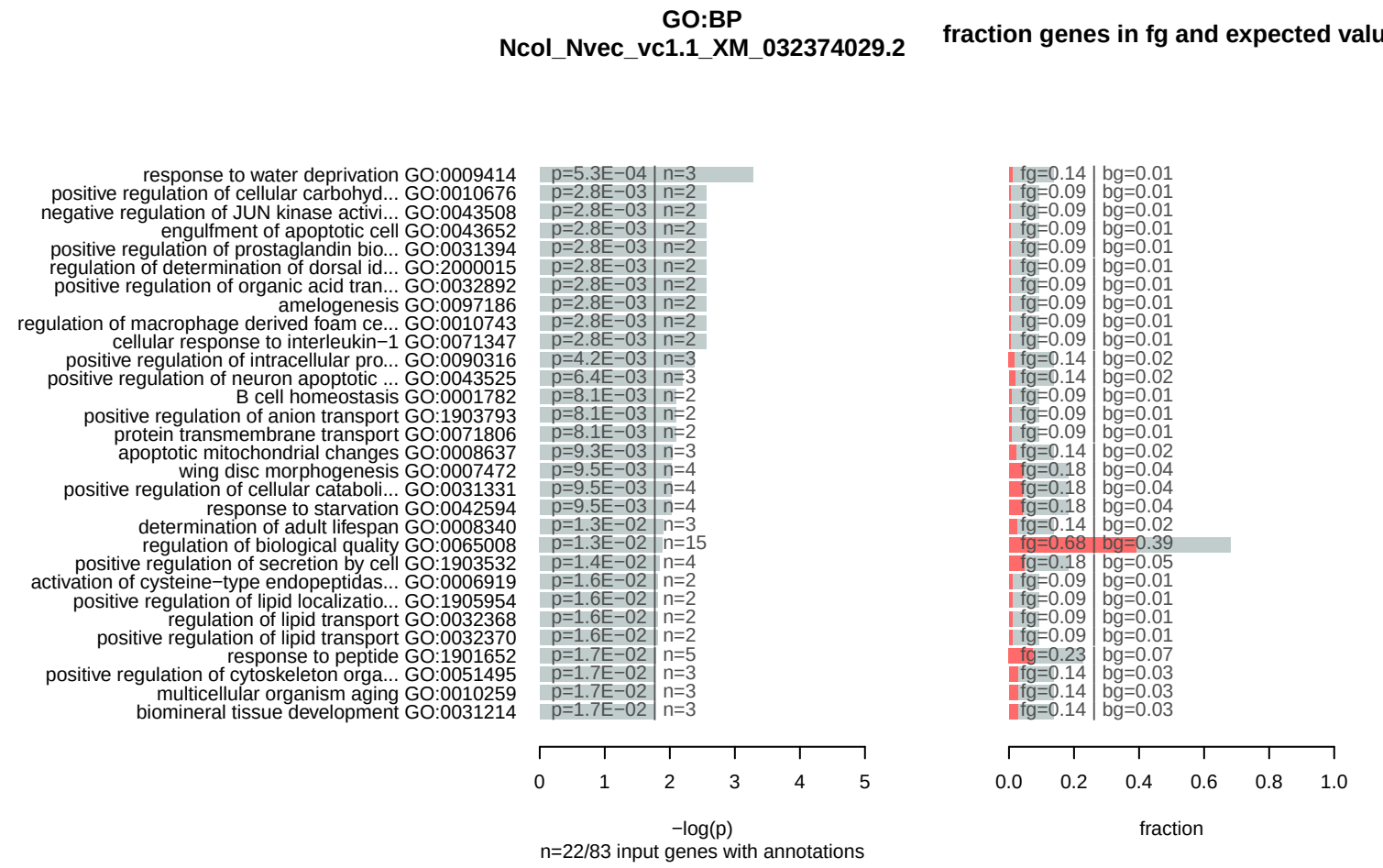
GO:BP
Ncol_Nvec_vc1.1_XM_032374029.2
fraction genes in fg and expected valu
response to water deprivation GO:0009414 p=5.3E−04 n=3 fg=0.14 bg=0.01
positive regulation of cellular carbohyd... GO:0010676 p=2.8E−03 n=2 fg=0.09 bg=0.01
negative regulation of JUN kinase activi... GO:0043508 p=2.8E−03 n=2 fg=0.09 bg=0.01
engulfment of apoptotic cell GO:0043652 p=2.8E−03 n=2 fg=0.09 bg=0.01
positive regulation of prostaglandin bio... GO:0031394 p=2.8E−03 n=2 fg=0.09 bg=0.01
regulation of determination of dorsal id... GO:2000015 p=2.8E−03 n=2 fg=0.09 bg=0.01
positive regulation of organic acid tran... GO:0032892 p=2.8E−03 n=2 fg=0.09 bg=0.01
amelogenesis GO:0097186 p=2.8E−03 n=2 fg=0.09 bg=0.01
regulation of macrophage derived foam ce... GO:0010743 p=2.8E−03 n=2 fg=0.09 bg=0.01
cellular response to interleukin−1 GO:0071347 p=2.8E−03 n=2 fg=0.09 bg=0.01
positive regulation of intracellular pro... GO:0090316 p=4.2E−03 n=3 fg=0.14 bg=0.02
positive regulation of neuron apoptotic ... GO:0043525 p=6.4E−03 n=3 fg=0.14 bg=0.02
B cell homeostasis GO:0001782 p=8.1E−03 n=2 fg=0.09 bg=0.01
positive regulation of anion transport GO:1903793 p=8.1E−03 n=2 fg=0.09 bg=0.01
protein transmembrane transport GO:0071806 p=8.1E−03 n=2 fg=0.09 bg=0.01
apoptotic mitochondrial changes GO:0008637 p=9.3E−03 n=3 fg=0.14 bg=0.02
wing disc morphogenesis GO:0007472 p=9.5E−03 n=4 fg=0.18 bg=0.04
positive regulation of cellular catabolic... GO:0031331 p=9.5E−03 n=4 fg=0.18 bg=0.04
response to starvation GO:0042594 p=9.5E−03 n=4 fg=0.18 bg=0.04
determination of adult lifespan GO:0008340 p=1.3E−02 n=3 fg=0.14 bg=0.02
regulation of biological quality GO:0065008 p=1.3E−02 n=15 fg=0.68 bg=0.39
positive regulation of secretion by cell GO:1903532 p=1.4E−02 n=4 fg=0.18 bg=0.05
activation of cysteine−type endopeptidas... GO:0006919 p=1.6E−02 n=2 fg=0.09 bg=0.01
positive regulation of lipid localizatio... GO:1905954 p=1.6E−02 n=2 fg=0.09 bg=0.01
regulation of lipid transport GO:0032368 p=1.6E−02 n=2 fg=0.09 bg=0.01
positive regulation of lipid transport GO:0032370 p=1.6E−02 n=2 fg=0.09 bg=0.01
response to peptide GO:1901652 p=1.7E−02 n=5 fg=0.23 bg=0.07
positive regulation of cytoskeleton orga... GO:0051495 p=1.7E−02 n=3 fg=0.14 bg=0.03
multicellular organism aging GO:0010259 p=1.7E−02 n=3 fg=0.14 bg=0.03
biomineral tissue development GO:0031214 p=1.7E−02 n=3 fg=0.14 bg=0.03
0 1 2 3 4 5
−log(p)
n=22/83 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032374029.2
fraction genes in fg and expected valu
ATP binding GO:0005524 p=6.8E−03 n=4 fg=0.18 bg=0.04
voltage−gated potassium channel activity GO:0005249 p=1.3E−02 n=3 fg=0.14 bg=0.02
transmembrane transporter activity GO:0022857 p=2.5E−02 n=7 fg=0.32 bg=0.14
potassium channel activity GO:0005267 p=3.0E−02 n=3 fg=0.14 bg=0.03
potassium ion transmembrane transporter ... GO:0015079 p=3.0E−02 n=3 fg=0.14 bg=0.03
transporter activity GO:0005215 p=4.4E−02 n=7 fg=0.32 bg=0.16
voltage−gated cation channel activity GO:0022843 p=4.5E−02 n=3 fg=0.14 bg=0.04
channel activity GO:0015267 p=5.4E−02 n=5 fg=0.23 bg=0.10
passive transmembrane transporter activi... GO:0022803 p=5.4E−02 n=5 fg=0.23 bg=0.10
voltage−gated ion channel activity GO:0005244 p=5.4E−02 n=3 fg=0.14 bg=0.04
voltage−gated channel activity GO:0022832 p=5.4E−02 n=3 fg=0.14 bg=0.04
inorganic molecular entity transmembrane... GO:0015318 p=5.4E−02 n=6 fg=0.27 bg=0.13
tricarboxylate secondary active transmem... GO:0005371 p=6.0E−02 n=1 fg=0.05 bg=0.00
BH3 domain binding GO:0051434 p=6.0E−02 n=1 fg=0.05 bg=0.00
nucleotidyltransferase activity GO:0016779 p=6.0E−02 n=1 fg=0.05 bg=0.00
V1A vasopressin receptor binding GO:0031894 p=6.0E−02 n=1 fg=0.05 bg=0.00
cysteine−type endopeptidase activator ac... GO:0008656 p=6.0E−02 n=1 fg=0.05 bg=0.00
open rectifier potassium channel activit... GO:0005252 p=6.0E−02 n=1 fg=0.05 bg=0.00
choline−phosphate cytidylyltransferase a... GO:0004105 p=6.0E−02 n=1 fg=0.05 bg=0.00
cytidylyltransferase activity GO:0070567 p=6.0E−02 n=1 fg=0.05 bg=0.00
macromolecule transmembrane transporter ... GO:0022884 p=6.0E−02 n=1 fg=0.05 bg=0.00
fructose−6−phosphate binding GO:0070095 p=6.0E−02 n=1 fg=0.05 bg=0.00
protein phosphatase activator activity GO:0072542 p=6.0E−02 n=1 fg=0.05 bg=0.00
histone deacetylase regulator activity GO:0035033 p=6.0E−02 n=1 fg=0.05 bg=0.00
JUN kinase activity GO:0004705 p=6.0E−02 n=1 fg=0.05 bg=0.00
MAP kinase activity GO:0004707 p=6.0E−02 n=1 fg=0.05 bg=0.00
glucuronosyltransferase activity GO:0015020 p=6.0E−02 n=1 fg=0.05 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=6.0E−02 n=1 fg=0.05 bg=0.00
carbohydrate kinase activity GO:0019200 p=6.0E−02 n=1 fg=0.05 bg=0.00
carbohydrate phosphatase activity GO:0019203 p=6.0E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=22/83 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032374029.2
fraction genes in fg and expected valu
Golgi lumen GO:0005796 p=3.7E−03 n=2 fg=0.08 bg=0.00
anchored component of membrane GO:0031225 p=3.7E−03 n=2 fg=0.08 bg=0.00
organelle envelope GO:0031967 p=2.3E−02 n=5 fg=0.20 bg=0.07
envelope GO:0031975 p=2.3E−02 n=5 fg=0.20 bg=0.07
intrinsic component of plasma membrane GO:0031226 p=3.0E−02 n=8 fg=0.32 bg=0.16
mitochondrion GO:0005739 p=3.4E−02 n=5 fg=0.20 bg=0.08
organelle outer membrane GO:0031968 p=4.8E−02 n=2 fg=0.08 bg=0.01
outer membrane GO:0019867 p=4.8E−02 n=2 fg=0.08 bg=0.01
mitochondrial outer membrane GO:0005741 p=4.8E−02 n=2 fg=0.08 bg=0.01
mitochondrial membrane GO:0031966 p=4.9E−02 n=3 fg=0.12 bg=0.03
anchored component of plasma membrane GO:0046658 p=6.2E−02 n=1 fg=0.04 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=6.2E−02 n=1 fg=0.04 bg=0.00
glycogen granule GO:0042587 p=6.2E−02 n=1 fg=0.04 bg=0.00
Bcl−2 family protein complex GO:0097136 p=6.2E−02 n=1 fg=0.04 bg=0.00
dendrite cytoplasm GO:0032839 p=6.2E−02 n=1 fg=0.04 bg=0.00
podosome GO:0002102 p=6.2E−02 n=1 fg=0.04 bg=0.00
neuron projection cytoplasm GO:0120111 p=6.2E−02 n=1 fg=0.04 bg=0.00
muscle cell projection GO:0036194 p=6.2E−02 n=1 fg=0.04 bg=0.00
muscle cell projection membrane GO:0036195 p=6.2E−02 n=1 fg=0.04 bg=0.00
sarcoplasmic reticulum membrane GO:0033017 p=6.2E−02 n=1 fg=0.04 bg=0.00
mitochondrial envelope GO:0005740 p=7.0E−02 n=3 fg=0.12 bg=0.04
voltage−gated potassium channel complex GO:0008076 p=8.3E−02 n=2 fg=0.08 bg=0.02
potassium channel complex GO:0034705 p=8.3E−02 n=2 fg=0.08 bg=0.02
sarcoplasm GO:0016528 p=1.2E−01 n=1 fg=0.04 bg=0.00
sarcoplasmic reticulum GO:0016529 p=1.2E−01 n=1 fg=0.04 bg=0.00
cortical endoplasmic reticulum GO:0032541 p=1.2E−01 n=1 fg=0.04 bg=0.00
site of double−strand break GO:0035861 p=1.2E−01 n=1 fg=0.04 bg=0.00
site of DNA damage GO:0090734 p=1.2E−01 n=1 fg=0.04 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=1.2E−01 n=1 fg=0.04 bg=0.00
endoplasmic reticulum tubular network GO:0071782 p=1.2E−01 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=25/83 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction