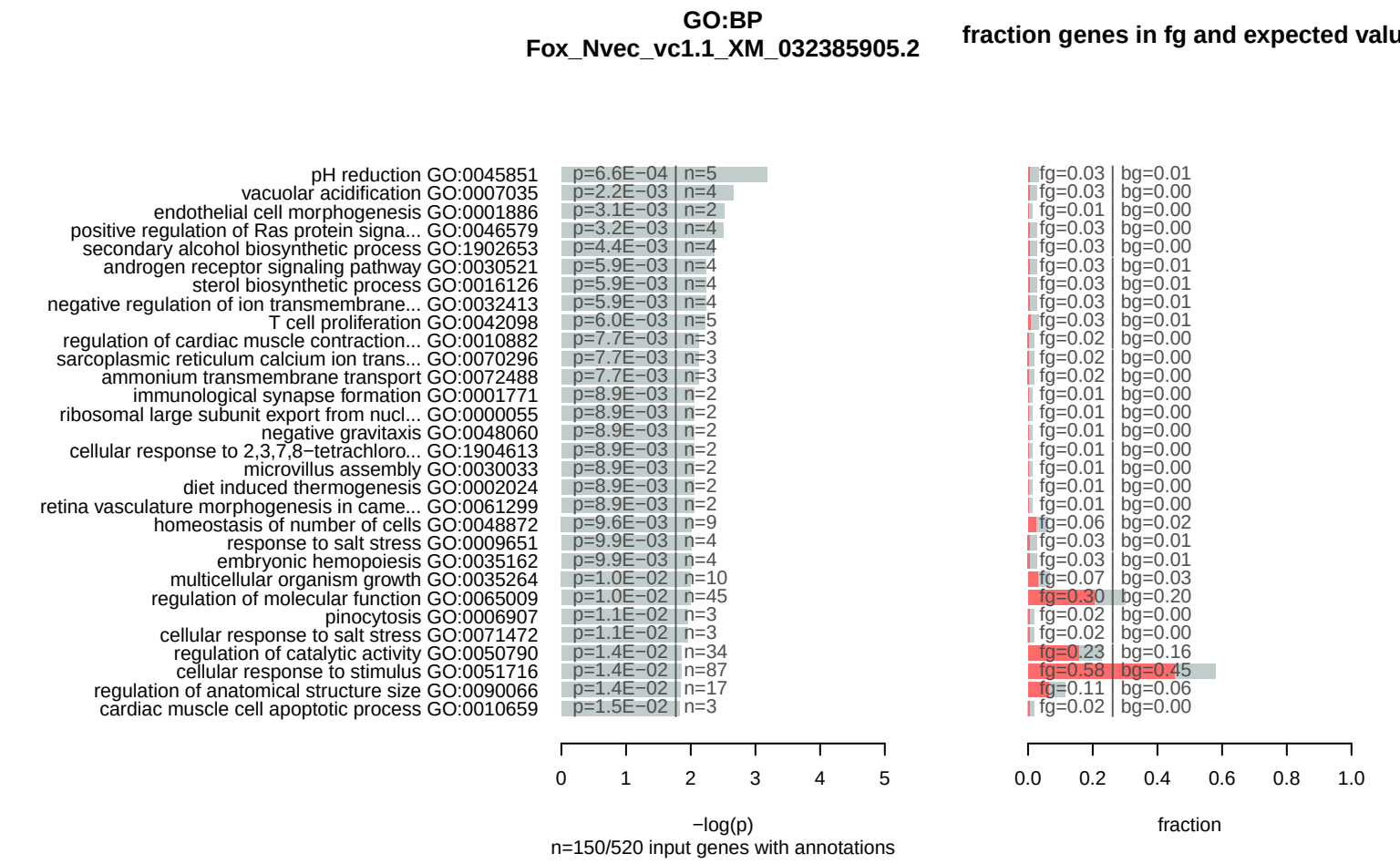
GO:BP
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
pH reduction GO:0045851 p=6.6E−04 n=5 fg=0.03 bg=0.01
vacuolar acidification GO:0007035 p=2.2E−03 n=4 fg=0.03 bg=0.00
endothelial cell morphogenesis GO:0001886 p=3.1E−03 n=2 fg=0.01 bg=0.00
positive regulation of Ras protein signa... GO:0046579 p=3.2E−03 n=4 fg=0.03 bg=0.00
secondary alcohol biosynthetic process GO:1902653 p=4.4E−03 n=4 fg=0.03 bg=0.00
androgen receptor signaling pathway GO:0030521 p=5.9E−03 n=4 fg=0.03 bg=0.01
sterol biosynthetic process GO:0016126 p=5.9E−03 n=4 fg=0.03 bg=0.01
negative regulation of ion transmembrane... GO:0032413 p=5.9E−03 n=4 fg=0.03 bg=0.01
T cell proliferation GO:0042098 p=6.0E−03 n=5 fg=0.03 bg=0.01
regulation of cardiac muscle contraction... GO:0010882 p=7.7E−03 n=3 fg=0.02 bg=0.00
sarcoplasmic reticulum calcium ion trans... GO:0070296 p=7.7E−03 n=3 fg=0.02 bg=0.00
ammonium transmembrane transport GO:0072488 p=7.7E−03 n=3 fg=0.02 bg=0.00
immunological synapse formation GO:0001771 p=8.9E−03 n=2 fg=0.01 bg=0.00
ribosomal large subunit export from nucl... GO:0000055 p=8.9E−03 n=2 fg=0.01 bg=0.00
negative gravitaxis GO:0048060 p=8.9E−03 n=2 fg=0.01 bg=0.00
cellular response to 2,3,7,8−tetrachloro... GO:1904613 p=8.9E−03 n=2 fg=0.01 bg=0.00
microvillus assembly GO:0030033 p=8.9E−03 n=2 fg=0.01 bg=0.00
diet induced thermogenesis GO:0002024 p=8.9E−03 n=2 fg=0.01 bg=0.00
retina vasculature morphogenesis in came... GO:0061299 p=8.9E−03 n=2 fg=0.01 bg=0.00
homeostasis of number of cells GO:0048872 p=9.6E−03 n=9 fg=0.06 bg=0.02
response to salt stress GO:0009651 p=9.9E−03 n=4 fg=0.03 bg=0.01
embryonic hemopoiesis GO:0035162 p=9.9E−03 n=4 fg=0.03 bg=0.01
multicellular organism growth GO:0035264 p=1.0E−02 n=10 fg=0.07 bg=0.03
regulation of molecular function GO:0065009 p=1.0E−02 n=45 fg=0.30 bg=0.20
pinocytosis GO:0006907 p=1.1E−02 n=3 fg=0.02 bg=0.00
cellular response to salt stress GO:0071472 p=1.1E−02 n=3 fg=0.02 bg=0.00
regulation of catalytic activity GO:0050790 p=1.4E−02 n=34 fg=0.23 bg=0.16
cellular response to stimulus GO:0051716 p=1.4E−02 n=87 fg=0.58 bg=0.45
regulation of anatomical structure size GO:0090066 p=1.4E−02 n=17 fg=0.11 bg=0.06
cardiac muscle cell apoptotic process GO:0010659 p=1.5E−02 n=3 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=150/520 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
WW domain binding GO:0050699 p=6.6E−04 n=3 fg=0.02 bg=0.00
peroxidase activity GO:0004601 p=3.1E−03 n=3 fg=0.02 bg=0.00
D3 dopamine receptor binding GO:0031750 p=3.1E−03 n=2 fg=0.02 bg=0.00
D4 dopamine receptor binding GO:0031751 p=3.1E−03 n=2 fg=0.02 bg=0.00
eukaryotic initiation factor 4E binding GO:0008190 p=3.1E−03 n=2 fg=0.02 bg=0.00
cyclin binding GO:0030332 p=5.1E−03 n=3 fg=0.02 bg=0.00
ammonium transmembrane transporter activ... GO:0008519 p=7.9E−03 n=3 fg=0.02 bg=0.00
U2 snRNA binding GO:0030620 p=9.0E−03 n=2 fg=0.02 bg=0.00
D2 dopamine receptor binding GO:0031749 p=9.0E−03 n=2 fg=0.02 bg=0.00
potassium:chloride symporter activity GO:0015379 p=9.0E−03 n=2 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=9.0E−03 n=2 fg=0.02 bg=0.00
signaling receptor binding GO:0005102 p=1.4E−02 n=23 fg=0.17 bg=0.10
protein domain specific binding GO:0019904 p=1.5E−02 n=21 fg=0.16 bg=0.08
phosphatase regulator activity GO:0019208 p=1.6E−02 n=4 fg=0.03 bg=0.01
G protein−coupled receptor binding GO:0001664 p=1.6E−02 n=8 fg=0.06 bg=0.02
glutathione peroxidase activity GO:0004602 p=1.7E−02 n=2 fg=0.02 bg=0.00
xylosyltransferase activity GO:0042285 p=1.7E−02 n=2 fg=0.02 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=1.7E−02 n=2 fg=0.02 bg=0.00
cAMP binding GO:0030552 p=1.7E−02 n=2 fg=0.02 bg=0.00
hexosaminidase activity GO:0015929 p=1.7E−02 n=2 fg=0.02 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=1.7E−02 n=2 fg=0.02 bg=0.00
nucleotidyltransferase activity GO:0016779 p=2.0E−02 n=6 fg=0.05 bg=0.02
phospholipid binding GO:0005543 p=2.3E−02 n=10 fg=0.08 bg=0.04
molecular function regulator activity GO:0098772 p=2.6E−02 n=22 fg=0.17 bg=0.11
phosphatidylinositol−4−phosphate binding GO:0070273 p=2.6E−02 n=3 fg=0.02 bg=0.01
pentosyltransferase activity GO:0016763 p=2.6E−02 n=3 fg=0.02 bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.7E−02 n=7 fg=0.05 bg=0.02
phosphatidylinositol−5−phosphate binding GO:0010314 p=2.8E−02 n=2 fg=0.02 bg=0.00
cyclic nucleotide binding GO:0030551 p=2.8E−02 n=2 fg=0.02 bg=0.00
enzyme regulator activity GO:0030234 p=3.1E−02 n=19 fg=0.14 bg=0.09
0 1 2 3 4 5
−log(p)
n=133/520 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
perinuclear region of cytoplasm GO:0048471 p=2.1E−03 n=19 fg=0.13 bg=0.06
brush border GO:0005903 p=2.2E−03 n=7 fg=0.05 bg=0.01
heterotrimeric G−protein complex GO:0005834 p=2.7E−03 n=3 fg=0.02 bg=0.00
DNA polymerase III complex GO:0009360 p=2.9E−03 n=2 fg=0.01 bg=0.00
neuronal cell body GO:0043025 p=5.1E−03 n=17 fg=0.12 bg=0.06
stereocilium GO:0032420 p=5.4E−03 n=4 fg=0.03 bg=0.01
extracellular exosome GO:0070062 p=6.6E−03 n=5 fg=0.03 bg=0.01
midbody GO:0030496 p=8.3E−03 n=7 fg=0.05 bg=0.02
muscle cell projection membrane GO:0036195 p=8.4E−03 n=2 fg=0.01 bg=0.00
cell leading edge GO:0031252 p=1.3E−02 n=11 fg=0.08 bg=0.04
dendrite GO:0030425 p=1.4E−02 n=16 fg=0.11 bg=0.06
dendritic tree GO:0097447 p=1.5E−02 n=16 fg=0.11 bg=0.06
manchette GO:0002177 p=1.6E−02 n=2 fg=0.01 bg=0.00
ruffle GO:0001726 p=1.8E−02 n=5 fg=0.03 bg=0.01
growth cone GO:0030426 p=1.8E−02 n=7 fg=0.05 bg=0.02
RNA polymerase II transcription regulato... GO:0090575 p=2.4E−02 n=6 fg=0.04 bg=0.02
microvillus GO:0005902 p=2.4E−02 n=4 fg=0.03 bg=0.01
site of polarized growth GO:0030427 p=2.4E−02 n=7 fg=0.05 bg=0.02
guanyl−nucleotide exchange factor comple... GO:0032045 p=2.6E−02 n=2 fg=0.01 bg=0.00
phagocytic cup GO:0001891 p=2.6E−02 n=2 fg=0.01 bg=0.00
cytoplasmic side of apical plasma membra... GO:0098592 p=2.6E−02 n=2 fg=0.01 bg=0.00
filopodium GO:0030175 p=2.8E−02 n=4 fg=0.03 bg=0.01
apical plasma membrane GO:0016324 p=2.8E−02 n=10 fg=0.07 bg=0.03
polysome GO:0005844 p=3.7E−02 n=4 fg=0.03 bg=0.01
cytoplasmic ribonucleoprotein granule GO:0036464 p=3.8E−02 n=7 fg=0.05 bg=0.02
astrocyte projection GO:0097449 p=3.8E−02 n=2 fg=0.01 bg=0.00
glial cell projection GO:0097386 p=3.8E−02 n=2 fg=0.01 bg=0.00
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=3.9E−02 n=6 fg=0.04 bg=0.02
extrinsic component of plasma membrane GO:0019897 p=4.0E−02 n=7 fg=0.05 bg=0.01
9+2 motile cilium GO:0097729 p=4.2E−02 n=5 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=146/520 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction