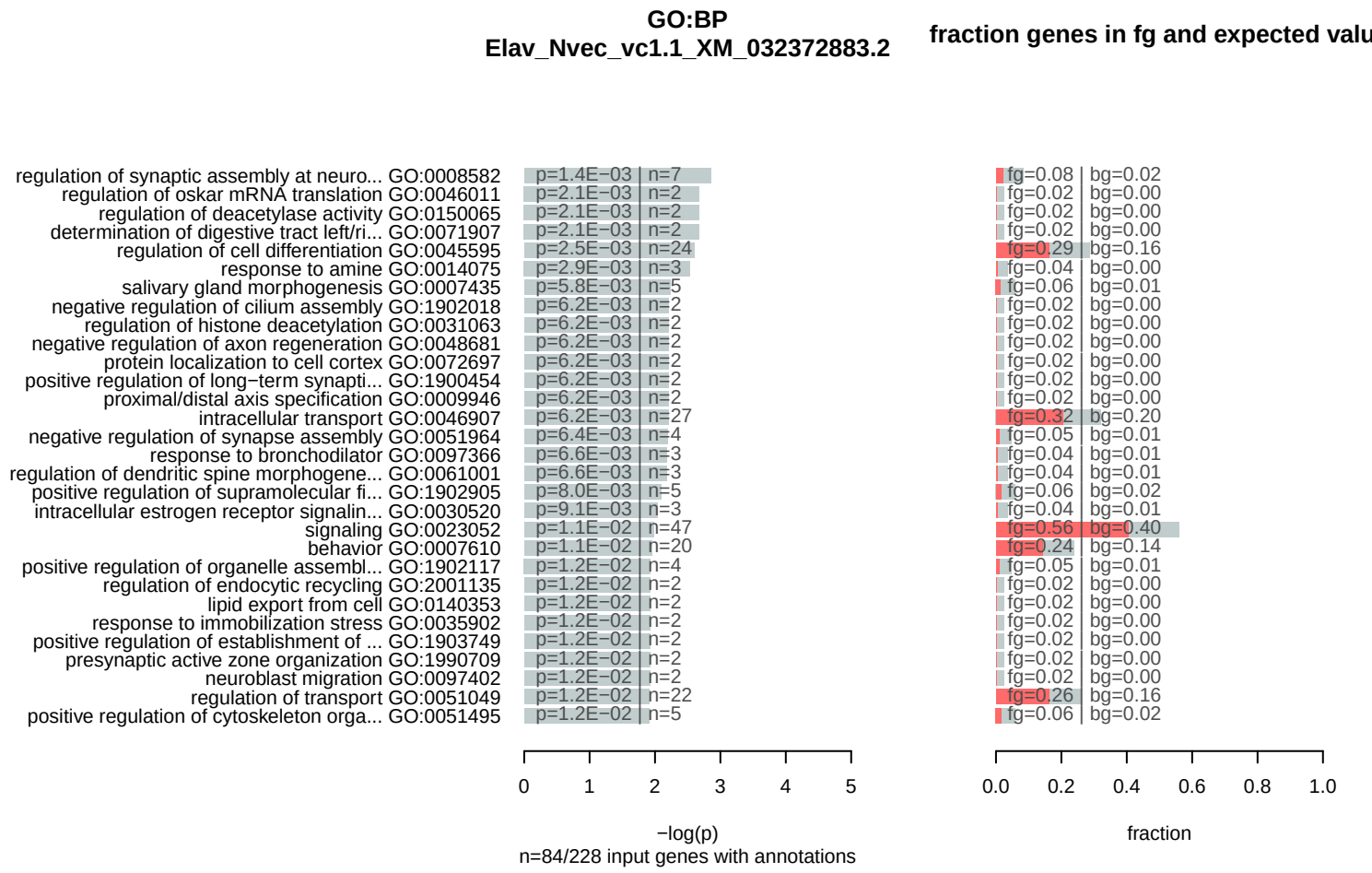
GO:BP
Elav_Nvec_vc1.1_XM_032372883.2
fraction genes in fg and expected valu
regulation of synaptic assembly at neuro... GO:0008582 p=1.4E−03 n=7 fg=0.08 bg=0.02
regulation of oskar mRNA translation GO:0046011 p=2.1E−03 n=2 fg=0.02 bg=0.00
regulation of deacetylase activity GO:0150065 p=2.1E−03 n=2 fg=0.02 bg=0.00
determination of digestive tract left/ri... GO:0071907 p=2.1E−03 n=2 fg=0.02 bg=0.00
regulation of cell differentiation GO:0045595 p=2.5E−03 n=24 fg=0.29 bg=0.16
response to amine GO:0014075 p=2.9E−03 n=3 fg=0.04 bg=0.00
salivary gland morphogenesis GO:0007435 p=5.8E−03 n=5 fg=0.06 bg=0.01
negative regulation of cilium assembly GO:1902018 p=6.2E−03 n=2 fg=0.02 bg=0.00
regulation of histone deacetylation GO:0031063 p=6.2E−03 n=2 fg=0.02 bg=0.00
negative regulation of axon regeneration GO:0048681 p=6.2E−03 n=2 fg=0.02 bg=0.00
protein localization to cell cortex GO:0072697 p=6.2E−03 n=2 fg=0.02 bg=0.00
positive regulation of long−term synapti... GO:1900454 p=6.2E−03 n=2 fg=0.02 bg=0.00
proximal/distal axis specification GO:0009946 p=6.2E−03 n=2 fg=0.02 bg=0.00
intracellular transport GO:0046907 p=6.2E−03 n=27 fg=0.32 bg=0.20
negative regulation of synapse assembly GO:0051964 p=6.4E−03 n=4 fg=0.05 bg=0.01
response to bronchodilator GO:0097366 p=6.6E−03 n=3 fg=0.04 bg=0.01
regulation of dendritic spine morphogene... GO:0061001 p=6.6E−03 n=3 fg=0.04 bg=0.01
positive regulation of supramolecular fi... GO:1902905 p=8.0E−03 n=5 fg=0.06 bg=0.02
intracellular estrogen receptor signalin... GO:0030520 p=9.1E−03 n=3 fg=0.04 bg=0.01
signaling GO:0023052 p=1.1E−02 n=47 fg=0.56 bg=0.40
behavior GO:0007610 p=1.1E−02 n=20 fg=0.24 bg=0.14
positive regulation of organelle assembl... GO:1902117 p=1.2E−02 n=4 fg=0.05 bg=0.01
regulation of endocytic recycling GO:2001135 p=1.2E−02 n=2 fg=0.02 bg=0.00
lipid export from cell GO:0140353 p=1.2E−02 n=2 fg=0.02 bg=0.00
response to immobilization stress GO:0035902 p=1.2E−02 n=2 fg=0.02 bg=0.00
positive regulation of establishment of ... GO:1903749 p=1.2E−02 n=2 fg=0.02 bg=0.00
presynaptic active zone organization GO:1990709 p=1.2E−02 n=2 fg=0.02 bg=0.00
neuroblast migration GO:0097402 p=1.2E−02 n=2 fg=0.02 bg=0.00
regulation of transport GO:0051049 p=1.2E−02 n=22 fg=0.26 bg=0.16
positive regulation of cytoskeleton orga... GO:0051495 p=1.2E−02 n=5 fg=0.06 bg=0.02
0 1 2 3 4 5
−log(p)
n=84/228 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032372883.2
fraction genes in fg and expected valu
protein phosphatase 1 binding GO:0008157 p=2.2E−04 n=4 fg=0.06 bg=0.01
mitogen−activated protein kinase binding GO:0051019 p=6.2E−04 n=4 fg=0.06 bg=0.01
transcription factor binding GO:0008134 p=5.0E−03 n=12 fg=0.17 bg=0.07
actin binding GO:0003779 p=1.4E−02 n=5 fg=0.07 bg=0.02
protein phosphatase regulator activity GO:0019888 p=1.8E−02 n=3 fg=0.04 bg=0.01
cation channel activity GO:0005261 p=1.8E−02 n=6 fg=0.08 bg=0.03
MAP kinase activity GO:0004707 p=1.8E−02 n=2 fg=0.03 bg=0.00
kinesin binding GO:0019894 p=2.2E−02 n=3 fg=0.04 bg=0.01
RNA polymerase II−specific DNA−binding t... GO:0061629 p=2.4E−02 n=5 fg=0.07 bg=0.02
phospholipid binding GO:0005543 p=2.5E−02 n=7 fg=0.10 bg=0.04
phosphatase regulator activity GO:0019208 p=2.6E−02 n=3 fg=0.04 bg=0.01
lipid binding GO:0008289 p=2.8E−02 n=8 fg=0.11 bg=0.05
DNA−binding transcription factor binding GO:0140297 p=3.3E−02 n=5 fg=0.07 bg=0.03
nuclear estrogen receptor binding GO:0030331 p=3.6E−02 n=2 fg=0.03 bg=0.00
potassium ion transmembrane transporter ... GO:0015079 p=3.7E−02 n=3 fg=0.04 bg=0.01
protein kinase binding GO:0019901 p=3.8E−02 n=13 fg=0.18 bg=0.08
metal ion transmembrane transporter acti... GO:0046873 p=4.1E−02 n=6 fg=0.08 bg=0.04
histone deacetylase binding GO:0042826 p=4.3E−02 n=3 fg=0.04 bg=0.01
transcription coactivator activity GO:0003713 p=4.4E−02 n=6 fg=0.08 bg=0.04
type I transforming growth factor beta r... GO:0034713 p=4.5E−02 n=1 fg=0.01 bg=0.00
lipoate synthase activity GO:0016992 p=4.5E−02 n=1 fg=0.01 bg=0.00
histone deacetylase regulator activity GO:0035033 p=4.5E−02 n=1 fg=0.01 bg=0.00
insulin−like growth factor−activated rec... GO:0005010 p=4.5E−02 n=1 fg=0.01 bg=0.00
pre−mRNA 5'−splice site binding GO:0030627 p=4.5E−02 n=1 fg=0.01 bg=0.00
glycogen binding GO:2001069 p=4.5E−02 n=1 fg=0.01 bg=0.00
myosin II binding GO:0045159 p=4.5E−02 n=1 fg=0.01 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=4.5E−02 n=1 fg=0.01 bg=0.00
polypeptide N−acetylgalactosaminyltransf... GO:0004653 p=4.5E−02 n=1 fg=0.01 bg=0.00
insulin−like growth factor II binding GO:0031995 p=4.5E−02 n=1 fg=0.01 bg=0.00
transmembrane receptor protein tyrosine ... GO:0005001 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/228 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032372883.2
fraction genes in fg and expected valu
endolysosome membrane GO:0036020 p=6.1E−03 n=2 fg=0.02 bg=0.00
cytoplasmic region GO:0099568 p=9.8E−03 n=10 fg=0.12 bg=0.05
neuronal cell body GO:0043025 p=1.1E−02 n=12 fg=0.14 bg=0.07
perikaryon GO:0043204 p=1.4E−02 n=4 fg=0.05 bg=0.01
cell cortex GO:0005938 p=1.8E−02 n=8 fg=0.10 bg=0.04
midbody GO:0030496 p=1.9E−02 n=4 fg=0.05 bg=0.01
protein phosphatase type 1 complex GO:0000164 p=1.9E−02 n=2 fg=0.02 bg=0.00
cortical actin cytoskeleton GO:0030864 p=1.9E−02 n=3 fg=0.04 bg=0.01
cell body GO:0044297 p=2.0E−02 n=12 fg=0.14 bg=0.08
cell periphery GO:0071944 p=2.1E−02 n=33 fg=0.40 bg=0.29
cell junction GO:0030054 p=2.4E−02 n=18 fg=0.22 bg=0.13
axon GO:0030424 p=2.4E−02 n=12 fg=0.14 bg=0.08
plasma membrane GO:0005886 p=2.5E−02 n=31 fg=0.37 bg=0.27
plasma membrane region GO:0098590 p=2.6E−02 n=14 fg=0.17 bg=0.10
dendrite membrane GO:0032590 p=2.8E−02 n=2 fg=0.02 bg=0.00
Cajal body GO:0015030 p=2.8E−02 n=2 fg=0.02 bg=0.00
cortical cytoskeleton GO:0030863 p=2.8E−02 n=3 fg=0.04 bg=0.01
synapse GO:0045202 p=2.9E−02 n=14 fg=0.17 bg=0.10
dendrite GO:0030425 p=3.2E−02 n=11 fg=0.13 bg=0.07
dendritic tree GO:0097447 p=3.2E−02 n=11 fg=0.13 bg=0.07
membrane GO:0016020 p=3.3E−02 n=48 fg=0.58 bg=0.46
apicolateral plasma membrane GO:0016327 p=3.8E−02 n=2 fg=0.02 bg=0.00
asymmetric synapse GO:0032279 p=4.4E−02 n=5 fg=0.06 bg=0.02
katanin complex GO:0008352 p=4.6E−02 n=1 fg=0.01 bg=0.00
integrin alpha9−beta1 complex GO:0034679 p=4.6E−02 n=1 fg=0.01 bg=0.00
keratin filament GO:0045095 p=4.6E−02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=4.6E−02 n=1 fg=0.01 bg=0.00
integral component of lysosomal membrane GO:1905103 p=4.6E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=4.6E−02 n=1 fg=0.01 bg=0.00
ciliary transition fiber GO:0097539 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=83/228 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction