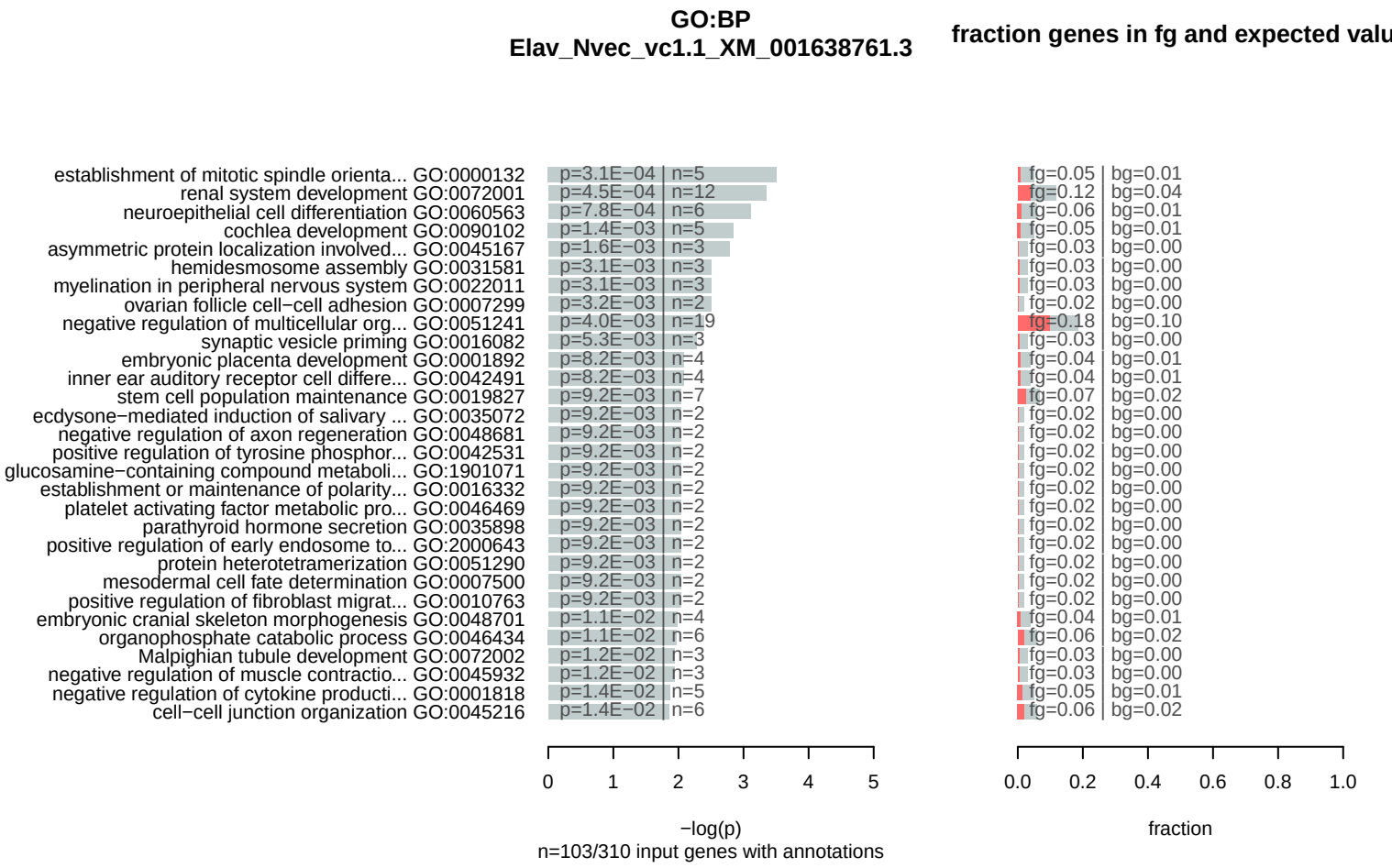
GO:BP
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
establishment of mitotic spindle orienta... GO:0000132 p=3.1E−04 n=5 fg=0.05 bg=0.01
renal system development GO:0072001 p=4.5E−04 n=12 fg=0.12 bg=0.04
neuroepithelial cell differentiation GO:0060563 p=7.8E−04 n=6 fg=0.06 bg=0.01
cochlea development GO:0090102 p=1.4E−03 n=5 fg=0.05 bg=0.01
asymmetric protein localization involved... GO:0045167 p=1.6E−03 n=3 fg=0.03 bg=0.00
hemidesmosome assembly GO:0031581 p=3.1E−03 n=3 fg=0.03 bg=0.00
myelination in peripheral nervous system GO:0022011 p=3.1E−03 n=3 fg=0.03 bg=0.00
ovarian follicle cell−cell adhesion GO:0007299 p=3.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of multicellular org... GO:0051241 p=4.0E−03 n=19 fg=0.18 bg=0.10
synaptic vesicle priming GO:0016082 p=5.3E−03 n=3 fg=0.03 bg=0.00
embryonic placenta development GO:0001892 p=8.2E−03 n=4 fg=0.04 bg=0.01
inner ear auditory receptor cell differe... GO:0042491 p=8.2E−03 n=4 fg=0.04 bg=0.01
stem cell population maintenance GO:0019827 p=9.2E−03 n=7 fg=0.07 bg=0.02
ecdysone−mediated induction of salivary ... GO:0035072 p=9.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of axon regeneration GO:0048681 p=9.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of tyrosine phosphor... GO:0042531 p=9.2E−03 n=2 fg=0.02 bg=0.00
glucosamine−containing compound metaboli... GO:1901071 p=9.2E−03 n=2 fg=0.02 bg=0.00
establishment or maintenance of polarity... GO:0016332 p=9.2E−03 n=2 fg=0.02 bg=0.00
platelet activating factor metabolic pro... GO:0046469 p=9.2E−03 n=2 fg=0.02 bg=0.00
parathyroid hormone secretion GO:0035898 p=9.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of early endosome to... GO:2000643 p=9.2E−03 n=2 fg=0.02 bg=0.00
protein heterotetramerization GO:0051290 p=9.2E−03 n=2 fg=0.02 bg=0.00
mesodermal cell fate determination GO:0007500 p=9.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of fibroblast migrat... GO:0010763 p=9.2E−03 n=2 fg=0.02 bg=0.00
embryonic cranial skeleton morphogenesis GO:0048701 p=1.1E−02 n=4 fg=0.04 bg=0.01
organophosphate catabolic process GO:0046434 p=1.1E−02 n=6 fg=0.06 bg=0.02
Malpighian tubule development GO:0072002 p=1.2E−02 n=3 fg=0.03 bg=0.00
negative regulation of muscle contractio... GO:0045932 p=1.2E−02 n=3 fg=0.03 bg=0.00
negative regulation of cytokine producti... GO:0001818 p=1.4E−02 n=5 fg=0.05 bg=0.01
cell−cell junction organization GO:0045216 p=1.4E−02 n=6 fg=0.06 bg=0.02
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−log(p)
n=103/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
E−box binding GO:0070888 p=9.3E−04 n=4 fg=0.04 bg=0.01
HMG box domain binding GO:0071837 p=3.0E−03 n=3 fg=0.03 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=8.9E−03 n=2 fg=0.02 bg=0.00
phosphoric diester hydrolase activity GO:0008081 p=1.5E−02 n=4 fg=0.04 bg=0.01
phosphatidylinositol phosphate 5−phospha... GO:0034595 p=1.7E−02 n=2 fg=0.02 bg=0.00
small GTPase binding GO:0031267 p=1.9E−02 n=10 fg=0.11 bg=0.05
cell adhesion molecule binding GO:0050839 p=2.0E−02 n=5 fg=0.06 bg=0.02
GTPase regulator activity GO:0030695 p=2.1E−02 n=9 fg=0.10 bg=0.05
inositol phosphate phosphatase activity GO:0052745 p=2.8E−02 n=2 fg=0.02 bg=0.00
phospholipase binding GO:0043274 p=2.8E−02 n=2 fg=0.02 bg=0.00
phosphatidylinositol−3−phosphate binding GO:0032266 p=2.8E−02 n=2 fg=0.02 bg=0.00
DNA−binding transcription factor activit... GO:0000981 p=3.2E−02 n=11 fg=0.12 bg=0.07
phosphoric ester hydrolase activity GO:0042578 p=3.6E−02 n=7 fg=0.08 bg=0.04
potassium channel activity GO:0005267 p=3.9E−02 n=3 fg=0.03 bg=0.01
phosphatidylinositol phosphate phosphata... GO:0052866 p=4.0E−02 n=2 fg=0.02 bg=0.00
ubiquitin−specific protease binding GO:1990381 p=4.0E−02 n=2 fg=0.02 bg=0.00
nucleoside−triphosphatase regulator acti... GO:0060589 p=4.3E−02 n=9 fg=0.10 bg=0.05
manganese ion binding GO:0030145 p=4.7E−02 n=3 fg=0.03 bg=0.01
DNA−binding transcription activator acti... GO:0001228 p=5.0E−02 n=7 fg=0.08 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=5.0E−02 n=7 fg=0.08 bg=0.04
heparin binding GO:0008201 p=5.4E−02 n=2 fg=0.02 bg=0.00
polyubiquitin modification−dependent pro... GO:0031593 p=5.4E−02 n=2 fg=0.02 bg=0.00
single−stranded DNA binding GO:0003697 p=5.6E−02 n=3 fg=0.03 bg=0.01
core promoter sequence−specific DNA bind... GO:0001046 p=5.6E−02 n=3 fg=0.03 bg=0.01
sphingomyelin phosphodiesterase D activi... GO:0050290 p=5.6E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=5.6E−02 n=1 fg=0.01 bg=0.00
myosin II binding GO:0045159 p=5.6E−02 n=1 fg=0.01 bg=0.00
glyceraldehyde−3−phosphate dehydrogenase... GO:0004365 p=5.6E−02 n=1 fg=0.01 bg=0.00
MDM2/MDM4 family protein binding GO:0097371 p=5.6E−02 n=1 fg=0.01 bg=0.00
chitin binding GO:0008061 p=5.6E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=89/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001638761.3
fraction genes in fg and expected valu
M band GO:0031430 p=1.5E−03 n=4 fg=0.04 bg=0.01
U5 snRNP GO:0005682 p=3.1E−03 n=2 fg=0.02 bg=0.00
intraciliary transport particle A GO:0030991 p=9.1E−03 n=2 fg=0.02 bg=0.00
ruffle GO:0001726 p=1.6E−02 n=4 fg=0.04 bg=0.01
endomembrane system GO:0012505 p=1.7E−02 n=45 fg=0.44 bg=0.34
zonula adherens GO:0005915 p=1.8E−02 n=2 fg=0.02 bg=0.00
adherens junction GO:0005912 p=2.2E−02 n=6 fg=0.06 bg=0.02
myelin sheath GO:0043209 p=2.7E−02 n=5 fg=0.05 bg=0.02
presynaptic active zone membrane GO:0048787 p=2.8E−02 n=2 fg=0.02 bg=0.00
mitotic spindle pole GO:0097431 p=2.8E−02 n=2 fg=0.02 bg=0.00
vesicle GO:0031982 p=3.6E−02 n=27 fg=0.26 bg=0.19
early endosome GO:0005769 p=3.7E−02 n=8 fg=0.08 bg=0.04
spindle pole GO:0000922 p=4.2E−02 n=4 fg=0.04 bg=0.01
extracellular exosome GO:0070062 p=4.8E−02 n=3 fg=0.03 bg=0.01
apicolateral plasma membrane GO:0016327 p=5.5E−02 n=2 fg=0.02 bg=0.00
ciliary tip GO:0097542 p=5.5E−02 n=2 fg=0.02 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=5.6E−02 n=1 fg=0.01 bg=0.00
omegasome GO:1990462 p=5.6E−02 n=1 fg=0.01 bg=0.00
ER membrane insertion complex GO:0072379 p=5.6E−02 n=1 fg=0.01 bg=0.00
interphase microtubule organizing center GO:0031021 p=5.6E−02 n=1 fg=0.01 bg=0.00
astral microtubule GO:0000235 p=5.6E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=5.6E−02 n=1 fg=0.01 bg=0.00
phenylalanine−tRNA ligase complex GO:0009328 p=5.6E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=5.6E−02 n=1 fg=0.01 bg=0.00
protein kinase CK2 complex GO:0005956 p=5.6E−02 n=1 fg=0.01 bg=0.00
smooth septate junction GO:0005920 p=5.6E−02 n=1 fg=0.01 bg=0.00
intrinsic component of omegasome membran... GO:0097630 p=5.6E−02 n=1 fg=0.01 bg=0.00
integral component of omegasome membrane GO:0097631 p=5.6E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=5.6E−02 n=1 fg=0.01 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=5.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=102/310 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction