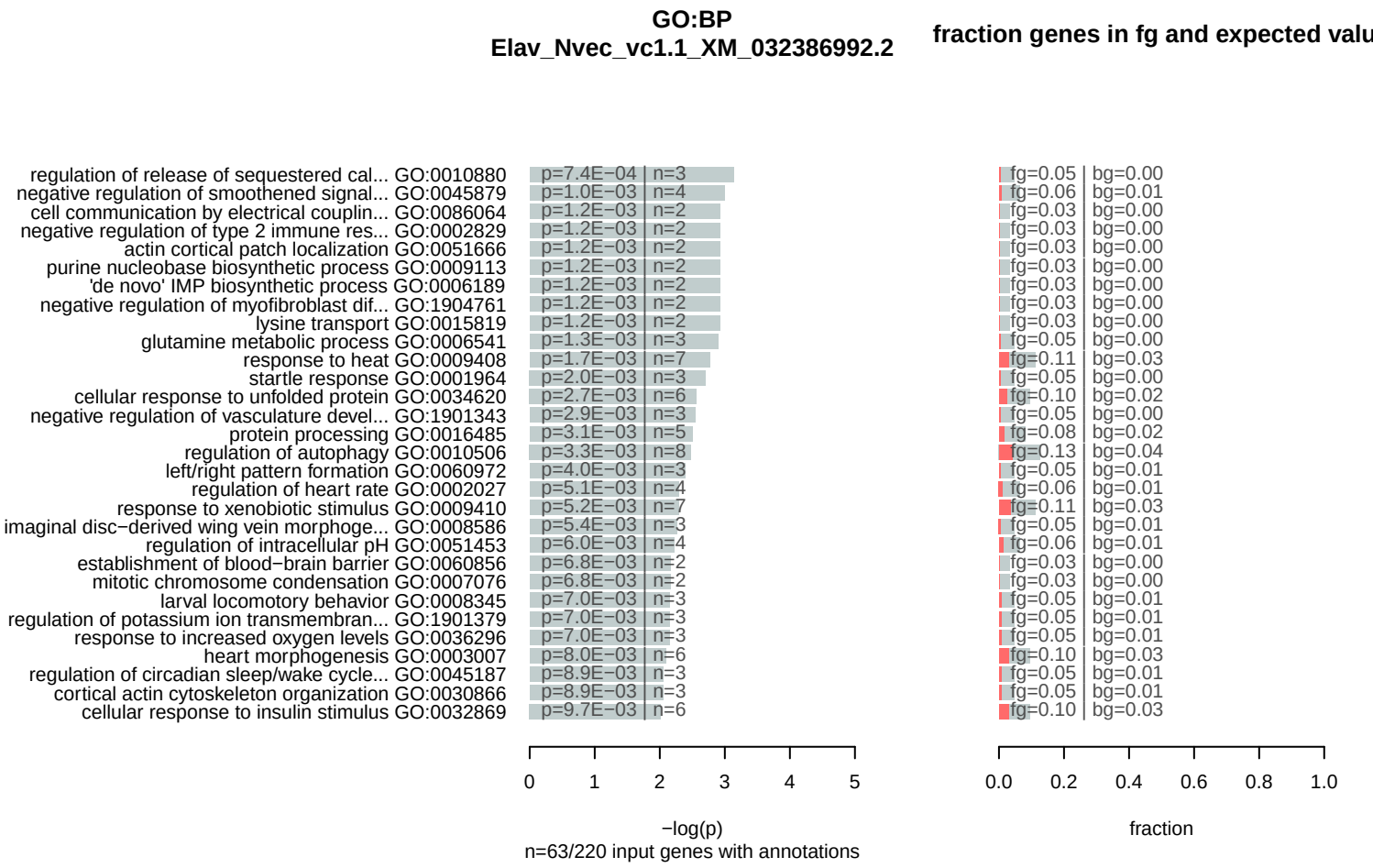
GO:BP
Elav_Nvec_vc1.1_XM_032386992.2
fraction genes in fg and expected valu
regulation of release of sequestered cal... GO:0010880 p=7.4E−04 n=3 fg=0.05 bg=0.00
negative regulation of smoothened signal... GO:0045879 p=1.0E−03 n=4 fg=0.06 bg=0.01
cell communication by electrical couplin... GO:0086064 p=1.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of type 2 immune res... GO:0002829 p=1.2E−03 n=2 fg=0.03 bg=0.00
actin cortical patch localization GO:0051666 p=1.2E−03 n=2 fg=0.03 bg=0.00
purine nucleobase biosynthetic process GO:0009113 p=1.2E−03 n=2 fg=0.03 bg=0.00
'de novo' IMP biosynthetic process GO:0006189 p=1.2E−03 n=2 fg=0.03 bg=0.00
negative regulation of myofibroblast dif... GO:1904761 p=1.2E−03 n=2 fg=0.03 bg=0.00
lysine transport GO:0015819 p=1.2E−03 n=2 fg=0.03 bg=0.00
glutamine metabolic process GO:0006541 p=1.3E−03 n=3 fg=0.05 bg=0.00
response to heat GO:0009408 p=1.7E−03 n=7 fg=0.11 bg=0.03
startle response GO:0001964 p=2.0E−03 n=3 fg=0.05 bg=0.00
cellular response to unfolded protein GO:0034620 p=2.7E−03 n=6 fg=0.10 bg=0.02
negative regulation of vasculature devel... GO:1901343 p=2.9E−03 n=3 fg=0.05 bg=0.00
protein processing GO:0016485 p=3.1E−03 n=5 fg=0.08 bg=0.02
regulation of autophagy GO:0010506 p=3.3E−03 n=8 fg=0.13 bg=0.04
left/right pattern formation GO:0060972 p=4.0E−03 n=3 fg=0.05 bg=0.01
regulation of heart rate GO:0002027 p=5.1E−03 n=4 fg=0.06 bg=0.01
response to xenobiotic stimulus GO:0009410 p=5.2E−03 n=7 fg=0.11 bg=0.03
imaginal disc−derived wing vein morphoge... GO:0008586 p=5.4E−03 n=3 fg=0.05 bg=0.01
regulation of intracellular pH GO:0051453 p=6.0E−03 n=4 fg=0.06 bg=0.01
establishment of blood−brain barrier GO:0060856 p=6.8E−03 n=2 fg=0.03 bg=0.00
mitotic chromosome condensation GO:0007076 p=6.8E−03 n=2 fg=0.03 bg=0.00
larval locomotory behavior GO:0008345 p=7.0E−03 n=3 fg=0.05 bg=0.01
regulation of potassium ion transmembran... GO:1901379 p=7.0E−03 n=3 fg=0.05 bg=0.01
response to increased oxygen levels GO:0036296 p=7.0E−03 n=3 fg=0.05 bg=0.01
heart morphogenesis GO:0003007 p=8.0E−03 n=6 fg=0.10 bg=0.03
regulation of circadian sleep/wake cycle... GO:0045187 p=8.9E−03 n=3 fg=0.05 bg=0.01
cortical actin cytoskeleton organization GO:0030866 p=8.9E−03 n=3 fg=0.05 bg=0.01
cellular response to insulin stimulus GO:0032869 p=9.7E−03 n=6 fg=0.10 bg=0.03
0 1 2 3 4 5
−log(p)
n=63/220 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032386992.2
fraction genes in fg and expected valu
mRNA 3'−UTR AU−rich region binding GO:0035925 p=1.2E−03 n=2 fg=0.04 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=1.2E−03 n=3 fg=0.05 bg=0.00
ligase activity, forming carbon−nitrogen... GO:0016879 p=1.9E−03 n=3 fg=0.05 bg=0.01
potassium channel regulator activity GO:0015459 p=5.3E−03 n=3 fg=0.05 bg=0.01
kinase binding GO:0019900 p=9.1E−03 n=10 fg=0.18 bg=0.08
kinesin binding GO:0019894 p=1.1E−02 n=3 fg=0.05 bg=0.01
proton−transporting ATPase activity, rot... GO:0046961 p=1.1E−02 n=2 fg=0.04 bg=0.00
cyclic nucleotide−gated ion channel acti... GO:0043855 p=1.1E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086008 p=1.1E−02 n=2 fg=0.04 bg=0.00
delayed rectifier potassium channel acti... GO:0005251 p=1.1E−02 n=2 fg=0.04 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=1.1E−02 n=2 fg=0.04 bg=0.00
intracellular cyclic nucleotide activate... GO:0005221 p=1.1E−02 n=2 fg=0.04 bg=0.00
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=1.1E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086090 p=1.1E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086087 p=1.1E−02 n=2 fg=0.04 bg=0.00
voltage−gated potassium channel activity... GO:0086089 p=1.1E−02 n=2 fg=0.04 bg=0.00
aspartic−type endopeptidase activity GO:0004190 p=1.6E−02 n=2 fg=0.04 bg=0.00
aspartic−type peptidase activity GO:0070001 p=1.6E−02 n=2 fg=0.04 bg=0.00
potassium channel inhibitor activity GO:0019870 p=1.6E−02 n=2 fg=0.04 bg=0.00
protein kinase binding GO:0019901 p=1.9E−02 n=9 fg=0.16 bg=0.08
protein−disulfide reductase (NAD(P)) act... GO:0047134 p=2.2E−02 n=2 fg=0.04 bg=0.00
oxidoreductase activity, acting on a sul... GO:0016668 p=2.2E−02 n=2 fg=0.04 bg=0.00
actinin binding GO:0042805 p=2.9E−02 n=2 fg=0.04 bg=0.01
alpha−actinin binding GO:0051393 p=2.9E−02 n=2 fg=0.04 bg=0.01
purine nucleotide binding GO:0017076 p=3.2E−02 n=8 fg=0.15 bg=0.07
cyclic nucleotide−dependent protein kina... GO:0004690 p=3.5E−02 n=1 fg=0.02 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=3.5E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase activity GO:0004691 p=3.5E−02 n=1 fg=0.02 bg=0.00
tRNA pseudouridine synthase activity GO:0106029 p=3.5E−02 n=1 fg=0.02 bg=0.00
pseudophosphatase activity GO:0001691 p=3.5E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=55/220 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032386992.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=1.6E−04 n=4 fg=0.06 bg=0.01
Z disc GO:0030018 p=1.6E−04 n=6 fg=0.09 bg=0.01
vacuolar proton−transporting V−type ATPa... GO:0000220 p=1.2E−03 n=2 fg=0.03 bg=0.00
endosome membrane GO:0010008 p=5.7E−03 n=7 fg=0.11 bg=0.03
fungal−type vacuole membrane GO:0000329 p=7.1E−03 n=2 fg=0.03 bg=0.00
integral component of lumenal side of en... GO:0071556 p=7.1E−03 n=2 fg=0.03 bg=0.00
cell tip GO:0051286 p=7.1E−03 n=2 fg=0.03 bg=0.00
intracellular canaliculus GO:0046691 p=1.1E−02 n=2 fg=0.03 bg=0.00
juxtaparanode region of axon GO:0044224 p=1.1E−02 n=2 fg=0.03 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=1.7E−02 n=2 fg=0.03 bg=0.00
acrosomal vesicle GO:0001669 p=1.7E−02 n=2 fg=0.03 bg=0.00
main axon GO:0044304 p=1.7E−02 n=3 fg=0.05 bg=0.01
paranode region of axon GO:0033270 p=2.3E−02 n=2 fg=0.03 bg=0.00
intrinsic component of postsynaptic memb... GO:0098936 p=2.3E−02 n=2 fg=0.03 bg=0.00
intrinsic component of synaptic membrane GO:0099240 p=2.3E−02 n=2 fg=0.03 bg=0.00
integral component of synaptic membrane GO:0099699 p=2.3E−02 n=2 fg=0.03 bg=0.00
intrinsic component of presynaptic membr... GO:0098889 p=2.3E−02 n=2 fg=0.03 bg=0.00
integral component of postsynaptic membr... GO:0099055 p=2.3E−02 n=2 fg=0.03 bg=0.00
integral component of presynaptic membra... GO:0099056 p=2.3E−02 n=2 fg=0.03 bg=0.00
magnesium−dependent protein serine/threo... GO:0005963 p=2.3E−02 n=2 fg=0.03 bg=0.00
Golgi−associated vesicle lumen GO:0070931 p=3.5E−02 n=1 fg=0.02 bg=0.00
protein phosphatase 4 complex GO:0030289 p=3.5E−02 n=1 fg=0.02 bg=0.00
apical cytoplasm GO:0090651 p=3.5E−02 n=1 fg=0.02 bg=0.00
sarcoplasmic reticulum lumen GO:0033018 p=3.5E−02 n=1 fg=0.02 bg=0.00
integral component of endoplasmic reticu... GO:0030176 p=3.6E−02 n=6 fg=0.09 bg=0.02
intrinsic component of endoplasmic retic... GO:0031227 p=3.6E−02 n=6 fg=0.09 bg=0.02
Golgi apparatus GO:0005794 p=3.6E−02 n=14 fg=0.22 bg=0.13
membrane raft GO:0045121 p=3.7E−02 n=5 fg=0.08 bg=0.03
membrane microdomain GO:0098857 p=3.7E−02 n=5 fg=0.08 bg=0.03
phagocytic vesicle membrane GO:0030670 p=3.8E−02 n=2 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=64/220 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction