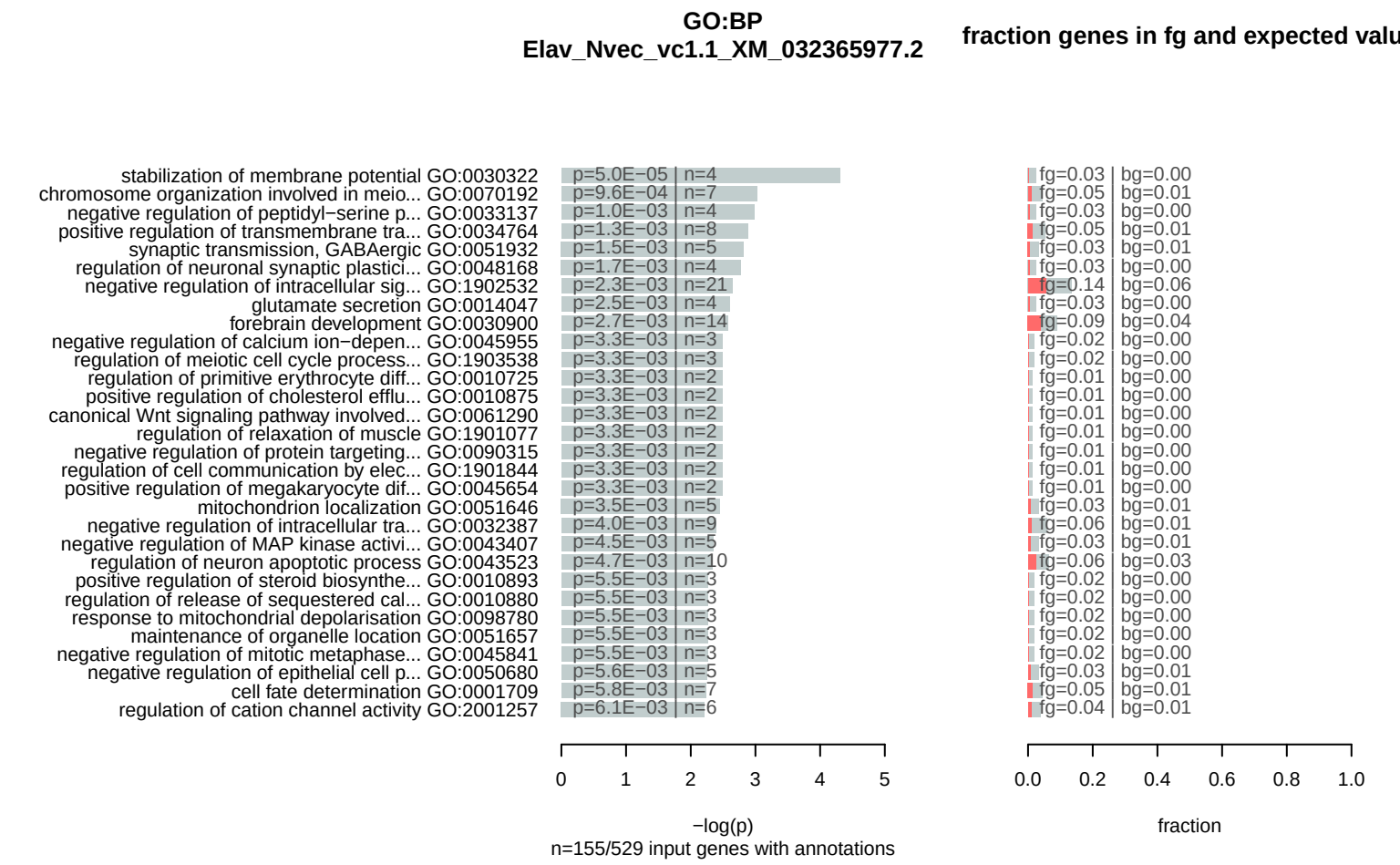
GO:BP
Elav_Nvec_vc1.1_XM_032365977.2
fraction genes in fg and expected valu
stabilization of membrane potential GO:0030322 p=5.0E−05 n=4 fg=0.03 bg=0.00
chromosome organization involved in meio... GO:0070192 p=9.6E−04 n=7 fg=0.05 bg=0.01
negative regulation of peptidyl−serine p... GO:0033137 p=1.0E−03 n=4 fg=0.03 bg=0.00
positive regulation of transmembrane tra... GO:0034764 p=1.3E−03 n=8 fg=0.05 bg=0.01
synaptic transmission, GABAergic GO:0051932 p=1.5E−03 n=5 fg=0.03 bg=0.01
regulation of neuronal synaptic plastici... GO:0048168 p=1.7E−03 n=4 fg=0.03 bg=0.00
negative regulation of intracellular sig... GO:1902532 p=2.3E−03 n=21 fg=0.14 bg=0.06
glutamate secretion GO:0014047 p=2.5E−03 n=4 fg=0.03 bg=0.00
forebrain development GO:0030900 p=2.7E−03 n=14 fg=0.09 bg=0.04
negative regulation of calcium ion−depen... GO:0045955 p=3.3E−03 n=3 fg=0.02 bg=0.00
regulation of meiotic cell cycle process... GO:1903538 p=3.3E−03 n=3 fg=0.02 bg=0.00
regulation of primitive erythrocyte diff... GO:0010725 p=3.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of cholesterol efflu... GO:0010875 p=3.3E−03 n=2 fg=0.01 bg=0.00
canonical Wnt signaling pathway involved... GO:0061290 p=3.3E−03 n=2 fg=0.01 bg=0.00
regulation of relaxation of muscle GO:1901077 p=3.3E−03 n=2 fg=0.01 bg=0.00
negative regulation of protein targeting... GO:0090315 p=3.3E−03 n=2 fg=0.01 bg=0.00
regulation of cell communication by elec... GO:1901844 p=3.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of megakaryocyte dif... GO:0045654 p=3.3E−03 n=2 fg=0.01 bg=0.00
mitochondrion localization GO:0051646 p=3.5E−03 n=5 fg=0.03 bg=0.01
negative regulation of intracellular tra... GO:0032387 p=4.0E−03 n=9 fg=0.06 bg=0.01
negative regulation of MAP kinase activi... GO:0043407 p=4.5E−03 n=5 fg=0.03 bg=0.01
regulation of neuron apoptotic process GO:0043523 p=4.7E−03 n=10 fg=0.06 bg=0.03
positive regulation of steroid biosynthe... GO:0010893 p=5.5E−03 n=3 fg=0.02 bg=0.00
regulation of release of sequestered cal... GO:0010880 p=5.5E−03 n=3 fg=0.02 bg=0.00
response to mitochondrial depolarisation GO:0098780 p=5.5E−03 n=3 fg=0.02 bg=0.00
maintenance of organelle location GO:0051657 p=5.5E−03 n=3 fg=0.02 bg=0.00
negative regulation of mitotic metaphase... GO:0045841 p=5.5E−03 n=3 fg=0.02 bg=0.00
negative regulation of epithelial cell p... GO:0050680 p=5.6E−03 n=5 fg=0.03 bg=0.01
cell fate determination GO:0001709 p=5.8E−03 n=7 fg=0.05 bg=0.01
regulation of cation channel activity GO:2001257 p=6.1E−03 n=6 fg=0.04 bg=0.01
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n=155/529 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032365977.2
fraction genes in fg and expected valu
cysteine−type endopeptidase activity GO:0004197 p=7.9E−04 n=5 fg=0.04 bg=0.01
potassium ion leak channel activity GO:0022841 p=1.7E−03 n=3 fg=0.02 bg=0.00
armadillo repeat domain binding GO:0070016 p=3.3E−03 n=2 fg=0.01 bg=0.00
caspase binding GO:0089720 p=9.6E−03 n=2 fg=0.01 bg=0.00
S100 protein binding GO:0044548 p=9.6E−03 n=2 fg=0.01 bg=0.00
translation initiation factor activity GO:0003743 p=1.1E−02 n=4 fg=0.03 bg=0.01
ion channel regulator activity GO:0099106 p=1.2E−02 n=6 fg=0.04 bg=0.01
protein domain specific binding GO:0019904 p=1.2E−02 n=21 fg=0.15 bg=0.08
tubulin binding GO:0015631 p=1.5E−02 n=10 fg=0.07 bg=0.03
channel regulator activity GO:0016247 p=1.5E−02 n=6 fg=0.04 bg=0.02
ATPase−coupled transmembrane transporter... GO:0042626 p=1.7E−02 n=5 fg=0.04 bg=0.01
transmembrane transporter binding GO:0044325 p=1.7E−02 n=4 fg=0.03 bg=0.01
microtubule binding GO:0008017 p=1.8E−02 n=8 fg=0.06 bg=0.02
calcium−dependent cysteine−type endopept... GO:0004198 p=1.8E−02 n=2 fg=0.01 bg=0.00
cAMP binding GO:0030552 p=1.8E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol phosphate 4−phospha... GO:0034596 p=1.8E−02 n=2 fg=0.01 bg=0.00
translation factor activity, RNA binding GO:0008135 p=2.0E−02 n=5 fg=0.04 bg=0.01
phosphatidylinositol phosphate phosphata... GO:0052866 p=2.2E−02 n=3 fg=0.02 bg=0.00
solute:sodium symporter activity GO:0015370 p=2.2E−02 n=3 fg=0.02 bg=0.00
chromatin binding GO:0003682 p=2.4E−02 n=13 fg=0.09 bg=0.05
translation regulator activity, nucleic ... GO:0090079 p=2.7E−02 n=5 fg=0.04 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=2.7E−02 n=9 fg=0.07 bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.7E−02 n=9 fg=0.07 bg=0.03
phospholipid binding GO:0005543 p=2.8E−02 n=10 fg=0.07 bg=0.04
demethylase activity GO:0032451 p=2.8E−02 n=3 fg=0.02 bg=0.01
nucleobase−containing compound transmemb... GO:0015932 p=2.8E−02 n=3 fg=0.02 bg=0.01
cyclic nucleotide binding GO:0030551 p=3.0E−02 n=2 fg=0.01 bg=0.00
AP−2 adaptor complex binding GO:0035612 p=3.0E−02 n=2 fg=0.01 bg=0.00
histone H3−methyl−lysine−4 demethylase a... GO:0032453 p=3.0E−02 n=2 fg=0.01 bg=0.00
phosphatidylinositol−4,5−bisphosphate ph... GO:0106019 p=3.0E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=137/529 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032365977.2
fraction genes in fg and expected valu
dendrite GO:0030425 p=4.8E−04 n=24 fg=0.16 bg=0.06
integral component of plasma membrane GO:0005887 p=3.1E−03 n=19 fg=0.12 bg=0.06
presynaptic active zone membrane GO:0048787 p=5.2E−03 n=3 fg=0.02 bg=0.00
dendritic shaft GO:0043198 p=6.4E−03 n=5 fg=0.03 bg=0.01
dendritic spine GO:0043197 p=7.6E−03 n=8 fg=0.05 bg=0.02
axon GO:0030424 p=1.0E−02 n=18 fg=0.12 bg=0.07
chromosome, centromeric region GO:0000775 p=1.5E−02 n=7 fg=0.05 bg=0.02
sarcoplasmic reticulum GO:0016529 p=1.6E−02 n=3 fg=0.02 bg=0.00
intrinsic component of peroxisomal membr... GO:0031231 p=1.8E−02 n=2 fg=0.01 bg=0.00
integral component of peroxisomal membra... GO:0005779 p=1.8E−02 n=2 fg=0.01 bg=0.00
sarcoplasm GO:0016528 p=2.1E−02 n=3 fg=0.02 bg=0.00
spindle microtubule GO:0005876 p=2.3E−02 n=4 fg=0.03 bg=0.01
condensed chromosome GO:0000793 p=2.3E−02 n=8 fg=0.05 bg=0.02
exocytic vesicle GO:0070382 p=2.3E−02 n=8 fg=0.05 bg=0.02
distal axon GO:0150034 p=2.4E−02 n=11 fg=0.07 bg=0.04
eukaryotic translation initiation factor... GO:0005851 p=2.8E−02 n=2 fg=0.01 bg=0.00
kinetochore microtubule GO:0005828 p=2.8E−02 n=2 fg=0.01 bg=0.00
phagocytic cup GO:0001891 p=2.8E−02 n=2 fg=0.01 bg=0.00
zymogen granule GO:0042588 p=2.8E−02 n=2 fg=0.01 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=2.8E−02 n=2 fg=0.01 bg=0.00
chromosomal region GO:0098687 p=3.4E−02 n=9 fg=0.06 bg=0.03
neuronal cell body GO:0043025 p=3.4E−02 n=15 fg=0.10 bg=0.06
sarcoplasmic reticulum membrane GO:0033017 p=4.1E−02 n=2 fg=0.01 bg=0.00
astrocyte projection GO:0097449 p=4.1E−02 n=2 fg=0.01 bg=0.00
aster GO:0005818 p=4.1E−02 n=2 fg=0.01 bg=0.00
glial cell projection GO:0097386 p=4.1E−02 n=2 fg=0.01 bg=0.00
exocytic vesicle membrane GO:0099501 p=4.3E−02 n=4 fg=0.03 bg=0.01
extracellular vesicle GO:1903561 p=4.3E−02 n=4 fg=0.03 bg=0.01
extracellular membrane−bounded organelle GO:0065010 p=4.3E−02 n=4 fg=0.03 bg=0.01
extracellular organelle GO:0043230 p=4.3E−02 n=4 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=152/529 input genes with annotations
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fraction