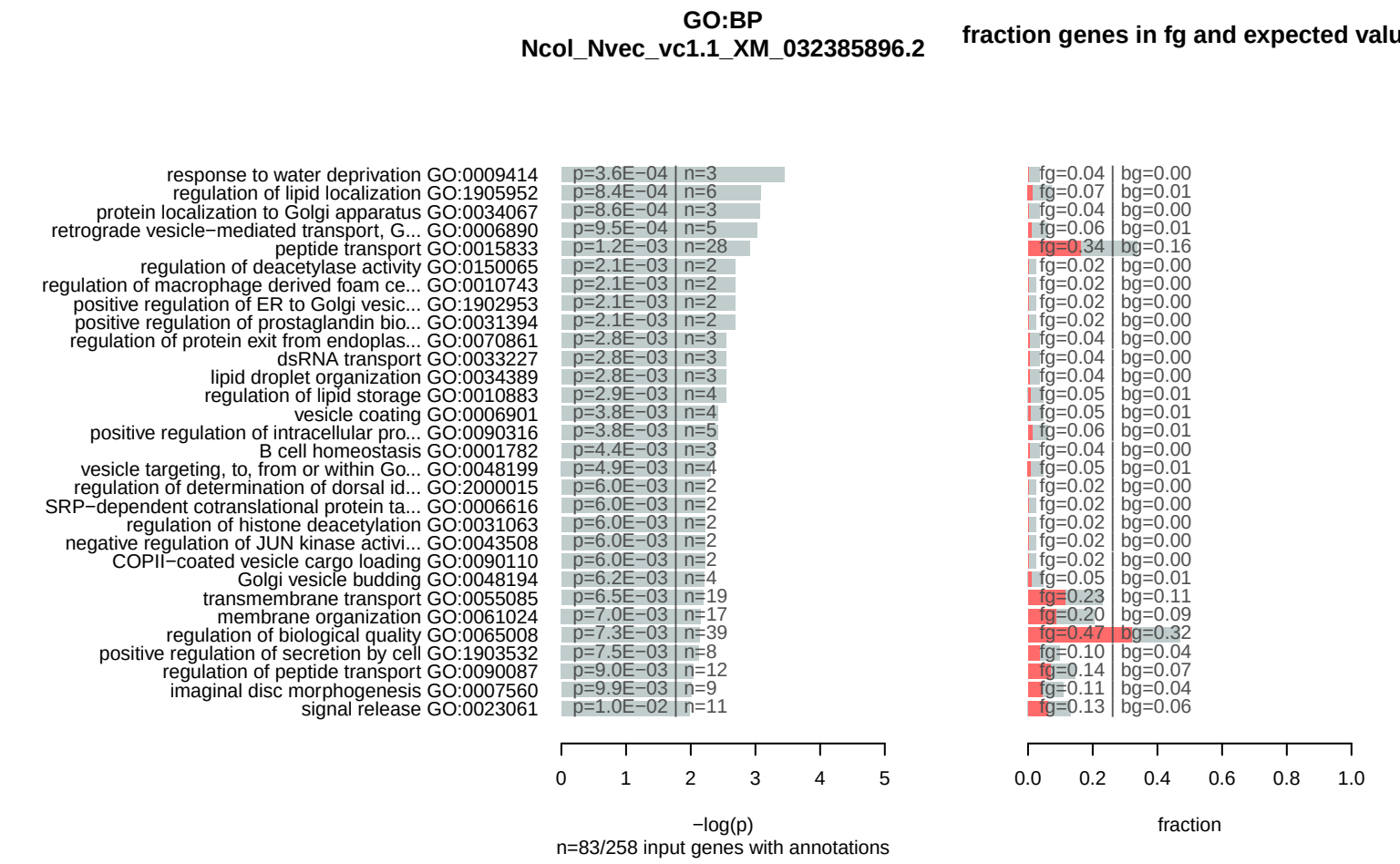
GO:BP
Ncol_Nvec_vc1.1_XM_032385896.2
fraction genes in fg and expected valu
response to water deprivation GO:0009414 p=3.6E−04 n=3 fg=0.04 bg=0.00
regulation of lipid localization GO:1905952 p=8.4E−04 n=6 fg=0.07 bg=0.01
protein localization to Golgi apparatus GO:0034067 p=8.6E−04 n=3 fg=0.04 bg=0.00
retrograde vesicle−mediated transport, G... GO:0006890 p=9.5E−04 n=5 fg=0.06 bg=0.01
peptide transport GO:0015833 p=1.2E−03 n=28 fg=0.34 bg=0.16
regulation of deacetylase activity GO:0150065 p=2.1E−03 n=2 fg=0.02 bg=0.00
regulation of macrophage derived foam ce... GO:0010743 p=2.1E−03 n=2 fg=0.02 bg=0.00
positive regulation of ER to Golgi vesic... GO:1902953 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
regulation of protein exit from endoplas... GO:0070861 p=2.8E−03 n=3 fg=0.04 bg=0.00
dsRNA transport GO:0033227 p=2.8E−03 n=3 fg=0.04 bg=0.00
lipid droplet organization GO:0034389 p=2.8E−03 n=3 fg=0.04 bg=0.00
regulation of lipid storage GO:0010883 p=2.9E−03 n=4 fg=0.05 bg=0.01
vesicle coating GO:0006901 p=3.8E−03 n=4 fg=0.05 bg=0.01
positive regulation of intracellular pro... GO:0090316 p=3.8E−03 n=5 fg=0.06 bg=0.01
B cell homeostasis GO:0001782 p=4.4E−03 n=3 fg=0.04 bg=0.00
vesicle targeting, to, from or within Go... GO:0048199 p=4.9E−03 n=4 fg=0.05 bg=0.01
regulation of determination of dorsal id... GO:2000015 p=6.0E−03 n=2 fg=0.02 bg=0.00
SRP−dependent cotranslational protein ta... GO:0006616 p=6.0E−03 n=2 fg=0.02 bg=0.00
regulation of histone deacetylation GO:0031063 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
COPII−coated vesicle cargo loading GO:0090110 p=6.0E−03 n=2 fg=0.02 bg=0.00
Golgi vesicle budding GO:0048194 p=6.2E−03 n=4 fg=0.05 bg=0.01
transmembrane transport GO:0055085 p=6.5E−03 n=19 fg=0.23 bg=0.11
membrane organization GO:0061024 p=7.0E−03 n=17 fg=0.20 bg=0.09
regulation of biological quality GO:0065008 p=7.3E−03 n=39 fg=0.47 bg=0.32
positive regulation of secretion by cell GO:1903532 p=7.5E−03 n=8 fg=0.10 bg=0.04
regulation of peptide transport GO:0090087 p=9.0E−03 n=12 fg=0.14 bg=0.07
imaginal disc morphogenesis GO:0007560 p=9.9E−03 n=9 fg=0.11 bg=0.04
signal release GO:0023061 p=1.0E−02 n=11 fg=0.13 bg=0.06
0 1 2 3 4 5
−log(p)
n=83/258 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032385896.2
fraction genes in fg and expected valu
cysteine−type endopeptidase activator ac... GO:0008656 p=6.5E−03 n=2 fg=0.03 bg=0.00
triglyceride lipase activity GO:0004806 p=6.5E−03 n=2 fg=0.03 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=9.8E−03 n=3 fg=0.04 bg=0.01
acyltransferase activity, transferring g... GO:0016747 p=1.5E−02 n=4 fg=0.05 bg=0.01
small GTPase binding GO:0031267 p=1.8E−02 n=9 fg=0.12 bg=0.05
dynactin binding GO:0034452 p=2.1E−02 n=2 fg=0.03 bg=0.00
acyltransferase activity GO:0016746 p=2.1E−02 n=4 fg=0.05 bg=0.01
GTPase activity GO:0003924 p=2.6E−02 n=5 fg=0.07 bg=0.02
DNA−binding transcription factor activit... GO:0000981 p=2.7E−02 n=10 fg=0.13 bg=0.07
enzyme binding GO:0019899 p=3.0E−02 n=26 fg=0.34 bg=0.24
DNA−binding transcription factor activit... GO:0003700 p=4.0E−02 n=11 fg=0.14 bg=0.08
GTP binding GO:0005525 p=4.6E−02 n=4 fg=0.05 bg=0.02
purine ribonucleoside binding GO:0032550 p=4.6E−02 n=4 fg=0.05 bg=0.02
ribonucleoside binding GO:0032549 p=4.6E−02 n=4 fg=0.05 bg=0.02
3'−phosphoadenosine 5'−phosphosulfate tr... GO:0046964 p=4.8E−02 n=1 fg=0.01 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=4.8E−02 n=1 fg=0.01 bg=0.00
low−density lipoprotein particle binding GO:0030169 p=4.8E−02 n=1 fg=0.01 bg=0.00
taste receptor binding GO:0031883 p=4.8E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=4.8E−02 n=1 fg=0.01 bg=0.00
glutamate−ammonia ligase activity GO:0004356 p=4.8E−02 n=1 fg=0.01 bg=0.00
D−xylose 1−dehydrogenase (NADP+) activit... GO:0047837 p=4.8E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=4.8E−02 n=1 fg=0.01 bg=0.00
mono−olein transacylation activity GO:0051264 p=4.8E−02 n=1 fg=0.01 bg=0.00
diolein transacylation activity GO:0051265 p=4.8E−02 n=1 fg=0.01 bg=0.00
ABC−type sterol transporter activity GO:0034041 p=4.8E−02 n=1 fg=0.01 bg=0.00
protein−membrane adaptor activity GO:0043495 p=4.8E−02 n=1 fg=0.01 bg=0.00
C−acyltransferase activity GO:0016408 p=4.8E−02 n=1 fg=0.01 bg=0.00
tricarboxylate secondary active transmem... GO:0005371 p=4.8E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=4.8E−02 n=1 fg=0.01 bg=0.00
steroid dehydrogenase activity GO:0016229 p=4.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/258 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032385896.2
fraction genes in fg and expected valu
Golgi membrane GO:0000139 p=4.2E−04 n=14 fg=0.16 bg=0.06
Golgi apparatus subcompartment GO:0098791 p=3.0E−03 n=15 fg=0.17 bg=0.08
endoplasmic reticulum−Golgi intermediate... GO:0033116 p=7.1E−03 n=3 fg=0.03 bg=0.01
cytoplasmic vesicle membrane GO:0030659 p=7.3E−03 n=14 fg=0.16 bg=0.08
endoplasmic reticulum GO:0005783 p=8.5E−03 n=21 fg=0.24 bg=0.14
endoplasmic reticulum membrane GO:0005789 p=1.2E−02 n=13 fg=0.15 bg=0.08
basal dendrite GO:0097441 p=1.3E−02 n=2 fg=0.02 bg=0.00
transport vesicle GO:0030133 p=1.3E−02 n=9 fg=0.10 bg=0.04
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.3E−02 n=13 fg=0.15 bg=0.08
transport vesicle membrane GO:0030658 p=1.4E−02 n=5 fg=0.06 bg=0.02
endosome GO:0005768 p=1.5E−02 n=14 fg=0.16 bg=0.09
endoplasmic reticulum subcompartment GO:0098827 p=1.6E−02 n=13 fg=0.15 bg=0.08
anchored component of membrane GO:0031225 p=2.0E−02 n=2 fg=0.02 bg=0.00
endosome membrane GO:0010008 p=2.7E−02 n=7 fg=0.08 bg=0.03
cell division site GO:0032153 p=3.1E−02 n=3 fg=0.03 bg=0.01
intrinsic component of plasma membrane GO:0031226 p=3.9E−02 n=12 fg=0.14 bg=0.08
vesicle coat GO:0030120 p=4.0E−02 n=2 fg=0.02 bg=0.00
Golgi stack GO:0005795 p=4.2E−02 n=5 fg=0.06 bg=0.02
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=4.8E−02 n=1 fg=0.01 bg=0.00
signal recognition particle GO:0048500 p=4.8E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=4.8E−02 n=1 fg=0.01 bg=0.00
intrinsic component of autophagosome mem... GO:0097636 p=4.8E−02 n=1 fg=0.01 bg=0.00
integral component of autophagosome memb... GO:0097637 p=4.8E−02 n=1 fg=0.01 bg=0.00
actin cortical patch GO:0030479 p=4.8E−02 n=1 fg=0.01 bg=0.00
signal recognition particle, endoplasmic... GO:0005786 p=4.8E−02 n=1 fg=0.01 bg=0.00
endocytic patch GO:0061645 p=4.8E−02 n=1 fg=0.01 bg=0.00
periciliary membrane compartment GO:1990075 p=4.8E−02 n=1 fg=0.01 bg=0.00
apoptosome GO:0043293 p=4.8E−02 n=1 fg=0.01 bg=0.00
Golgi lumen GO:0005796 p=5.2E−02 n=2 fg=0.02 bg=0.00
proton−transporting V−type ATPase comple... GO:0033176 p=5.2E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=86/258 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction