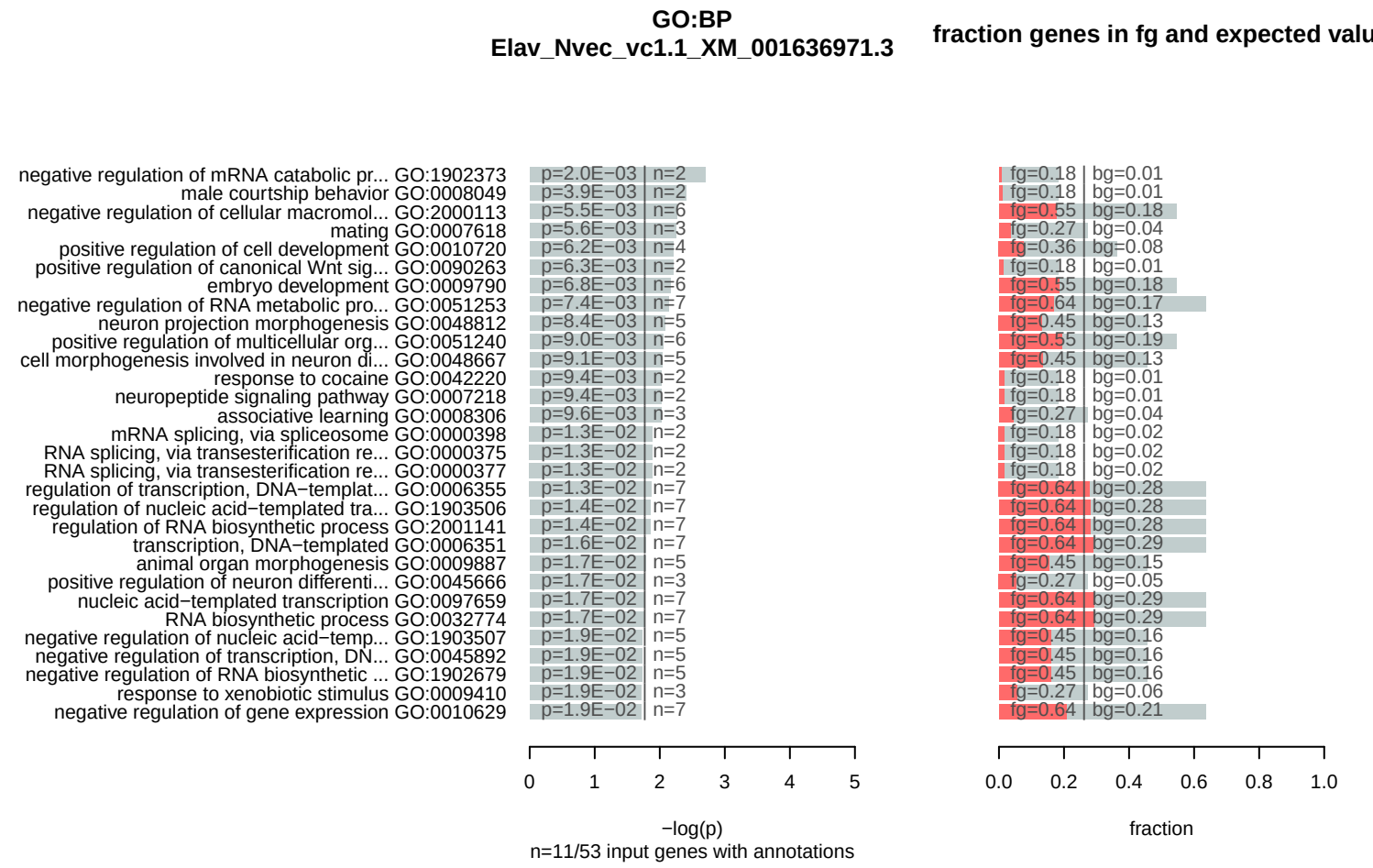
GO:BP
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
negative regulation of mRNA catabolic pr... GO:1902373 p=2.0E−03 n=2 fg=0.18 bg=0.01
male courtship behavior GO:0008049 p=3.9E−03 n=2 fg=0.18 bg=0.01
negative regulation of cellular macromol... GO:2000113 p=5.5E−03 n=6 fg=0.55 bg=0.18
mating GO:0007618 p=5.6E−03 n=3 fg=0.27 bg=0.04
positive regulation of cell development GO:0010720 p=6.2E−03 n=4 fg=0.36 bg=0.08
positive regulation of canonical Wnt sig... GO:0090263 p=6.3E−03 n=2 fg=0.18 bg=0.01
embryo development GO:0009790 p=6.8E−03 n=6 fg=0.55 bg=0.18
negative regulation of RNA metabolic pro... GO:0051253 p=7.4E−03 n=7 fg=0.64 bg=0.17
neuron projection morphogenesis GO:0048812 p=8.4E−03 n=5 fg=0.45 bg=0.13
positive regulation of multicellular org... GO:0051240 p=9.0E−03 n=6 fg=0.55 bg=0.19
cell morphogenesis involved in neuron di... GO:0048667 p=9.1E−03 n=5 fg=0.45 bg=0.13
response to cocaine GO:0042220 p=9.4E−03 n=2 fg=0.18 bg=0.01
neuropeptide signaling pathway GO:0007218 p=9.4E−03 n=2 fg=0.18 bg=0.01
associative learning GO:0008306 p=9.6E−03 n=3 fg=0.27 bg=0.04
mRNA splicing, via spliceosome GO:0000398 p=1.3E−02 n=2 fg=0.18 bg=0.02
RNA splicing, via transesterification re... GO:0000375 p=1.3E−02 n=2 fg=0.18 bg=0.02
RNA splicing, via transesterification re... GO:0000377 p=1.3E−02 n=2 fg=0.18 bg=0.02
regulation of transcription, DNA−templat... GO:0006355 p=1.3E−02 n=7 fg=0.64 bg=0.28
regulation of nucleic acid−templated tra... GO:1903506 p=1.4E−02 n=7 fg=0.64 bg=0.28
regulation of RNA biosynthetic process GO:2001141 p=1.4E−02 n=7 fg=0.64 bg=0.28
transcription, DNA−templated GO:0006351 p=1.6E−02 n=7 fg=0.64 bg=0.29
animal organ morphogenesis GO:0009887 p=1.7E−02 n=5 fg=0.45 bg=0.15
positive regulation of neuron differenti... GO:0045666 p=1.7E−02 n=3 fg=0.27 bg=0.05
nucleic acid−templated transcription GO:0097659 p=1.7E−02 n=7 fg=0.64 bg=0.29
RNA biosynthetic process GO:0032774 p=1.7E−02 n=7 fg=0.64 bg=0.29
negative regulation of nucleic acid−temp... GO:1903507 p=1.9E−02 n=5 fg=0.45 bg=0.16
negative regulation of transcription, DN... GO:0045892 p=1.9E−02 n=5 fg=0.45 bg=0.16
negative regulation of RNA biosynthetic ... GO:1902679 p=1.9E−02 n=5 fg=0.45 bg=0.16
response to xenobiotic stimulus GO:0009410 p=1.9E−02 n=3 fg=0.27 bg=0.06
negative regulation of gene expression GO:0010629 p=1.9E−02 n=7 fg=0.64 bg=0.21
0 1 2 3 4 5
−log(p)
n=11/53 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
neuropeptide receptor activity GO:0008188 p=9.6E−03 n=2 fg=0.20 bg=0.02
protein homodimerization activity GO:0042803 p=2.3E−02 n=4 fg=0.40 bg=0.12
identical protein binding GO:0042802 p=2.3E−02 n=5 fg=0.50 bg=0.19
poly(U) RNA binding GO:0008266 p=2.8E−02 n=1 fg=0.10 bg=0.00
proline−rich region binding GO:0070064 p=2.8E−02 n=1 fg=0.10 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=2.8E−02 n=1 fg=0.10 bg=0.00
protein kinase A catalytic subunit bindi... GO:0034236 p=2.8E−02 n=1 fg=0.10 bg=0.00
poly−pyrimidine tract binding GO:0008187 p=2.8E−02 n=1 fg=0.10 bg=0.00
protein serine/threonine kinase inhibito... GO:0030291 p=2.8E−02 n=1 fg=0.10 bg=0.00
cAMP−dependent protein kinase inhibitor ... GO:0004862 p=2.8E−02 n=1 fg=0.10 bg=0.00
cAMP−dependent protein kinase regulator ... GO:0008603 p=2.8E−02 n=1 fg=0.10 bg=0.00
tau protein binding GO:0048156 p=2.8E−02 n=1 fg=0.10 bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925 p=2.8E−02 n=1 fg=0.10 bg=0.00
miRNA binding GO:0035198 p=5.4E−02 n=1 fg=0.10 bg=0.01
substance P receptor activity GO:0016496 p=5.4E−02 n=1 fg=0.10 bg=0.01
substance K receptor activity GO:0016497 p=5.4E−02 n=1 fg=0.10 bg=0.01
regulatory RNA binding GO:0061980 p=5.4E−02 n=1 fg=0.10 bg=0.01
double−stranded RNA binding GO:0003725 p=5.4E−02 n=1 fg=0.10 bg=0.01
protein−hormone receptor activity GO:0016500 p=5.4E−02 n=1 fg=0.10 bg=0.01
protein dimerization activity GO:0046983 p=7.9E−02 n=4 fg=0.40 bg=0.18
protein kinase A binding GO:0051018 p=8.0E−02 n=1 fg=0.10 bg=0.01
translation regulator activity GO:0045182 p=8.0E−02 n=1 fg=0.10 bg=0.01
translation repressor activity GO:0030371 p=8.0E−02 n=1 fg=0.10 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=8.0E−02 n=1 fg=0.10 bg=0.01
kinase inhibitor activity GO:0019210 p=8.0E−02 n=1 fg=0.10 bg=0.01
protein kinase inhibitor activity GO:0004860 p=8.0E−02 n=1 fg=0.10 bg=0.01
mRNA regulatory element binding translat... GO:0000900 p=8.0E−02 n=1 fg=0.10 bg=0.01
single−stranded RNA binding GO:0003727 p=8.0E−02 n=1 fg=0.10 bg=0.01
cAMP binding GO:0030552 p=8.0E−02 n=1 fg=0.10 bg=0.01
nucleic acid binding GO:0003676 p=8.7E−02 n=4 fg=0.40 bg=0.18
0 1 2 3 4 5
−log(p)
n=10/53 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001636971.3
fraction genes in fg and expected valu
nuclear speck GO:0016607 p=1.4E−02 n=2 fg=0.20 bg=0.02
neuronal cell body GO:0043025 p=1.7E−02 n=4 fg=0.40 bg=0.11
cell body GO:0044297 p=2.4E−02 n=4 fg=0.40 bg=0.12
polysomal ribosome GO:0042788 p=2.5E−02 n=1 fg=0.10 bg=0.00
Dsl1/NZR complex GO:0070939 p=2.5E−02 n=1 fg=0.10 bg=0.00
growth cone filopodium GO:1990812 p=2.5E−02 n=1 fg=0.10 bg=0.00
growth cone lamellipodium GO:1990761 p=2.5E−02 n=1 fg=0.10 bg=0.00
Cajal body GO:0015030 p=2.5E−02 n=1 fg=0.10 bg=0.00
vesicle tethering complex GO:0099023 p=2.5E−02 n=1 fg=0.10 bg=0.00
dendrite GO:0030425 p=2.5E−02 n=4 fg=0.40 bg=0.12
dendritic tree GO:0097447 p=2.5E−02 n=4 fg=0.40 bg=0.12
nucleus GO:0005634 p=2.9E−02 n=8 fg=0.80 bg=0.46
growth cone GO:0030426 p=3.8E−02 n=2 fg=0.20 bg=0.03
trans−Golgi network GO:0005802 p=3.8E−02 n=2 fg=0.20 bg=0.03
site of polarized growth GO:0030427 p=4.3E−02 n=2 fg=0.20 bg=0.03
intracellular membrane−bounded organelle GO:0043231 p=4.7E−02 n=10 fg=1.00 bg=0.74
ribosome GO:0005840 p=4.9E−02 n=1 fg=0.10 bg=0.01
polysome GO:0005844 p=4.9E−02 n=1 fg=0.10 bg=0.01
nucleotide−activated protein kinase comp... GO:0031588 p=4.9E−02 n=1 fg=0.10 bg=0.01
female germ cell nucleus GO:0001674 p=4.9E−02 n=1 fg=0.10 bg=0.01
cAMP−dependent protein kinase complex GO:0005952 p=4.9E−02 n=1 fg=0.10 bg=0.01
germinal vesicle GO:0042585 p=4.9E−02 n=1 fg=0.10 bg=0.01
cytoplasmic stress granule GO:0010494 p=4.9E−02 n=1 fg=0.10 bg=0.01
nuclear body GO:0016604 p=4.9E−02 n=2 fg=0.20 bg=0.04
membrane−bounded organelle GO:0043227 p=5.2E−02 n=10 fg=1.00 bg=0.75
somatodendritic compartment GO:0036477 p=5.2E−02 n=4 fg=0.40 bg=0.15
intracellular organelle GO:0043229 p=7.2E−02 n=10 fg=1.00 bg=0.77
germ cell nucleus GO:0043073 p=7.3E−02 n=1 fg=0.10 bg=0.01
endoplasmic reticulum protein−containing... GO:0140534 p=7.3E−02 n=1 fg=0.10 bg=0.01
filopodium GO:0030175 p=7.3E−02 n=1 fg=0.10 bg=0.01
0 1 2 3 4 5
−log(p)
n=10/53 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction