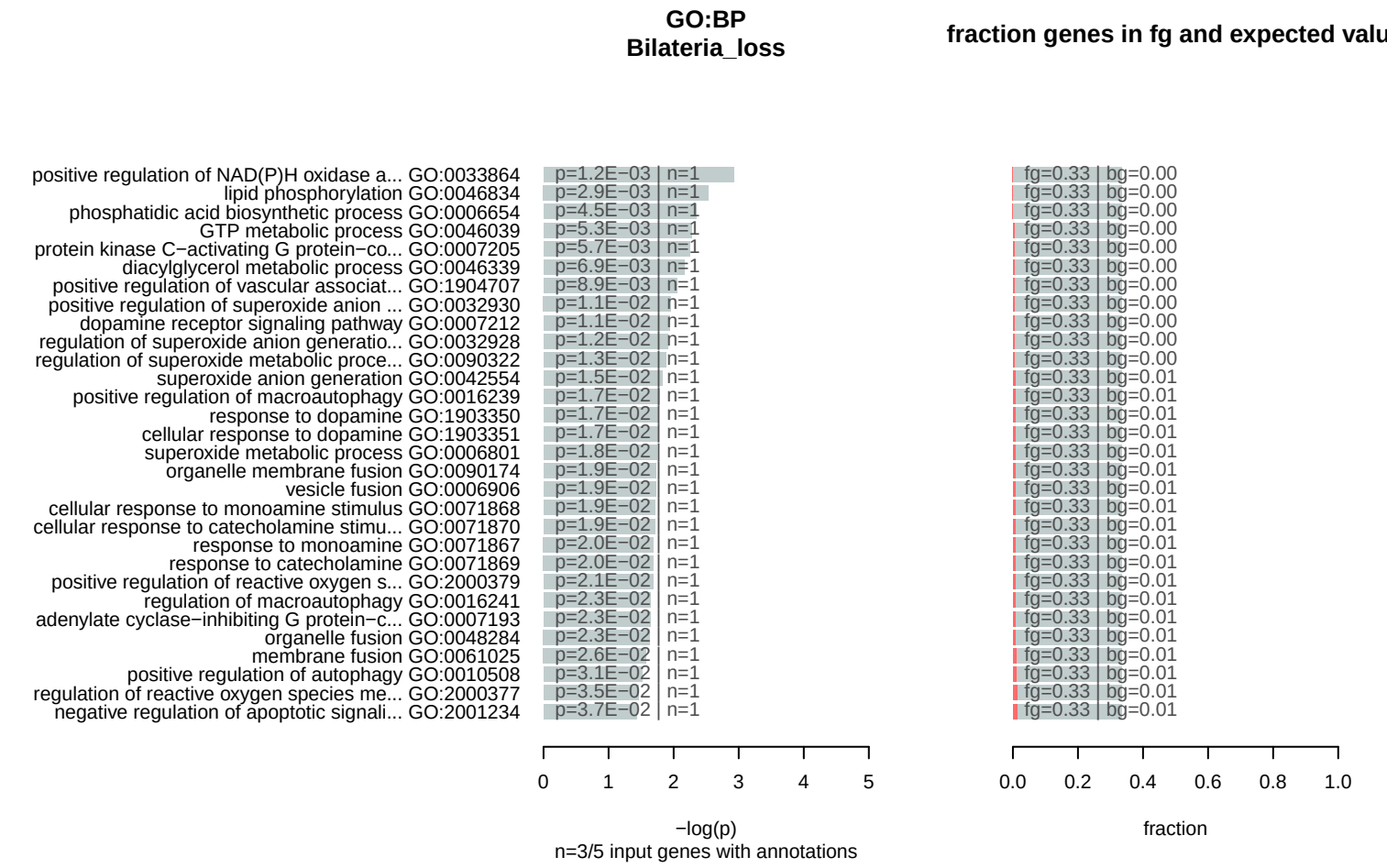
GO:BP
Bilateria_loss
fraction genes in fg and expected valu
positive regulation of NAD(P)H oxidase a... GO:0033864 p=1.2E−03 n=1 fg=0.33 bg=0.00
lipid phosphorylation GO:0046834 p=2.9E−03 n=1 fg=0.33 bg=0.00
phosphatidic acid biosynthetic process GO:0006654 p=4.5E−03 n=1 fg=0.33 bg=0.00
GTP metabolic process GO:0046039 p=5.3E−03 n=1 fg=0.33 bg=0.00
protein kinase C−activating G protein−co... GO:0007205 p=5.7E−03 n=1 fg=0.33 bg=0.00
diacylglycerol metabolic process GO:0046339 p=6.9E−03 n=1 fg=0.33 bg=0.00
positive regulation of vascular associat... GO:1904707 p=8.9E−03 n=1 fg=0.33 bg=0.00
positive regulation of superoxide anion ... GO:0032930 p=1.1E−02 n=1 fg=0.33 bg=0.00
dopamine receptor signaling pathway GO:0007212 p=1.1E−02 n=1 fg=0.33 bg=0.00
regulation of superoxide anion generatio... GO:0032928 p=1.2E−02 n=1 fg=0.33 bg=0.00
regulation of superoxide metabolic proce... GO:0090322 p=1.3E−02 n=1 fg=0.33 bg=0.00
superoxide anion generation GO:0042554 p=1.5E−02 n=1 fg=0.33 bg=0.01
positive regulation of macroautophagy GO:0016239 p=1.7E−02 n=1 fg=0.33 bg=0.01
response to dopamine GO:1903350 p=1.7E−02 n=1 fg=0.33 bg=0.01
cellular response to dopamine GO:1903351 p=1.7E−02 n=1 fg=0.33 bg=0.01
superoxide metabolic process GO:0006801 p=1.8E−02 n=1 fg=0.33 bg=0.01
organelle membrane fusion GO:0090174 p=1.9E−02 n=1 fg=0.33 bg=0.01
vesicle fusion GO:0006906 p=1.9E−02 n=1 fg=0.33 bg=0.01
cellular response to monoamine stimulus GO:0071868 p=1.9E−02 n=1 fg=0.33 bg=0.01
cellular response to catecholamine stimu... GO:0071870 p=1.9E−02 n=1 fg=0.33 bg=0.01
response to monoamine GO:0071867 p=2.0E−02 n=1 fg=0.33 bg=0.01
response to catecholamine GO:0071869 p=2.0E−02 n=1 fg=0.33 bg=0.01
positive regulation of reactive oxygen s... GO:2000379 p=2.1E−02 n=1 fg=0.33 bg=0.01
regulation of macroautophagy GO:0016241 p=2.3E−02 n=1 fg=0.33 bg=0.01
adenylate cyclase−inhibiting G protein−c... GO:0007193 p=2.3E−02 n=1 fg=0.33 bg=0.01
organelle fusion GO:0048284 p=2.3E−02 n=1 fg=0.33 bg=0.01
membrane fusion GO:0061025 p=2.6E−02 n=1 fg=0.33 bg=0.01
positive regulation of autophagy GO:0010508 p=3.1E−02 n=1 fg=0.33 bg=0.01
regulation of reactive oxygen species me... GO:2000377 p=3.5E−02 n=1 fg=0.33 bg=0.01
negative regulation of apoptotic signali... GO:2001234 p=3.7E−02 n=1 fg=0.33 bg=0.01
0 1 2 3 4 5
−log(p)
n=3/5 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Bilateria_loss
fraction genes in fg and expected valu
G protein−coupled serotonin receptor bin... GO:0031821 p=2.0E−03 n=1 fg=0.33 bg=0.00
diacylglycerol kinase activity GO:0004143 p=2.8E−03 n=1 fg=0.33 bg=0.00
NAD+ kinase activity GO:0003951 p=3.6E−03 n=1 fg=0.33 bg=0.00
glutathione peroxidase activity GO:0004602 p=6.1E−03 n=1 fg=0.33 bg=0.00
GTPase activating protein binding GO:0032794 p=6.5E−03 n=1 fg=0.33 bg=0.00
G−protein beta/gamma−subunit complex bin... GO:0031683 p=8.9E−03 n=1 fg=0.33 bg=0.00
GDP binding GO:0019003 p=2.0E−02 n=1 fg=0.33 bg=0.01
purine ribonucleoside triphosphate bindi... GO:0035639 p=3.7E−02 n=2 fg=0.67 bg=0.12
purine ribonucleotide binding GO:0032555 p=4.1E−02 n=2 fg=0.67 bg=0.12
purine nucleotide binding GO:0017076 p=4.1E−02 n=2 fg=0.67 bg=0.12
ribonucleotide binding GO:0032553 p=4.1E−02 n=2 fg=0.67 bg=0.12
nucleoside phosphate binding GO:1901265 p=4.8E−02 n=2 fg=0.67 bg=0.13
nucleotide binding GO:0000166 p=4.8E−02 n=2 fg=0.67 bg=0.13
carbohydrate derivative binding GO:0097367 p=5.5E−02 n=2 fg=0.67 bg=0.14
anion binding GO:0043168 p=6.2E−02 n=2 fg=0.67 bg=0.15
GTPase activity GO:0003924 p=6.8E−02 n=1 fg=0.33 bg=0.02
small molecule binding GO:0036094 p=6.8E−02 n=2 fg=0.67 bg=0.16
GTP binding GO:0005525 p=7.1E−02 n=1 fg=0.33 bg=0.02
guanyl nucleotide binding GO:0019001 p=7.7E−02 n=1 fg=0.33 bg=0.03
guanyl ribonucleotide binding GO:0032561 p=7.7E−02 n=1 fg=0.33 bg=0.03
phospholipid binding GO:0005543 p=9.6E−02 n=1 fg=0.33 bg=0.03
nucleoside−triphosphatase activity GO:0017111 p=1.1E−01 n=1 fg=0.33 bg=0.04
pyrophosphatase activity GO:0016462 p=1.2E−01 n=1 fg=0.33 bg=0.04
hydrolase activity, acting on acid anhyd... GO:0016817 p=1.2E−01 n=1 fg=0.33 bg=0.04
hydrolase activity, acting on acid anhyd... GO:0016818 p=1.2E−01 n=1 fg=0.33 bg=0.04
metal ion binding GO:0046872 p=1.3E−01 n=2 fg=0.67 bg=0.22
calcium ion binding GO:0005509 p=1.3E−01 n=1 fg=0.33 bg=0.05
cation binding GO:0043169 p=1.4E−01 n=2 fg=0.67 bg=0.23
protein domain specific binding GO:0019904 p=1.7E−01 n=1 fg=0.33 bg=0.06
lipid binding GO:0008289 p=1.7E−01 n=1 fg=0.33 bg=0.06
0 1 2 3 4 5
−log(p)
n=3/5 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Bilateria_loss
fraction genes in fg and expected valu
zymogen granule GO:0042588 p=8.8E−03 n=1 fg=0.33 bg=0.00
heterotrimeric G−protein complex GO:0005834 p=1.1E−02 n=1 fg=0.33 bg=0.00
GTPase complex GO:1905360 p=1.2E−02 n=1 fg=0.33 bg=0.00
midbody GO:0030496 p=2.2E−02 n=1 fg=0.33 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=2.4E−02 n=1 fg=0.33 bg=0.01
extrinsic component of plasma membrane GO:0019897 p=4.4E−02 n=1 fg=0.33 bg=0.01
cytoplasmic side of plasma membrane GO:0009898 p=4.6E−02 n=1 fg=0.33 bg=0.02
cytoplasmic side of membrane GO:0098562 p=4.8E−02 n=1 fg=0.33 bg=0.02
Golgi membrane GO:0000139 p=5.0E−02 n=1 fg=0.33 bg=0.02
extrinsic component of membrane GO:0019898 p=6.7E−02 n=1 fg=0.33 bg=0.02
centrosome GO:0005813 p=8.1E−02 n=1 fg=0.33 bg=0.03
membrane raft GO:0045121 p=9.0E−02 n=1 fg=0.33 bg=0.03
membrane microdomain GO:0098857 p=9.0E−02 n=1 fg=0.33 bg=0.03
microtubule organizing center GO:0005815 p=9.9E−02 n=1 fg=0.33 bg=0.03
endoplasmic reticulum membrane GO:0005789 p=1.0E−01 n=1 fg=0.33 bg=0.03
endoplasmic reticulum subcompartment GO:0098827 p=1.0E−01 n=1 fg=0.33 bg=0.04
nuclear outer membrane−endoplasmic retic... GO:0042175 p=1.1E−01 n=1 fg=0.33 bg=0.04
plasma membrane protein complex GO:0098797 p=1.3E−01 n=1 fg=0.33 bg=0.04
side of membrane GO:0098552 p=1.3E−01 n=1 fg=0.33 bg=0.05
organelle subcompartment GO:0031984 p=1.6E−01 n=1 fg=0.33 bg=0.06
microtubule cytoskeleton GO:0015630 p=1.7E−01 n=1 fg=0.33 bg=0.06
bounding membrane of organelle GO:0098588 p=2.0E−01 n=1 fg=0.33 bg=0.07
catalytic complex GO:1902494 p=2.1E−01 n=1 fg=0.33 bg=0.07
membrane protein complex GO:0098796 p=2.1E−01 n=1 fg=0.33 bg=0.08
Golgi apparatus GO:0005794 p=2.6E−01 n=1 fg=0.33 bg=0.10
endoplasmic reticulum GO:0005783 p=2.9E−01 n=1 fg=0.33 bg=0.11
plasma membrane GO:0005886 p=3.2E−01 n=2 fg=0.67 bg=0.38
cytoskeleton GO:0005856 p=3.4E−01 n=1 fg=0.33 bg=0.13
organelle membrane GO:0031090 p=3.4E−01 n=1 fg=0.33 bg=0.13
extracellular region GO:0005576 p=3.5E−01 n=1 fg=0.33 bg=0.13
0 1 2 3 4 5
−log(p)
n=3/5 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction