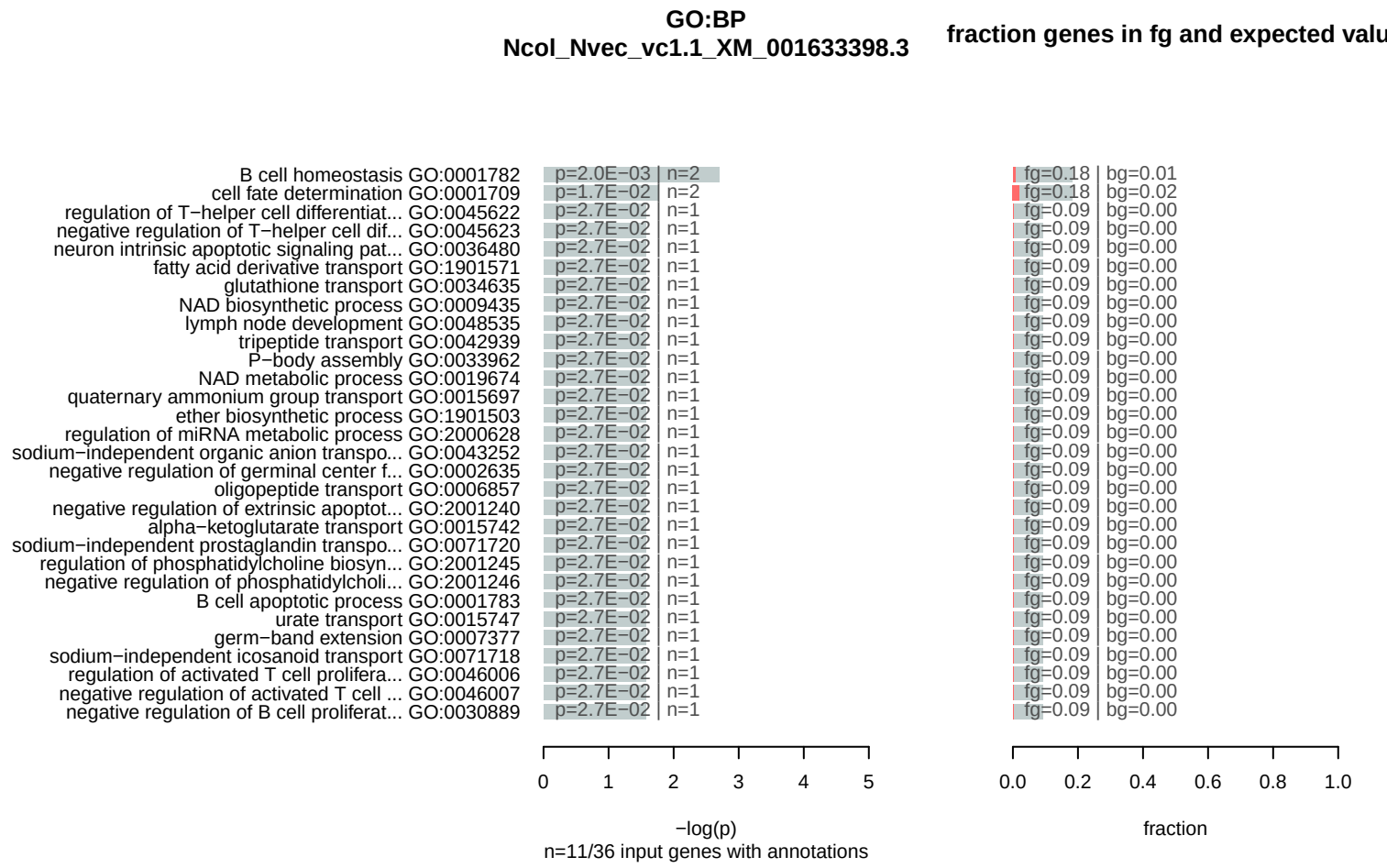
GO:BP
Ncol_Nvec_vc1.1_XM_001633398.3
fraction genes in fg and expected valu
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cell fate determination GO:0001709 p=1.7E−02 n=2 fg=0.18 bg=0.02
regulation of T−helper cell differentiat... GO:0045622 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of T−helper cell dif... GO:0045623 p=2.7E−02 n=1 fg=0.09 bg=0.00
neuron intrinsic apoptotic signaling pat... GO:0036480 p=2.7E−02 n=1 fg=0.09 bg=0.00
fatty acid derivative transport GO:1901571 p=2.7E−02 n=1 fg=0.09 bg=0.00
glutathione transport GO:0034635 p=2.7E−02 n=1 fg=0.09 bg=0.00
NAD biosynthetic process GO:0009435 p=2.7E−02 n=1 fg=0.09 bg=0.00
lymph node development GO:0048535 p=2.7E−02 n=1 fg=0.09 bg=0.00
tripeptide transport GO:0042939 p=2.7E−02 n=1 fg=0.09 bg=0.00
P−body assembly GO:0033962 p=2.7E−02 n=1 fg=0.09 bg=0.00
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quaternary ammonium group transport GO:0015697 p=2.7E−02 n=1 fg=0.09 bg=0.00
ether biosynthetic process GO:1901503 p=2.7E−02 n=1 fg=0.09 bg=0.00
regulation of miRNA metabolic process GO:2000628 p=2.7E−02 n=1 fg=0.09 bg=0.00
sodium−independent organic anion transpo... GO:0043252 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of germinal center f... GO:0002635 p=2.7E−02 n=1 fg=0.09 bg=0.00
oligopeptide transport GO:0006857 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of extrinsic apoptot... GO:2001240 p=2.7E−02 n=1 fg=0.09 bg=0.00
alpha−ketoglutarate transport GO:0015742 p=2.7E−02 n=1 fg=0.09 bg=0.00
sodium−independent prostaglandin transpo... GO:0071720 p=2.7E−02 n=1 fg=0.09 bg=0.00
regulation of phosphatidylcholine biosyn... GO:2001245 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of phosphatidylcholi... GO:2001246 p=2.7E−02 n=1 fg=0.09 bg=0.00
B cell apoptotic process GO:0001783 p=2.7E−02 n=1 fg=0.09 bg=0.00
urate transport GO:0015747 p=2.7E−02 n=1 fg=0.09 bg=0.00
germ−band extension GO:0007377 p=2.7E−02 n=1 fg=0.09 bg=0.00
sodium−independent icosanoid transport GO:0071718 p=2.7E−02 n=1 fg=0.09 bg=0.00
regulation of activated T cell prolifera... GO:0046006 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of activated T cell ... GO:0046007 p=2.7E−02 n=1 fg=0.09 bg=0.00
negative regulation of B cell proliferat... GO:0030889 p=2.7E−02 n=1 fg=0.09 bg=0.00
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−log(p)
n=11/36 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001633398.3
fraction genes in fg and expected valu
ion channel activity GO:0005216 p=1.0E−02 n=4 fg=0.40 bg=0.10
passive transmembrane transporter activi... GO:0022803 p=1.8E−02 n=5 fg=0.50 bg=0.10
channel activity GO:0015267 p=1.8E−02 n=5 fg=0.50 bg=0.10
voltage−gated potassium channel activity GO:0005249 p=2.2E−02 n=2 fg=0.20 bg=0.03
quaternary ammonium group transmembrane ... GO:0015651 p=2.7E−02 n=1 fg=0.10 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=2.7E−02 n=1 fg=0.10 bg=0.00
gamma−glutamylaminecyclotransferase acti... GO:0061929 p=2.7E−02 n=1 fg=0.10 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=2.7E−02 n=1 fg=0.10 bg=0.00
vitamin transmembrane transporter activi... GO:0090482 p=2.7E−02 n=1 fg=0.10 bg=0.00
O−acyltransferase activity GO:0008374 p=2.7E−02 n=1 fg=0.10 bg=0.00
icosanoid receptor activity GO:0004953 p=2.7E−02 n=1 fg=0.10 bg=0.00
prostanoid receptor activity GO:0004954 p=2.7E−02 n=1 fg=0.10 bg=0.00
prostaglandin receptor activity GO:0004955 p=2.7E−02 n=1 fg=0.10 bg=0.00
protein transmembrane transporter activi... GO:0008320 p=2.7E−02 n=1 fg=0.10 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.7E−02 n=1 fg=0.10 bg=0.00
fatty acid transmembrane transporter act... GO:0015245 p=2.7E−02 n=1 fg=0.10 bg=0.00
amide transmembrane transporter activity GO:0042887 p=2.7E−02 n=1 fg=0.10 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=2.7E−02 n=1 fg=0.10 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=2.7E−02 n=1 fg=0.10 bg=0.00
BH3 domain binding GO:0051434 p=2.7E−02 n=1 fg=0.10 bg=0.00
urate transmembrane transporter activity GO:0015143 p=2.7E−02 n=1 fg=0.10 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=2.7E−02 n=1 fg=0.10 bg=0.00
nicotinate transmembrane transporter act... GO:0090416 p=2.7E−02 n=1 fg=0.10 bg=0.00
ammonium transmembrane transporter activ... GO:0008519 p=2.7E−02 n=1 fg=0.10 bg=0.00
S100 protein binding GO:0044548 p=2.7E−02 n=1 fg=0.10 bg=0.00
death domain binding GO:0070513 p=2.7E−02 n=1 fg=0.10 bg=0.00
peptide transmembrane transporter activi... GO:1904680 p=2.7E−02 n=1 fg=0.10 bg=0.00
salt transmembrane transporter activity GO:1901702 p=2.7E−02 n=1 fg=0.10 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.7E−02 n=1 fg=0.10 bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=2.7E−02 n=1 fg=0.10 bg=0.00
0 1 2 3 4 5
−log(p)
n=10/36 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001633398.3
fraction genes in fg and expected valu
Bcl−2 family protein complex GO:0097136 p=2.5E−02 n=1 fg=0.10 bg=0.00
muscle cell projection GO:0036194 p=2.5E−02 n=1 fg=0.10 bg=0.00
muscle cell projection membrane GO:0036195 p=2.5E−02 n=1 fg=0.10 bg=0.00
integral component of plasma membrane GO:0005887 p=4.4E−02 n=4 fg=0.40 bg=0.15
supramolecular complex GO:0099080 p=4.7E−02 n=3 fg=0.30 bg=0.09
P−body GO:0000932 p=4.9E−02 n=1 fg=0.10 bg=0.01
striated muscle dense body GO:0055120 p=4.9E−02 n=1 fg=0.10 bg=0.01
azurophil granule membrane GO:0035577 p=4.9E−02 n=1 fg=0.10 bg=0.01
cytoplasmic stress granule GO:0010494 p=4.9E−02 n=1 fg=0.10 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=5.8E−02 n=4 fg=0.40 bg=0.16
cell surface GO:0009986 p=7.6E−02 n=2 fg=0.20 bg=0.05
membrane GO:0016020 p=9.4E−02 n=8 fg=0.80 bg=0.55
brush border membrane GO:0031526 p=9.6E−02 n=1 fg=0.10 bg=0.01
cytoplasmic microtubule GO:0005881 p=9.6E−02 n=1 fg=0.10 bg=0.01
external side of plasma membrane GO:0009897 p=9.6E−02 n=1 fg=0.10 bg=0.01
apical plasma membrane GO:0016324 p=1.2E−01 n=2 fg=0.20 bg=0.06
cytoplasmic ribonucleoprotein granule GO:0036464 p=1.2E−01 n=1 fg=0.10 bg=0.01
secretory granule membrane GO:0030667 p=1.2E−01 n=1 fg=0.10 bg=0.01
cell projection membrane GO:0031253 p=1.3E−01 n=2 fg=0.20 bg=0.07
apical part of cell GO:0045177 p=1.4E−01 n=2 fg=0.20 bg=0.07
mitochondrial outer membrane GO:0005741 p=1.4E−01 n=1 fg=0.10 bg=0.01
lysosomal membrane GO:0005765 p=1.4E−01 n=1 fg=0.10 bg=0.01
ribonucleoprotein granule GO:0035770 p=1.4E−01 n=1 fg=0.10 bg=0.01
outer membrane GO:0019867 p=1.4E−01 n=1 fg=0.10 bg=0.01
lipid droplet GO:0005811 p=1.4E−01 n=1 fg=0.10 bg=0.01
brush border GO:0005903 p=1.4E−01 n=1 fg=0.10 bg=0.01
organelle outer membrane GO:0031968 p=1.4E−01 n=1 fg=0.10 bg=0.01
plasma membrane GO:0005886 p=1.6E−01 n=6 fg=0.60 bg=0.40
supramolecular fiber GO:0099512 p=1.6E−01 n=2 fg=0.20 bg=0.07
supramolecular polymer GO:0099081 p=1.6E−01 n=2 fg=0.20 bg=0.07
0 1 2 3 4 5
−log(p)
n=10/36 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction