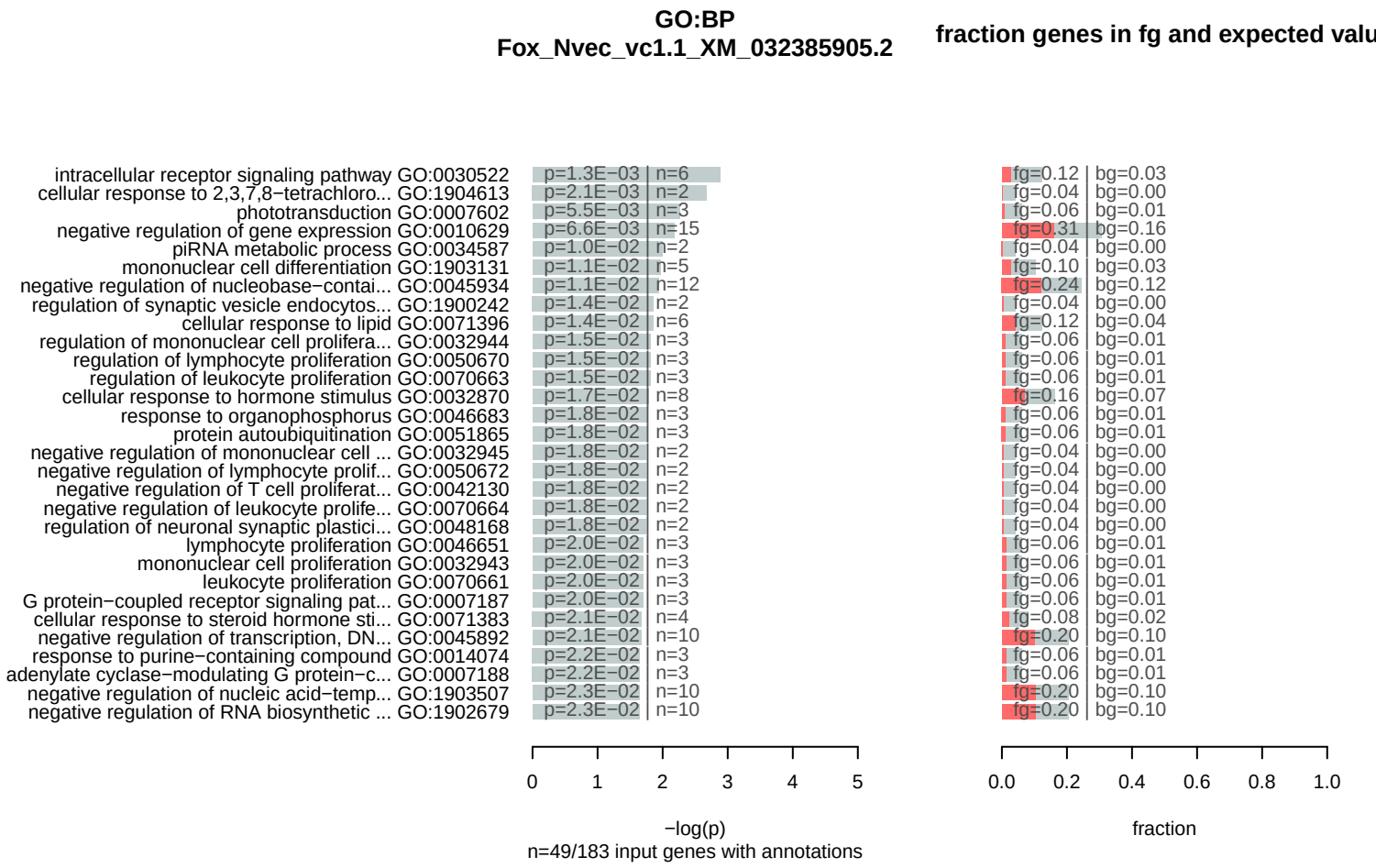
GO:BP
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
intracellular receptor signaling pathway GO:0030522 p=1.3E−03 n=6 fg=0.12 bg=0.03
cellular response to 2,3,7,8−tetrachloro... GO:1904613 p=2.1E−03 n=2 fg=0.04 bg=0.00
phototransduction GO:0007602 p=5.5E−03 n=3 fg=0.06 bg=0.01
negative regulation of gene expression GO:0010629 p=6.6E−03 n=15 fg=0.31 bg=0.16
piRNA metabolic process GO:0034587 p=1.0E−02 n=2 fg=0.04 bg=0.00
mononuclear cell differentiation GO:1903131 p=1.1E−02 n=5 fg=0.10 bg=0.03
negative regulation of nucleobase−contai... GO:0045934 p=1.1E−02 n=12 fg=0.24 bg=0.12
regulation of synaptic vesicle endocytos... GO:1900242 p=1.4E−02 n=2 fg=0.04 bg=0.00
cellular response to lipid GO:0071396 p=1.4E−02 n=6 fg=0.12 bg=0.04
regulation of mononuclear cell prolifera... GO:0032944 p=1.5E−02 n=3 fg=0.06 bg=0.01
regulation of lymphocyte proliferation GO:0050670 p=1.5E−02 n=3 fg=0.06 bg=0.01
regulation of leukocyte proliferation GO:0070663 p=1.5E−02 n=3 fg=0.06 bg=0.01
cellular response to hormone stimulus GO:0032870 p=1.7E−02 n=8 fg=0.16 bg=0.07
response to organophosphorus GO:0046683 p=1.8E−02 n=3 fg=0.06 bg=0.01
protein autoubiquitination GO:0051865 p=1.8E−02 n=3 fg=0.06 bg=0.01
negative regulation of mononuclear cell ... GO:0032945 p=1.8E−02 n=2 fg=0.04 bg=0.00
negative regulation of lymphocyte prolif... GO:0050672 p=1.8E−02 n=2 fg=0.04 bg=0.00
negative regulation of T cell proliferat... GO:0042130 p=1.8E−02 n=2 fg=0.04 bg=0.00
negative regulation of leukocyte prolife... GO:0070664 p=1.8E−02 n=2 fg=0.04 bg=0.00
regulation of neuronal synaptic plastici... GO:0048168 p=1.8E−02 n=2 fg=0.04 bg=0.00
lymphocyte proliferation GO:0046651 p=2.0E−02 n=3 fg=0.06 bg=0.01
mononuclear cell proliferation GO:0032943 p=2.0E−02 n=3 fg=0.06 bg=0.01
leukocyte proliferation GO:0070661 p=2.0E−02 n=3 fg=0.06 bg=0.01
G protein−coupled receptor signaling pat... GO:0007187 p=2.0E−02 n=3 fg=0.06 bg=0.01
cellular response to steroid hormone sti... GO:0071383 p=2.1E−02 n=4 fg=0.08 bg=0.02
negative regulation of transcription, DN... GO:0045892 p=2.1E−02 n=10 fg=0.20 bg=0.10
response to purine−containing compound GO:0014074 p=2.2E−02 n=3 fg=0.06 bg=0.01
adenylate cyclase−modulating G protein−c... GO:0007188 p=2.2E−02 n=3 fg=0.06 bg=0.01
negative regulation of nucleic acid−temp... GO:1903507 p=2.3E−02 n=10 fg=0.20 bg=0.10
negative regulation of RNA biosynthetic ... GO:1902679 p=2.3E−02 n=10 fg=0.20 bg=0.10
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−log(p)
n=49/183 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
cyclin binding GO:0030332 p=1.8E−03 n=2 fg=0.05 bg=0.00
protein self−association GO:0043621 p=2.1E−03 n=3 fg=0.07 bg=0.01
TBP−class protein binding GO:0017025 p=2.8E−03 n=3 fg=0.07 bg=0.01
cAMP binding GO:0030552 p=3.6E−03 n=2 fg=0.05 bg=0.00
ligase activity, forming carbon−sulfur b... GO:0016877 p=5.9E−03 n=2 fg=0.05 bg=0.00
dolichyl−diphosphooligosaccharide−protei... GO:0004579 p=2.5E−02 n=1 fg=0.03 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=2.5E−02 n=1 fg=0.03 bg=0.00
SMC family protein binding GO:0043221 p=2.5E−02 n=1 fg=0.03 bg=0.00
aminophospholipid flippase activity GO:0015247 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylglycerol binding GO:1901611 p=2.5E−02 n=1 fg=0.03 bg=0.00
cardiolipin binding GO:1901612 p=2.5E−02 n=1 fg=0.03 bg=0.00
UFM1 activating enzyme activity GO:0071566 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−malate dehydrogenase activity GO:0030060 p=2.5E−02 n=1 fg=0.03 bg=0.00
DNA binding, bending GO:0008301 p=2.5E−02 n=1 fg=0.03 bg=0.00
cGMP−stimulated cyclic−nucleotide phosph... GO:0004118 p=2.5E−02 n=1 fg=0.03 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=2.5E−02 n=1 fg=0.03 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=2.5E−02 n=1 fg=0.03 bg=0.00
flippase activity GO:0140327 p=2.5E−02 n=1 fg=0.03 bg=0.00
alkylglycerophosphoethanolamine phosphod... GO:0047391 p=2.5E−02 n=1 fg=0.03 bg=0.00
non−sequence−specific DNA binding, bendi... GO:0044378 p=2.5E−02 n=1 fg=0.03 bg=0.00
signaling receptor binding GO:0005102 p=4.8E−02 n=8 fg=0.20 bg=0.10
nucleoside kinase activity GO:0019206 p=5.0E−02 n=1 fg=0.03 bg=0.00
dynein heavy chain binding GO:0045504 p=5.0E−02 n=1 fg=0.03 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=5.0E−02 n=1 fg=0.03 bg=0.00
acetylation−dependent protein binding GO:0140033 p=5.0E−02 n=1 fg=0.03 bg=0.00
LIM domain binding GO:0030274 p=5.0E−02 n=1 fg=0.03 bg=0.00
chemokine receptor binding GO:0042379 p=5.0E−02 n=1 fg=0.03 bg=0.00
malate dehydrogenase activity GO:0016615 p=5.0E−02 n=1 fg=0.03 bg=0.00
lysine−acetylated histone binding GO:0070577 p=5.0E−02 n=1 fg=0.03 bg=0.00
vitamin E binding GO:0008431 p=5.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=40/183 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385905.2
fraction genes in fg and expected valu
heterotrimeric G−protein complex GO:0005834 p=2.7E−04 n=3 fg=0.07 bg=0.00
P granule GO:0043186 p=2.7E−03 n=3 fg=0.07 bg=0.01
MLL1 complex GO:0071339 p=5.8E−03 n=2 fg=0.04 bg=0.00
transcription regulator complex GO:0005667 p=1.1E−02 n=6 fg=0.13 bg=0.04
dendrite GO:0030425 p=1.3E−02 n=8 fg=0.18 bg=0.07
dendritic tree GO:0097447 p=1.3E−02 n=8 fg=0.18 bg=0.07
perinuclear region of cytoplasm GO:0048471 p=1.4E−02 n=8 fg=0.18 bg=0.07
endoplasmic reticulum protein−containing... GO:0140534 p=2.3E−02 n=3 fg=0.07 bg=0.01
dense core granule membrane GO:0032127 p=2.5E−02 n=1 fg=0.02 bg=0.00
microvesicle GO:1990742 p=2.5E−02 n=1 fg=0.02 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=2.5E−02 n=1 fg=0.02 bg=0.00
dense core granule GO:0031045 p=2.5E−02 n=1 fg=0.02 bg=0.00
bleb GO:0032059 p=2.5E−02 n=1 fg=0.02 bg=0.00
PET complex GO:1990923 p=2.5E−02 n=1 fg=0.02 bg=0.00
hippocampal mossy fiber GO:0097457 p=2.5E−02 n=1 fg=0.02 bg=0.00
molybdopterin synthase complex GO:0019008 p=2.5E−02 n=1 fg=0.02 bg=0.00
piP−body GO:0071547 p=2.5E−02 n=1 fg=0.02 bg=0.00
postsynaptic endosome GO:0098845 p=2.5E−02 n=1 fg=0.02 bg=0.00
postsynaptic recycling endosome GO:0098837 p=2.5E−02 n=1 fg=0.02 bg=0.00
integral component of Golgi membrane GO:0030173 p=2.9E−02 n=2 fg=0.04 bg=0.01
somatodendritic compartment GO:0036477 p=2.9E−02 n=9 fg=0.20 bg=0.10
catalytic complex GO:1902494 p=3.0E−02 n=15 fg=0.33 bg=0.14
intracellular protein−containing complex GO:0140535 p=3.3E−02 n=8 fg=0.18 bg=0.09
intrinsic component of Golgi membrane GO:0031228 p=3.4E−02 n=2 fg=0.04 bg=0.01
polysome GO:0005844 p=3.4E−02 n=2 fg=0.04 bg=0.01
protein−containing complex GO:0032991 p=4.5E−02 n=27 fg=0.60 bg=0.41
protein kinase complex GO:1902911 p=4.6E−02 n=2 fg=0.04 bg=0.01
RNA polymerase II transcription regulato... GO:0090575 p=4.7E−02 n=3 fg=0.07 bg=0.02
cell body GO:0044297 p=4.9E−02 n=7 fg=0.16 bg=0.08
inner dynein arm GO:0036156 p=4.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=45/183 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction