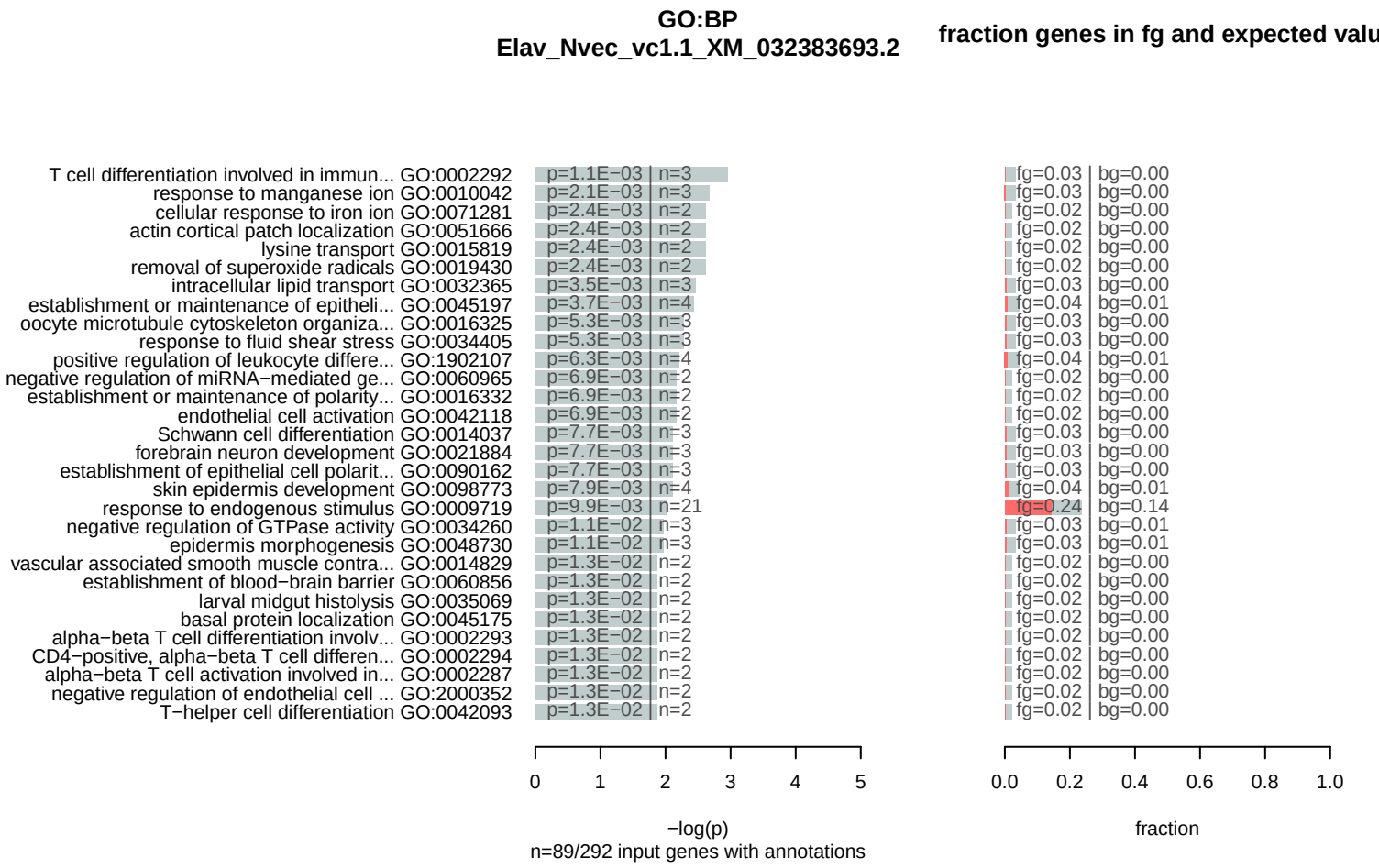
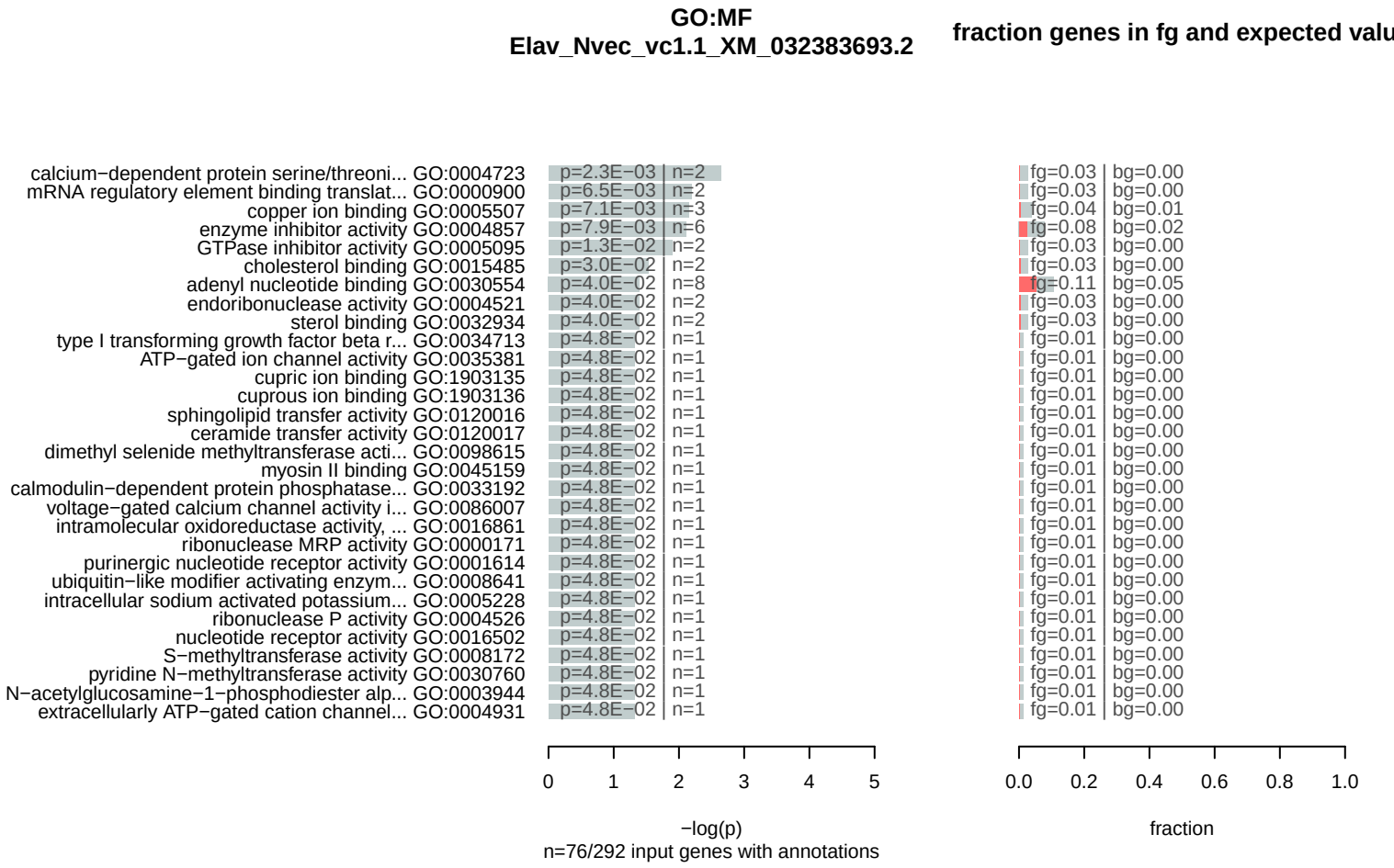
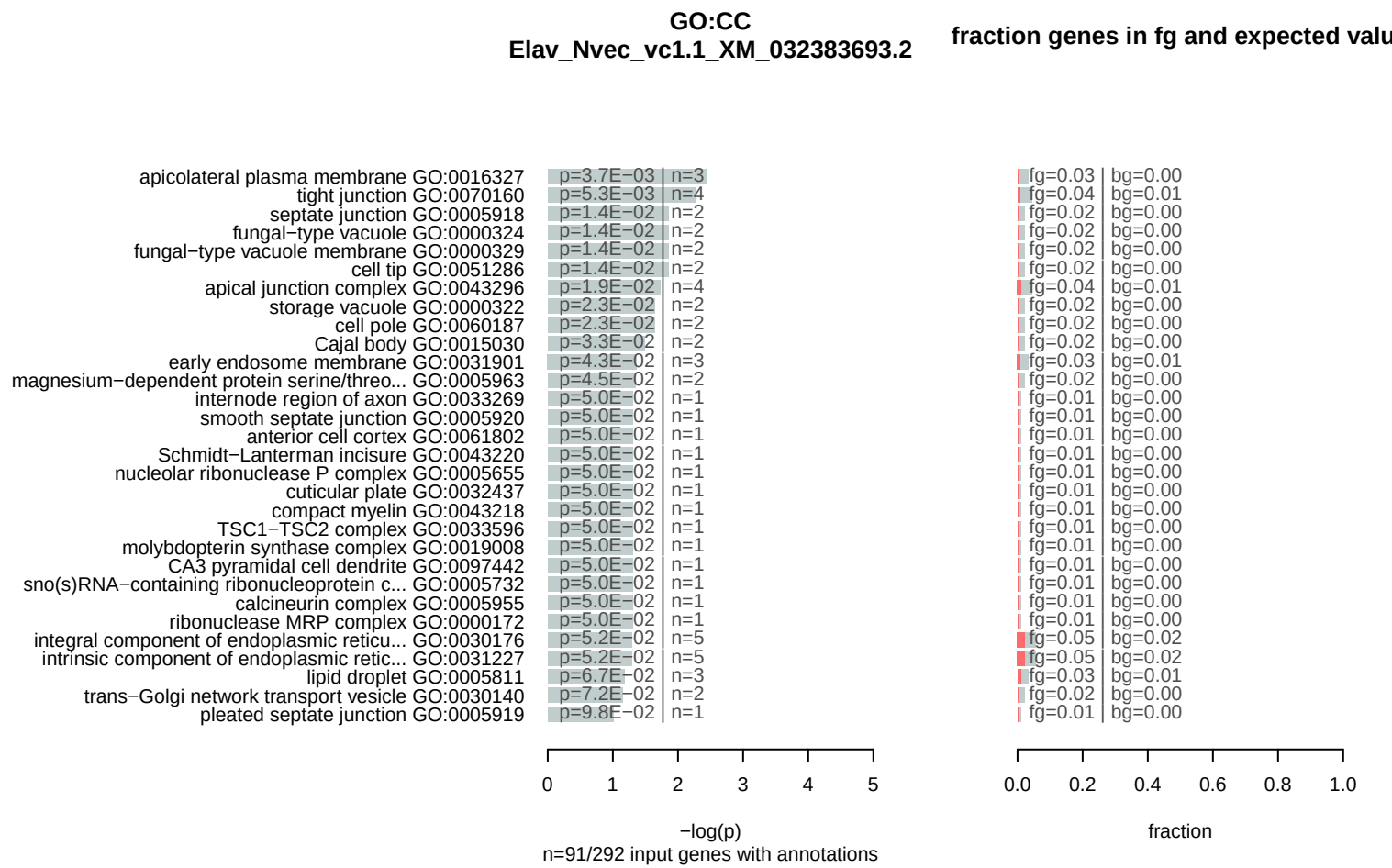

GO:BP
Elav_Nvec_vc1.1_XM_032383693.2
fraction genes in fg and expected valu
T cell differentiation involved in immun... GO:0002292 p=1.1E−03 n=3 fg=0.03 bg=0.00
response to manganese ion GO:0010042 p=2.1E−03 n=3 fg=0.03 bg=0.00
cellular response to iron ion GO:0071281 p=2.4E−03 n=2 fg=0.02 bg=0.00
actin cortical patch localization GO:0051666 p=2.4E−03 n=2 fg=0.02 bg=0.00
lysine transport GO:0015819 p=2.4E−03 n=2 fg=0.02 bg=0.00
removal of superoxide radicals GO:0019430 p=2.4E−03 n=2 fg=0.02 bg=0.00
intracellular lipid transport GO:0032365 p=3.5E−03 n=3 fg=0.03 bg=0.00
establishment or maintenance of epitheli... GO:0045197 p=3.7E−03 n=4 fg=0.04 bg=0.01
oocyte microtubule cytoskeleton organiza... GO:0016325 p=5.3E−03 n=3 fg=0.03 bg=0.00
response to fluid shear stress GO:0034405 p=5.3E−03 n=3 fg=0.03 bg=0.00
positive regulation of leukocyte differe... GO:1902107 p=6.3E−03 n=4 fg=0.04 bg=0.01
negative regulation of miRNA−mediated ge... GO:0060965 p=6.9E−03 n=2 fg=0.02 bg=0.00
establishment or maintenance of polarity... GO:0016332 p=6.9E−03 n=2 fg=0.02 bg=0.00
endothelial cell activation GO:0042118 p=6.9E−03 n=2 fg=0.02 bg=0.00
Schwann cell differentiation GO:0014037 p=7.7E−03 n=3 fg=0.03 bg=0.00
forebrain neuron development GO:0021884 p=7.7E−03 n=3 fg=0.03 bg=0.00
establishment of epithelial cell polarit... GO:0090162 p=7.7E−03 n=3 fg=0.03 bg=0.00
skin epidermis development GO:0098773 p=7.9E−03 n=4 fg=0.04 bg=0.01
response to endogenous stimulus GO:0009719 p=9.9E−03 n=21 fg=0.24 bg=0.14
negative regulation of GTPase activity GO:0034260 p=1.1E−02 n=3 fg=0.03 bg=0.01
epidermis morphogenesis GO:0048730 p=1.1E−02 n=3 fg=0.03 bg=0.01
vascular associated smooth muscle contra... GO:0014829 p=1.3E−02 n=2 fg=0.02 bg=0.00
establishment of blood−brain barrier GO:0060856 p=1.3E−02 n=2 fg=0.02 bg=0.00
larval midgut histolysis GO:0035069 p=1.3E−02 n=2 fg=0.02 bg=0.00
basal protein localization GO:0045175 p=1.3E−02 n=2 fg=0.02 bg=0.00
alpha−beta T cell differentiation involv... GO:0002293 p=1.3E−02 n=2 fg=0.02 bg=0.00
CD4−positive, alpha−beta T cell differen... GO:0002294 p=1.3E−02 n=2 fg=0.02 bg=0.00
alpha−beta T cell activation involved in... GO:0002287 p=1.3E−02 n=2 fg=0.02 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=1.3E−02 n=2 fg=0.02 bg=0.00
T−helper cell differentiation GO:0042093 p=1.3E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=89/292 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Elav_Nvec_vc1.1_XM_032383693.2
fraction genes in fg and expected valu
calcium−dependent protein serine/threoni... GO:0004723 p=2.3E−03 n=2 fg=0.03 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=6.5E−03 n=2 fg=0.03 bg=0.00
copper ion binding GO:0005507 p=7.1E−03 n=3 fg=0.04 bg=0.01
enzyme inhibitor activity GO:0004857 p=7.9E−03 n=6 fg=0.08 bg=0.02
GTPase inhibitor activity GO:0005095 p=1.3E−02 n=2 fg=0.03 bg=0.00
cholesterol binding GO:0015485 p=3.0E−02 n=2 fg=0.03 bg=0.00
adenyl nucleotide binding GO:0030554 p=4.0E−02 n=8 fg=0.11 bg=0.05
endoribonuclease activity GO:0004521 p=4.0E−02 n=2 fg=0.03 bg=0.00
sterol binding GO:0032934 p=4.0E−02 n=2 fg=0.03 bg=0.00
type I transforming growth factor beta r... GO:0034713 p=4.8E−02 n=1 fg=0.01 bg=0.00
ATP−gated ion channel activity GO:0035381 p=4.8E−02 n=1 fg=0.01 bg=0.00
cupric ion binding GO:1903135 p=4.8E−02 n=1 fg=0.01 bg=0.00
cuprous ion binding GO:1903136 p=4.8E−02 n=1 fg=0.01 bg=0.00
sphingolipid transfer activity GO:0120016 p=4.8E−02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=4.8E−02 n=1 fg=0.01 bg=0.00
dimethyl selenide methyltransferase acti... GO:0098615 p=4.8E−02 n=1 fg=0.01 bg=0.00
myosin II binding GO:0045159 p=4.8E−02 n=1 fg=0.01 bg=0.00
calmodulin−dependent protein phosphatase... GO:0033192 p=4.8E−02 n=1 fg=0.01 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=4.8E−02 n=1 fg=0.01 bg=0.00
intramolecular oxidoreductase activity, ... GO:0016861 p=4.8E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP activity GO:0000171 p=4.8E−02 n=1 fg=0.01 bg=0.00
purinergic nucleotide receptor activity GO:0001614 p=4.8E−02 n=1 fg=0.01 bg=0.00
ubiquitin−like modifier activating enzym... GO:0008641 p=4.8E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=4.8E−02 n=1 fg=0.01 bg=0.00
ribonuclease P activity GO:0004526 p=4.8E−02 n=1 fg=0.01 bg=0.00
nucleotide receptor activity GO:0016502 p=4.8E−02 n=1 fg=0.01 bg=0.00
S−methyltransferase activity GO:0008172 p=4.8E−02 n=1 fg=0.01 bg=0.00
pyridine N−methyltransferase activity GO:0030760 p=4.8E−02 n=1 fg=0.01 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=4.8E−02 n=1 fg=0.01 bg=0.00
extracellularly ATP−gated cation channel... GO:0004931 p=4.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=76/292 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Elav_Nvec_vc1.1_XM_032383693.2
fraction genes in fg and expected valu
apicolateral plasma membrane GO:0016327 p=3.7E−03 n=3 fg=0.03 bg=0.00
tight junction GO:0070160 p=5.3E−03 n=4 fg=0.04 bg=0.01
septate junction GO:0005918 p=1.4E−02 n=2 fg=0.02 bg=0.00
fungal−type vacuole GO:0000324 p=1.4E−02 n=2 fg=0.02 bg=0.00
fungal−type vacuole membrane GO:0000329 p=1.4E−02 n=2 fg=0.02 bg=0.00
cell tip GO:0051286 p=1.4E−02 n=2 fg=0.02 bg=0.00
apical junction complex GO:0043296 p=1.9E−02 n=4 fg=0.04 bg=0.01
storage vacuole GO:0000322 p=2.3E−02 n=2 fg=0.02 bg=0.00
cell pole GO:0060187 p=2.3E−02 n=2 fg=0.02 bg=0.00
Cajal body GO:0015030 p=3.3E−02 n=2 fg=0.02 bg=0.00
early endosome membrane GO:0031901 p=4.3E−02 n=3 fg=0.03 bg=0.01
magnesium−dependent protein serine/threo... GO:0005963 p=4.5E−02 n=2 fg=0.02 bg=0.00
internode region of axon GO:0033269 p=5.0E−02 n=1 fg=0.01 bg=0.00
smooth septate junction GO:0005920 p=5.0E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=5.0E−02 n=1 fg=0.01 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=5.0E−02 n=1 fg=0.01 bg=0.00
nucleolar ribonuclease P complex GO:0005655 p=5.0E−02 n=1 fg=0.01 bg=0.00
cuticular plate GO:0032437 p=5.0E−02 n=1 fg=0.01 bg=0.00
compact myelin GO:0043218 p=5.0E−02 n=1 fg=0.01 bg=0.00
TSC1−TSC2 complex GO:0033596 p=5.0E−02 n=1 fg=0.01 bg=0.00
molybdopterin synthase complex GO:0019008 p=5.0E−02 n=1 fg=0.01 bg=0.00
CA3 pyramidal cell dendrite GO:0097442 p=5.0E−02 n=1 fg=0.01 bg=0.00
sno(s)RNA−containing ribonucleoprotein c... GO:0005732 p=5.0E−02 n=1 fg=0.01 bg=0.00
calcineurin complex GO:0005955 p=5.0E−02 n=1 fg=0.01 bg=0.00
ribonuclease MRP complex GO:0000172 p=5.0E−02 n=1 fg=0.01 bg=0.00
integral component of endoplasmic reticu... GO:0030176 p=5.2E−02 n=5 fg=0.05 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=5.2E−02 n=5 fg=0.05 bg=0.02
lipid droplet GO:0005811 p=6.7E−02 n=3 fg=0.03 bg=0.01
trans−Golgi network transport vesicle GO:0030140 p=7.2E−02 n=2 fg=0.02 bg=0.00
pleated septate junction GO:0005919 p=9.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=91/292 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction