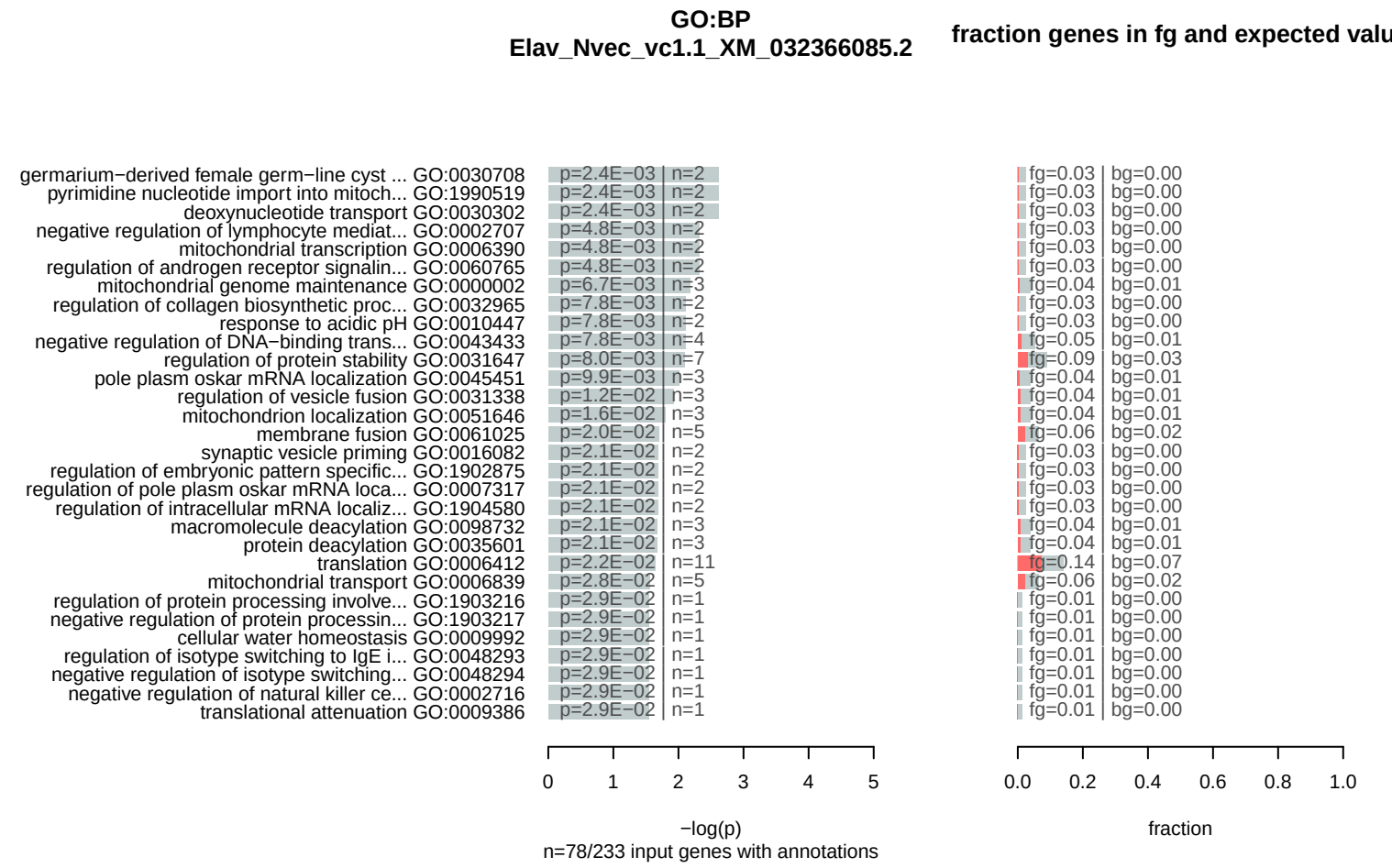
GO:BP
Elav_Nvec_vc1.1_XM_032366085.2
fraction genes in fg and expected valu
germarium−derived female germ−line cyst ... GO:0030708 p=2.4E−03 n=2 fg=0.03 bg=0.00
pyrimidine nucleotide import into mitoch... GO:1990519 p=2.4E−03 n=2 fg=0.03 bg=0.00
deoxynucleotide transport GO:0030302 p=2.4E−03 n=2 fg=0.03 bg=0.00
negative regulation of lymphocyte mediat... GO:0002707 p=4.8E−03 n=2 fg=0.03 bg=0.00
mitochondrial transcription GO:0006390 p=4.8E−03 n=2 fg=0.03 bg=0.00
regulation of androgen receptor signalin... GO:0060765 p=4.8E−03 n=2 fg=0.03 bg=0.00
mitochondrial genome maintenance GO:0000002 p=6.7E−03 n=3 fg=0.04 bg=0.01
regulation of collagen biosynthetic proc... GO:0032965 p=7.8E−03 n=2 fg=0.03 bg=0.00
response to acidic pH GO:0010447 p=7.8E−03 n=2 fg=0.03 bg=0.00
negative regulation of DNA−binding trans... GO:0043433 p=7.8E−03 n=4 fg=0.05 bg=0.01
regulation of protein stability GO:0031647 p=8.0E−03 n=7 fg=0.09 bg=0.03
pole plasm oskar mRNA localization GO:0045451 p=9.9E−03 n=3 fg=0.04 bg=0.01
regulation of vesicle fusion GO:0031338 p=1.2E−02 n=3 fg=0.04 bg=0.01
mitochondrion localization GO:0051646 p=1.6E−02 n=3 fg=0.04 bg=0.01
membrane fusion GO:0061025 p=2.0E−02 n=5 fg=0.06 bg=0.02
synaptic vesicle priming GO:0016082 p=2.1E−02 n=2 fg=0.03 bg=0.00
regulation of embryonic pattern specific... GO:1902875 p=2.1E−02 n=2 fg=0.03 bg=0.00
regulation of pole plasm oskar mRNA loca... GO:0007317 p=2.1E−02 n=2 fg=0.03 bg=0.00
regulation of intracellular mRNA localiz... GO:1904580 p=2.1E−02 n=2 fg=0.03 bg=0.00
macromolecule deacylation GO:0098732 p=2.1E−02 n=3 fg=0.04 bg=0.01
protein deacylation GO:0035601 p=2.1E−02 n=3 fg=0.04 bg=0.01
translation GO:0006412 p=2.2E−02 n=11 fg=0.14 bg=0.07
mitochondrial transport GO:0006839 p=2.8E−02 n=5 fg=0.06 bg=0.02
regulation of protein processing involve... GO:1903216 p=2.9E−02 n=1 fg=0.01 bg=0.00
negative regulation of protein processin... GO:1903217 p=2.9E−02 n=1 fg=0.01 bg=0.00
cellular water homeostasis GO:0009992 p=2.9E−02 n=1 fg=0.01 bg=0.00
regulation of isotype switching to IgE i... GO:0048293 p=2.9E−02 n=1 fg=0.01 bg=0.00
negative regulation of isotype switching... GO:0048294 p=2.9E−02 n=1 fg=0.01 bg=0.00
negative regulation of natural killer ce... GO:0002716 p=2.9E−02 n=1 fg=0.01 bg=0.00
translational attenuation GO:0009386 p=2.9E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=78/233 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_032366085.2
fraction genes in fg and expected valu
pyrimidine nucleotide transmembrane tran... GO:0015218 p=2.3E−03 n=2 fg=0.03 bg=0.00
cysteine−type endopeptidase inhibitor ac... GO:0004869 p=4.6E−03 n=2 fg=0.03 bg=0.00
opsin binding GO:0002046 p=2.8E−02 n=1 fg=0.01 bg=0.00
biotinidase activity GO:0047708 p=2.8E−02 n=1 fg=0.01 bg=0.00
mediator complex binding GO:0036033 p=2.8E−02 n=1 fg=0.01 bg=0.00
L−leucine transmembrane transporter acti... GO:0015190 p=2.8E−02 n=1 fg=0.01 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=2.8E−02 n=1 fg=0.01 bg=0.00
ankyrin repeat binding GO:0071532 p=2.8E−02 n=1 fg=0.01 bg=0.00
methionine transmembrane transporter act... GO:0043865 p=2.8E−02 n=1 fg=0.01 bg=0.00
muscle alpha−actinin binding GO:0051371 p=2.8E−02 n=1 fg=0.01 bg=0.00
L−asparagine transmembrane transporter a... GO:0015182 p=2.8E−02 n=1 fg=0.01 bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186 p=2.8E−02 n=1 fg=0.01 bg=0.00
HLH domain binding GO:0043398 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=2.8E−02 n=1 fg=0.01 bg=0.00
V2 vasopressin receptor binding GO:0031896 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.8E−02 n=1 fg=0.01 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=2.8E−02 n=1 fg=0.01 bg=0.00
inositol oxygenase activity GO:0050113 p=2.8E−02 n=1 fg=0.01 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=2.8E−02 n=1 fg=0.01 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=2.8E−02 n=1 fg=0.01 bg=0.00
plus−end directed microfilament motor ac... GO:0060002 p=2.8E−02 n=1 fg=0.01 bg=0.00
type 2A serotonin receptor binding GO:0031826 p=2.8E−02 n=1 fg=0.01 bg=0.00
lipoamidase activity GO:0061690 p=2.8E−02 n=1 fg=0.01 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=2.8E−02 n=1 fg=0.01 bg=0.00
methionine adenosyltransferase regulator... GO:0048270 p=2.8E−02 n=1 fg=0.01 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=2.8E−02 n=1 fg=0.01 bg=0.00
branched−chain amino acid transmembrane ... GO:0015658 p=2.8E−02 n=1 fg=0.01 bg=0.00
histone deacetylase activity GO:0004407 p=3.1E−02 n=2 fg=0.03 bg=0.00
NADP binding GO:0050661 p=3.1E−02 n=2 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=67/233 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_032366085.2
fraction genes in fg and expected valu
mitochondrial inner membrane GO:0005743 p=3.5E−03 n=9 fg=0.12 bg=0.04
Set1C/COMPASS complex GO:0048188 p=7.6E−03 n=2 fg=0.03 bg=0.00
ciliary membrane GO:0060170 p=1.1E−02 n=3 fg=0.04 bg=0.01
endocytic vesicle GO:0030139 p=1.9E−02 n=5 fg=0.06 bg=0.02
cytoplasmic side of endoplasmic reticulu... GO:0098554 p=2.0E−02 n=2 fg=0.03 bg=0.00
bounding membrane of organelle GO:0098588 p=2.0E−02 n=17 fg=0.22 bg=0.13
large ribosomal subunit GO:0015934 p=2.2E−02 n=4 fg=0.05 bg=0.01
clathrin−coated pit GO:0005905 p=2.5E−02 n=2 fg=0.03 bg=0.00
organelle membrane GO:0031090 p=2.8E−02 n=30 fg=0.39 bg=0.24
ACF complex GO:0016590 p=2.9E−02 n=1 fg=0.01 bg=0.00
nuclear meiotic cohesin complex GO:0034991 p=2.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=2.9E−02 n=1 fg=0.01 bg=0.00
meiotic cohesin complex GO:0030893 p=2.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=2.9E−02 n=1 fg=0.01 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=2.9E−02 n=1 fg=0.01 bg=0.00
TIM22 mitochondrial import inner membran... GO:0042721 p=2.9E−02 n=1 fg=0.01 bg=0.00
polycystin complex GO:0002133 p=2.9E−02 n=1 fg=0.01 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=2.9E−02 n=1 fg=0.01 bg=0.00
organellar large ribosomal subunit GO:0000315 p=3.7E−02 n=2 fg=0.03 bg=0.00
mitochondrial large ribosomal subunit GO:0005762 p=3.7E−02 n=2 fg=0.03 bg=0.00
F−actin capping protein complex GO:0008290 p=5.6E−02 n=1 fg=0.01 bg=0.00
THO complex GO:0000347 p=5.6E−02 n=1 fg=0.01 bg=0.00
RSF complex GO:0031213 p=5.6E−02 n=1 fg=0.01 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=5.6E−02 n=1 fg=0.01 bg=0.00
mitochondrial pyruvate dehydrogenase (li... GO:0019910 p=5.6E−02 n=1 fg=0.01 bg=0.00
THO complex part of transcription export... GO:0000445 p=5.6E−02 n=1 fg=0.01 bg=0.00
pyruvate dehydrogenase (lipoamide) phosp... GO:0045253 p=5.6E−02 n=1 fg=0.01 bg=0.00
eukaryotic translation elongation factor... GO:0005853 p=5.6E−02 n=1 fg=0.01 bg=0.00
chromatin GO:0000785 p=7.0E−02 n=7 fg=0.09 bg=0.05
P granule GO:0043186 p=7.4E−02 n=2 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=77/233 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction