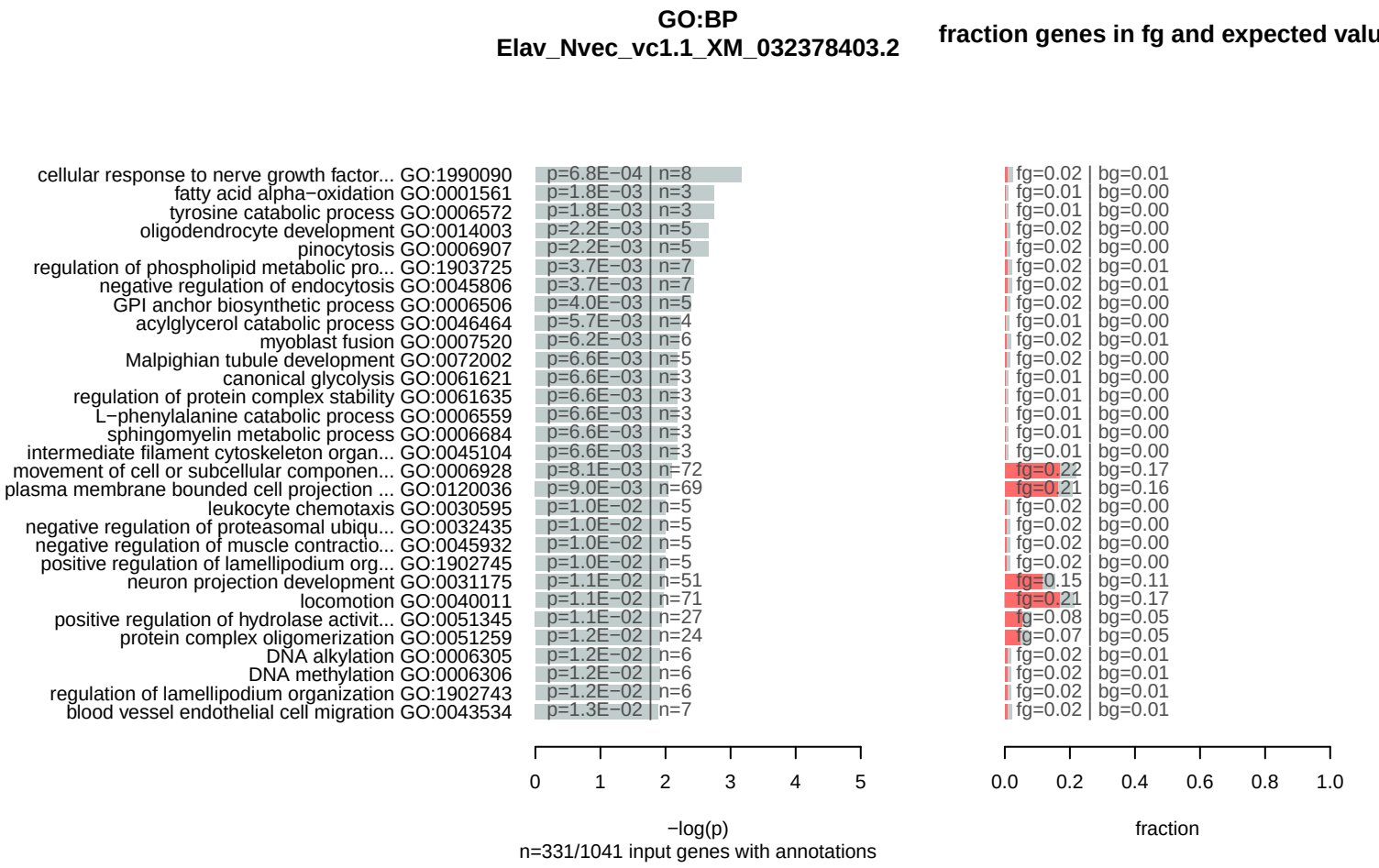
GO:BP
Elav_Nvec_vc1.1_XM_032378403.2
fraction genes in fg and expected valu
cellular response to nerve growth factor... GO:1990090 p=6.8E−04 n=8 fg=0.02 bg=0.01
fatty acid alpha−oxidation GO:0001561 p=1.8E−03 n=3 fg=0.01 bg=0.00
tyrosine catabolic process GO:0006572 p=1.8E−03 n=3 fg=0.01 bg=0.00
oligodendrocyte development GO:0014003 p=2.2E−03 n=5 fg=0.02 bg=0.00
pinocytosis GO:0006907 p=2.2E−03 n=5 fg=0.02 bg=0.00
regulation of phospholipid metabolic pro... GO:1903725 p=3.7E−03 n=7 fg=0.02 bg=0.01
negative regulation of endocytosis GO:0045806 p=3.7E−03 n=7 fg=0.02 bg=0.01
GPI anchor biosynthetic process GO:0006506 p=4.0E−03 n=5 fg=0.02 bg=0.00
acylglycerol catabolic process GO:0046464 p=5.7E−03 n=4 fg=0.01 bg=0.00
myoblast fusion GO:0007520 p=6.2E−03 n=6 fg=0.02 bg=0.01
Malpighian tubule development GO:0072002 p=6.6E−03 n=5 fg=0.02 bg=0.00
canonical glycolysis GO:0061621 p=6.6E−03 n=3 fg=0.01 bg=0.00
regulation of protein complex stability GO:0061635 p=6.6E−03 n=3 fg=0.01 bg=0.00
L−phenylalanine catabolic process GO:0006559 p=6.6E−03 n=3 fg=0.01 bg=0.00
sphingomyelin metabolic process GO:0006684 p=6.6E−03 n=3 fg=0.01 bg=0.00
intermediate filament cytoskeleton organ... GO:0045104 p=6.6E−03 n=3 fg=0.01 bg=0.00
movement of cell or subcellular componen... GO:0006928 p=8.1E−03 n=72 fg=0.22 bg=0.17
plasma membrane bounded cell projection ... GO:0120036 p=9.0E−03 n=69 fg=0.21 bg=0.16
leukocyte chemotaxis GO:0030595 p=1.0E−02 n=5 fg=0.02 bg=0.00
negative regulation of proteasomal ubiqu... GO:0032435 p=1.0E−02 n=5 fg=0.02 bg=0.00
negative regulation of muscle contractio... GO:0045932 p=1.0E−02 n=5 fg=0.02 bg=0.00
positive regulation of lamellipodium org... GO:1902745 p=1.0E−02 n=5 fg=0.02 bg=0.00
neuron projection development GO:0031175 p=1.1E−02 n=51 fg=0.15 bg=0.11
locomotion GO:0040011 p=1.1E−02 n=71 fg=0.21 bg=0.17
positive regulation of hydrolase activit... GO:0051345 p=1.1E−02 n=27 fg=0.08 bg=0.05
protein complex oligomerization GO:0051259 p=1.2E−02 n=24 fg=0.07 bg=0.05
DNA alkylation GO:0006305 p=1.2E−02 n=6 fg=0.02 bg=0.01
DNA methylation GO:0006306 p=1.2E−02 n=6 fg=0.02 bg=0.01
regulation of lamellipodium organization GO:1902743 p=1.2E−02 n=6 fg=0.02 bg=0.01
blood vessel endothelial cell migration GO:0043534 p=1.3E−02 n=7 fg=0.02 bg=0.01
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n=331/1041 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032378403.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=2.1E−03 n=3 fg=0.01 bg=0.00
WW domain binding GO:0050699 p=7.4E−03 n=3 fg=0.01 bg=0.00
translation initiation factor activity GO:0003743 p=1.1E−02 n=6 fg=0.02 bg=0.01
ion channel inhibitor activity GO:0008200 p=1.2E−02 n=5 fg=0.02 bg=0.01
phospholipid binding GO:0005543 p=1.3E−02 n=19 fg=0.06 bg=0.04
ATP−dependent protein binding GO:0043008 p=1.6E−02 n=2 fg=0.01 bg=0.00
gamma−butyrobetaine dioxygenase activity GO:0008336 p=1.6E−02 n=2 fg=0.01 bg=0.00
nucleobase transmembrane transporter act... GO:0015205 p=1.6E−02 n=2 fg=0.01 bg=0.00
calcium channel inhibitor activity GO:0019855 p=1.6E−02 n=2 fg=0.01 bg=0.00
1,4−alpha−oligoglucan phosphorylase acti... GO:0004645 p=1.6E−02 n=2 fg=0.01 bg=0.00
N4−(beta−N−acetylglucosaminyl)−L−asparag... GO:0003948 p=1.6E−02 n=2 fg=0.01 bg=0.00
purine nucleobase transmembrane transpor... GO:0005345 p=1.6E−02 n=2 fg=0.01 bg=0.00
K48−linked polyubiquitin modification−de... GO:0036435 p=1.6E−02 n=2 fg=0.01 bg=0.00
channel inhibitor activity GO:0016248 p=1.8E−02 n=5 fg=0.02 bg=0.01
translation regulator activity GO:0045182 p=2.7E−02 n=9 fg=0.03 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=3.0E−02 n=8 fg=0.03 bg=0.01
GTPase regulator activity GO:0030695 p=3.0E−02 n=19 fg=0.06 bg=0.04
BH domain binding GO:0051400 p=3.0E−02 n=3 fg=0.01 bg=0.00
proteoglycan binding GO:0043394 p=3.0E−02 n=3 fg=0.01 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.0E−02 n=3 fg=0.01 bg=0.00
GTPase binding GO:0051020 p=3.2E−02 n=24 fg=0.08 bg=0.05
molecular function inhibitor activity GO:0140678 p=3.3E−02 n=5 fg=0.02 bg=0.01
nucleoside−triphosphatase regulator acti... GO:0060589 p=3.4E−02 n=21 fg=0.07 bg=0.05
phosphatidylinositol phosphate phosphata... GO:0052866 p=4.1E−02 n=4 fg=0.01 bg=0.00
triglyceride lipase activity GO:0004806 p=4.4E−02 n=2 fg=0.01 bg=0.00
tRNA−specific ribonuclease activity GO:0004549 p=4.4E−02 n=2 fg=0.01 bg=0.00
Arp2/3 complex binding GO:0071933 p=4.4E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on singl... GO:0016702 p=4.4E−02 n=2 fg=0.01 bg=0.00
acylglycerol lipase activity GO:0047372 p=4.4E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=4.4E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=302/1041 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032378403.2
fraction genes in fg and expected valu
caveola GO:0005901 p=1.6E−04 n=10 fg=0.03 bg=0.01
axon cytoplasm GO:1904115 p=2.6E−03 n=4 fg=0.01 bg=0.00
lipid droplet GO:0005811 p=5.4E−03 n=8 fg=0.02 bg=0.01
nuclear membrane GO:0031965 p=5.6E−03 n=15 fg=0.05 bg=0.02
cytoplasmic dynein complex GO:0005868 p=9.9E−03 n=4 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0005851 p=1.5E−02 n=3 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.5E−02 n=2 fg=0.01 bg=0.00
cytoplasmic vesicle GO:0031410 p=2.0E−02 n=64 fg=0.20 bg=0.15
intracellular vesicle GO:0097708 p=2.0E−02 n=64 fg=0.20 bg=0.15
cis−Golgi network GO:0005801 p=2.1E−02 n=6 fg=0.02 bg=0.01
vesicle GO:0031982 p=2.1E−02 n=67 fg=0.20 bg=0.16
primary lysosome GO:0005766 p=2.3E−02 n=8 fg=0.02 bg=0.01
azurophil granule GO:0042582 p=2.3E−02 n=8 fg=0.02 bg=0.01
lysosome GO:0005764 p=2.5E−02 n=22 fg=0.07 bg=0.04
endonuclease complex GO:1905348 p=2.7E−02 n=3 fg=0.01 bg=0.00
endoribonuclease complex GO:1902555 p=2.7E−02 n=3 fg=0.01 bg=0.00
plasma membrane proton−transporting V−ty... GO:0033181 p=2.7E−02 n=3 fg=0.01 bg=0.00
cell leading edge GO:0031252 p=3.6E−02 n=18 fg=0.06 bg=0.04
vacuole GO:0005773 p=3.6E−02 n=27 fg=0.08 bg=0.06
actin−based cell projection GO:0098858 p=3.8E−02 n=11 fg=0.03 bg=0.02
lytic vacuole GO:0000323 p=3.9E−02 n=22 fg=0.07 bg=0.05
plasma membrane protein complex GO:0098797 p=3.9E−02 n=15 fg=0.05 bg=0.03
EARP complex GO:1990745 p=4.0E−02 n=2 fg=0.01 bg=0.00
vacuolar proton−transporting V−type ATPa... GO:0000221 p=4.0E−02 n=2 fg=0.01 bg=0.00
GARP complex GO:0000938 p=4.0E−02 n=2 fg=0.01 bg=0.00
multimeric ribonuclease P complex GO:0030681 p=4.0E−02 n=2 fg=0.01 bg=0.00
caspase complex GO:0008303 p=4.0E−02 n=2 fg=0.01 bg=0.00
ribonuclease P complex GO:0030677 p=4.0E−02 n=2 fg=0.01 bg=0.00
GPI−anchor transamidase complex GO:0042765 p=4.0E−02 n=2 fg=0.01 bg=0.00
proton−transporting V−type ATPase, V1 do... GO:0033180 p=4.0E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=327/1041 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction