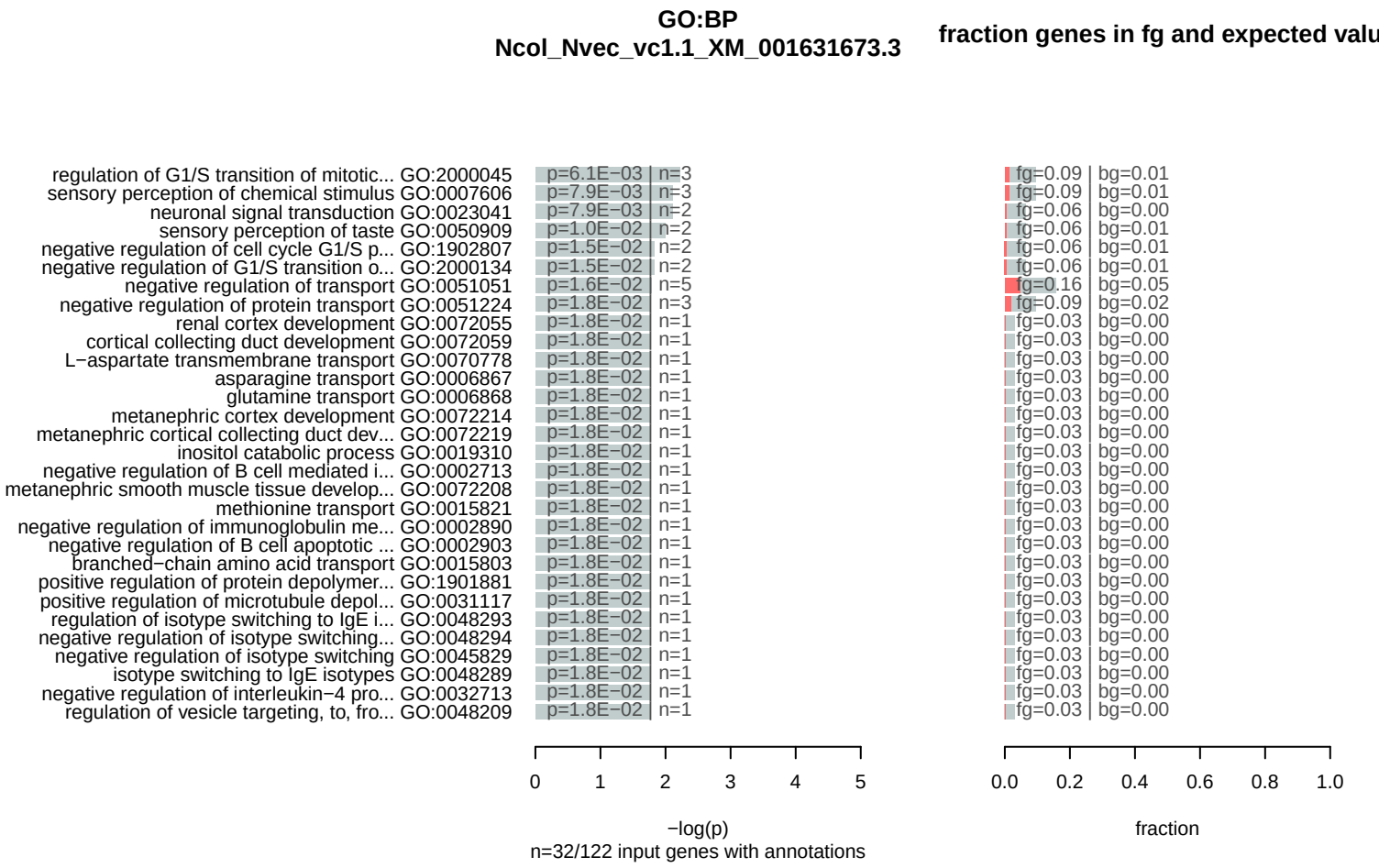
GO:BP
Ncol_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
regulation of G1/S transition of mitotic... GO:2000045 p=6.1E−03 n=3 fg=0.09 bg=0.01
sensory perception of chemical stimulus GO:0007606 p=7.9E−03 n=3 fg=0.09 bg=0.01
neuronal signal transduction GO:0023041 p=7.9E−03 n=2 fg=0.06 bg=0.00
sensory perception of taste GO:0050909 p=1.0E−02 n=2 fg=0.06 bg=0.01
negative regulation of cell cycle G1/S p... GO:1902807 p=1.5E−02 n=2 fg=0.06 bg=0.01
negative regulation of G1/S transition o... GO:2000134 p=1.5E−02 n=2 fg=0.06 bg=0.01
negative regulation of transport GO:0051051 p=1.6E−02 n=5 fg=0.16 bg=0.05
negative regulation of protein transport GO:0051224 p=1.8E−02 n=3 fg=0.09 bg=0.02
renal cortex development GO:0072055 p=1.8E−02 n=1 fg=0.03 bg=0.00
cortical collecting duct development GO:0072059 p=1.8E−02 n=1 fg=0.03 bg=0.00
L−aspartate transmembrane transport GO:0070778 p=1.8E−02 n=1 fg=0.03 bg=0.00
asparagine transport GO:0006867 p=1.8E−02 n=1 fg=0.03 bg=0.00
glutamine transport GO:0006868 p=1.8E−02 n=1 fg=0.03 bg=0.00
metanephric cortex development GO:0072214 p=1.8E−02 n=1 fg=0.03 bg=0.00
metanephric cortical collecting duct dev... GO:0072219 p=1.8E−02 n=1 fg=0.03 bg=0.00
inositol catabolic process GO:0019310 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of B cell mediated i... GO:0002713 p=1.8E−02 n=1 fg=0.03 bg=0.00
metanephric smooth muscle tissue develop... GO:0072208 p=1.8E−02 n=1 fg=0.03 bg=0.00
methionine transport GO:0015821 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of immunoglobulin me... GO:0002890 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of B cell apoptotic ... GO:0002903 p=1.8E−02 n=1 fg=0.03 bg=0.00
branched−chain amino acid transport GO:0015803 p=1.8E−02 n=1 fg=0.03 bg=0.00
positive regulation of protein depolymer... GO:1901881 p=1.8E−02 n=1 fg=0.03 bg=0.00
positive regulation of microtubule depol... GO:0031117 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of isotype switching to IgE i... GO:0048293 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of isotype switching... GO:0048294 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of isotype switching GO:0045829 p=1.8E−02 n=1 fg=0.03 bg=0.00
isotype switching to IgE isotypes GO:0048289 p=1.8E−02 n=1 fg=0.03 bg=0.00
negative regulation of interleukin−4 pro... GO:0032713 p=1.8E−02 n=1 fg=0.03 bg=0.00
regulation of vesicle targeting, to, fro... GO:0048209 p=1.8E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=32/122 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
outward rectifier potassium channel acti... GO:0015271 p=5.5E−03 n=2 fg=0.07 bg=0.00
ligand−gated ion channel activity GO:0015276 p=6.1E−03 n=3 fg=0.11 bg=0.01
alpha−actinin binding GO:0051393 p=7.3E−03 n=2 fg=0.07 bg=0.01
amide transmembrane transporter activity GO:0042887 p=9.3E−03 n=2 fg=0.07 bg=0.01
intracellular ligand−gated ion channel a... GO:0005217 p=1.1E−02 n=2 fg=0.07 bg=0.01
ubiquitin conjugating enzyme binding GO:0031624 p=1.1E−02 n=2 fg=0.07 bg=0.01
ubiquitin−like protein conjugating enzym... GO:0044390 p=1.7E−02 n=2 fg=0.07 bg=0.01
methionine transmembrane transporter act... GO:0043865 p=1.7E−02 n=1 fg=0.04 bg=0.00
ankyrin repeat binding GO:0071532 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−leucine transmembrane transporter acti... GO:0015190 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=1.7E−02 n=1 fg=0.04 bg=0.00
ferric iron binding GO:0008199 p=1.7E−02 n=1 fg=0.04 bg=0.00
inositol oxygenase activity GO:0050113 p=1.7E−02 n=1 fg=0.04 bg=0.00
HLH domain binding GO:0043398 p=1.7E−02 n=1 fg=0.04 bg=0.00
glycogen binding GO:2001069 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−asparagine transmembrane transporter a... GO:0015182 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183 p=1.7E−02 n=1 fg=0.04 bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186 p=1.7E−02 n=1 fg=0.04 bg=0.00
acidic amino acid transmembrane transpor... GO:0015172 p=1.7E−02 n=1 fg=0.04 bg=0.00
muscle alpha−actinin binding GO:0051371 p=1.7E−02 n=1 fg=0.04 bg=0.00
[phosphorylase] phosphatase activity GO:0050196 p=1.7E−02 n=1 fg=0.04 bg=0.00
branched−chain amino acid transmembrane ... GO:0015658 p=1.7E−02 n=1 fg=0.04 bg=0.00
ligand−gated cation channel activity GO:0099094 p=2.5E−02 n=2 fg=0.07 bg=0.01
ion gated channel activity GO:0022839 p=3.2E−02 n=3 fg=0.11 bg=0.03
BH3 domain binding GO:0051434 p=3.4E−02 n=1 fg=0.04 bg=0.00
alanine transmembrane transporter activi... GO:0022858 p=3.4E−02 n=1 fg=0.04 bg=0.00
monooxygenase activity GO:0004497 p=3.4E−02 n=1 fg=0.04 bg=0.00
serine transmembrane transporter activit... GO:0022889 p=3.4E−02 n=1 fg=0.04 bg=0.00
L−serine transmembrane transporter activ... GO:0015194 p=3.4E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=27/122 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
microtubule GO:0005874 p=1.5E−02 n=3 fg=0.10 bg=0.02
anchored component of synaptic vesicle m... GO:0098993 p=1.7E−02 n=1 fg=0.03 bg=0.00
axonemal microtubule GO:0005879 p=1.7E−02 n=1 fg=0.03 bg=0.00
katanin complex GO:0008352 p=1.7E−02 n=1 fg=0.03 bg=0.00
polycystin complex GO:0002133 p=1.7E−02 n=1 fg=0.03 bg=0.00
polymeric cytoskeletal fiber GO:0099513 p=2.9E−02 n=3 fg=0.10 bg=0.02
intrinsic component of organelle membran... GO:0031300 p=3.7E−02 n=4 fg=0.13 bg=0.04
cation channel complex GO:0034703 p=4.6E−02 n=2 fg=0.07 bg=0.01
glycogen granule GO:0042587 p=4.9E−02 n=1 fg=0.03 bg=0.00
Bcl−2 family protein complex GO:0097136 p=4.9E−02 n=1 fg=0.03 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=4.9E−02 n=1 fg=0.03 bg=0.00
cytolytic granule GO:0044194 p=4.9E−02 n=1 fg=0.03 bg=0.00
spindle GO:0005819 p=5.3E−02 n=3 fg=0.10 bg=0.03
ion channel complex GO:0034702 p=5.4E−02 n=2 fg=0.07 bg=0.01
supramolecular fiber GO:0099512 p=5.6E−02 n=4 fg=0.13 bg=0.05
supramolecular polymer GO:0099081 p=5.6E−02 n=4 fg=0.13 bg=0.05
basal cortex GO:0045180 p=6.5E−02 n=1 fg=0.03 bg=0.00
integral component of lumenal side of en... GO:0071556 p=6.5E−02 n=1 fg=0.03 bg=0.00
eukaryotic translation initiation factor... GO:0005851 p=6.5E−02 n=1 fg=0.03 bg=0.00
lumenal side of endoplasmic reticulum me... GO:0098553 p=6.5E−02 n=1 fg=0.03 bg=0.00
microtubule cytoskeleton GO:0015630 p=7.0E−02 n=6 fg=0.20 bg=0.10
axon GO:0030424 p=7.8E−02 n=5 fg=0.17 bg=0.08
sensory dendrite GO:0071683 p=8.0E−02 n=1 fg=0.03 bg=0.00
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=8.0E−02 n=1 fg=0.03 bg=0.00
anchored component of membrane GO:0031225 p=8.0E−02 n=1 fg=0.03 bg=0.00
septin cytoskeleton GO:0032156 p=8.0E−02 n=1 fg=0.03 bg=0.00
juxtaparanode region of axon GO:0044224 p=8.0E−02 n=1 fg=0.03 bg=0.00
protein phosphatase type 1 complex GO:0000164 p=8.0E−02 n=1 fg=0.03 bg=0.00
intracellular canaliculus GO:0046691 p=8.0E−02 n=1 fg=0.03 bg=0.00
lumenal side of membrane GO:0098576 p=8.0E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=30/122 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction