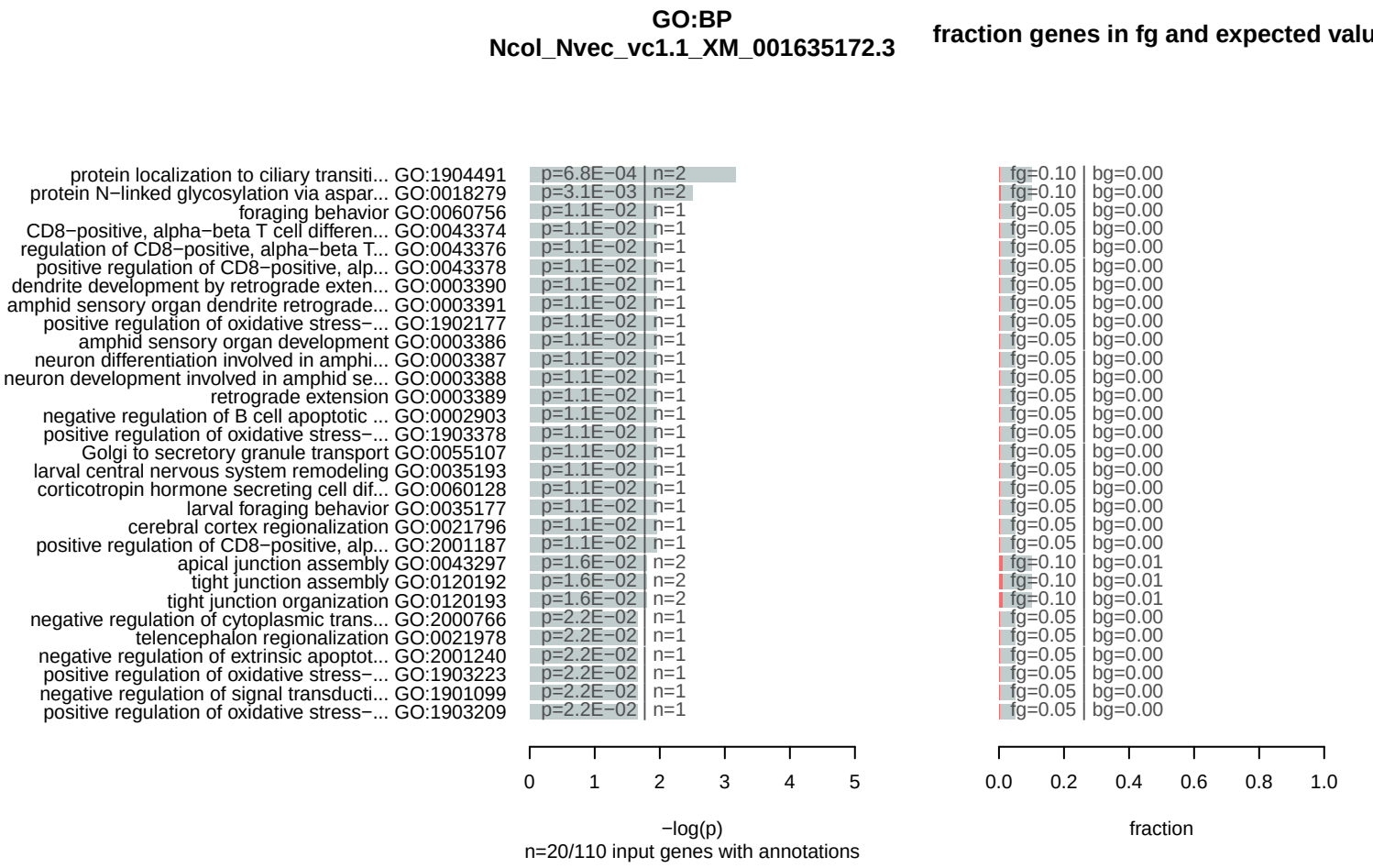
GO:BP
Ncol_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
protein localization to ciliary transiti... GO:1904491 p=6.8E−04 n=2 fg=0.10 bg=0.00
protein N−linked glycosylation via aspar... GO:0018279 p=3.1E−03 n=2 fg=0.10 bg=0.00
foraging behavior GO:0060756 p=1.1E−02 n=1 fg=0.05 bg=0.00
CD8−positive, alpha−beta T cell differen... GO:0043374 p=1.1E−02 n=1 fg=0.05 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:0043376 p=1.1E−02 n=1 fg=0.05 bg=0.00
positive regulation of CD8−positive, alp... GO:0043378 p=1.1E−02 n=1 fg=0.05 bg=0.00
dendrite development by retrograde exten... GO:0003390 p=1.1E−02 n=1 fg=0.05 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=1.1E−02 n=1 fg=0.05 bg=0.00
positive regulation of oxidative stress−... GO:1902177 p=1.1E−02 n=1 fg=0.05 bg=0.00
amphid sensory organ development GO:0003386 p=1.1E−02 n=1 fg=0.05 bg=0.00
neuron differentiation involved in amphi... GO:0003387 p=1.1E−02 n=1 fg=0.05 bg=0.00
neuron development involved in amphid se... GO:0003388 p=1.1E−02 n=1 fg=0.05 bg=0.00
retrograde extension GO:0003389 p=1.1E−02 n=1 fg=0.05 bg=0.00
negative regulation of B cell apoptotic ... GO:0002903 p=1.1E−02 n=1 fg=0.05 bg=0.00
positive regulation of oxidative stress−... GO:1903378 p=1.1E−02 n=1 fg=0.05 bg=0.00
Golgi to secretory granule transport GO:0055107 p=1.1E−02 n=1 fg=0.05 bg=0.00
larval central nervous system remodeling GO:0035193 p=1.1E−02 n=1 fg=0.05 bg=0.00
corticotropin hormone secreting cell dif... GO:0060128 p=1.1E−02 n=1 fg=0.05 bg=0.00
larval foraging behavior GO:0035177 p=1.1E−02 n=1 fg=0.05 bg=0.00
cerebral cortex regionalization GO:0021796 p=1.1E−02 n=1 fg=0.05 bg=0.00
positive regulation of CD8−positive, alp... GO:2001187 p=1.1E−02 n=1 fg=0.05 bg=0.00
apical junction assembly GO:0043297 p=1.6E−02 n=2 fg=0.10 bg=0.01
tight junction assembly GO:0120192 p=1.6E−02 n=2 fg=0.10 bg=0.01
tight junction organization GO:0120193 p=1.6E−02 n=2 fg=0.10 bg=0.01
negative regulation of cytoplasmic trans... GO:2000766 p=2.2E−02 n=1 fg=0.05 bg=0.00
telencephalon regionalization GO:0021978 p=2.2E−02 n=1 fg=0.05 bg=0.00
negative regulation of extrinsic apoptot... GO:2001240 p=2.2E−02 n=1 fg=0.05 bg=0.00
positive regulation of oxidative stress−... GO:1903223 p=2.2E−02 n=1 fg=0.05 bg=0.00
negative regulation of signal transducti... GO:1901099 p=2.2E−02 n=1 fg=0.05 bg=0.00
positive regulation of oxidative stress−... GO:1903209 p=2.2E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=20/110 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=1.3E−02 n=1 fg=0.05 bg=0.00
dynein light intermediate chain binding GO:0051959 p=1.3E−02 n=1 fg=0.05 bg=0.00
hedgehog receptor activity GO:0008158 p=1.3E−02 n=1 fg=0.05 bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581 p=1.3E−02 n=1 fg=0.05 bg=0.00
UDP−glycosyltransferase activity GO:0008194 p=2.5E−02 n=2 fg=0.10 bg=0.01
caspase binding GO:0089720 p=2.5E−02 n=1 fg=0.05 bg=0.00
oligosaccharyl transferase activity GO:0004576 p=2.5E−02 n=1 fg=0.05 bg=0.00
BH3 domain binding GO:0051434 p=2.5E−02 n=1 fg=0.05 bg=0.00
protein transporter activity GO:0140318 p=3.7E−02 n=1 fg=0.05 bg=0.00
GABA−A receptor activity GO:0004890 p=3.7E−02 n=1 fg=0.05 bg=0.00
catalytic activity, acting on a glycopro... GO:0140103 p=3.7E−02 n=1 fg=0.05 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=3.7E−02 n=1 fg=0.05 bg=0.00
UDP−glucosyltransferase activity GO:0035251 p=3.7E−02 n=1 fg=0.05 bg=0.00
GABA−gated chloride ion channel activity GO:0022851 p=3.7E−02 n=1 fg=0.05 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=3.7E−02 n=1 fg=0.05 bg=0.00
death domain binding GO:0070513 p=3.7E−02 n=1 fg=0.05 bg=0.00
GABA receptor activity GO:0016917 p=3.7E−02 n=1 fg=0.05 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=3.7E−02 n=1 fg=0.05 bg=0.00
benzodiazepine receptor activity GO:0008503 p=3.7E−02 n=1 fg=0.05 bg=0.00
hexosyltransferase activity GO:0016758 p=4.4E−02 n=2 fg=0.10 bg=0.02
actin monomer binding GO:0003785 p=4.9E−02 n=1 fg=0.05 bg=0.00
translation repressor activity GO:0030371 p=4.9E−02 n=1 fg=0.05 bg=0.00
aminopeptidase activity GO:0004177 p=4.9E−02 n=1 fg=0.05 bg=0.00
glucosyltransferase activity GO:0046527 p=4.9E−02 n=1 fg=0.05 bg=0.00
transmitter−gated channel activity GO:0022835 p=6.1E+02 n=1 fg=0.05 bg=0.00
RNA polymerase II complex binding GO:0000993 p=6.1E+02 n=1 fg=0.05 bg=0.00
transmitter−gated ion channel activity GO:0022824 p=6.1E+02 n=1 fg=0.05 bg=0.00
acetylglucosaminyltransferase activity GO:0008375 p=6.1E+02 n=1 fg=0.05 bg=0.00
BH domain binding GO:0051400 p=6.1E+02 n=1 fg=0.05 bg=0.00
ubiquitin−ubiquitin ligase activity GO:0034450 p=6.1E+02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=20/110 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001635172.3
fraction genes in fg and expected valu
core−binding factor complex GO:0016513 p=1.3E−02 n=1 fg=0.04 bg=0.00
synaptic vesicle membrane GO:0030672 p=2.3E−02 n=2 fg=0.09 bg=0.01
anchored component of plasma membrane GO:0046658 p=2.5E−02 n=1 fg=0.04 bg=0.00
exocytic vesicle membrane GO:0099501 p=2.6E−02 n=2 fg=0.09 bg=0.01
centrosome GO:0005813 p=2.6E−02 n=4 fg=0.17 bg=0.05
spot adherens junction GO:0005914 p=3.8E−02 n=1 fg=0.04 bg=0.00
Bcl−2 family protein complex GO:0097136 p=3.8E−02 n=1 fg=0.04 bg=0.00
ciliary basal body GO:0036064 p=4.5E−02 n=2 fg=0.09 bg=0.01
zonula adherens GO:0005915 p=5.0E−02 n=1 fg=0.04 bg=0.00
transport vesicle membrane GO:0030658 p=5.8E+02 n=2 fg=0.09 bg=0.02
microtubule organizing center GO:0005815 p=6.1E+02 n=4 fg=0.17 bg=0.07
messenger ribonucleoprotein complex GO:1990124 p=6.2E+02 n=1 fg=0.04 bg=0.00
anchored component of membrane GO:0031225 p=6.2E+02 n=1 fg=0.04 bg=0.00
sensory dendrite GO:0071683 p=6.2E+02 n=1 fg=0.04 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=6.4E+02 n=2 fg=0.09 bg=0.02
microtubule cytoskeleton GO:0015630 p=7.1E−02 n=5 fg=0.22 bg=0.10
MKS complex GO:0036038 p=9.7E−02 n=1 fg=0.04 bg=0.00
cytoplasmic microtubule GO:0005881 p=9.7E−02 n=1 fg=0.04 bg=0.00
Golgi lumen GO:0005796 p=9.7E−02 n=1 fg=0.04 bg=0.00
synaptic vesicle GO:0008021 p=1.2E−01 n=2 fg=0.09 bg=0.03
integral component of synaptic vesicle m... GO:0030285 p=1.3E−01 n=1 fg=0.04 bg=0.01
intrinsic component of synaptic vesicle ... GO:0098563 p=1.4E−01 n=1 fg=0.04 bg=0.01
exocytic vesicle GO:0070382 p=1.5E−01 n=2 fg=0.09 bg=0.03
Golgi medial cisterna GO:0005797 p=1.5E−01 n=1 fg=0.04 bg=0.01
neuronal cell body membrane GO:0032809 p=1.7E−01 n=1 fg=0.04 bg=0.01
neuron projection membrane GO:0032589 p=1.7E−01 n=1 fg=0.04 bg=0.01
extracellular exosome GO:0070062 p=1.7E−01 n=1 fg=0.04 bg=0.01
cell body membrane GO:0044298 p=1.7E−01 n=1 fg=0.04 bg=0.01
Golgi apparatus GO:0005794 p=1.8E−01 n=5 fg=0.22 bg=0.13
extracellular membrane−bounded organelle GO:0065010 p=1.9E−01 n=1 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=23/110 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction