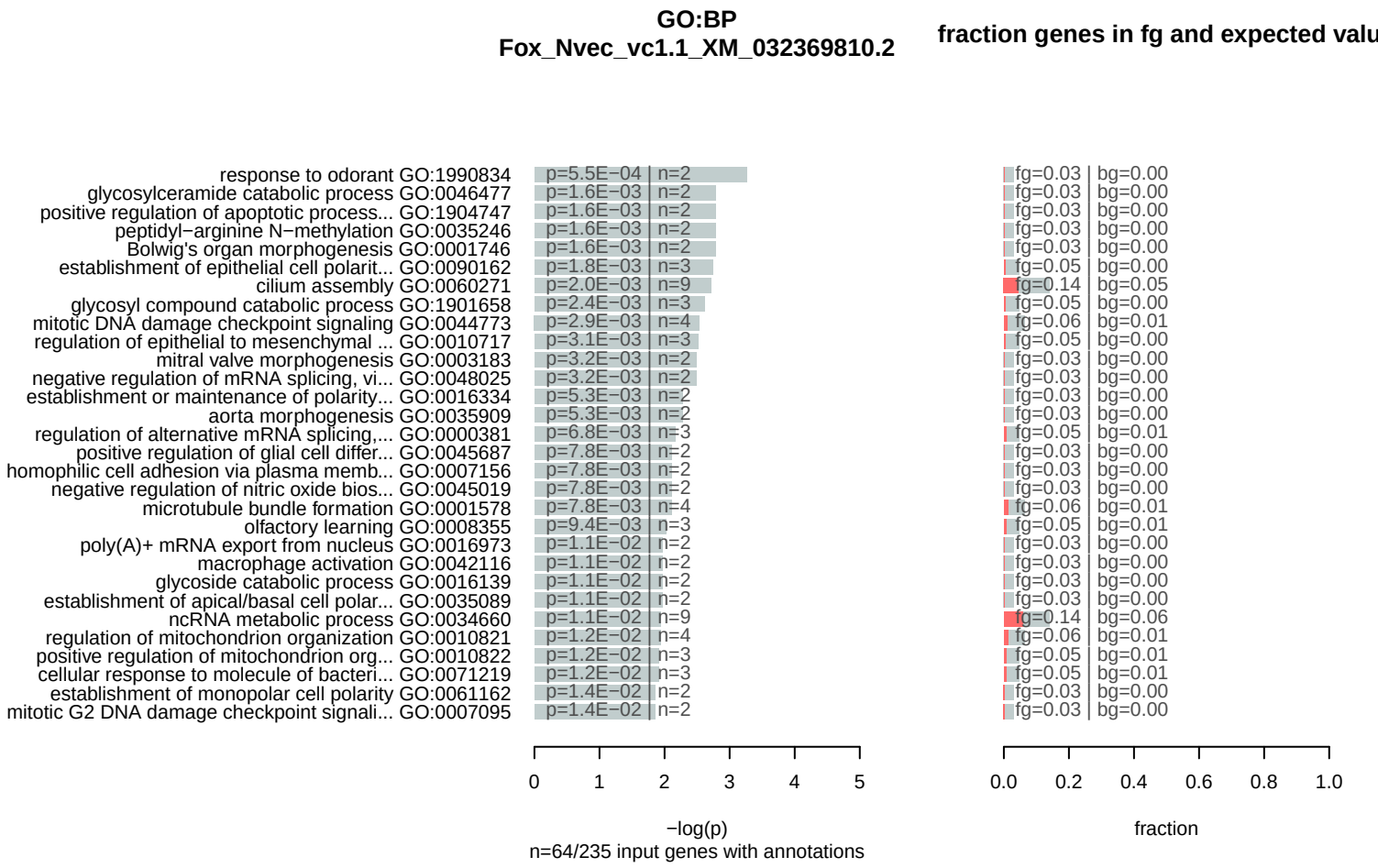
GO:BP
Fox_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
response to odorant GO:1990834 p=5.5E−04 n=2 fg=0.03 bg=0.00
glycosylceramide catabolic process GO:0046477 p=1.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of apoptotic process... GO:1904747 p=1.6E−03 n=2 fg=0.03 bg=0.00
peptidyl−arginine N−methylation GO:0035246 p=1.6E−03 n=2 fg=0.03 bg=0.00
Bolwig's organ morphogenesis GO:0001746 p=1.6E−03 n=2 fg=0.03 bg=0.00
establishment of epithelial cell polarit... GO:0090162 p=1.8E−03 n=3 fg=0.05 bg=0.00
cilium assembly GO:0060271 p=2.0E−03 n=9 fg=0.14 bg=0.05
glycosyl compound catabolic process GO:1901658 p=2.4E−03 n=3 fg=0.05 bg=0.00
mitotic DNA damage checkpoint signaling GO:0044773 p=2.9E−03 n=4 fg=0.06 bg=0.01
regulation of epithelial to mesenchymal ... GO:0010717 p=3.1E−03 n=3 fg=0.05 bg=0.00
mitral valve morphogenesis GO:0003183 p=3.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of mRNA splicing, vi... GO:0048025 p=3.2E−03 n=2 fg=0.03 bg=0.00
establishment or maintenance of polarity... GO:0016334 p=5.3E−03 n=2 fg=0.03 bg=0.00
aorta morphogenesis GO:0035909 p=5.3E−03 n=2 fg=0.03 bg=0.00
regulation of alternative mRNA splicing,... GO:0000381 p=6.8E−03 n=3 fg=0.05 bg=0.01
positive regulation of glial cell differ... GO:0045687 p=7.8E−03 n=2 fg=0.03 bg=0.00
homophilic cell adhesion via plasma memb... GO:0007156 p=7.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of nitric oxide bios... GO:0045019 p=7.8E−03 n=2 fg=0.03 bg=0.00
microtubule bundle formation GO:0001578 p=7.8E−03 n=4 fg=0.06 bg=0.01
olfactory learning GO:0008355 p=9.4E−03 n=3 fg=0.05 bg=0.01
poly(A)+ mRNA export from nucleus GO:0016973 p=1.1E−02 n=2 fg=0.03 bg=0.00
macrophage activation GO:0042116 p=1.1E−02 n=2 fg=0.03 bg=0.00
glycoside catabolic process GO:0016139 p=1.1E−02 n=2 fg=0.03 bg=0.00
establishment of apical/basal cell polar... GO:0035089 p=1.1E−02 n=2 fg=0.03 bg=0.00
ncRNA metabolic process GO:0034660 p=1.1E−02 n=9 fg=0.14 bg=0.06
regulation of mitochondrion organization GO:0010821 p=1.2E−02 n=4 fg=0.06 bg=0.01
positive regulation of mitochondrion org... GO:0010822 p=1.2E−02 n=3 fg=0.05 bg=0.01
cellular response to molecule of bacteri... GO:0071219 p=1.2E−02 n=3 fg=0.05 bg=0.01
establishment of monopolar cell polarity GO:0061162 p=1.4E−02 n=2 fg=0.03 bg=0.00
mitotic G2 DNA damage checkpoint signali... GO:0007095 p=1.4E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=64/235 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
alpha−galactosidase activity GO:0004557 p=5.3E−04 n=2 fg=0.04 bg=0.00
alpha−N−acetylgalactosaminidase activity GO:0008456 p=5.3E−04 n=2 fg=0.04 bg=0.00
protein−arginine N−methyltransferase act... GO:0016274 p=1.6E−03 n=2 fg=0.04 bg=0.00
microtubule plus−end binding GO:0051010 p=3.1E−03 n=2 fg=0.04 bg=0.00
O−methyltransferase activity GO:0008171 p=7.5E−03 n=2 fg=0.04 bg=0.00
RNA binding GO:0003723 p=2.2E−02 n=11 fg=0.20 bg=0.10
interleukin−5 receptor binding GO:0005137 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein−arginine omega−N symmetric methy... GO:0035243 p=2.3E−02 n=1 fg=0.02 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=2.3E−02 n=1 fg=0.02 bg=0.00
light−activated ion channel activity GO:0010461 p=2.3E−02 n=1 fg=0.02 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.3E−02 n=1 fg=0.02 bg=0.00
rRNA (guanosine−2'−O−)−methyltransferase... GO:0070039 p=2.3E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.3E−02 n=1 fg=0.02 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=2.3E−02 n=1 fg=0.02 bg=0.00
dystroglycan binding GO:0002162 p=2.3E−02 n=1 fg=0.02 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=2.3E−02 n=1 fg=0.02 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulatory region RNA binding GO:0001069 p=2.3E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.3E−02 n=1 fg=0.02 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=2.3E−02 n=1 fg=0.02 bg=0.00
guanyl nucleotide exchange factor inhibi... GO:1990624 p=2.3E−02 n=1 fg=0.02 bg=0.00
inositol oxygenase activity GO:0050113 p=2.3E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.3E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.3E−02 n=1 fg=0.02 bg=0.00
myosin II binding GO:0045159 p=2.3E−02 n=1 fg=0.02 bg=0.00
mRNA binding GO:0003729 p=2.8E−02 n=5 fg=0.09 bg=0.03
transcription regulatory region nucleic ... GO:0001067 p=2.9E−02 n=7 fg=0.13 bg=0.05
transcription coactivator activity GO:0003713 p=3.1E−02 n=5 fg=0.09 bg=0.03
microtubule motor activity GO:0003777 p=3.5E−02 n=2 fg=0.04 bg=0.01
nucleic acid binding GO:0003676 p=4.4E−02 n=17 fg=0.31 bg=0.21
0 1 2 3 4 5
−log(p)
n=55/235 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032369810.2
fraction genes in fg and expected valu
membrane−bounded organelle GO:0043227 p=2.1E−03 n=59 fg=0.94 bg=0.80
cytoplasmic stress granule GO:0010494 p=2.3E−03 n=3 fg=0.05 bg=0.00
microtubule cytoskeleton GO:0015630 p=9.8E−03 n=13 fg=0.21 bg=0.10
apicolateral plasma membrane GO:0016327 p=1.0E−02 n=2 fg=0.03 bg=0.00
ciliary basal body GO:0036064 p=1.5E−02 n=4 fg=0.06 bg=0.02
plasma membrane bounded cell projection ... GO:0032838 p=2.0E−02 n=4 fg=0.06 bg=0.02
microtubule organizing center GO:0005815 p=2.3E−02 n=9 fg=0.14 bg=0.07
smooth septate junction GO:0005920 p=2.3E−02 n=1 fg=0.02 bg=0.00
fungal biofilm matrix GO:0062040 p=2.3E−02 n=1 fg=0.02 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=2.3E−02 n=1 fg=0.02 bg=0.00
cortical microtubule plus−end GO:1903754 p=2.3E−02 n=1 fg=0.02 bg=0.00
biofilm matrix GO:0062039 p=2.3E−02 n=1 fg=0.02 bg=0.00
cortical microtubule GO:0055028 p=2.3E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor complex GO:0005895 p=2.3E−02 n=1 fg=0.02 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=2.3E−02 n=1 fg=0.02 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=2.3E−02 n=1 fg=0.02 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=2.3E−02 n=1 fg=0.02 bg=0.00
centrosomal corona GO:0031592 p=2.3E−02 n=1 fg=0.02 bg=0.00
rhabdomere membrane GO:0033583 p=2.3E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.3E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus GO:0035996 p=2.3E−02 n=1 fg=0.02 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=2.3E−02 n=1 fg=0.02 bg=0.00
cytosol GO:0005829 p=3.1E−02 n=33 fg=0.52 bg=0.40
cytoplasmic region GO:0099568 p=3.7E−02 n=7 fg=0.11 bg=0.05
centrosome GO:0005813 p=4.2E−02 n=7 fg=0.11 bg=0.05
axoneme GO:0005930 p=4.3E−02 n=3 fg=0.05 bg=0.01
intracellular organelle GO:0043229 p=4.5E−02 n=59 fg=0.94 bg=0.83
Rb−E2F complex GO:0035189 p=4.6E−02 n=1 fg=0.02 bg=0.00
H zone GO:0031673 p=4.6E−02 n=1 fg=0.02 bg=0.00
radial spoke GO:0001534 p=4.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=63/235 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction