P complex GO:0030681 p=6.6E−02 n=2 fg=0.00 bg=0.00
ribonuclease P complex GO:0030677 p=6.6E−02 n=2 fg=0.00 bg=0.00
DNA replication factor C complex GO:0005663 p=6.6E−02 n=2 fg=0.00 bg=0.00
0 1 2 3 4 5
−log(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=425/1433 input genes with annotations