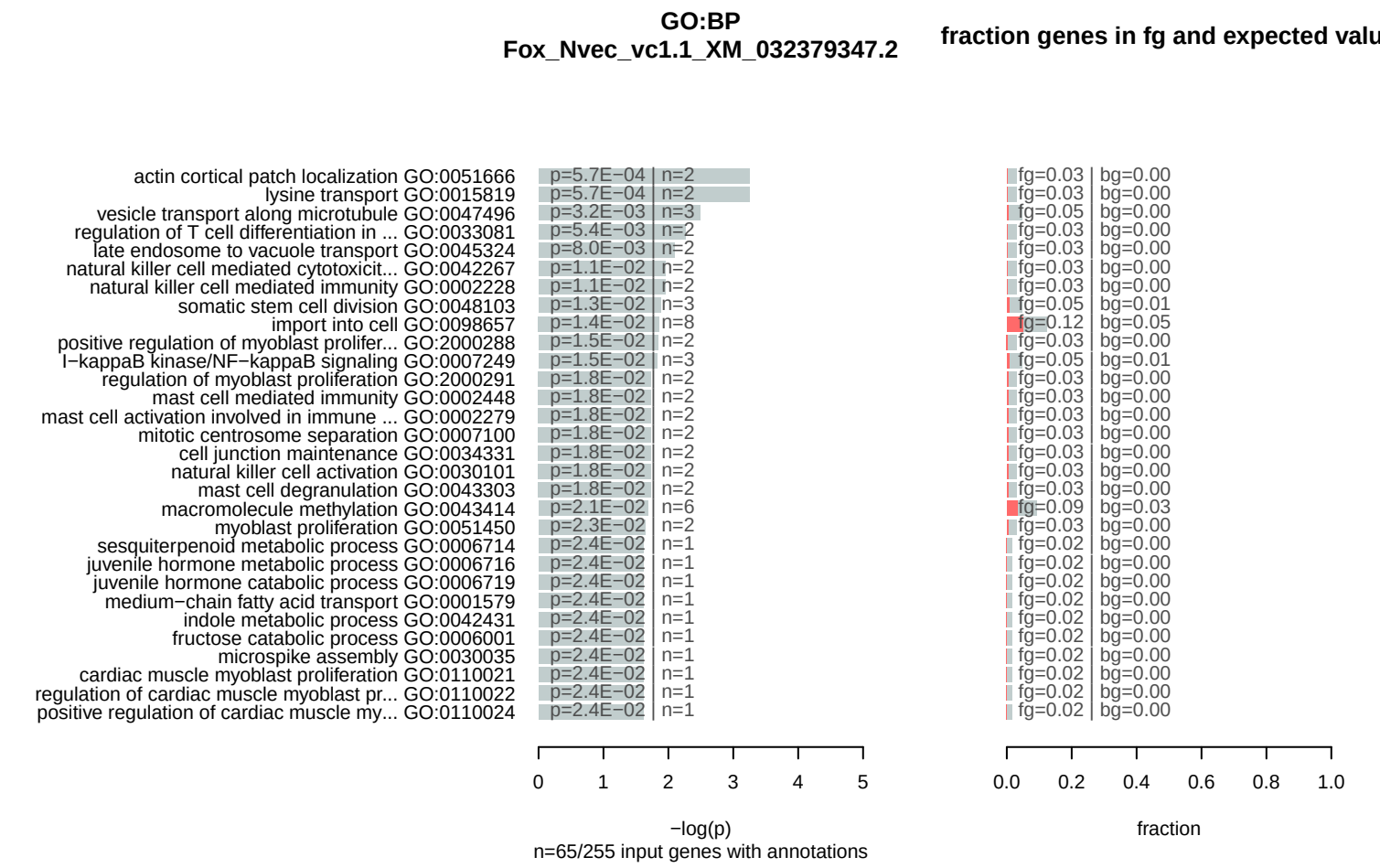
GO:BP
Fox_Nvec_vc1.1_XM_032379347.2
fraction genes in fg and expected valu
actin cortical patch localization GO:0051666 p=5.7E−04 n=2 fg=0.03 bg=0.00
lysine transport GO:0015819 p=5.7E−04 n=2 fg=0.03 bg=0.00
vesicle transport along microtubule GO:0047496 p=3.2E−03 n=3 fg=0.05 bg=0.00
regulation of T cell differentiation in ... GO:0033081 p=5.4E−03 n=2 fg=0.03 bg=0.00
late endosome to vacuole transport GO:0045324 p=8.0E−03 n=2 fg=0.03 bg=0.00
natural killer cell mediated cytotoxicit... GO:0042267 p=1.1E−02 n=2 fg=0.03 bg=0.00
natural killer cell mediated immunity GO:0002228 p=1.1E−02 n=2 fg=0.03 bg=0.00
somatic stem cell division GO:0048103 p=1.3E−02 n=3 fg=0.05 bg=0.01
import into cell GO:0098657 p=1.4E−02 n=8 fg=0.12 bg=0.05
positive regulation of myoblast prolifer... GO:2000288 p=1.5E−02 n=2 fg=0.03 bg=0.00
I−kappaB kinase/NF−kappaB signaling GO:0007249 p=1.5E−02 n=3 fg=0.05 bg=0.01
regulation of myoblast proliferation GO:2000291 p=1.8E−02 n=2 fg=0.03 bg=0.00
mast cell mediated immunity GO:0002448 p=1.8E−02 n=2 fg=0.03 bg=0.00
mast cell activation involved in immune ... GO:0002279 p=1.8E−02 n=2 fg=0.03 bg=0.00
mitotic centrosome separation GO:0007100 p=1.8E−02 n=2 fg=0.03 bg=0.00
cell junction maintenance GO:0034331 p=1.8E−02 n=2 fg=0.03 bg=0.00
natural killer cell activation GO:0030101 p=1.8E−02 n=2 fg=0.03 bg=0.00
mast cell degranulation GO:0043303 p=1.8E−02 n=2 fg=0.03 bg=0.00
macromolecule methylation GO:0043414 p=2.1E−02 n=6 fg=0.09 bg=0.03
myoblast proliferation GO:0051450 p=2.3E−02 n=2 fg=0.03 bg=0.00
sesquiterpenoid metabolic process GO:0006714 p=2.4E−02 n=1 fg=0.02 bg=0.00
juvenile hormone metabolic process GO:0006716 p=2.4E−02 n=1 fg=0.02 bg=0.00
juvenile hormone catabolic process GO:0006719 p=2.4E−02 n=1 fg=0.02 bg=0.00
medium−chain fatty acid transport GO:0001579 p=2.4E−02 n=1 fg=0.02 bg=0.00
indole metabolic process GO:0042431 p=2.4E−02 n=1 fg=0.02 bg=0.00
fructose catabolic process GO:0006001 p=2.4E−02 n=1 fg=0.02 bg=0.00
microspike assembly GO:0030035 p=2.4E−02 n=1 fg=0.02 bg=0.00
cardiac muscle myoblast proliferation GO:0110021 p=2.4E−02 n=1 fg=0.02 bg=0.00
regulation of cardiac muscle myoblast pr... GO:0110022 p=2.4E−02 n=1 fg=0.02 bg=0.00
positive regulation of cardiac muscle my... GO:0110024 p=2.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Fox_Nvec_vc1.1_XM_032379347.2
fraction genes in fg and expected valu
phosphatidylinositol−3,4−bisphosphate bi... GO:0043325 p=5.4E−03 n=2 fg=0.04 bg=0.00
methyltransferase activity GO:0008168 p=5.7E−03 n=5 fg=0.09 bg=0.02
S−adenosylmethionine−dependent methyltra... GO:0008757 p=1.6E−02 n=4 fg=0.07 bg=0.02
RNA methyltransferase activity GO:0008173 p=1.7E−02 n=3 fg=0.05 bg=0.01
actin filament binding GO:0051015 p=2.3E−02 n=3 fg=0.05 bg=0.01
inositol 1,3,4,5 tetrakisphosphate bindi... GO:0043533 p=2.4E−02 n=1 fg=0.02 bg=0.00
juvenile hormone epoxide hydrolase activ... GO:0008096 p=2.4E−02 n=1 fg=0.02 bg=0.00
racemase and epimerase activity, acting ... GO:0016857 p=2.4E−02 n=1 fg=0.02 bg=0.00
FAD−AMP lyase (cyclizing) activity GO:0034012 p=2.4E−02 n=1 fg=0.02 bg=0.00
cis−stilbene−oxide hydrolase activity GO:0033961 p=2.4E−02 n=1 fg=0.02 bg=0.00
phosphotransferase activity, nitrogenous... GO:0016775 p=2.4E−02 n=1 fg=0.02 bg=0.00
long−chain fatty acid−CoA ligase activit... GO:0004467 p=2.4E−02 n=1 fg=0.02 bg=0.00
chondroitin−glucuronate 5−epimerase acti... GO:0047757 p=2.4E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=2.4E−02 n=1 fg=0.02 bg=0.00
DNA clamp loader activity GO:0003689 p=2.4E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=2.4E−02 n=1 fg=0.02 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=2.4E−02 n=1 fg=0.02 bg=0.00
carbonyl reductase (NADPH) activity GO:0004090 p=2.4E−02 n=1 fg=0.02 bg=0.00
glycerone kinase activity GO:0004371 p=2.4E−02 n=1 fg=0.02 bg=0.00
very long−chain fatty acid−CoA ligase ac... GO:0031957 p=2.4E−02 n=1 fg=0.02 bg=0.00
triokinase activity GO:0050354 p=2.4E−02 n=1 fg=0.02 bg=0.00
C−methyltransferase activity GO:0008169 p=2.4E−02 n=1 fg=0.02 bg=0.00
arginine kinase activity GO:0004054 p=2.4E−02 n=1 fg=0.02 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=2.4E−02 n=1 fg=0.02 bg=0.00
leucine zipper domain binding GO:0043522 p=2.4E−02 n=1 fg=0.02 bg=0.00
actin binding GO:0003779 p=3.7E−02 n=4 fg=0.07 bg=0.02
PDZ domain binding GO:0030165 p=4.3E−02 n=3 fg=0.05 bg=0.01
cAMP response element binding protein bi... GO:0008140 p=4.8E−02 n=1 fg=0.02 bg=0.00
sodium:phosphate symporter activity GO:0005436 p=4.8E−02 n=1 fg=0.02 bg=0.00
phosphate ion binding GO:0042301 p=4.8E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=57/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032379347.2
fraction genes in fg and expected valu
fungal−type vacuole membrane GO:0000329 p=5.3E−03 n=2 fg=0.03 bg=0.00
cell tip GO:0051286 p=7.8E−03 n=2 fg=0.03 bg=0.00
cell division site GO:0032153 p=9.4E−03 n=3 fg=0.05 bg=0.01
synaptic vesicle membrane GO:0030672 p=1.6E−02 n=3 fg=0.05 bg=0.01
exocytic vesicle membrane GO:0099501 p=1.8E−02 n=3 fg=0.05 bg=0.01
site of double−strand break GO:0035861 p=2.2E−02 n=2 fg=0.03 bg=0.00
site of DNA damage GO:0090734 p=2.2E−02 n=2 fg=0.03 bg=0.00
organelle subcompartment GO:0031984 p=2.2E−02 n=14 fg=0.22 bg=0.12
Dsl1/NZR complex GO:0070939 p=2.4E−02 n=1 fg=0.02 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=2.4E−02 n=1 fg=0.02 bg=0.00
SMC loading complex GO:0032116 p=2.4E−02 n=1 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=2.4E−02 n=1 fg=0.02 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=2.4E−02 n=1 fg=0.02 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=2.4E−02 n=1 fg=0.02 bg=0.00
intracellular anatomical structure GO:0005622 p=2.6E−02 n=64 fg=1.00 bg=0.94
integral component of organelle membrane GO:0031301 p=2.7E−02 n=6 fg=0.09 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=3.2E−02 n=6 fg=0.09 bg=0.04
integral component of synaptic vesicle m... GO:0030285 p=3.6E−02 n=2 fg=0.03 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=4.0E−02 n=9 fg=0.14 bg=0.07
intrinsic component of synaptic vesicle ... GO:0098563 p=4.2E−02 n=2 fg=0.03 bg=0.01
synaptic vesicle GO:0008021 p=4.2E−02 n=4 fg=0.06 bg=0.02
nuclear outer membrane−endoplasmic retic... GO:0042175 p=4.5E−02 n=9 fg=0.14 bg=0.07
endoplasmic reticulum subcompartment GO:0098827 p=4.6E−02 n=9 fg=0.14 bg=0.07
IkappaB kinase complex GO:0008385 p=4.7E−02 n=1 fg=0.02 bg=0.00
Elg1 RFC−like complex GO:0031391 p=4.7E−02 n=1 fg=0.02 bg=0.00
translation preinitiation complex GO:0070993 p=4.7E−02 n=1 fg=0.02 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=4.7E−02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=4.7E−02 n=1 fg=0.02 bg=0.00
presynaptic cytoskeleton GO:0099569 p=4.7E−02 n=1 fg=0.02 bg=0.00
transport vesicle membrane GO:0030658 p=5.6E−02 n=3 fg=0.05 bg=0.01
0 1 2 3 4 5
−log(p)
n=64/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction