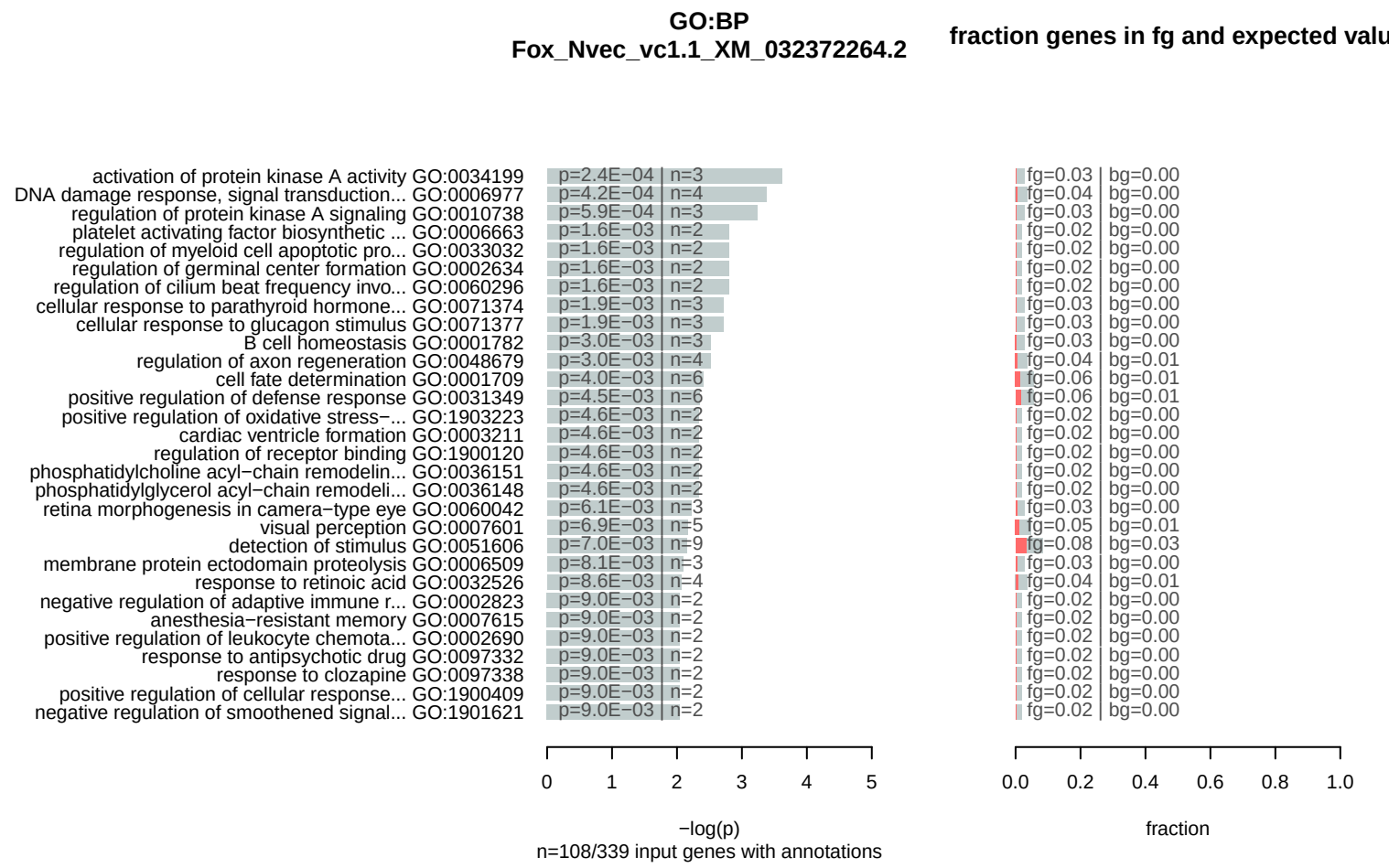
GO:BP
Fox_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
activation of protein kinase A activity GO:0034199 p=2.4E−04 n=3 fg=0.03 bg=0.00
DNA damage response, signal transduction... GO:0006977 p=4.2E−04 n=4 fg=0.04 bg=0.00
regulation of protein kinase A signaling GO:0010738 p=5.9E−04 n=3 fg=0.03 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=1.6E−03 n=2 fg=0.02 bg=0.00
regulation of myeloid cell apoptotic pro... GO:0033032 p=1.6E−03 n=2 fg=0.02 bg=0.00
regulation of germinal center formation GO:0002634 p=1.6E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=1.6E−03 n=2 fg=0.02 bg=0.00
cellular response to parathyroid hormone... GO:0071374 p=1.9E−03 n=3 fg=0.03 bg=0.00
cellular response to glucagon stimulus GO:0071377 p=1.9E−03 n=3 fg=0.03 bg=0.00
B cell homeostasis GO:0001782 p=3.0E−03 n=3 fg=0.03 bg=0.00
regulation of axon regeneration GO:0048679 p=3.0E−03 n=4 fg=0.04 bg=0.01
cell fate determination GO:0001709 p=4.0E−03 n=6 fg=0.06 bg=0.01
positive regulation of defense response GO:0031349 p=4.5E−03 n=6 fg=0.06 bg=0.01
positive regulation of oxidative stress−... GO:1903223 p=4.6E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=4.6E−03 n=2 fg=0.02 bg=0.00
regulation of receptor binding GO:1900120 p=4.6E−03 n=2 fg=0.02 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=4.6E−03 n=2 fg=0.02 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=4.6E−03 n=2 fg=0.02 bg=0.00
retina morphogenesis in camera−type eye GO:0060042 p=6.1E−03 n=3 fg=0.03 bg=0.00
visual perception GO:0007601 p=6.9E−03 n=5 fg=0.05 bg=0.01
detection of stimulus GO:0051606 p=7.0E−03 n=9 fg=0.08 bg=0.03
membrane protein ectodomain proteolysis GO:0006509 p=8.1E−03 n=3 fg=0.03 bg=0.00
response to retinoic acid GO:0032526 p=8.6E−03 n=4 fg=0.04 bg=0.01
negative regulation of adaptive immune r... GO:0002823 p=9.0E−03 n=2 fg=0.02 bg=0.00
anesthesia−resistant memory GO:0007615 p=9.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of leukocyte chemota... GO:0002690 p=9.0E−03 n=2 fg=0.02 bg=0.00
response to antipsychotic drug GO:0097332 p=9.0E−03 n=2 fg=0.02 bg=0.00
response to clozapine GO:0097338 p=9.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of cellular response... GO:1900409 p=9.0E−03 n=2 fg=0.02 bg=0.00
negative regulation of smoothened signal... GO:1901621 p=9.0E−03 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=108/339 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
protein kinase A regulatory subunit bind... GO:0034237 p=5.5E−04 n=3 fg=0.03 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=1.5E−03 n=2 fg=0.02 bg=0.00
mRNA binding GO:0003729 p=2.2E−03 n=9 fg=0.10 bg=0.03
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=4.5E−03 n=2 fg=0.02 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=4.5E−03 n=2 fg=0.02 bg=0.00
WW domain binding GO:0050699 p=8.7E−03 n=2 fg=0.02 bg=0.00
protein domain specific binding GO:0019904 p=1.3E−02 n=16 fg=0.17 bg=0.08
ephrin receptor binding GO:0046875 p=1.4E−02 n=2 fg=0.02 bg=0.00
phospholipid transporter activity GO:0005548 p=1.6E−02 n=3 fg=0.03 bg=0.01
lipid transporter activity GO:0005319 p=1.7E−02 n=4 fg=0.04 bg=0.01
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.9E−02 n=3 fg=0.03 bg=0.01
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=2.1E−02 n=2 fg=0.02 bg=0.00
coreceptor activity GO:0015026 p=2.1E−02 n=2 fg=0.02 bg=0.00
lipid transfer activity GO:0120013 p=2.1E−02 n=2 fg=0.02 bg=0.00
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.3E−02 n=3 fg=0.03 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=2.3E−02 n=3 fg=0.03 bg=0.01
carbohydrate derivative binding GO:0097367 p=2.6E−02 n=13 fg=0.14 bg=0.08
GTP binding GO:0005525 p=2.7E−02 n=5 fg=0.05 bg=0.02
acylglycerol O−acyltransferase activity GO:0016411 p=2.8E−02 n=2 fg=0.02 bg=0.00
peptidase activator activity GO:0016504 p=2.8E−02 n=2 fg=0.02 bg=0.00
HMG box domain binding GO:0071837 p=2.8E−02 n=2 fg=0.02 bg=0.00
purine ribonucleoside binding GO:0032550 p=3.2E−02 n=5 fg=0.05 bg=0.02
ribonucleoside binding GO:0032549 p=3.2E−02 n=5 fg=0.05 bg=0.02
nucleotide binding GO:0000166 p=3.5E−02 n=13 fg=0.14 bg=0.08
nucleoside phosphate binding GO:1901265 p=3.5E−02 n=13 fg=0.14 bg=0.08
snRNA binding GO:0017069 p=3.7E−02 n=2 fg=0.02 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=3.7E−02 n=2 fg=0.02 bg=0.00
purine nucleoside binding GO:0001883 p=3.8E−02 n=5 fg=0.05 bg=0.02
phosphatidylcholine transporter activity GO:0008525 p=3.9E−02 n=1 fg=0.01 bg=0.00
protein−arginine omega−N asymmetric meth... GO:0035242 p=3.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=93/339 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032372264.2
fraction genes in fg and expected valu
cAMP−dependent protein kinase complex GO:0005952 p=4.5E−03 n=2 fg=0.02 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=8.9E−03 n=2 fg=0.02 bg=0.00
photoreceptor inner segment GO:0001917 p=1.3E−02 n=3 fg=0.03 bg=0.00
lipid droplet GO:0005811 p=1.3E−02 n=4 fg=0.04 bg=0.01
secretory granule membrane GO:0030667 p=1.4E−02 n=6 fg=0.06 bg=0.02
anchored component of plasma membrane GO:0046658 p=1.4E−02 n=2 fg=0.02 bg=0.00
neuromuscular junction GO:0031594 p=2.6E−02 n=5 fg=0.05 bg=0.02
germinal vesicle GO:0042585 p=2.9E−02 n=2 fg=0.02 bg=0.00
azurophil granule GO:0042582 p=2.9E−02 n=4 fg=0.04 bg=0.01
primary lysosome GO:0005766 p=2.9E−02 n=4 fg=0.04 bg=0.01
female germ cell nucleus GO:0001674 p=3.7E−02 n=2 fg=0.02 bg=0.00
anchored component of membrane GO:0031225 p=3.7E−02 n=2 fg=0.02 bg=0.00
host cell nucleus GO:0042025 p=4.0E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=4.0E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=4.0E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=4.0E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=4.0E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=4.0E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=4.0E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=4.0E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=4.0E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=4.0E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=4.0E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=4.0E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=4.0E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=4.0E−02 n=1 fg=0.01 bg=0.00
anchored component of the cytoplasmic si... GO:0098753 p=4.0E−02 n=1 fg=0.01 bg=0.00
host cell nuclear part GO:0044094 p=4.0E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=4.0E−02 n=1 fg=0.01 bg=0.00
ACF complex GO:0016590 p=4.0E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=107/339 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction