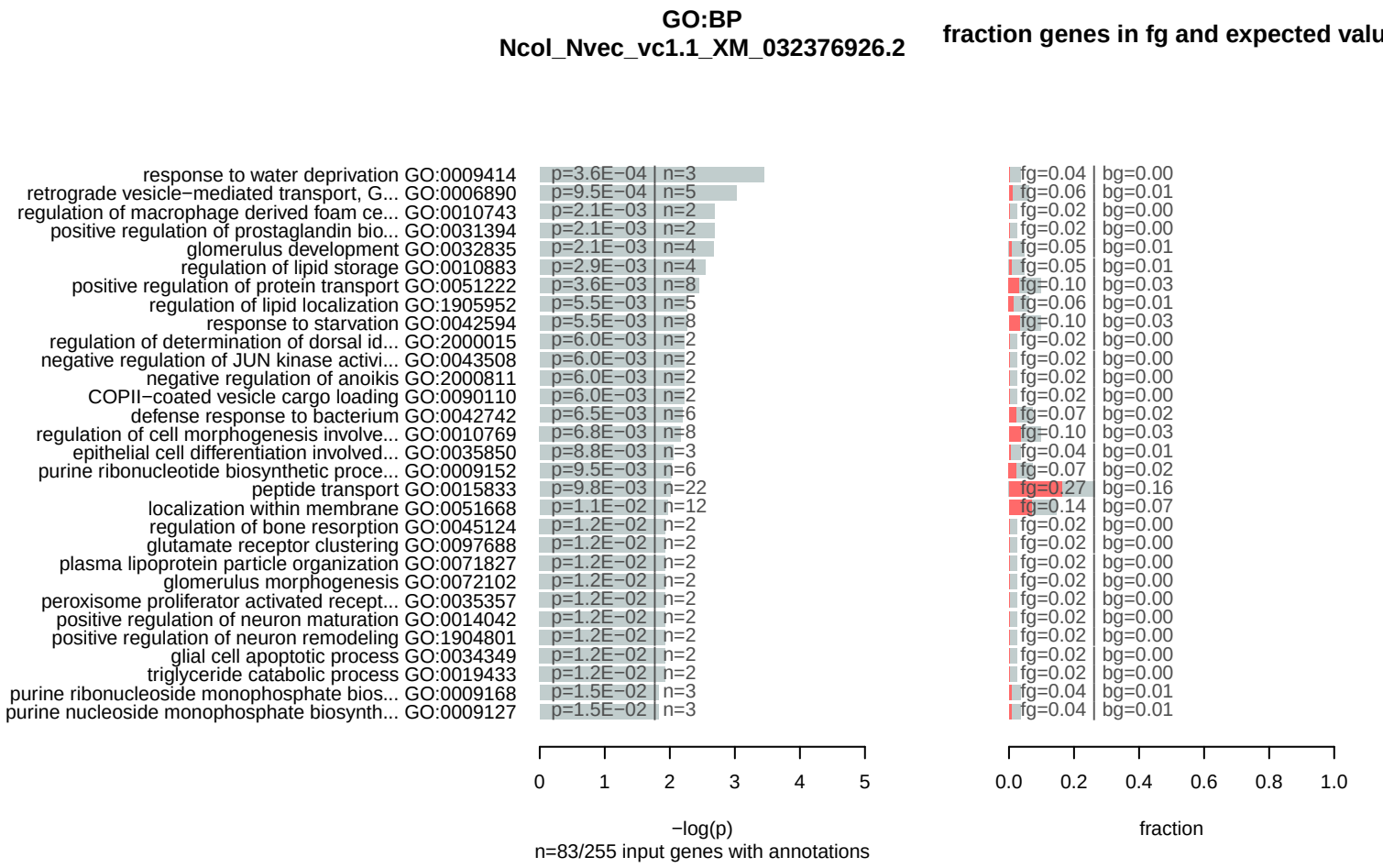
GO:BP
Ncol_Nvec_vc1.1_XM_032376926.2
fraction genes in fg and expected valu
response to water deprivation GO:0009414 p=3.6E−04 n=3 fg=0.04 bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890 p=9.5E−04 n=5 fg=0.06 bg=0.01
regulation of macrophage derived foam ce... GO:0010743 p=2.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of prostaglandin bio... GO:0031394 p=2.1E−03 n=2 fg=0.02 bg=0.00
glomerulus development GO:0032835 p=2.1E−03 n=4 fg=0.05 bg=0.01
regulation of lipid storage GO:0010883 p=2.9E−03 n=4 fg=0.05 bg=0.01
positive regulation of protein transport GO:0051222 p=3.6E−03 n=8 fg=0.10 bg=0.03
regulation of lipid localization GO:1905952 p=5.5E−03 n=5 fg=0.06 bg=0.01
response to starvation GO:0042594 p=5.5E−03 n=8 fg=0.10 bg=0.03
regulation of determination of dorsal id... GO:2000015 p=6.0E−03 n=2 fg=0.02 bg=0.00
negative regulation of JUN kinase activi... GO:0043508 p=6.0E−03 n=2 fg=0.02 bg=0.00
negative regulation of anoikis GO:2000811 p=6.0E−03 n=2 fg=0.02 bg=0.00
COPII−coated vesicle cargo loading GO:0090110 p=6.0E−03 n=2 fg=0.02 bg=0.00
defense response to bacterium GO:0042742 p=6.5E−03 n=6 fg=0.07 bg=0.02
regulation of cell morphogenesis involve... GO:0010769 p=6.8E−03 n=8 fg=0.10 bg=0.03
epithelial cell differentiation involved... GO:0035850 p=8.8E−03 n=3 fg=0.04 bg=0.01
purine ribonucleotide biosynthetic proce... GO:0009152 p=9.5E−03 n=6 fg=0.07 bg=0.02
peptide transport GO:0015833 p=9.8E−03 n=22 fg=0.27 bg=0.16
localization within membrane GO:0051668 p=1.1E−02 n=12 fg=0.14 bg=0.07
regulation of bone resorption GO:0045124 p=1.2E−02 n=2 fg=0.02 bg=0.00
glutamate receptor clustering GO:0097688 p=1.2E−02 n=2 fg=0.02 bg=0.00
plasma lipoprotein particle organization GO:0071827 p=1.2E−02 n=2 fg=0.02 bg=0.00
glomerulus morphogenesis GO:0072102 p=1.2E−02 n=2 fg=0.02 bg=0.00
peroxisome proliferator activated recept... GO:0035357 p=1.2E−02 n=2 fg=0.02 bg=0.00
positive regulation of neuron maturation GO:0014042 p=1.2E−02 n=2 fg=0.02 bg=0.00
positive regulation of neuron remodeling GO:1904801 p=1.2E−02 n=2 fg=0.02 bg=0.00
glial cell apoptotic process GO:0034349 p=1.2E−02 n=2 fg=0.02 bg=0.00
triglyceride catabolic process GO:0019433 p=1.2E−02 n=2 fg=0.02 bg=0.00
purine ribonucleoside monophosphate bios... GO:0009168 p=1.5E−02 n=3 fg=0.04 bg=0.01
purine nucleoside monophosphate biosynth... GO:0009127 p=1.5E−02 n=3 fg=0.04 bg=0.01
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−log(p)
n=83/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032376926.2
fraction genes in fg and expected valu
cysteine−type endopeptidase activator ac... GO:0008656 p=6.2E−03 n=2 fg=0.03 bg=0.00
triglyceride lipase activity GO:0004806 p=6.2E−03 n=2 fg=0.03 bg=0.00
transporter activity GO:0005215 p=1.3E−02 n=15 fg=0.20 bg=0.11
acyltransferase activity, transferring g... GO:0016747 p=1.4E−02 n=4 fg=0.05 bg=0.01
transmembrane transporter activity GO:0022857 p=1.4E−02 n=13 fg=0.18 bg=0.09
acyltransferase activity GO:0016746 p=1.9E−02 n=4 fg=0.05 bg=0.01
dynactin binding GO:0034452 p=1.9E−02 n=2 fg=0.03 bg=0.00
inorganic molecular entity transmembrane... GO:0015318 p=3.1E−02 n=10 fg=0.14 bg=0.07
phospholipase activity GO:0004620 p=3.5E−02 n=3 fg=0.04 bg=0.01
ion transmembrane transporter activity GO:0015075 p=3.8E−02 n=10 fg=0.14 bg=0.07
3'−phosphoadenosine 5'−phosphosulfate tr... GO:0046964 p=4.6E−02 n=1 fg=0.01 bg=0.00
tropomyosin binding GO:0005523 p=4.6E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=4.6E−02 n=1 fg=0.01 bg=0.00
taste receptor binding GO:0031883 p=4.6E−02 n=1 fg=0.01 bg=0.00
neurotrophin binding GO:0043121 p=4.6E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=4.6E−02 n=1 fg=0.01 bg=0.00
glutamate−ammonia ligase activity GO:0004356 p=4.6E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=4.6E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=4.6E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=4.6E−02 n=1 fg=0.01 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=4.6E−02 n=1 fg=0.01 bg=0.00
protein−membrane adaptor activity GO:0043495 p=4.6E−02 n=1 fg=0.01 bg=0.00
C−acyltransferase activity GO:0016408 p=4.6E−02 n=1 fg=0.01 bg=0.00
tricarboxylate secondary active transmem... GO:0005371 p=4.6E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=4.6E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity GO:0016229 p=4.6E−02 n=1 fg=0.01 bg=0.00
adenosine−phosphate deaminase activity GO:0047623 p=4.6E−02 n=1 fg=0.01 bg=0.00
ammonia ligase activity GO:0016211 p=4.6E−02 n=1 fg=0.01 bg=0.00
7S RNA binding GO:0008312 p=4.6E−02 n=1 fg=0.01 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032376926.2
fraction genes in fg and expected valu
transport vesicle membrane GO:0030658 p=3.6E−04 n=7 fg=0.08 bg=0.02
Golgi membrane GO:0000139 p=9.3E−03 n=11 fg=0.13 bg=0.06
exocytic vesicle membrane GO:0099501 p=1.1E−02 n=4 fg=0.05 bg=0.01
basal dendrite GO:0097441 p=1.2E−02 n=2 fg=0.02 bg=0.00
Golgi−associated vesicle membrane GO:0030660 p=2.4E−02 n=3 fg=0.04 bg=0.01
endosome GO:0005768 p=2.6E−02 n=13 fg=0.16 bg=0.09
Golgi apparatus subcompartment GO:0098791 p=3.2E−02 n=12 fg=0.14 bg=0.08
Golgi stack GO:0005795 p=3.7E−02 n=5 fg=0.06 bg=0.02
exocytic vesicle GO:0070382 p=3.7E−02 n=6 fg=0.07 bg=0.03
vesicle coat GO:0030120 p=3.8E−02 n=2 fg=0.02 bg=0.00
neuron projection cytoplasm GO:0120111 p=3.8E−02 n=2 fg=0.02 bg=0.00
apical dendrite GO:0097440 p=3.8E−02 n=2 fg=0.02 bg=0.00
organelle subcompartment GO:0031984 p=4.1E−02 n=18 fg=0.22 bg=0.14
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.6E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=4.6E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=4.6E−02 n=1 fg=0.01 bg=0.00
apoptosome GO:0043293 p=4.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase com... GO:0005967 p=4.6E−02 n=1 fg=0.01 bg=0.00
kinesin I complex GO:0016938 p=4.6E−02 n=1 fg=0.01 bg=0.00
endoplasmic reticulum membrane GO:0005789 p=4.9E−02 n=11 fg=0.13 bg=0.08
Golgi lumen GO:0005796 p=4.9E−02 n=2 fg=0.02 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=4.9E−02 n=2 fg=0.02 bg=0.00
cytoplasmic microtubule GO:0005881 p=4.9E−02 n=2 fg=0.02 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=4.9E−02 n=2 fg=0.02 bg=0.00
nuclear outer membrane−endoplasmic retic... GO:0042175 p=5.3E−02 n=11 fg=0.13 bg=0.08
synaptic vesicle membrane GO:0030672 p=5.3E−02 n=3 fg=0.04 bg=0.01
microtubule GO:0005874 p=5.6E−02 n=4 fg=0.05 bg=0.02
endoplasmic reticulum subcompartment GO:0098827 p=6.0E−02 n=11 fg=0.13 bg=0.08
endoplasmic reticulum−Golgi intermediate... GO:0005793 p=6.0E−02 n=3 fg=0.04 bg=0.01
melanosome GO:0042470 p=6.1E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/255 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction