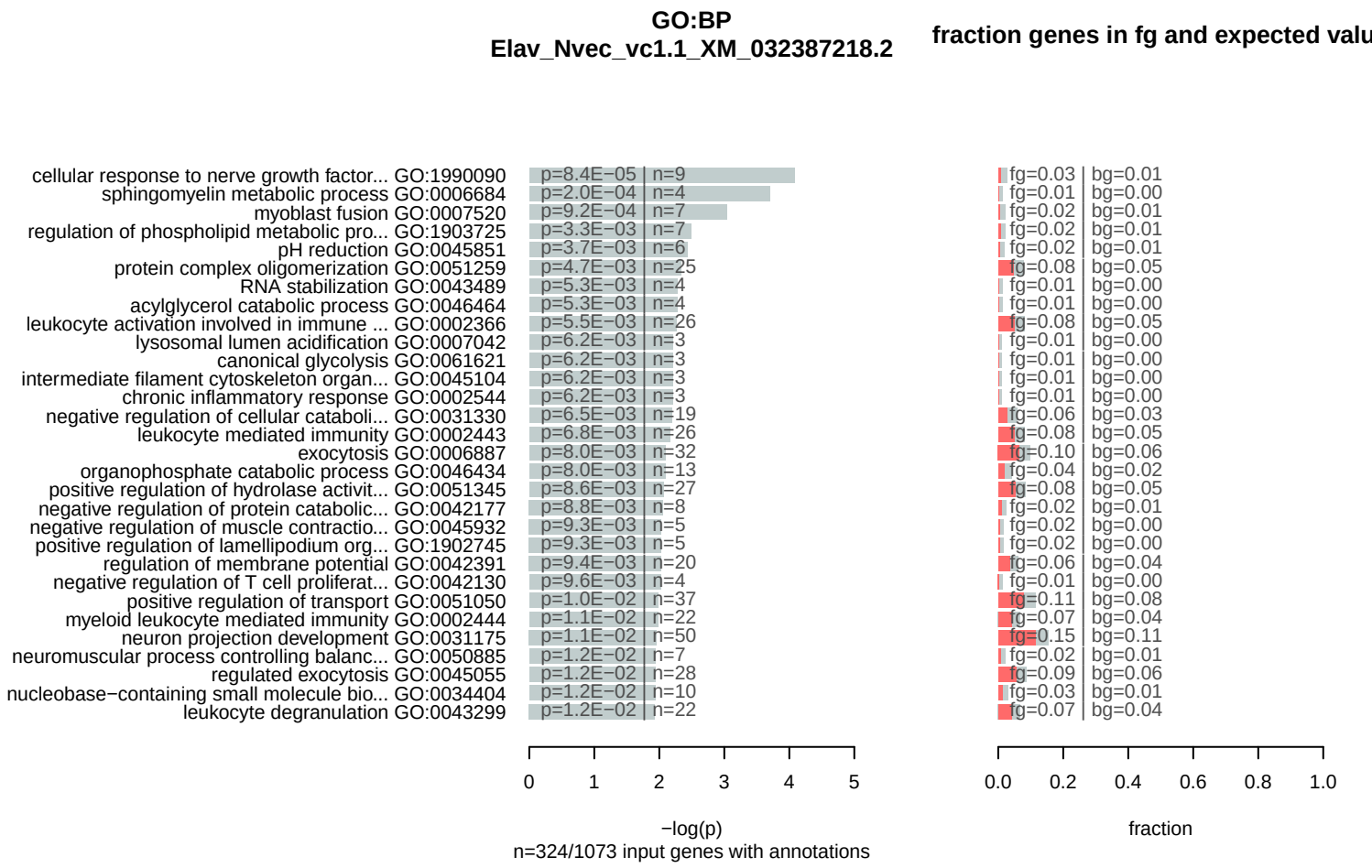
GO:BP
Elav_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
cellular response to nerve growth factor... GO:1990090 p=8.4E−05 n=9 fg=0.03 bg=0.01
sphingomyelin metabolic process GO:0006684 p=2.0E−04 n=4 fg=0.01 bg=0.00
myoblast fusion GO:0007520 p=9.2E−04 n=7 fg=0.02 bg=0.01
regulation of phospholipid metabolic pro... GO:1903725 p=3.3E−03 n=7 fg=0.02 bg=0.01
pH reduction GO:0045851 p=3.7E−03 n=6 fg=0.02 bg=0.01
protein complex oligomerization GO:0051259 p=4.7E−03 n=25 fg=0.08 bg=0.05
RNA stabilization GO:0043489 p=5.3E−03 n=4 fg=0.01 bg=0.00
acylglycerol catabolic process GO:0046464 p=5.3E−03 n=4 fg=0.01 bg=0.00
leukocyte activation involved in immune ... GO:0002366 p=5.5E−03 n=26 fg=0.08 bg=0.05
lysosomal lumen acidification GO:0007042 p=6.2E−03 n=3 fg=0.01 bg=0.00
canonical glycolysis GO:0061621 p=6.2E−03 n=3 fg=0.01 bg=0.00
intermediate filament cytoskeleton organ... GO:0045104 p=6.2E−03 n=3 fg=0.01 bg=0.00
chronic inflammatory response GO:0002544 p=6.2E−03 n=3 fg=0.01 bg=0.00
negative regulation of cellular catabolí... GO:0031330 p=6.5E−03 n=19 fg=0.06 bg=0.03
leukocyte mediated immunity GO:0002443 p=6.8E−03 n=26 fg=0.08 bg=0.05
exocytosis GO:0006887 p=8.0E−03 n=32 fg=0.10 bg=0.06
organophosphate catabolic process GO:0046434 p=8.0E−03 n=13 fg=0.04 bg=0.02
positive regulation of hydrolase activit... GO:0051345 p=8.6E−03 n=27 fg=0.08 bg=0.05
negative regulation of protein catabolic... GO:0042177 p=8.8E−03 n=8 fg=0.02 bg=0.01
negative regulation of muscle contractio... GO:0045932 p=9.3E−03 n=5 fg=0.02 bg=0.00
positive regulation of lamellipodium org... GO:1902745 p=9.3E−03 n=5 fg=0.02 bg=0.00
regulation of membrane potential GO:0042391 p=9.4E−03 n=20 fg=0.06 bg=0.04
negative regulation of T cell proliferat... GO:0042130 p=9.6E−03 n=4 fg=0.01 bg=0.00
positive regulation of transport GO:0051050 p=1.0E−02 n=37 fg=0.11 bg=0.08
myeloid leukocyte mediated immunity GO:0002444 p=1.1E−02 n=22 fg=0.07 bg=0.04
neuron projection development GO:0031175 p=1.1E−02 n=50 fg=0.15 bg=0.11
neuromuscular process controlling balanc... GO:0050885 p=1.2E−02 n=7 fg=0.02 bg=0.01
regulated exocytosis GO:0045055 p=1.2E−02 n=28 fg=0.09 bg=0.06
nucleobase−containing small molecule bio... GO:0034404 p=1.2E−02 n=10 fg=0.03 bg=0.01
leukocyte degranulation GO:0043299 p=1.2E−02 n=22 fg=0.07 bg=0.04
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n=324/1073 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
miRNA binding GO:0035198 p=2.0E−03 n=3 fg=0.01 bg=0.00
GTPase binding GO:0051020 p=2.0E−03 n=28 fg=0.09 bg=0.05
GTPase regulator activity GO:0030695 p=2.9E−03 n=22 fg=0.07 bg=0.04
WW domain binding GO:0050699 p=7.2E−03 n=3 fg=0.01 bg=0.00
small GTPase binding GO:0031267 p=1.0E−02 n=22 fg=0.07 bg=0.04
ATP−dependent protein binding GO:0043008 p=1.6E−02 n=2 fg=0.01 bg=0.00
nucleotide diphosphatase activity GO:0004551 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
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.6E−02 n=2 fg=0.01 bg=0.00
bis(5'−nucleosyl)−tetraphosphatase activ... GO:0008796 p=1.6E−02 n=2 fg=0.01 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.6E−02 n=2 fg=0.01 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 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
bis(5'−nucleosyl)−tetraphosphatase (asym... GO:0004081 p=1.6E−02 n=2 fg=0.01 bg=0.00
sphingomyelin phosphodiesterase activity GO:0004767 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
K48−linked polyubiquitin modification−de... GO:0036435 p=1.6E−02 n=2 fg=0.01 bg=0.00
double−stranded RNA binding GO:0003725 p=1.7E−02 n=5 fg=0.02 bg=0.01
phospholipid binding GO:0005543 p=2.2E−02 n=18 fg=0.06 bg=0.04
guanyl−nucleotide exchange factor activi... GO:0005085 p=2.3E−02 n=10 fg=0.03 bg=0.02
GTPase activator activity GO:0005096 p=2.8E−02 n=12 fg=0.04 bg=0.02
BH domain binding GO:0051400 p=2.9E−02 n=3 fg=0.01 bg=0.00
dynein intermediate chain binding GO:0045505 p=2.9E−02 n=3 fg=0.01 bg=0.00
phosphoric diester hydrolase activity GO:0008081 p=3.1E−02 n=6 fg=0.02 bg=0.01
triglyceride lipase activity GO:0004806 p=4.3E−02 n=2 fg=0.01 bg=0.00
Arp2/3 complex binding GO:0071933 p=4.3E−02 n=2 fg=0.01 bg=0.00
acylglycerol lipase activity GO:0047372 p=4.3E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=4.3E−02 n=2 fg=0.01 bg=0.00
intermediate filament binding GO:0019215 p=4.3E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=298/1073 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032387218.2
fraction genes in fg and expected valu
caveola GO:0005901 p=1.2E−04 n=10 fg=0.03 bg=0.01
axon cytoplasm GO:1904115 p=2.3E−03 n=4 fg=0.01 bg=0.00
lysosome GO:0005764 p=4.6E−03 n=24 fg=0.08 bg=0.04
presynaptic active zone membrane GO:0048787 p=4.9E−03 n=4 fg=0.01 bg=0.00
cell cortex GO:0005938 p=5.1E−03 n=20 fg=0.06 bg=0.03
secretory vesicle GO:0099503 p=7.6E−03 n=36 fg=0.11 bg=0.07
vacuolar membrane GO:0005774 p=7.6E−03 n=16 fg=0.05 bg=0.03
cytoplasmic dynein complex GO:0005868 p=8.9E−03 n=4 fg=0.01 bg=0.00
tertiary granule membrane GO:0070821 p=8.9E−03 n=4 fg=0.01 bg=0.00
cell−substrate junction GO:0030055 p=9.8E−03 n=8 fg=0.03 bg=0.01
cytoplasmic region GO:0099568 p=1.3E−02 n=28 fg=0.09 bg=0.05
cytoplasmic side of apical plasma membra... GO:0098592 p=1.3E−02 n=3 fg=0.01 bg=0.00
Gtr1−Gtr2 GTPase complex GO:1990131 p=1.4E−02 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.4E−02 n=2 fg=0.01 bg=0.00
cytoplasmic vesicle GO:0031410 p=1.9E−02 n=72 fg=0.23 bg=0.15
intracellular vesicle GO:0097708 p=1.9E−02 n=72 fg=0.23 bg=0.15
vesicle GO:0031982 p=2.0E−02 n=75 fg=0.24 bg=0.16
lysosomal membrane GO:0005765 p=2.0E−02 n=11 fg=0.03 bg=0.02
synaptic vesicle GO:0008021 p=2.6E−02 n=12 fg=0.04 bg=0.02
apical part of cell GO:0045177 p=2.6E−02 n=23 fg=0.07 bg=0.05
phagocytic vesicle GO:0045335 p=2.6E−02 n=7 fg=0.02 bg=0.01
microvillus GO:0005902 p=2.9E−02 n=6 fg=0.02 bg=0.01
secretory granule GO:0030141 p=3.0E−02 n=27 fg=0.09 bg=0.05
actin−based cell projection GO:0098858 p=3.1E−02 n=11 fg=0.03 bg=0.02
recycling endosome membrane GO:0055038 p=3.1E−02 n=4 fg=0.01 bg=0.00
nuclear speck GO:0016607 p=3.2E−02 n=16 fg=0.05 bg=0.03
EARP complex GO:1990745 p=3.8E−02 n=2 fg=0.01 bg=0.00
GARP complex GO:0000938 p=3.8E−02 n=2 fg=0.01 bg=0.00
caspase complex GO:0008303 p=3.8E−02 n=2 fg=0.01 bg=0.00
extrinsic component of endoplasmic retic... GO:0042406 p=3.8E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=317/1073 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction