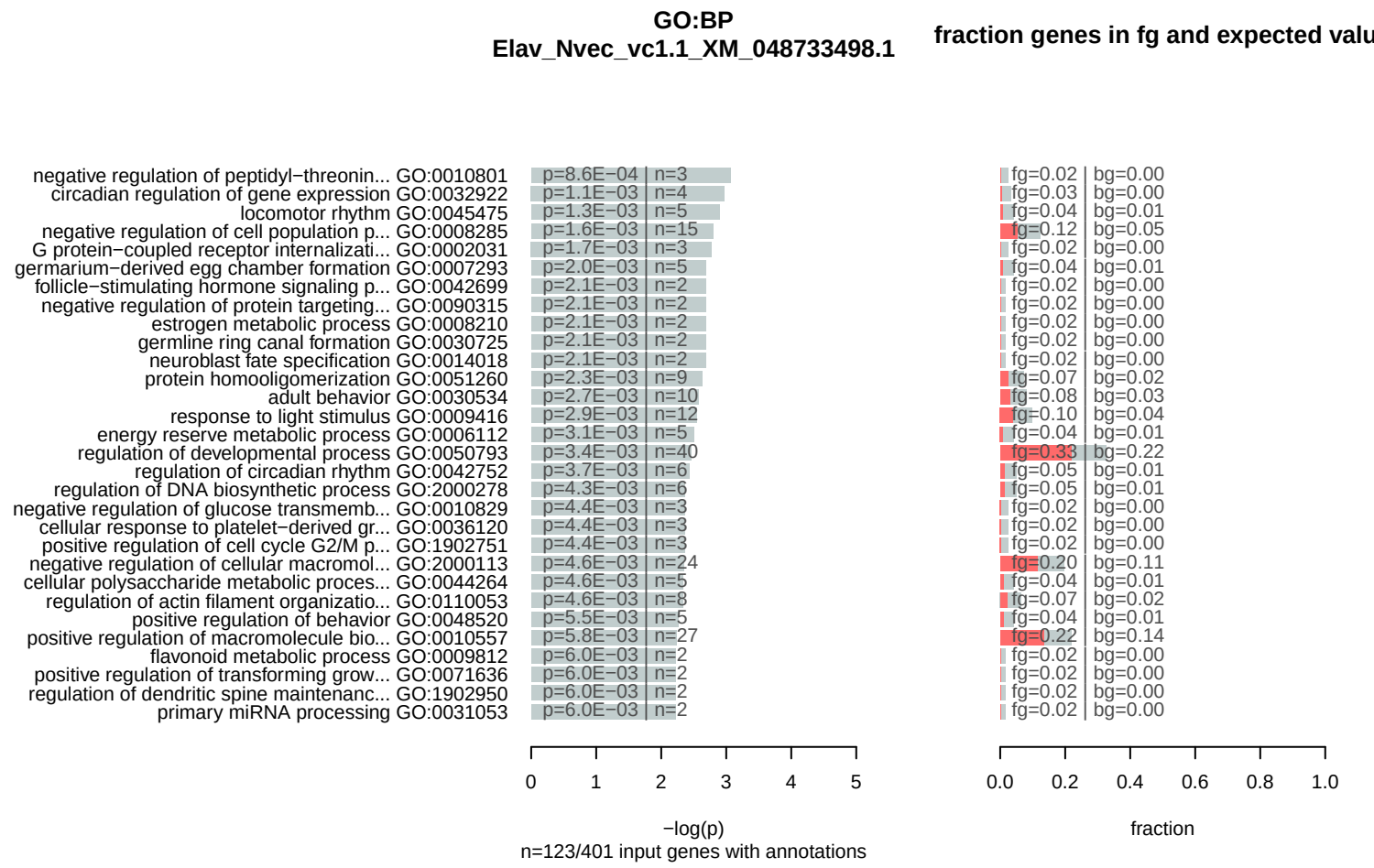
GO:BP
Elav_Nvec_vc1.1_XM_048733498.1
fraction genes in fg and expected valu
negative regulation of peptidyl−threonin... GO:0010801 p=8.6E−04 n=3 fg=0.02 bg=0.00
circadian regulation of gene expression GO:0032922 p=1.1E−03 n=4 fg=0.03 bg=0.00
locomotor rhythm GO:0045475 p=1.3E−03 n=5 fg=0.04 bg=0.01
negative regulation of cell population p... GO:0008285 p=1.6E−03 n=15 fg=0.12 bg=0.05
G protein−coupled receptor internalizati... GO:0002031 p=1.7E−03 n=3 fg=0.02 bg=0.00
germarium−derived egg chamber formation GO:0007293 p=2.0E−03 n=5 fg=0.04 bg=0.01
follicle−stimulating hormone signaling p... GO:0042699 p=2.1E−03 n=2 fg=0.02 bg=0.00
negative regulation of protein targeting... GO:0090315 p=2.1E−03 n=2 fg=0.02 bg=0.00
estrogen metabolic process GO:0008210 p=2.1E−03 n=2 fg=0.02 bg=0.00
germline ring canal formation GO:0030725 p=2.1E−03 n=2 fg=0.02 bg=0.00
neuroblast fate specification GO:0014018 p=2.1E−03 n=2 fg=0.02 bg=0.00
protein homooligomerization GO:0051260 p=2.3E−03 n=9 fg=0.07 bg=0.02
adult behavior GO:0030534 p=2.7E−03 n=10 fg=0.08 bg=0.03
response to light stimulus GO:0009416 p=2.9E−03 n=12 fg=0.10 bg=0.04
energy reserve metabolic process GO:0006112 p=3.1E−03 n=5 fg=0.04 bg=0.01
regulation of developmental process GO:0050793 p=3.4E−03 n=40 fg=0.33 bg=0.22
regulation of circadian rhythm GO:0042752 p=3.7E−03 n=6 fg=0.05 bg=0.01
regulation of DNA biosynthetic process GO:2000278 p=4.3E−03 n=6 fg=0.05 bg=0.01
negative regulation of glucose transmemb... GO:0010829 p=4.4E−03 n=3 fg=0.02 bg=0.00
cellular response to platelet−derived gr... GO:0036120 p=4.4E−03 n=3 fg=0.02 bg=0.00
positive regulation of cell cycle G2/M p... GO:1902751 p=4.4E−03 n=3 fg=0.02 bg=0.00
negative regulation of cellular macromol... GO:2000113 p=4.6E−03 n=24 fg=0.20 bg=0.11
cellular polysaccharide metabolic proces... GO:0044264 p=4.6E−03 n=5 fg=0.04 bg=0.01
regulation of actin filament organizatio... GO:0110053 p=4.6E−03 n=8 fg=0.07 bg=0.02
positive regulation of behavior GO:0048520 p=5.5E−03 n=5 fg=0.04 bg=0.01
positive regulation of macromolecule bio... GO:0010557 p=5.8E−03 n=27 fg=0.22 bg=0.14
flavonoid metabolic process GO:0009812 p=6.0E−03 n=2 fg=0.02 bg=0.00
positive regulation of transforming grow... GO:0071636 p=6.0E−03 n=2 fg=0.02 bg=0.00
regulation of dendritic spine maintenanc... GO:1902950 p=6.0E−03 n=2 fg=0.02 bg=0.00
primary miRNA processing GO:0031053 p=6.0E−03 n=2 fg=0.02 bg=0.00
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−log(p)
n=123/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048733498.1
fraction genes in fg and expected valu
cAMP response element binding GO:0035497 p=1.0E−04 n=3 fg=0.03 bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485 p=2.2E−03 n=2 fg=0.02 bg=0.00
cAMP response element binding protein bi... GO:0008140 p=2.2E−03 n=2 fg=0.02 bg=0.00
primary miRNA binding GO:0070878 p=2.2E−03 n=2 fg=0.02 bg=0.00
double−stranded RNA binding GO:0003725 p=2.4E−03 n=4 fg=0.04 bg=0.01
D1 dopamine receptor binding GO:0031748 p=6.4E−03 n=2 fg=0.02 bg=0.00
inositol−1,3,4,5−tetrakisphosphate 5−pho... GO:0052659 p=6.4E−03 n=2 fg=0.02 bg=0.00
inositol−polyphosphate 5−phosphatase act... GO:0004445 p=6.4E−03 n=2 fg=0.02 bg=0.00
DNA−binding transcription repressor acti... GO:0001227 p=7.6E−03 n=5 fg=0.04 bg=0.01
phosphatidylinositol−3,4,5−trisphosphate... GO:0005547 p=8.7E−03 n=4 fg=0.04 bg=0.01
identical protein binding GO:0042802 p=1.2E−02 n=29 fg=0.26 bg=0.17
protein kinase B binding GO:0043422 p=1.3E−02 n=2 fg=0.02 bg=0.00
sequence−specific single stranded DNA bi... GO:0098847 p=2.0E−02 n=2 fg=0.02 bg=0.00
acetylcholine receptor binding GO:0033130 p=2.0E−02 n=2 fg=0.02 bg=0.00
arrestin family protein binding GO:1990763 p=2.0E−02 n=2 fg=0.02 bg=0.00
DNA−binding transcription activator acti... GO:0001228 p=2.1E−02 n=8 fg=0.07 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=2.1E−02 n=8 fg=0.07 bg=0.03
GTPase activity GO:0003924 p=2.4E−02 n=6 fg=0.05 bg=0.02
ribonuclease activity GO:0004540 p=3.6E−02 n=4 fg=0.04 bg=0.01
mRNA 3'−UTR binding GO:0003730 p=3.7E−02 n=3 fg=0.03 bg=0.01
SMAD binding GO:0046332 p=3.7E−02 n=3 fg=0.03 bg=0.01
enzyme inhibitor activity GO:0004857 p=4.0E−02 n=6 fg=0.05 bg=0.02
DEAD/H−box RNA helicase binding GO:0017151 p=4.0E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=4.0E−02 n=2 fg=0.02 bg=0.00
ferrous iron binding GO:0008198 p=4.0E−02 n=2 fg=0.02 bg=0.00
lysophospholipase activity GO:0004622 p=4.0E−02 n=2 fg=0.02 bg=0.00
potassium channel inhibitor activity GO:0019870 p=4.0E−02 n=2 fg=0.02 bg=0.00
protein kinase binding GO:0019901 p=4.2E−02 n=13 fg=0.12 bg=0.07
sodium:dicarboxylate symporter activity GO:0017153 p=4.7E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on metal... GO:0016724 p=4.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=112/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048733498.1
fraction genes in fg and expected valu
perinuclear region of cytoplasm GO:0048471 p=7.5E−04 n=18 fg=0.15 bg=0.06
dendritic shaft GO:0043198 p=2.6E−03 n=5 fg=0.04 bg=0.01
euchromatin GO:0000791 p=3.9E−03 n=4 fg=0.03 bg=0.01
main axon GO:0044304 p=9.6E−03 n=4 fg=0.03 bg=0.01
mitotic spindle pole GO:0097431 p=1.2E−02 n=3 fg=0.02 bg=0.00
protein phosphatase type 1 complex GO:0000164 p=1.9E−02 n=2 fg=0.02 bg=0.00
PML body GO:0016605 p=1.9E−02 n=3 fg=0.02 bg=0.00
spindle GO:0005819 p=2.3E−02 n=9 fg=0.07 bg=0.03
actin−based cell projection GO:0098858 p=2.7E−02 n=6 fg=0.05 bg=0.02
autophagosome membrane GO:0000421 p=2.8E−02 n=2 fg=0.02 bg=0.00
chromosomal region GO:0098687 p=2.8E−02 n=8 fg=0.06 bg=0.03
intrinsic component of Golgi membrane GO:0031228 p=2.9E−02 n=3 fg=0.02 bg=0.01
spindle midzone GO:0051233 p=2.9E−02 n=3 fg=0.02 bg=0.01
neuron spine GO:0044309 p=3.0E−02 n=6 fg=0.05 bg=0.02
dendritic spine GO:0043197 p=3.0E−02 n=6 fg=0.05 bg=0.02
cell leading edge GO:0031252 p=3.0E−02 n=9 fg=0.07 bg=0.04
cytoskeleton GO:0005856 p=3.4E−02 n=26 fg=0.21 bg=0.15
protein serine/threonine phosphatase com... GO:0008287 p=3.4E−02 n=3 fg=0.02 bg=0.01
spindle pole GO:0000922 p=3.4E−02 n=5 fg=0.04 bg=0.01
transcription regulator complex GO:0005667 p=3.8E−02 n=9 fg=0.07 bg=0.04
postsynapse GO:0098794 p=3.8E−02 n=9 fg=0.07 bg=0.04
intermediate−density lipoprotein particl... GO:0034363 p=4.6E−02 n=1 fg=0.01 bg=0.00
high−density lipoprotein particle GO:0034364 p=4.6E−02 n=1 fg=0.01 bg=0.00
lipoprotein particle GO:1990777 p=4.6E−02 n=1 fg=0.01 bg=0.00
ATF4−CREB1 transcription factor complex GO:1990589 p=4.6E−02 n=1 fg=0.01 bg=0.00
plasma lipoprotein particle GO:0034358 p=4.6E−02 n=1 fg=0.01 bg=0.00
triglyceride−rich plasma lipoprotein par... GO:0034385 p=4.6E−02 n=1 fg=0.01 bg=0.00
amyloid−beta complex GO:0106003 p=4.6E−02 n=1 fg=0.01 bg=0.00
nuclear mitotic cohesin complex GO:0034990 p=4.6E−02 n=1 fg=0.01 bg=0.00
clathrin−sculpted gamma−aminobutyric aci... GO:0061200 p=4.6E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=124/401 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction