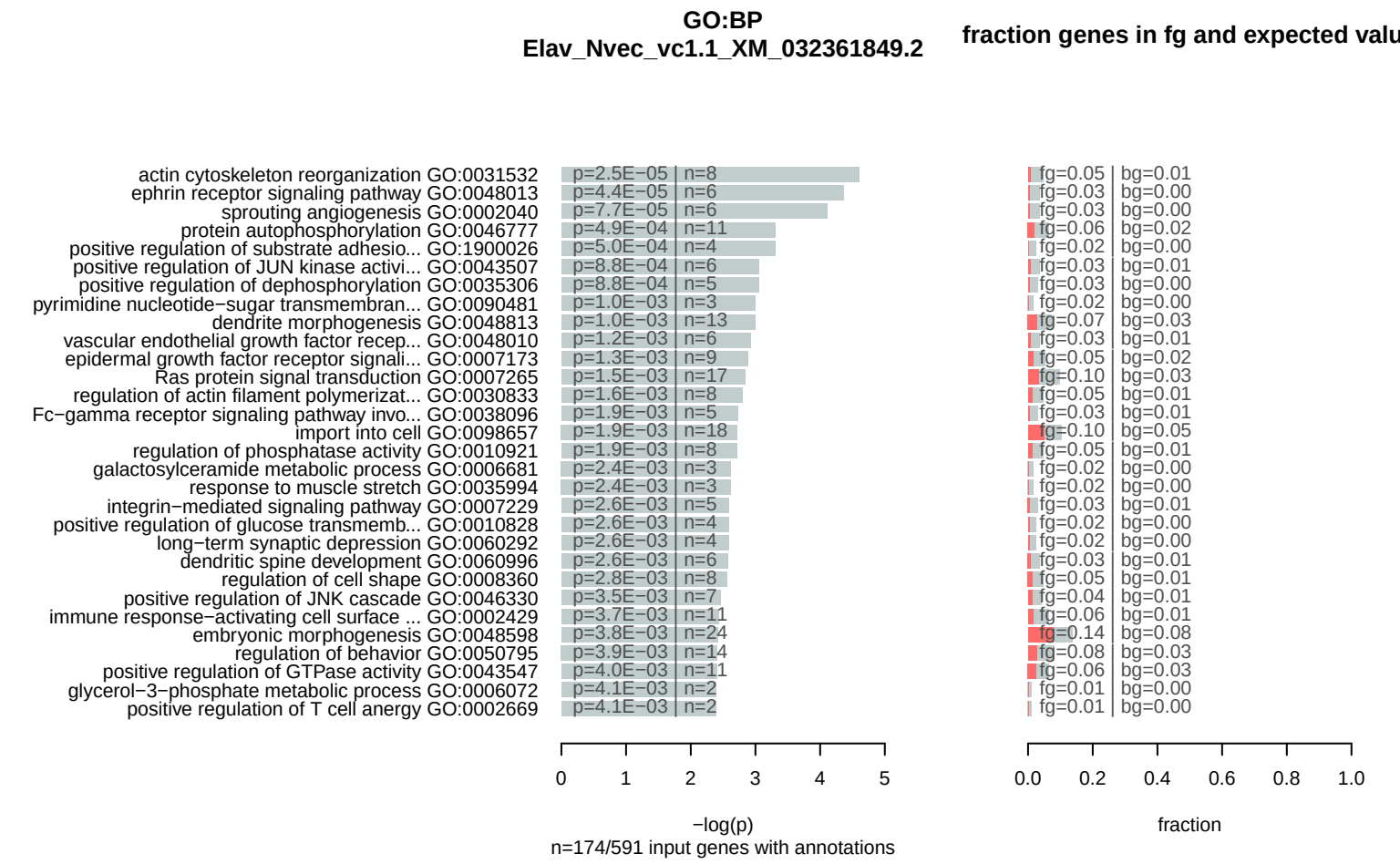
GO:BP
Elav_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
actin cytoskeleton reorganization GO:0031532 p=2.5E−05 n=8 fg=0.05 bg=0.01
ephrin receptor signaling pathway GO:0048013 p=4.4E−05 n=6 fg=0.03 bg=0.00
sprouting angiogenesis GO:0002040 p=7.7E−05 n=6 fg=0.03 bg=0.00
protein autophosphorylation GO:0046777 p=4.9E−04 n=11 fg=0.06 bg=0.02
positive regulation of substrate adhesio... GO:1900026 p=5.0E−04 n=4 fg=0.02 bg=0.00
positive regulation of JUN kinase activi... GO:0043507 p=8.8E−04 n=6 fg=0.03 bg=0.01
positive regulation of dephosphorylation GO:0035306 p=8.8E−04 n=5 fg=0.03 bg=0.00
pyrimidine nucleotide−sugar transmembran... GO:0090481 p=1.0E−03 n=3 fg=0.02 bg=0.00
dendrite morphogenesis GO:0048813 p=1.0E−03 n=13 fg=0.07 bg=0.03
vascular endothelial growth factor recep... GO:0048010 p=1.2E−03 n=6 fg=0.03 bg=0.01
epidermal growth factor receptor signali... GO:0007173 p=1.3E−03 n=9 fg=0.05 bg=0.02
Ras protein signal transduction GO:0007265 p=1.5E−03 n=17 fg=0.10 bg=0.03
regulation of actin filament polymerizat... GO:0030833 p=1.6E−03 n=8 fg=0.05 bg=0.01
Fc−gamma receptor signaling pathway invo... GO:0038096 p=1.9E−03 n=5 fg=0.03 bg=0.01
import into cell GO:0098657 p=1.9E−03 n=18 fg=0.10 bg=0.05
regulation of phosphatase activity GO:0010921 p=1.9E−03 n=8 fg=0.05 bg=0.01
galactosylceramide metabolic process GO:0006681 p=2.4E−03 n=3 fg=0.02 bg=0.00
response to muscle stretch GO:0035994 p=2.4E−03 n=3 fg=0.02 bg=0.00
integrin−mediated signaling pathway GO:0007229 p=2.6E−03 n=5 fg=0.03 bg=0.01
positive regulation of glucose transmemb... GO:0010828 p=2.6E−03 n=4 fg=0.02 bg=0.00
long−term synaptic depression GO:0060292 p=2.6E−03 n=4 fg=0.02 bg=0.00
dendritic spine development GO:0060996 p=2.6E−03 n=6 fg=0.03 bg=0.01
regulation of cell shape GO:0008360 p=2.8E−03 n=8 fg=0.05 bg=0.01
positive regulation of JNK cascade GO:0046330 p=3.5E−03 n=7 fg=0.04 bg=0.01
immune response−activating cell surface ... GO:0002429 p=3.7E−03 n=11 fg=0.06 bg=0.01
embryonic morphogenesis GO:0048598 p=3.8E−03 n=24 fg=0.14 bg=0.08
regulation of behavior GO:0050795 p=3.9E−03 n=14 fg=0.08 bg=0.03
positive regulation of GTPase activity GO:0043547 p=4.0E−03 n=11 fg=0.06 bg=0.03
glycerol−3−phosphate metabolic process GO:0006072 p=4.1E−03 n=2 fg=0.01 bg=0.00
positive regulation of T cell anergy GO:0002669 p=4.1E−03 n=2 fg=0.01 bg=0.00
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−log(p)
n=174/591 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
signaling receptor complex adaptor activ... GO:0030159 p=2.0E−03 n=4 fg=0.02 bg=0.00
protein kinase activity GO:0004672 p=3.5E−03 n=17 fg=0.11 bg=0.05
small GTPase binding GO:0031267 p=4.4E−03 n=15 fg=0.09 bg=0.04
GTPase regulator activity GO:0030695 p=4.5E−03 n=14 fg=0.09 bg=0.04
glycerol−3−phosphate dehydrogenase [NAD+... GO:0004367 p=4.6E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate dehydrogenase (quin... GO:0004368 p=4.6E−03 n=2 fg=0.01 bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183 p=4.6E−03 n=2 fg=0.01 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=4.6E−03 n=2 fg=0.01 bg=0.00
phosphatase regulator activity GO:0019208 p=5.7E−03 n=5 fg=0.03 bg=0.01
enzyme activator activity GO:0008047 p=6.3E−03 n=15 fg=0.09 bg=0.05
actin filament binding GO:0051015 p=6.6E−03 n=6 fg=0.04 bg=0.01
amide transmembrane transporter activity GO:0042887 p=6.6E−03 n=4 fg=0.02 bg=0.01
protein tyrosine kinase activity GO:0004713 p=1.1E−02 n=5 fg=0.03 bg=0.01
vinculin binding GO:0017166 p=1.3E−02 n=2 fg=0.01 bg=0.00
pre−mRNA 3'−splice site binding GO:0030628 p=1.3E−02 n=2 fg=0.01 bg=0.00
pyrimidine nucleotide−sugar transmembran... GO:0015165 p=1.3E−02 n=2 fg=0.01 bg=0.00
miRNA binding GO:0035198 p=1.3E−02 n=2 fg=0.01 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=1.3E−02 n=2 fg=0.01 bg=0.00
protein phosphatase regulator activity GO:0019888 p=1.5E−02 n=4 fg=0.02 bg=0.01
guanyl−nucleotide exchange factor activi... GO:0005085 p=1.6E−02 n=7 fg=0.04 bg=0.02
sodium ion transmembrane transporter act... GO:0015081 p=1.7E−02 n=5 fg=0.03 bg=0.01
signaling adaptor activity GO:0035591 p=1.8E−02 n=7 fg=0.04 bg=0.01
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DNA secondary structure binding GO:0000217 p=1.9E−02 n=3 fg=0.02 bg=0.00
pre−mRNA binding GO:0036002 p=1.9E−02 n=3 fg=0.02 bg=0.00
GTPase activator activity GO:0005096 p=2.5E−02 n=8 fg=0.05 bg=0.02
nucleotide−sugar transmembrane transport... GO:0005338 p=2.5E−02 n=2 fg=0.01 bg=0.00
minor groove of adenine−thymine−rich DNA... GO:0003680 p=2.5E−02 n=2 fg=0.01 bg=0.00
translation repressor activity GO:0030371 p=2.5E−02 n=2 fg=0.01 bg=0.00
regulatory RNA binding GO:0061980 p=2.5E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=161/591 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032361849.2
fraction genes in fg and expected valu
stress fiber GO:0001725 p=1.8E−04 n=5 fg=0.03 bg=0.00
cell cortex GO:0005938 p=1.8E−03 n=14 fg=0.08 bg=0.03
podosome GO:0002102 p=2.2E−03 n=3 fg=0.02 bg=0.00
focal adhesion GO:0005925 p=2.3E−03 n=6 fg=0.04 bg=0.01
cell leading edge GO:0031252 p=2.8E−03 n=16 fg=0.09 bg=0.04
cytoplasmic ribonucleoprotein granule GO:0036464 p=3.2E−03 n=10 fg=0.06 bg=0.02
Arp2/3 protein complex GO:0005885 p=3.9E−03 n=2 fg=0.01 bg=0.00
U2AF complex GO:0089701 p=3.9E−03 n=2 fg=0.01 bg=0.00
glycerol−3−phosphate dehydrogenase compl... GO:0009331 p=3.9E−03 n=2 fg=0.01 bg=0.00
peripheral region of growth cone GO:0090725 p=3.9E−03 n=2 fg=0.01 bg=0.00
axolemma GO:0030673 p=7.1E−03 n=3 fg=0.02 bg=0.00
axon terminus GO:0043679 p=8.2E−03 n=9 fg=0.05 bg=0.02
cleavage furrow GO:0032154 p=9.2E−03 n=4 fg=0.02 bg=0.01
growth cone GO:0030426 p=9.6E−03 n=10 fg=0.06 bg=0.02
extrinsic component of plasma membrane GO:0019897 p=1.1E−02 n=6 fg=0.04 bg=0.01
septin ring GO:0005940 p=1.1E−02 n=2 fg=0.01 bg=0.00
sperm annulus GO:0097227 p=1.1E−02 n=2 fg=0.01 bg=0.00
septin complex GO:0031105 p=1.1E−02 n=2 fg=0.01 bg=0.00
type Ib terminal bouton GO:0061176 p=1.1E−02 n=2 fg=0.01 bg=0.00
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lamellipodium GO:0030027 p=1.6E−02 n=8 fg=0.05 bg=0.02
cytoplasmic region GO:0099568 p=2.2E−02 n=15 fg=0.09 bg=0.05
Golgi apparatus subcompartment GO:0098791 p=2.6E−02 n=18 fg=0.11 bg=0.07
adherens junction GO:0005912 p=2.7E−02 n=8 fg=0.05 bg=0.02
cell body GO:0044297 p=3.1E−02 n=18 fg=0.11 bg=0.07
ruffle GO:0001726 p=3.2E−02 n=5 fg=0.03 bg=0.01
protein phosphatase type 2A complex GO:0000159 p=3.5E−02 n=2 fg=0.01 bg=0.00
septin cytoskeleton GO:0032156 p=3.5E−02 n=2 fg=0.01 bg=0.00
M band GO:0031430 p=3.5E−02 n=3 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=170/591 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction