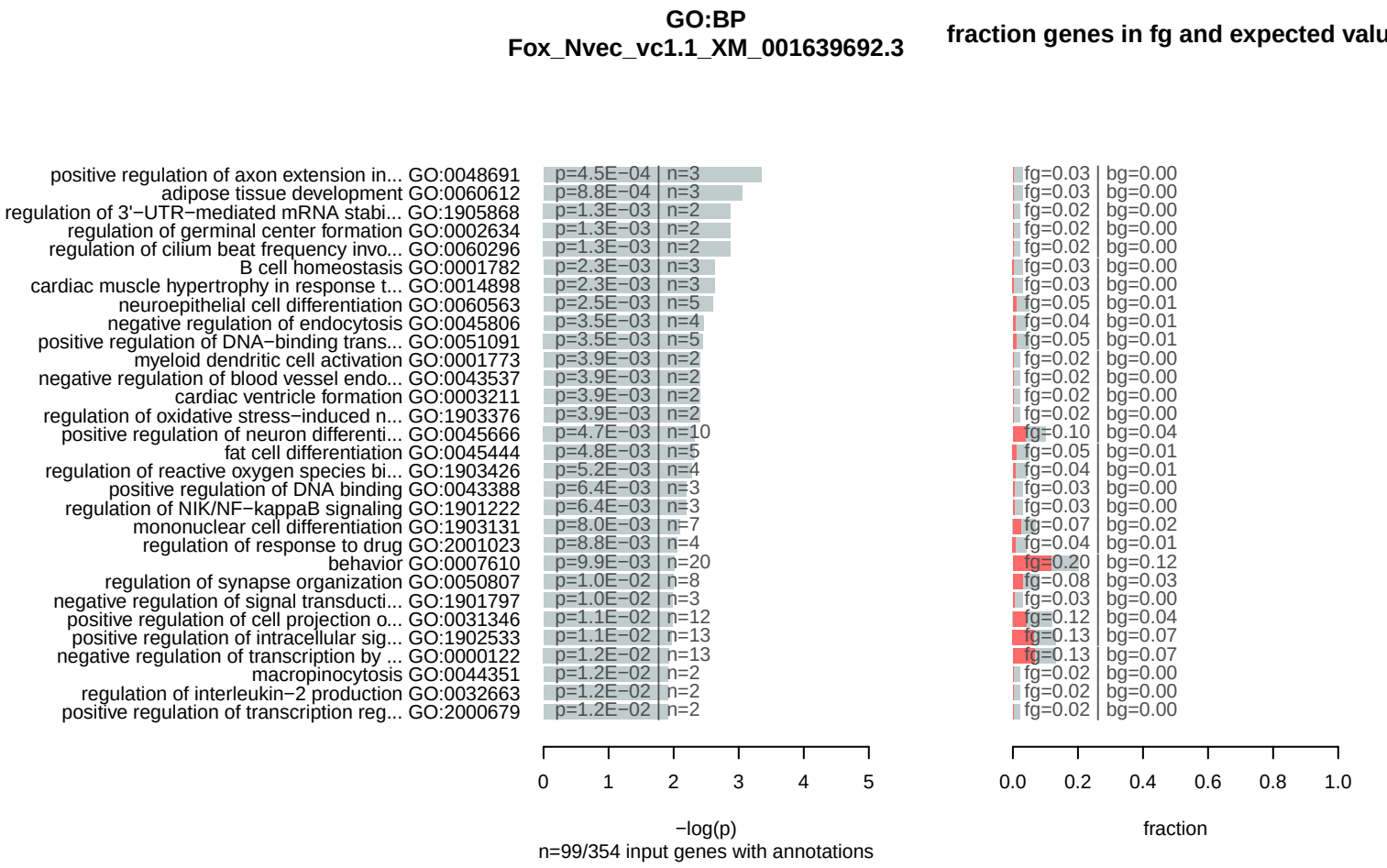
GO:BP
Fox_Nvec_vc1.1_XM_001639692.3
fraction genes in fg and expected valu
positive regulation of axon extension in... GO:0048691 p=4.5E−04 n=3 fg=0.03 bg=0.00
adipose tissue development GO:0060612 p=8.8E−04 n=3 fg=0.03 bg=0.00
regulation of 3'−UTR−mediated mRNA stabi... GO:1905868 p=1.3E−03 n=2 fg=0.02 bg=0.00
regulation of germinal center formation GO:0002634 p=1.3E−03 n=2 fg=0.02 bg=0.00
regulation of cilium beat frequency invo... GO:0060296 p=1.3E−03 n=2 fg=0.02 bg=0.00
B cell homeostasis GO:0001782 p=2.3E−03 n=3 fg=0.03 bg=0.00
cardiac muscle hypertrophy in response t... GO:0014898 p=2.3E−03 n=3 fg=0.03 bg=0.00
neuroepithelial cell differentiation GO:0060563 p=2.5E−03 n=5 fg=0.05 bg=0.01
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positive regulation of DNA−binding trans... GO:0051091 p=3.5E−03 n=5 fg=0.05 bg=0.01
myeloid dendritic cell activation GO:0001773 p=3.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of blood vessel endo... GO:0043537 p=3.9E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=3.9E−03 n=2 fg=0.02 bg=0.00
regulation of oxidative stress−induced n... GO:1903376 p=3.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of neuron differenti... GO:0045666 p=4.7E−03 n=10 fg=0.10 bg=0.04
fat cell differentiation GO:0045444 p=4.8E−03 n=5 fg=0.05 bg=0.01
regulation of reactive oxygen species bi... GO:1903426 p=5.2E−03 n=4 fg=0.04 bg=0.01
positive regulation of DNA binding GO:0043388 p=6.4E−03 n=3 fg=0.03 bg=0.00
regulation of NIK/NF−kappaB signaling GO:1901222 p=6.4E−03 n=3 fg=0.03 bg=0.00
mononuclear cell differentiation GO:1903131 p=8.0E−03 n=7 fg=0.07 bg=0.02
regulation of response to drug GO:2001023 p=8.8E−03 n=4 fg=0.04 bg=0.01
behavior GO:0007610 p=9.9E−03 n=20 fg=0.20 bg=0.12
regulation of synapse organization GO:0050807 p=1.0E−02 n=8 fg=0.08 bg=0.03
negative regulation of signal transducti... GO:1901797 p=1.0E−02 n=3 fg=0.03 bg=0.00
positive regulation of cell projection o... GO:0031346 p=1.1E−02 n=12 fg=0.12 bg=0.04
positive regulation of intracellular sig... GO:1902533 p=1.1E−02 n=13 fg=0.13 bg=0.07
negative regulation of transcription by ... GO:0000122 p=1.2E−02 n=13 fg=0.13 bg=0.07
macropinocytosis GO:0044351 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of interleukin−2 production GO:0032663 p=1.2E−02 n=2 fg=0.02 bg=0.00
positive regulation of transcription reg... GO:2000679 p=1.2E−02 n=2 fg=0.02 bg=0.00
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−log(p)
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_001639692.3
fraction genes in fg and expected valu
DNA−binding transcription activator acti... GO:0001228 p=1.1E−03 n=9 fg=0.11 bg=0.03
cAMP response element binding GO:0035497 p=3.7E−03 n=2 fg=0.02 bg=0.00
structural constituent of nuclear pore GO:0017056 p=4.5E−03 n=3 fg=0.04 bg=0.00
sequence−specific DNA binding GO:0043565 p=5.2E−03 n=14 fg=0.16 bg=0.06
promoter−specific chromatin binding GO:1990841 p=6.0E−03 n=3 fg=0.04 bg=0.00
bHLH transcription factor binding GO:0043425 p=7.3E−03 n=2 fg=0.02 bg=0.00
transcription corepressor activity GO:0003714 p=9.3E−03 n=5 fg=0.06 bg=0.02
microtubule motor activity GO:0003777 p=9.8E−03 n=3 fg=0.04 bg=0.01
glutamate receptor binding GO:0035254 p=9.8E−03 n=3 fg=0.04 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=1.2E−02 n=9 fg=0.11 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=1.2E−02 n=9 fg=0.11 bg=0.03
transcription cis−regulatory region bind... GO:0000976 p=1.3E−02 n=11 fg=0.13 bg=0.05
histone deacetylase binding GO:0042826 p=1.3E−02 n=4 fg=0.05 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=1.8E−02 n=10 fg=0.12 bg=0.04
SMAD binding GO:0046332 p=1.8E−02 n=3 fg=0.04 bg=0.01
sequence−specific double−stranded DNA bi... GO:1990837 p=2.0E−02 n=11 fg=0.13 bg=0.05
HMG box domain binding GO:0071837 p=2.4E−02 n=2 fg=0.02 bg=0.00
ubiquitin−specific protease binding GO:1990381 p=2.4E−02 n=2 fg=0.02 bg=0.00
MAP kinase kinase kinase activity GO:0004709 p=2.4E−02 n=2 fg=0.02 bg=0.00
acetyltransferase activity GO:0016407 p=2.5E−02 n=3 fg=0.04 bg=0.01
cullin family protein binding GO:0097602 p=3.1E−02 n=2 fg=0.02 bg=0.00
transcription regulatory region nucleic ... GO:0001067 p=3.1E−02 n=11 fg=0.13 bg=0.05
protein−arginine omega−N symmetric methy... GO:0035243 p=3.6E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.6E−02 n=1 fg=0.01 bg=0.00
ATP−dependent DNA/DNA annealing activity GO:0036310 p=3.6E−02 n=1 fg=0.01 bg=0.00
volume−sensitive chloride channel activi... GO:0072320 p=3.6E−02 n=1 fg=0.01 bg=0.00
galactose binding GO:0005534 p=3.6E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=3.6E−02 n=1 fg=0.01 bg=0.00
3−oxo−5−alpha−steroid 4−dehydrogenase ac... GO:0003865 p=3.6E−02 n=1 fg=0.01 bg=0.00
[myelin basic protein]−arginine N−methyl... GO:0016277 p=3.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=85/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_001639692.3
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=4.9E−03 n=3 fg=0.03 bg=0.00
exon−exon junction complex GO:0035145 p=7.8E−03 n=2 fg=0.02 bg=0.00
synapse GO:0045202 p=1.4E−02 n=15 fg=0.15 bg=0.08
endoplasmic reticulum subcompartment GO:0098827 p=1.5E−02 n=14 fg=0.14 bg=0.07
actomyosin GO:0042641 p=2.3E−02 n=3 fg=0.03 bg=0.01
exocytic vesicle GO:0070382 p=2.7E−02 n=6 fg=0.06 bg=0.02
endoplasmic reticulum membrane GO:0005789 p=2.8E−02 n=13 fg=0.13 bg=0.07
transcription regulator complex GO:0005667 p=3.0E−02 n=8 fg=0.08 bg=0.04
nuclear outer membrane−endoplasmic retic... GO:0042175 p=3.2E−02 n=13 fg=0.13 bg=0.07
DNA repair complex GO:1990391 p=3.3E−02 n=2 fg=0.02 bg=0.00
XPC complex GO:0071942 p=3.7E−02 n=1 fg=0.01 bg=0.00
insulin−responsive compartment GO:0032593 p=3.7E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=3.7E−02 n=1 fg=0.01 bg=0.00
nucleotide−excision repair complex GO:0000109 p=3.7E−02 n=1 fg=0.01 bg=0.00
nuclear pore inner ring GO:0044611 p=3.7E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=3.7E−02 n=1 fg=0.01 bg=0.00
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transport vesicle GO:0030133 p=5.4E−02 n=7 fg=0.07 bg=0.03
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intrinsic component of vacuolar membrane GO:0031310 p=7.3E−02 n=1 fg=0.01 bg=0.00
RNA polymerase III transcription regulat... GO:0090576 p=7.3E−02 n=1 fg=0.01 bg=0.00
integral component of vacuolar membrane GO:0031166 p=7.3E−02 n=1 fg=0.01 bg=0.00
spermatoproteasome complex GO:1990111 p=7.3E−02 n=1 fg=0.01 bg=0.00
transcription factor TFIIIC complex GO:0000127 p=7.3E−02 n=1 fg=0.01 bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=7.3E−02 n=1 fg=0.01 bg=0.00
BBSome GO:0034464 p=7.3E−02 n=1 fg=0.01 bg=0.00
tRNA−splicing ligase complex GO:0072669 p=7.3E−02 n=1 fg=0.01 bg=0.00
Lewy body GO:0097413 p=7.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=100/354 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction