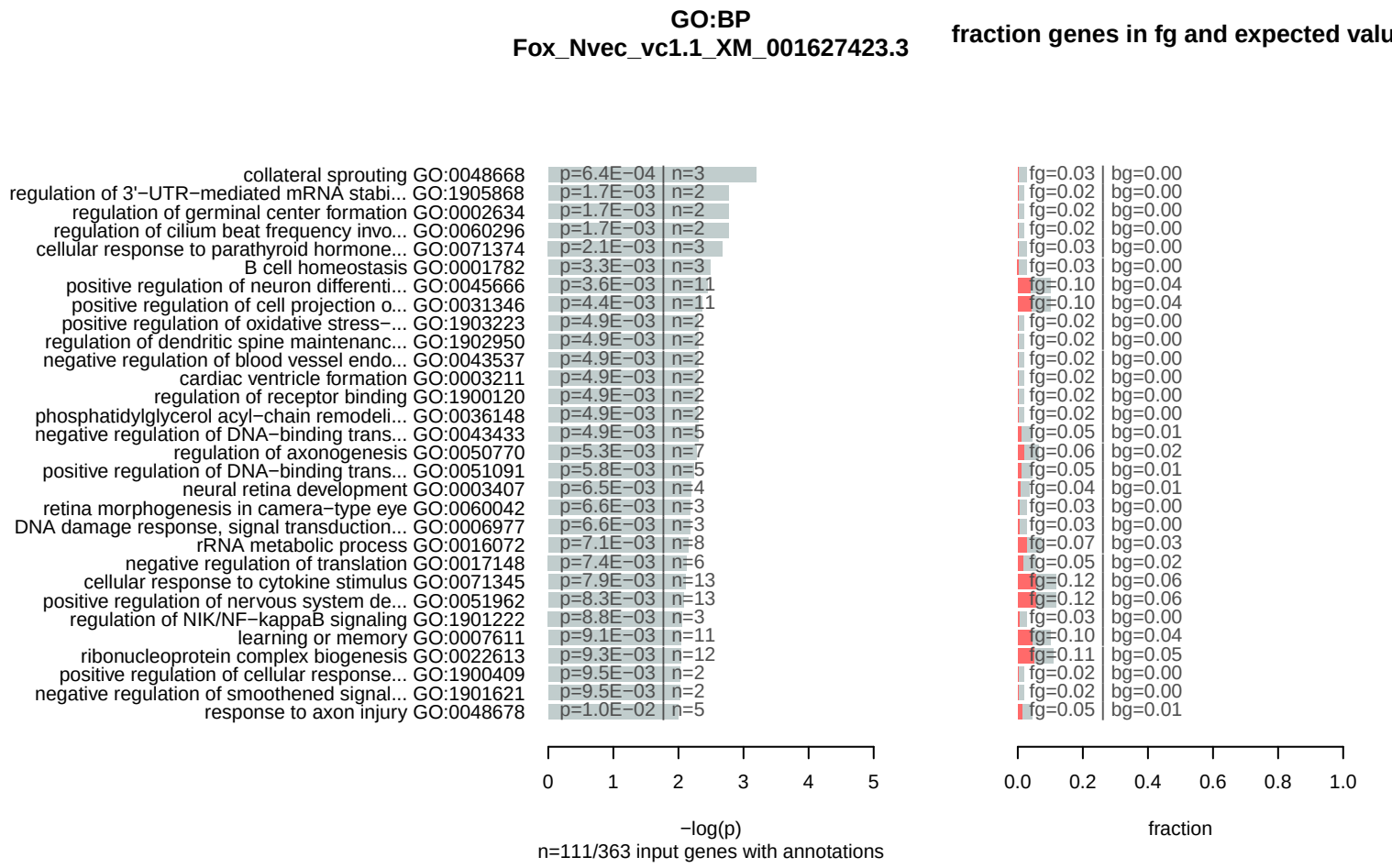
GO:BP
Fox_Nvec_vc1.1_XM_001627423.3
fraction genes in fg and expected valu
collateral sprouting GO:0048668 p=6.4E−04 n=3 fg=0.03 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=1.7E−03 n=2 fg=0.02 bg=0.00
regulation of germinal center formation GO:0002634 p=1.7E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=1.7E−03 n=2 fg=0.02 bg=0.00
cellular response to parathyroid hormone... GO:0071374 p=2.1E−03 n=3 fg=0.03 bg=0.00
B cell homeostasis GO:0001782 p=3.3E−03 n=3 fg=0.03 bg=0.00
positive regulation of neuron differenti... GO:0045666 p=3.6E−03 n=11 fg=0.10 bg=0.04
positive regulation of cell projection o... GO:0031346 p=4.4E−03 n=11 fg=0.10 bg=0.04
positive regulation of oxidative stress−... GO:1903223 p=4.9E−03 n=2 fg=0.02 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=4.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=4.9E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=4.9E−03 n=2 fg=0.02 bg=0.00
regulation of receptor binding GO:1900120 p=4.9E−03 n=2 fg=0.02 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=4.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of DNA−binding trans... GO:0043433 p=4.9E−03 n=5 fg=0.05 bg=0.01
regulation of axonogenesis GO:0050770 p=5.3E−03 n=7 fg=0.06 bg=0.02
positive regulation of DNA−binding trans... GO:0051091 p=5.8E−03 n=5 fg=0.05 bg=0.01
neural retina development GO:0003407 p=6.5E−03 n=4 fg=0.04 bg=0.01
retina morphogenesis in camera−type eye GO:0060042 p=6.6E−03 n=3 fg=0.03 bg=0.00
DNA damage response, signal transduction... GO:0006977 p=6.6E−03 n=3 fg=0.03 bg=0.00
rRNA metabolic process GO:0016072 p=7.1E−03 n=8 fg=0.07 bg=0.03
negative regulation of translation GO:0017148 p=7.4E−03 n=6 fg=0.05 bg=0.02
cellular response to cytokine stimulus GO:0071345 p=7.9E−03 n=13 fg=0.12 bg=0.06
positive regulation of nervous system de... GO:0051962 p=8.3E−03 n=13 fg=0.12 bg=0.06
regulation of NIK/NF−kappaB signaling GO:1901222 p=8.8E−03 n=3 fg=0.03 bg=0.00
learning or memory GO:0007611 p=9.1E−03 n=11 fg=0.10 bg=0.04
ribonucleoprotein complex biogenesis GO:0022613 p=9.3E−03 n=12 fg=0.11 bg=0.05
positive regulation of cellular response... GO:1900409 p=9.5E−03 n=2 fg=0.02 bg=0.00
negative regulation of smoothened signal... GO:1901621 p=9.5E−03 n=2 fg=0.02 bg=0.00
response to axon injury GO:0048678 p=1.0E−02 n=5 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=111/363 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_001627423.3
fraction genes in fg and expected valu
DNA−binding transcription factor activit... GO:0000981 p=1.2E−03 n=14 fg=0.14 bg=0.06
mRNA 3'−UTR binding GO:0003730 p=3.3E−03 n=4 fg=0.04 bg=0.01
miRNA binding GO:0035198 p=4.8E−03 n=2 fg=0.02 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=4.8E−03 n=2 fg=0.02 bg=0.00
bHLH transcription factor binding GO:0043425 p=9.4E−03 n=2 fg=0.02 bg=0.00
ephrin receptor binding GO:0046875 p=1.5E−02 n=2 fg=0.02 bg=0.00
phospholipid transporter activity GO:0005548 p=1.7E−02 n=3 fg=0.03 bg=0.01
lipid transporter activity GO:0005319 p=2.0E−02 n=4 fg=0.04 bg=0.01
ATPase−coupled cation transmembrane tran... GO:0019829 p=2.1E−02 n=3 fg=0.03 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=2.5E−02 n=3 fg=0.03 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=3.0E−02 n=7 fg=0.07 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=3.0E−02 n=7 fg=0.07 bg=0.03
HMG box domain binding GO:0071837 p=3.0E−02 n=2 fg=0.02 bg=0.00
acetyl−CoA C−acetyltransferase activity GO:0003985 p=4.1E−02 n=1 fg=0.01 bg=0.00
acetyl−CoA C−acyltransferase activity GO:0003988 p=4.1E−02 n=1 fg=0.01 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=4.1E−02 n=1 fg=0.01 bg=0.00
UDP−glucose:hexose−1−phosphate uridylylt... GO:0008108 p=4.1E−02 n=1 fg=0.01 bg=0.00
galactose binding GO:0005534 p=4.1E−02 n=1 fg=0.01 bg=0.00
IMP cyclohydrolase activity GO:0003937 p=4.1E−02 n=1 fg=0.01 bg=0.00
phorbol ester receptor activity GO:0001565 p=4.1E−02 n=1 fg=0.01 bg=0.00
C−acetyltransferase activity GO:0016453 p=4.1E−02 n=1 fg=0.01 bg=0.00
laminin receptor activity GO:0005055 p=4.1E−02 n=1 fg=0.01 bg=0.00
heparan sulfate binding GO:1904399 p=4.1E−02 n=1 fg=0.01 bg=0.00
telomeric repeat−containing RNA binding GO:0061752 p=4.1E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=4.1E−02 n=1 fg=0.01 bg=0.00
DNA clamp loader activity GO:0003689 p=4.1E−02 n=1 fg=0.01 bg=0.00
calcitonin family binding GO:0097644 p=4.1E−02 n=1 fg=0.01 bg=0.00
amylin binding GO:0097645 p=4.1E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=4.1E−02 n=1 fg=0.01 bg=0.00
mevalonate kinase activity GO:0004496 p=4.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=97/363 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001627423.3
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=6.7E−03 n=3 fg=0.03 bg=0.00
nuclear body GO:0016604 p=6.8E−03 n=14 fg=0.12 bg=0.06
RNA polymerase II transcription represso... GO:0090571 p=9.7E−03 n=2 fg=0.02 bg=0.00
nuclear speck GO:0016607 p=2.1E−02 n=8 fg=0.07 bg=0.03
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=2.3E−02 n=2 fg=0.02 bg=0.00
actomyosin GO:0042641 p=3.1E−02 n=3 fg=0.03 bg=0.01
ciliary membrane GO:0060170 p=3.1E−02 n=3 fg=0.03 bg=0.01
host cell nucleus GO:0042025 p=4.2E−02 n=1 fg=0.01 bg=0.00
endosome to plasma membrane transport ve... GO:0070381 p=4.2E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=4.2E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=4.2E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=4.2E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=4.2E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=4.2E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=4.2E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=4.2E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=4.2E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=4.2E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=4.2E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=4.2E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=4.2E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=4.2E−02 n=1 fg=0.01 bg=0.00
host cell nuclear part GO:0044094 p=4.2E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=4.2E−02 n=1 fg=0.01 bg=0.00
intermediate−density lipoprotein particl... GO:0034363 p=4.2E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=4.2E−02 n=1 fg=0.01 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=4.2E−02 n=1 fg=0.01 bg=0.00
plasma lipoprotein particle GO:0034358 p=4.2E−02 n=1 fg=0.01 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=4.2E−02 n=1 fg=0.01 bg=0.00
azurophil granule membrane GO:0035577 p=5.1E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=112/363 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction