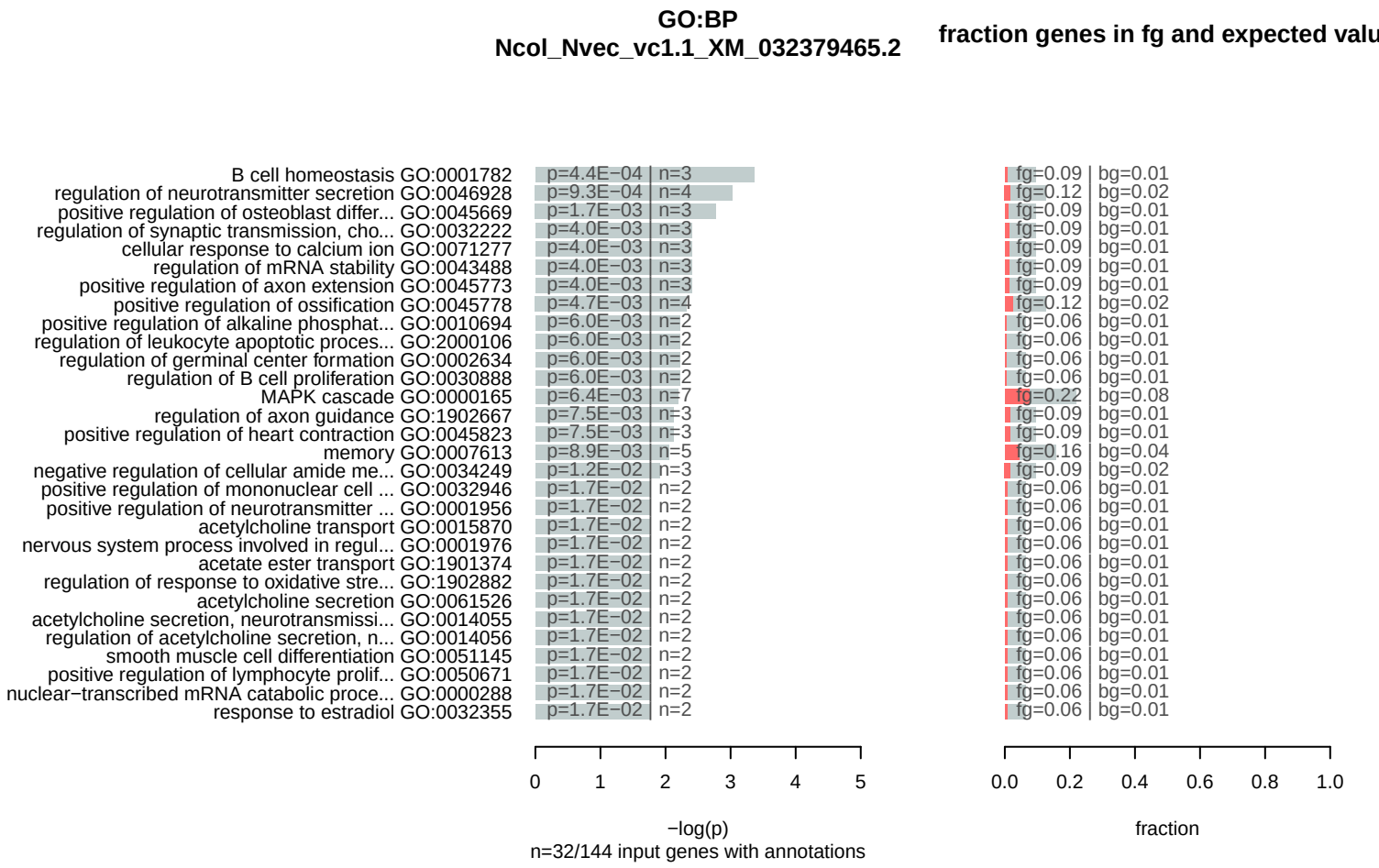
GO:BP
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
B cell homeostasis GO:0001782 p=4.4E−04 n=3 fg=0.09 bg=0.01
regulation of neurotransmitter secretion GO:0046928 p=9.3E−04 n=4 fg=0.12 bg=0.02
positive regulation of osteoblast differ... GO:0045669 p=1.7E−03 n=3 fg=0.09 bg=0.01
regulation of synaptic transmission, cho... GO:0032222 p=4.0E−03 n=3 fg=0.09 bg=0.01
cellular response to calcium ion GO:0071277 p=4.0E−03 n=3 fg=0.09 bg=0.01
regulation of mRNA stability GO:0043488 p=4.0E−03 n=3 fg=0.09 bg=0.01
positive regulation of axon extension GO:0045773 p=4.0E−03 n=3 fg=0.09 bg=0.01
positive regulation of ossification GO:0045778 p=4.7E−03 n=4 fg=0.12 bg=0.02
positive regulation of alkaline phosphat... GO:0010694 p=6.0E−03 n=2 fg=0.06 bg=0.01
regulation of leukocyte apoptotic proces... GO:2000106 p=6.0E−03 n=2 fg=0.06 bg=0.01
regulation of germinal center formation GO:0002634 p=6.0E−03 n=2 fg=0.06 bg=0.01
regulation of B cell proliferation GO:0030888 p=6.0E−03 n=2 fg=0.06 bg=0.01
MAPK cascade GO:0000165 p=6.4E−03 n=7 fg=0.22 bg=0.08
regulation of axon guidance GO:1902667 p=7.5E−03 n=3 fg=0.09 bg=0.01
positive regulation of heart contraction GO:0045823 p=7.5E−03 n=3 fg=0.09 bg=0.01
memory GO:0007613 p=8.9E−03 n=5 fg=0.16 bg=0.04
negative regulation of cellular amide me... GO:0034249 p=1.2E−02 n=3 fg=0.09 bg=0.02
positive regulation of mononuclear cell ... GO:0032946 p=1.7E−02 n=2 fg=0.06 bg=0.01
positive regulation of neurotransmitter ... GO:0001956 p=1.7E−02 n=2 fg=0.06 bg=0.01
acetylcholine transport GO:0015870 p=1.7E−02 n=2 fg=0.06 bg=0.01
nervous system process involved in regul... GO:0001976 p=1.7E−02 n=2 fg=0.06 bg=0.01
acetate ester transport GO:1901374 p=1.7E−02 n=2 fg=0.06 bg=0.01
regulation of response to oxidative stre... GO:1902882 p=1.7E−02 n=2 fg=0.06 bg=0.01
acetylcholine secretion GO:0061526 p=1.7E−02 n=2 fg=0.06 bg=0.01
acetylcholine secretion, neurotransmissi... GO:0014055 p=1.7E−02 n=2 fg=0.06 bg=0.01
regulation of acetylcholine secretion, n... GO:0014056 p=1.7E−02 n=2 fg=0.06 bg=0.01
smooth muscle cell differentiation GO:0051145 p=1.7E−02 n=2 fg=0.06 bg=0.01
positive regulation of lymphocyte prolif... GO:0050671 p=1.7E−02 n=2 fg=0.06 bg=0.01
nuclear−transcribed mRNA catabolic proce... GO:0000288 p=1.7E−02 n=2 fg=0.06 bg=0.01
response to estradiol GO:0032355 p=1.7E−02 n=2 fg=0.06 bg=0.01
0 1 2 3 4 5
−log(p)
n=32/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
ion gated channel activity GO:0022839 p=9.4E−03 n=6 fg=0.22 bg=0.07
extracellular ligand−gated ion channel a... GO:0005230 p=1.6E−02 n=3 fg=0.11 bg=0.02
voltage−gated potassium channel activity GO:0005249 p=2.3E−02 n=3 fg=0.11 bg=0.02
transmitter−gated ion channel activity GO:0022824 p=2.9E−02 n=2 fg=0.07 bg=0.01
transmitter−gated channel activity GO:0022835 p=2.9E−02 n=2 fg=0.07 bg=0.01
ion channel activity GO:0005216 p=3.4E−02 n=6 fg=0.22 bg=0.10
excitatory extracellular ligand−gated io... GO:0005231 p=4.6E−02 n=2 fg=0.07 bg=0.01
DNA−binding transcription factor activit... GO:0000981 p=4.9E−02 n=7 fg=0.26 bg=0.13
potassium channel activity GO:0005267 p=5.1E−02 n=3 fg=0.11 bg=0.03
potassium ion transmembrane transporter ... GO:0015079 p=5.1E−02 n=3 fg=0.11 bg=0.03
cis−regulatory region sequence−specific ... GO:0000987 p=5.1E−02 n=4 fg=0.15 bg=0.05
RNA polymerase II cis−regulatory region ... GO:0000978 p=5.1E−02 n=4 fg=0.15 bg=0.05
DNA−binding transcription factor activit... GO:0003700 p=5.2E−02 n=8 fg=0.30 bg=0.16
protein C−terminus binding GO:0008022 p=6.6E−02 n=2 fg=0.07 bg=0.02
neurotransmitter receptor activity GO:0030594 p=6.6E−02 n=2 fg=0.07 bg=0.02
BH3 domain binding GO:0051434 p=7.4E−02 n=1 fg=0.04 bg=0.00
exonuclease activity GO:0004527 p=7.4E−02 n=1 fg=0.04 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=7.4E−02 n=1 fg=0.04 bg=0.00
nuclear steroid receptor activity GO:0003707 p=7.4E−02 n=1 fg=0.04 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=7.4E−02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=7.4E−02 n=1 fg=0.04 bg=0.00
nuclease activity GO:0004518 p=7.4E−02 n=1 fg=0.04 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=7.4E−02 n=1 fg=0.04 bg=0.00
ribonuclease activity GO:0004540 p=7.4E−02 n=1 fg=0.04 bg=0.00
transmitter−gated ion channel activity i... GO:1904315 p=7.4E−02 n=1 fg=0.04 bg=0.00
exoribonuclease activity GO:0004532 p=7.4E−02 n=1 fg=0.04 bg=0.00
3'−5' exonuclease activity GO:0008408 p=7.4E−02 n=1 fg=0.04 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=7.4E−02 n=1 fg=0.04 bg=0.00
toxic substance binding GO:0015643 p=7.4E−02 n=1 fg=0.04 bg=0.00
histone methyltransferase activity GO:0042054 p=7.4E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=27/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=2.0E−02 n=3 fg=0.09 bg=0.02
potassium channel complex GO:0034705 p=2.0E−02 n=3 fg=0.09 bg=0.02
synaptic vesicle GO:0008021 p=2.4E−02 n=4 fg=0.12 bg=0.04
transporter complex GO:1990351 p=3.1E−02 n=4 fg=0.12 bg=0.04
transmembrane transporter complex GO:1902495 p=3.1E−02 n=4 fg=0.12 bg=0.04
ion channel complex GO:0034702 p=3.1E−02 n=4 fg=0.12 bg=0.04
exocytic vesicle GO:0070382 p=3.1E−02 n=4 fg=0.12 bg=0.04
neuron projection membrane GO:0032589 p=3.8E−02 n=3 fg=0.09 bg=0.03
neuron projection GO:0043005 p=5.3E−02 n=10 fg=0.31 bg=0.19
transport vesicle GO:0030133 p=6.5E−02 n=4 fg=0.12 bg=0.05
acetylcholine−gated channel complex GO:0005892 p=8.0E−02 n=1 fg=0.03 bg=0.00
anchored component of plasma membrane GO:0046658 p=8.0E−02 n=1 fg=0.03 bg=0.00
muscle cell projection GO:0036194 p=8.0E−02 n=1 fg=0.03 bg=0.00
muscle cell projection membrane GO:0036195 p=8.0E−02 n=1 fg=0.03 bg=0.00
septin collar GO:0032173 p=8.0E−02 n=1 fg=0.03 bg=0.00
Bcl−2 family protein complex GO:0097136 p=8.0E−02 n=1 fg=0.03 bg=0.00
9+2 non−motile cilium GO:0097732 p=8.0E−02 n=1 fg=0.03 bg=0.00
smooth muscle contractile fiber GO:0030485 p=8.0E−02 n=1 fg=0.03 bg=0.00
kinocilium GO:0060091 p=8.0E−02 n=1 fg=0.03 bg=0.00
plasma membrane protein complex GO:0098797 p=8.7E−02 n=4 fg=0.12 bg=0.05
leading edge membrane GO:0031256 p=9.1E−02 n=3 fg=0.09 bg=0.03
9+2 motile cilium GO:0097729 p=1.0E−01 n=2 fg=0.06 bg=0.02
sperm flagellum GO:0036126 p=1.0E−01 n=2 fg=0.06 bg=0.02
cation channel complex GO:0034703 p=1.1E−01 n=3 fg=0.09 bg=0.04
cell projection GO:0042995 p=1.1E−01 n=11 fg=0.34 bg=0.24
plasma membrane bounded cell projection GO:0120025 p=1.1E−01 n=11 fg=0.34 bg=0.24
intrinsic component of plasma membrane GO:0031226 p=1.2E−01 n=8 fg=0.25 bg=0.16
secretory vesicle GO:0099503 p=1.2E−01 n=5 fg=0.16 bg=0.08
presynapse GO:0098793 p=1.2E−01 n=5 fg=0.16 bg=0.08
motile cilium GO:0031514 p=1.3E−01 n=2 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=32/144 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction