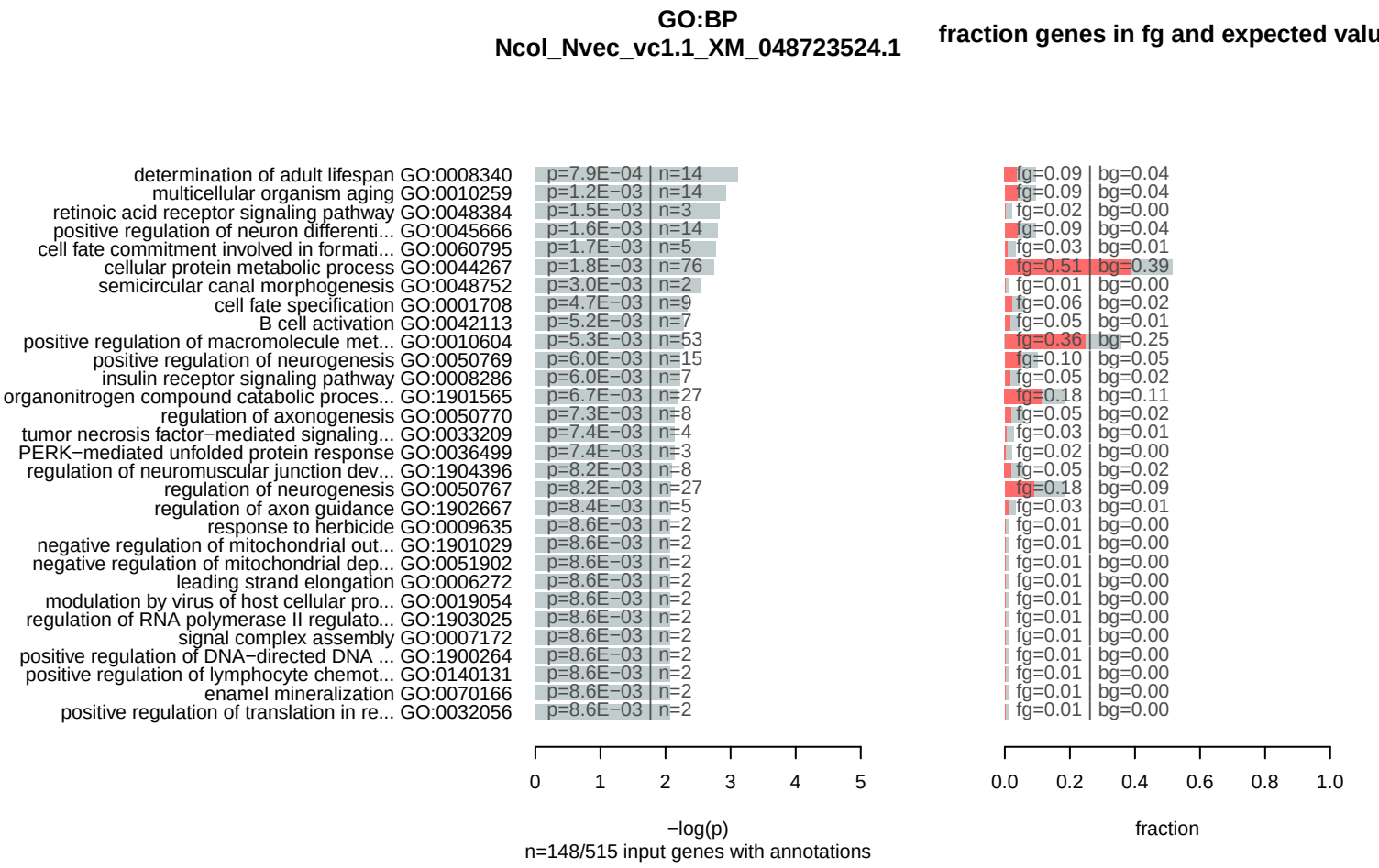
GO:BP
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
determination of adult lifespan GO:0008340 p=7.9E−04 n=14 fg=0.09 bg=0.04
multicellular organism aging GO:0010259 p=1.2E−03 n=14 fg=0.09 bg=0.04
retinoic acid receptor signaling pathway GO:0048384 p=1.5E−03 n=3 fg=0.02 bg=0.00
positive regulation of neuron differenti... GO:0045666 p=1.6E−03 n=14 fg=0.09 bg=0.04
cell fate commitment involved in formati... GO:0060795 p=1.7E−03 n=5 fg=0.03 bg=0.01
cellular protein metabolic process GO:0044267 p=1.8E−03 n=76 fg=0.51 bg=0.39
semicircular canal morphogenesis GO:0048752 p=3.0E−03 n=2 fg=0.01 bg=0.00
cell fate specification GO:0001708 p=4.7E−03 n=9 fg=0.06 bg=0.02
B cell activation GO:0042113 p=5.2E−03 n=7 fg=0.05 bg=0.01
positive regulation of macromolecule met... GO:0010604 p=5.3E−03 n=53 fg=0.36 bg=0.25
positive regulation of neurogenesis GO:0050769 p=6.0E−03 n=15 fg=0.10 bg=0.05
insulin receptor signaling pathway GO:0008286 p=6.0E−03 n=7 fg=0.05 bg=0.02
organonitrogen compound catabolic proces... GO:1901565 p=6.7E−03 n=27 fg=0.18 bg=0.11
regulation of axonogenesis GO:0050770 p=7.3E−03 n=8 fg=0.05 bg=0.02
tumor necrosis factor−mediated signaling... GO:0033209 p=7.4E−03 n=4 fg=0.03 bg=0.01
PERK−mediated unfolded protein response GO:0036499 p=7.4E−03 n=3 fg=0.02 bg=0.00
regulation of neuromuscular junction dev... GO:1904396 p=8.2E−03 n=8 fg=0.05 bg=0.02
regulation of neurogenesis GO:0050767 p=8.2E−03 n=27 fg=0.18 bg=0.09
regulation of axon guidance GO:1902667 p=8.4E−03 n=5 fg=0.03 bg=0.01
response to herbicide GO:0009635 p=8.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of mitochondrial out... GO:1901029 p=8.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of mitochondrial dep... GO:0051902 p=8.6E−03 n=2 fg=0.01 bg=0.00
leading strand elongation GO:0006272 p=8.6E−03 n=2 fg=0.01 bg=0.00
modulation by virus of host cellular pro... GO:0019054 p=8.6E−03 n=2 fg=0.01 bg=0.00
regulation of RNA polymerase II regulato... GO:1903025 p=8.6E−03 n=2 fg=0.01 bg=0.00
signal complex assembly GO:0007172 p=8.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of DNA−directed DNA ... GO:1900264 p=8.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of lymphocyte chemot... GO:0140131 p=8.6E−03 n=2 fg=0.01 bg=0.00
enamel mineralization GO:0070166 p=8.6E−03 n=2 fg=0.01 bg=0.00
positive regulation of translation in re... GO:0032056 p=8.6E−03 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=148/515 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
protease binding GO:0002020 p=7.1E−03 n=5 fg=0.04 bg=0.01
Notch binding GO:0005112 p=8.5E−03 n=3 fg=0.02 bg=0.00
oxo−acid−lyase activity GO:0016833 p=9.6E−03 n=2 fg=0.01 bg=0.00
nuclear retinoic acid receptor binding GO:0042974 p=9.6E−03 n=2 fg=0.01 bg=0.00
transcription coregulator binding GO:0001221 p=1.2E−02 n=3 fg=0.02 bg=0.00
heme binding GO:0020037 p=1.7E−02 n=3 fg=0.02 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=1.7E−02 n=5 fg=0.04 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=1.7E−02 n=5 fg=0.04 bg=0.01
endopeptidase activity GO:0004175 p=1.8E−02 n=6 fg=0.04 bg=0.02
tetrapyrrole binding GO:0046906 p=2.2E−02 n=3 fg=0.02 bg=0.00
eukaryotic initiation factor eIF2 bindin... GO:0071074 p=3.0E−02 n=2 fg=0.01 bg=0.00
misfolded protein binding GO:0051787 p=3.0E−02 n=2 fg=0.01 bg=0.00
JUN kinase binding GO:0008432 p=3.0E−02 n=2 fg=0.01 bg=0.00
transcription coactivator binding GO:0001223 p=3.0E−02 n=2 fg=0.01 bg=0.00
Hsp70 protein binding GO:0030544 p=3.0E−02 n=4 fg=0.03 bg=0.01
transcription coregulator activity GO:0003712 p=3.9E−02 n=12 fg=0.09 bg=0.05
aspartic−type endopeptidase activity GO:0004190 p=4.3E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol phosphate 5−phospha... GO:0034595 p=4.3E−02 n=2 fg=0.01 bg=0.00
Wnt−protein binding GO:0017147 p=4.3E−02 n=2 fg=0.01 bg=0.00
aspartic−type peptidase activity GO:0070001 p=4.3E−02 n=2 fg=0.01 bg=0.00
organic cation transmembrane transporter... GO:0015101 p=4.3E−02 n=2 fg=0.01 bg=0.00
glucuronosyltransferase activity GO:0015020 p=4.3E−02 n=2 fg=0.01 bg=0.00
coreceptor activity GO:0015026 p=4.3E−02 n=2 fg=0.01 bg=0.00
cysteine−type endopeptidase activity GO:0004197 p=4.3E−02 n=3 fg=0.02 bg=0.01
translation initiation factor binding GO:0031369 p=4.3E−02 n=3 fg=0.02 bg=0.01
structural constituent of ribosome GO:0003735 p=4.3E−02 n=7 fg=0.05 bg=0.02
heat shock protein binding GO:0031072 p=5.1E−02 n=6 fg=0.04 bg=0.02
ubiquitin protein ligase binding GO:0031625 p=5.4E−02 n=9 fg=0.07 bg=0.04
calcium−release channel activity GO:0015278 p=5.8E−02 n=2 fg=0.01 bg=0.00
MAP kinase activity GO:0004707 p=5.8E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=137/515 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048723524.1
fraction genes in fg and expected valu
endoplasmic reticulum quality control co... GO:0044322 p=6.3E−04 n=3 fg=0.02 bg=0.00
ribosome GO:0005840 p=1.3E−03 n=11 fg=0.07 bg=0.03
Elg1 RFC−like complex GO:0031391 p=3.0E−03 n=2 fg=0.01 bg=0.00
integral component of mitochondrial memb... GO:0032592 p=3.1E−03 n=4 fg=0.03 bg=0.00
ribonucleoprotein complex GO:1990904 p=5.2E−03 n=23 fg=0.15 bg=0.09
DNA replication factor C complex GO:0005663 p=8.8E−03 n=2 fg=0.01 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=8.8E−03 n=2 fg=0.01 bg=0.00
Cul3−RING ubiquitin ligase complex GO:0031463 p=1.1E−02 n=3 fg=0.02 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=1.7E−02 n=2 fg=0.01 bg=0.00
integral component of lumenal side of en... GO:0071556 p=1.7E−02 n=2 fg=0.01 bg=0.00
cortical endoplasmic reticulum GO:0032541 p=1.7E−02 n=2 fg=0.01 bg=0.00
organellar large ribosomal subunit GO:0000315 p=2.0E−02 n=3 fg=0.02 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=2.0E−02 n=3 fg=0.02 bg=0.00
early endosome membrane GO:0031901 p=2.6E−02 n=4 fg=0.03 bg=0.01
late endosome membrane GO:0031902 p=2.6E−02 n=4 fg=0.03 bg=0.01
lumenal side of membrane GO:0098576 p=2.7E−02 n=2 fg=0.01 bg=0.00
integral component of Golgi membrane GO:0030173 p=3.1E−02 n=3 fg=0.02 bg=0.00
cytosolic ribosome GO:0022626 p=3.8E−02 n=6 fg=0.04 bg=0.02
intrinsic component of mitochondrial inn... GO:0031304 p=3.9E−02 n=2 fg=0.01 bg=0.00
integral component of mitochondrial inne... GO:0031305 p=3.9E−02 n=2 fg=0.01 bg=0.00
intracellular membrane−bounded organelle GO:0043231 p=4.0E−02 n=125 fg=0.84 bg=0.77
integral component of organelle membrane GO:0031301 p=4.0E−02 n=13 fg=0.09 bg=0.04
intracellular organelle GO:0043229 p=4.5E−02 n=134 fg=0.90 bg=0.83
intrinsic component of Golgi membrane GO:0031228 p=4.6E−02 n=3 fg=0.02 bg=0.01
ribosomal subunit GO:0044391 p=4.8E−02 n=7 fg=0.05 bg=0.02
intrinsic component of organelle membran... GO:0031300 p=5.1E−02 n=13 fg=0.09 bg=0.04
cytoplasmic ubiquitin ligase complex GO:0000153 p=5.3E−02 n=2 fg=0.01 bg=0.00
Cul2−RING ubiquitin ligase complex GO:0031462 p=5.3E−02 n=2 fg=0.01 bg=0.00
large ribosomal subunit GO:0015934 p=5.5E−02 n=5 fg=0.03 bg=0.01
Gemini of coiled bodies GO:0097504 p=5.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=149/515 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction