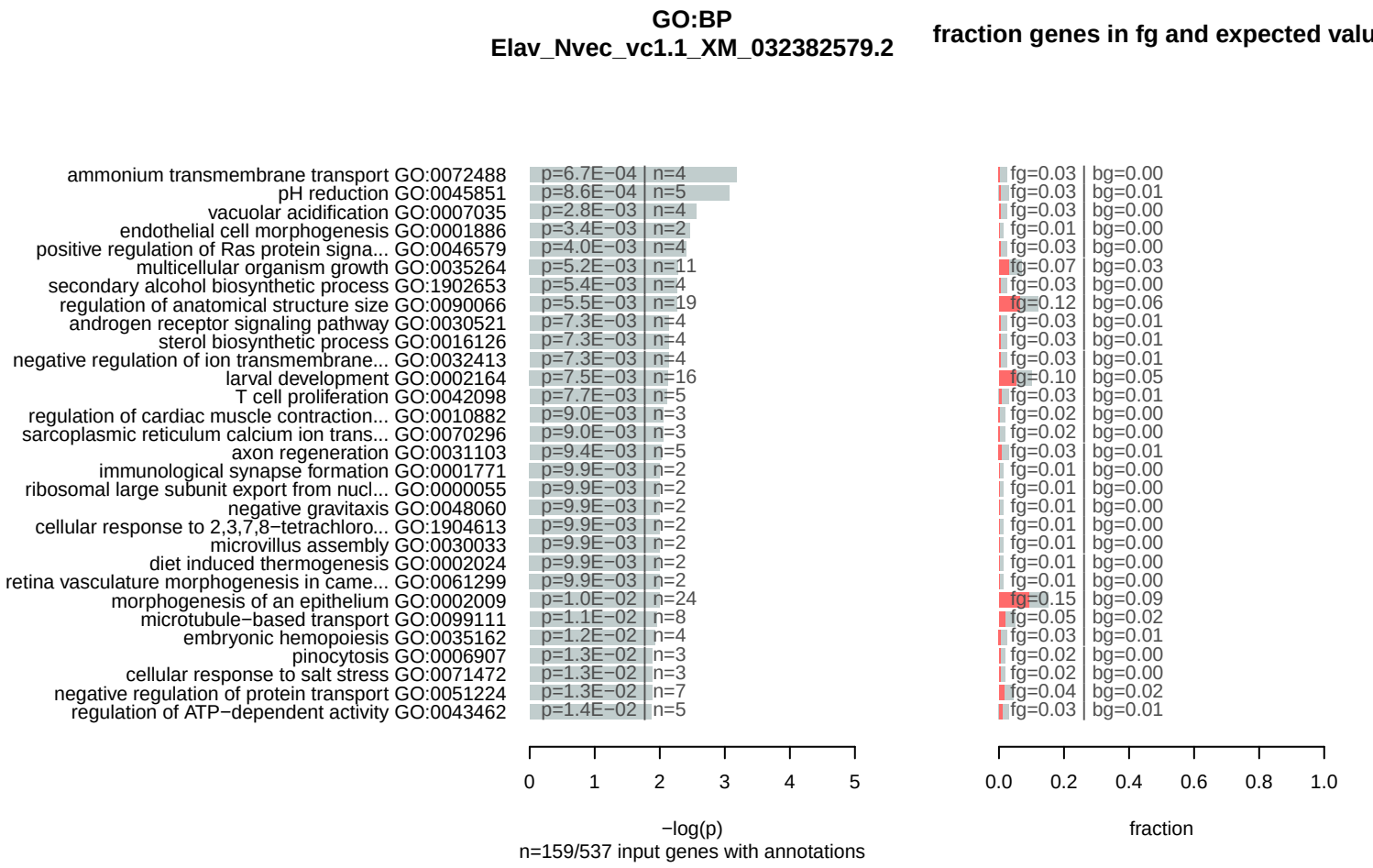
GO:BP
Elav_Nvec_vc1.1_XM_032382579.2
fraction genes in fg and expected valu
ammonium transmembrane transport GO:0072488 p=6.7E−04 n=4 fg=0.03 bg=0.00
pH reduction GO:0045851 p=8.6E−04 n=5 fg=0.03 bg=0.01
vacuolar acidification GO:0007035 p=2.8E−03 n=4 fg=0.03 bg=0.00
endothelial cell morphogenesis GO:0001886 p=3.4E−03 n=2 fg=0.01 bg=0.00
positive regulation of Ras protein signa... GO:0046579 p=4.0E−03 n=4 fg=0.03 bg=0.00
multicellular organism growth GO:0035264 p=5.2E−03 n=11 fg=0.07 bg=0.03
secondary alcohol biosynthetic process GO:1902653 p=5.4E−03 n=4 fg=0.03 bg=0.00
regulation of anatomical structure size GO:0090066 p=5.5E−03 n=19 fg=0.12 bg=0.06
androgen receptor signaling pathway GO:0030521 p=7.3E−03 n=4 fg=0.03 bg=0.01
sterol biosynthetic process GO:0016126 p=7.3E−03 n=4 fg=0.03 bg=0.01
negative regulation of ion transmembrane... GO:0032413 p=7.3E−03 n=4 fg=0.03 bg=0.01
larval development GO:0002164 p=7.5E−03 n=16 fg=0.10 bg=0.05
T cell proliferation GO:0042098 p=7.7E−03 n=5 fg=0.03 bg=0.01
regulation of cardiac muscle contraction... GO:0010882 p=9.0E−03 n=3 fg=0.02 bg=0.00
sarcoplasmic reticulum calcium ion trans... GO:0070296 p=9.0E−03 n=3 fg=0.02 bg=0.00
axon regeneration GO:0031103 p=9.4E−03 n=5 fg=0.03 bg=0.01
immunological synapse formation GO:0001771 p=9.9E−03 n=2 fg=0.01 bg=0.00
ribosomal large subunit export from nucl... GO:0000055 p=9.9E−03 n=2 fg=0.01 bg=0.00
negative gravitaxis GO:0048060 p=9.9E−03 n=2 fg=0.01 bg=0.00
cellular response to 2,3,7,8−tetrachloro... GO:1904613 p=9.9E−03 n=2 fg=0.01 bg=0.00
microvillus assembly GO:0030033 p=9.9E−03 n=2 fg=0.01 bg=0.00
diet induced thermogenesis GO:0002024 p=9.9E−03 n=2 fg=0.01 bg=0.00
retina vasculature morphogenesis in came... GO:0061299 p=9.9E−03 n=2 fg=0.01 bg=0.00
morphogenesis of an epithelium GO:0002009 p=1.0E−02 n=24 fg=0.15 bg=0.09
microtubule−based transport GO:0099111 p=1.1E−02 n=8 fg=0.05 bg=0.02
embryonic hemopoiesis GO:0035162 p=1.2E−02 n=4 fg=0.03 bg=0.01
pinocytosis GO:0006907 p=1.3E−02 n=3 fg=0.02 bg=0.00
cellular response to salt stress GO:0071472 p=1.3E−02 n=3 fg=0.02 bg=0.00
negative regulation of protein transport GO:0051224 p=1.3E−02 n=7 fg=0.04 bg=0.02
regulation of ATP−dependent activity GO:0043462 p=1.4E−02 n=5 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=159/537 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032382579.2
fraction genes in fg and expected valu
ammonium transmembrane transporter activ... GO:0008519 p=6.8E−04 n=4 fg=0.03 bg=0.00
protein domain specific binding GO:0019904 p=1.9E−03 n=22 fg=0.16 bg=0.08
eukaryotic initiation factor 4E binding GO:0008190 p=3.5E−03 n=2 fg=0.01 bg=0.00
D3 dopamine receptor binding GO:0031750 p=3.5E−03 n=2 fg=0.01 bg=0.00
D4 dopamine receptor binding GO:0031751 p=3.5E−03 n=2 fg=0.01 bg=0.00
peroxidase activity GO:0004601 p=3.5E−03 n=3 fg=0.02 bg=0.00
cyclin binding GO:0030332 p=5.9E−03 n=3 fg=0.02 bg=0.00
snRNA binding GO:0017069 p=9.1E−03 n=3 fg=0.02 bg=0.00
D2 dopamine receptor binding GO:0031749 p=1.0E−02 n=2 fg=0.01 bg=0.00
cation:chloride symporter activity GO:0015377 p=1.0E−02 n=2 fg=0.01 bg=0.00
potassium:chloride symporter activity GO:0015379 p=1.0E−02 n=2 fg=0.01 bg=0.00
anion:cation symporter activity GO:0015296 p=1.0E−02 n=2 fg=0.01 bg=0.00
S100 protein binding GO:0044548 p=1.0E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=1.0E−02 n=2 fg=0.01 bg=0.00
signaling receptor binding GO:0005102 p=1.4E−02 n=24 fg=0.17 bg=0.10
cAMP binding GO:0030552 p=1.9E−02 n=2 fg=0.01 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=1.9E−02 n=2 fg=0.01 bg=0.00
WW domain binding GO:0050699 p=1.9E−02 n=2 fg=0.01 bg=0.00
xylosyltransferase activity GO:0042285 p=1.9E−02 n=2 fg=0.01 bg=0.00
glutathione peroxidase activity GO:0004602 p=1.9E−02 n=2 fg=0.01 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=1.9E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=3.0E−02 n=3 fg=0.02 bg=0.01
pentosyltransferase activity GO:0016763 p=3.0E−02 n=3 fg=0.02 bg=0.01
cyclic nucleotide binding GO:0030551 p=3.1E−02 n=2 fg=0.01 bg=0.00
AP−2 adaptor complex binding GO:0035612 p=3.1E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol−5−phosphate binding GO:0010314 p=3.1E−02 n=2 fg=0.01 bg=0.00
phospholipid binding GO:0005543 p=3.2E−02 n=10 fg=0.07 bg=0.04
RNA polymerase II−specific DNA−binding t... GO:0061629 p=3.4E−02 n=7 fg=0.05 bg=0.02
nuclear androgen receptor binding GO:0050681 p=3.7E−02 n=3 fg=0.02 bg=0.01
inorganic anion transmembrane transporte... GO:0015103 p=4.2E−02 n=5 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=140/537 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032382579.2
fraction genes in fg and expected valu
brush border GO:0005903 p=6.1E−04 n=8 fg=0.05 bg=0.01
perinuclear region of cytoplasm GO:0048471 p=7.0E−04 n=21 fg=0.14 bg=0.06
DNA polymerase III complex GO:0009360 p=3.3E−03 n=2 fg=0.01 bg=0.00
ruffle GO:0001726 p=5.1E−03 n=6 fg=0.04 bg=0.01
stereocilium GO:0032420 p=6.6E−03 n=4 fg=0.03 bg=0.01
filopodium GO:0030175 p=6.9E−03 n=5 fg=0.03 bg=0.01
extrinsic component of plasma membrane GO:0019897 p=7.2E−03 n=6 fg=0.04 bg=0.01
muscle cell projection membrane GO:0036195 p=9.5E−03 n=2 fg=0.01 bg=0.00
extracellular vesicle GO:1903561 p=1.0E−02 n=5 fg=0.03 bg=0.01
extracellular membrane−bounded organelle GO:0065010 p=1.0E−02 n=5 fg=0.03 bg=0.01
extracellular organelle GO:0043230 p=1.0E−02 n=5 fg=0.03 bg=0.01
dendrite GO:0030425 p=1.1E−02 n=17 fg=0.11 bg=0.06
midbody GO:0030496 p=1.1E−02 n=7 fg=0.05 bg=0.02
dendritic tree GO:0097447 p=1.2E−02 n=17 fg=0.11 bg=0.06
vesicle GO:0031982 p=1.4E−02 n=36 fg=0.23 bg=0.16
intracellular vesicle GO:0097708 p=1.8E−02 n=34 fg=0.22 bg=0.15
cytoplasmic vesicle GO:0031410 p=1.8E−02 n=34 fg=0.22 bg=0.15
manchette GO:0002177 p=1.8E−02 n=2 fg=0.01 bg=0.00
basal part of cell GO:0045178 p=1.9E−02 n=9 fg=0.06 bg=0.03
somatodendritic compartment GO:0036477 p=2.1E−02 n=21 fg=0.14 bg=0.09
cytoplasmic side of membrane GO:0098562 p=2.4E−02 n=8 fg=0.05 bg=0.02
basolateral plasma membrane GO:0016323 p=2.4E−02 n=8 fg=0.05 bg=0.02
basal plasma membrane GO:0009925 p=2.4E−02 n=8 fg=0.05 bg=0.02
growth cone GO:0030426 p=2.5E−02 n=7 fg=0.05 bg=0.02
lysosomal lumen GO:0043202 p=2.5E−02 n=4 fg=0.03 bg=0.01
cell body GO:0044297 p=2.6E−02 n=17 fg=0.11 bg=0.07
distal axon GO:0150034 p=2.8E−02 n=11 fg=0.07 bg=0.04
microvillus GO:0005902 p=2.9E−02 n=4 fg=0.03 bg=0.01
extrinsic component of cytoplasmic side ... GO:0031234 p=2.9E−02 n=4 fg=0.03 bg=0.01
guanyl−nucleotide exchange factor comple... GO:0032045 p=2.9E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=155/537 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction