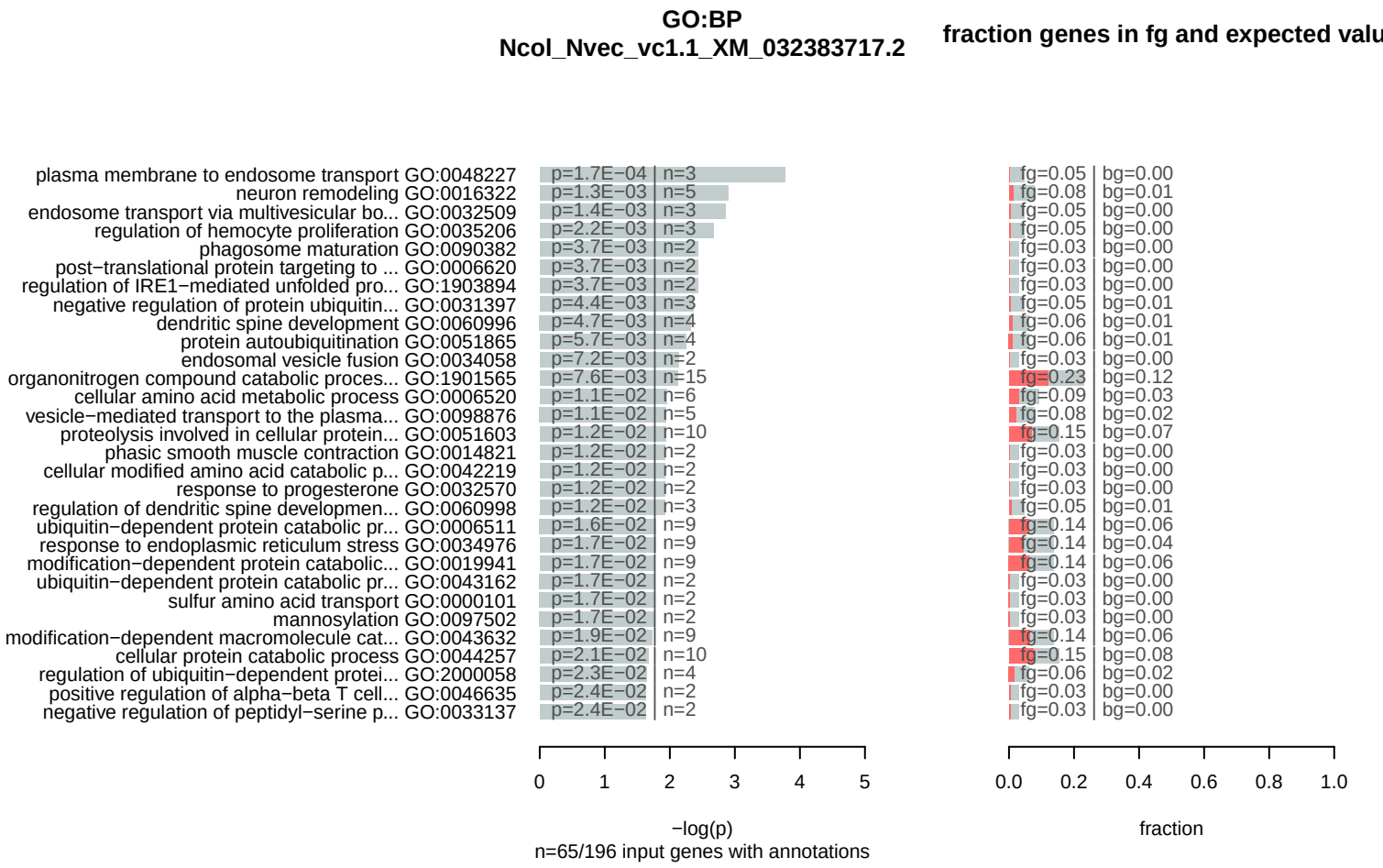
GO:BP
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
plasma membrane to endosome transport GO:0048227 p=1.7E−04 n=3 fg=0.05 bg=0.00
neuron remodeling GO:0016322 p=1.3E−03 n=5 fg=0.08 bg=0.01
endosome transport via multivesicular bo... GO:0032509 p=1.4E−03 n=3 fg=0.05 bg=0.00
regulation of hemocyte proliferation GO:0035206 p=2.2E−03 n=3 fg=0.05 bg=0.00
phagosome maturation GO:0090382 p=3.7E−03 n=2 fg=0.03 bg=0.00
post−translational protein targeting to ... GO:0006620 p=3.7E−03 n=2 fg=0.03 bg=0.00
regulation of IRE1−mediated unfolded pro... GO:1903894 p=3.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of protein ubiquitin... GO:0031397 p=4.4E−03 n=3 fg=0.05 bg=0.01
dendritic spine development GO:0060996 p=4.7E−03 n=4 fg=0.06 bg=0.01
protein autoubiquitination GO:0051865 p=5.7E−03 n=4 fg=0.06 bg=0.01
endosomal vesicle fusion GO:0034058 p=7.2E−03 n=2 fg=0.03 bg=0.00
organonitrogen compound catabolic proces... GO:1901565 p=7.6E−03 n=15 fg=0.23 bg=0.12
cellular amino acid metabolic process GO:0006520 p=1.1E−02 n=6 fg=0.09 bg=0.03
vesicle−mediated transport to the plasma... GO:0098876 p=1.1E−02 n=5 fg=0.08 bg=0.02
proteolysis involved in cellular protein... GO:0051603 p=1.2E−02 n=10 fg=0.15 bg=0.07
phasic smooth muscle contraction GO:0014821 p=1.2E−02 n=2 fg=0.03 bg=0.00
cellular modified amino acid catabolic p... GO:0042219 p=1.2E−02 n=2 fg=0.03 bg=0.00
response to progesterone GO:0032570 p=1.2E−02 n=2 fg=0.03 bg=0.00
regulation of dendritic spine developmen... GO:0060998 p=1.2E−02 n=3 fg=0.05 bg=0.01
ubiquitin−dependent protein catabolic pr... GO:0006511 p=1.6E−02 n=9 fg=0.14 bg=0.06
response to endoplasmic reticulum stress GO:0034976 p=1.7E−02 n=9 fg=0.14 bg=0.04
modification−dependent protein catabolic... GO:0019941 p=1.7E−02 n=9 fg=0.14 bg=0.06
ubiquitin−dependent protein catabolic pr... GO:0043162 p=1.7E−02 n=2 fg=0.03 bg=0.00
sulfur amino acid transport GO:0000101 p=1.7E−02 n=2 fg=0.03 bg=0.00
mannosylation GO:0097502 p=1.7E−02 n=2 fg=0.03 bg=0.00
modification−dependent macromolecule cat... GO:0043632 p=1.9E−02 n=9 fg=0.14 bg=0.06
cellular protein catabolic process GO:0044257 p=2.1E−02 n=10 fg=0.15 bg=0.08
regulation of ubiquitin−dependent protei... GO:2000058 p=2.3E−02 n=4 fg=0.06 bg=0.02
positive regulation of alpha−beta T cell... GO:0046635 p=2.4E−02 n=2 fg=0.03 bg=0.00
negative regulation of peptidyl−serine p... GO:0033137 p=2.4E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/196 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
acetyltransferase activity GO:0016407 p=9.5E−04 n=4 fg=0.07 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=3.5E−03 n=4 fg=0.07 bg=0.01
UDP−glycosyltransferase activity GO:0008194 p=5.3E−03 n=4 fg=0.07 bg=0.01
acetylglucosaminyltransferase activity GO:0008375 p=1.3E−02 n=2 fg=0.03 bg=0.00
hexosyltransferase activity GO:0016758 p=1.6E−02 n=4 fg=0.07 bg=0.02
sulfur amino acid transmembrane transpor... GO:0000099 p=1.8E−02 n=2 fg=0.03 bg=0.00
translation factor activity, RNA binding GO:0008135 p=1.9E−02 n=3 fg=0.05 bg=0.01
N−acetyltransferase activity GO:0008080 p=2.5E−02 n=2 fg=0.03 bg=0.00
neutral amino acid transmembrane transpo... GO:0015175 p=3.3E−02 n=2 fg=0.03 bg=0.01
ligase activity, forming carbon−oxygen b... GO:0016875 p=3.3E−02 n=2 fg=0.03 bg=0.01
N−acyltransferase activity GO:0016410 p=3.3E−02 n=2 fg=0.03 bg=0.01
GTPase activating protein binding GO:0032794 p=3.3E−02 n=2 fg=0.03 bg=0.01
aminoacyl−tRNA ligase activity GO:0004812 p=3.3E−02 n=2 fg=0.03 bg=0.01
L−leucine transmembrane transporter acti... GO:0015190 p=3.7E−02 n=1 fg=0.02 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=3.7E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.7E−02 n=1 fg=0.02 bg=0.00
acyl−CoA desaturase activity GO:0016215 p=3.7E−02 n=1 fg=0.02 bg=0.00
ankyrin repeat binding GO:0071532 p=3.7E−02 n=1 fg=0.02 bg=0.00
methionine transmembrane transporter act... GO:0043865 p=3.7E−02 n=1 fg=0.02 bg=0.00
macrophage migration inhibitory factor b... GO:0035718 p=3.7E−02 n=1 fg=0.02 bg=0.00
glutamate 5−kinase activity GO:0004349 p=3.7E−02 n=1 fg=0.02 bg=0.00
translation release factor activity GO:0003747 p=3.7E−02 n=1 fg=0.02 bg=0.00
ubiquitin modification−dependent histone... GO:0061649 p=3.7E−02 n=1 fg=0.02 bg=0.00
L−asparagine transmembrane transporter a... GO:0015182 p=3.7E−02 n=1 fg=0.02 bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183 p=3.7E−02 n=1 fg=0.02 bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186 p=3.7E−02 n=1 fg=0.02 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=3.7E−02 n=1 fg=0.02 bg=0.00
phospholipase D activator activity GO:1990583 p=3.7E−02 n=1 fg=0.02 bg=0.00
acidic amino acid transmembrane transpor... GO:0015172 p=3.7E−02 n=1 fg=0.02 bg=0.00
4−hydroxy−2−oxoglutarate aldolase activi... GO:0008700 p=3.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=59/196 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032383717.2
fraction genes in fg and expected valu
anchored component of membrane GO:0031225 p=1.2E−02 n=2 fg=0.03 bg=0.00
endoplasmic reticulum subcompartment GO:0098827 p=1.3E−02 n=11 fg=0.17 bg=0.08
endocytic vesicle GO:0030139 p=2.6E−02 n=5 fg=0.08 bg=0.03
endoplasmic reticulum membrane GO:0005789 p=2.6E−02 n=10 fg=0.15 bg=0.08
nuclear outer membrane−endoplasmic retic... GO:0042175 p=2.9E−02 n=10 fg=0.15 bg=0.08
fibrillar center GO:0001650 p=3.0E−02 n=3 fg=0.05 bg=0.01
fusome GO:0045169 p=3.2E−02 n=2 fg=0.03 bg=0.00
periciliary membrane compartment GO:1990075 p=3.6E−02 n=1 fg=0.02 bg=0.00
translation preinitiation complex GO:0070993 p=3.6E−02 n=1 fg=0.02 bg=0.00
core−binding factor complex GO:0016513 p=3.6E−02 n=1 fg=0.02 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=3.6E−02 n=1 fg=0.02 bg=0.00
endocytic vesicle lumen GO:0071682 p=3.6E−02 n=1 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=3.6E−02 n=1 fg=0.02 bg=0.00
cytoplasmic vesicle lumen GO:0060205 p=4.7E−02 n=4 fg=0.06 bg=0.02
vesicle lumen GO:0031983 p=4.7E−02 n=4 fg=0.06 bg=0.02
ESCRT complex GO:0036452 p=4.9E−02 n=2 fg=0.03 bg=0.01
azurophil granule GO:0042582 p=5.4E−02 n=3 fg=0.05 bg=0.01
primary lysosome GO:0005766 p=5.4E−02 n=3 fg=0.05 bg=0.01
secretory vesicle GO:0099503 p=5.9E−02 n=9 fg=0.14 bg=0.08
cytoplasmic vesicle GO:0031410 p=7.1E−02 n=17 fg=0.26 bg=0.18
intracellular vesicle GO:0097708 p=7.1E−02 n=17 fg=0.26 bg=0.18
anchored component of plasma membrane GO:0046658 p=7.2E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005850 p=7.2E−02 n=1 fg=0.02 bg=0.00
eukaryotic translation initiation factor... GO:0005852 p=7.2E−02 n=1 fg=0.02 bg=0.00
HULC complex GO:0033503 p=7.2E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=7.2E−02 n=1 fg=0.02 bg=0.00
COP9 signalosome GO:0008180 p=7.2E−02 n=1 fg=0.02 bg=0.00
ESCRT I complex GO:0000813 p=7.2E−02 n=1 fg=0.02 bg=0.00
endosome membrane GO:0010008 p=7.6E−02 n=5 fg=0.08 bg=0.03
organelle subcompartment GO:0031984 p=7.8E−02 n=14 fg=0.21 bg=0.14
0 1 2 3 4 5
−log(p)
n=66/196 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction