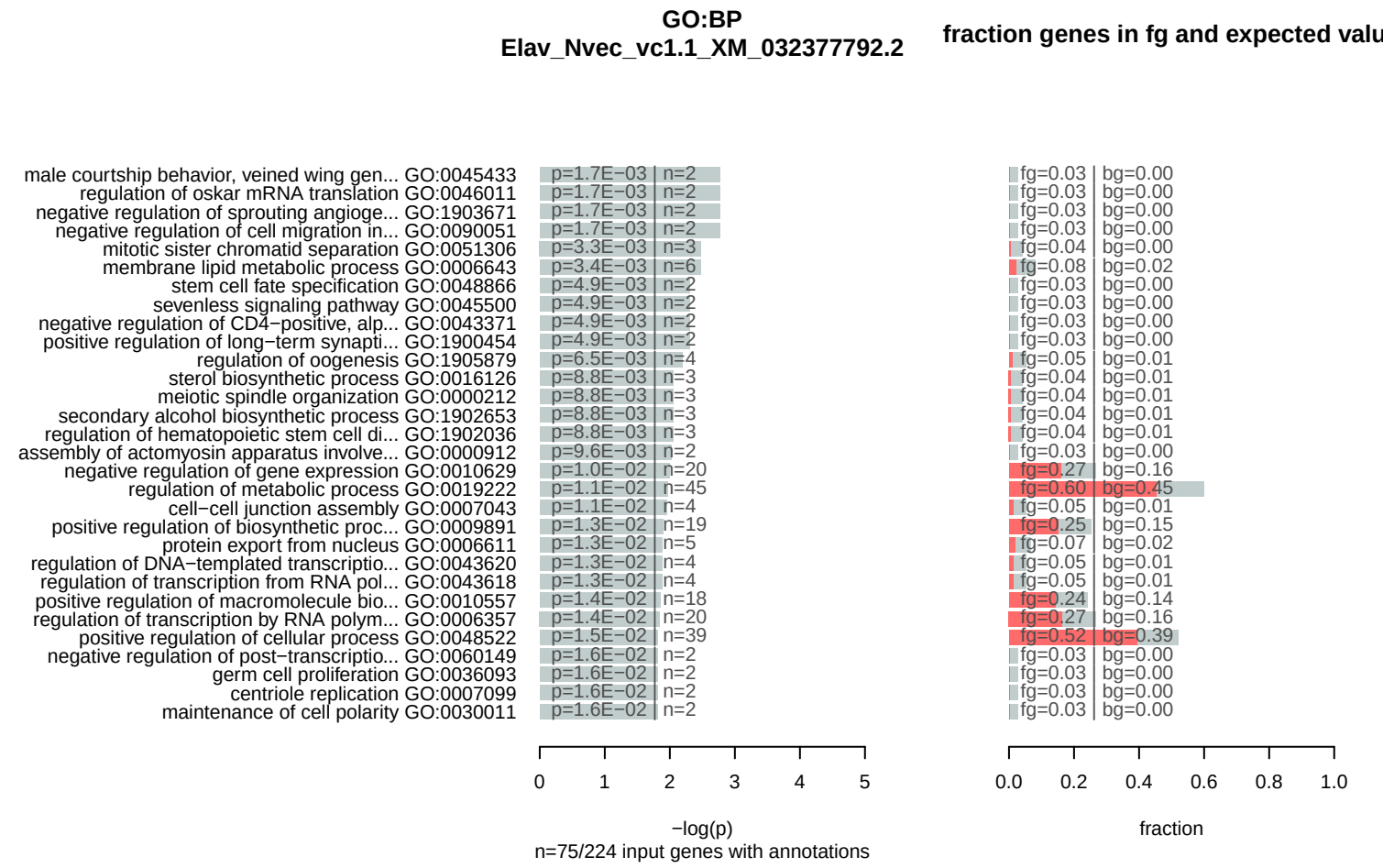
GO:BP
Elav_Nvec_vc1.1_XM_032377792.2
fraction genes in fg and expected valu
male courtship behavior, veined wing gen... GO:0045433 p=1.7E−03 n=2 fg=0.03 bg=0.00
regulation of oskar mRNA translation GO:0046011 p=1.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of sprouting angioge... GO:1903671 p=1.7E−03 n=2 fg=0.03 bg=0.00
negative regulation of cell migration in... GO:0090051 p=1.7E−03 n=2 fg=0.03 bg=0.00
mitotic sister chromatid separation GO:0051306 p=3.3E−03 n=3 fg=0.04 bg=0.00
membrane lipid metabolic process GO:0006643 p=3.4E−03 n=6 fg=0.08 bg=0.02
stem cell fate specification GO:0048866 p=4.9E−03 n=2 fg=0.03 bg=0.00
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negative regulation of CD4−positive, alp... GO:0043371 p=4.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of long−term synapti... GO:1900454 p=4.9E−03 n=2 fg=0.03 bg=0.00
regulation of oogenesis GO:1905879 p=6.5E−03 n=4 fg=0.05 bg=0.01
sterol biosynthetic process GO:0016126 p=8.8E−03 n=3 fg=0.04 bg=0.01
meiotic spindle organization GO:0000212 p=8.8E−03 n=3 fg=0.04 bg=0.01
secondary alcohol biosynthetic process GO:1902653 p=8.8E−03 n=3 fg=0.04 bg=0.01
regulation of hematopoietic stem cell di... GO:1902036 p=8.8E−03 n=3 fg=0.04 bg=0.01
assembly of actomyosin apparatus involve... GO:0000912 p=9.6E−03 n=2 fg=0.03 bg=0.00
negative regulation of gene expression GO:0010629 p=1.0E−02 n=20 fg=0.27 bg=0.16
regulation of metabolic process GO:0019222 p=1.1E−02 n=45 fg=0.60 bg=0.45
cell−cell junction assembly GO:0007043 p=1.1E−02 n=4 fg=0.05 bg=0.01
positive regulation of biosynthetic proc... GO:0009891 p=1.3E−02 n=19 fg=0.25 bg=0.15
protein export from nucleus GO:0006611 p=1.3E−02 n=5 fg=0.07 bg=0.02
regulation of DNA−templated transcriptio... GO:0043620 p=1.3E−02 n=4 fg=0.05 bg=0.01
regulation of transcription from RNA pol... GO:0043618 p=1.3E−02 n=4 fg=0.05 bg=0.01
positive regulation of macromolecule bio... GO:0010557 p=1.4E−02 n=18 fg=0.24 bg=0.14
regulation of transcription by RNA polym... GO:0006357 p=1.4E−02 n=20 fg=0.27 bg=0.16
positive regulation of cellular process GO:0048522 p=1.5E−02 n=39 fg=0.52 bg=0.39
negative regulation of post−transcriptio... GO:0060149 p=1.6E−02 n=2 fg=0.03 bg=0.00
germ cell proliferation GO:0036093 p=1.6E−02 n=2 fg=0.03 bg=0.00
centriole replication GO:0007099 p=1.6E−02 n=2 fg=0.03 bg=0.00
maintenance of cell polarity GO:0030011 p=1.6E−02 n=2 fg=0.03 bg=0.00
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n=75/224 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
transcription corepressor activity GO:0003714 p=9.3E−03 n=5 fg=0.07 bg=0.02
DNA−binding transcription activator acti... GO:0001228 p=1.4E−02 n=7 fg=0.10 bg=0.04
DNA−binding transcription activator acti... GO:0001216 p=1.4E−02 n=7 fg=0.10 bg=0.04
DNA−binding transcription factor activit... GO:0000981 p=1.5E−02 n=10 fg=0.14 bg=0.07
structural constituent of nuclear pore GO:0017056 p=1.7E−02 n=2 fg=0.03 bg=0.00
cis−regulatory region sequence−specific ... GO:0000987 p=3.4E−02 n=6 fg=0.09 bg=0.04
RNA polymerase II cis−regulatory region ... GO:0000978 p=3.4E−02 n=6 fg=0.09 bg=0.04
spermine:oxygen oxidoreductase (spermidi... GO:0052901 p=4.3E−02 n=1 fg=0.01 bg=0.00
N1−acetylspermidine:oxygen oxidoreductas... GO:0052904 p=4.3E−02 n=1 fg=0.01 bg=0.00
large conductance calcium−activated pota... GO:0060072 p=4.3E−02 n=1 fg=0.01 bg=0.00
SMC family protein binding GO:0043221 p=4.3E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0016647 p=4.3E−02 n=1 fg=0.01 bg=0.00
proteinase activated receptor binding GO:0031871 p=4.3E−02 n=1 fg=0.01 bg=0.00
5'−3' DNA helicase activity GO:0043139 p=4.3E−02 n=1 fg=0.01 bg=0.00
polyamine oxidase activity GO:0046592 p=4.3E−02 n=1 fg=0.01 bg=0.00
CoA carboxylase activity GO:0016421 p=4.3E−02 n=1 fg=0.01 bg=0.00
farnesyltranstransferase activity GO:0004311 p=4.3E−02 n=1 fg=0.01 bg=0.00
protein farnesyltransferase activity GO:0004660 p=4.3E−02 n=1 fg=0.01 bg=0.00
7SK snRNA binding GO:0097322 p=4.3E−02 n=1 fg=0.01 bg=0.00
propionyl−CoA carboxylase activity GO:0004658 p=4.3E−02 n=1 fg=0.01 bg=0.00
DNA−binding transcription factor activit... GO:0003700 p=4.9E−02 n=10 fg=0.14 bg=0.08
transcription coregulator binding GO:0001221 p=5.5E−02 n=2 fg=0.03 bg=0.01
SH2 domain binding GO:0042169 p=5.5E−02 n=2 fg=0.03 bg=0.01
mRNA binding GO:0003729 p=5.7E−02 n=5 fg=0.07 bg=0.03
RNA helicase activity GO:0003724 p=6.7E−02 n=2 fg=0.03 bg=0.01
nucleoside−triphosphatase regulator acti... GO:0060589 p=7.0E−02 n=7 fg=0.10 bg=0.05
RNA binding GO:0003723 p=7.7E−02 n=10 fg=0.14 bg=0.09
enzyme regulator activity GO:0030234 p=7.8E−02 n=11 fg=0.16 bg=0.10
mRNA 3'−UTR binding GO:0003730 p=7.9E−02 n=2 fg=0.03 bg=0.01
ATPase regulator activity GO:0060590 p=7.9E−02 n=2 fg=0.03 bg=0.01
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−log(p)
n=69/224 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032377792.2
fraction genes in fg and expected valu
nuclear envelope GO:0005635 p=1.5E−03 n=9 fg=0.13 bg=0.04
endoplasmic reticulum exit site GO:0070971 p=4.4E−03 n=2 fg=0.03 bg=0.00
cytoplasmic ribonucleoprotein granule GO:0036464 p=6.4E−03 n=6 fg=0.08 bg=0.02
basolateral plasma membrane GO:0016323 p=8.9E−03 n=6 fg=0.08 bg=0.03
polysome GO:0005844 p=9.9E−03 n=3 fg=0.04 bg=0.01
germ plasm GO:0060293 p=1.3E−02 n=3 fg=0.04 bg=0.01
pole plasm GO:0045495 p=1.3E−02 n=3 fg=0.04 bg=0.01
nuclear membrane GO:0031965 p=1.3E−02 n=5 fg=0.07 bg=0.02
protein phosphatase type 2A complex GO:0000159 p=1.4E−02 n=2 fg=0.03 bg=0.00
magnesium−dependent protein serine/threo... GO:0005963 p=2.8E−02 n=2 fg=0.03 bg=0.00
nuclear speck GO:0016607 p=3.0E−02 n=6 fg=0.08 bg=0.03
fibrillar center GO:0001650 p=3.6E−02 n=3 fg=0.04 bg=0.01
nuclear pore inner ring GO:0044611 p=3.9E−02 n=1 fg=0.01 bg=0.00
apical cytoplasm GO:0090651 p=3.9E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=3.9E−02 n=1 fg=0.01 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=3.9E−02 n=1 fg=0.01 bg=0.00
RES complex GO:0070274 p=3.9E−02 n=1 fg=0.01 bg=0.00
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protein farnesyltransferase complex GO:0005965 p=3.9E−02 n=1 fg=0.01 bg=0.00
melanosome GO:0042470 p=4.6E−02 n=2 fg=0.03 bg=0.00
sex chromosome GO:0000803 p=4.6E−02 n=2 fg=0.03 bg=0.00
cytoplasmic stress granule GO:0010494 p=5.6E−02 n=2 fg=0.03 bg=0.01
nuclear pore GO:0005643 p=5.6E−02 n=2 fg=0.03 bg=0.01
pigment granule GO:0048770 p=5.6E−02 n=2 fg=0.03 bg=0.01
Golgi trans cisterna GO:0000138 p=6.6E−02 n=2 fg=0.03 bg=0.01
ribosome GO:0005840 p=7.2E−02 n=3 fg=0.04 bg=0.01
Barr body GO:0001740 p=7.7E−02 n=1 fg=0.01 bg=0.00
TRAMP complex GO:0031499 p=7.7E−02 n=1 fg=0.01 bg=0.00
meiotic spindle GO:0072687 p=7.7E−02 n=1 fg=0.01 bg=0.00
cytosolic region GO:0099522 p=7.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=71/224 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction