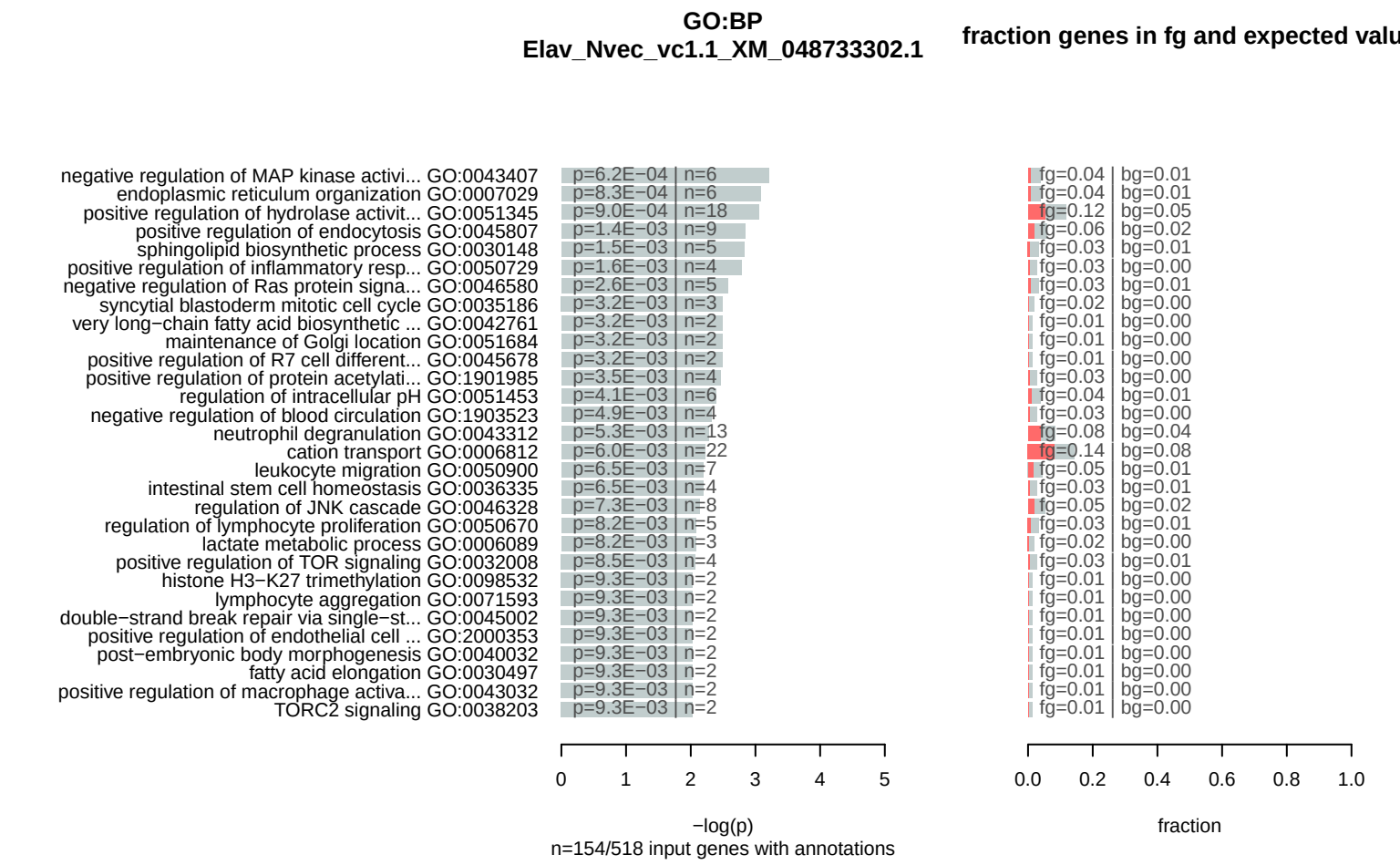
GO:BP
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
negative regulation of MAP kinase activi... GO:0043407 p=6.2E−04 n=6 fg=0.04 bg=0.01
endoplasmic reticulum organization GO:0007029 p=8.3E−04 n=6 fg=0.04 bg=0.01
positive regulation of hydrolase activit... GO:0051345 p=9.0E−04 n=18 fg=0.12 bg=0.05
positive regulation of endocytosis GO:0045807 p=1.4E−03 n=9 fg=0.06 bg=0.02
sphingolipid biosynthetic process GO:0030148 p=1.5E−03 n=5 fg=0.03 bg=0.01
positive regulation of inflammatory resp... GO:0050729 p=1.6E−03 n=4 fg=0.03 bg=0.00
negative regulation of Ras protein signa... GO:0046580 p=2.6E−03 n=5 fg=0.03 bg=0.01
syncytial blastoderm mitotic cell cycle GO:0035186 p=3.2E−03 n=3 fg=0.02 bg=0.00
very long−chain fatty acid biosynthetic ... GO:0042761 p=3.2E−03 n=2 fg=0.01 bg=0.00
maintenance of Golgi location GO:0051684 p=3.2E−03 n=2 fg=0.01 bg=0.00
positive regulation of R7 cell different... GO:0045678 p=3.2E−03 n=2 fg=0.01 bg=0.00
positive regulation of protein acetylati... GO:1901985 p=3.5E−03 n=4 fg=0.03 bg=0.00
regulation of intracellular pH GO:0051453 p=4.1E−03 n=6 fg=0.04 bg=0.01
negative regulation of blood circulation GO:1903523 p=4.9E−03 n=4 fg=0.03 bg=0.00
neutrophil degranulation GO:0043312 p=5.3E−03 n=13 fg=0.08 bg=0.04
cation transport GO:0006812 p=6.0E−03 n=22 fg=0.14 bg=0.08
leukocyte migration GO:0050900 p=6.5E−03 n=7 fg=0.05 bg=0.01
intestinal stem cell homeostasis GO:0036335 p=6.5E−03 n=4 fg=0.03 bg=0.01
regulation of JNK cascade GO:0046328 p=7.3E−03 n=8 fg=0.05 bg=0.02
regulation of lymphocyte proliferation GO:0050670 p=8.2E−03 n=5 fg=0.03 bg=0.01
lactate metabolic process GO:0006089 p=8.2E−03 n=3 fg=0.02 bg=0.00
positive regulation of TOR signaling GO:0032008 p=8.5E−03 n=4 fg=0.03 bg=0.01
histone H3−K27 trimethylation GO:0098532 p=9.3E−03 n=2 fg=0.01 bg=0.00
lymphocyte aggregation GO:0071593 p=9.3E−03 n=2 fg=0.01 bg=0.00
double−strand break repair via single−st... GO:0045002 p=9.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of endothelial cell ... GO:2000353 p=9.3E−03 n=2 fg=0.01 bg=0.00
post−embryonic body morphogenesis GO:0040032 p=9.3E−03 n=2 fg=0.01 bg=0.00
fatty acid elongation GO:0030497 p=9.3E−03 n=2 fg=0.01 bg=0.00
positive regulation of macrophage activa... GO:0043032 p=9.3E−03 n=2 fg=0.01 bg=0.00
TORC2 signaling GO:0038203 p=9.3E−03 n=2 fg=0.01 bg=0.00
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n=154/518 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
bicarbonate transmembrane transporter ac... GO:0015106 p=2.9E−03 n=3 fg=0.02 bg=0.00
myosin V binding GO:0031489 p=3.0E−03 n=2 fg=0.02 bg=0.00
active ion transmembrane transporter act... GO:0022853 p=5.3E−03 n=8 fg=0.06 bg=0.02
phosphotyrosine residue binding GO:0001784 p=7.5E−03 n=3 fg=0.02 bg=0.00
nucleotide−sugar transmembrane transport... GO:0005338 p=1.7E−02 n=2 fg=0.02 bg=0.00
nucleobase−containing compound transmemb... GO:0015932 p=2.5E−02 n=3 fg=0.02 bg=0.01
inorganic cation transmembrane transport... GO:0022890 p=2.5E−02 n=12 fg=0.09 bg=0.05
proton transmembrane transporter activit... GO:0015078 p=2.6E−02 n=4 fg=0.03 bg=0.01
SNAP receptor activity GO:0005484 p=3.1E−02 n=3 fg=0.02 bg=0.01
inorganic anion transmembrane transporte... GO:0015103 p=3.3E−02 n=5 fg=0.04 bg=0.01
cation transmembrane transporter activit... GO:0008324 p=3.4E−02 n=12 fg=0.09 bg=0.05
pyrophosphate hydrolysis−driven proton t... GO:0009678 p=3.9E−02 n=2 fg=0.02 bg=0.00
ATPase activity, coupled to transmembran... GO:0044769 p=3.9E−02 n=2 fg=0.02 bg=0.00
proton−transporting ATPase activity, rot... GO:0046961 p=3.9E−02 n=2 fg=0.02 bg=0.00
ATPase−coupled cation transmembrane tran... GO:0019829 p=4.6E−02 n=3 fg=0.02 bg=0.01
signaling receptor activity GO:0038023 p=4.9E−02 n=10 fg=0.08 bg=0.04
molecular transducer activity GO:0060089 p=5.2E−02 n=10 fg=0.08 bg=0.04
calcium−release channel activity GO:0015278 p=5.3E−02 n=2 fg=0.02 bg=0.00
peptidase activator activity GO:0016504 p=5.3E−02 n=2 fg=0.02 bg=0.00
inorganic anion exchanger activity GO:0005452 p=5.3E−02 n=2 fg=0.02 bg=0.00
anion:anion antiporter activity GO:0015301 p=5.3E−02 n=2 fg=0.02 bg=0.00
solute:anion antiporter activity GO:0140323 p=5.3E−02 n=2 fg=0.02 bg=0.00
ATPase−coupled ion transmembrane transpo... GO:0042625 p=5.4E−02 n=3 fg=0.02 bg=0.01
receptor tyrosine kinase−like orphan rec... GO:0005115 p=5.5E−02 n=1 fg=0.01 bg=0.00
sphingolipid transfer activity GO:0120016 p=5.5E−02 n=1 fg=0.01 bg=0.00
ceramide transfer activity GO:0120017 p=5.5E−02 n=1 fg=0.01 bg=0.00
leucine binding GO:0070728 p=5.5E−02 n=1 fg=0.01 bg=0.00
neuregulin binding GO:0038132 p=5.5E−02 n=1 fg=0.01 bg=0.00
transmembrane receptor protein phosphata... GO:0019198 p=5.5E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=5.5E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=131/518 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048733302.1
fraction genes in fg and expected valu
perinuclear region of cytoplasm GO:0048471 p=4.5E−04 n=21 fg=0.14 bg=0.06
cytoplasmic vesicle membrane GO:0030659 p=1.4E−03 n=22 fg=0.15 bg=0.07
collagen and cuticulin−based cuticle ext... GO:0060102 p=3.1E−03 n=2 fg=0.01 bg=0.00
secretory granule GO:0030141 p=4.2E−03 n=16 fg=0.11 bg=0.05
preribosome, small subunit precursor GO:0030688 p=5.0E−03 n=3 fg=0.02 bg=0.00
plasma membrane GO:0005886 p=5.1E−03 n=49 fg=0.33 bg=0.23
endolysosome membrane GO:0036020 p=8.9E−03 n=2 fg=0.01 bg=0.00
endocytic vesicle GO:0030139 p=9.9E−03 n=8 fg=0.05 bg=0.02
synaptonemal structure GO:0099086 p=1.1E−02 n=3 fg=0.02 bg=0.00
synaptonemal complex GO:0000795 p=1.1E−02 n=3 fg=0.02 bg=0.00
clathrin−coated vesicle GO:0030136 p=1.1E−02 n=6 fg=0.04 bg=0.01
secretory granule membrane GO:0030667 p=2.1E−02 n=7 fg=0.05 bg=0.02
bounding membrane of organelle GO:0098588 p=2.5E−02 n=30 fg=0.20 bg=0.13
late endosome membrane GO:0031902 p=2.6E−02 n=4 fg=0.03 bg=0.01
RNA polymerase II, core complex GO:0005665 p=2.7E−02 n=2 fg=0.01 bg=0.00
membrane protein complex GO:0098796 p=3.1E−02 n=18 fg=0.12 bg=0.08
vacuolar membrane GO:0005774 p=3.3E−02 n=10 fg=0.07 bg=0.03
lysosomal membrane GO:0005765 p=3.4E−02 n=8 fg=0.05 bg=0.02
clathrin−coated endocytic vesicle membra... GO:0030669 p=4.0E−02 n=2 fg=0.01 bg=0.00
aster GO:0005818 p=4.0E−02 n=2 fg=0.01 bg=0.00
filopodium membrane GO:0031527 p=4.0E−02 n=2 fg=0.01 bg=0.00
endocytic vesicle membrane GO:0030666 p=4.1E−02 n=4 fg=0.03 bg=0.01
lipid droplet GO:0005811 p=4.1E−02 n=4 fg=0.03 bg=0.01
tertiary granule GO:0070820 p=4.7E−02 n=4 fg=0.03 bg=0.01
condensed nuclear chromosome GO:0000794 p=4.7E−02 n=4 fg=0.03 bg=0.01
phagocytic vesicle GO:0045335 p=5.3E−02 n=4 fg=0.03 bg=0.01
lytic vacuole membrane GO:0098852 p=5.3E−02 n=8 fg=0.05 bg=0.02
vacuolar proton−transporting V−type ATPa... GO:0016471 p=5.4E−02 n=2 fg=0.01 bg=0.00
intrinsic component of organelle membran... GO:0031300 p=5.4E−02 n=10 fg=0.07 bg=0.04
SNARE complex GO:0031201 p=5.5E−02 n=3 fg=0.02 bg=0.01
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−log(p)
n=150/518 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction