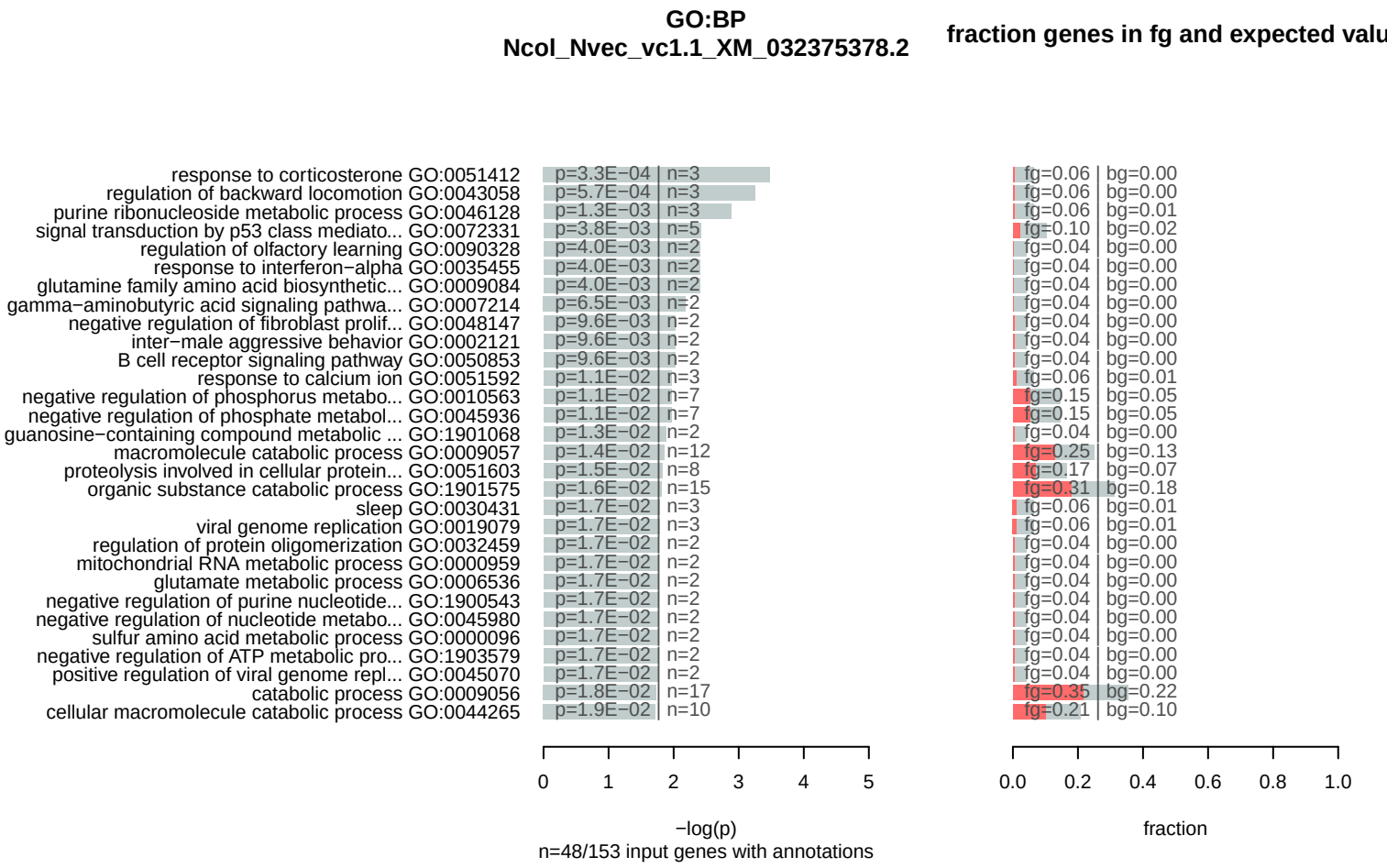
GO:BP
Ncol_Nvec_vc1.1_XM_032375378.2
fraction genes in fg and expected valu
response to corticosterone GO:0051412 p=3.3E−04 n=3 fg=0.06 bg=0.00
regulation of backward locomotion GO:0043058 p=5.7E−04 n=3 fg=0.06 bg=0.00
purine ribonucleoside metabolic process GO:0046128 p=1.3E−03 n=3 fg=0.06 bg=0.01
signal transduction by p53 class mediato... GO:0072331 p=3.8E−03 n=5 fg=0.10 bg=0.02
regulation of olfactory learning GO:0090328 p=4.0E−03 n=2 fg=0.04 bg=0.00
response to interferon−alpha GO:0035455 p=4.0E−03 n=2 fg=0.04 bg=0.00
glutamine family amino acid biosynthetic... GO:0009084 p=4.0E−03 n=2 fg=0.04 bg=0.00
gamma−aminobutyric acid signaling pathwa... GO:0007214 p=6.5E−03 n=2 fg=0.04 bg=0.00
negative regulation of fibroblast prolif... GO:0048147 p=9.6E−03 n=2 fg=0.04 bg=0.00
inter−male aggressive behavior GO:0002121 p=9.6E−03 n=2 fg=0.04 bg=0.00
B cell receptor signaling pathway GO:0050853 p=9.6E−03 n=2 fg=0.04 bg=0.00
response to calcium ion GO:0051592 p=1.1E−02 n=3 fg=0.06 bg=0.01
negative regulation of phosphorus metabo... GO:0010563 p=1.1E−02 n=7 fg=0.15 bg=0.05
negative regulation of phosphate metabol... GO:0045936 p=1.1E−02 n=7 fg=0.15 bg=0.05
guanosine−containing compound metabolic ... GO:1901068 p=1.3E−02 n=2 fg=0.04 bg=0.00
macromolecule catabolic process GO:0009057 p=1.4E−02 n=12 fg=0.25 bg=0.13
proteolysis involved in cellular protein... GO:0051603 p=1.5E−02 n=8 fg=0.17 bg=0.07
organic substance catabolic process GO:1901575 p=1.6E−02 n=15 fg=0.31 bg=0.18
sleep GO:0030431 p=1.7E−02 n=3 fg=0.06 bg=0.01
viral genome replication GO:0019079 p=1.7E−02 n=3 fg=0.06 bg=0.01
regulation of protein oligomerization GO:0032459 p=1.7E−02 n=2 fg=0.04 bg=0.00
mitochondrial RNA metabolic process GO:0000959 p=1.7E−02 n=2 fg=0.04 bg=0.00
glutamate metabolic process GO:0006536 p=1.7E−02 n=2 fg=0.04 bg=0.00
negative regulation of purine nucleotide... GO:1900543 p=1.7E−02 n=2 fg=0.04 bg=0.00
negative regulation of nucleotide metabo... GO:0045980 p=1.7E−02 n=2 fg=0.04 bg=0.00
sulfur amino acid metabolic process GO:0000096 p=1.7E−02 n=2 fg=0.04 bg=0.00
negative regulation of ATP metabolic pro... GO:1903579 p=1.7E−02 n=2 fg=0.04 bg=0.00
positive regulation of viral genome repl... GO:0045070 p=1.7E−02 n=2 fg=0.04 bg=0.00
catabolic process GO:0009056 p=1.8E−02 n=17 fg=0.35 bg=0.22
cellular macromolecule catabolic process GO:0044265 p=1.9E−02 n=10 fg=0.21 bg=0.10
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−log(p)
n=48/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032375378.2
fraction genes in fg and expected valu
GABA−gated chloride ion channel activity GO:0022851 p=2.5E−03 n=2 fg=0.04 bg=0.00
GABA−A receptor activity GO:0004890 p=2.5E−03 n=2 fg=0.04 bg=0.00
benzodiazepine receptor activity GO:0008503 p=2.5E−03 n=2 fg=0.04 bg=0.00
protein binding GO:0005515 p=4.2E−03 n=37 fg=0.79 bg=0.60
identical protein binding GO:0042802 p=1.8E−02 n=14 fg=0.30 bg=0.17
tricarboxylate secondary active transmem... GO:0005371 p=2.9E−02 n=1 fg=0.02 bg=0.00
cysteine−tRNA ligase activity GO:0004817 p=2.9E−02 n=1 fg=0.02 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=2.9E−02 n=1 fg=0.02 bg=0.00
ammonia ligase activity GO:0016211 p=2.9E−02 n=1 fg=0.02 bg=0.00
myosin VI binding GO:0070853 p=2.9E−02 n=1 fg=0.02 bg=0.00
myosin VI heavy chain binding GO:0070854 p=2.9E−02 n=1 fg=0.02 bg=0.00
interferon binding GO:0019961 p=2.9E−02 n=1 fg=0.02 bg=0.00
interferon−gamma binding GO:0019964 p=2.9E−02 n=1 fg=0.02 bg=0.00
mannosyl−oligosaccharide mannosidase act... GO:0015924 p=2.9E−02 n=1 fg=0.02 bg=0.00
glutamate−5−semialdehyde dehydrogenase a... GO:0004350 p=2.9E−02 n=1 fg=0.02 bg=0.00
amino acid kinase activity GO:0019202 p=2.9E−02 n=1 fg=0.02 bg=0.00
carbohydrate phosphatase activity GO:0019203 p=2.9E−02 n=1 fg=0.02 bg=0.00
glutamate−ammonia ligase activity GO:0004356 p=2.9E−02 n=1 fg=0.02 bg=0.00
low−density lipoprotein particle binding GO:0030169 p=2.9E−02 n=1 fg=0.02 bg=0.00
delta1−pyrroline−5−carboxylate synthetas... GO:0017084 p=2.9E−02 n=1 fg=0.02 bg=0.00
sugar−phosphatase activity GO:0050308 p=2.9E−02 n=1 fg=0.02 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=2.9E−02 n=1 fg=0.02 bg=0.00
C−rich single−stranded DNA binding GO:1990829 p=2.9E−02 n=1 fg=0.02 bg=0.00
glutamate 5−kinase activity GO:0004349 p=2.9E−02 n=1 fg=0.02 bg=0.00
fructose−2,6−bisphosphate 2−phosphatase ... GO:0004331 p=2.9E−02 n=1 fg=0.02 bg=0.00
cysteine desulfurase activity GO:0031071 p=2.9E−02 n=1 fg=0.02 bg=0.00
RNA polymerase I core binding GO:0001042 p=2.9E−02 n=1 fg=0.02 bg=0.00
lipoprotein particle receptor activity GO:0030228 p=2.9E−02 n=1 fg=0.02 bg=0.00
7SK snRNA binding GO:0097322 p=2.9E−02 n=1 fg=0.02 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=2.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=47/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032375378.2
fraction genes in fg and expected valu
Cul3−RING ubiquitin ligase complex GO:0031463 p=6.8E−03 n=2 fg=0.04 bg=0.00
membrane−bounded organelle GO:0043227 p=8.0E−03 n=46 fg=0.94 bg=0.81
PML body GO:0016605 p=1.4E−02 n=2 fg=0.04 bg=0.00
cytoplasmic microtubule GO:0005881 p=1.8E−02 n=2 fg=0.04 bg=0.00
BAX complex GO:0097144 p=2.7E−02 n=1 fg=0.02 bg=0.00
Sec61 translocon complex GO:0005784 p=2.7E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=2.7E−02 n=1 fg=0.02 bg=0.00
9+2 non−motile cilium GO:0097732 p=2.7E−02 n=1 fg=0.02 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=2.7E−02 n=1 fg=0.02 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=2.7E−02 n=1 fg=0.02 bg=0.00
translocon complex GO:0071256 p=2.7E−02 n=1 fg=0.02 bg=0.00
L−cysteine desulfurase complex GO:1990221 p=2.7E−02 n=1 fg=0.02 bg=0.00
podocyte foot GO:0098846 p=2.7E−02 n=1 fg=0.02 bg=0.00
dendritic microtubule GO:1901588 p=2.7E−02 n=1 fg=0.02 bg=0.00
kinocilium GO:0060091 p=2.7E−02 n=1 fg=0.02 bg=0.00
condensed nuclear chromosome GO:0000794 p=2.8E−02 n=2 fg=0.04 bg=0.01
integral component of synaptic vesicle m... GO:0030285 p=3.4E−02 n=2 fg=0.04 bg=0.01
endomembrane system GO:0012505 p=3.8E−02 n=23 fg=0.47 bg=0.34
synaptic vesicle GO:0008021 p=3.8E−02 n=4 fg=0.08 bg=0.03
intrinsic component of synaptic vesicle ... GO:0098563 p=4.0E−02 n=2 fg=0.04 bg=0.01
condensed chromosome GO:0000793 p=4.9E−02 n=3 fg=0.06 bg=0.02
neuronal cell body membrane GO:0032809 p=5.3E−02 n=2 fg=0.04 bg=0.01
microtubule GO:0005874 p=5.3E−02 n=3 fg=0.06 bg=0.02
endoplasmic reticulum chaperone complex GO:0034663 p=5.3E−02 n=1 fg=0.02 bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=5.3E−02 n=1 fg=0.02 bg=0.00
mitochondrial permeability transition po... GO:0005757 p=5.3E−02 n=1 fg=0.02 bg=0.00
proteasome regulatory particle, lid subc... GO:0008541 p=5.3E−02 n=1 fg=0.02 bg=0.00
pore complex GO:0046930 p=5.3E−02 n=1 fg=0.02 bg=0.00
U2AF complex GO:0089701 p=5.3E−02 n=1 fg=0.02 bg=0.00
transcription factor AP−1 complex GO:0035976 p=5.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction