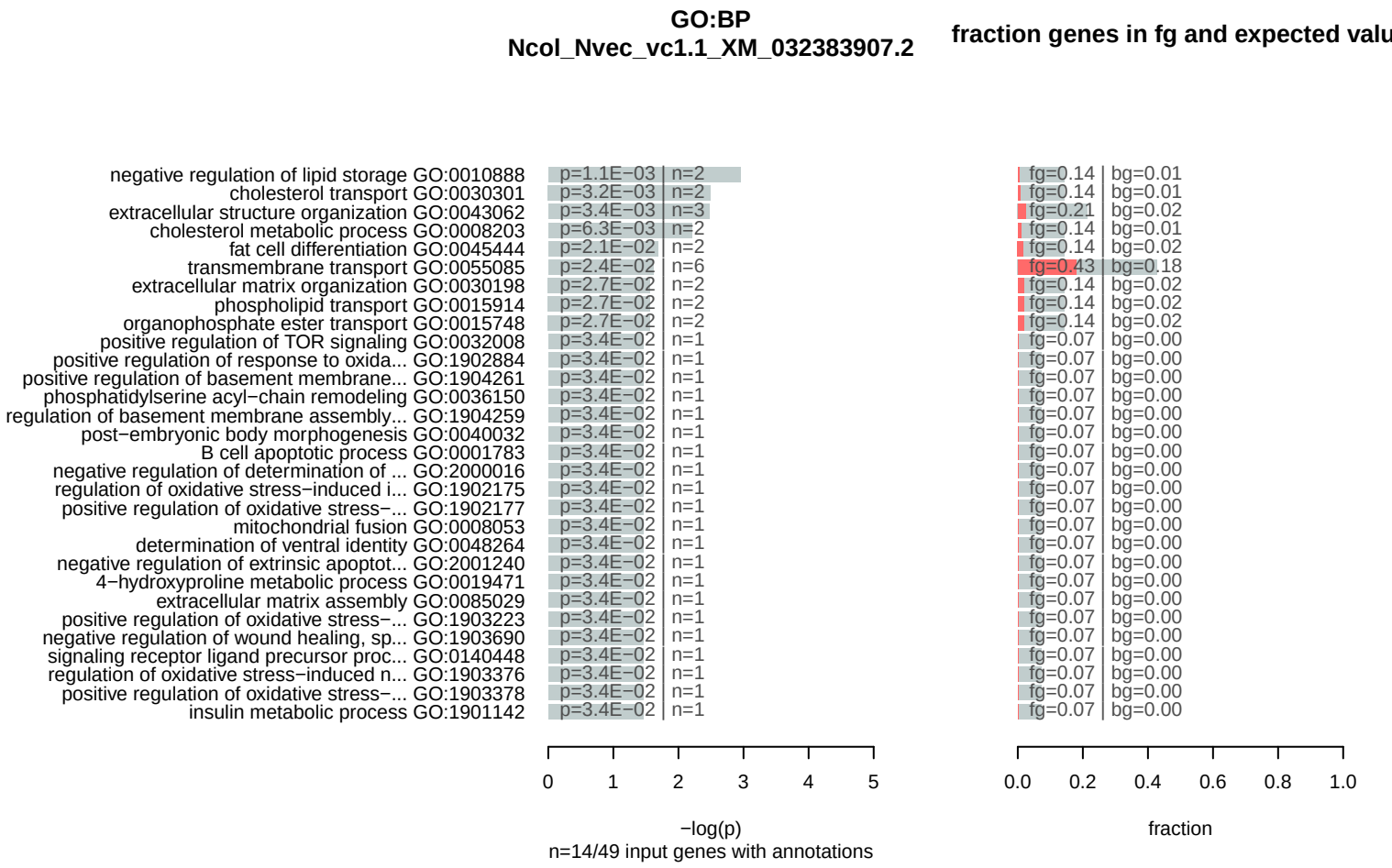
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fraction genes in fg and expected valu
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cholesterol transport GO:0030301 p=3.2E−03 n=2 fg=0.14 bg=0.01
extracellular structure organization GO:0043062 p=3.4E−03 n=3 fg=0.21 bg=0.02
cholesterol metabolic process GO:0008203 p=6.3E−03 n=2 fg=0.14 bg=0.01
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extracellular matrix organization GO:0030198 p=2.7E−02 n=2 fg=0.14 bg=0.02
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organophosphate ester transport GO:0015748 p=2.7E−02 n=2 fg=0.14 bg=0.02
positive regulation of TOR signaling GO:0032008 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of response to oxida... GO:1902884 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of basement membrane... GO:1904261 p=3.4E−02 n=1 fg=0.07 bg=0.00
phosphatidylserine acyl−chain remodeling GO:0036150 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of basement membrane assembly... GO:1904259 p=3.4E−02 n=1 fg=0.07 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=3.4E−02 n=1 fg=0.07 bg=0.00
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negative regulation of determination of ... GO:2000016 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of oxidative stress−induced i... GO:1902175 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of oxidative stress−... GO:1902177 p=3.4E−02 n=1 fg=0.07 bg=0.00
mitochondrial fusion GO:0008053 p=3.4E−02 n=1 fg=0.07 bg=0.00
determination of ventral identity GO:0048264 p=3.4E−02 n=1 fg=0.07 bg=0.00
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extracellular matrix assembly GO:0085029 p=3.4E−02 n=1 fg=0.07 bg=0.00
positive regulation of oxidative stress−... GO:1903223 p=3.4E−02 n=1 fg=0.07 bg=0.00
negative regulation of wound healing, sp... GO:1903690 p=3.4E−02 n=1 fg=0.07 bg=0.00
signaling receptor ligand precursor proc... GO:0140448 p=3.4E−02 n=1 fg=0.07 bg=0.00
regulation of oxidative stress−induced n... GO:1903376 p=3.4E−02 n=1 fg=0.07 bg=0.00
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insulin metabolic process GO:1901142 p=3.4E−02 n=1 fg=0.07 bg=0.00
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n=14/49 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032383907.2
fraction genes in fg and expected valu
cholesterol binding GO:0015485 p=1.0E−03 n=2 fg=0.17 bg=0.01
phospholipid binding GO:0005543 p=6.9E−03 n=4 fg=0.33 bg=0.07
phosphatidylinositol binding GO:0035091 p=1.2E−02 n=3 fg=0.25 bg=0.04
phospholipid transporter activity GO:0005548 p=2.5E−02 n=2 fg=0.17 bg=0.02
glycerophosphoinositol glycerophosphodie... GO:0047395 p=3.3E−02 n=1 fg=0.08 bg=0.00
oxysterol binding GO:0008142 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=3.3E−02 n=1 fg=0.08 bg=0.00
amide transmembrane transporter activity GO:0042887 p=3.3E−02 n=1 fg=0.08 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=3.3E−02 n=1 fg=0.08 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=3.3E−02 n=1 fg=0.08 bg=0.00
BH3 domain binding GO:0051434 p=3.3E−02 n=1 fg=0.08 bg=0.00
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dystroglycan binding GO:0002162 p=3.3E−02 n=1 fg=0.08 bg=0.00
death domain binding GO:0070513 p=3.3E−02 n=1 fg=0.08 bg=0.00
peptide transmembrane transporter activi... GO:1904680 p=3.3E−02 n=1 fg=0.08 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016864 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein disulfide isomerase activity GO:0003756 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=3.3E−02 n=1 fg=0.08 bg=0.00
modified amino acid binding GO:0072341 p=3.3E−02 n=1 fg=0.08 bg=0.00
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kinetochore binding GO:0043515 p=3.3E−02 n=1 fg=0.08 bg=0.00
protein transporter activity GO:0140318 p=3.3E−02 n=1 fg=0.08 bg=0.00
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calcium ion binding GO:0005509 p=6.4E−02 n=2 fg=0.17 bg=0.04
toxin transmembrane transporter activity GO:0019534 p=6.5E−02 n=1 fg=0.08 bg=0.01
ADP binding GO:0043531 p=6.5E−02 n=1 fg=0.08 bg=0.01
calcium−dependent phospholipid binding GO:0005544 p=6.5E−02 n=1 fg=0.08 bg=0.01
phosphatidylethanolamine binding GO:0008429 p=6.5E−02 n=1 fg=0.08 bg=0.01
caspase binding GO:0089720 p=6.5E−02 n=1 fg=0.08 bg=0.01
sterol transporter activity GO:0015248 p=6.5E−02 n=1 fg=0.08 bg=0.01
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−log(p)
n=12/49 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032383907.2
fraction genes in fg and expected valu
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kinetochore microtubule GO:0005828 p=3.5E−02 n=1 fg=0.07 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.5E−02 n=1 fg=0.07 bg=0.00
kinetochore GO:0000776 p=3.5E−02 n=1 fg=0.07 bg=0.00
microtubule plus−end GO:0035371 p=3.5E−02 n=1 fg=0.07 bg=0.00
Bcl−2 family protein complex GO:0097136 p=3.5E−02 n=1 fg=0.07 bg=0.00
Seh1−associated complex GO:0035859 p=3.5E−02 n=1 fg=0.07 bg=0.00
cortical microtubule plus−end GO:1903754 p=3.5E−02 n=1 fg=0.07 bg=0.00
centrosomal corona GO:0031592 p=3.5E−02 n=1 fg=0.07 bg=0.00
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spindle microtubule GO:0005876 p=3.5E−02 n=1 fg=0.07 bg=0.00
integral component of endoplasmic reticu... GO:0030176 p=5.2E−02 n=2 fg=0.14 bg=0.03
intrinsic component of endoplasmic retic... GO:0031227 p=5.2E−02 n=2 fg=0.14 bg=0.03
membrane GO:0016020 p=5.7E−02 n=11 fg=0.79 bg=0.55
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myosin V complex GO:0031475 p=6.9E−02 n=1 fg=0.07 bg=0.01
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myosin VII complex GO:0031477 p=6.9E−02 n=1 fg=0.07 bg=0.01
cell cortex region GO:0099738 p=6.9E−02 n=1 fg=0.07 bg=0.01
endoplasmic reticulum tubular network GO:0071782 p=6.9E−02 n=1 fg=0.07 bg=0.01
chromosome, centromeric region GO:0000775 p=6.9E−02 n=1 fg=0.07 bg=0.01
condensed chromosome, centromeric region GO:0000779 p=6.9E−02 n=1 fg=0.07 bg=0.01
microtubule end GO:1990752 p=6.9E−02 n=1 fg=0.07 bg=0.01
myosin II complex GO:0016460 p=6.9E−02 n=1 fg=0.07 bg=0.01
unconventional myosin complex GO:0016461 p=6.9E−02 n=1 fg=0.07 bg=0.01
basal cortex GO:0045180 p=6.9E−02 n=1 fg=0.07 bg=0.01
myosin complex GO:0016459 p=6.9E−02 n=1 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=14/49 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction