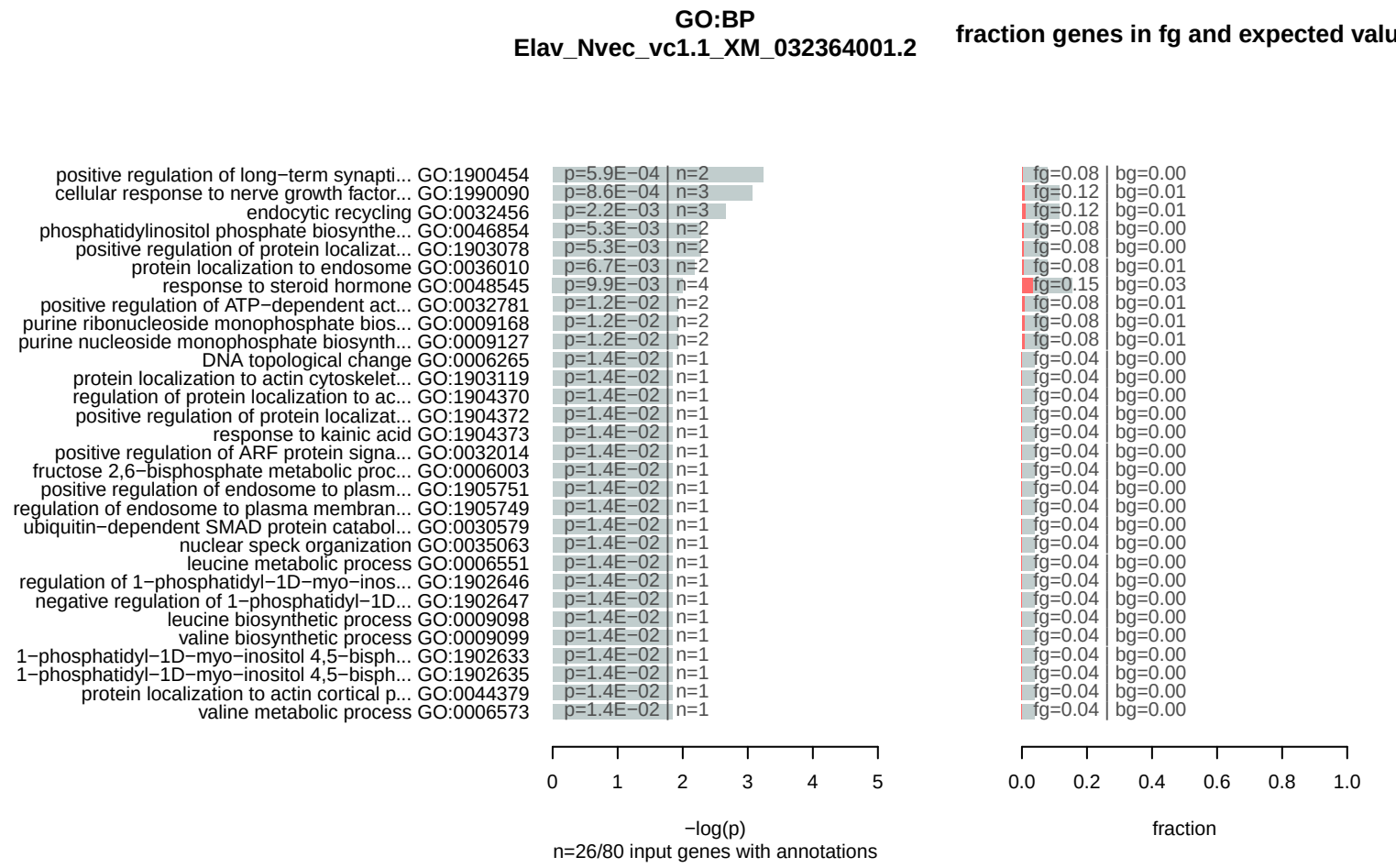
GO:BP
Elav_Nvec_vc1.1_XM_032364001.2
fraction genes in fg and expected valu
positive regulation of long−term synapti... GO:1900454 p=5.9E−04 n=2 fg=0.08 bg=0.00
cellular response to nerve growth factor... GO:1990090 p=8.6E−04 n=3 fg=0.12 bg=0.01
endocytic recycling GO:0032456 p=2.2E−03 n=3 fg=0.12 bg=0.01
phosphatidylinositol phosphate biosynthe... GO:0046854 p=5.3E−03 n=2 fg=0.08 bg=0.00
positive regulation of protein localizat... GO:1903078 p=5.3E−03 n=2 fg=0.08 bg=0.00
protein localization to endosome GO:0036010 p=6.7E−03 n=2 fg=0.08 bg=0.01
response to steroid hormone GO:0048545 p=9.9E−03 n=4 fg=0.15 bg=0.03
positive regulation of ATP−dependent act... GO:0032781 p=1.2E−02 n=2 fg=0.08 bg=0.01
purine ribonucleoside monophosphate bios... GO:0009168 p=1.2E−02 n=2 fg=0.08 bg=0.01
purine nucleoside monophosphate biosynth... GO:0009127 p=1.2E−02 n=2 fg=0.08 bg=0.01
DNA topological change GO:0006265 p=1.4E−02 n=1 fg=0.04 bg=0.00
protein localization to actin cytoskelet... GO:1903119 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of protein localization to ac... GO:1904370 p=1.4E−02 n=1 fg=0.04 bg=0.00
positive regulation of protein localizat... GO:1904372 p=1.4E−02 n=1 fg=0.04 bg=0.00
response to kainic acid GO:1904373 p=1.4E−02 n=1 fg=0.04 bg=0.00
positive regulation of ARF protein signa... GO:0032014 p=1.4E−02 n=1 fg=0.04 bg=0.00
fructose 2,6−bisphosphate metabolic proc... GO:0006003 p=1.4E−02 n=1 fg=0.04 bg=0.00
positive regulation of endosome to plasm... GO:1905751 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of endosome to plasma membran... GO:1905749 p=1.4E−02 n=1 fg=0.04 bg=0.00
ubiquitin−dependent SMAD protein catabol... GO:0030579 p=1.4E−02 n=1 fg=0.04 bg=0.00
nuclear speck organization GO:0035063 p=1.4E−02 n=1 fg=0.04 bg=0.00
leucine metabolic process GO:0006551 p=1.4E−02 n=1 fg=0.04 bg=0.00
regulation of 1−phosphatidyl−1D−myo−inos... GO:1902646 p=1.4E−02 n=1 fg=0.04 bg=0.00
negative regulation of 1−phosphatidyl−1D... GO:1902647 p=1.4E−02 n=1 fg=0.04 bg=0.00
leucine biosynthetic process GO:0009098 p=1.4E−02 n=1 fg=0.04 bg=0.00
valine biosynthetic process GO:0009099 p=1.4E−02 n=1 fg=0.04 bg=0.00
1−phosphatidyl−1D−myo−inositol 4,5−bisph... GO:1902633 p=1.4E−02 n=1 fg=0.04 bg=0.00
1−phosphatidyl−1D−myo−inositol 4,5−bisph... GO:1902635 p=1.4E−02 n=1 fg=0.04 bg=0.00
protein localization to actin cortical p... GO:0044379 p=1.4E−02 n=1 fg=0.04 bg=0.00
valine metabolic process GO:0006573 p=1.4E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=26/80 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032364001.2
fraction genes in fg and expected valu
phospholipid binding GO:0005543 p=2.9E−03 n=5 fg=0.20 bg=0.04
anion binding GO:0043168 p=8.7E−03 n=8 fg=0.32 bg=0.13
cell adhesion molecule binding GO:0050839 p=9.6E−03 n=3 fg=0.12 bg=0.02
branched−chain−amino−acid transaminase a... GO:0004084 p=1.6E−02 n=1 fg=0.04 bg=0.00
neuropilin binding GO:0038191 p=1.6E−02 n=1 fg=0.04 bg=0.00
Roundabout binding GO:0048495 p=1.6E−02 n=1 fg=0.04 bg=0.00
phosphofructokinase activity GO:0008443 p=1.6E−02 n=1 fg=0.04 bg=0.00
fructose−2,6−bisphosphate 2−phosphatase ... GO:0004331 p=1.6E−02 n=1 fg=0.04 bg=0.00
BH4 domain binding GO:0051435 p=1.6E−02 n=1 fg=0.04 bg=0.00
sugar−phosphatase activity GO:0050308 p=1.6E−02 n=1 fg=0.04 bg=0.00
ankyrin repeat binding GO:0071532 p=1.6E−02 n=1 fg=0.04 bg=0.00
carbohydrate phosphatase activity GO:0019203 p=1.6E−02 n=1 fg=0.04 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=1.6E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol−4,5−bisphosphate bi... GO:0005546 p=2.5E−02 n=2 fg=0.08 bg=0.01
proton transmembrane transporter activit... GO:0015078 p=2.8E−02 n=2 fg=0.08 bg=0.01
vinculin binding GO:0017166 p=3.1E−02 n=1 fg=0.04 bg=0.00
phosphatidylinositol−3,5−bisphosphate bi... GO:0080025 p=3.1E−02 n=1 fg=0.04 bg=0.00
fructose−6−phosphate binding GO:0070095 p=3.1E−02 n=1 fg=0.04 bg=0.00
GPI anchor binding GO:0034235 p=3.1E−02 n=1 fg=0.04 bg=0.00
translation elongation factor activity GO:0003746 p=3.1E−02 n=1 fg=0.04 bg=0.00
ISG15 transferase activity GO:0042296 p=3.1E−02 n=1 fg=0.04 bg=0.00
enzyme regulator activity GO:0030234 p=3.3E−02 n=6 fg=0.24 bg=0.10
phosphatidylinositol binding GO:0035091 p=3.3E−02 n=3 fg=0.12 bg=0.03
phosphatidylinositol bisphosphate bindin... GO:1902936 p=3.8E−02 n=2 fg=0.08 bg=0.01
syntaxin binding GO:0019905 p=3.8E−02 n=2 fg=0.08 bg=0.01
nucleoside−triphosphatase regulator acti... GO:0060589 p=4.1E−02 n=4 fg=0.16 bg=0.05
carbohydrate derivative binding GO:0097367 p=4.3E−02 n=5 fg=0.20 bg=0.08
I−SMAD binding GO:0070411 p=4.6E−02 n=1 fg=0.04 bg=0.00
glycolipid binding GO:0051861 p=4.6E−02 n=1 fg=0.04 bg=0.00
protein folding chaperone GO:0044183 p=4.6E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=25/80 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032364001.2
fraction genes in fg and expected valu
stress fiber GO:0001725 p=7.2E−03 n=2 fg=0.07 bg=0.00
recycling endosome membrane GO:0055038 p=7.2E−03 n=2 fg=0.07 bg=0.00
intrinsic component of synaptic vesicle ... GO:0098563 p=1.3E−02 n=2 fg=0.07 bg=0.01
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=1.5E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of dendritic spine plas... GO:1990780 p=1.5E−02 n=1 fg=0.04 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=1.5E−02 n=1 fg=0.04 bg=0.00
ACF complex GO:0016590 p=1.5E−02 n=1 fg=0.04 bg=0.00
CHRAC GO:0008623 p=1.5E−02 n=1 fg=0.04 bg=0.00
dendritic spine neck GO:0044326 p=1.5E−02 n=1 fg=0.04 bg=0.00
dendritic spine head GO:0044327 p=1.5E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of plasma membrane GO:0009898 p=2.3E−02 n=3 fg=0.11 bg=0.02
ruffle GO:0001726 p=2.8E−02 n=2 fg=0.07 bg=0.01
RSF complex GO:0031213 p=3.0E−02 n=1 fg=0.04 bg=0.00
chaperonin−containing T−complex GO:0005832 p=3.0E−02 n=1 fg=0.04 bg=0.00
NURF complex GO:0016589 p=3.0E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of membrane GO:0098562 p=3.1E−02 n=3 fg=0.11 bg=0.03
synaptic vesicle membrane GO:0030672 p=3.1E−02 n=2 fg=0.07 bg=0.01
exocytic vesicle membrane GO:0099501 p=3.5E−02 n=2 fg=0.07 bg=0.01
extracellular region GO:0005576 p=3.5E−02 n=5 fg=0.19 bg=0.07
exon−exon junction complex GO:0035145 p=4.4E−02 n=1 fg=0.04 bg=0.00
growth cone lamellipodium GO:1990761 p=4.4E−02 n=1 fg=0.04 bg=0.00
dendritic spine membrane GO:0032591 p=4.4E−02 n=1 fg=0.04 bg=0.00
endoplasmic reticulum exit site GO:0070971 p=4.4E−02 n=1 fg=0.04 bg=0.00
respiratory chain complex IV GO:0045277 p=4.4E−02 n=1 fg=0.04 bg=0.00
mitochondria−associated endoplasmic reti... GO:0044233 p=4.4E−02 n=1 fg=0.04 bg=0.00
mitochondrial respiratory chain complex ... GO:0005751 p=4.4E−02 n=1 fg=0.04 bg=0.00
ISWI−type complex GO:0031010 p=4.4E−02 n=1 fg=0.04 bg=0.00
chaperone complex GO:0101031 p=4.4E−02 n=1 fg=0.04 bg=0.00
podosome GO:0002102 p=4.4E−02 n=1 fg=0.04 bg=0.00
cytoplasmic side of apical plasma membra... GO:0098592 p=5.8E−02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=27/80 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction