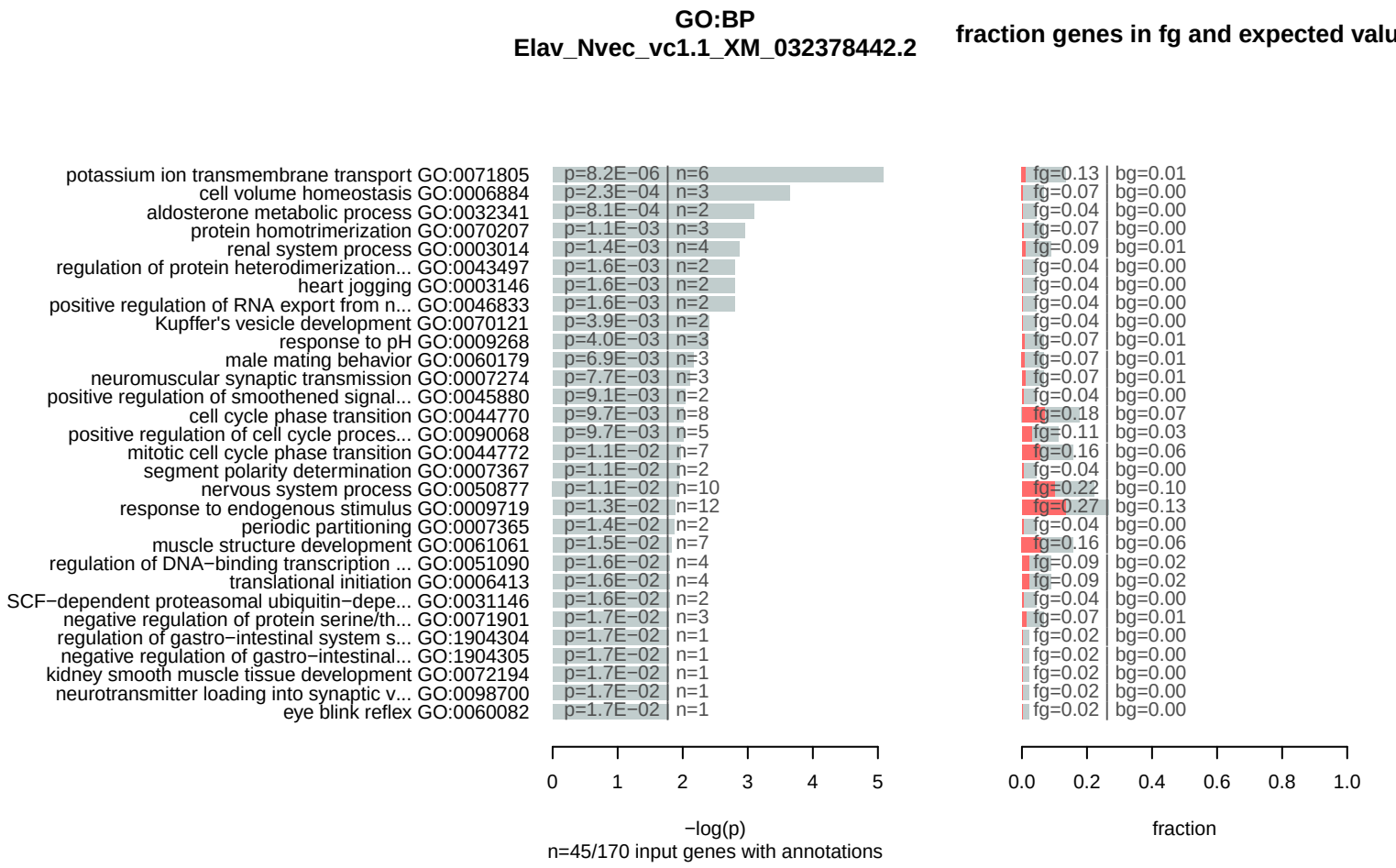
GO:BP
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
potassium ion transmembrane transport GO:0071805 p=8.2E−06 n=6 fg=0.13 bg=0.01
cell volume homeostasis GO:0006884 p=2.3E−04 n=3 fg=0.07 bg=0.00
aldosterone metabolic process GO:0032341 p=8.1E−04 n=2 fg=0.04 bg=0.00
protein homotrimerization GO:0070207 p=1.1E−03 n=3 fg=0.07 bg=0.00
renal system process GO:0003014 p=1.4E−03 n=4 fg=0.09 bg=0.01
regulation of protein heterodimerization... GO:0043497 p=1.6E−03 n=2 fg=0.04 bg=0.00
heart jogging GO:0003146 p=1.6E−03 n=2 fg=0.04 bg=0.00
positive regulation of RNA export from n... GO:0046833 p=1.6E−03 n=2 fg=0.04 bg=0.00
Kupffer's vesicle development GO:0070121 p=3.9E−03 n=2 fg=0.04 bg=0.00
response to pH GO:0009268 p=4.0E−03 n=3 fg=0.07 bg=0.01
male mating behavior GO:0060179 p=6.9E−03 n=3 fg=0.07 bg=0.01
neuromuscular synaptic transmission GO:0007274 p=7.7E−03 n=3 fg=0.07 bg=0.01
positive regulation of smoothened signal... GO:0045880 p=9.1E−03 n=2 fg=0.04 bg=0.00
cell cycle phase transition GO:0044770 p=9.7E−03 n=8 fg=0.18 bg=0.07
positive regulation of cell cycle proces... GO:0090068 p=9.7E−03 n=5 fg=0.11 bg=0.03
mitotic cell cycle phase transition GO:0044772 p=1.1E−02 n=7 fg=0.16 bg=0.06
segment polarity determination GO:0007367 p=1.1E−02 n=2 fg=0.04 bg=0.00
nervous system process GO:0050877 p=1.1E−02 n=10 fg=0.22 bg=0.10
response to endogenous stimulus GO:0009719 p=1.3E−02 n=12 fg=0.27 bg=0.13
periodic partitioning GO:0007365 p=1.4E−02 n=2 fg=0.04 bg=0.00
muscle structure development GO:0061061 p=1.5E−02 n=7 fg=0.16 bg=0.06
regulation of DNA−binding transcription ... GO:0051090 p=1.6E−02 n=4 fg=0.09 bg=0.02
translational initiation GO:0006413 p=1.6E−02 n=4 fg=0.09 bg=0.02
SCF−dependent proteasomal ubiquitin−depe... GO:0031146 p=1.6E−02 n=2 fg=0.04 bg=0.00
negative regulation of protein serine/th... GO:0071901 p=1.7E−02 n=3 fg=0.07 bg=0.01
regulation of gastro−intestinal system s... GO:1904304 p=1.7E−02 n=1 fg=0.02 bg=0.00
negative regulation of gastro−intestinal... GO:1904305 p=1.7E−02 n=1 fg=0.02 bg=0.00
kidney smooth muscle tissue development GO:0072194 p=1.7E−02 n=1 fg=0.02 bg=0.00
neurotransmitter loading into synaptic v... GO:0098700 p=1.7E−02 n=1 fg=0.02 bg=0.00
eye blink reflex GO:0060082 p=1.7E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=45/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
calcium−activated potassium channel acti... GO:0015269 p=5.8E−05 n=3 fg=0.07 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=9.2E−04 n=4 fg=0.09 bg=0.00
voltage−gated sodium channel activity GO:0005248 p=2.0E−03 n=2 fg=0.05 bg=0.00
outward rectifier potassium channel acti... GO:0015271 p=8.8E−03 n=2 fg=0.05 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=1.2E−02 n=6 fg=0.14 bg=0.01
voltage−gated calcium channel activity GO:0005245 p=1.4E−02 n=2 fg=0.05 bg=0.00
translation factor activity, RNA binding GO:0008135 p=1.4E−02 n=3 fg=0.07 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=1.7E−02 n=3 fg=0.07 bg=0.01
2',3'−cyclic GMP−AMP synthase activity GO:0061501 p=1.9E−02 n=1 fg=0.02 bg=0.00
cytosine C−5 DNA demethylase activity GO:0051747 p=1.9E−02 n=1 fg=0.02 bg=0.00
RNA−3'−phosphate cyclase activity GO:0003963 p=1.9E−02 n=1 fg=0.02 bg=0.00
GBD domain binding GO:0032427 p=1.9E−02 n=1 fg=0.02 bg=0.00
large conductance calcium−activated pota... GO:0060072 p=1.9E−02 n=1 fg=0.02 bg=0.00
HLH domain binding GO:0043398 p=1.9E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=1.9E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=1.9E−02 n=1 fg=0.02 bg=0.00
steryl−sulfatase activity GO:0004773 p=1.9E−02 n=1 fg=0.02 bg=0.00
muscle alpha−actinin binding GO:0051371 p=1.9E−02 n=1 fg=0.02 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=1.9E−02 n=1 fg=0.02 bg=0.00
apolipoprotein receptor binding GO:0034190 p=1.9E−02 n=1 fg=0.02 bg=0.00
apolipoprotein A−I receptor binding GO:0034191 p=1.9E−02 n=1 fg=0.02 bg=0.00
ABC−type guanine transporter activity GO:0008558 p=1.9E−02 n=1 fg=0.02 bg=0.00
guanine transmembrane transporter activi... GO:0015208 p=1.9E−02 n=1 fg=0.02 bg=0.00
ferric−chelate reductase activity GO:0000293 p=1.9E−02 n=1 fg=0.02 bg=0.00
cyclic GMP−AMP synthase activity GO:0140699 p=1.9E−02 n=1 fg=0.02 bg=0.00
ABC−type 3',5'−cyclic GMP transmembrane ... GO:1905948 p=1.9E−02 n=1 fg=0.02 bg=0.00
Rho GDP−dissociation inhibitor binding GO:0051022 p=1.9E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=1.9E−02 n=1 fg=0.02 bg=0.00
amine transmembrane transporter activity GO:0005275 p=1.9E−02 n=1 fg=0.02 bg=0.00
inositol oxygenase activity GO:0050113 p=1.9E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=44/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378442.2
fraction genes in fg and expected valu
voltage−gated potassium channel complex GO:0008076 p=5.4E−04 n=3 fg=0.06 bg=0.00
calcium channel complex GO:0034704 p=9.9E−03 n=2 fg=0.04 bg=0.00
plasma membrane region GO:0098590 p=1.3E−02 n=9 fg=0.19 bg=0.08
plasma membrane raft GO:0044853 p=1.4E−02 n=3 fg=0.06 bg=0.01
eukaryotic translation initiation factor... GO:0071540 p=1.7E−02 n=1 fg=0.02 bg=0.00
integral component of pigment granule me... GO:0090740 p=1.7E−02 n=1 fg=0.02 bg=0.00
pigment granule membrane GO:0090741 p=1.7E−02 n=1 fg=0.02 bg=0.00
cytoskeleton of presynaptic active zone GO:0048788 p=1.7E−02 n=1 fg=0.02 bg=0.00
polycystin complex GO:0002133 p=1.7E−02 n=1 fg=0.02 bg=0.00
Grb2−Sos complex GO:0070618 p=1.7E−02 n=1 fg=0.02 bg=0.00
presynaptic active zone cytoplasmic comp... GO:0098831 p=1.7E−02 n=1 fg=0.02 bg=0.00
basal plasma membrane GO:0009925 p=2.2E−02 n=4 fg=0.09 bg=0.02
basolateral plasma membrane GO:0016323 p=2.2E−02 n=4 fg=0.09 bg=0.02
apical part of cell GO:0045177 p=2.3E−02 n=6 fg=0.13 bg=0.05
inclusion body GO:0016234 p=2.7E−02 n=2 fg=0.04 bg=0.01
mitotic spindle GO:0072686 p=2.7E−02 n=3 fg=0.06 bg=0.01
postsynapse GO:0098794 p=2.8E−02 n=5 fg=0.11 bg=0.04
SCF ubiquitin ligase complex GO:0019005 p=3.0E−02 n=2 fg=0.04 bg=0.01
basal part of cell GO:0045178 p=3.3E−02 n=4 fg=0.09 bg=0.03
IkappaB kinase complex GO:0008385 p=3.5E−02 n=1 fg=0.02 bg=0.00
Hedgehog signaling complex GO:0035301 p=3.5E−02 n=1 fg=0.02 bg=0.00
nuclear stress granule GO:0097165 p=3.5E−02 n=1 fg=0.02 bg=0.00
presynaptic cytoskeleton GO:0099569 p=3.5E−02 n=1 fg=0.02 bg=0.00
cell cortex region GO:0099738 p=5.0E−02 n=2 fg=0.04 bg=0.01
eukaryotic translation initiation factor... GO:0005850 p=5.1E−02 n=1 fg=0.02 bg=0.00
integral component of cytoplasmic side o... GO:0071458 p=5.1E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=5.1E−02 n=1 fg=0.02 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=5.1E−02 n=1 fg=0.02 bg=0.00
ribonucleoprotein complex GO:1990904 p=5.2E−02 n=8 fg=0.17 bg=0.09
caveola GO:0005901 p=6.0E−02 n=2 fg=0.04 bg=0.01
0 1 2 3 4 5
−log(p)
n=47/170 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction