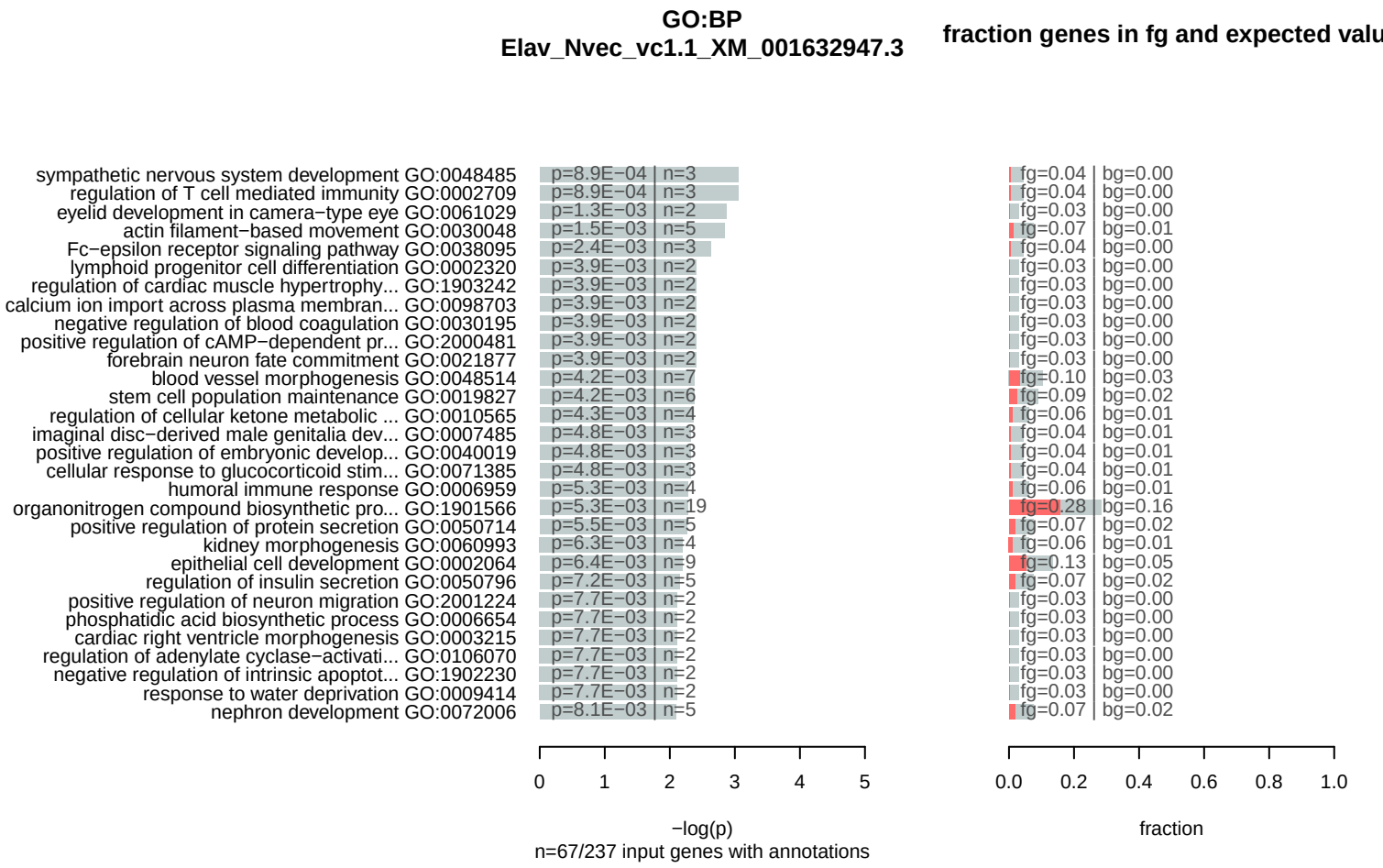
GO:BP
Elav_Nvec_vc1.1_XM_001632947.3
fraction genes in fg and expected valu
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regulation of T cell mediated immunity GO:0002709 p=8.9E−04 n=3 fg=0.04 bg=0.00
eyelid development in camera−type eye GO:0061029 p=1.3E−03 n=2 fg=0.03 bg=0.00
actin filament−based movement GO:0030048 p=1.5E−03 n=5 fg=0.07 bg=0.01
Fc−epsilon receptor signaling pathway GO:0038095 p=2.4E−03 n=3 fg=0.04 bg=0.00
lymphoid progenitor cell differentiation GO:0002320 p=3.9E−03 n=2 fg=0.03 bg=0.00
regulation of cardiac muscle hypertrophy... GO:1903242 p=3.9E−03 n=2 fg=0.03 bg=0.00
calcium ion import across plasma membran... GO:0098703 p=3.9E−03 n=2 fg=0.03 bg=0.00
negative regulation of blood coagulation GO:0030195 p=3.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of cAMP−dependent pr... GO:2000481 p=3.9E−03 n=2 fg=0.03 bg=0.00
forebrain neuron fate commitment GO:0021877 p=3.9E−03 n=2 fg=0.03 bg=0.00
blood vessel morphogenesis GO:0048514 p=4.2E−03 n=7 fg=0.10 bg=0.03
stem cell population maintenance GO:0019827 p=4.2E−03 n=6 fg=0.09 bg=0.02
regulation of cellular ketone metabolic ... GO:0010565 p=4.3E−03 n=4 fg=0.06 bg=0.01
imaginal disc−derived male genitalia dev... GO:0007485 p=4.8E−03 n=3 fg=0.04 bg=0.01
positive regulation of embryonic develop... GO:0040019 p=4.8E−03 n=3 fg=0.04 bg=0.01
cellular response to glucocorticoid stim... GO:0071385 p=4.8E−03 n=3 fg=0.04 bg=0.01
humoral immune response GO:0006959 p=5.3E−03 n=4 fg=0.06 bg=0.01
organonitrogen compound biosynthetic pro... GO:1901566 p=5.3E−03 n=19 fg=0.28 bg=0.16
positive regulation of protein secretion GO:0050714 p=5.5E−03 n=5 fg=0.07 bg=0.02
kidney morphogenesis GO:0060993 p=6.3E−03 n=4 fg=0.06 bg=0.01
epithelial cell development GO:0002064 p=6.4E−03 n=9 fg=0.13 bg=0.05
regulation of insulin secretion GO:0050796 p=7.2E−03 n=5 fg=0.07 bg=0.02
positive regulation of neuron migration GO:2001224 p=7.7E−03 n=2 fg=0.03 bg=0.00
phosphatidic acid biosynthetic process GO:0006654 p=7.7E−03 n=2 fg=0.03 bg=0.00
cardiac right ventricle morphogenesis GO:0003215 p=7.7E−03 n=2 fg=0.03 bg=0.00
regulation of adenylate cyclase−activati... GO:0106070 p=7.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of intrinsic apoptot... GO:1902230 p=7.7E−03 n=2 fg=0.03 bg=0.00
response to water deprivation GO:0009414 p=7.7E−03 n=2 fg=0.03 bg=0.00
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−log(p)
n=67/237 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001632947.3
fraction genes in fg and expected valu
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protein serine/threonine phosphatase act... GO:0004722 p=2.3E−03 n=4 fg=0.06 bg=0.01
ion binding GO:0043167 p=2.9E−03 n=23 fg=0.36 bg=0.21
protein heterodimerization activity GO:0046982 p=2.9E−03 n=10 fg=0.16 bg=0.06
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=4.6E−03 n=2 fg=0.03 bg=0.00
glutamate receptor binding GO:0035254 p=8.1E−03 n=3 fg=0.05 bg=0.01
DNA−binding transcription repressor acti... GO:0001227 p=8.5E−03 n=4 fg=0.06 bg=0.01
nuclear receptor activity GO:0004879 p=9.1E−03 n=2 fg=0.03 bg=0.00
C2H2 zinc finger domain binding GO:0070742 p=9.1E−03 n=2 fg=0.03 bg=0.00
cation binding GO:0043169 p=1.1E−02 n=14 fg=0.22 bg=0.11
cysteine−type endopeptidase regulator ac... GO:0043028 p=1.5E−02 n=2 fg=0.03 bg=0.00
protein phosphatase 2B binding GO:0030346 p=1.5E−02 n=2 fg=0.03 bg=0.00
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2−oxoglutarate−dependent dioxygenase act... GO:0016706 p=2.1E−02 n=2 fg=0.03 bg=0.00
organic cyclic compound binding GO:0097159 p=2.2E−02 n=27 fg=0.42 bg=0.27
core promoter sequence−specific DNA bind... GO:0001046 p=2.4E−02 n=3 fg=0.05 bg=0.01
cis−regulatory region sequence−specific ... GO:0000987 p=2.4E−02 n=6 fg=0.09 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=2.4E−02 n=6 fg=0.09 bg=0.04
dioxygenase activity GO:0051213 p=2.9E−02 n=2 fg=0.03 bg=0.00
RNA methyltransferase activity GO:0008173 p=2.9E−02 n=2 fg=0.03 bg=0.00
metal ion binding GO:0046872 p=3.0E−02 n=12 fg=0.19 bg=0.10
DNA−binding transcription activator acti... GO:0001228 p=3.3E−02 n=6 fg=0.09 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=3.3E−02 n=6 fg=0.09 bg=0.04
histone deacetylase binding GO:0042826 p=3.3E−02 n=3 fg=0.05 bg=0.01
voltage−gated cation channel activity GO:0022843 p=3.3E−02 n=3 fg=0.05 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=3.6E−02 n=7 fg=0.11 bg=0.05
heterocyclic compound binding GO:1901363 p=3.6E−02 n=26 fg=0.41 bg=0.27
transcription regulatory region nucleic ... GO:0001067 p=3.9E−02 n=8 fg=0.12 bg=0.06
adiponectin binding GO:0055100 p=4.0E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=64/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001632947.3
fraction genes in fg and expected valu
filamentous actin GO:0031941 p=1.4E−03 n=2 fg=0.03 bg=0.00
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dendrite cytoplasm GO:0032839 p=7.7E−03 n=2 fg=0.03 bg=0.00
caveola GO:0005901 p=1.9E−02 n=3 fg=0.04 bg=0.01
euchromatin GO:0000791 p=3.3E−02 n=2 fg=0.03 bg=0.00
Dsl1/NZR complex GO:0070939 p=3.7E−02 n=1 fg=0.01 bg=0.00
cuticular plate GO:0032437 p=3.7E−02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=3.7E−02 n=1 fg=0.01 bg=0.00
integral component of pigment granule me... GO:0090740 p=3.7E−02 n=1 fg=0.01 bg=0.00
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calcineurin complex GO:0005955 p=3.7E−02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=3.7E−02 n=1 fg=0.01 bg=0.00
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cation channel complex GO:0034703 p=4.0E−02 n=3 fg=0.04 bg=0.01
voltage−gated potassium channel complex GO:0008076 p=4.1E−02 n=2 fg=0.03 bg=0.00
potassium channel complex GO:0034705 p=4.1E−02 n=2 fg=0.03 bg=0.00
T−tubule GO:0030315 p=5.0E−02 n=2 fg=0.03 bg=0.01
ion channel complex GO:0034702 p=5.1E−02 n=3 fg=0.04 bg=0.01
neuron spine GO:0044309 p=5.8E−02 n=4 fg=0.06 bg=0.02
dendritic spine GO:0043197 p=5.8E−02 n=4 fg=0.06 bg=0.02
transcription regulator complex GO:0005667 p=6.2E−02 n=6 fg=0.09 bg=0.04
catalytic step 2 spliceosome GO:0071013 p=7.0E−02 n=2 fg=0.03 bg=0.01
pre−snoRNP complex GO:0070761 p=7.3E−02 n=1 fg=0.01 bg=0.00
cytosolic aryl hydrocarbon receptor comp... GO:0034752 p=7.3E−02 n=1 fg=0.01 bg=0.00
GPI−anchor transamidase complex GO:0042765 p=7.3E−02 n=1 fg=0.01 bg=0.00
caspase complex GO:0008303 p=7.3E−02 n=1 fg=0.01 bg=0.00
meiotic spindle GO:0072687 p=7.3E−02 n=1 fg=0.01 bg=0.00
pyruvate dehydrogenase (lipoamide) phosp... GO:0045253 p=7.3E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase (li... GO:0019910 p=7.3E−02 n=1 fg=0.01 bg=0.00
neuronal cell body membrane GO:0032809 p=9.2E−02 n=2 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=67/237 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction