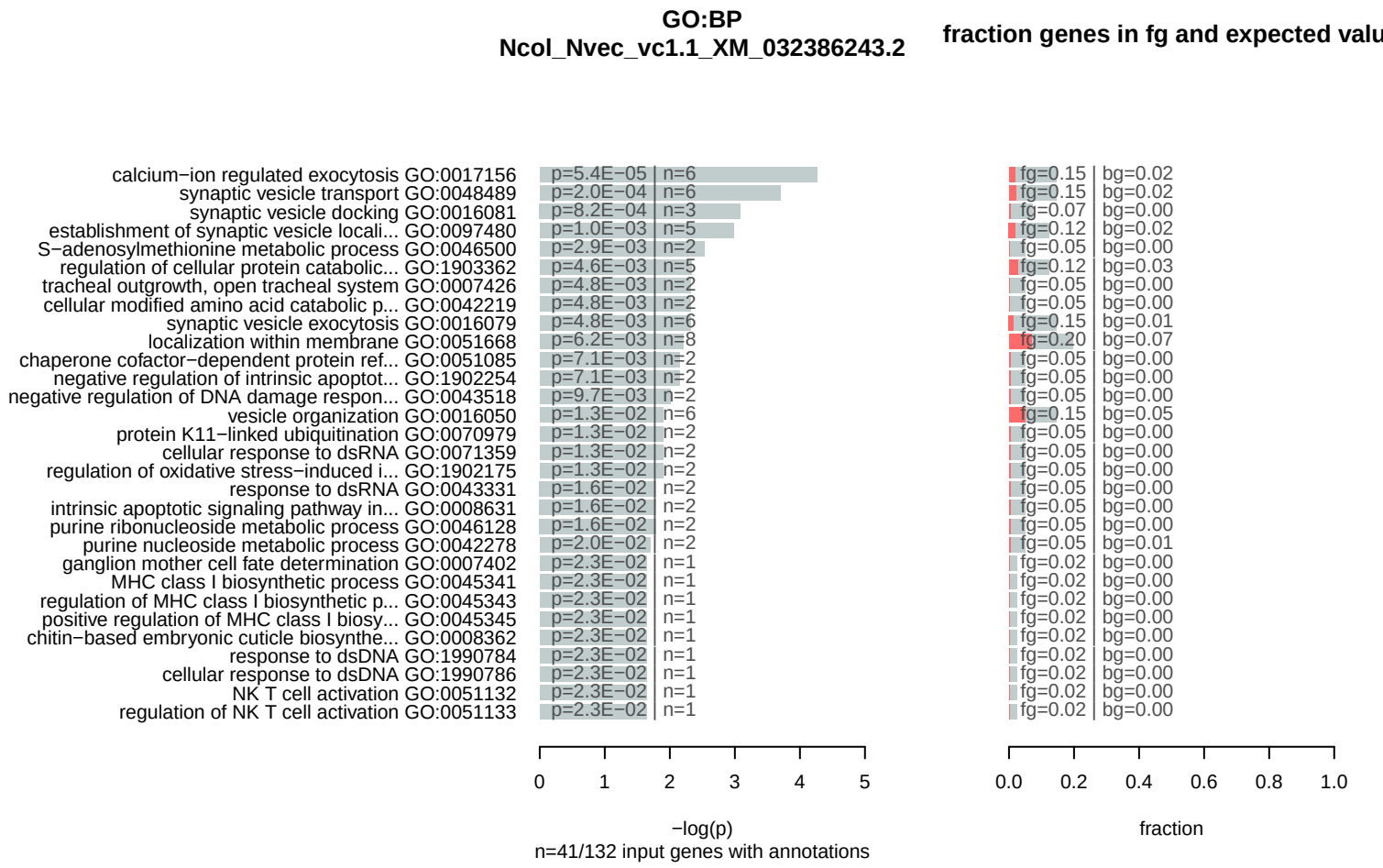
GO:BP
Ncol_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
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synaptic vesicle transport GO:0048489 p=2.0E−04 n=6 fg=0.15 bg=0.02
synaptic vesicle docking GO:0016081 p=8.2E−04 n=3 fg=0.07 bg=0.00
establishment of synaptic vesicle locali... GO:0097480 p=1.0E−03 n=5 fg=0.12 bg=0.02
S−adenosylmethionine metabolic process GO:0046500 p=2.9E−03 n=2 fg=0.05 bg=0.00
regulation of cellular protein catabolic... GO:1903362 p=4.6E−03 n=5 fg=0.12 bg=0.03
tracheal outgrowth, open tracheal system GO:0007426 p=4.8E−03 n=2 fg=0.05 bg=0.00
cellular modified amino acid catabolic p... GO:0042219 p=4.8E−03 n=2 fg=0.05 bg=0.00
synaptic vesicle exocytosis GO:0016079 p=4.8E−03 n=6 fg=0.15 bg=0.01
localization within membrane GO:0051668 p=6.2E−03 n=8 fg=0.20 bg=0.07
chaperone cofactor−dependent protein ref... GO:0051085 p=7.1E−03 n=2 fg=0.05 bg=0.00
negative regulation of intrinsic apoptot... GO:1902254 p=7.1E−03 n=2 fg=0.05 bg=0.00
negative regulation of DNA damage respon... GO:0043518 p=9.7E−03 n=2 fg=0.05 bg=0.00
vesicle organization GO:0016050 p=1.3E−02 n=6 fg=0.15 bg=0.05
protein K11−linked ubiquitination GO:0070979 p=1.3E−02 n=2 fg=0.05 bg=0.00
cellular response to dsRNA GO:0071359 p=1.3E−02 n=2 fg=0.05 bg=0.00
regulation of oxidative stress−induced i... GO:1902175 p=1.3E−02 n=2 fg=0.05 bg=0.00
response to dsRNA GO:0043331 p=1.6E−02 n=2 fg=0.05 bg=0.00
intrinsic apoptotic signaling pathway in... GO:0008631 p=1.6E−02 n=2 fg=0.05 bg=0.00
purine ribonucleoside metabolic process GO:0046128 p=1.6E−02 n=2 fg=0.05 bg=0.00
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ganglion mother cell fate determination GO:0007402 p=2.3E−02 n=1 fg=0.02 bg=0.00
MHC class I biosynthetic process GO:0045341 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of MHC class I biosynthetic p... GO:0045343 p=2.3E−02 n=1 fg=0.02 bg=0.00
positive regulation of MHC class I biosy... GO:0045345 p=2.3E−02 n=1 fg=0.02 bg=0.00
chitin−based embryonic cuticle biosynthe... GO:0008362 p=2.3E−02 n=1 fg=0.02 bg=0.00
response to dsDNA GO:1990784 p=2.3E−02 n=1 fg=0.02 bg=0.00
cellular response to dsDNA GO:1990786 p=2.3E−02 n=1 fg=0.02 bg=0.00
NK T cell activation GO:0051132 p=2.3E−02 n=1 fg=0.02 bg=0.00
regulation of NK T cell activation GO:0051133 p=2.3E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=41/132 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
caspase binding GO:0089720 p=5.6E−04 n=2 fg=0.05 bg=0.00
neurexin family protein binding GO:0042043 p=1.6E−03 n=2 fg=0.05 bg=0.00
ammonium ion binding GO:0070405 p=2.4E−03 n=3 fg=0.08 bg=0.01
phosphatidylethanolamine binding GO:0008429 p=3.2E−03 n=2 fg=0.05 bg=0.00
calcium−dependent phospholipid binding GO:0005544 p=3.2E−03 n=2 fg=0.05 bg=0.00
amidine−lyase activity GO:0016842 p=3.2E−03 n=2 fg=0.05 bg=0.00
protein disulfide isomerase activity GO:0003756 p=5.3E−03 n=2 fg=0.05 bg=0.00
quaternary ammonium group binding GO:0050997 p=1.1E−02 n=2 fg=0.05 bg=0.00
phosphatidylcholine binding GO:0031210 p=1.1E−02 n=2 fg=0.05 bg=0.00
channel activity GO:0015267 p=1.4E−02 n=5 fg=0.13 bg=0.04
passive transmembrane transporter activi... GO:0022803 p=1.4E−02 n=5 fg=0.13 bg=0.04
ion gated channel activity GO:0022839 p=1.6E−02 n=4 fg=0.11 bg=0.03
gated channel activity GO:0022836 p=1.9E−02 n=4 fg=0.11 bg=0.03
phosphatidylinositol binding GO:0035091 p=2.2E−02 n=4 fg=0.11 bg=0.03
thiol oxidase activity GO:0016972 p=2.4E−02 n=1 fg=0.03 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=2.4E−02 n=1 fg=0.03 bg=0.00
adenosylmethionine decarboxylase activit... GO:0004014 p=2.4E−02 n=1 fg=0.03 bg=0.00
polyamine binding GO:0019808 p=2.4E−02 n=1 fg=0.03 bg=0.00
interleukin−5 receptor binding GO:0005137 p=2.4E−02 n=1 fg=0.03 bg=0.00
putrescine binding GO:0019810 p=2.4E−02 n=1 fg=0.03 bg=0.00
tricarboxylate secondary active transmem... GO:0005371 p=2.4E−02 n=1 fg=0.03 bg=0.00
SNAP receptor activity GO:0005484 p=2.7E−02 n=2 fg=0.05 bg=0.01
ubiquitin conjugating enzyme activity GO:0061631 p=2.7E−02 n=2 fg=0.05 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0061650 p=3.2E−02 n=2 fg=0.05 bg=0.01
ubiquitin−like protein ligase activity GO:0061659 p=4.4E−02 n=4 fg=0.11 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=4.4E−02 n=4 fg=0.11 bg=0.04
gamma−glutamylcyclotransferase activity GO:0003839 p=4.7E−02 n=1 fg=0.03 bg=0.00
tricarboxylic acid transmembrane transpo... GO:0015142 p=4.7E−02 n=1 fg=0.03 bg=0.00
BH3 domain binding GO:0051434 p=4.7E−02 n=1 fg=0.03 bg=0.00
chloride channel inhibitor activity GO:0019869 p=4.7E−02 n=1 fg=0.03 bg=0.00
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−log(p)
n=38/132 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032386243.2
fraction genes in fg and expected valu
extrinsic component of cytoplasmic side ... GO:0031234 p=4.1E−03 n=3 fg=0.07 bg=0.01
presynapse GO:0098793 p=5.7E−03 n=7 fg=0.17 bg=0.05
organelle membrane contact site GO:0044232 p=7.1E−03 n=2 fg=0.05 bg=0.00
secretory vesicle GO:0099503 p=1.0E−02 n=8 fg=0.20 bg=0.08
synaptic vesicle GO:0008021 p=2.1E−02 n=4 fg=0.10 bg=0.03
endocytic vesicle lumen GO:0071682 p=2.3E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=2.3E−02 n=1 fg=0.02 bg=0.00
podocyte foot GO:0098846 p=2.3E−02 n=1 fg=0.02 bg=0.00
interleukin−5 receptor complex GO:0005895 p=2.3E−02 n=1 fg=0.02 bg=0.00
integral component of synaptic vesicle m... GO:0030285 p=2.4E−02 n=2 fg=0.05 bg=0.01
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transport vesicle membrane GO:0030658 p=3.1E−02 n=3 fg=0.07 bg=0.02
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transport vesicle GO:0030133 p=3.4E−02 n=5 fg=0.12 bg=0.04
exocytic vesicle GO:0070382 p=3.4E−02 n=4 fg=0.10 bg=0.03
vesicle GO:0031982 p=3.5E−02 n=13 fg=0.32 bg=0.19
nuclear outer membrane−endoplasmic retic... GO:0042175 p=3.6E−02 n=7 fg=0.17 bg=0.08
terminal bouton GO:0043195 p=3.7E−02 n=3 fg=0.07 bg=0.02
intrinsic component of membrane GO:0031224 p=3.8E−02 n=12 fg=0.29 bg=0.17
SNARE complex GO:0031201 p=3.8E−02 n=2 fg=0.05 bg=0.01
endoplasmic reticulum subcompartment GO:0098827 p=4.0E−02 n=7 fg=0.17 bg=0.08
intrinsic component of plasma membrane GO:0031226 p=4.2E−02 n=7 fg=0.17 bg=0.08
cytoplasmic vesicle membrane GO:0030659 p=4.2E−02 n=7 fg=0.17 bg=0.08
extracellular exosome GO:0070062 p=4.4E−02 n=2 fg=0.05 bg=0.01
organelle membrane GO:0031090 p=4.4E−02 n=16 fg=0.39 bg=0.26
HULC complex GO:0033503 p=4.5E−02 n=1 fg=0.02 bg=0.00
anchored component of plasma membrane GO:0046658 p=4.5E−02 n=1 fg=0.02 bg=0.00
endoplasmic reticulum chaperone complex GO:0034663 p=4.5E−02 n=1 fg=0.02 bg=0.00
platelet alpha granule membrane GO:0031092 p=4.5E−02 n=1 fg=0.02 bg=0.00
COPII vesicle coat GO:0030127 p=4.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=41/132 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction