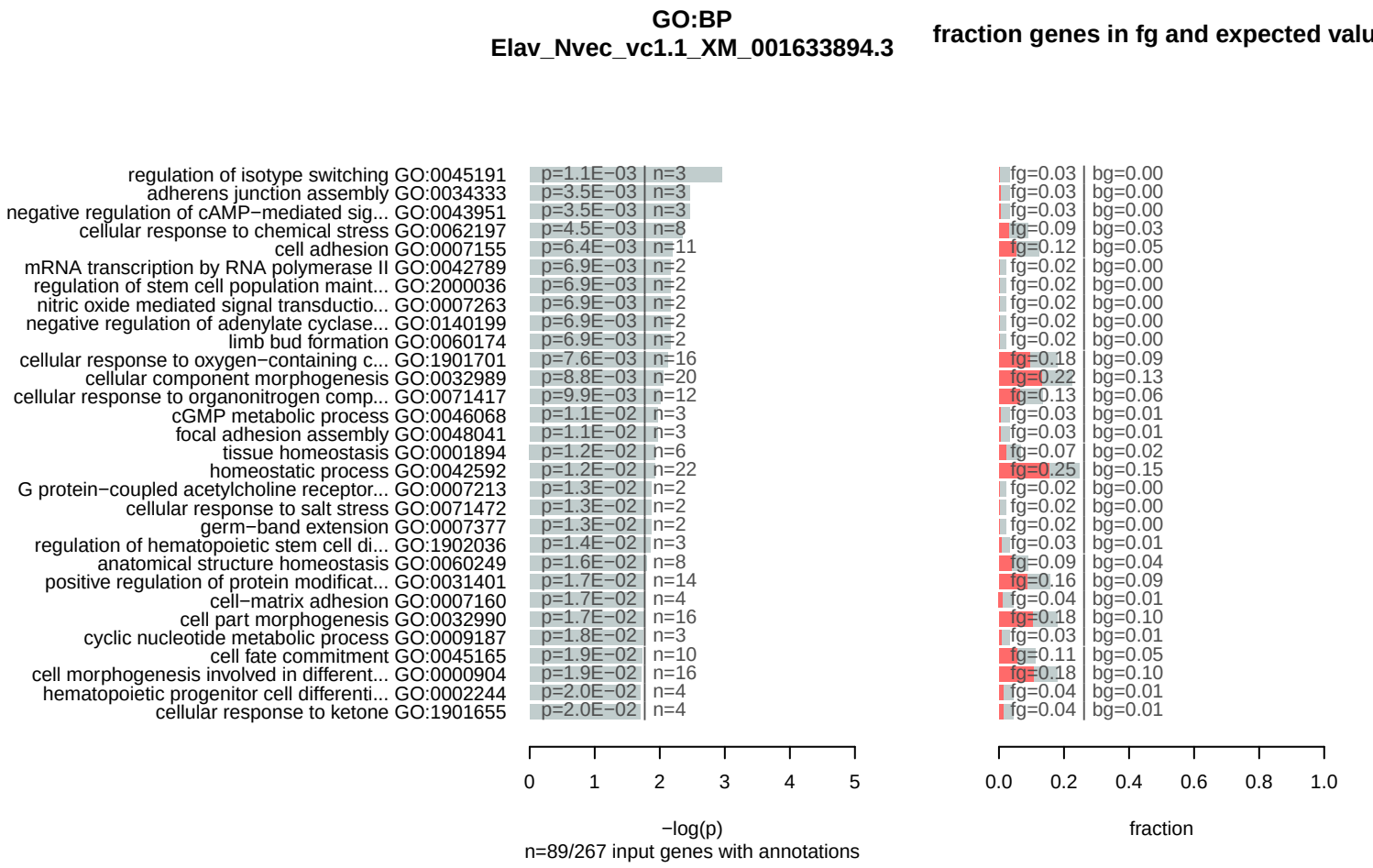
GO:BP
Elav_Nvec_vc1.1_XM_001633894.3
fraction genes in fg and expected valu
regulation of isotype switching GO:0045191 p=1.1E−03 n=3 fg=0.03 bg=0.00
adherens junction assembly GO:0034333 p=3.5E−03 n=3 fg=0.03 bg=0.00
negative regulation of cAMP−mediated sig... GO:0043951 p=3.5E−03 n=3 fg=0.03 bg=0.00
cellular response to chemical stress GO:0062197 p=4.5E−03 n=8 fg=0.09 bg=0.03
cell adhesion GO:0007155 p=6.4E−03 n=11 fg=0.12 bg=0.05
mRNA transcription by RNA polymerase II GO:0042789 p=6.9E−03 n=2 fg=0.02 bg=0.00
regulation of stem cell population maint... GO:2000036 p=6.9E−03 n=2 fg=0.02 bg=0.00
nitric oxide mediated signal transductio... GO:0007263 p=6.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of adenylate cyclase... GO:0140199 p=6.9E−03 n=2 fg=0.02 bg=0.00
limb bud formation GO:0060174 p=6.9E−03 n=2 fg=0.02 bg=0.00
cellular response to oxygen−containing c... GO:1901701 p=7.6E−03 n=16 fg=0.18 bg=0.09
cellular component morphogenesis GO:0032989 p=8.8E−03 n=20 fg=0.22 bg=0.13
cellular response to organonitrogen comp... GO:0071417 p=9.9E−03 n=12 fg=0.13 bg=0.06
cGMP metabolic process GO:0046068 p=1.1E−02 n=3 fg=0.03 bg=0.01
focal adhesion assembly GO:0048041 p=1.1E−02 n=3 fg=0.03 bg=0.01
tissue homeostasis GO:0001894 p=1.2E−02 n=6 fg=0.07 bg=0.02
homeostatic process GO:0042592 p=1.2E−02 n=22 fg=0.25 bg=0.15
G protein−coupled acetylcholine receptor... GO:0007213 p=1.3E−02 n=2 fg=0.02 bg=0.00
cellular response to salt stress GO:0071472 p=1.3E−02 n=2 fg=0.02 bg=0.00
germ−band extension GO:0007377 p=1.3E−02 n=2 fg=0.02 bg=0.00
regulation of hematopoietic stem cell di... GO:1902036 p=1.4E−02 n=3 fg=0.03 bg=0.01
anatomical structure homeostasis GO:0060249 p=1.6E−02 n=8 fg=0.09 bg=0.04
positive regulation of protein modificat... GO:0031401 p=1.7E−02 n=14 fg=0.16 bg=0.09
cell−matrix adhesion GO:0007160 p=1.7E−02 n=4 fg=0.04 bg=0.01
cell part morphogenesis GO:0032990 p=1.7E−02 n=16 fg=0.18 bg=0.10
cyclic nucleotide metabolic process GO:0009187 p=1.8E−02 n=3 fg=0.03 bg=0.01
cell fate commitment GO:0045165 p=1.9E−02 n=10 fg=0.11 bg=0.05
cell morphogenesis involved in different... GO:0000904 p=1.9E−02 n=16 fg=0.18 bg=0.10
hematopoietic progenitor cell differenti... GO:0002244 p=2.0E−02 n=4 fg=0.04 bg=0.01
cellular response to ketone GO:1901655 p=2.0E−02 n=4 fg=0.04 bg=0.01
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−log(p)
n=89/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001633894.3
fraction genes in fg and expected valu
vinculin binding GO:0017166 p=2.4E−03 n=2 fg=0.03 bg=0.00
proteasome binding GO:0070628 p=2.4E−03 n=2 fg=0.03 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=7.8E−03 n=4 fg=0.05 bg=0.01
poly(U) RNA binding GO:0008266 p=2.1E−02 n=2 fg=0.03 bg=0.00
BH domain binding GO:0051400 p=2.1E−02 n=2 fg=0.03 bg=0.00
voltage−gated channel activity GO:0022832 p=2.7E−02 n=4 fg=0.05 bg=0.02
voltage−gated ion channel activity GO:0005244 p=2.7E−02 n=4 fg=0.05 bg=0.02
cation channel activity GO:0005261 p=2.7E−02 n=6 fg=0.08 bg=0.03
potassium channel activity GO:0005267 p=2.8E−02 n=3 fg=0.04 bg=0.01
SMAD binding GO:0046332 p=2.8E−02 n=3 fg=0.04 bg=0.01
fibroblast growth factor binding GO:0017134 p=3.1E−02 n=2 fg=0.03 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=3.1E−02 n=2 fg=0.03 bg=0.00
protein heterodimerization activity GO:0046982 p=3.2E−02 n=9 fg=0.12 bg=0.06
calcium activated cation channel activit... GO:0005227 p=4.2E−02 n=2 fg=0.03 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=4.8E−02 n=11 fg=0.14 bg=0.08
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=4.9E−02 n=1 fg=0.01 bg=0.00
netrin receptor activity GO:0005042 p=4.9E−02 n=1 fg=0.01 bg=0.00
Roundabout binding GO:0048495 p=4.9E−02 n=1 fg=0.01 bg=0.00
BH4 domain binding GO:0051435 p=4.9E−02 n=1 fg=0.01 bg=0.00
neuropilin binding GO:0038191 p=4.9E−02 n=1 fg=0.01 bg=0.00
pyrroline−5−carboxylate reductase activi... GO:0004735 p=4.9E−02 n=1 fg=0.01 bg=0.00
alkylglycerophosphoethanolamine phosphod... GO:0047391 p=4.9E−02 n=1 fg=0.01 bg=0.00
intracellular sodium activated potassium... GO:0005228 p=4.9E−02 n=1 fg=0.01 bg=0.00
protein serine/threonine phosphatase inh... GO:0004865 p=4.9E−02 n=1 fg=0.01 bg=0.00
anion:cation symporter activity GO:0015296 p=4.9E−02 n=1 fg=0.01 bg=0.00
poly(G) binding GO:0034046 p=4.9E−02 n=1 fg=0.01 bg=0.00
cation:chloride symporter activity GO:0015377 p=4.9E−02 n=1 fg=0.01 bg=0.00
potassium:chloride symporter activity GO:0015379 p=4.9E−02 n=1 fg=0.01 bg=0.00
SMC family protein binding GO:0043221 p=4.9E−02 n=1 fg=0.01 bg=0.00
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=4.9E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=78/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001633894.3
fraction genes in fg and expected valu
lipid droplet GO:0005811 p=1.1E−02 n=4 fg=0.05 bg=0.01
side of membrane GO:0098552 p=1.2E−02 n=8 fg=0.09 bg=0.04
cytoplasmic side of plasma membrane GO:0009898 p=1.4E−02 n=6 fg=0.07 bg=0.02
polysome GO:0005844 p=1.7E−02 n=3 fg=0.03 bg=0.01
cytoplasmic side of membrane GO:0098562 p=2.3E−02 n=6 fg=0.07 bg=0.03
plasma membrane protein complex GO:0098797 p=2.7E−02 n=7 fg=0.08 bg=0.03
heterotrimeric G−protein complex GO:0005834 p=3.0E−02 n=2 fg=0.02 bg=0.00
dendrite membrane GO:0032590 p=3.0E−02 n=2 fg=0.02 bg=0.00
GTPase complex GO:1905360 p=3.0E−02 n=2 fg=0.02 bg=0.00
sarcoplasm GO:0016528 p=3.0E−02 n=2 fg=0.02 bg=0.00
sarcoplasmic reticulum GO:0016529 p=3.0E−02 n=2 fg=0.02 bg=0.00
focal adhesion GO:0005925 p=3.2E−02 n=3 fg=0.03 bg=0.01
nuclear outer membrane−endoplasmic retic... GO:0042175 p=3.4E−02 n=12 fg=0.14 bg=0.08
adherens junction GO:0005912 p=4.0E−02 n=5 fg=0.06 bg=0.02
vesicle coat GO:0030120 p=4.1E−02 n=2 fg=0.02 bg=0.00
cell periphery GO:0071944 p=4.2E−02 n=33 fg=0.38 bg=0.29
somatodendritic compartment GO:0036477 p=4.4E−02 n=14 fg=0.16 bg=0.10
basal part of cell GO:0045178 p=4.5E−02 n=6 fg=0.07 bg=0.03
intraciliary transport particle B GO:0030992 p=4.8E−02 n=1 fg=0.01 bg=0.00
internode region of axon GO:0033269 p=4.8E−02 n=1 fg=0.01 bg=0.00
integrin alpha9−beta1 complex GO:0034679 p=4.8E−02 n=1 fg=0.01 bg=0.00
BAT3 complex GO:0071818 p=4.8E−02 n=1 fg=0.01 bg=0.00
lumenal side of Golgi membrane GO:0098547 p=4.8E−02 n=1 fg=0.01 bg=0.00
ER membrane insertion complex GO:0072379 p=4.8E−02 n=1 fg=0.01 bg=0.00
nuclear outer membrane GO:0005640 p=4.8E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=4.8E−02 n=1 fg=0.01 bg=0.00
Schmidt−Lanterman incisure GO:0043220 p=4.8E−02 n=1 fg=0.01 bg=0.00
compact myelin GO:0043218 p=4.8E−02 n=1 fg=0.01 bg=0.00
anterior cell cortex GO:0061802 p=4.8E−02 n=1 fg=0.01 bg=0.00
plasma membrane GO:0005886 p=4.8E−02 n=31 fg=0.36 bg=0.27
0 1 2 3 4 5
−log(p)
n=87/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction