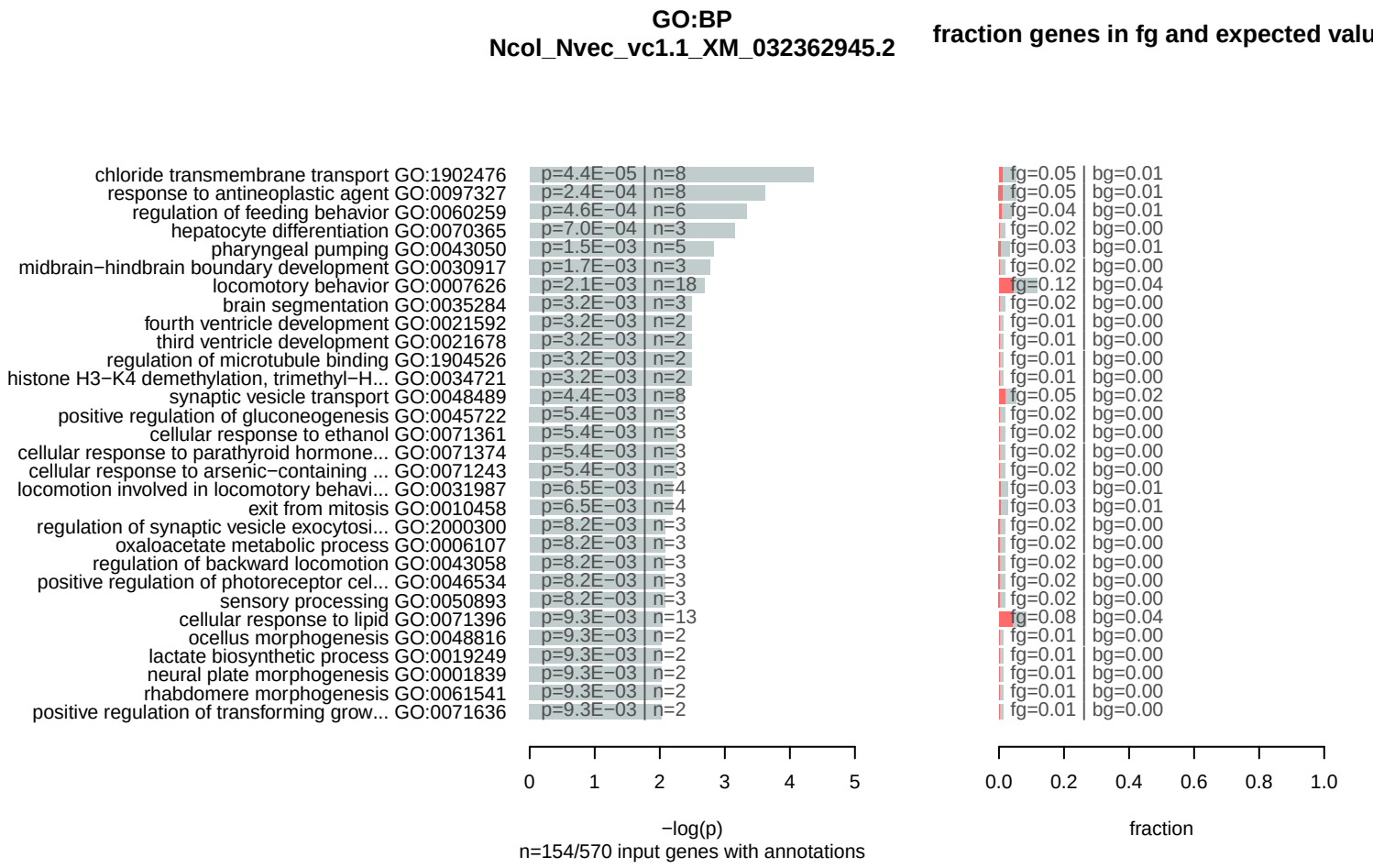
GO:BP
Ncol_Nvec_vc1.1_XM_032362945.2
fraction genes in fg and expected valu
chloride transmembrane transport GO:1902476 p=4.4E−05 n=8 fg=0.05 bg=0.01
response to antineoplastic agent GO:0097327 p=2.4E−04 n=8 fg=0.05 bg=0.01
regulation of feeding behavior GO:0060259 p=4.6E−04 n=6 fg=0.04 bg=0.01
hepatocyte differentiation GO:0070365 p=7.0E−04 n=3 fg=0.02 bg=0.00
pharyngeal pumping GO:0043050 p=1.5E−03 n=5 fg=0.03 bg=0.01
midbrain−hindbrain boundary development GO:0030917 p=1.7E−03 n=3 fg=0.02 bg=0.00
locomotory behavior GO:0007626 p=2.1E−03 n=18 fg=0.12 bg=0.04
brain segmentation GO:0035284 p=3.2E−03 n=3 fg=0.02 bg=0.00
fourth ventricle development GO:0021592 p=3.2E−03 n=2 fg=0.01 bg=0.00
third ventricle development GO:0021678 p=3.2E−03 n=2 fg=0.01 bg=0.00
regulation of microtubule binding GO:1904526 p=3.2E−03 n=2 fg=0.01 bg=0.00
histone H3−K4 demethylation, trimethyl−H... GO:0034721 p=3.2E−03 n=2 fg=0.01 bg=0.00
synaptic vesicle transport GO:0048489 p=4.4E−03 n=8 fg=0.05 bg=0.02
positive regulation of gluconeogenesis GO:0045722 p=5.4E−03 n=3 fg=0.02 bg=0.00
cellular response to ethanol GO:0071361 p=5.4E−03 n=3 fg=0.02 bg=0.00
cellular response to parathyroid hormone... GO:0071374 p=5.4E−03 n=3 fg=0.02 bg=0.00
cellular response to arsenic−containing ... GO:0071243 p=5.4E−03 n=3 fg=0.02 bg=0.00
locomotion involved in locomotory behavi... GO:0031987 p=6.5E−03 n=4 fg=0.03 bg=0.01
exit from mitosis GO:0010458 p=6.5E−03 n=4 fg=0.03 bg=0.01
regulation of synaptic vesicle exocytosi... GO:2000300 p=8.2E−03 n=3 fg=0.02 bg=0.00
oxaloacetate metabolic process GO:0006107 p=8.2E−03 n=3 fg=0.02 bg=0.00
regulation of backward locomotion GO:0043058 p=8.2E−03 n=3 fg=0.02 bg=0.00
positive regulation of photoreceptor cel... GO:0046534 p=8.2E−03 n=3 fg=0.02 bg=0.00
sensory processing GO:0050893 p=8.2E−03 n=3 fg=0.02 bg=0.00
cellular response to lipid GO:0071396 p=9.3E−03 n=13 fg=0.08 bg=0.04
ocellus morphogenesis GO:0048816 p=9.3E−03 n=2 fg=0.01 bg=0.00
lactate biosynthetic process GO:0019249 p=9.3E−03 n=2 fg=0.01 bg=0.00
neural plate morphogenesis GO:0001839 p=9.3E−03 n=2 fg=0.01 bg=0.00
rhabdomere morphogenesis GO:0061541 p=9.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of transforming grow... GO:0071636 p=9.3E−03 n=2 fg=0.01 bg=0.00
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−log(p)
n=154/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032362945.2
fraction genes in fg and expected valu
extracellularly glutamate−gated chloride... GO:0008068 p=7.3E−04 n=3 fg=0.02 bg=0.00
ion gated channel activity GO:0022839 p=1.1E−03 n=10 fg=0.07 bg=0.02
histone H3−tri/di/monomethyl−lysine−4 de... GO:0034647 p=3.3E−03 n=2 fg=0.01 bg=0.00
glutamate binding GO:0016595 p=3.3E−03 n=3 fg=0.02 bg=0.00
chloride transmembrane transporter activ... GO:0015108 p=5.3E−03 n=8 fg=0.06 bg=0.01
identical protein binding GO:0042802 p=7.6E−03 n=35 fg=0.26 bg=0.17
protein dimerization activity GO:0046983 p=8.3E−03 n=28 fg=0.20 bg=0.13
inosine kinase activity GO:0008906 p=9.6E−03 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=9.6E−03 n=2 fg=0.01 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=9.6E−03 n=2 fg=0.01 bg=0.00
tRNA (cytosine) methyltransferase activi... GO:0016427 p=9.6E−03 n=2 fg=0.01 bg=0.00
S100 protein binding GO:0044548 p=9.6E−03 n=2 fg=0.01 bg=0.00
magnesium ion binding GO:0000287 p=9.9E−03 n=8 fg=0.06 bg=0.02
chloride channel activity GO:0005254 p=1.1E−02 n=7 fg=0.05 bg=0.01
quaternary ammonium group binding GO:0050997 p=1.2E−02 n=3 fg=0.02 bg=0.00
anion channel activity GO:0005253 p=1.3E−02 n=7 fg=0.05 bg=0.01
myosin heavy chain binding GO:0032036 p=1.7E−02 n=3 fg=0.02 bg=0.00
phosphotransferase activity, phosphate g... GO:0016776 p=1.7E−02 n=3 fg=0.02 bg=0.00
ligand−gated anion channel activity GO:0099095 p=1.8E−02 n=5 fg=0.04 bg=0.00
phosphatidylethanolamine binding GO:0008429 p=1.8E−02 n=2 fg=0.01 bg=0.00
GABA−gated chloride ion channel activity GO:0022851 p=1.8E−02 n=2 fg=0.01 bg=0.00
acyl−CoA binding GO:0120227 p=1.8E−02 n=2 fg=0.01 bg=0.00
GABA−A receptor activity GO:0004890 p=1.8E−02 n=2 fg=0.01 bg=0.00
benzodiazepine receptor activity GO:0008503 p=1.8E−02 n=2 fg=0.01 bg=0.00
DNA binding domain binding GO:0050692 p=1.8E−02 n=2 fg=0.01 bg=0.00
tau−protein kinase activity GO:0050321 p=1.8E−02 n=2 fg=0.01 bg=0.00
GABA receptor activity GO:0016917 p=1.8E−02 n=2 fg=0.01 bg=0.00
fatty−acyl−CoA binding GO:0000062 p=1.8E−02 n=2 fg=0.01 bg=0.00
lactate dehydrogenase activity GO:0004457 p=1.8E−02 n=2 fg=0.01 bg=0.00
chromatin DNA binding GO:0031490 p=2.1E−02 n=4 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=137/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032362945.2
fraction genes in fg and expected valu
exocytic vesicle GO:0070382 p=7.7E−03 n=9 fg=0.06 bg=0.02
synaptic vesicle GO:0008021 p=1.2E−02 n=8 fg=0.05 bg=0.02
striated muscle dense body GO:0055120 p=1.6E−02 n=3 fg=0.02 bg=0.00
Golgi trans cisterna GO:0000138 p=2.6E−02 n=3 fg=0.02 bg=0.00
mitochondrial matrix GO:0005759 p=3.9E−02 n=12 fg=0.08 bg=0.05
sarcoplasmic reticulum membrane GO:0033017 p=4.1E−02 n=2 fg=0.01 bg=0.00
ESCRT III complex GO:0000815 p=4.1E−02 n=2 fg=0.01 bg=0.00
organelle membrane contact site GO:0044232 p=4.1E−02 n=2 fg=0.01 bg=0.00
euchromatin GO:0000791 p=4.8E−02 n=3 fg=0.02 bg=0.01
apical dendrite GO:0097440 p=5.5E−02 n=2 fg=0.01 bg=0.00
polytene chromosome band GO:0005704 p=5.6E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=5.6E−02 n=1 fg=0.01 bg=0.00
postsynaptic actin cytoskeleton GO:0098871 p=5.6E−02 n=1 fg=0.01 bg=0.00
microprocessor complex GO:0070877 p=5.6E−02 n=1 fg=0.01 bg=0.00
nuclear pore inner ring GO:0044611 p=5.6E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=5.6E−02 n=1 fg=0.01 bg=0.00
acrosomal membrane GO:0002080 p=5.6E−02 n=1 fg=0.01 bg=0.00
outer acrosomal membrane GO:0002081 p=5.6E−02 n=1 fg=0.01 bg=0.00
Ragulator complex GO:0071986 p=5.6E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070032 p=5.6E−02 n=1 fg=0.01 bg=0.00
synaptobrevin 2−SNAP−25−syntaxin−1a−comp... GO:0070033 p=5.6E−02 n=1 fg=0.01 bg=0.00
SUMO−targeted ubiquitin ligase complex GO:0033768 p=5.6E−02 n=1 fg=0.01 bg=0.00
ribonuclease III complex GO:1903095 p=5.6E−02 n=1 fg=0.01 bg=0.00
longitudinal sarcoplasmic reticulum GO:0014801 p=5.6E−02 n=1 fg=0.01 bg=0.00
KICSTOR complex GO:0140007 p=5.6E−02 n=1 fg=0.01 bg=0.00
ribbon synapse GO:0097470 p=5.6E−02 n=1 fg=0.01 bg=0.00
NatA complex GO:0031415 p=5.6E−02 n=1 fg=0.01 bg=0.00
kinesin I complex GO:0016938 p=5.6E−02 n=1 fg=0.01 bg=0.00
postsynaptic cytoskeleton GO:0099571 p=5.6E−02 n=1 fg=0.01 bg=0.00
platelet dense tubular network GO:0031094 p=5.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=152/570 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction