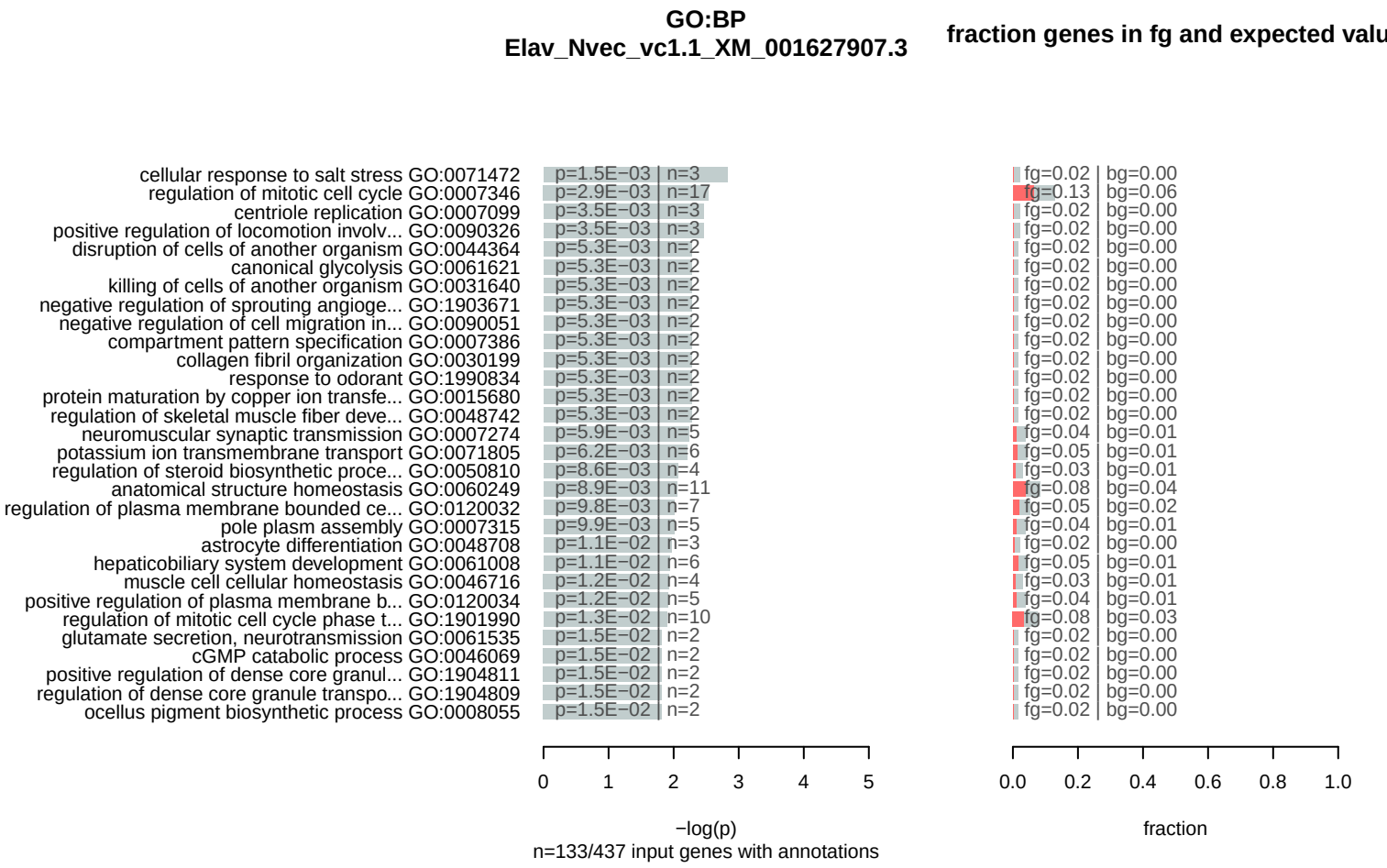
GO:BP
Elav_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
cellular response to salt stress GO:0071472 p=1.5E−03 n=3 fg=0.02 bg=0.00
regulation of mitotic cell cycle GO:0007346 p=2.9E−03 n=17 fg=0.13 bg=0.06
centriole replication GO:0007099 p=3.5E−03 n=3 fg=0.02 bg=0.00
positive regulation of locomotion involv... GO:0090326 p=3.5E−03 n=3 fg=0.02 bg=0.00
disruption of cells of another organism GO:0044364 p=5.3E−03 n=2 fg=0.02 bg=0.00
canonical glycolysis GO:0061621 p=5.3E−03 n=2 fg=0.02 bg=0.00
killing of cells of another organism GO:0031640 p=5.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of sprouting angioge... GO:1903671 p=5.3E−03 n=2 fg=0.02 bg=0.00
negative regulation of cell migration in... GO:0090051 p=5.3E−03 n=2 fg=0.02 bg=0.00
compartment pattern specification GO:0007386 p=5.3E−03 n=2 fg=0.02 bg=0.00
collagen fibril organization GO:0030199 p=5.3E−03 n=2 fg=0.02 bg=0.00
response to odorant GO:1990834 p=5.3E−03 n=2 fg=0.02 bg=0.00
protein maturation by copper ion transfe... GO:0015680 p=5.3E−03 n=2 fg=0.02 bg=0.00
regulation of skeletal muscle fiber deve... GO:0048742 p=5.3E−03 n=2 fg=0.02 bg=0.00
neuromuscular synaptic transmission GO:0007274 p=5.9E−03 n=5 fg=0.04 bg=0.01
potassium ion transmembrane transport GO:0071805 p=6.2E−03 n=6 fg=0.05 bg=0.01
regulation of steroid biosynthetic proce... GO:0050810 p=8.6E−03 n=4 fg=0.03 bg=0.01
anatomical structure homeostasis GO:0060249 p=8.9E−03 n=11 fg=0.08 bg=0.04
regulation of plasma membrane bounded ce... GO:0120032 p=9.8E−03 n=7 fg=0.05 bg=0.02
pole plasm assembly GO:0007315 p=9.9E−03 n=5 fg=0.04 bg=0.01
astrocyte differentiation GO:0048708 p=1.1E−02 n=3 fg=0.02 bg=0.00
hepaticobiliary system development GO:0061008 p=1.1E−02 n=6 fg=0.05 bg=0.01
muscle cell cellular homeostasis GO:0046716 p=1.2E−02 n=4 fg=0.03 bg=0.01
positive regulation of plasma membrane b... GO:0120034 p=1.2E−02 n=5 fg=0.04 bg=0.01
regulation of mitotic cell cycle phase t... GO:1901990 p=1.3E−02 n=10 fg=0.08 bg=0.03
glutamate secretion, neurotransmission GO:0061535 p=1.5E−02 n=2 fg=0.02 bg=0.00
cGMP catabolic process GO:0046069 p=1.5E−02 n=2 fg=0.02 bg=0.00
positive regulation of dense core granul... GO:1904811 p=1.5E−02 n=2 fg=0.02 bg=0.00
regulation of dense core granule transpo... GO:1904809 p=1.5E−02 n=2 fg=0.02 bg=0.00
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n=133/437 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
superoxide dismutase copper chaperone ac... GO:0016532 p=5.5E−03 n=2 fg=0.02 bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948 p=5.5E−03 n=2 fg=0.02 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=6.2E−03 n=5 fg=0.04 bg=0.01
3',5'−cyclic−AMP phosphodiesterase activ... GO:0004115 p=1.6E−02 n=2 fg=0.02 bg=0.00
cGMP binding GO:0030553 p=1.6E−02 n=2 fg=0.02 bg=0.00
calcium−activated potassium channel acti... GO:0015269 p=1.6E−02 n=2 fg=0.02 bg=0.00
potassium channel activity GO:0005267 p=1.6E−02 n=4 fg=0.03 bg=0.01
ADP binding GO:0043531 p=1.7E−02 n=3 fg=0.03 bg=0.01
microtubule motor activity GO:0003777 p=1.7E−02 n=3 fg=0.03 bg=0.01
translation factor activity, RNA binding GO:0008135 p=2.6E−02 n=4 fg=0.03 bg=0.01
carbohydrate kinase activity GO:0019200 p=3.0E−02 n=2 fg=0.02 bg=0.00
voltage−gated potassium channel activity GO:0005249 p=3.2E−02 n=3 fg=0.03 bg=0.01
ribonucleoprotein complex binding GO:0043021 p=3.3E−02 n=5 fg=0.04 bg=0.02
translation regulator activity, nucleic ... GO:0090079 p=3.9E−02 n=4 fg=0.03 bg=0.01
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cyclic nucleotide binding GO:0030551 p=4.7E−02 n=2 fg=0.02 bg=0.00
phospholipase binding GO:0043274 p=4.7E−02 n=2 fg=0.02 bg=0.00
dynactin binding GO:0034452 p=4.7E−02 n=2 fg=0.02 bg=0.00
ribonucleotide binding GO:0032553 p=4.7E−02 n=13 fg=0.11 bg=0.07
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cytoskeletal motor activity GO:0003774 p=5.3E−02 n=3 fg=0.03 bg=0.01
ubiquitin−like protein ligase activity GO:0061659 p=5.5E−02 n=8 fg=0.07 bg=0.04
ubiquitin protein ligase activity GO:0061630 p=5.5E−02 n=8 fg=0.07 bg=0.04
cis−regulatory region sequence−specific ... GO:0000987 p=5.5E−02 n=8 fg=0.07 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=5.5E−02 n=8 fg=0.07 bg=0.04
purine nucleotide binding GO:0017076 p=5.7E−02 n=13 fg=0.11 bg=0.07
nucleotide binding GO:0000166 p=6.0E−02 n=14 fg=0.12 bg=0.08
nucleoside phosphate binding GO:1901265 p=6.0E−02 n=14 fg=0.12 bg=0.08
GTPase activator activity GO:0005096 p=6.3E−02 n=6 fg=0.05 bg=0.02
signaling adaptor activity GO:0035591 p=6.6E−02 n=3 fg=0.03 bg=0.01
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−log(p)
n=118/437 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001627907.3
fraction genes in fg and expected valu
lipid droplet GO:0005811 p=1.9E−03 n=6 fg=0.04 bg=0.01
presynaptic active zone membrane GO:0048787 p=3.6E−03 n=3 fg=0.02 bg=0.00
A band GO:0031672 p=1.3E−02 n=4 fg=0.03 bg=0.01
membrane microdomain GO:0098857 p=1.4E−02 n=9 fg=0.07 bg=0.03
membrane raft GO:0045121 p=1.4E−02 n=9 fg=0.07 bg=0.03
EARP complex GO:1990745 p=1.6E−02 n=2 fg=0.01 bg=0.00
GARP complex GO:0000938 p=1.6E−02 n=2 fg=0.01 bg=0.00
centriole GO:0005814 p=1.7E−02 n=5 fg=0.04 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=2.5E−02 n=3 fg=0.02 bg=0.00
potassium channel complex GO:0034705 p=2.5E−02 n=3 fg=0.02 bg=0.00
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type I terminal bouton GO:0061174 p=3.3E−02 n=3 fg=0.02 bg=0.01
M band GO:0031430 p=3.3E−02 n=3 fg=0.02 bg=0.01
sarcomere GO:0030017 p=4.2E−02 n=6 fg=0.04 bg=0.02
bicellular tight junction GO:0005923 p=4.3E−02 n=3 fg=0.02 bg=0.01
sperm fibrous sheath GO:0035686 p=4.8E−02 n=2 fg=0.01 bg=0.00
vesicle GO:0031982 p=6.3E−02 n=33 fg=0.24 bg=0.19
perikaryon GO:0043204 p=6.6E−02 n=4 fg=0.03 bg=0.01
actomyosin GO:0042641 p=6.7E−02 n=3 fg=0.02 bg=0.01
desmosome GO:0030057 p=7.5E−02 n=1 fg=0.01 bg=0.00
ciliary transition fiber GO:0097539 p=7.5E−02 n=1 fg=0.01 bg=0.00
dentate gyrus mossy fiber GO:0044302 p=7.5E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=7.5E−02 n=1 fg=0.01 bg=0.00
interphase microtubule organizing center GO:0031021 p=7.5E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=7.5E−02 n=1 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0016281 p=7.5E−02 n=1 fg=0.01 bg=0.00
AP−3 adaptor complex GO:0030123 p=7.5E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted vesicle GO:0060198 p=7.5E−02 n=1 fg=0.01 bg=0.00
phenylalanine−tRNA ligase complex GO:0009328 p=7.5E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=7.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=135/437 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction