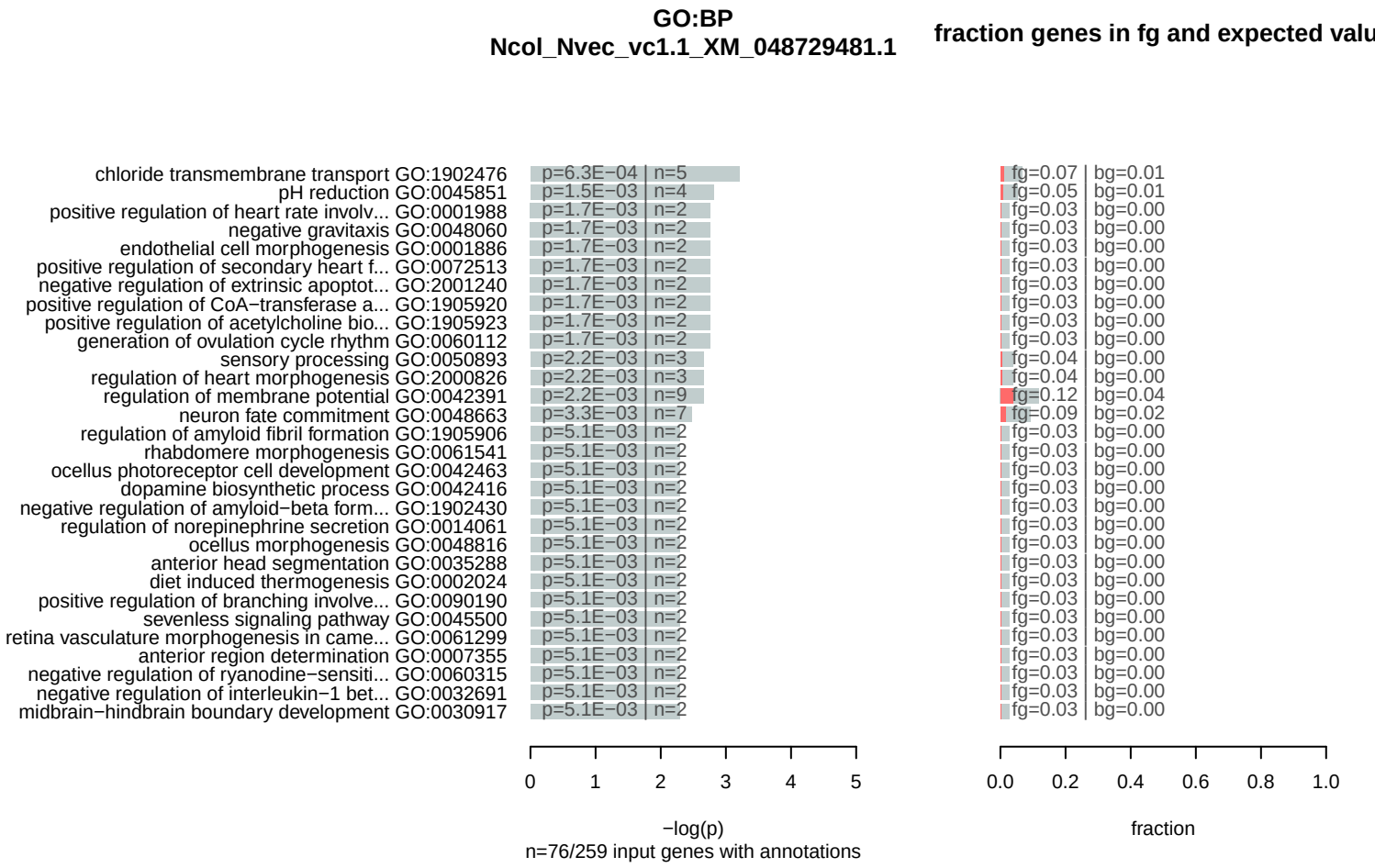
GO:BP
Ncol_Nvec_vc1.1_XM_048729481.1
fraction genes in fg and expected valu
chloride transmembrane transport GO:1902476 p=6.3E−04 n=5 fg=0.07 bg=0.01
pH reduction GO:0045851 p=1.5E−03 n=4 fg=0.05 bg=0.01
positive regulation of heart rate involv... GO:0001988 p=1.7E−03 n=2 fg=0.03 bg=0.00
negative gravitaxis GO:0048060 p=1.7E−03 n=2 fg=0.03 bg=0.00
endothelial cell morphogenesis GO:0001886 p=1.7E−03 n=2 fg=0.03 bg=0.00
positive regulation of secondary heart f... GO:0072513 p=1.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of extrinsic apoptot... GO:2001240 p=1.7E−03 n=2 fg=0.03 bg=0.00
positive regulation of CoA−transferase a... GO:1905920 p=1.7E−03 n=2 fg=0.03 bg=0.00
positive regulation of acetylcholine bio... GO:1905923 p=1.7E−03 n=2 fg=0.03 bg=0.00
generation of ovulation cycle rhythm GO:0060112 p=1.7E−03 n=2 fg=0.03 bg=0.00
sensory processing GO:0050893 p=2.2E−03 n=3 fg=0.04 bg=0.00
regulation of heart morphogenesis GO:2000826 p=2.2E−03 n=3 fg=0.04 bg=0.00
regulation of membrane potential GO:0042391 p=2.2E−03 n=9 fg=0.12 bg=0.04
neuron fate commitment GO:0048663 p=3.3E−03 n=7 fg=0.09 bg=0.02
regulation of amyloid fibril formation GO:1905906 p=5.1E−03 n=2 fg=0.03 bg=0.00
rhabdomere morphogenesis GO:0061541 p=5.1E−03 n=2 fg=0.03 bg=0.00
ocellus photoreceptor cell development GO:0042463 p=5.1E−03 n=2 fg=0.03 bg=0.00
dopamine biosynthetic process GO:0042416 p=5.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of amyloid−beta form... GO:1902430 p=5.1E−03 n=2 fg=0.03 bg=0.00
regulation of norepinephrine secretion GO:0014061 p=5.1E−03 n=2 fg=0.03 bg=0.00
ocellus morphogenesis GO:0048816 p=5.1E−03 n=2 fg=0.03 bg=0.00
anterior head segmentation GO:0035288 p=5.1E−03 n=2 fg=0.03 bg=0.00
diet induced thermogenesis GO:0002024 p=5.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of branching involve... GO:0090190 p=5.1E−03 n=2 fg=0.03 bg=0.00
sevenless signaling pathway GO:0045500 p=5.1E−03 n=2 fg=0.03 bg=0.00
retina vasculature morphogenesis in came... GO:0061299 p=5.1E−03 n=2 fg=0.03 bg=0.00
anterior region determination GO:0007355 p=5.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of ryanodine−sensiti... GO:0060315 p=5.1E−03 n=2 fg=0.03 bg=0.00
negative regulation of interleukin−1 bet... GO:0032691 p=5.1E−03 n=2 fg=0.03 bg=0.00
midbrain−hindbrain boundary development GO:0030917 p=5.1E−03 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/259 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048729481.1
fraction genes in fg and expected valu
protein disulfide isomerase activity GO:0003756 p=6.7E−04 n=3 fg=0.04 bg=0.00
voltage−gated chloride channel activity GO:0005247 p=1.3E−03 n=3 fg=0.04 bg=0.00
ion gated channel activity GO:0022839 p=1.4E−03 n=7 fg=0.10 bg=0.03
acetylcholine−gated cation−selective cha... GO:0022848 p=1.8E−03 n=2 fg=0.03 bg=0.00
acetylcholine receptor activity GO:0015464 p=1.8E−03 n=2 fg=0.03 bg=0.00
glutathione peroxidase activity GO:0004602 p=1.8E−03 n=2 fg=0.03 bg=0.00
D3 dopamine receptor binding GO:0031750 p=1.8E−03 n=2 fg=0.03 bg=0.00
D4 dopamine receptor binding GO:0031751 p=1.8E−03 n=2 fg=0.03 bg=0.00
acetylcholine binding GO:0042166 p=1.8E−03 n=2 fg=0.03 bg=0.00
D2 dopamine receptor binding GO:0031749 p=5.1E−03 n=2 fg=0.03 bg=0.00
toxic substance binding GO:0015643 p=9.9E−03 n=2 fg=0.03 bg=0.00
chloride channel regulator activity GO:0017081 p=9.9E−03 n=2 fg=0.03 bg=0.00
ammonium ion binding GO:0070405 p=1.2E−02 n=3 fg=0.04 bg=0.01
transcription coactivator binding GO:0001223 p=1.6E−02 n=2 fg=0.03 bg=0.00
ubiquitin−ubiquitin ligase activity GO:0034450 p=1.6E−02 n=2 fg=0.03 bg=0.00
adenylate cyclase binding GO:0008179 p=1.6E−02 n=2 fg=0.03 bg=0.00
phosphatase regulator activity GO:0019208 p=2.3E−02 n=3 fg=0.04 bg=0.01
identical protein binding GO:0042802 p=2.3E−02 n=18 fg=0.27 bg=0.17
neurotransmitter transmembrane transport... GO:0005326 p=2.3E−02 n=2 fg=0.03 bg=0.00
ligand−gated anion channel activity GO:0099095 p=3.2E−02 n=2 fg=0.03 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=3.2E−02 n=2 fg=0.03 bg=0.00
G protein−coupled receptor binding GO:0001664 p=3.5E−02 n=6 fg=0.09 bg=0.02
extracellular ligand−gated ion channel a... GO:0005230 p=3.9E−02 n=4 fg=0.06 bg=0.01
passive transmembrane transporter activi... GO:0022803 p=3.9E−02 n=10 fg=0.15 bg=0.04
channel activity GO:0015267 p=3.9E−02 n=10 fg=0.15 bg=0.04
Notch binding GO:0005112 p=4.1E−02 n=2 fg=0.03 bg=0.01
hormone binding GO:0042562 p=4.1E−02 n=2 fg=0.03 bg=0.01
CXCR chemokine receptor binding GO:0045236 p=4.2E−02 n=1 fg=0.01 bg=0.00
acetate ester transmembrane transporter ... GO:1901375 p=4.2E−02 n=1 fg=0.01 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=4.2E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/259 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048729481.1
fraction genes in fg and expected valu
Cul3−RING ubiquitin ligase complex GO:0031463 p=6.2E−04 n=3 fg=0.04 bg=0.00
extracellular space GO:0005615 p=1.4E−03 n=8 fg=0.11 bg=0.03
acetylcholine−gated channel complex GO:0005892 p=1.6E−03 n=2 fg=0.03 bg=0.00
external side of plasma membrane GO:0009897 p=4.1E−03 n=4 fg=0.05 bg=0.01
muscle cell projection membrane GO:0036195 p=4.8E−03 n=2 fg=0.03 bg=0.00
lysosomal lumen GO:0043202 p=5.1E−03 n=4 fg=0.05 bg=0.01
axolemma GO:0030673 p=1.5E−02 n=2 fg=0.03 bg=0.00
azurophil granule lumen GO:0035578 p=1.7E−02 n=3 fg=0.04 bg=0.01
membrane raft GO:0045121 p=1.9E−02 n=6 fg=0.08 bg=0.03
membrane microdomain GO:0098857 p=1.9E−02 n=6 fg=0.08 bg=0.03
neuron projection membrane GO:0032589 p=2.1E−02 n=3 fg=0.04 bg=0.01
extracellular exosome GO:0070062 p=2.1E−02 n=3 fg=0.04 bg=0.01
extracellular membrane−bounded organelle GO:0065010 p=2.5E−02 n=3 fg=0.04 bg=0.01
extracellular organelle GO:0043230 p=2.5E−02 n=3 fg=0.04 bg=0.01
extracellular vesicle GO:1903561 p=2.5E−02 n=3 fg=0.04 bg=0.01
Cul4−RING E3 ubiquitin ligase complex GO:0080008 p=3.0E−02 n=2 fg=0.03 bg=0.00
postsynaptic membrane GO:0045211 p=3.2E−02 n=4 fg=0.05 bg=0.02
endoplasmic reticulum lumen GO:0005788 p=3.2E−02 n=4 fg=0.05 bg=0.02
dendritic shaft GO:0043198 p=3.4E−02 n=3 fg=0.04 bg=0.01
postsynapse GO:0098794 p=3.5E−02 n=7 fg=0.09 bg=0.04
stereocilium GO:0032420 p=3.9E−02 n=2 fg=0.03 bg=0.00
stereocilium bundle GO:0032421 p=3.9E−02 n=2 fg=0.03 bg=0.00
striated muscle dense body GO:0055120 p=3.9E−02 n=2 fg=0.03 bg=0.00
equatorial microtubule organizing center GO:0000923 p=4.1E−02 n=1 fg=0.01 bg=0.00
syntrophin complex GO:0016013 p=4.1E−02 n=1 fg=0.01 bg=0.00
interleukin−5 receptor complex GO:0005895 p=4.1E−02 n=1 fg=0.01 bg=0.00
nuclear SCF ubiquitin ligase complex GO:0043224 p=4.1E−02 n=1 fg=0.01 bg=0.00
gamma−tubulin complex GO:0000930 p=4.1E−02 n=1 fg=0.01 bg=0.00
Cul5−RING ubiquitin ligase complex GO:0031466 p=4.1E−02 n=1 fg=0.01 bg=0.00
Cul7−RING ubiquitin ligase complex GO:0031467 p=4.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/259 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction