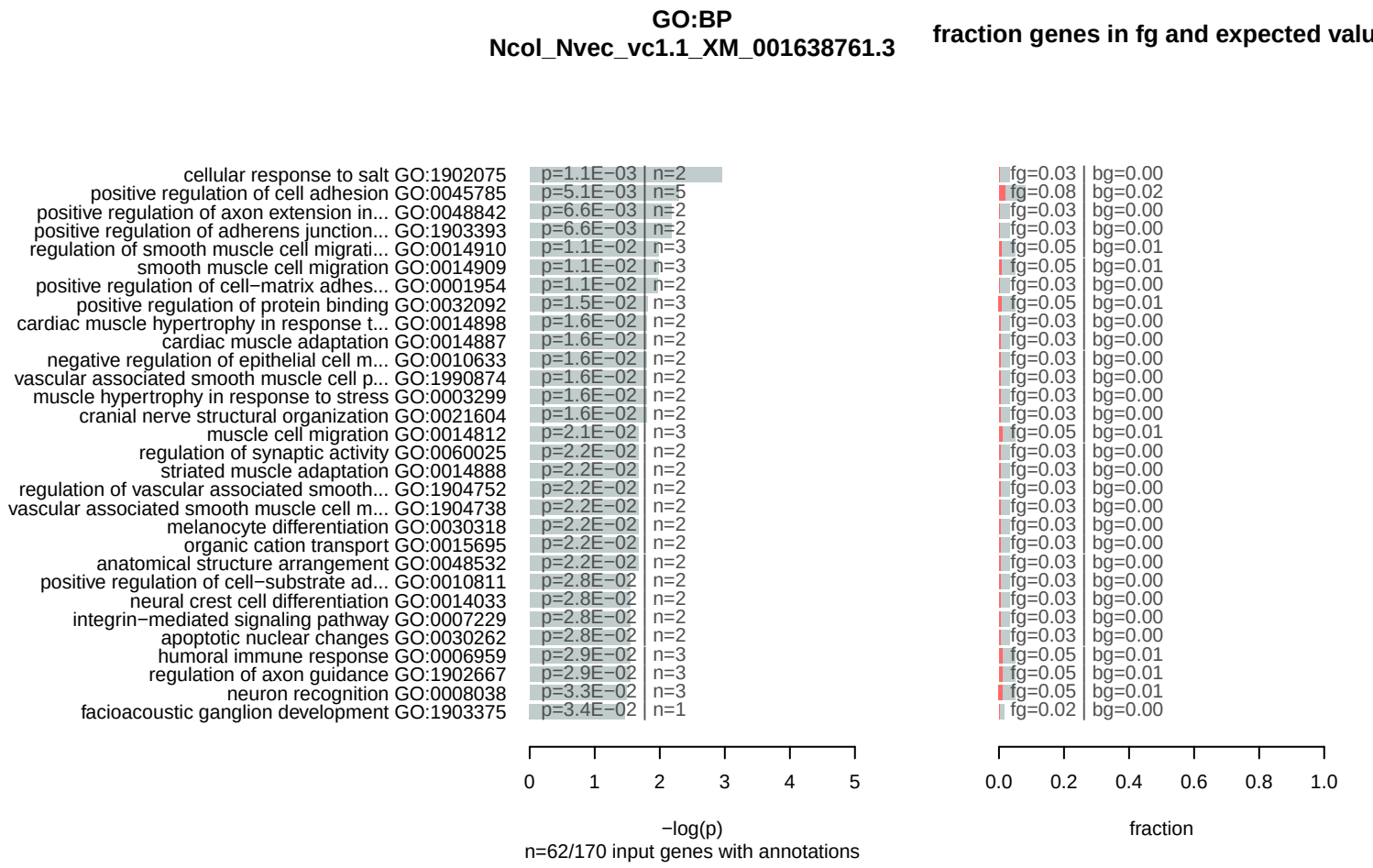
GO:BP
Ncol_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
cellular response to salt GO:1902075 p=1.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of cell adhesion GO:0045785 p=5.1E−03 n=5 fg=0.08 bg=0.02
positive regulation of axon extension in... GO:0048842 p=6.6E−03 n=2 fg=0.03 bg=0.00
positive regulation of adherens junction... GO:1903393 p=6.6E−03 n=2 fg=0.03 bg=0.00
regulation of smooth muscle cell migrati... GO:0014910 p=1.1E−02 n=3 fg=0.05 bg=0.01
smooth muscle cell migration GO:0014909 p=1.1E−02 n=3 fg=0.05 bg=0.01
positive regulation of cell−matrix adhes... GO:0001954 p=1.1E−02 n=2 fg=0.03 bg=0.00
positive regulation of protein binding GO:0032092 p=1.5E−02 n=3 fg=0.05 bg=0.01
cardiac muscle hypertrophy in response t... GO:0014898 p=1.6E−02 n=2 fg=0.03 bg=0.00
cardiac muscle adaptation GO:0014887 p=1.6E−02 n=2 fg=0.03 bg=0.00
negative regulation of epithelial cell m... GO:0010633 p=1.6E−02 n=2 fg=0.03 bg=0.00
vascular associated smooth muscle cell p... GO:1990874 p=1.6E−02 n=2 fg=0.03 bg=0.00
muscle hypertrophy in response to stress GO:0003299 p=1.6E−02 n=2 fg=0.03 bg=0.00
cranial nerve structural organization GO:0021604 p=1.6E−02 n=2 fg=0.03 bg=0.00
muscle cell migration GO:0014812 p=2.1E−02 n=3 fg=0.05 bg=0.01
regulation of synaptic activity GO:0060025 p=2.2E−02 n=2 fg=0.03 bg=0.00
striated muscle adaptation GO:0014888 p=2.2E−02 n=2 fg=0.03 bg=0.00
regulation of vascular associated smooth... GO:1904752 p=2.2E−02 n=2 fg=0.03 bg=0.00
vascular associated smooth muscle cell m... GO:1904738 p=2.2E−02 n=2 fg=0.03 bg=0.00
melanocyte differentiation GO:0030318 p=2.2E−02 n=2 fg=0.03 bg=0.00
organic cation transport GO:0015695 p=2.2E−02 n=2 fg=0.03 bg=0.00
anatomical structure arrangement GO:0048532 p=2.2E−02 n=2 fg=0.03 bg=0.00
positive regulation of cell−substrate ad... GO:0010811 p=2.8E−02 n=2 fg=0.03 bg=0.00
neural crest cell differentiation GO:0014033 p=2.8E−02 n=2 fg=0.03 bg=0.00
integrin−mediated signaling pathway GO:0007229 p=2.8E−02 n=2 fg=0.03 bg=0.00
apoptotic nuclear changes GO:0030262 p=2.8E−02 n=2 fg=0.03 bg=0.00
humoral immune response GO:0006959 p=2.9E−02 n=3 fg=0.05 bg=0.01
regulation of axon guidance GO:1902667 p=2.9E−02 n=3 fg=0.05 bg=0.01
neuron recognition GO:0008038 p=3.3E−02 n=3 fg=0.05 bg=0.01
facioacoustic ganglion development GO:1903375 p=3.4E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=62/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
oxidoreductase activity, acting on paire... GO:0016705 p=2.4E−03 n=3 fg=0.06 bg=0.01
enzyme binding GO:0019899 p=2.8E−03 n=22 fg=0.42 bg=0.24
protein kinase binding GO:0019901 p=1.3E−02 n=9 fg=0.17 bg=0.08
kinase binding GO:0019900 p=1.8E−02 n=9 fg=0.17 bg=0.08
histone deacetylase binding GO:0042826 p=1.9E−02 n=3 fg=0.06 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=2.9E−02 n=3 fg=0.06 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=2.9E−02 n=3 fg=0.06 bg=0.01
heme binding GO:0020037 p=3.3E−02 n=2 fg=0.04 bg=0.01
pentosyltransferase activity GO:0016763 p=3.3E−02 n=2 fg=0.04 bg=0.01
biotin−protein ligase activity GO:0018271 p=3.3E−02 n=1 fg=0.02 bg=0.00
RNA polymerase I core binding GO:0001042 p=3.3E−02 n=1 fg=0.02 bg=0.00
chloride ion binding GO:0031404 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
neurotrophin binding GO:0043121 p=3.3E−02 n=1 fg=0.02 bg=0.00
acyl−CoA desaturase activity GO:0016215 p=3.3E−02 n=1 fg=0.02 bg=0.00
semaphorin receptor activity GO:0017154 p=3.3E−02 n=1 fg=0.02 bg=0.00
translation release factor activity GO:0003747 p=3.3E−02 n=1 fg=0.02 bg=0.00
fatty acid transmembrane transporter act... GO:0015245 p=3.3E−02 n=1 fg=0.02 bg=0.00
short−chain fatty acid transmembrane tra... GO:0015636 p=3.3E−02 n=1 fg=0.02 bg=0.00
biotin binding GO:0009374 p=3.3E−02 n=1 fg=0.02 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=3.3E−02 n=1 fg=0.02 bg=0.00
nucleotide diphosphatase activity GO:0004551 p=3.3E−02 n=1 fg=0.02 bg=0.00
icosanoid receptor activity GO:0004953 p=3.3E−02 n=1 fg=0.02 bg=0.00
prostanoid receptor activity GO:0004954 p=3.3E−02 n=1 fg=0.02 bg=0.00
prostaglandin receptor activity GO:0004955 p=3.3E−02 n=1 fg=0.02 bg=0.00
urate transmembrane transporter activity GO:0015143 p=3.3E−02 n=1 fg=0.02 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=3.3E−02 n=1 fg=0.02 bg=0.00
nerve growth factor binding GO:0048406 p=3.3E−02 n=1 fg=0.02 bg=0.00
vascular endothelial growth factor bindi... GO:0038085 p=3.3E−02 n=1 fg=0.02 bg=0.00
salt transmembrane transporter activity GO:1901702 p=3.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=52/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
Golgi lumen GO:0005796 p=2.9E−02 n=2 fg=0.03 bg=0.00
early endosome GO:0005769 p=3.0E−02 n=6 fg=0.10 bg=0.04
intraciliary transport particle B GO:0030992 p=3.5E−02 n=1 fg=0.02 bg=0.00
Sin3 complex GO:0016580 p=3.5E−02 n=1 fg=0.02 bg=0.00
omegasome GO:1990462 p=3.5E−02 n=1 fg=0.02 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=3.5E−02 n=1 fg=0.02 bg=0.00
integral component of omegasome membrane GO:0097631 p=3.5E−02 n=1 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=3.5E−02 n=1 fg=0.02 bg=0.00
translation preinitiation complex GO:0070993 p=3.5E−02 n=1 fg=0.02 bg=0.00
omegasome membrane GO:1903349 p=3.5E−02 n=1 fg=0.02 bg=0.00
semaphorin receptor complex GO:0002116 p=3.5E−02 n=1 fg=0.02 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.5E−02 n=1 fg=0.02 bg=0.00
cell body fiber GO:0070852 p=6.8E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=6.8E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=6.8E−02 n=1 fg=0.02 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=6.8E−02 n=1 fg=0.02 bg=0.00
neurofilament GO:0005883 p=6.8E−02 n=1 fg=0.02 bg=0.00
cell hair GO:0070451 p=6.8E−02 n=1 fg=0.02 bg=0.00
trans−Golgi network transport vesicle me... GO:0012510 p=6.8E−02 n=1 fg=0.02 bg=0.00
sorting endosome GO:0097443 p=6.8E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=6.8E−02 n=1 fg=0.02 bg=0.00
sarcoplasmic reticulum membrane GO:0033017 p=6.8E−02 n=1 fg=0.02 bg=0.00
extracellular matrix GO:0031012 p=8.3E−02 n=2 fg=0.03 bg=0.01
external encapsulating structure GO:0030312 p=9.4E−02 n=2 fg=0.03 bg=0.01
intraciliary transport particle GO:0030990 p=1.0E−01 n=1 fg=0.02 bg=0.00
intraciliary transport particle A GO:0030991 p=1.0E−01 n=1 fg=0.02 bg=0.00
nuclear lamina GO:0005652 p=1.0E−01 n=1 fg=0.02 bg=0.00
Sin3−type complex GO:0070822 p=1.0E−01 n=1 fg=0.02 bg=0.00
intermediate filament GO:0005882 p=1.0E−01 n=1 fg=0.02 bg=0.00
growth cone membrane GO:0032584 p=1.0E−01 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=63/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction