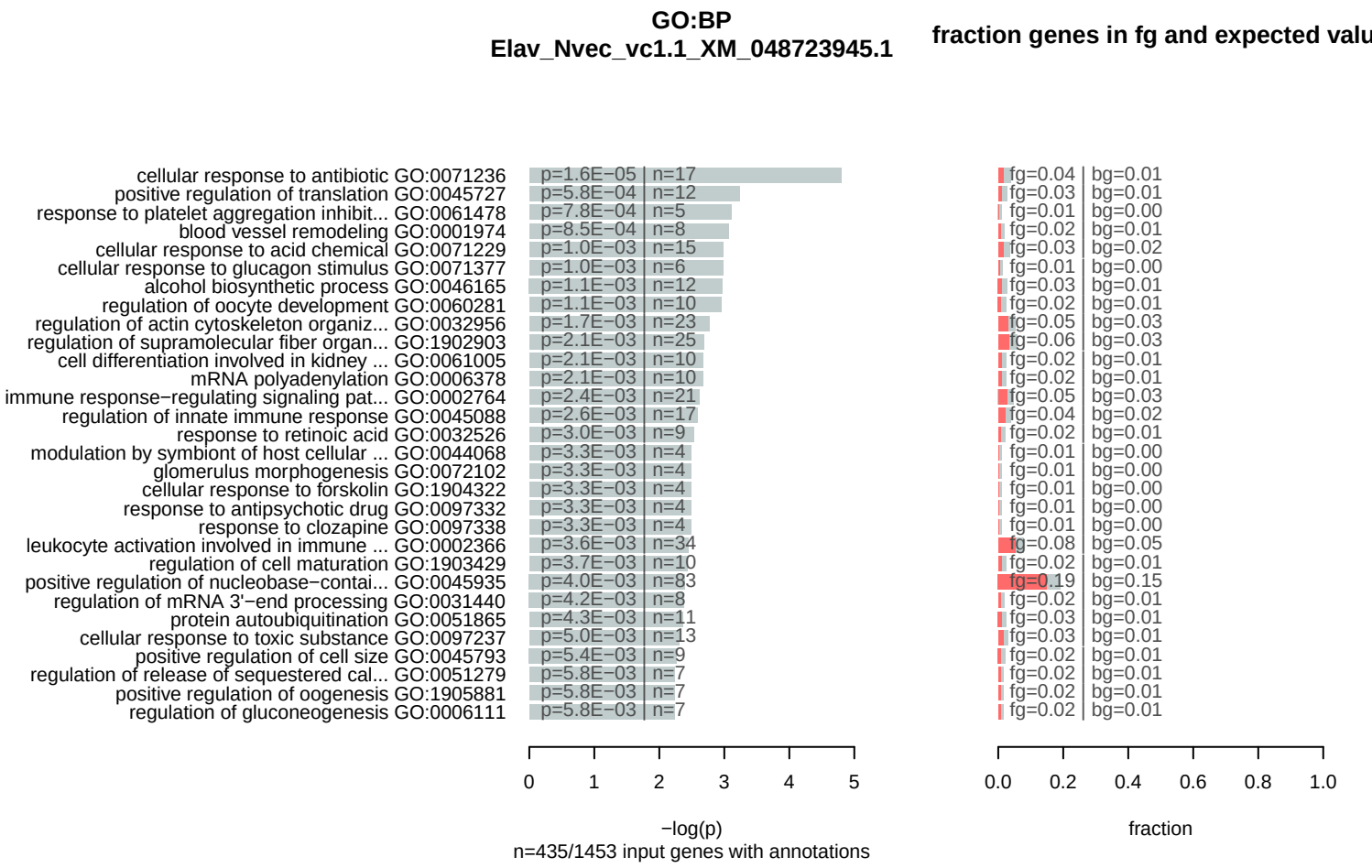
GO:BP
Elav_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
cellular response to antibiotic GO:0071236 p=1.6E−05 n=17 fg=0.04 bg=0.01
positive regulation of translation GO:0045727 p=5.8E−04 n=12 fg=0.03 bg=0.01
response to platelet aggregation inhibit... GO:0061478 p=7.8E−04 n=5 fg=0.01 bg=0.00
blood vessel remodeling GO:0001974 p=8.5E−04 n=8 fg=0.02 bg=0.01
cellular response to acid chemical GO:0071229 p=1.0E−03 n=15 fg=0.03 bg=0.02
cellular response to glucagon stimulus GO:0071377 p=1.0E−03 n=6 fg=0.01 bg=0.00
alcohol biosynthetic process GO:0046165 p=1.1E−03 n=12 fg=0.03 bg=0.01
regulation of oocyte development GO:0060281 p=1.1E−03 n=10 fg=0.02 bg=0.01
regulation of actin cytoskeleton organiz... GO:0032956 p=1.7E−03 n=23 fg=0.05 bg=0.03
regulation of supramolecular fiber organ... GO:1902903 p=2.1E−03 n=25 fg=0.06 bg=0.03
cell differentiation involved in kidney ... GO:0061005 p=2.1E−03 n=10 fg=0.02 bg=0.01
mRNA polyadenylation GO:0006378 p=2.1E−03 n=10 fg=0.02 bg=0.01
immune response−regulating signaling pat... GO:0002764 p=2.4E−03 n=21 fg=0.05 bg=0.03
regulation of innate immune response GO:0045088 p=2.6E−03 n=17 fg=0.04 bg=0.02
response to retinoic acid GO:0032526 p=3.0E−03 n=9 fg=0.02 bg=0.01
modulation by symbiont of host cellular ... GO:0044068 p=3.3E−03 n=4 fg=0.01 bg=0.00
glomerulus morphogenesis GO:0072102 p=3.3E−03 n=4 fg=0.01 bg=0.00
cellular response to forskolin GO:1904322 p=3.3E−03 n=4 fg=0.01 bg=0.00
response to antipsychotic drug GO:0097332 p=3.3E−03 n=4 fg=0.01 bg=0.00
response to clozapine GO:0097338 p=3.3E−03 n=4 fg=0.01 bg=0.00
leukocyte activation involved in immune ... GO:0002366 p=3.6E−03 n=34 fg=0.08 bg=0.05
regulation of cell maturation GO:1903429 p=3.7E−03 n=10 fg=0.02 bg=0.01
positive regulation of nucleobase−contai... GO:0045935 p=4.0E−03 n=83 fg=0.19 bg=0.15
regulation of mRNA 3'−end processing GO:0031440 p=4.2E−03 n=8 fg=0.02 bg=0.01
protein autoubiquitination GO:0051865 p=4.3E−03 n=11 fg=0.03 bg=0.01
cellular response to toxic substance GO:0097237 p=5.0E−03 n=13 fg=0.03 bg=0.01
positive regulation of cell size GO:0045793 p=5.4E−03 n=9 fg=0.02 bg=0.01
regulation of release of sequestered cal... GO:0051279 p=5.8E−03 n=7 fg=0.02 bg=0.01
positive regulation of oogenesis GO:1905881 p=5.8E−03 n=7 fg=0.02 bg=0.01
regulation of gluconeogenesis GO:0006111 p=5.8E−03 n=7 fg=0.02 bg=0.01
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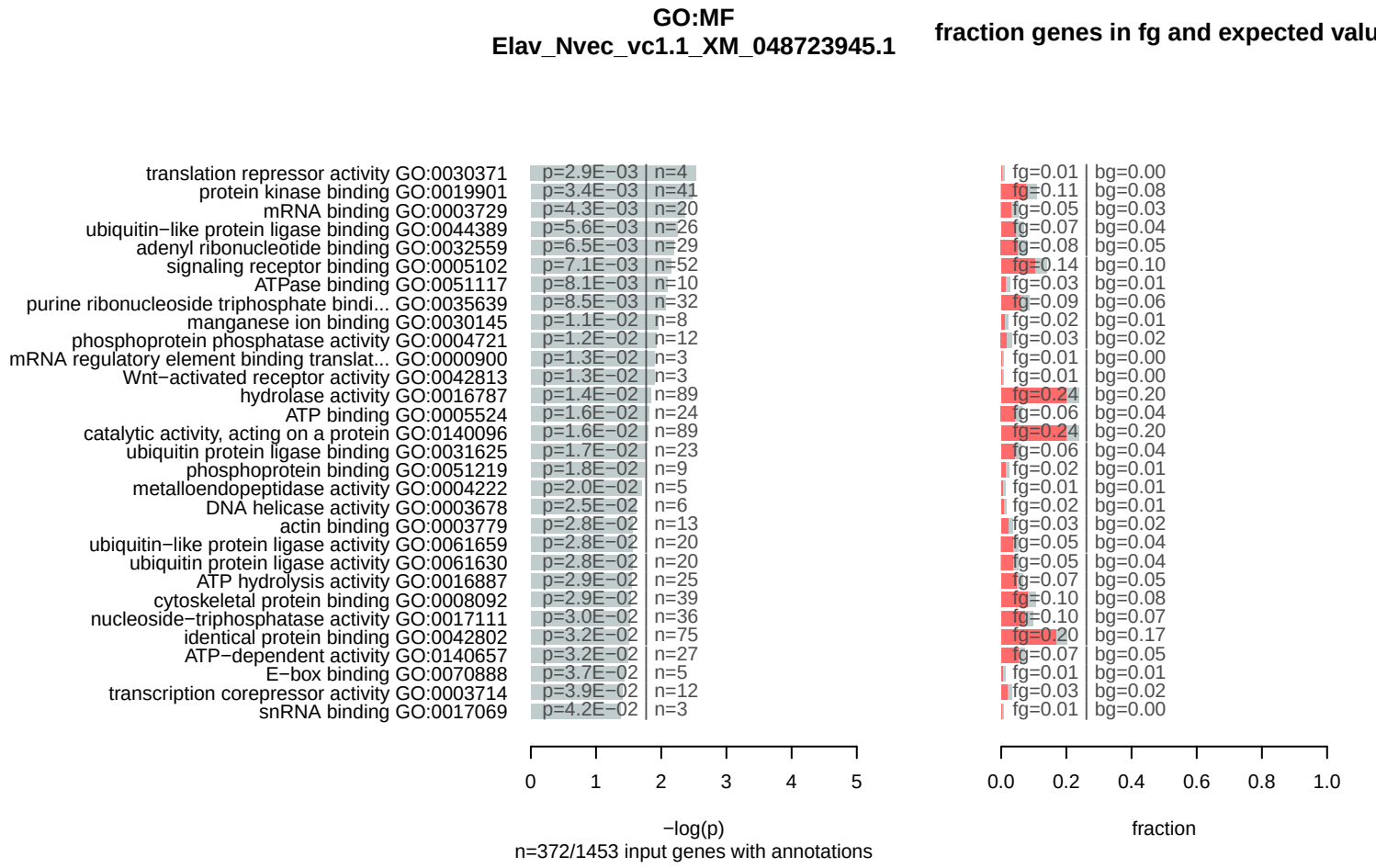
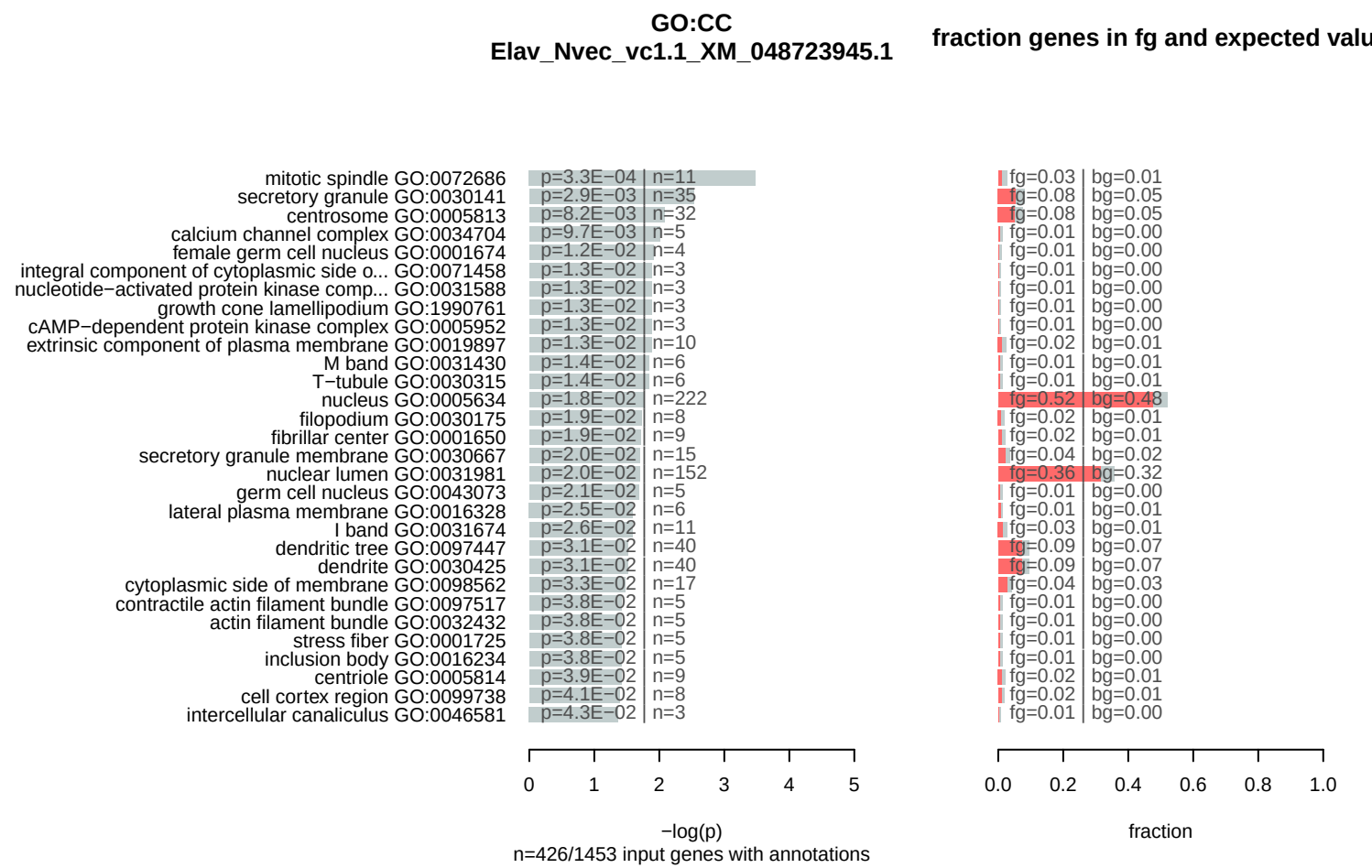
−log(p)
n=435/1453 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Elav_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
translation repressor activity GO:0030371 p=2.9E−03 n=4 fg=0.01 bg=0.00
protein kinase binding GO:0019901 p=3.4E−03 n=41 fg=0.11 bg=0.08
mRNA binding GO:0003729 p=4.3E−03 n=20 fg=0.05 bg=0.03
ubiquitin−like protein ligase binding GO:0044389 p=5.6E−03 n=26 fg=0.07 bg=0.04
adenyl ribonucleotide binding GO:0032559 p=6.5E−03 n=29 fg=0.08 bg=0.05
signaling receptor binding GO:0005102 p=7.1E−03 n=52 fg=0.14 bg=0.10
ATPase binding GO:0051117 p=8.1E−03 n=10 fg=0.03 bg=0.01
purine ribonucleoside triphosphate bindi... GO:0035639 p=8.5E−03 n=32 fg=0.09 bg=0.06
manganese ion binding GO:0030145 p=1.1E−02 n=8 fg=0.02 bg=0.01
phosphoprotein phosphatase activity GO:0004721 p=1.2E−02 n=12 fg=0.03 bg=0.02
mRNA regulatory element binding translat... GO:0000900 p=1.3E−02 n=3 fg=0.01 bg=0.00
Wnt−activated receptor activity GO:0042813 p=1.3E−02 n=3 fg=0.01 bg=0.00
hydrolase activity GO:0016787 p=1.4E−02 n=89 fg=0.24 bg=0.20
ATP binding GO:0005524 p=1.6E−02 n=24 fg=0.06 bg=0.04
catalytic activity, acting on a protein GO:0140096 p=1.6E−02 n=89 fg=0.24 bg=0.20
ubiquitin protein ligase binding GO:0031625 p=1.7E−02 n=23 fg=0.06 bg=0.04
phosphoprotein binding GO:0051219 p=1.8E−02 n=9 fg=0.02 bg=0.01
metalloendopeptidase activity GO:0004222 p=2.0E−02 n=5 fg=0.01 bg=0.01
DNA helicase activity GO:0003678 p=2.5E−02 n=6 fg=0.02 bg=0.01
actin binding GO:0003779 p=2.8E−02 n=13 fg=0.03 bg=0.02
ubiquitin−like protein ligase activity GO:0061659 p=2.8E−02 n=20 fg=0.05 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=2.8E−02 n=20 fg=0.05 bg=0.04
ATP hydrolysis activity GO:0016887 p=2.9E−02 n=25 fg=0.07 bg=0.05
cytoskeletal protein binding GO:0008092 p=2.9E−02 n=39 fg=0.10 bg=0.08
nucleoside−triphosphatase activity GO:0017111 p=3.0E−02 n=36 fg=0.10 bg=0.07
identical protein binding GO:0042802 p=3.2E−02 n=75 fg=0.20 bg=0.17
ATP−dependent activity GO:0140657 p=3.2E−02 n=27 fg=0.07 bg=0.05
E−box binding GO:0070888 p=3.7E−02 n=5 fg=0.01 bg=0.01
transcription corepressor activity GO:0003714 p=3.9E−02 n=12 fg=0.03 bg=0.02
snRNA binding GO:0017069 p=4.2E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=372/1453 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Elav_Nvec_vc1.1_XM_048723945.1
fraction genes in fg and expected valu
mitotic spindle GO:0072686 p=3.3E−04 n=11 fg=0.03 bg=0.01
secretory granule GO:0030141 p=2.9E−03 n=35 fg=0.08 bg=0.05
centrosome GO:0005813 p=8.2E−03 n=32 fg=0.08 bg=0.05
calcium channel complex GO:0034704 p=9.7E−03 n=5 fg=0.01 bg=0.00
female germ cell nucleus GO:0001674 p=1.2E−02 n=4 fg=0.01 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=1.3E−02 n=3 fg=0.01 bg=0.00
nucleotide−activated protein kinase comp... GO:0031588 p=1.3E−02 n=3 fg=0.01 bg=0.00
growth cone lamellipodium GO:1990761 p=1.3E−02 n=3 fg=0.01 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=1.3E−02 n=3 fg=0.01 bg=0.00
extrinsic component of plasma membrane GO:0019897 p=1.3E−02 n=10 fg=0.02 bg=0.01
M band GO:0031430 p=1.4E−02 n=6 fg=0.01 bg=0.01
T−tubule GO:0030315 p=1.4E−02 n=6 fg=0.01 bg=0.01
nucleus GO:0005634 p=1.8E−02 n=222 fg=0.52 bg=0.48
filopodium GO:0030175 p=1.9E−02 n=8 fg=0.02 bg=0.01
fibrillar center GO:0001650 p=1.9E−02 n=9 fg=0.02 bg=0.01
secretory granule membrane GO:0030667 p=2.0E−02 n=15 fg=0.04 bg=0.02
nuclear lumen GO:0031981 p=2.0E−02 n=152 fg=0.36 bg=0.32
germ cell nucleus GO:0043073 p=2.1E−02 n=5 fg=0.01 bg=0.00
lateral plasma membrane GO:0016328 p=2.5E−02 n=6 fg=0.01 bg=0.01
I band GO:0031674 p=2.6E−02 n=11 fg=0.03 bg=0.01
dendritic tree GO:0097447 p=3.1E−02 n=40 fg=0.09 bg=0.07
dendrite GO:0030425 p=3.1E−02 n=40 fg=0.09 bg=0.07
cytoplasmic side of membrane GO:0098562 p=3.3E−02 n=17 fg=0.04 bg=0.03
contractile actin filament bundle GO:0097517 p=3.8E−02 n=5 fg=0.01 bg=0.00
actin filament bundle GO:0032432 p=3.8E−02 n=5 fg=0.01 bg=0.00
stress fiber GO:0001725 p=3.8E−02 n=5 fg=0.01 bg=0.00
inclusion body GO:0016234 p=3.8E−02 n=5 fg=0.01 bg=0.00
centriole GO:0005814 p=3.9E−02 n=9 fg=0.02 bg=0.01
cell cortex region GO:0099738 p=4.1E−02 n=8 fg=0.02 bg=0.01
intercellular canaliculus GO:0046581 p=4.3E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=426/1453 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction