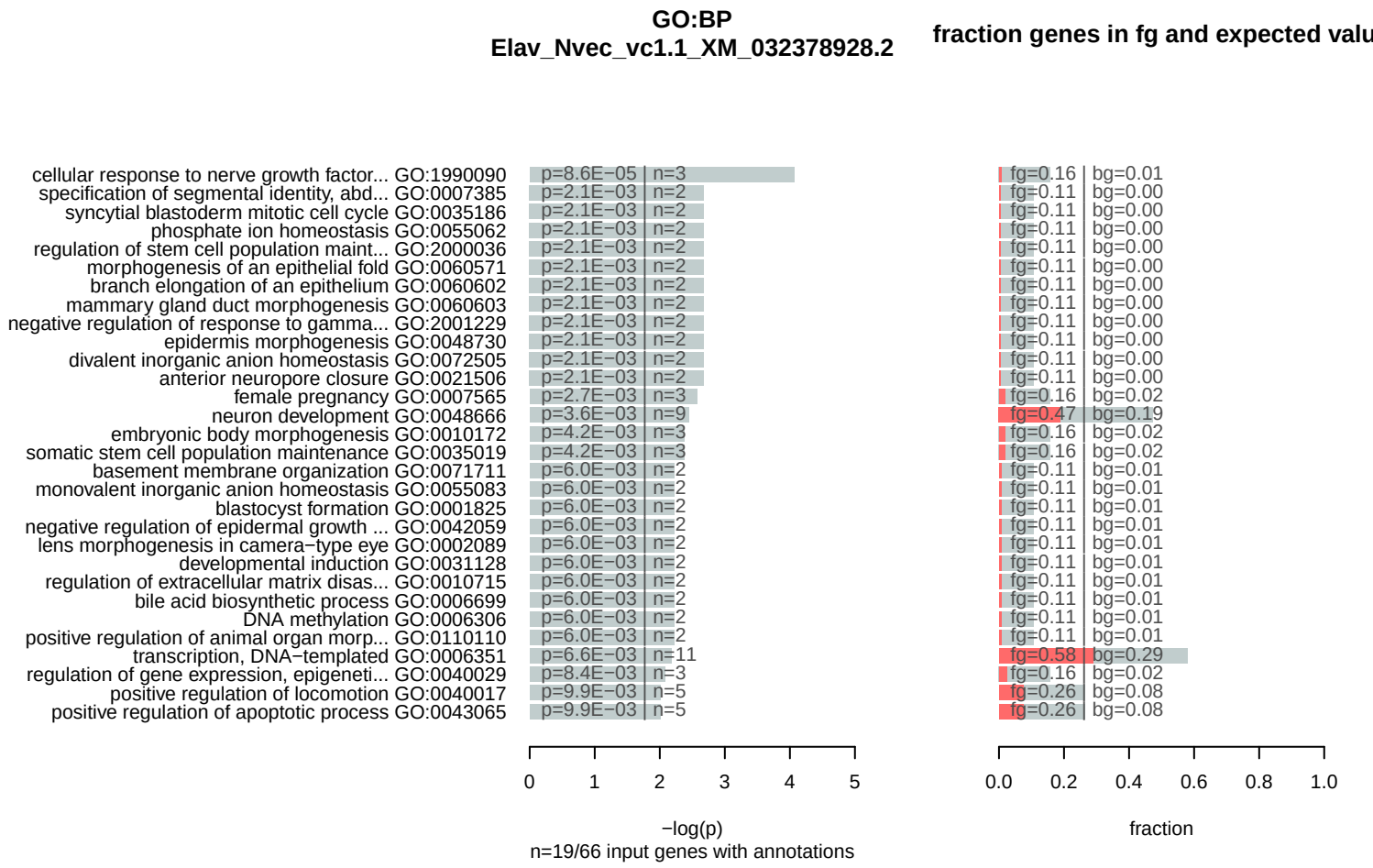
GO:BP
Elav_Nvec_vc1.1_XM_032378928.2
fraction genes in fg and expected valu
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specification of segmental identity, abd... GO:0007385 p=2.1E−03 n=2 fg=0.11 bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186 p=2.1E−03 n=2 fg=0.11 bg=0.00
phosphate ion homeostasis GO:0055062 p=2.1E−03 n=2 fg=0.11 bg=0.00
regulation of stem cell population maint... GO:2000036 p=2.1E−03 n=2 fg=0.11 bg=0.00
morphogenesis of an epithelial fold GO:0060571 p=2.1E−03 n=2 fg=0.11 bg=0.00
branch elongation of an epithelium GO:0060602 p=2.1E−03 n=2 fg=0.11 bg=0.00
mammary gland duct morphogenesis GO:0060603 p=2.1E−03 n=2 fg=0.11 bg=0.00
negative regulation of response to gamma... GO:2001229 p=2.1E−03 n=2 fg=0.11 bg=0.00
epidermis morphogenesis GO:0048730 p=2.1E−03 n=2 fg=0.11 bg=0.00
divalent inorganic anion homeostasis GO:0072505 p=2.1E−03 n=2 fg=0.11 bg=0.00
anterior neuropore closure GO:0021506 p=2.1E−03 n=2 fg=0.11 bg=0.00
female pregnancy GO:0007565 p=2.7E−03 n=3 fg=0.16 bg=0.02
neuron development GO:0048666 p=3.6E−03 n=9 fg=0.47 bg=0.19
embryonic body morphogenesis GO:0010172 p=4.2E−03 n=3 fg=0.16 bg=0.02
somatic stem cell population maintenance GO:0035019 p=4.2E−03 n=3 fg=0.16 bg=0.02
basement membrane organization GO:0071711 p=6.0E−03 n=2 fg=0.11 bg=0.01
monovalent inorganic anion homeostasis GO:0055083 p=6.0E−03 n=2 fg=0.11 bg=0.01
blastocyst formation GO:0001825 p=6.0E−03 n=2 fg=0.11 bg=0.01
negative regulation of epidermal growth ... GO:0042059 p=6.0E−03 n=2 fg=0.11 bg=0.01
lens morphogenesis in camera−type eye GO:0002089 p=6.0E−03 n=2 fg=0.11 bg=0.01
developmental induction GO:0031128 p=6.0E−03 n=2 fg=0.11 bg=0.01
regulation of extracellular matrix disas... GO:0010715 p=6.0E−03 n=2 fg=0.11 bg=0.01
bile acid biosynthetic process GO:0006699 p=6.0E−03 n=2 fg=0.11 bg=0.01
DNA methylation GO:0006306 p=6.0E−03 n=2 fg=0.11 bg=0.01
positive regulation of animal organ morp... GO:0110110 p=6.0E−03 n=2 fg=0.11 bg=0.01
transcription, DNA−templated GO:0006351 p=6.6E−03 n=11 fg=0.58 bg=0.29
regulation of gene expression, epigeneti... GO:0040029 p=8.4E−03 n=3 fg=0.16 bg=0.02
positive regulation of locomotion GO:0040017 p=9.9E−03 n=5 fg=0.26 bg=0.08
positive regulation of apoptotic process GO:0043065 p=9.9E−03 n=5 fg=0.26 bg=0.08
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n=19/66 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032378928.2
fraction genes in fg and expected valu
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single−stranded RNA binding GO:0003727 p=6.7E−03 n=2 fg=0.11 bg=0.01
protein tyrosine kinase binding GO:1990782 p=3.1E−02 n=2 fg=0.11 bg=0.02
protein C−terminus binding GO:0008022 p=3.1E−02 n=2 fg=0.11 bg=0.02
chromatin binding GO:0003682 p=3.2E−02 n=4 fg=0.22 bg=0.07
enzyme regulator activity GO:0030234 p=3.3E−02 n=5 fg=0.28 bg=0.11
guanyl−nucleotide exchange factor activi... GO:0005085 p=4.2E−02 n=2 fg=0.11 bg=0.02
phosphatidylinositol bisphosphate kinase... GO:0052813 p=5.0E−02 n=1 fg=0.06 bg=0.00
beta−1 adrenergic receptor binding GO:0031697 p=5.0E−02 n=1 fg=0.06 bg=0.00
dystroglycan binding GO:0002162 p=5.0E−02 n=1 fg=0.06 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=5.0E−02 n=1 fg=0.06 bg=0.00
P−type sodium transporter activity GO:0008554 p=5.0E−02 n=1 fg=0.06 bg=0.00
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mRNA 3'−UTR AU−rich region binding GO:0035925 p=5.0E−02 n=1 fg=0.06 bg=0.00
bile acid transmembrane transporter acti... GO:0015125 p=5.0E−02 n=1 fg=0.06 bg=0.00
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poly(U) RNA binding GO:0008266 p=5.0E−02 n=1 fg=0.06 bg=0.00
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chromatin DNA binding GO:0031490 p=5.0E−02 n=1 fg=0.06 bg=0.00
rRNA primary transcript binding GO:0042134 p=5.0E−02 n=1 fg=0.06 bg=0.00
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GDP−dissociation inhibitor activity GO:0005092 p=5.0E−02 n=1 fg=0.06 bg=0.00
ATPase−coupled monocarboxylic acid trans... GO:0033285 p=5.0E−02 n=1 fg=0.06 bg=0.00
ubiquitin−protein transferase activator ... GO:0097027 p=5.0E−02 n=1 fg=0.06 bg=0.00
ubiquitin−protein transferase regulator ... GO:0055106 p=5.0E−02 n=1 fg=0.06 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=5.0E−02 n=1 fg=0.06 bg=0.00
acylglycerol lipase activity GO:0047372 p=5.0E−02 n=1 fg=0.06 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=5.0E−02 n=1 fg=0.06 bg=0.00
phosphatidylinositol kinase activity GO:0052742 p=5.0E−02 n=1 fg=0.06 bg=0.00
0 1 2 3 4 5
−log(p)
n=18/66 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378928.2
fraction genes in fg and expected valu
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cell cortex GO:0005938 p=5.8E−03 n=4 fg=0.21 bg=0.04
PRC1 complex GO:0035102 p=6.2E−03 n=2 fg=0.11 bg=0.01
cytoplasmic region GO:0099568 p=7.2E−03 n=4 fg=0.21 bg=0.04
nuclear lumen GO:0031981 p=1.2E−02 n=10 fg=0.53 bg=0.27
Golgi apparatus GO:0005794 p=1.4E−02 n=7 fg=0.37 bg=0.15
nucleoplasm GO:0005654 p=1.6E−02 n=9 fg=0.47 bg=0.23
growth cone GO:0030426 p=1.9E−02 n=3 fg=0.16 bg=0.03
site of polarized growth GO:0030427 p=2.4E−02 n=3 fg=0.16 bg=0.03
distal axon GO:0150034 p=2.7E−02 n=4 fg=0.21 bg=0.06
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Golgi apparatus subcompartment GO:0098791 p=4.4E−02 n=4 fg=0.21 bg=0.07
microtubule plus−end GO:0035371 p=4.7E−02 n=1 fg=0.05 bg=0.00
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RNA polymerase III transcription regulat... GO:0090576 p=4.7E−02 n=1 fg=0.05 bg=0.00
gut granule GO:0044840 p=4.7E−02 n=1 fg=0.05 bg=0.00
gut granule membrane GO:0044841 p=4.7E−02 n=1 fg=0.05 bg=0.00
hippocampal mossy fiber to CA3 synapse GO:0098686 p=4.7E−02 n=1 fg=0.05 bg=0.00
type I terminal bouton GO:0061174 p=4.7E−02 n=1 fg=0.05 bg=0.00
excitatory synapse GO:0060076 p=4.7E−02 n=1 fg=0.05 bg=0.00
PML body GO:0016605 p=4.7E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=19/66 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction