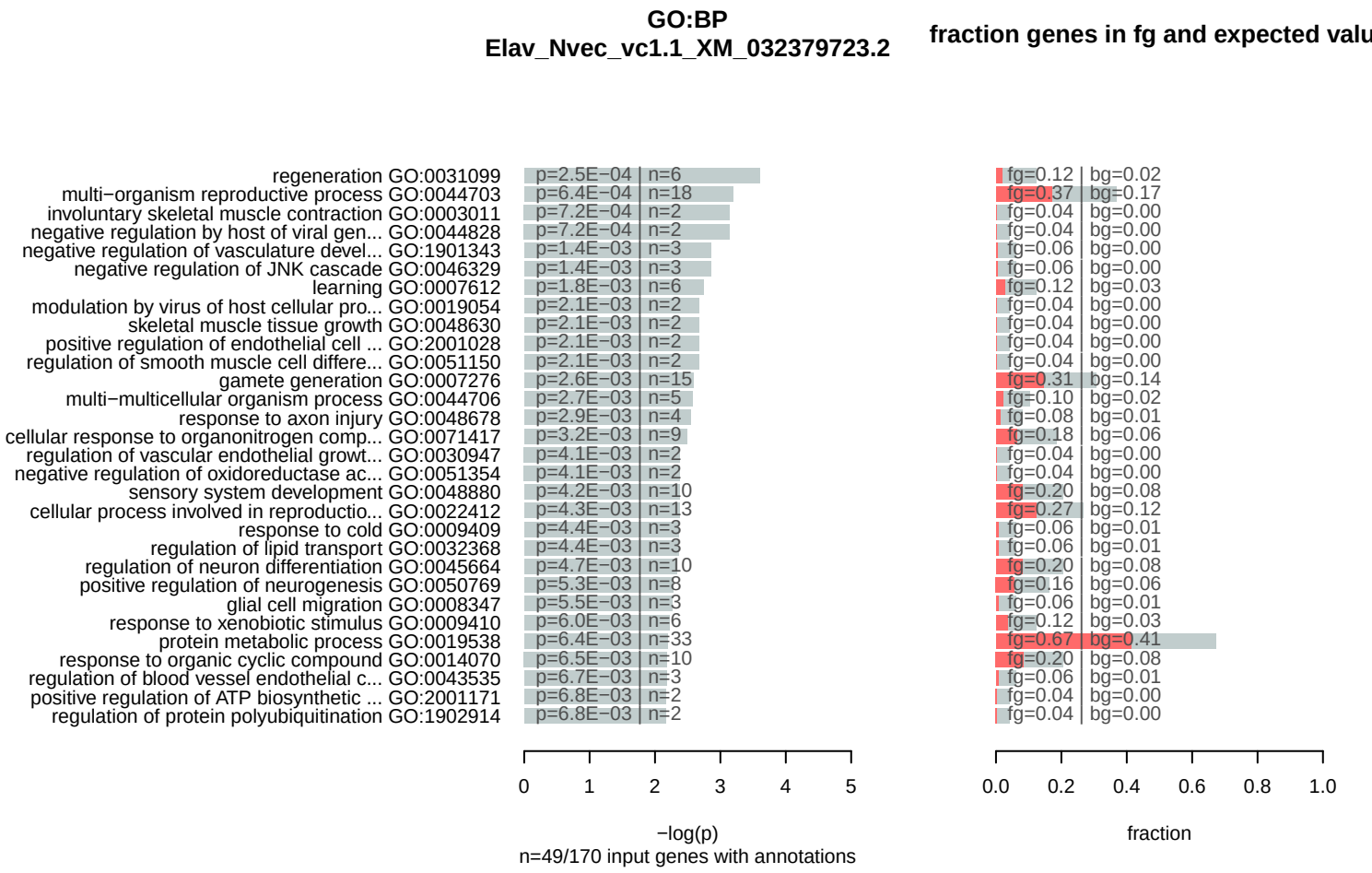
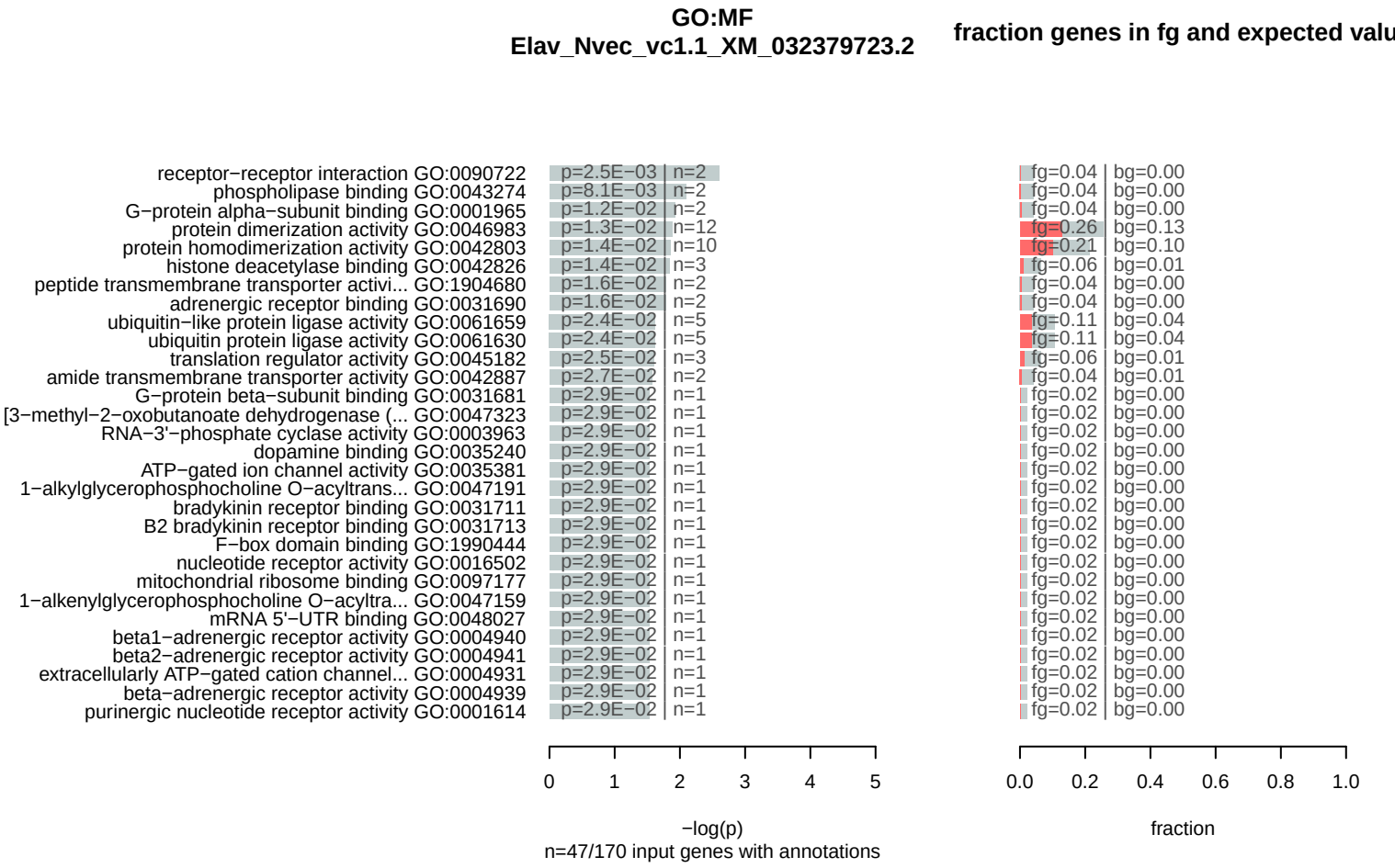
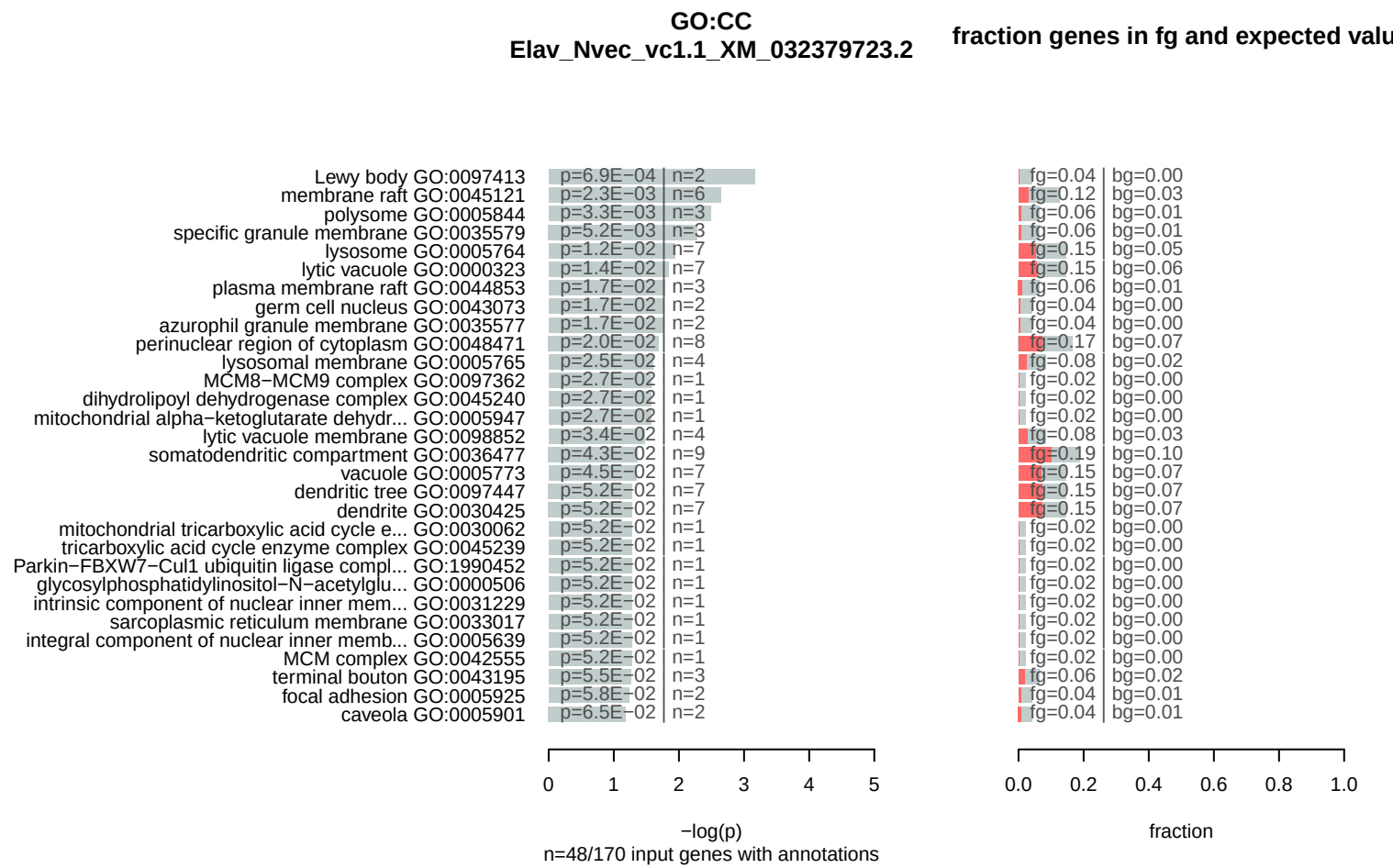

GO:BP
Elav_Nvec_vc1.1_XM_032379723.2
fraction genes in fg and expected valu
regeneration GO:0031099 p=2.5E−04 n=6 fg=0.12 bg=0.02
multi−organism reproductive process GO:0044703 p=6.4E−04 n=18 fg=0.37 bg=0.17
involuntary skeletal muscle contraction GO:0003011 p=7.2E−04 n=2 fg=0.04 bg=0.00
negative regulation by host of viral gen... GO:0044828 p=7.2E−04 n=2 fg=0.04 bg=0.00
negative regulation of vasculature devel... GO:1901343 p=1.4E−03 n=3 fg=0.06 bg=0.00
negative regulation of JNK cascade GO:0046329 p=1.4E−03 n=3 fg=0.06 bg=0.00
learning GO:0007612 p=1.8E−03 n=6 fg=0.12 bg=0.03
modulation by virus of host cellular pro... GO:0019054 p=2.1E−03 n=2 fg=0.04 bg=0.00
skeletal muscle tissue growth GO:0048630 p=2.1E−03 n=2 fg=0.04 bg=0.00
positive regulation of endothelial cell ... GO:2001028 p=2.1E−03 n=2 fg=0.04 bg=0.00
regulation of smooth muscle cell differe... GO:0051150 p=2.1E−03 n=2 fg=0.04 bg=0.00
gamete generation GO:0007276 p=2.6E−03 n=15 fg=0.31 bg=0.14
multi−multicellular organism process GO:0044706 p=2.7E−03 n=5 fg=0.10 bg=0.02
response to axon injury GO:0048678 p=2.9E−03 n=4 fg=0.08 bg=0.01
cellular response to organonitrogen comp... GO:0071417 p=3.2E−03 n=9 fg=0.18 bg=0.06
regulation of vascular endothelial growt... GO:0030947 p=4.1E−03 n=2 fg=0.04 bg=0.00
negative regulation of oxidoreductase ac... GO:0051354 p=4.1E−03 n=2 fg=0.04 bg=0.00
sensory system development GO:0048880 p=4.2E−03 n=10 fg=0.20 bg=0.08
cellular process involved in reproductio... GO:0022412 p=4.3E−03 n=13 fg=0.27 bg=0.12
response to cold GO:0009409 p=4.4E−03 n=3 fg=0.06 bg=0.01
regulation of lipid transport GO:0032368 p=4.4E−03 n=3 fg=0.06 bg=0.01
regulation of neuron differentiation GO:0045664 p=4.7E−03 n=10 fg=0.20 bg=0.08
positive regulation of neurogenesis GO:0050769 p=5.3E−03 n=8 fg=0.16 bg=0.06
glial cell migration GO:0008347 p=5.5E−03 n=3 fg=0.06 bg=0.01
response to xenobiotic stimulus GO:0009410 p=6.0E−03 n=6 fg=0.12 bg=0.03
protein metabolic process GO:0019538 p=6.4E−03 n=33 fg=0.67 bg=0.41
response to organic cyclic compound GO:0014070 p=6.5E−03 n=10 fg=0.20 bg=0.08
regulation of blood vessel endothelial c... GO:0043535 p=6.7E−03 n=3 fg=0.06 bg=0.01
positive regulation of ATP biosynthetic ... GO:2001171 p=6.8E−03 n=2 fg=0.04 bg=0.00
regulation of protein polyubiquitination GO:1902914 p=6.8E−03 n=2 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=49/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Elav_Nvec_vc1.1_XM_032379723.2
fraction genes in fg and expected valu
receptor−receptor interaction GO:0090722 p=2.5E−03 n=2 fg=0.04 bg=0.00
phospholipase binding GO:0043274 p=8.1E−03 n=2 fg=0.04 bg=0.00
G−protein alpha−subunit binding GO:0001965 p=1.2E−02 n=2 fg=0.04 bg=0.00
protein dimerization activity GO:0046983 p=1.3E−02 n=12 fg=0.26 bg=0.13
protein homodimerization activity GO:0042803 p=1.4E−02 n=10 fg=0.21 bg=0.10
histone deacetylase binding GO:0042826 p=1.4E−02 n=3 fg=0.06 bg=0.01
peptide transmembrane transporter activi... GO:1904680 p=1.6E−02 n=2 fg=0.04 bg=0.00
adrenergic receptor binding GO:0031690 p=1.6E−02 n=2 fg=0.04 bg=0.00
ubiquitin−like protein ligase activity GO:0061659 p=2.4E−02 n=5 fg=0.11 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=2.4E−02 n=5 fg=0.11 bg=0.04
translation regulator activity GO:0045182 p=2.5E−02 n=3 fg=0.06 bg=0.01
amide transmembrane transporter activity GO:0042887 p=2.7E−02 n=2 fg=0.04 bg=0.01
G−protein beta−subunit binding GO:0031681 p=2.9E−02 n=1 fg=0.02 bg=0.00
[3−methyl−2−oxobutanoate dehydrogenase (... GO:0047323 p=2.9E−02 n=1 fg=0.02 bg=0.00
RNA−3'−phosphate cyclase activity GO:0003963 p=2.9E−02 n=1 fg=0.02 bg=0.00
dopamine binding GO:0035240 p=2.9E−02 n=1 fg=0.02 bg=0.00
ATP−gated ion channel activity GO:0035381 p=2.9E−02 n=1 fg=0.02 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=2.9E−02 n=1 fg=0.02 bg=0.00
bradykinin receptor binding GO:0031711 p=2.9E−02 n=1 fg=0.02 bg=0.00
B2 bradykinin receptor binding GO:0031713 p=2.9E−02 n=1 fg=0.02 bg=0.00
F−box domain binding GO:1990444 p=2.9E−02 n=1 fg=0.02 bg=0.00
nucleotide receptor activity GO:0016502 p=2.9E−02 n=1 fg=0.02 bg=0.00
mitochondrial ribosome binding GO:0097177 p=2.9E−02 n=1 fg=0.02 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=2.9E−02 n=1 fg=0.02 bg=0.00
mRNA 5'−UTR binding GO:0048027 p=2.9E−02 n=1 fg=0.02 bg=0.00
beta1−adrenergic receptor activity GO:0004940 p=2.9E−02 n=1 fg=0.02 bg=0.00
beta2−adrenergic receptor activity GO:0004941 p=2.9E−02 n=1 fg=0.02 bg=0.00
extracellularly ATP−gated cation channel... GO:0004931 p=2.9E−02 n=1 fg=0.02 bg=0.00
beta−adrenergic receptor activity GO:0004939 p=2.9E−02 n=1 fg=0.02 bg=0.00
purinergic nucleotide receptor activity GO:0001614 p=2.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=47/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Elav_Nvec_vc1.1_XM_032379723.2
fraction genes in fg and expected valu
Lewy body GO:0097413 p=6.9E−04 n=2 fg=0.04 bg=0.00
membrane raft GO:0045121 p=2.3E−03 n=6 fg=0.12 bg=0.03
polysome GO:0005844 p=3.3E−03 n=3 fg=0.06 bg=0.01
specific granule membrane GO:0035579 p=5.2E−03 n=3 fg=0.06 bg=0.01
lysosome GO:0005764 p=1.2E−02 n=7 fg=0.15 bg=0.05
lytic vacuole GO:0000323 p=1.4E−02 n=7 fg=0.15 bg=0.06
plasma membrane raft GO:0044853 p=1.7E−02 n=3 fg=0.06 bg=0.01
germ cell nucleus GO:0043073 p=1.7E−02 n=2 fg=0.04 bg=0.00
azurophil granule membrane GO:0035577 p=1.7E−02 n=2 fg=0.04 bg=0.00
perinuclear region of cytoplasm GO:0048471 p=2.0E−02 n=8 fg=0.17 bg=0.07
lysosomal membrane GO:0005765 p=2.5E−02 n=4 fg=0.08 bg=0.02
MCM8−MCM9 complex GO:0097362 p=2.7E−02 n=1 fg=0.02 bg=0.00
dihydrolipoyl dehydrogenase complex GO:0045240 p=2.7E−02 n=1 fg=0.02 bg=0.00
mitochondrial alpha−ketoglutarate dehydr... GO:0005947 p=2.7E−02 n=1 fg=0.02 bg=0.00
lytic vacuole membrane GO:0098852 p=3.4E−02 n=4 fg=0.08 bg=0.03
somatodendritic compartment GO:0036477 p=4.3E−02 n=9 fg=0.19 bg=0.10
vacuole GO:0005773 p=4.5E−02 n=7 fg=0.15 bg=0.07
dendritic tree GO:0097447 p=5.2E−02 n=7 fg=0.15 bg=0.07
dendrite GO:0030425 p=5.2E−02 n=7 fg=0.15 bg=0.07
mitochondrial tricarboxylic acid cycle e... GO:0030062 p=5.2E−02 n=1 fg=0.02 bg=0.00
tricarboxylic acid cycle enzyme complex GO:0045239 p=5.2E−02 n=1 fg=0.02 bg=0.00
Parkin−FBXW7−Cul1 ubiquitin ligase compl... GO:1990452 p=5.2E−02 n=1 fg=0.02 bg=0.00
glycosylphosphatidylinositol−N−acetylglu... GO:0000506 p=5.2E−02 n=1 fg=0.02 bg=0.00
intrinsic component of nuclear inner mem... GO:0031229 p=5.2E−02 n=1 fg=0.02 bg=0.00
sarcoplasmic reticulum membrane GO:0033017 p=5.2E−02 n=1 fg=0.02 bg=0.00
integral component of nuclear inner memb... GO:0005639 p=5.2E−02 n=1 fg=0.02 bg=0.00
MCM complex GO:0042555 p=5.2E−02 n=1 fg=0.02 bg=0.00
terminal bouton GO:0043195 p=5.5E−02 n=3 fg=0.06 bg=0.02
focal adhesion GO:0005925 p=5.8E−02 n=2 fg=0.04 bg=0.01
caveola GO:0005901 p=6.5E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=48/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction