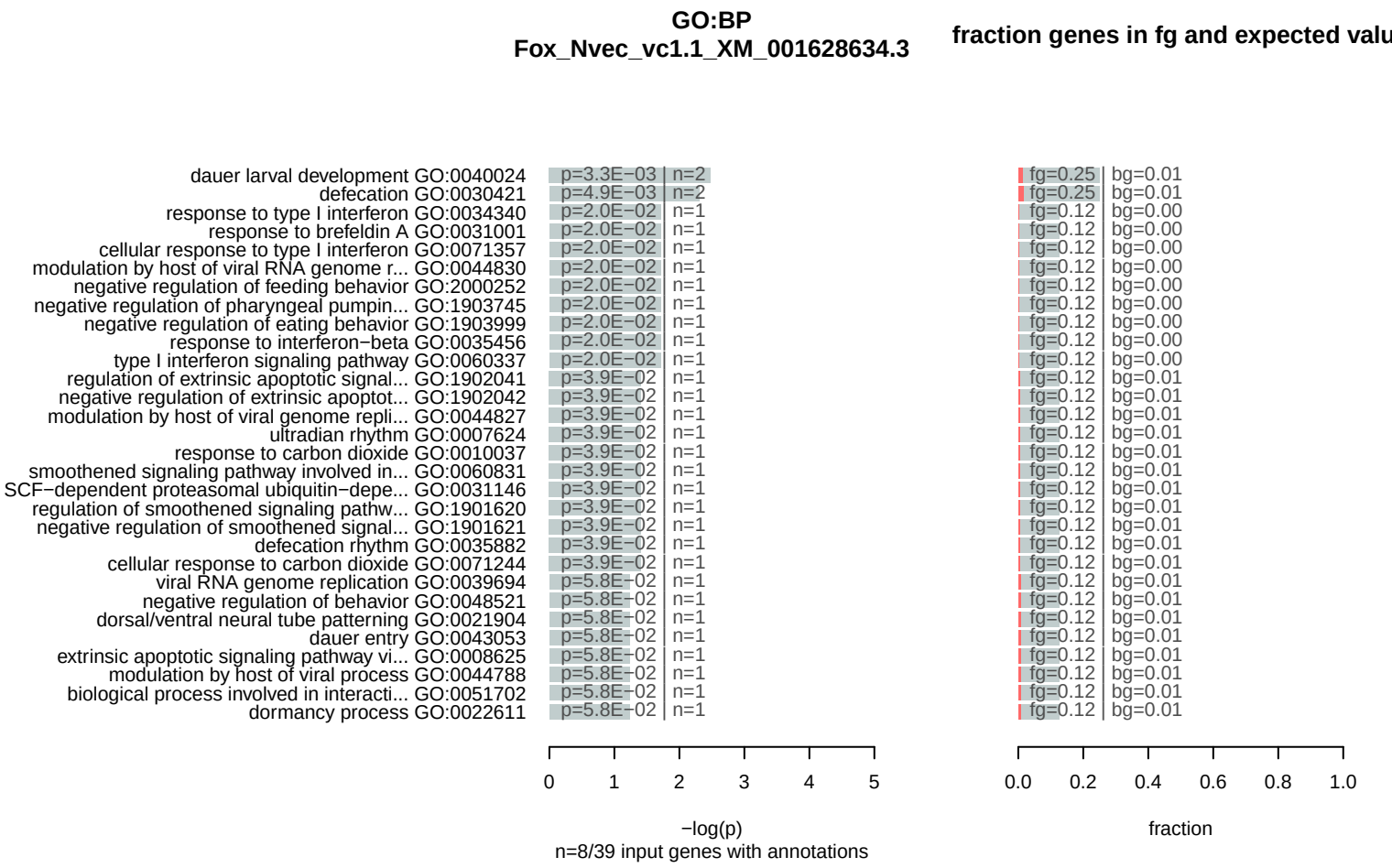
GO:BP
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
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defecation GO:0030421 p=4.9E−03 n=2 fg=0.25 bg=0.01
response to type I interferon GO:0034340 p=2.0E−02 n=1 fg=0.12 bg=0.00
response to brefeldin A GO:0031001 p=2.0E−02 n=1 fg=0.12 bg=0.00
cellular response to type I interferon GO:0071357 p=2.0E−02 n=1 fg=0.12 bg=0.00
modulation by host of viral RNA genome r... GO:0044830 p=2.0E−02 n=1 fg=0.12 bg=0.00
negative regulation of feeding behavior GO:2000252 p=2.0E−02 n=1 fg=0.12 bg=0.00
negative regulation of pharyngeal pumpin... GO:1903745 p=2.0E−02 n=1 fg=0.12 bg=0.00
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response to interferon−beta GO:0035456 p=2.0E−02 n=1 fg=0.12 bg=0.00
type I interferon signaling pathway GO:0060337 p=2.0E−02 n=1 fg=0.12 bg=0.00
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modulation by host of viral genome repli... GO:0044827 p=3.9E−02 n=1 fg=0.12 bg=0.01
ultradian rhythm GO:0007624 p=3.9E−02 n=1 fg=0.12 bg=0.01
response to carbon dioxide GO:0010037 p=3.9E−02 n=1 fg=0.12 bg=0.01
smoothened signaling pathway involved in... GO:0060831 p=3.9E−02 n=1 fg=0.12 bg=0.01
SCF−dependent proteasomal ubiquitin−depe... GO:0031146 p=3.9E−02 n=1 fg=0.12 bg=0.01
regulation of smoothened signaling pathw... GO:1901620 p=3.9E−02 n=1 fg=0.12 bg=0.01
negative regulation of smoothened signal... GO:1901621 p=3.9E−02 n=1 fg=0.12 bg=0.01
defecation rhythm GO:0035882 p=3.9E−02 n=1 fg=0.12 bg=0.01
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negative regulation of behavior GO:0048521 p=5.8E+02 n=1 fg=0.12 bg=0.01
dorsal/ventral neural tube patterning GO:0021904 p=5.8E+02 n=1 fg=0.12 bg=0.01
dauer entry GO:0043053 p=5.8E+02 n=1 fg=0.12 bg=0.01
extrinsic apoptotic signaling pathway vi... GO:0008625 p=5.8E+02 n=1 fg=0.12 bg=0.01
modulation by host of viral process GO:0044788 p=5.8E+02 n=1 fg=0.12 bg=0.01
biological process involved in interacti... GO:0051702 p=5.8E+02 n=1 fg=0.12 bg=0.01
dormancy process GO:0022611 p=5.8E+02 n=1 fg=0.12 bg=0.01
0 1 2 3 4 5
−log(p)
n=8/39 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
phosphatidylinositol 3−kinase binding GO:0043548 p=3.3E−02 n=1 fg=0.17 bg=0.01
phosphatidylinositol 3−kinase regulatory... GO:0036312 p=3.3E−02 n=1 fg=0.17 bg=0.01
protein phosphatase binding GO:0019903 p=6.5E+02 n=1 fg=0.17 bg=0.01
leak channel activity GO:0022840 p=6.5E+02 n=1 fg=0.17 bg=0.01
potassium ion leak channel activity GO:0022841 p=6.5E+02 n=1 fg=0.17 bg=0.01
narrow pore channel activity GO:0022842 p=6.5E+02 n=1 fg=0.17 bg=0.01
phosphatase binding GO:0019902 p=1.1E−01 n=1 fg=0.17 bg=0.02
DNA−binding transcription repressor acti... GO:0001227 p=1.3E−01 n=1 fg=0.17 bg=0.02
DNA−binding transcription repressor acti... GO:0001217 p=1.3E−01 n=1 fg=0.17 bg=0.02
mRNA binding GO:0003729 p=1.4E−01 n=1 fg=0.17 bg=0.02
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DNA−binding transcription factor activit... GO:0003700 p=2.5E−01 n=2 fg=0.33 bg=0.16
ubiquitin−protein transferase activity GO:0004842 p=2.6E−01 n=1 fg=0.17 bg=0.05
G protein−coupled receptor activity GO:0004930 p=2.8E−01 n=1 fg=0.17 bg=0.05
ubiquitin−like protein transferase activ... GO:0019787 p=2.8E−01 n=1 fg=0.17 bg=0.05
RNA binding GO:0003723 p=2.9E−01 n=1 fg=0.17 bg=0.06
nucleic acid binding GO:0003676 p=3.0E−01 n=2 fg=0.33 bg=0.18
transcription regulator activity GO:0140110 p=3.0E−01 n=2 fg=0.33 bg=0.18
cation channel activity GO:0005261 p=3.6E−01 n=1 fg=0.17 bg=0.07
metal ion transmembrane transporter acti... GO:0046873 p=3.8E−01 n=1 fg=0.17 bg=0.08
transmembrane signaling receptor activit... GO:0004888 p=4.1E−01 n=1 fg=0.17 bg=0.08
RNA polymerase II transcription regulato... GO:0000977 p=4.1E−01 n=1 fg=0.17 bg=0.08
transcription cis−regulatory region bind... GO:0000976 p=4.3E−01 n=1 fg=0.17 bg=0.09
signaling receptor activity GO:0038023 p=4.4E−01 n=1 fg=0.17 bg=0.09
sequence−specific double−stranded DNA bi... GO:1990837 p=4.4E−01 n=1 fg=0.17 bg=0.09
molecular transducer activity GO:0060089 p=4.4E−01 n=1 fg=0.17 bg=0.09
double−stranded DNA binding GO:0003690 p=4.5E−01 n=1 fg=0.17 bg=0.09
transcription regulatory region nucleic ... GO:0001067 p=4.5E−01 n=1 fg=0.17 bg=0.09
ion channel activity GO:0005216 p=4.6E−01 n=1 fg=0.17 bg=0.10
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−log(p)
n=6/39 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001628634.3
fraction genes in fg and expected valu
extrinsic component of Golgi membrane GO:0090498 p=2.0E−02 n=1 fg=0.12 bg=0.00
SCF ubiquitin ligase complex GO:0019005 p=3.9E−02 n=1 fg=0.12 bg=0.01
extrinsic component of organelle membran... GO:0031312 p=3.9E−02 n=1 fg=0.12 bg=0.01
Golgi medial cisterna GO:0005797 p=3.9E−02 n=1 fg=0.12 bg=0.01
ciliary membrane GO:0060170 p=5.9E+02 n=1 fg=0.12 bg=0.01
cytoplasmic microtubule GO:0005881 p=7.8E−02 n=1 fg=0.12 bg=0.01
cullin−RING ubiquitin ligase complex GO:0031461 p=7.8E−02 n=1 fg=0.12 bg=0.01
Golgi trans cisterna GO:0000138 p=7.8E−02 n=1 fg=0.12 bg=0.01
endocytic vesicle membrane GO:0030666 p=9.6E−02 n=1 fg=0.12 bg=0.01
Golgi cisterna GO:0031985 p=9.6E−02 n=1 fg=0.12 bg=0.01
Golgi stack GO:0005795 p=1.3E−01 n=1 fg=0.12 bg=0.02
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polymeric cytoskeletal fiber GO:0099513 p=2.0E−01 n=1 fg=0.12 bg=0.03
extrinsic component of membrane GO:0019898 p=2.0E−01 n=1 fg=0.12 bg=0.03
ubiquitin ligase complex GO:0000151 p=2.6E−01 n=1 fg=0.12 bg=0.04
nuclear body GO:0016604 p=2.6E−01 n=1 fg=0.12 bg=0.04
nuclear chromosome GO:0000228 p=2.9E−01 n=1 fg=0.12 bg=0.04
Golgi membrane GO:0000139 p=3.2E−01 n=1 fg=0.12 bg=0.05
chromatin GO:0000785 p=3.4E−01 n=1 fg=0.12 bg=0.05
bounding membrane of organelle GO:0098588 p=3.6E−01 n=2 fg=0.25 bg=0.15
cilium GO:0005929 p=3.8E−01 n=1 fg=0.12 bg=0.06
intracellular protein−containing complex GO:0140535 p=3.9E−01 n=1 fg=0.12 bg=0.06
cell projection membrane GO:0031253 p=4.2E−01 n=1 fg=0.12 bg=0.07
transferase complex GO:1990234 p=4.4E−01 n=1 fg=0.12 bg=0.07
chromosome GO:0005694 p=4.5E−01 n=1 fg=0.12 bg=0.07
supramolecular fiber GO:0099512 p=4.5E−01 n=1 fg=0.12 bg=0.07
microtubule cytoskeleton GO:0015630 p=4.5E−01 n=1 fg=0.12 bg=0.07
supramolecular polymer GO:0099081 p=4.5E−01 n=1 fg=0.12 bg=0.07
0 1 2 3 4 5
−log(p)
n=8/39 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction