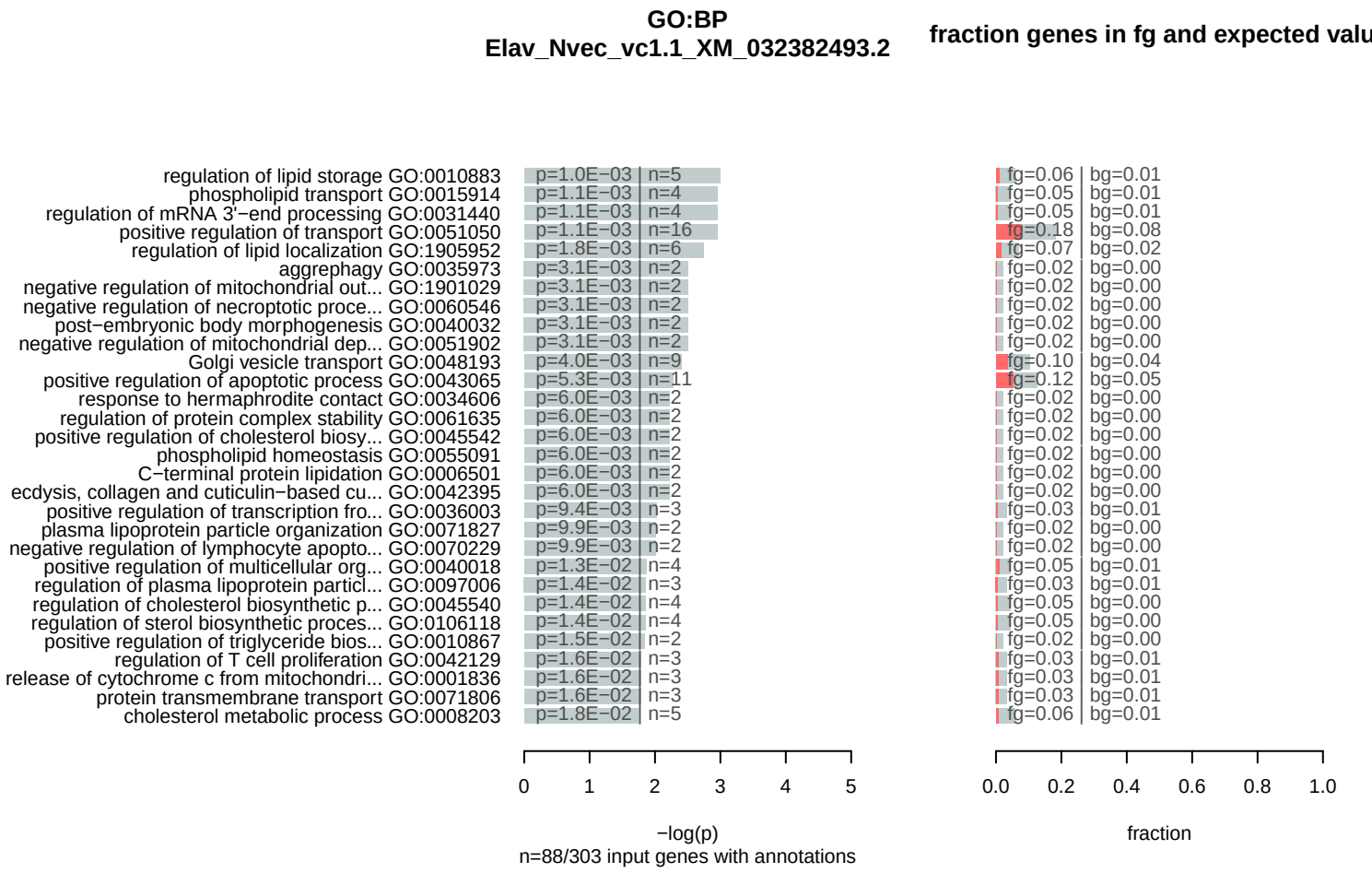
GO:BP
Elav_Nvec_vc1.1_XM_032382493.2
fraction genes in fg and expected valu
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phospholipid transport GO:0015914 p=1.1E−03 n=4 fg=0.05 bg=0.01
regulation of mRNA 3'−end processing GO:0031440 p=1.1E−03 n=4 fg=0.05 bg=0.01
positive regulation of transport GO:0051050 p=1.1E−03 n=16 fg=0.18 bg=0.08
regulation of lipid localization GO:1905952 p=1.8E−03 n=6 fg=0.07 bg=0.02
aggrephagy GO:0035973 p=3.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitochondrial out... GO:1901029 p=3.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of necroptotic proce... GO:0060546 p=3.1E−03 n=2 fg=0.02 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=3.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of mitochondrial dep... GO:0051902 p=3.1E−03 n=2 fg=0.02 bg=0.00
Golgi vesicle transport GO:0048193 p=4.0E−03 n=9 fg=0.10 bg=0.04
positive regulation of apoptotic process GO:0043065 p=5.3E−03 n=11 fg=0.12 bg=0.05
response to hermaphrodite contact GO:0034606 p=6.0E−03 n=2 fg=0.02 bg=0.00
regulation of protein complex stability GO:0061635 p=6.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of cholesterol biosy... GO:0045542 p=6.0E−03 n=2 fg=0.02 bg=0.00
phospholipid homeostasis GO:0055091 p=6.0E−03 n=2 fg=0.02 bg=0.00
C−terminal protein lipidation GO:0006501 p=6.0E−03 n=2 fg=0.02 bg=0.00
ecdysis, collagen and cuticulin−based cu... GO:0042395 p=6.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of transcription fro... GO:0036003 p=9.4E−03 n=3 fg=0.03 bg=0.01
plasma lipoprotein particle organization GO:0071827 p=9.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of lymphocyte apopto... GO:0070229 p=9.9E−03 n=2 fg=0.02 bg=0.00
positive regulation of multicellular org... GO:0040018 p=1.3E−02 n=4 fg=0.05 bg=0.01
regulation of plasma lipoprotein particl... GO:0097006 p=1.4E−02 n=3 fg=0.03 bg=0.01
regulation of cholesterol biosynthetic p... GO:0045540 p=1.4E−02 n=4 fg=0.05 bg=0.00
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positive regulation of triglyceride bios... GO:0010867 p=1.5E−02 n=2 fg=0.02 bg=0.00
regulation of T cell proliferation GO:0042129 p=1.6E−02 n=3 fg=0.03 bg=0.01
release of cytochrome c from mitochondri... GO:0001836 p=1.6E−02 n=3 fg=0.03 bg=0.01
protein transmembrane transport GO:0071806 p=1.6E−02 n=3 fg=0.03 bg=0.01
cholesterol metabolic process GO:0008203 p=1.8E−02 n=5 fg=0.06 bg=0.01
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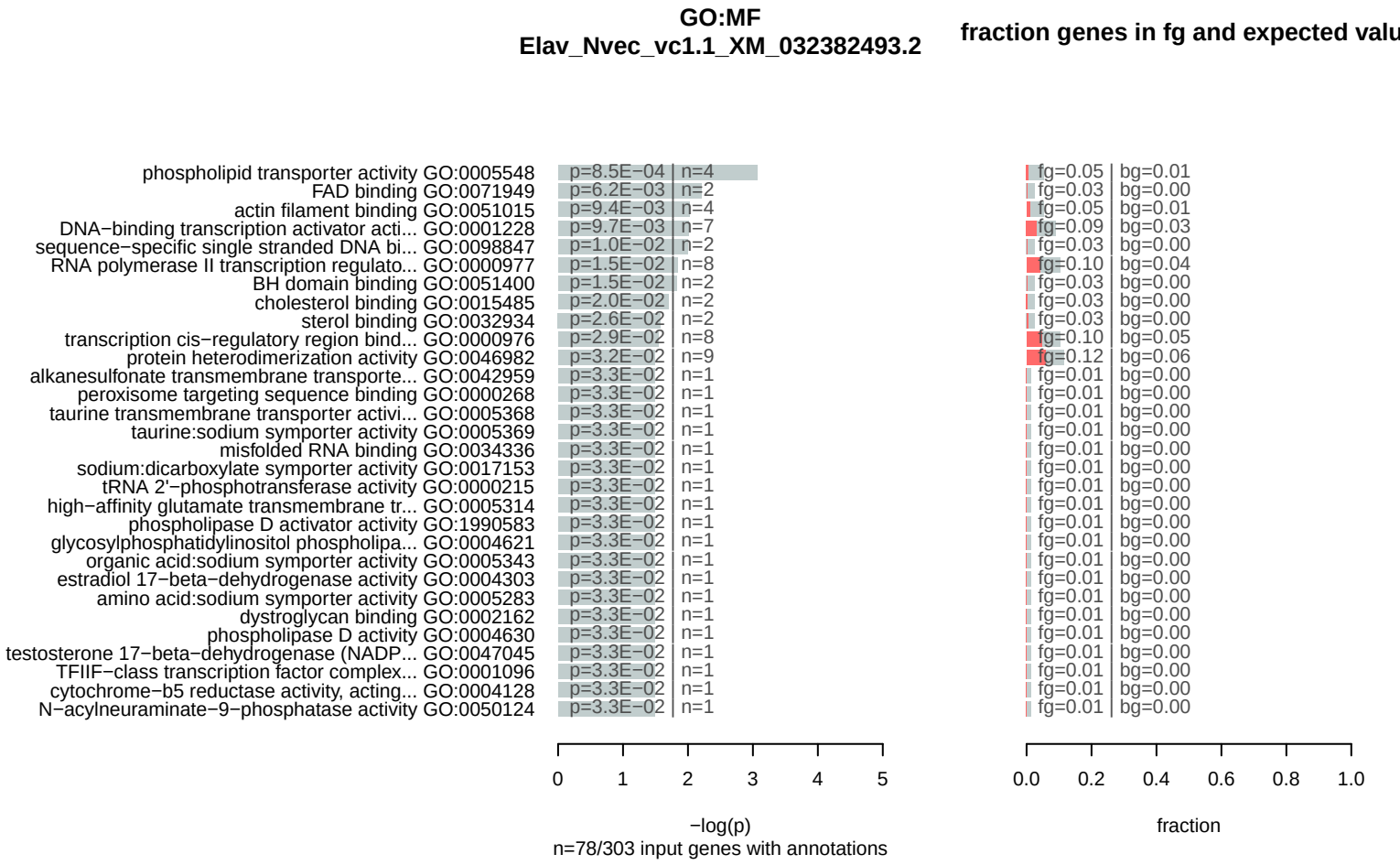
−log(p)
n=88/303 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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FAD binding GO:0071949 p=6.2E−03 n=2 fg=0.03 bg=0.00
actin filament binding GO:0051015 p=9.4E−03 n=4 fg=0.05 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=9.7E−03 n=7 fg=0.09 bg=0.03
sequence−specific single stranded DNA bi... GO:0098847 p=1.0E−02 n=2 fg=0.03 bg=0.00
RNA polymerase II transcription regulato... GO:0000977 p=1.5E−02 n=8 fg=0.10 bg=0.04
BH domain binding GO:0051400 p=1.5E−02 n=2 fg=0.03 bg=0.00
cholesterol binding GO:0015485 p=2.0E−02 n=2 fg=0.03 bg=0.00
sterol binding GO:0032934 p=2.6E−02 n=2 fg=0.03 bg=0.00
transcription cis−regulatory region bind... GO:0000976 p=2.9E−02 n=8 fg=0.10 bg=0.05
protein heterodimerization activity GO:0046982 p=3.2E−02 n=9 fg=0.12 bg=0.06
alkanesulfonate transmembrane transporte... GO:0042959 p=3.3E−02 n=1 fg=0.01 bg=0.00
peroxisome targeting sequence binding GO:0000268 p=3.3E−02 n=1 fg=0.01 bg=0.00
taurine transmembrane transporter activi... GO:0005368 p=3.3E−02 n=1 fg=0.01 bg=0.00
taurine:sodium symporter activity GO:0005369 p=3.3E−02 n=1 fg=0.01 bg=0.00
misfolded RNA binding GO:0034336 p=3.3E−02 n=1 fg=0.01 bg=0.00
sodium:dicarboxylate symporter activity GO:0017153 p=3.3E−02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=3.3E−02 n=1 fg=0.01 bg=0.00
high−affinity glutamate transmembrane tr... GO:0005314 p=3.3E−02 n=1 fg=0.01 bg=0.00
phospholipase D activator activity GO:1990583 p=3.3E−02 n=1 fg=0.01 bg=0.00
glycosylphosphatidylinositol phospholipa... GO:0004621 p=3.3E−02 n=1 fg=0.01 bg=0.00
organic acid:sodium symporter activity GO:0005343 p=3.3E−02 n=1 fg=0.01 bg=0.00
estradiol 17−beta−dehydrogenase activity GO:0004303 p=3.3E−02 n=1 fg=0.01 bg=0.00
amino acid:sodium symporter activity GO:0005283 p=3.3E−02 n=1 fg=0.01 bg=0.00
dystroglycan binding GO:0002162 p=3.3E−02 n=1 fg=0.01 bg=0.00
phospholipase D activity GO:0004630 p=3.3E−02 n=1 fg=0.01 bg=0.00
testosterone 17−beta−dehydrogenase (NADP... GO:0047045 p=3.3E−02 n=1 fg=0.01 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=3.3E−02 n=1 fg=0.01 bg=0.00
cytochrome−b5 reductase activity, acting... GO:0004128 p=3.3E−02 n=1 fg=0.01 bg=0.00
N−acylneuraminate−9−phosphatase activity GO:0050124 p=3.3E−02 n=1 fg=0.01 bg=0.00
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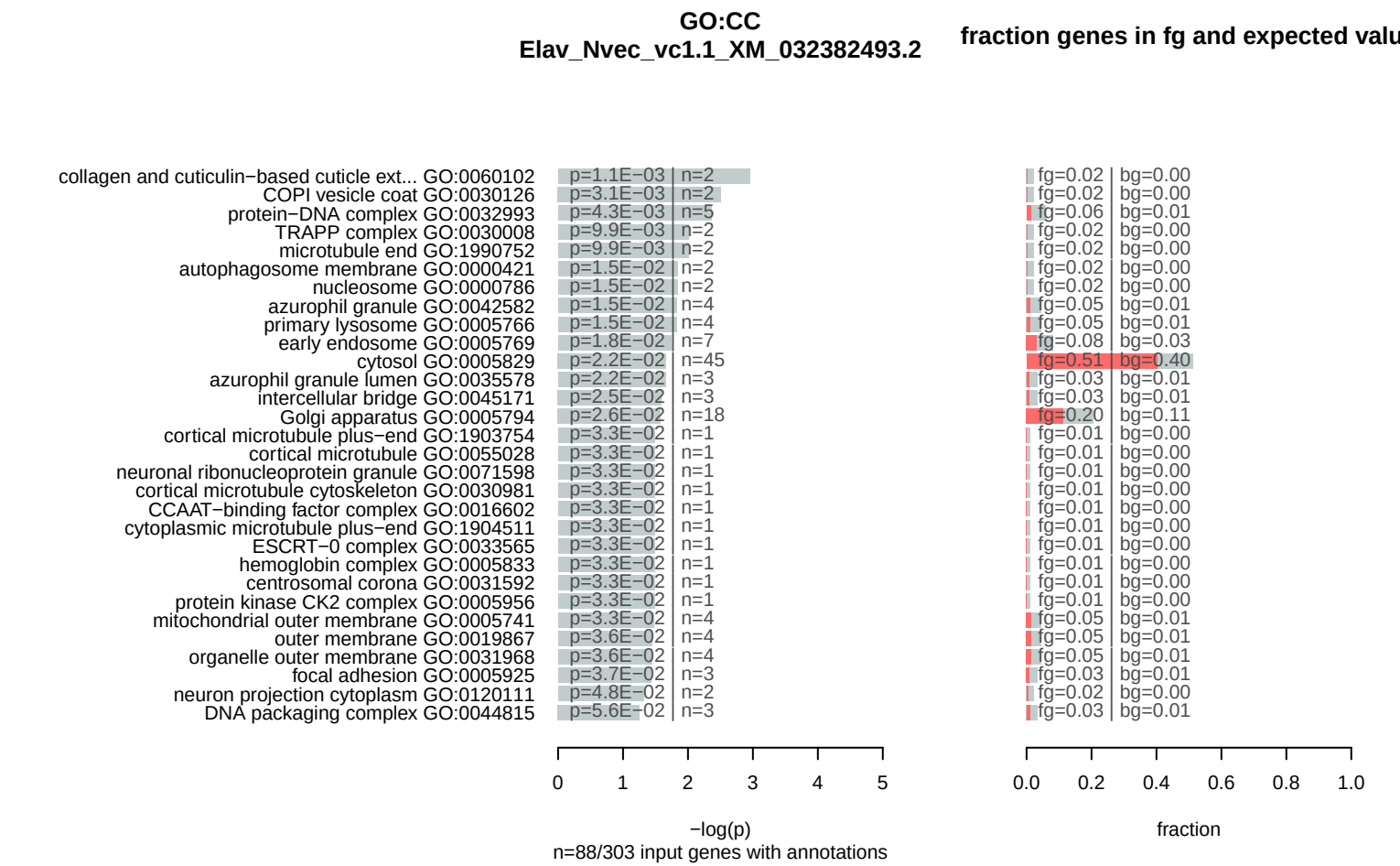
−log(p)
n=78/303 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction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fraction genes in fg and expected valu
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.1E−03 n=2 fg=0.02 bg=0.00
COPI vesicle coat GO:0030126 p=3.1E−03 n=2 fg=0.02 bg=0.00
protein−DNA complex GO:0032993 p=4.3E−03 n=5 fg=0.06 bg=0.01
TRAPP complex GO:0030008 p=9.9E−03 n=2 fg=0.02 bg=0.00
microtubule end GO:1990752 p=9.9E−03 n=2 fg=0.02 bg=0.00
autophagosome membrane GO:0000421 p=1.5E−02 n=2 fg=0.02 bg=0.00
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azurophil granule GO:0042582 p=1.5E−02 n=4 fg=0.05 bg=0.01
primary lysosome GO:0005766 p=1.5E−02 n=4 fg=0.05 bg=0.01
early endosome GO:0005769 p=1.8E−02 n=7 fg=0.08 bg=0.03
cytosol GO:0005829 p=2.2E−02 n=45 fg=0.51 bg=0.40
azurophil granule lumen GO:0035578 p=2.2E−02 n=3 fg=0.03 bg=0.01
intercellular bridge GO:0045171 p=2.5E−02 n=3 fg=0.03 bg=0.01
Golgi apparatus GO:0005794 p=2.6E−02 n=18 fg=0.20 bg=0.11
cortical microtubule plus−end GO:1903754 p=3.3E−02 n=1 fg=0.01 bg=0.00
cortical microtubule GO:0055028 p=3.3E−02 n=1 fg=0.01 bg=0.00
neuronal ribonucleoprotein granule GO:0071598 p=3.3E−02 n=1 fg=0.01 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=3.3E−02 n=1 fg=0.01 bg=0.00
CCAAT−binding factor complex GO:0016602 p=3.3E−02 n=1 fg=0.01 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=3.3E−02 n=1 fg=0.01 bg=0.00
ESCRT−0 complex GO:0033565 p=3.3E−02 n=1 fg=0.01 bg=0.00
hemoglobin complex GO:0005833 p=3.3E−02 n=1 fg=0.01 bg=0.00
centrosomal corona GO:0031592 p=3.3E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=3.3E−02 n=1 fg=0.01 bg=0.00
mitochondrial outer membrane GO:0005741 p=3.3E−02 n=4 fg=0.05 bg=0.01
outer membrane GO:0019867 p=3.6E−02 n=4 fg=0.05 bg=0.01
organelle outer membrane GO:0031968 p=3.6E−02 n=4 fg=0.05 bg=0.01
focal adhesion GO:0005925 p=3.7E−02 n=3 fg=0.03 bg=0.01
neuron projection cytoplasm GO:0120111 p=4.8E−02 n=2 fg=0.02 bg=0.00
DNA packaging complex GO:0044815 p=5.6E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=88/303 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction