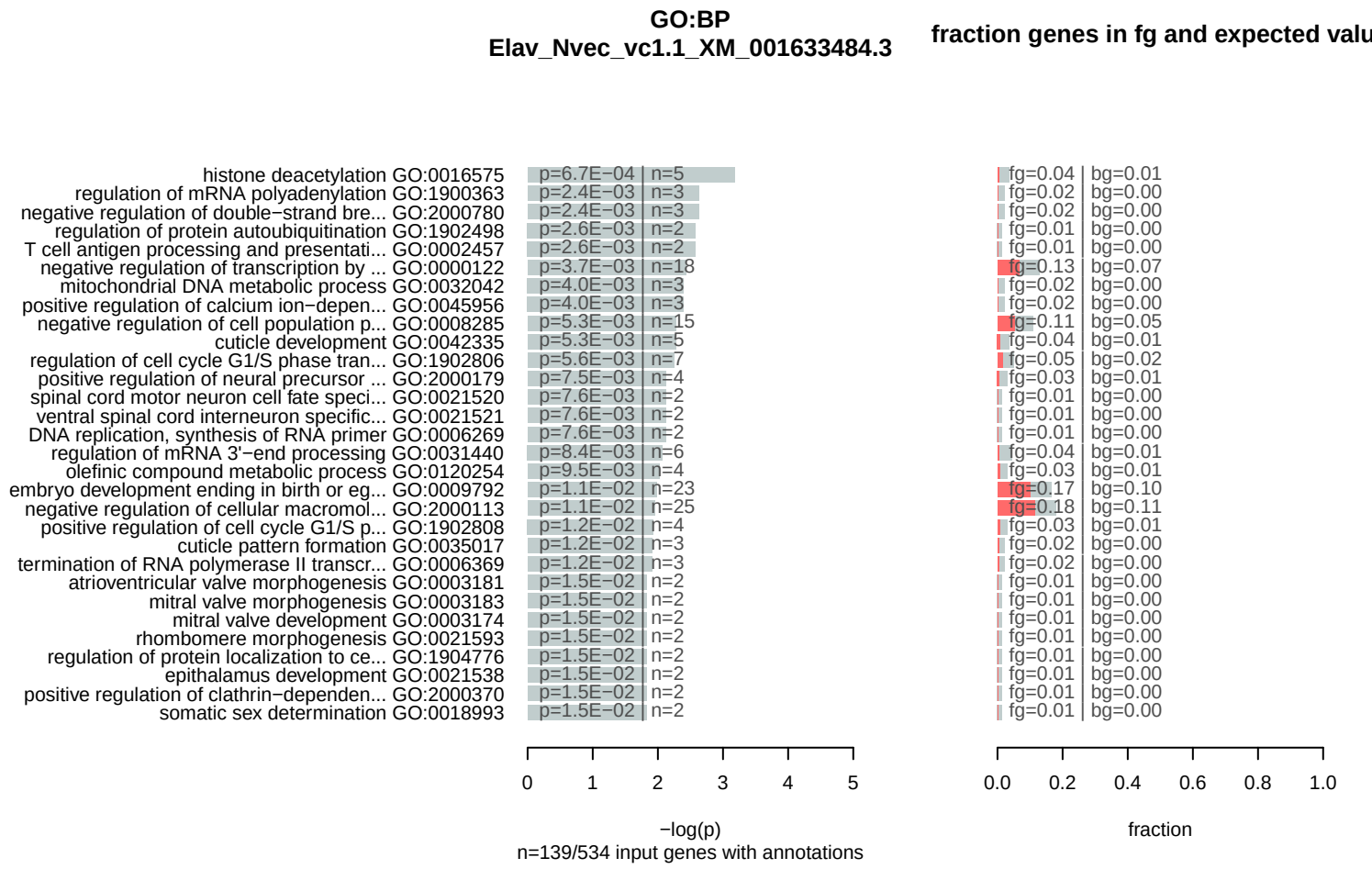
GO:BP
Elav_Nvec_vc1.1_XM_001633484.3
fraction genes in fg and expected valu
histone deacetylation GO:0016575 p=6.7E−04 n=5 fg=0.04 bg=0.01
regulation of mRNA polyadenylation GO:1900363 p=2.4E−03 n=3 fg=0.02 bg=0.00
negative regulation of double−strand bre... GO:2000780 p=2.4E−03 n=3 fg=0.02 bg=0.00
regulation of protein autoubiquitination GO:1902498 p=2.6E−03 n=2 fg=0.01 bg=0.00
T cell antigen processing and presentati... GO:0002457 p=2.6E−03 n=2 fg=0.01 bg=0.00
negative regulation of transcription by ... GO:0000122 p=3.7E−03 n=18 fg=0.13 bg=0.07
mitochondrial DNA metabolic process GO:0032042 p=4.0E−03 n=3 fg=0.02 bg=0.00
positive regulation of calcium ion−depen... GO:0045956 p=4.0E−03 n=3 fg=0.02 bg=0.00
negative regulation of cell population p... GO:0008285 p=5.3E−03 n=15 fg=0.11 bg=0.05
cuticle development GO:0042335 p=5.3E−03 n=5 fg=0.04 bg=0.01
regulation of cell cycle G1/S phase tran... GO:1902806 p=5.6E−03 n=7 fg=0.05 bg=0.02
positive regulation of neural precursor ... GO:2000179 p=7.5E−03 n=4 fg=0.03 bg=0.01
spinal cord motor neuron cell fate speci... GO:0021520 p=7.6E−03 n=2 fg=0.01 bg=0.00
ventral spinal cord interneuron specific... GO:0021521 p=7.6E−03 n=2 fg=0.01 bg=0.00
DNA replication, synthesis of RNA primer GO:0006269 p=7.6E−03 n=2 fg=0.01 bg=0.00
regulation of mRNA 3'−end processing GO:0031440 p=8.4E−03 n=6 fg=0.04 bg=0.01
olefinic compound metabolic process GO:0120254 p=9.5E−03 n=4 fg=0.03 bg=0.01
embryo development ending in birth or eg... GO:0009792 p=1.1E−02 n=23 fg=0.17 bg=0.10
negative regulation of cellular macromol... GO:2000113 p=1.1E−02 n=25 fg=0.18 bg=0.11
positive regulation of cell cycle G1/S p... GO:1902808 p=1.2E−02 n=4 fg=0.03 bg=0.01
cuticle pattern formation GO:0035017 p=1.2E−02 n=3 fg=0.02 bg=0.00
termination of RNA polymerase II transcr... GO:0006369 p=1.2E−02 n=3 fg=0.02 bg=0.00
atrioventricular valve morphogenesis GO:0003181 p=1.5E−02 n=2 fg=0.01 bg=0.00
mitral valve morphogenesis GO:0003183 p=1.5E−02 n=2 fg=0.01 bg=0.00
mitral valve development GO:0003174 p=1.5E−02 n=2 fg=0.01 bg=0.00
rhombomere morphogenesis GO:0021593 p=1.5E−02 n=2 fg=0.01 bg=0.00
regulation of protein localization to ce... GO:1904776 p=1.5E−02 n=2 fg=0.01 bg=0.00
epithalamus development GO:0021538 p=1.5E−02 n=2 fg=0.01 bg=0.00
positive regulation of clathrin−dependen... GO:2000370 p=1.5E−02 n=2 fg=0.01 bg=0.00
somatic sex determination GO:0018993 p=1.5E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=139/534 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001633484.3
fraction genes in fg and expected valu
DNA−binding transcription factor activit... GO:0000981 p=4.0E−04 n=18 fg=0.14 bg=0.06
core promoter sequence−specific DNA bind... GO:0001046 p=1.3E−03 n=7 fg=0.05 bg=0.01
glutathione binding GO:0043295 p=2.9E−03 n=3 fg=0.02 bg=0.00
prostaglandin−E synthase activity GO:0050220 p=3.0E−03 n=2 fg=0.02 bg=0.00
prostaglandin−D synthase activity GO:0004667 p=3.0E−03 n=2 fg=0.02 bg=0.00
microtubule binding GO:0008017 p=4.1E−03 n=9 fg=0.07 bg=0.02
manganese ion binding GO:0030145 p=4.6E−03 n=5 fg=0.04 bg=0.01
phospholipase binding GO:0043274 p=4.8E−03 n=3 fg=0.02 bg=0.00
polynucleotide adenylyltransferase activ... GO:0004652 p=4.8E−03 n=3 fg=0.02 bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978 p=6.8E−03 n=10 fg=0.08 bg=0.03
magnesium ion binding GO:0000287 p=7.2E−03 n=8 fg=0.06 bg=0.02
RNA polymerase II core promoter sequence... GO:0000979 p=7.4E−03 n=3 fg=0.02 bg=0.00
RNA polymerase II intronic transcription... GO:0001162 p=8.6E−03 n=2 fg=0.02 bg=0.00
transcription corepressor activity GO:0003714 p=1.4E−02 n=6 fg=0.05 bg=0.02
DNA−binding transcription repressor acti... GO:0001227 p=1.4E−02 n=5 fg=0.04 bg=0.01
DNA−binding transcription repressor acti... GO:0001217 p=1.4E−02 n=5 fg=0.04 bg=0.01
histone deacetylase activity GO:0004407 p=1.5E−02 n=3 fg=0.02 bg=0.00
oxidoreductase activity, acting on singl... GO:0016701 p=1.7E−02 n=2 fg=0.02 bg=0.00
[pyruvate dehydrogenase (lipoamide)] pho... GO:0004741 p=1.7E−02 n=2 fg=0.02 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=1.8E−02 n=9 fg=0.07 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=1.8E−02 n=9 fg=0.07 bg=0.03
protein lysine deacetylase activity GO:0033558 p=1.9E−02 n=3 fg=0.02 bg=0.00
histone binding GO:0042393 p=2.0E−02 n=6 fg=0.05 bg=0.02
deacetylase activity GO:0019213 p=2.5E−02 n=3 fg=0.02 bg=0.01
phosphatidylinositol−5−phosphate binding GO:0010314 p=2.7E−02 n=2 fg=0.02 bg=0.00
histone acetyltransferase binding GO:0035035 p=3.1E−02 n=3 fg=0.02 bg=0.01
histone deacetylase binding GO:0042826 p=5.1E−02 n=4 fg=0.03 bg=0.01
oxidoreductase activity, acting on perox... GO:0016684 p=5.2E−02 n=2 fg=0.02 bg=0.00
leucine binding GO:0070728 p=5.5E−02 n=1 fg=0.01 bg=0.00
double−stranded methylated DNA binding GO:0010385 p=5.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=130/534 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001633484.3
fraction genes in fg and expected valu
cytoplasmic microtubule GO:0005881 p=3.6E−03 n=4 fg=0.03 bg=0.00
histone deacetylase complex GO:0000118 p=3.6E−03 n=4 fg=0.03 bg=0.00
caveola GO:0005901 p=5.8E−03 n=5 fg=0.04 bg=0.01
transcription repressor complex GO:0017053 p=1.3E−02 n=4 fg=0.03 bg=0.01
NuRD complex GO:0016581 p=1.5E−02 n=2 fg=0.01 bg=0.00
spot adherens junction GO:0005914 p=1.5E−02 n=2 fg=0.01 bg=0.00
CHD−type complex GO:0090545 p=1.5E−02 n=2 fg=0.01 bg=0.00
mitotic spindle pole GO:0097431 p=1.7E−02 n=3 fg=0.02 bg=0.00
zymogen granule GO:0042588 p=2.5E−02 n=2 fg=0.01 bg=0.00
adherens junction GO:0005912 p=3.0E−02 n=7 fg=0.05 bg=0.02
brush border GO:0005903 p=3.4E−02 n=5 fg=0.04 bg=0.01
microtubule associated complex GO:0005875 p=3.4E−02 n=6 fg=0.04 bg=0.02
Golgi medial cisterna GO:0005797 p=4.1E−02 n=3 fg=0.02 bg=0.01
nuclear body GO:0016604 p=4.6E−02 n=14 fg=0.10 bg=0.06
SCF ubiquitin ligase complex GO:0019005 p=4.8E−02 n=3 fg=0.02 bg=0.01
host cell nucleus GO:0042025 p=5.3E−02 n=1 fg=0.01 bg=0.00
cytoplasmic periphery of the nuclear por... GO:1990723 p=5.3E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=5.3E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=5.3E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=5.3E−02 n=1 fg=0.01 bg=0.00
trans−synaptic protein complex GO:0098820 p=5.3E−02 n=1 fg=0.01 bg=0.00
nuclear pore cytoplasmic filaments GO:0044614 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=5.3E−02 n=1 fg=0.01 bg=0.00
protein farnesyltransferase complex GO:0005965 p=5.3E−02 n=1 fg=0.01 bg=0.00
macropinocytic cup GO:0070685 p=5.3E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=5.3E−02 n=1 fg=0.01 bg=0.00
host intracellular part GO:0033646 p=5.3E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=5.3E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=142/534 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction