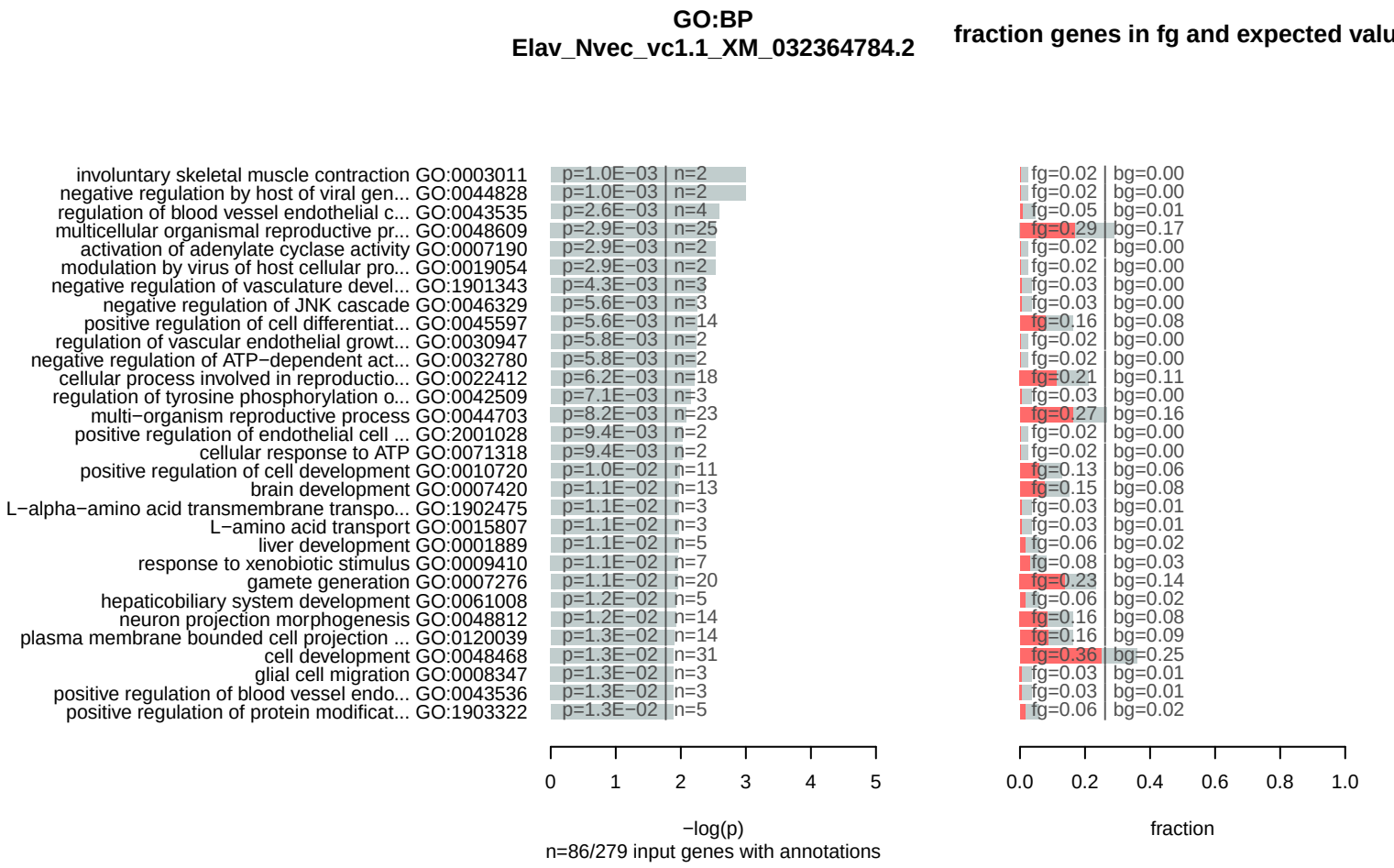
GO:BP
Elav_Nvec_vc1.1_XM_032364784.2
fraction genes in fg and expected valu
involuntary skeletal muscle contraction GO:0003011 p=1.0E−03 n=2 fg=0.02 bg=0.00
negative regulation by host of viral gen... GO:0044828 p=1.0E−03 n=2 fg=0.02 bg=0.00
regulation of blood vessel endothelial c... GO:0043535 p=2.6E−03 n=4 fg=0.05 bg=0.01
multicellular organismal reproductive pr... GO:0048609 p=2.9E−03 n=25 fg=0.29 bg=0.17
activation of adenylate cyclase activity GO:0007190 p=2.9E−03 n=2 fg=0.02 bg=0.00
modulation by virus of host cellular pro... GO:0019054 p=2.9E−03 n=2 fg=0.02 bg=0.00
negative regulation of vasculature devel... GO:1901343 p=4.3E−03 n=3 fg=0.03 bg=0.00
negative regulation of JNK cascade GO:0046329 p=5.6E−03 n=3 fg=0.03 bg=0.00
positive regulation of cell differentiat... GO:0045597 p=5.6E−03 n=14 fg=0.16 bg=0.08
regulation of vascular endothelial growt... GO:0030947 p=5.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of ATP−dependent act... GO:0032780 p=5.8E−03 n=2 fg=0.02 bg=0.00
cellular process involved in reproductio... GO:0022412 p=6.2E−03 n=18 fg=0.21 bg=0.11
regulation of tyrosine phosphorylation o... GO:0042509 p=7.1E−03 n=3 fg=0.03 bg=0.00
multi−organism reproductive process GO:0044703 p=8.2E−03 n=23 fg=0.27 bg=0.16
positive regulation of endothelial cell ... GO:2001028 p=9.4E−03 n=2 fg=0.02 bg=0.00
cellular response to ATP GO:0071318 p=9.4E−03 n=2 fg=0.02 bg=0.00
positive regulation of cell development GO:0010720 p=1.0E−02 n=11 fg=0.13 bg=0.06
brain development GO:0007420 p=1.1E−02 n=13 fg=0.15 bg=0.08
L−alpha−amino acid transmembrane transpo... GO:1902475 p=1.1E−02 n=3 fg=0.03 bg=0.01
L−amino acid transport GO:0015807 p=1.1E−02 n=3 fg=0.03 bg=0.01
liver development GO:0001889 p=1.1E−02 n=5 fg=0.06 bg=0.02
response to xenobiotic stimulus GO:0009410 p=1.1E−02 n=7 fg=0.08 bg=0.03
gamete generation GO:0007276 p=1.1E−02 n=20 fg=0.23 bg=0.14
hepaticobiliary system development GO:0061008 p=1.2E−02 n=5 fg=0.06 bg=0.02
neuron projection morphogenesis GO:0048812 p=1.2E−02 n=14 fg=0.16 bg=0.08
plasma membrane bounded cell projection ... GO:0120039 p=1.3E−02 n=14 fg=0.16 bg=0.09
cell development GO:0048468 p=1.3E−02 n=31 fg=0.36 bg=0.25
glial cell migration GO:0008347 p=1.3E−02 n=3 fg=0.03 bg=0.01
positive regulation of blood vessel endo... GO:0043536 p=1.3E−02 n=3 fg=0.03 bg=0.01
positive regulation of protein modificat... GO:1903322 p=1.3E−02 n=5 fg=0.06 bg=0.02
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n=86/279 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032364784.2
fraction genes in fg and expected valu
receptor−receptor interaction GO:0090722 p=6.6E−03 n=2 fg=0.02 bg=0.00
L−amino acid transmembrane transporter a... GO:0015179 p=1.1E−02 n=3 fg=0.04 bg=0.01
amino acid transmembrane transporter act... GO:0015171 p=1.3E−02 n=3 fg=0.04 bg=0.01
cell adhesion molecule binding GO:0050839 p=1.6E−02 n=5 fg=0.06 bg=0.02
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.6E−02 n=2 fg=0.02 bg=0.00
peptide antigen binding GO:0042605 p=1.6E−02 n=2 fg=0.02 bg=0.00
L−cystine transmembrane transporter acti... GO:0015184 p=1.6E−02 n=2 fg=0.02 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=2.2E−02 n=2 fg=0.02 bg=0.00
sulfur amino acid transmembrane transpor... GO:0000099 p=2.2E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=2.2E−02 n=2 fg=0.02 bg=0.00
nuclear receptor activity GO:0004879 p=2.2E−02 n=2 fg=0.02 bg=0.00
adenylate cyclase binding GO:0008179 p=2.2E−02 n=2 fg=0.02 bg=0.00
phospholipase binding GO:0043274 p=2.2E−02 n=2 fg=0.02 bg=0.00
ligand−activated transcription factor ac... GO:0098531 p=2.2E−02 n=2 fg=0.02 bg=0.00
acetyltransferase activity GO:0016407 p=2.2E−02 n=3 fg=0.04 bg=0.01
lysophosphatidic acid acyltransferase ac... GO:0042171 p=2.8E−02 n=2 fg=0.02 bg=0.00
modified amino acid transmembrane transp... GO:0072349 p=2.8E−02 n=2 fg=0.02 bg=0.00
G−protein alpha−subunit binding GO:0001965 p=2.8E−02 n=2 fg=0.02 bg=0.00
lysophospholipid acyltransferase activit... GO:0071617 p=2.8E−02 n=2 fg=0.02 bg=0.00
cullin family protein binding GO:0097602 p=2.8E−02 n=2 fg=0.02 bg=0.00
integrin binding GO:0005178 p=2.9E−02 n=3 fg=0.04 bg=0.01
translation regulator activity GO:0045182 p=3.0E−02 n=4 fg=0.05 bg=0.01
acyltransferase activity, transferring g... GO:0016747 p=3.3E−02 n=4 fg=0.05 bg=0.02
dopamine binding GO:0035240 p=3.4E−02 n=1 fg=0.01 bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.4E−02 n=1 fg=0.01 bg=0.00
icosanoid binding GO:0050542 p=3.4E−02 n=1 fg=0.01 bg=0.00
icosatetraenoic acid binding GO:0050543 p=3.4E−02 n=1 fg=0.01 bg=0.00
arachidonic acid binding GO:0050544 p=3.4E−02 n=1 fg=0.01 bg=0.00
arginine kinase activity GO:0004054 p=3.4E−02 n=1 fg=0.01 bg=0.00
F−box domain binding GO:1990444 p=3.4E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=81/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032364784.2
fraction genes in fg and expected valu
Lewy body GO:0097413 p=1.0E−03 n=2 fg=0.02 bg=0.00
Cul4A−RING E3 ubiquitin ligase complex GO:0031464 p=5.9E−03 n=2 fg=0.02 bg=0.00
polysome GO:0005844 p=6.5E−03 n=4 fg=0.05 bg=0.01
U2−type prespliceosome GO:0071004 p=9.6E−03 n=2 fg=0.02 bg=0.00
lysosome GO:0005764 p=1.3E−02 n=9 fg=0.10 bg=0.04
azurophil granule GO:0042582 p=1.5E−02 n=4 fg=0.05 bg=0.01
primary lysosome GO:0005766 p=1.5E−02 n=4 fg=0.05 bg=0.01
lytic vacuole GO:0000323 p=1.7E−02 n=9 fg=0.10 bg=0.05
lysosomal membrane GO:0005765 p=1.8E−02 n=5 fg=0.06 bg=0.02
cortical actin cytoskeleton GO:0030864 p=2.5E−02 n=3 fg=0.03 bg=0.01
specific granule membrane GO:0035579 p=2.5E−02 n=3 fg=0.03 bg=0.01
lytic vacuole membrane GO:0098852 p=2.6E−02 n=5 fg=0.06 bg=0.02
membrane raft GO:0045121 p=2.8E−02 n=6 fg=0.07 bg=0.03
membrane microdomain GO:0098857 p=2.8E−02 n=6 fg=0.07 bg=0.03
azurophil granule membrane GO:0035577 p=3.2E−02 n=2 fg=0.02 bg=0.00
eukaryotic 43S preinitiation complex GO:0016282 p=3.2E−02 n=1 fg=0.01 bg=0.00
sperm mitochondrial sheath GO:0097226 p=3.2E−02 n=1 fg=0.01 bg=0.00
MCM8−MCM9 complex GO:0097362 p=3.2E−02 n=1 fg=0.01 bg=0.00
NatA complex GO:0031415 p=3.2E−02 n=1 fg=0.01 bg=0.00
cortical cytoskeleton GO:0030863 p=3.6E−02 n=3 fg=0.03 bg=0.01
organelle envelope GO:0031967 p=3.6E−02 n=15 fg=0.17 bg=0.11
envelope GO:0031975 p=3.6E−02 n=15 fg=0.17 bg=0.11
polysomal ribosome GO:0042788 p=3.9E−02 n=2 fg=0.02 bg=0.00
terminal bouton GO:0043195 p=4.1E−02 n=4 fg=0.05 bg=0.02
organellar large ribosomal subunit GO:0000315 p=4.7E−02 n=2 fg=0.02 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=4.7E−02 n=2 fg=0.02 bg=0.00
Cajal body GO:0015030 p=4.7E−02 n=2 fg=0.02 bg=0.00
cell−substrate junction GO:0030055 p=5.4E−02 n=3 fg=0.03 bg=0.01
sarcolemma GO:0042383 p=5.4E−02 n=3 fg=0.03 bg=0.01
RNA polymerase III transcription regulat... GO:0090576 p=6.3E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=87/279 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction