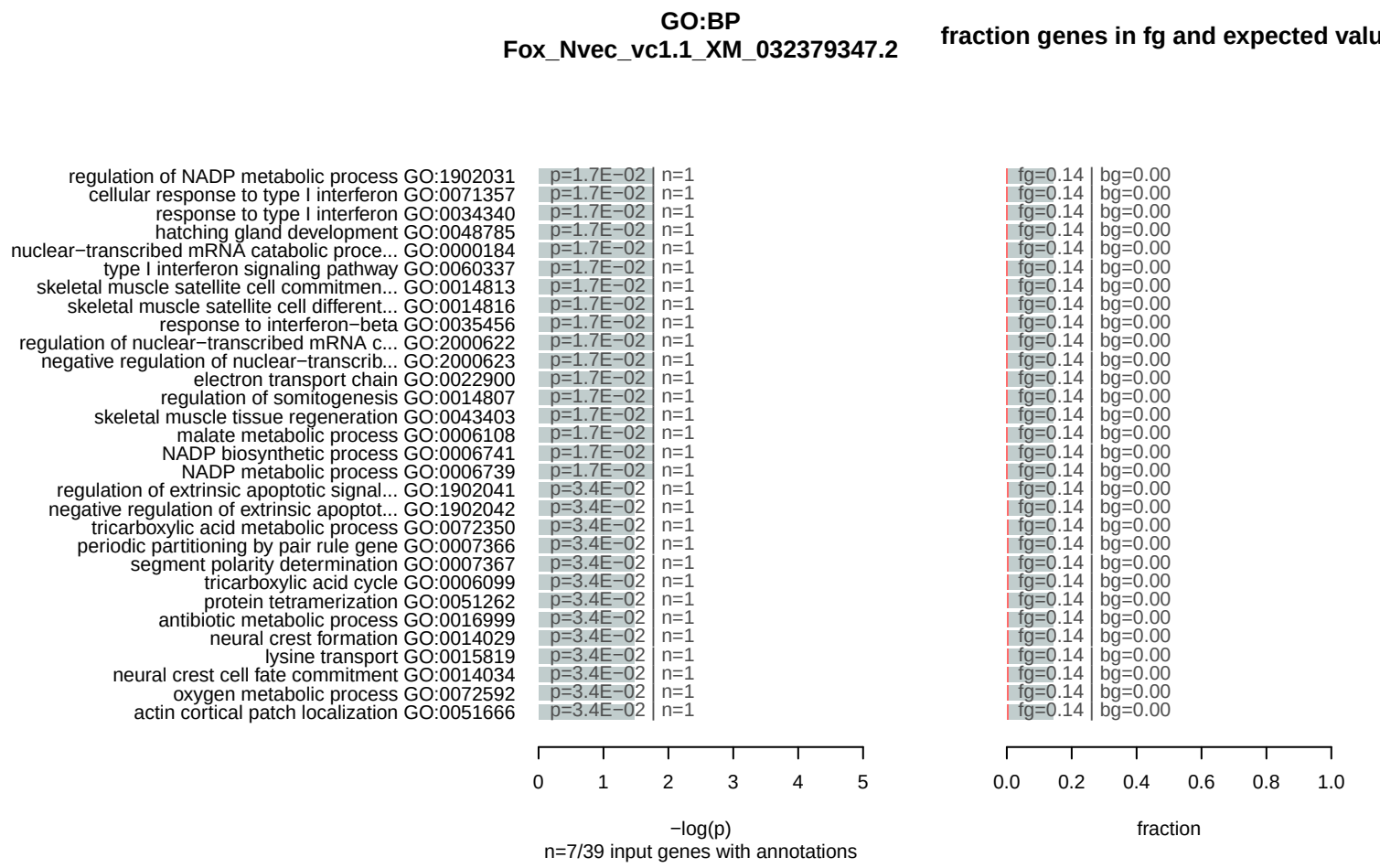
GO:BP
Fox_Nvec_vc1.1_XM_032379347.2
fraction genes in fg and expected valu
regulation of NADP metabolic process GO:1902031 p=1.7E−02 n=1 fg=0.14 bg=0.00
cellular response to type I interferon GO:0071357 p=1.7E−02 n=1 fg=0.14 bg=0.00
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hatching gland development GO:0048785 p=1.7E−02 n=1 fg=0.14 bg=0.00
nuclear−transcribed mRNA catabolic proce... GO:0000184 p=1.7E−02 n=1 fg=0.14 bg=0.00
type I interferon signaling pathway GO:0060337 p=1.7E−02 n=1 fg=0.14 bg=0.00
skeletal muscle satellite cell commitmen... GO:0014813 p=1.7E−02 n=1 fg=0.14 bg=0.00
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response to interferon−beta GO:0035456 p=1.7E−02 n=1 fg=0.14 bg=0.00
regulation of nuclear−transcribed mRNA c... GO:2000622 p=1.7E−02 n=1 fg=0.14 bg=0.00
negative regulation of nuclear−transcrib... GO:2000623 p=1.7E−02 n=1 fg=0.14 bg=0.00
electron transport chain GO:0022900 p=1.7E−02 n=1 fg=0.14 bg=0.00
regulation of somitogenesis GO:0014807 p=1.7E−02 n=1 fg=0.14 bg=0.00
skeletal muscle tissue regeneration GO:0043403 p=1.7E−02 n=1 fg=0.14 bg=0.00
malate metabolic process GO:0006108 p=1.7E−02 n=1 fg=0.14 bg=0.00
NADP biosynthetic process GO:0006741 p=1.7E−02 n=1 fg=0.14 bg=0.00
NADP metabolic process GO:0006739 p=1.7E−02 n=1 fg=0.14 bg=0.00
regulation of extrinsic apoptotic signal... GO:1902041 p=3.4E−02 n=1 fg=0.14 bg=0.00
negative regulation of extrinsic apoptot... GO:1902042 p=3.4E−02 n=1 fg=0.14 bg=0.00
tricarboxylic acid metabolic process GO:0072350 p=3.4E−02 n=1 fg=0.14 bg=0.00
periodic partitioning by pair rule gene GO:0007366 p=3.4E−02 n=1 fg=0.14 bg=0.00
segment polarity determination GO:0007367 p=3.4E−02 n=1 fg=0.14 bg=0.00
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neural crest formation GO:0014029 p=3.4E−02 n=1 fg=0.14 bg=0.00
lysine transport GO:0015819 p=3.4E−02 n=1 fg=0.14 bg=0.00
neural crest cell fate commitment GO:0014034 p=3.4E−02 n=1 fg=0.14 bg=0.00
oxygen metabolic process GO:0072592 p=3.4E−02 n=1 fg=0.14 bg=0.00
actin cortical patch localization GO:0051666 p=3.4E−02 n=1 fg=0.14 bg=0.00
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−log(p)
n=7/39 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
malic enzyme activity GO:0004470 p=1.4E−02 n=1 fg=0.20 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004471 p=1.4E−02 n=1 fg=0.20 bg=0.00
NADP binding GO:0050661 p=1.4E−02 n=1 fg=0.20 bg=0.00
malate dehydrogenase (decarboxylating) (... GO:0004473 p=1.4E−02 n=1 fg=0.20 bg=0.00
NAD binding GO:0051287 p=1.4E−02 n=1 fg=0.20 bg=0.00
oxidoreductase activity, acting on CH−OH... GO:0016614 p=1.4E−02 n=1 fg=0.20 bg=0.00
electron transfer activity GO:0009055 p=1.4E−02 n=1 fg=0.20 bg=0.00
malate dehydrogenase activity GO:0016615 p=1.4E−02 n=1 fg=0.20 bg=0.00
oxidoreductase activity, acting on the C... GO:0016616 p=1.4E−02 n=1 fg=0.20 bg=0.00
transition metal ion binding GO:0046914 p=1.5E−02 n=2 fg=0.40 bg=0.04
manganese ion binding GO:0030145 p=2.7E−02 n=1 fg=0.20 bg=0.01
ADP binding GO:0043531 p=2.7E−02 n=1 fg=0.20 bg=0.01
HMG box domain binding GO:0071837 p=5.4E−02 n=1 fg=0.20 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=5.6E−02 n=2 fg=0.40 bg=0.08
metal ion binding GO:0046872 p=6.3E−02 n=2 fg=0.40 bg=0.09
transcription cis−regulatory region bind... GO:0000976 p=6.3E−02 n=2 fg=0.40 bg=0.09
sequence−specific double−stranded DNA bi... GO:1990837 p=6.7E−02 n=2 fg=0.40 bg=0.09
SNARE binding GO:0000149 p=6.7E−02 n=1 fg=0.20 bg=0.01
double−stranded DNA binding GO:0003690 p=7.1E−02 n=2 fg=0.40 bg=0.09
transcription regulatory region nucleic ... GO:0001067 p=7.1E−02 n=2 fg=0.40 bg=0.09
sequence−specific DNA binding GO:0043565 p=8.3E−02 n=2 fg=0.40 bg=0.10
cation binding GO:0043169 p=8.3E−02 n=2 fg=0.40 bg=0.10
oxidoreductase activity GO:0016491 p=9.3E−02 n=1 fg=0.20 bg=0.02
DNA−binding transcription repressor acti... GO:0001227 p=1.1E−01 n=1 fg=0.20 bg=0.02
DNA−binding transcription repressor acti... GO:0001217 p=1.1E−01 n=1 fg=0.20 bg=0.02
heterocyclic compound binding GO:1901363 p=1.1E−01 n=3 fg=0.60 bg=0.26
organic cyclic compound binding GO:0097159 p=1.3E−01 n=3 fg=0.60 bg=0.27
DNA−binding transcription factor activit... GO:0000981 p=1.3E−01 n=2 fg=0.40 bg=0.13
DNA binding GO:0003677 p=1.4E−01 n=2 fg=0.40 bg=0.14
zinc ion binding GO:0008270 p=1.4E−01 n=1 fg=0.20 bg=0.03
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−log(p)
n=5/39 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032379347.2
fraction genes in fg and expected valu
Dsl1/NZR complex GO:0070939 p=1.7E−02 n=1 fg=0.14 bg=0.00
vesicle tethering complex GO:0099023 p=1.7E−02 n=1 fg=0.14 bg=0.00
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cell tip GO:0051286 p=3.5E−02 n=1 fg=0.14 bg=0.00
intrinsic component of organelle membran... GO:0031300 p=3.5E−02 n=2 fg=0.29 bg=0.04
integral component of organelle membrane GO:0031301 p=3.5E−02 n=2 fg=0.29 bg=0.04
endoplasmic reticulum protein−containing... GO:0140534 p=5.1E−02 n=1 fg=0.14 bg=0.01
storage vacuole GO:0000322 p=5.1E−02 n=1 fg=0.14 bg=0.01
fungal−type vacuole GO:0000324 p=5.1E−02 n=1 fg=0.14 bg=0.01
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early endosome membrane GO:0031901 p=6.8E−02 n=1 fg=0.14 bg=0.01
intrinsic component of synaptic vesicle ... GO:0098563 p=8.4E−02 n=1 fg=0.14 bg=0.01
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integral component of synaptic vesicle m... GO:0030285 p=8.4E−02 n=1 fg=0.14 bg=0.01
mitochondrion GO:0005739 p=9.5E−02 n=2 fg=0.29 bg=0.08
intracellular membrane−bounded organelle GO:0043231 p=1.2E−01 n=7 fg=1.00 bg=0.74
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synaptic vesicle membrane GO:0030672 p=1.3E−01 n=1 fg=0.14 bg=0.02
exocytic vesicle membrane GO:0099501 p=1.5E−01 n=1 fg=0.14 bg=0.02
mitochondrial matrix GO:0005759 p=1.5E−01 n=1 fg=0.14 bg=0.02
lytic vacuole membrane GO:0098852 p=1.5E−01 n=1 fg=0.14 bg=0.02
intracellular organelle GO:0043229 p=1.6E−01 n=7 fg=1.00 bg=0.77
transport vesicle membrane GO:0030658 p=1.6E−01 n=1 fg=0.14 bg=0.02
vacuolar membrane GO:0005774 p=1.8E−01 n=1 fg=0.14 bg=0.03
integral component of endoplasmic reticu... GO:0030176 p=1.8E−01 n=1 fg=0.14 bg=0.03
intrinsic component of endoplasmic retic... GO:0031227 p=1.8E−01 n=1 fg=0.14 bg=0.03
organelle GO:0043226 p=1.8E−01 n=7 fg=1.00 bg=0.78
endosome membrane GO:0010008 p=2.1E−01 n=1 fg=0.14 bg=0.03
early endosome GO:0005769 p=2.2E−01 n=1 fg=0.14 bg=0.03
synaptic vesicle GO:0008021 p=2.3E−01 n=1 fg=0.14 bg=0.04
0 1 2 3 4 5
−log(p)
n=7/39 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction