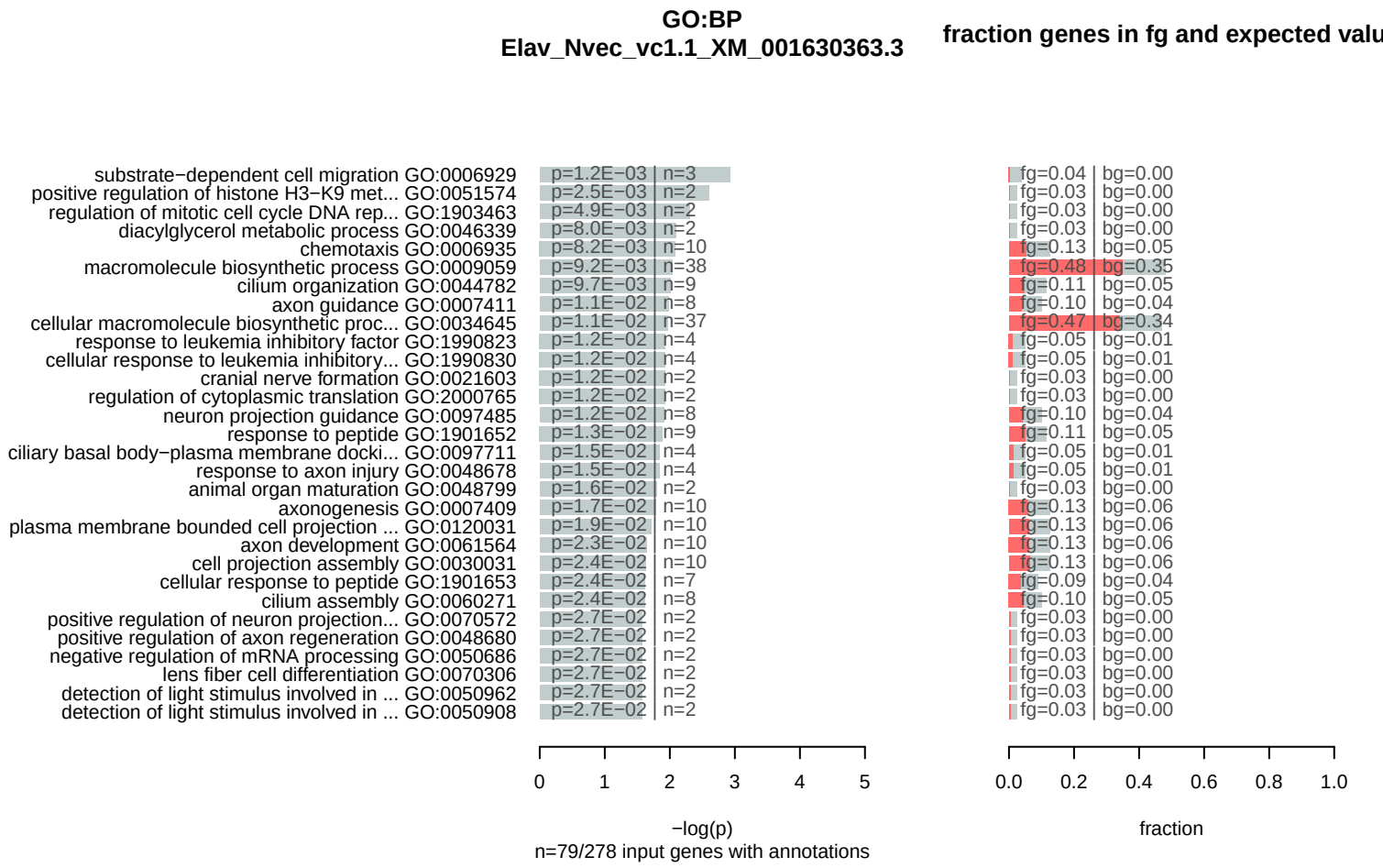
GO:BP
Elav_Nvec_vc1.1_XM_001630363.3
fraction genes in fg and expected valu
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positive regulation of histone H3−K9 met... GO:0051574 p=2.5E−03 n=2 fg=0.03 bg=0.00
regulation of mitotic cell cycle DNA rep... GO:1903463 p=4.9E−03 n=2 fg=0.03 bg=0.00
diacylglycerol metabolic process GO:0046339 p=8.0E−03 n=2 fg=0.03 bg=0.00
chemotaxis GO:0006935 p=8.2E−03 n=10 fg=0.13 bg=0.05
macromolecule biosynthetic process GO:0009059 p=9.2E−03 n=38 fg=0.48 bg=0.35
cilium organization GO:0044782 p=9.7E−03 n=9 fg=0.11 bg=0.05
axon guidance GO:0007411 p=1.1E−02 n=8 fg=0.10 bg=0.04
cellular macromolecule biosynthetic proc... GO:0034645 p=1.1E−02 n=37 fg=0.47 bg=0.34
response to leukemia inhibitory factor GO:1990823 p=1.2E−02 n=4 fg=0.05 bg=0.01
cellular response to leukemia inhibitory... GO:1990830 p=1.2E−02 n=4 fg=0.05 bg=0.01
cranial nerve formation GO:0021603 p=1.2E−02 n=2 fg=0.03 bg=0.00
regulation of cytoplasmic translation GO:2000765 p=1.2E−02 n=2 fg=0.03 bg=0.00
neuron projection guidance GO:0097485 p=1.2E−02 n=8 fg=0.10 bg=0.04
response to peptide GO:1901652 p=1.3E−02 n=9 fg=0.11 bg=0.05
ciliary basal body−plasma membrane docki... GO:0097711 p=1.5E−02 n=4 fg=0.05 bg=0.01
response to axon injury GO:0048678 p=1.5E−02 n=4 fg=0.05 bg=0.01
animal organ maturation GO:0048799 p=1.6E−02 n=2 fg=0.03 bg=0.00
axonogenesis GO:0007409 p=1.7E−02 n=10 fg=0.13 bg=0.06
plasma membrane bounded cell projection ... GO:0120031 p=1.9E−02 n=10 fg=0.13 bg=0.06
axon development GO:0061564 p=2.3E−02 n=10 fg=0.13 bg=0.06
cell projection assembly GO:0030031 p=2.4E−02 n=10 fg=0.13 bg=0.06
cellular response to peptide GO:1901653 p=2.4E−02 n=7 fg=0.09 bg=0.04
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positive regulation of neuron projection... GO:0070572 p=2.7E−02 n=2 fg=0.03 bg=0.00
positive regulation of axon regeneration GO:0048680 p=2.7E−02 n=2 fg=0.03 bg=0.00
negative regulation of mRNA processing GO:0050686 p=2.7E−02 n=2 fg=0.03 bg=0.00
lens fiber cell differentiation GO:0070306 p=2.7E−02 n=2 fg=0.03 bg=0.00
detection of light stimulus involved in ... GO:0050962 p=2.7E−02 n=2 fg=0.03 bg=0.00
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−log(p)
n=79/278 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001630363.3
fraction genes in fg and expected valu
mRNA regulatory element binding translat... GO:0000900 p=2.5E−03 n=2 fg=0.03 bg=0.00
tau−protein kinase activity GO:0050321 p=5.0E−03 n=2 fg=0.03 bg=0.00
insulin receptor binding GO:0005158 p=1.6E−02 n=2 fg=0.03 bg=0.00
protein tyrosine kinase activity GO:0004713 p=2.2E−02 n=3 fg=0.04 bg=0.01
poly(U) RNA binding GO:0008266 p=2.7E−02 n=2 fg=0.03 bg=0.00
guanyl−nucleotide exchange factor activi... GO:0005085 p=2.9E−02 n=4 fg=0.06 bg=0.02
D−glucose transmembrane transporter acti... GO:0055056 p=2.9E−02 n=1 fg=0.01 bg=0.00
alanine−oxo−acid transaminase activity GO:0047635 p=2.9E−02 n=1 fg=0.01 bg=0.00
carbohydrate:proton symporter activity GO:0005351 p=2.9E−02 n=1 fg=0.01 bg=0.00
glucose transmembrane transporter activi... GO:0005355 p=2.9E−02 n=1 fg=0.01 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=2.9E−02 n=1 fg=0.01 bg=0.00
nickel cation binding GO:0016151 p=2.9E−02 n=1 fg=0.01 bg=0.00
angiostatin binding GO:0043532 p=2.9E−02 n=1 fg=0.01 bg=0.00
carbohydrate:cation symporter activity GO:0005402 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphopantetheine−dependent carrier act... GO:0140414 p=2.9E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase activit... GO:0046933 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphomannomutase activity GO:0004615 p=2.9E−02 n=1 fg=0.01 bg=0.00
prosthetic group binding GO:0051192 p=2.9E−02 n=1 fg=0.01 bg=0.00
carbohydrate transmembrane transporter a... GO:0015144 p=2.9E−02 n=1 fg=0.01 bg=0.00
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hexose transmembrane transporter activit... GO:0015149 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphopantetheine binding GO:0031177 p=2.9E−02 n=1 fg=0.01 bg=0.00
phenanthrene−epoxide hydrolase activity GO:0019118 p=2.9E−02 n=1 fg=0.01 bg=0.00
phenanthrene−9,10−epoxide hydrolase acti... GO:0019119 p=2.9E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.9E−02 n=1 fg=0.01 bg=0.00
MHC class I protein binding GO:0042288 p=2.9E−02 n=1 fg=0.01 bg=0.00
ACP phosphopantetheine attachment site b... GO:0044620 p=2.9E−02 n=1 fg=0.01 bg=0.00
L−alanine:2−oxoglutarate aminotransferas... GO:0004021 p=2.9E−02 n=1 fg=0.01 bg=0.00
sugar transmembrane transporter activity GO:0051119 p=2.9E−02 n=1 fg=0.01 bg=0.00
acyl binding GO:0000035 p=2.9E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=70/278 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_001630363.3
fraction genes in fg and expected valu
presynaptic active zone GO:0048786 p=3.9E−03 n=4 fg=0.05 bg=0.01
intracellular membrane−bounded organelle GO:0043231 p=6.2E−03 n=70 fg=0.89 bg=0.77
transcription factor TFTC complex GO:0033276 p=1.2E−02 n=2 fg=0.03 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=1.2E−02 n=2 fg=0.03 bg=0.00
excitatory synapse GO:0060076 p=1.6E−02 n=2 fg=0.03 bg=0.00
membrane−bounded organelle GO:0043227 p=1.8E−02 n=74 fg=0.94 bg=0.80
nuclear body GO:0016604 p=1.9E−02 n=10 fg=0.13 bg=0.06
vesicle coat GO:0030120 p=2.1E−02 n=2 fg=0.03 bg=0.00
SAGA−type complex GO:0070461 p=2.1E−02 n=2 fg=0.03 bg=0.00
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COPI−coated vesicle GO:0030137 p=2.7E−02 n=2 fg=0.03 bg=0.00
ACF complex GO:0016590 p=2.9E−02 n=1 fg=0.01 bg=0.00
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mitochondrial proton−transporting ATP sy... GO:0005754 p=2.9E−02 n=1 fg=0.01 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=2.9E−02 n=1 fg=0.01 bg=0.00
polytene chromosome band GO:0005704 p=2.9E−02 n=1 fg=0.01 bg=0.00
Ric1−Rgp1 guanyl−nucleotide exchange fac... GO:0034066 p=2.9E−02 n=1 fg=0.01 bg=0.00
proton−transporting ATP synthase, cataly... GO:0045267 p=2.9E−02 n=1 fg=0.01 bg=0.00
polysomal ribosome GO:0042788 p=3.3E−02 n=2 fg=0.03 bg=0.00
RNA polymerase II transcription regulato... GO:0090575 p=3.3E−02 n=4 fg=0.05 bg=0.02
mitochondrial protein−containing complex GO:0098798 p=3.5E−02 n=5 fg=0.06 bg=0.02
organellar large ribosomal subunit GO:0000315 p=3.9E−02 n=2 fg=0.03 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=3.9E−02 n=2 fg=0.03 bg=0.00
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mitochondrial inner membrane GO:0005743 p=4.0E−02 n=7 fg=0.09 bg=0.04
sarcolemma GO:0042383 p=4.3E−02 n=3 fg=0.04 bg=0.01
nucleus GO:0005634 p=5.1E−02 n=47 fg=0.59 bg=0.50
ribosome GO:0005840 p=5.2E−02 n=5 fg=0.06 bg=0.03
T−tubule GO:0030315 p=5.3E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=79/278 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction