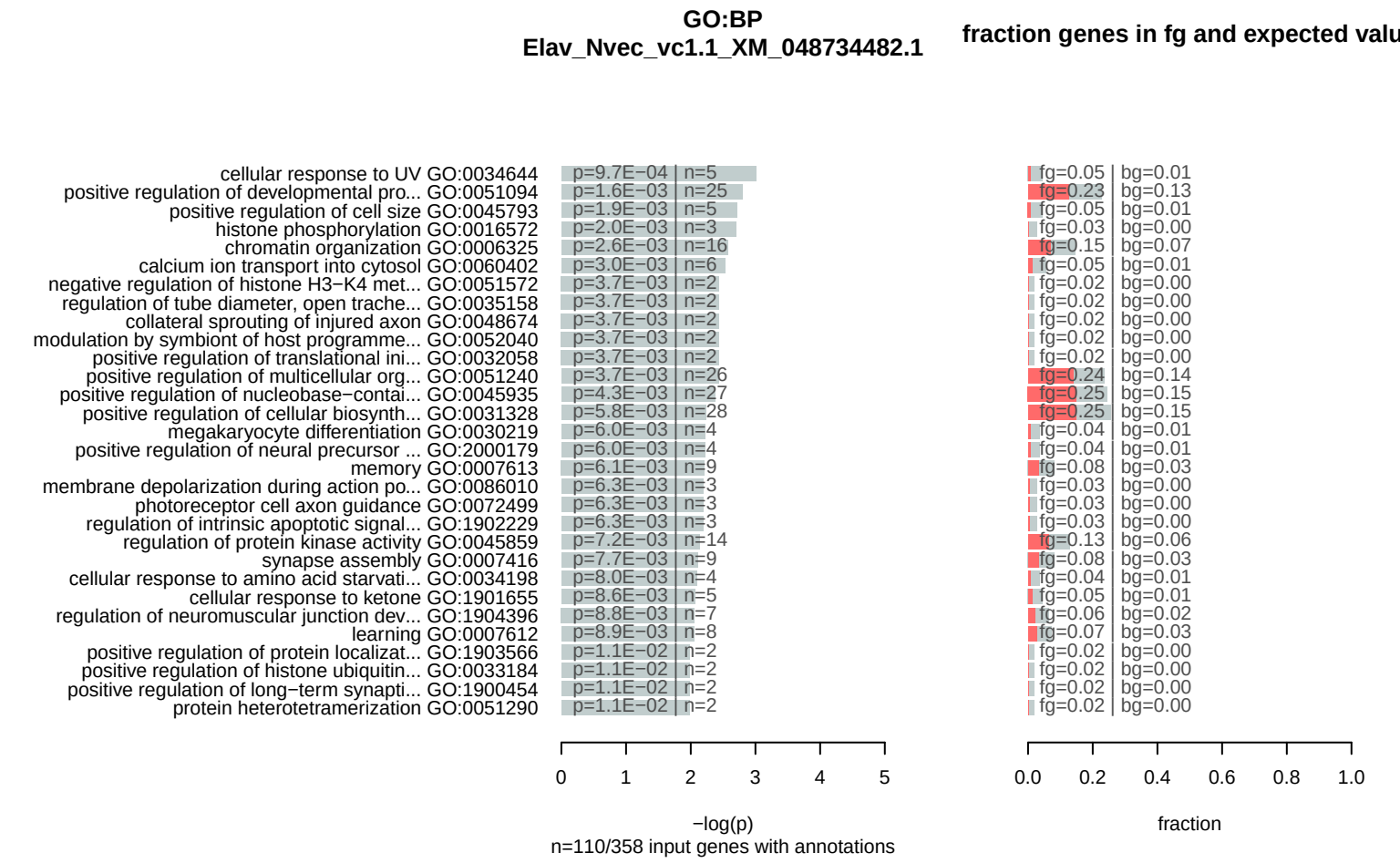
GO:BP
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
cellular response to UV GO:0034644 p=9.7E−04 n=5 fg=0.05 bg=0.01
positive regulation of developmental pro... GO:0051094 p=1.6E−03 n=25 fg=0.23 bg=0.13
positive regulation of cell size GO:0045793 p=1.9E−03 n=5 fg=0.05 bg=0.01
histone phosphorylation GO:0016572 p=2.0E−03 n=3 fg=0.03 bg=0.00
chromatin organization GO:0006325 p=2.6E−03 n=16 fg=0.15 bg=0.07
calcium ion transport into cytosol GO:0060402 p=3.0E−03 n=6 fg=0.05 bg=0.01
negative regulation of histone H3−K4 met... GO:0051572 p=3.7E−03 n=2 fg=0.02 bg=0.00
regulation of tube diameter, open trache... GO:0035158 p=3.7E−03 n=2 fg=0.02 bg=0.00
collateral sprouting of injured axon GO:0048674 p=3.7E−03 n=2 fg=0.02 bg=0.00
modulation by symbiont of host programme... GO:0052040 p=3.7E−03 n=2 fg=0.02 bg=0.00
positive regulation of translational ini... GO:0032058 p=3.7E−03 n=2 fg=0.02 bg=0.00
positive regulation of multicellular org... GO:0051240 p=3.7E−03 n=26 fg=0.24 bg=0.14
positive regulation of nucleobase−contai... GO:0045935 p=4.3E−03 n=27 fg=0.25 bg=0.15
positive regulation of cellular biosynth... GO:0031328 p=5.8E−03 n=28 fg=0.25 bg=0.15
megakaryocyte differentiation GO:0030219 p=6.0E−03 n=4 fg=0.04 bg=0.01
positive regulation of neural precursor ... GO:2000179 p=6.0E−03 n=4 fg=0.04 bg=0.01
memory GO:0007613 p=6.1E−03 n=9 fg=0.08 bg=0.03
membrane depolarization during action po... GO:0086010 p=6.3E−03 n=3 fg=0.03 bg=0.00
photoreceptor cell axon guidance GO:0072499 p=6.3E−03 n=3 fg=0.03 bg=0.00
regulation of intrinsic apoptotic signal... GO:1902229 p=6.3E−03 n=3 fg=0.03 bg=0.00
regulation of protein kinase activity GO:0045859 p=7.2E−03 n=14 fg=0.13 bg=0.06
synapse assembly GO:0007416 p=7.7E−03 n=9 fg=0.08 bg=0.03
cellular response to amino acid starvati... GO:0034198 p=8.0E−03 n=4 fg=0.04 bg=0.01
cellular response to ketone GO:1901655 p=8.6E−03 n=5 fg=0.05 bg=0.01
regulation of neuromuscular junction dev... GO:1904396 p=8.8E−03 n=7 fg=0.06 bg=0.02
learning GO:0007612 p=8.9E−03 n=8 fg=0.07 bg=0.03
positive regulation of protein localizat... GO:1903566 p=1.1E−02 n=2 fg=0.02 bg=0.00
positive regulation of histone ubiquitin... GO:0033184 p=1.1E−02 n=2 fg=0.02 bg=0.00
positive regulation of long−term synapti... GO:1900454 p=1.1E−02 n=2 fg=0.02 bg=0.00
protein heterotetramerization GO:0051290 p=1.1E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=110/358 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
transcription coactivator activity GO:0003713 p=1.2E−03 n=10 fg=0.11 bg=0.04
low voltage−gated calcium channel activi... GO:0008332 p=3.1E−03 n=2 fg=0.02 bg=0.00
nucleosomal DNA binding GO:0031492 p=3.1E−03 n=2 fg=0.02 bg=0.00
RNA polymerase II cis−regulatory region ... GO:0000978 p=3.5E−03 n=9 fg=0.10 bg=0.04
protein kinase inhibitor activity GO:0004860 p=5.9E−03 n=4 fg=0.04 bg=0.01
protein serine/threonine kinase activity GO:0004674 p=8.5E−03 n=9 fg=0.10 bg=0.04
Wnt−activated receptor activity GO:0042813 p=8.9E−03 n=2 fg=0.02 bg=0.00
deaminase activity GO:0019239 p=8.9E−03 n=2 fg=0.02 bg=0.00
bHLH transcription factor binding GO:0043425 p=8.9E−03 n=2 fg=0.02 bg=0.00
nuclear receptor coactivator activity GO:0030374 p=1.1E−02 n=3 fg=0.03 bg=0.01
p53 binding GO:0002039 p=1.2E−02 n=4 fg=0.04 bg=0.01
nuclear receptor activity GO:0004879 p=1.7E−02 n=2 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016814 p=1.7E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=1.7E−02 n=2 fg=0.02 bg=0.00
hydrolase activity, acting on carbon−nit... GO:0016810 p=2.6E−02 n=4 fg=0.04 bg=0.01
exoribonuclease activity GO:0004532 p=2.8E−02 n=2 fg=0.02 bg=0.00
exoribonuclease activity, producing 5'−p... GO:0016896 p=2.8E−02 n=2 fg=0.02 bg=0.00
calcium−release channel activity GO:0015278 p=2.8E−02 n=2 fg=0.02 bg=0.00
3'−5'−exoribonuclease activity GO:0000175 p=2.8E−02 n=2 fg=0.02 bg=0.00
Wnt−protein binding GO:0017147 p=2.8E−02 n=2 fg=0.02 bg=0.00
misfolded protein binding GO:0051787 p=2.8E−02 n=2 fg=0.02 bg=0.00
MAP kinase kinase activity GO:0004708 p=2.8E−02 n=2 fg=0.02 bg=0.00
galactosyltransferase activity GO:0008378 p=4.0E−02 n=2 fg=0.02 bg=0.00
HMG box domain binding GO:0071837 p=4.0E−02 n=2 fg=0.02 bg=0.00
UDP−galactose:beta−N−acetylglucosamine b... GO:0008499 p=4.0E−02 n=2 fg=0.02 bg=0.00
beta−1,3−galactosyltransferase activity GO:0048531 p=4.0E−02 n=2 fg=0.02 bg=0.00
ligand−gated calcium channel activity GO:0099604 p=4.0E−02 n=2 fg=0.02 bg=0.00
dopamine receptor binding GO:0050780 p=4.0E−02 n=2 fg=0.02 bg=0.00
UDP−galactosyltransferase activity GO:0035250 p=4.0E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=5.4E−02 n=2 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=89/358 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048734482.1
fraction genes in fg and expected valu
presynaptic periactive zone GO:0036062 p=7.7E−04 n=3 fg=0.03 bg=0.00
Barr body GO:0001740 p=3.5E−03 n=2 fg=0.02 bg=0.00
nucleosome GO:0000786 p=1.9E−02 n=2 fg=0.02 bg=0.00
methyltransferase complex GO:0034708 p=2.2E−02 n=4 fg=0.04 bg=0.01
polysome GO:0005844 p=3.0E−02 n=3 fg=0.03 bg=0.01
transcription factor TFTC complex GO:0033276 p=3.1E−02 n=2 fg=0.02 bg=0.00
pericentric heterochromatin GO:0005721 p=3.1E−02 n=2 fg=0.02 bg=0.00
female germ cell nucleus GO:0001674 p=3.1E−02 n=2 fg=0.02 bg=0.00
voltage−gated calcium channel complex GO:0005891 p=3.1E−02 n=2 fg=0.02 bg=0.00
DNA packaging complex GO:0044815 p=3.7E−02 n=3 fg=0.03 bg=0.01
neuromuscular junction GO:0031594 p=4.2E−02 n=5 fg=0.05 bg=0.02
eukaryotic translation initiation factor... GO:0016281 p=5.9E+02 n=1 fg=0.01 bg=0.00
SAM complex GO:0001401 p=5.9E+02 n=1 fg=0.01 bg=0.00
spectrosome GO:0045170 p=5.9E+02 n=1 fg=0.01 bg=0.00
mitochondrial outer membrane translocase... GO:0005742 p=5.9E+02 n=1 fg=0.01 bg=0.00
single−stranded DNA−dependent ATP−depend... GO:0017117 p=5.9E+02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=5.9E+02 n=1 fg=0.01 bg=0.00
exoribonuclease complex GO:1905354 p=5.9E+02 n=1 fg=0.01 bg=0.00
exosome (RNase complex) GO:0000178 p=5.9E+02 n=1 fg=0.01 bg=0.00
outer mitochondrial membrane protein com... GO:0098799 p=5.9E+02 n=1 fg=0.01 bg=0.00
dendritic spine neck GO:0044326 p=5.9E+02 n=1 fg=0.01 bg=0.00
dendritic spine head GO:0044327 p=5.9E+02 n=1 fg=0.01 bg=0.00
spectrin GO:0008091 p=5.9E+02 n=1 fg=0.01 bg=0.00
CCR4−NOT complex GO:0030014 p=5.9E+02 n=1 fg=0.01 bg=0.00
CCR4−NOT core complex GO:0030015 p=5.9E+02 n=1 fg=0.01 bg=0.00
autosome GO:0030849 p=5.9E+02 n=1 fg=0.01 bg=0.00
RCAF complex GO:0035059 p=5.9E+02 n=1 fg=0.01 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=5.9E+02 n=1 fg=0.01 bg=0.00
FACT complex GO:0035101 p=5.9E+02 n=1 fg=0.01 bg=0.00
Dbf4−dependent protein kinase complex GO:0031431 p=5.9E+02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=107/358 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction