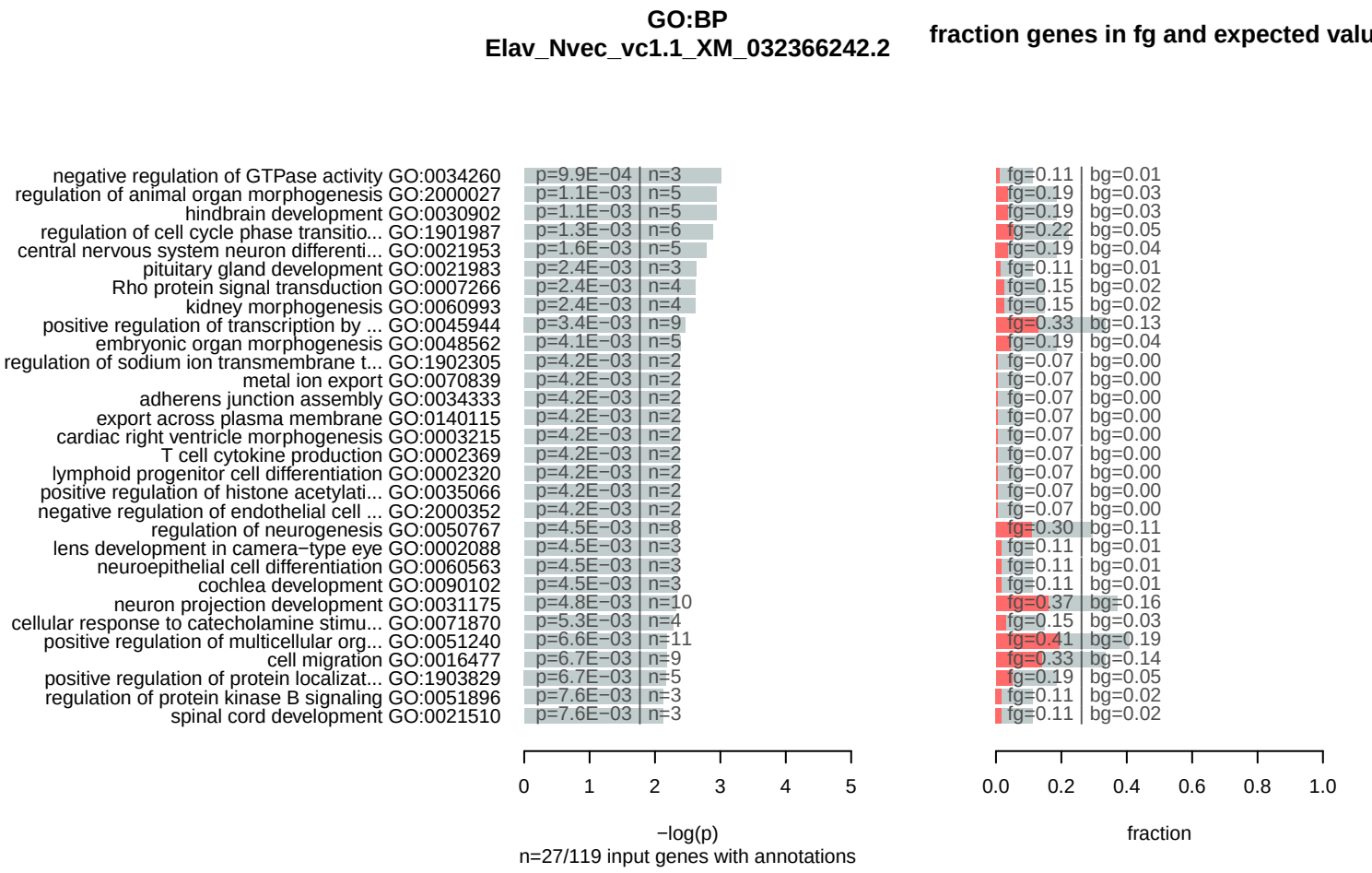
GO:BP
Elav_Nvec_vc1.1_XM_032366242.2
fraction genes in fg and expected valu
negative regulation of GTPase activity GO:0034260 p=9.9E−04 n=3 fg=0.11 bg=0.01
regulation of animal organ morphogenesis GO:2000027 p=1.1E−03 n=5 fg=0.19 bg=0.03
hindbrain development GO:0030902 p=1.1E−03 n=5 fg=0.19 bg=0.03
regulation of cell cycle phase transitio... GO:1901987 p=1.3E−03 n=6 fg=0.22 bg=0.05
central nervous system neuron differenti... GO:0021953 p=1.6E−03 n=5 fg=0.19 bg=0.04
pituitary gland development GO:0021983 p=2.4E−03 n=3 fg=0.11 bg=0.01
Rho protein signal transduction GO:0007266 p=2.4E−03 n=4 fg=0.15 bg=0.02
kidney morphogenesis GO:0060993 p=2.4E−03 n=4 fg=0.15 bg=0.02
positive regulation of transcription by ... GO:0045944 p=3.4E−03 n=9 fg=0.33 bg=0.13
embryonic organ morphogenesis GO:0048562 p=4.1E−03 n=5 fg=0.19 bg=0.04
regulation of sodium ion transmembrane t... GO:1902305 p=4.2E−03 n=2 fg=0.07 bg=0.00
metal ion export GO:0070839 p=4.2E−03 n=2 fg=0.07 bg=0.00
adherens junction assembly GO:0034333 p=4.2E−03 n=2 fg=0.07 bg=0.00
export across plasma membrane GO:0140115 p=4.2E−03 n=2 fg=0.07 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=4.2E−03 n=2 fg=0.07 bg=0.00
T cell cytokine production GO:0002369 p=4.2E−03 n=2 fg=0.07 bg=0.00
lymphoid progenitor cell differentiation GO:0002320 p=4.2E−03 n=2 fg=0.07 bg=0.00
positive regulation of histone acetylati... GO:0035066 p=4.2E−03 n=2 fg=0.07 bg=0.00
negative regulation of endothelial cell ... GO:2000352 p=4.2E−03 n=2 fg=0.07 bg=0.00
regulation of neurogenesis GO:0050767 p=4.5E−03 n=8 fg=0.30 bg=0.11
lens development in camera−type eye GO:0002088 p=4.5E−03 n=3 fg=0.11 bg=0.01
neuroepithelial cell differentiation GO:0060563 p=4.5E−03 n=3 fg=0.11 bg=0.01
cochlea development GO:0090102 p=4.5E−03 n=3 fg=0.11 bg=0.01
neuron projection development GO:0031175 p=4.8E−03 n=10 fg=0.37 bg=0.16
cellular response to catecholamine stimu... GO:0071870 p=5.3E−03 n=4 fg=0.15 bg=0.03
positive regulation of multicellular org... GO:0051240 p=6.6E−03 n=11 fg=0.41 bg=0.19
cell migration GO:0016477 p=6.7E−03 n=9 fg=0.33 bg=0.14
positive regulation of protein localizat... GO:1903829 p=6.7E−03 n=5 fg=0.19 bg=0.05
regulation of protein kinase B signaling GO:0051896 p=7.6E−03 n=3 fg=0.11 bg=0.02
spinal cord development GO:0021510 p=7.6E−03 n=3 fg=0.11 bg=0.02
0 1 2 3 4 5
−log(p)
n=27/119 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366242.2
fraction genes in fg and expected valu
DNA−binding transcription activator acti... GO:0001228 p=1.4E−03 n=7 fg=0.27 bg=0.07
protein domain specific binding GO:0019904 p=2.6E−03 n=8 fg=0.31 bg=0.10
acetylcholine receptor binding GO:0033130 p=4.9E−03 n=2 fg=0.08 bg=0.01
molecular function regulator activity GO:0098772 p=5.7E−03 n=9 fg=0.35 bg=0.14
transcription coactivator activity GO:0003713 p=1.3E−02 n=4 fg=0.15 bg=0.04
transcription coregulator binding GO:0001221 p=1.4E−02 n=2 fg=0.08 bg=0.01
enzyme inhibitor activity GO:0004857 p=1.4E−02 n=3 fg=0.12 bg=0.02
potassium channel regulator activity GO:0015459 p=2.0E−02 n=3 fg=0.12 bg=0.02
transcription regulatory region nucleic ... GO:0001067 p=2.5E−02 n=6 fg=0.23 bg=0.09
mitogen−activated protein kinase kinase ... GO:0031434 p=2.7E−02 n=2 fg=0.08 bg=0.01
HMG box domain binding GO:0071837 p=2.7E−02 n=2 fg=0.08 bg=0.01
scaffold protein binding GO:0097110 p=2.8E−02 n=3 fg=0.12 bg=0.03
enzyme binding GO:0019899 p=3.5E−02 n=11 fg=0.42 bg=0.25
sequence−specific DNA binding GO:0043565 p=3.7E−02 n=6 fg=0.23 bg=0.10
transmembrane transporter binding GO:0044325 p=4.3E−02 n=2 fg=0.08 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=4.5E−02 n=4 fg=0.15 bg=0.06
RNA polymerase II cis−regulatory region ... GO:0000978 p=4.5E−02 n=4 fg=0.15 bg=0.06
enzyme regulator activity GO:0030234 p=4.6E−02 n=6 fg=0.23 bg=0.11
DNA binding GO:0003677 p=5.0E−02 n=7 fg=0.27 bg=0.14
RNA polymerase II transcription regulato... GO:0000977 p=5.1E−02 n=5 fg=0.19 bg=0.08
GTPase regulator activity GO:0030695 p=5.3E−02 n=4 fg=0.15 bg=0.06
channel regulator activity GO:0016247 p=5.7E−02 n=3 fg=0.12 bg=0.04
ion channel regulator activity GO:0099106 p=5.7E−02 n=3 fg=0.12 bg=0.04
transcription factor binding GO:0008134 p=5.8E−02 n=5 fg=0.19 bg=0.08
core promoter sequence−specific DNA bind... GO:0001046 p=6.2E−02 n=2 fg=0.08 bg=0.02
hormone receptor binding GO:0051427 p=6.2E−02 n=2 fg=0.08 bg=0.02
protein C−terminus binding GO:0008022 p=6.2E−02 n=2 fg=0.08 bg=0.02
glutamate receptor binding GO:0035254 p=6.2E−02 n=2 fg=0.08 bg=0.02
signaling receptor binding GO:0005102 p=6.2E−02 n=8 fg=0.31 bg=0.13
transcription cis−regulatory region bind... GO:0000976 p=6.6E−02 n=5 fg=0.19 bg=0.09
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−log(p)
n=26/119 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366242.2
fraction genes in fg and expected valu
postsynaptic membrane GO:0045211 p=2.9E−03 n=5 fg=0.18 bg=0.04
photoreceptor inner segment GO:0001917 p=4.7E−03 n=2 fg=0.07 bg=0.01
cell projection membrane GO:0031253 p=5.7E−03 n=6 fg=0.21 bg=0.06
membrane raft GO:0045121 p=1.3E−02 n=5 fg=0.18 bg=0.05
membrane microdomain GO:0098857 p=1.3E−02 n=5 fg=0.18 bg=0.05
microvillus GO:0005902 p=1.3E−02 n=2 fg=0.07 bg=0.01
basolateral plasma membrane GO:0016323 p=2.4E−02 n=4 fg=0.14 bg=0.04
basal plasma membrane GO:0009925 p=2.4E−02 n=4 fg=0.14 bg=0.04
T−tubule GO:0030315 p=2.6E−02 n=2 fg=0.07 bg=0.01
cell leading edge GO:0031252 p=2.7E−02 n=5 fg=0.18 bg=0.06
intermediate filament cytoskeleton GO:0045111 p=4.1E−02 n=2 fg=0.07 bg=0.01
asymmetric synapse GO:0032279 p=4.2E−02 n=4 fg=0.14 bg=0.05
basal part of cell GO:0045178 p=4.2E−02 n=4 fg=0.14 bg=0.05
cell body membrane GO:0044298 p=4.4E−02 n=3 fg=0.11 bg=0.03
neuronal cell body membrane GO:0032809 p=4.4E−02 n=3 fg=0.11 bg=0.03
dendrite GO:0030425 p=4.5E−02 n=7 fg=0.25 bg=0.12
dendritic tree GO:0097447 p=4.5E−02 n=7 fg=0.25 bg=0.12
neuron to neuron synapse GO:0098984 p=4.9E−02 n=4 fg=0.14 bg=0.05
plasma membrane protein complex GO:0098797 p=5.8E−02 n=4 fg=0.14 bg=0.05
transcription regulator complex GO:0005667 p=5.8E−02 n=4 fg=0.14 bg=0.05
sarcolemma GO:0042383 p=5.9E−02 n=2 fg=0.07 bg=0.01
paranode region of axon GO:0033270 p=5.9E−02 n=2 fg=0.07 bg=0.01
leading edge membrane GO:0031256 p=6.6E−02 n=3 fg=0.11 bg=0.03
lateral loop GO:0043219 p=7.0E−02 n=1 fg=0.04 bg=0.00
postsynaptic specialization membrane GO:0099634 p=7.0E−02 n=1 fg=0.04 bg=0.00
clathrin−coated pit GO:0005905 p=7.0E−02 n=1 fg=0.04 bg=0.00
sperm principal piece GO:0097228 p=7.0E−02 n=1 fg=0.04 bg=0.00
immunological synapse GO:0001772 p=7.0E−02 n=1 fg=0.04 bg=0.00
node of Ranvier GO:0033268 p=7.0E−02 n=1 fg=0.04 bg=0.00
dendritic spine membrane GO:0032591 p=7.0E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=28/119 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction