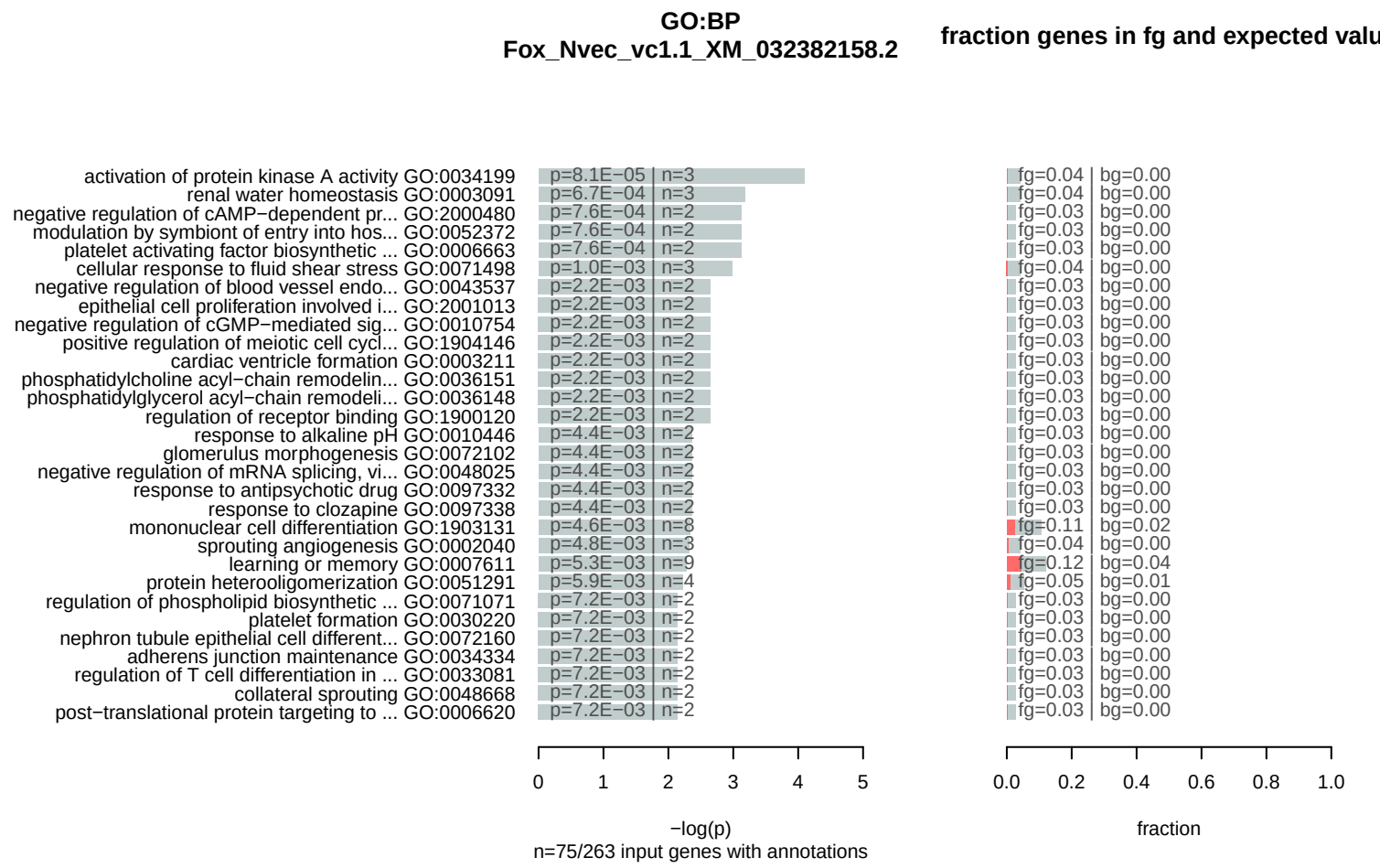
GO:BP
Fox_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
activation of protein kinase A activity GO:0034199 p=8.1E−05 n=3 fg=0.04 bg=0.00
renal water homeostasis GO:0003091 p=6.7E−04 n=3 fg=0.04 bg=0.00
negative regulation of cAMP−dependent pr... GO:2000480 p=7.6E−04 n=2 fg=0.03 bg=0.00
modulation by symbiont of entry into hos... GO:0052372 p=7.6E−04 n=2 fg=0.03 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=7.6E−04 n=2 fg=0.03 bg=0.00
cellular response to fluid shear stress GO:0071498 p=1.0E−03 n=3 fg=0.04 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=2.2E−03 n=2 fg=0.03 bg=0.00
epithelial cell proliferation involved i... GO:2001013 p=2.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of cGMP−mediated sig... GO:0010754 p=2.2E−03 n=2 fg=0.03 bg=0.00
positive regulation of meiotic cell cycl... GO:1904146 p=2.2E−03 n=2 fg=0.03 bg=0.00
cardiac ventricle formation GO:0003211 p=2.2E−03 n=2 fg=0.03 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=2.2E−03 n=2 fg=0.03 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=2.2E−03 n=2 fg=0.03 bg=0.00
regulation of receptor binding GO:1900120 p=2.2E−03 n=2 fg=0.03 bg=0.00
response to alkaline pH GO:0010446 p=4.4E−03 n=2 fg=0.03 bg=0.00
glomerulus morphogenesis GO:0072102 p=4.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of mRNA splicing, vi... GO:0048025 p=4.4E−03 n=2 fg=0.03 bg=0.00
response to antipsychotic drug GO:0097332 p=4.4E−03 n=2 fg=0.03 bg=0.00
response to clozapine GO:0097338 p=4.4E−03 n=2 fg=0.03 bg=0.00
mononuclear cell differentiation GO:1903131 p=4.6E−03 n=8 fg=0.11 bg=0.02
sprouting angiogenesis GO:0002040 p=4.8E−03 n=3 fg=0.04 bg=0.00
learning or memory GO:0007611 p=5.3E−03 n=9 fg=0.12 bg=0.04
protein heterooligomerization GO:0051291 p=5.9E−03 n=4 fg=0.05 bg=0.01
regulation of phospholipid biosynthetic ... GO:0071071 p=7.2E−03 n=2 fg=0.03 bg=0.00
platelet formation GO:0030220 p=7.2E−03 n=2 fg=0.03 bg=0.00
nephron tubule epithelial cell different... GO:0072160 p=7.2E−03 n=2 fg=0.03 bg=0.00
adherens junction maintenance GO:0034334 p=7.2E−03 n=2 fg=0.03 bg=0.00
regulation of T cell differentiation in ... GO:0033081 p=7.2E−03 n=2 fg=0.03 bg=0.00
collateral sprouting GO:0048668 p=7.2E−03 n=2 fg=0.03 bg=0.00
post−translational protein targeting to ... GO:0006620 p=7.2E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=75/263 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
cAMP binding GO:0030552 p=7.7E−05 n=3 fg=0.05 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=7.4E−04 n=2 fg=0.03 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=7.4E−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
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.2E−03 n=2 fg=0.03 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=4.3E−03 n=2 fg=0.03 bg=0.00
peptide hormone binding GO:0017046 p=4.3E−03 n=2 fg=0.03 bg=0.00
ephrin receptor binding GO:0046875 p=7.0E−03 n=2 fg=0.03 bg=0.00
3',5'−cyclic−GMP phosphodiesterase activ... GO:0047555 p=1.0E−02 n=2 fg=0.03 bg=0.00
cyclic−nucleotide phosphodiesterase acti... GO:0004112 p=1.0E−02 n=2 fg=0.03 bg=0.00
3',5'−cyclic−nucleotide phosphodiesteras... GO:0004114 p=1.0E−02 n=2 fg=0.03 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.0E−02 n=2 fg=0.03 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=1.4E−02 n=2 fg=0.03 bg=0.00
carbohydrate derivative binding GO:0097367 p=1.7E−02 n=13 fg=0.20 bg=0.08
anion binding GO:0043168 p=1.9E−02 n=17 fg=0.26 bg=0.13
metalloendopeptidase activity GO:0004222 p=2.4E−02 n=2 fg=0.03 bg=0.00
monosaccharide binding GO:0048029 p=2.4E−02 n=2 fg=0.03 bg=0.00
protein−membrane adaptor activity GO:0043495 p=2.7E−02 n=1 fg=0.02 bg=0.00
heparan sulfate binding GO:1904399 p=2.7E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−2 demethylase... GO:0033746 p=2.7E−02 n=1 fg=0.02 bg=0.00
histone H3−methyl−arginine−3 demethylase... GO:0033749 p=2.7E−02 n=1 fg=0.02 bg=0.00
signal recognition particle binding GO:0005047 p=2.7E−02 n=1 fg=0.02 bg=0.00
calcitonin family binding GO:0097644 p=2.7E−02 n=1 fg=0.02 bg=0.00
peptidyl−lysine 5−dioxygenase activity GO:0070815 p=2.7E−02 n=1 fg=0.02 bg=0.00
amylin binding GO:0097645 p=2.7E−02 n=1 fg=0.02 bg=0.00
pantetheine hydrolase activity GO:0017159 p=2.7E−02 n=1 fg=0.02 bg=0.00
7S RNA binding GO:0008312 p=2.7E−02 n=1 fg=0.02 bg=0.00
beta−endorphin binding GO:0031626 p=2.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/263 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032382158.2
fraction genes in fg and expected valu
germinal vesicle GO:0042585 p=6.9E−04 n=3 fg=0.04 bg=0.00
azurophil granule membrane GO:0035577 p=1.6E−03 n=3 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=2.3E−03 n=2 fg=0.03 bg=0.00
dendritic shaft GO:0043198 p=2.9E−03 n=4 fg=0.05 bg=0.01
RNA polymerase II transcription represso... GO:0090571 p=4.5E−03 n=2 fg=0.03 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=4.5E−03 n=2 fg=0.03 bg=0.00
T−tubule GO:0030315 p=5.0E−03 n=3 fg=0.04 bg=0.00
actomyosin GO:0042641 p=1.1E−02 n=3 fg=0.04 bg=0.01
filopodium GO:0030175 p=2.2E−02 n=3 fg=0.04 bg=0.01
fusome GO:0045169 p=2.5E−02 n=2 fg=0.03 bg=0.00
host cell nuclear part GO:0044094 p=2.8E−02 n=1 fg=0.01 bg=0.00
DNA ligase III−XRCC1 complex GO:0070421 p=2.8E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=2.8E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=2.8E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=2.8E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=2.8E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=2.8E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=2.8E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=2.8E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=2.8E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=2.8E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=2.8E−02 n=1 fg=0.01 bg=0.00
mitochondrial electron transfer flavopro... GO:0017133 p=2.8E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.8E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=2.8E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=2.8E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=2.8E−02 n=1 fg=0.01 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=2.8E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=2.8E−02 n=1 fg=0.01 bg=0.00
acrosomal membrane GO:0002080 p=2.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/263 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction