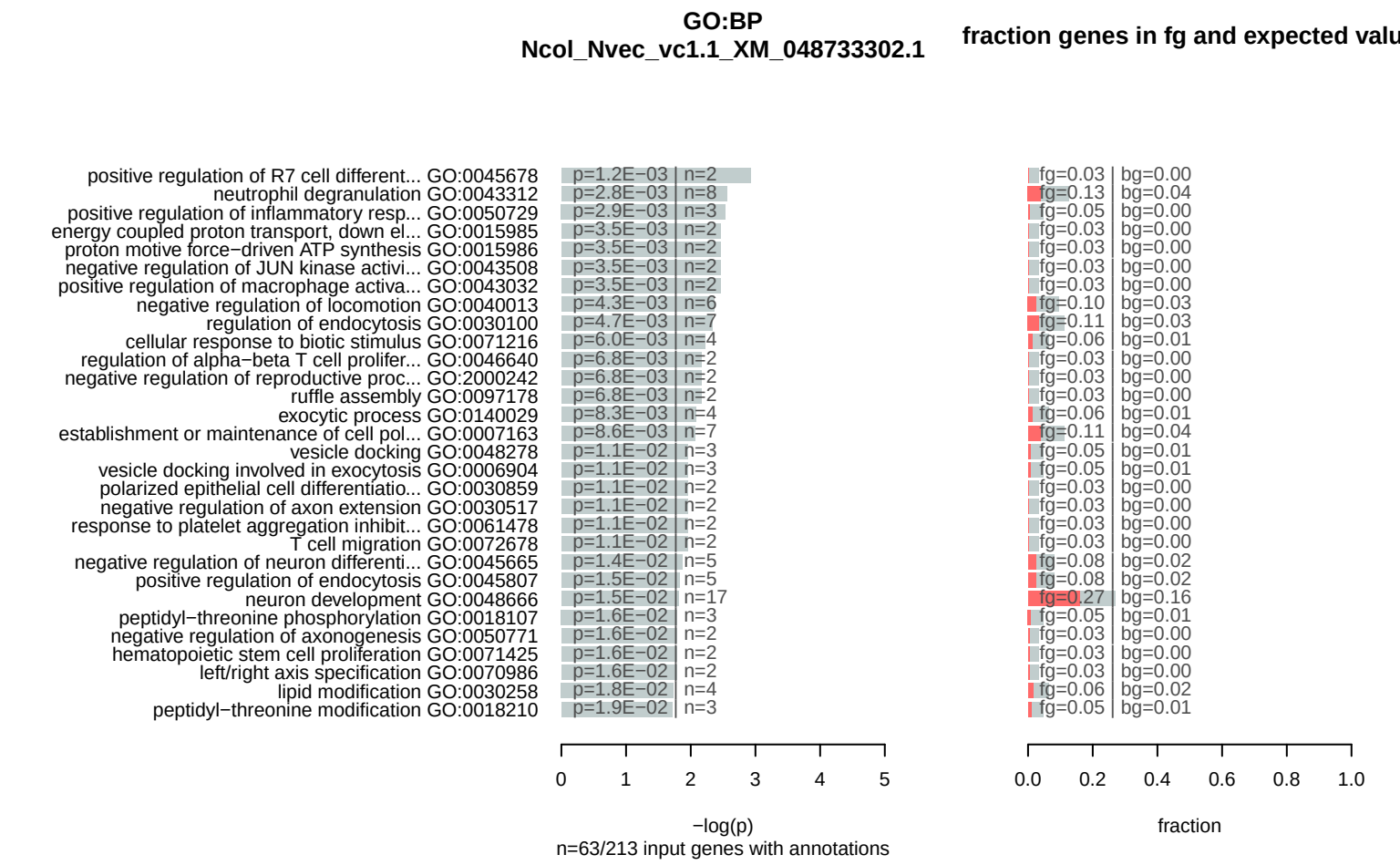
GO:BP
Ncol_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
positive regulation of R7 cell different... GO:0045678 p=1.2E−03 n=2 fg=0.03 bg=0.00
neutrophil degranulation GO:0043312 p=2.8E−03 n=8 fg=0.13 bg=0.04
positive regulation of inflammatory resp... GO:0050729 p=2.9E−03 n=3 fg=0.05 bg=0.00
energy coupled proton transport, down el... GO:0015985 p=3.5E−03 n=2 fg=0.03 bg=0.00
proton motive force−driven ATP synthesis GO:0015986 p=3.5E−03 n=2 fg=0.03 bg=0.00
negative regulation of JUN kinase activi... GO:0043508 p=3.5E−03 n=2 fg=0.03 bg=0.00
positive regulation of macrophage activa... GO:0043032 p=3.5E−03 n=2 fg=0.03 bg=0.00
negative regulation of locomotion GO:0040013 p=4.3E−03 n=6 fg=0.10 bg=0.03
regulation of endocytosis GO:0030100 p=4.7E−03 n=7 fg=0.11 bg=0.03
cellular response to biotic stimulus GO:0071216 p=6.0E−03 n=4 fg=0.06 bg=0.01
regulation of alpha−beta T cell prolifer... GO:0046640 p=6.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of reproductive proc... GO:2000242 p=6.8E−03 n=2 fg=0.03 bg=0.00
ruffle assembly GO:0097178 p=6.8E−03 n=2 fg=0.03 bg=0.00
exocytic process GO:0140029 p=8.3E−03 n=4 fg=0.06 bg=0.01
establishment or maintenance of cell pol... GO:0007163 p=8.6E−03 n=7 fg=0.11 bg=0.04
vesicle docking GO:0048278 p=1.1E−02 n=3 fg=0.05 bg=0.01
vesicle docking involved in exocytosis GO:0006904 p=1.1E−02 n=3 fg=0.05 bg=0.01
polarized epithelial cell differentiatio... GO:0030859 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of axon extension GO:0030517 p=1.1E−02 n=2 fg=0.03 bg=0.00
response to platelet aggregation inhibit... GO:0061478 p=1.1E−02 n=2 fg=0.03 bg=0.00
T cell migration GO:0072678 p=1.1E−02 n=2 fg=0.03 bg=0.00
negative regulation of neuron differenti... GO:0045665 p=1.4E−02 n=5 fg=0.08 bg=0.02
positive regulation of endocytosis GO:0045807 p=1.5E−02 n=5 fg=0.08 bg=0.02
neuron development GO:0048666 p=1.5E−02 n=17 fg=0.27 bg=0.16
peptidyl−threonine phosphorylation GO:0018107 p=1.6E−02 n=3 fg=0.05 bg=0.01
negative regulation of axonogenesis GO:0050771 p=1.6E−02 n=2 fg=0.03 bg=0.00
hematopoietic stem cell proliferation GO:0071425 p=1.6E−02 n=2 fg=0.03 bg=0.00
left/right axis specification GO:0070986 p=1.6E−02 n=2 fg=0.03 bg=0.00
lipid modification GO:0030258 p=1.8E−02 n=4 fg=0.06 bg=0.02
peptidyl−threonine modification GO:0018210 p=1.9E−02 n=3 fg=0.05 bg=0.01
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−log(p)
n=63/213 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
gated channel activity GO:0022836 p=1.4E−02 n=5 fg=0.09 bg=0.03
passive transmembrane transporter activi... GO:0022803 p=1.5E−02 n=6 fg=0.11 bg=0.04
channel activity GO:0015267 p=1.5E−02 n=6 fg=0.11 bg=0.04
transmembrane transporter activity GO:0022857 p=1.9E−02 n=10 fg=0.19 bg=0.09
phosphotyrosine residue binding GO:0001784 p=2.7E−02 n=2 fg=0.04 bg=0.01
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=3.3E−02 n=1 fg=0.02 bg=0.00
aldehyde dehydrogenase (NAD+) activity GO:0004029 p=3.3E−02 n=1 fg=0.02 bg=0.00
aldehyde dehydrogenase [NAD(P)+] activit... GO:0004030 p=3.3E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=3.3E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=3.3E−02 n=1 fg=0.02 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=3.3E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=3.3E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=3.3E−02 n=1 fg=0.02 bg=0.00
chemoattractant activity involved in axo... GO:1902379 p=3.3E−02 n=1 fg=0.02 bg=0.00
Toll−like receptor binding GO:0035325 p=3.3E−02 n=1 fg=0.02 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=3.3E−02 n=1 fg=0.02 bg=0.00
S100 protein binding GO:0044548 p=3.3E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=3.3E−02 n=1 fg=0.02 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=3.3E−02 n=1 fg=0.02 bg=0.00
GDP−dissociation inhibitor binding GO:0051021 p=3.3E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.3E−02 n=1 fg=0.02 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=3.3E−02 n=1 fg=0.02 bg=0.00
inositol bisphosphate phosphatase activi... GO:0016312 p=3.3E−02 n=1 fg=0.02 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=3.3E−02 n=1 fg=0.02 bg=0.00
receptor tyrosine kinase−like orphan rec... GO:0005115 p=3.3E−02 n=1 fg=0.02 bg=0.00
short−branched−chain−acyl−CoA dehydrogen... GO:0016937 p=3.3E−02 n=1 fg=0.02 bg=0.00
protein phosphorylated amino acid bindin... GO:0045309 p=4.1E−02 n=2 fg=0.04 bg=0.01
voltage−gated channel activity GO:0022832 p=4.3E−02 n=3 fg=0.06 bg=0.02
voltage−gated ion channel activity GO:0005244 p=4.3E−02 n=3 fg=0.06 bg=0.02
ion channel activity GO:0005216 p=4.6E−02 n=5 fg=0.09 bg=0.04
0 1 2 3 4 5
−log(p)
n=53/213 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
muscle cell projection membrane GO:0036195 p=3.3E−03 n=2 fg=0.03 bg=0.00
presynapse GO:0098793 p=4.9E−03 n=9 fg=0.15 bg=0.05
phagocytic vesicle GO:0045335 p=5.4E−03 n=4 fg=0.07 bg=0.01
secretory granule membrane GO:0030667 p=7.9E−03 n=5 fg=0.08 bg=0.02
cell periphery GO:0071944 p=8.4E−03 n=28 fg=0.46 bg=0.29
exocytic vesicle GO:0070382 p=9.1E−03 n=6 fg=0.10 bg=0.03
immunological synapse GO:0001772 p=1.1E−02 n=2 fg=0.03 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=1.1E−02 n=10 fg=0.16 bg=0.07
lysosomal membrane GO:0005765 p=1.3E−02 n=5 fg=0.08 bg=0.02
plasma membrane GO:0005886 p=1.5E−02 n=26 fg=0.43 bg=0.27
lytic vacuole membrane GO:0098852 p=1.9E−02 n=5 fg=0.08 bg=0.03
synaptic vesicle GO:0008021 p=2.1E−02 n=5 fg=0.08 bg=0.03
synaptic vesicle membrane GO:0030672 p=2.4E−02 n=3 fg=0.05 bg=0.01
secretory vesicle GO:0099503 p=2.4E−02 n=14 fg=0.23 bg=0.08
striated muscle dense body GO:0055120 p=2.8E−02 n=2 fg=0.03 bg=0.00
exocytic vesicle membrane GO:0099501 p=2.8E−02 n=3 fg=0.05 bg=0.01
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.4E−02 n=1 fg=0.02 bg=0.00
insulin−responsive compartment GO:0032593 p=3.4E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=3.4E−02 n=1 fg=0.02 bg=0.00
actin cortical patch GO:0030479 p=3.4E−02 n=1 fg=0.02 bg=0.00
immunoglobulin complex GO:0019814 p=3.4E−02 n=1 fg=0.02 bg=0.00
B cell receptor complex GO:0019815 p=3.4E−02 n=1 fg=0.02 bg=0.00
endocytic patch GO:0061645 p=3.4E−02 n=1 fg=0.02 bg=0.00
apoptosome GO:0043293 p=3.4E−02 n=1 fg=0.02 bg=0.00
secretory granule GO:0030141 p=3.6E−02 n=10 fg=0.16 bg=0.05
recycling endosome GO:0055037 p=4.0E−02 n=4 fg=0.07 bg=0.02
membrane GO:0016020 p=4.4E−02 n=38 fg=0.62 bg=0.46
integral component of synaptic vesicle m... GO:0030285 p=5.1E−02 n=2 fg=0.03 bg=0.01
Golgi apparatus GO:0005794 p=5.2E−02 n=13 fg=0.21 bg=0.13
vacuolar membrane GO:0005774 p=5.5E−02 n=5 fg=0.08 bg=0.03
0 1 2 3 4 5
−log(p)
n=61/213 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction