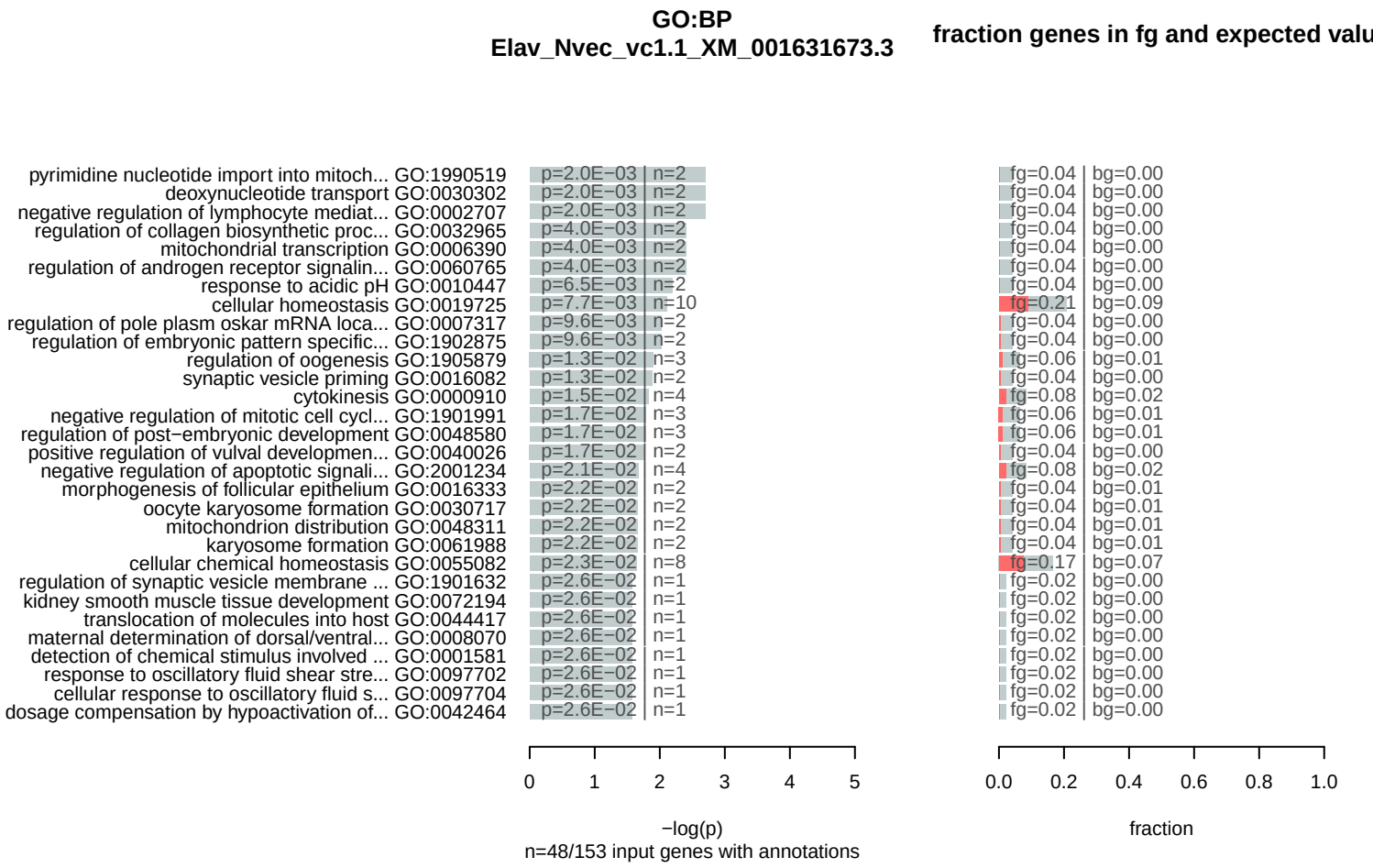
GO:BP
Elav_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
pyrimidine nucleotide import into mitoch... GO:1990519 p=2.0E−03 n=2 fg=0.04 bg=0.00
deoxynucleotide transport GO:0030302 p=2.0E−03 n=2 fg=0.04 bg=0.00
negative regulation of lymphocyte mediat... GO:0002707 p=2.0E−03 n=2 fg=0.04 bg=0.00
regulation of collagen biosynthetic proc... GO:0032965 p=4.0E−03 n=2 fg=0.04 bg=0.00
mitochondrial transcription GO:0006390 p=4.0E−03 n=2 fg=0.04 bg=0.00
regulation of androgen receptor signalin... GO:0060765 p=4.0E−03 n=2 fg=0.04 bg=0.00
response to acidic pH GO:0010447 p=6.5E−03 n=2 fg=0.04 bg=0.00
cellular homeostasis GO:0019725 p=7.7E−03 n=10 fg=0.21 bg=0.09
regulation of pole plasm oskar mRNA loca... GO:0007317 p=9.6E−03 n=2 fg=0.04 bg=0.00
regulation of embryonic pattern specific... GO:1902875 p=9.6E−03 n=2 fg=0.04 bg=0.00
regulation of oogenesis GO:1905879 p=1.3E−02 n=3 fg=0.06 bg=0.01
synaptic vesicle priming GO:0016082 p=1.3E−02 n=2 fg=0.04 bg=0.00
cytokinesis GO:0000910 p=1.5E−02 n=4 fg=0.08 bg=0.02
negative regulation of mitotic cell cycl... GO:1901991 p=1.7E−02 n=3 fg=0.06 bg=0.01
regulation of post−embryonic development GO:0048580 p=1.7E−02 n=3 fg=0.06 bg=0.01
positive regulation of vulval developmen... GO:0040026 p=1.7E−02 n=2 fg=0.04 bg=0.00
negative regulation of apoptotic signali... GO:2001234 p=2.1E−02 n=4 fg=0.08 bg=0.02
morphogenesis of follicular epithelium GO:0016333 p=2.2E−02 n=2 fg=0.04 bg=0.01
oocyte karyosome formation GO:0030717 p=2.2E−02 n=2 fg=0.04 bg=0.01
mitochondrion distribution GO:0048311 p=2.2E−02 n=2 fg=0.04 bg=0.01
karyosome formation GO:0061988 p=2.2E−02 n=2 fg=0.04 bg=0.01
cellular chemical homeostasis GO:0055082 p=2.3E−02 n=8 fg=0.17 bg=0.07
regulation of synaptic vesicle membrane ... GO:1901632 p=2.6E−02 n=1 fg=0.02 bg=0.00
kidney smooth muscle tissue development GO:0072194 p=2.6E−02 n=1 fg=0.02 bg=0.00
translocation of molecules into host GO:0044417 p=2.6E−02 n=1 fg=0.02 bg=0.00
maternal determination of dorsal/ventral... GO:0008070 p=2.6E−02 n=1 fg=0.02 bg=0.00
detection of chemical stimulus involved ... GO:0001581 p=2.6E−02 n=1 fg=0.02 bg=0.00
response to oscillatory fluid shear stre... GO:0097702 p=2.6E−02 n=1 fg=0.02 bg=0.00
cellular response to oscillatory fluid s... GO:0097704 p=2.6E−02 n=1 fg=0.02 bg=0.00
dosage compensation by hypoactivation of... GO:0042464 p=2.6E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=48/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
cysteine−type endopeptidase inhibitor ac... GO:0004869 p=1.8E−03 n=2 fg=0.05 bg=0.00
pyrimidine nucleotide transmembrane tran... GO:0015218 p=1.8E−03 n=2 fg=0.05 bg=0.00
ADP binding GO:0043531 p=1.6E−02 n=2 fg=0.05 bg=0.01
methionine adenosyltransferase regulator... GO:0048270 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphoglycerate kinase activity GO:0004618 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−asparagine transmembrane transporter a... GO:0015182 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−aspartate transmembrane transporter ac... GO:0015183 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−glutamine transmembrane transporter ac... GO:0015186 p=2.5E−02 n=1 fg=0.03 bg=0.00
HLH domain binding GO:0043398 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphopantothenate−−cysteine ligase act... GO:0004632 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−glutamate transmembrane transporter ac... GO:0005313 p=2.5E−02 n=1 fg=0.03 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=2.5E−02 n=1 fg=0.03 bg=0.00
acidic amino acid transmembrane transpor... GO:0015172 p=2.5E−02 n=1 fg=0.03 bg=0.00
follicle−stimulating hormone receptor bi... GO:0031762 p=2.5E−02 n=1 fg=0.03 bg=0.00
muscle alpha−actinin binding GO:0051371 p=2.5E−02 n=1 fg=0.03 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=2.5E−02 n=1 fg=0.03 bg=0.00
type 2A serotonin receptor binding GO:0031826 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylserine decarboxylase activit... GO:0004609 p=2.5E−02 n=1 fg=0.03 bg=0.00
opsin binding GO:0002046 p=2.5E−02 n=1 fg=0.03 bg=0.00
branched−chain amino acid transmembrane ... GO:0015658 p=2.5E−02 n=1 fg=0.03 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=2.5E−02 n=1 fg=0.03 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=2.5E−02 n=1 fg=0.03 bg=0.00
ankyrin repeat binding GO:0071532 p=2.5E−02 n=1 fg=0.03 bg=0.00
methionine transmembrane transporter act... GO:0043865 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−leucine transmembrane transporter acti... GO:0015190 p=2.5E−02 n=1 fg=0.03 bg=0.00
L−methionine transmembrane transporter a... GO:0015191 p=2.5E−02 n=1 fg=0.03 bg=0.00
V2 vasopressin receptor binding GO:0031896 p=2.5E−02 n=1 fg=0.03 bg=0.00
ATP binding GO:0005524 p=2.5E−02 n=5 fg=0.12 bg=0.04
purine ribonucleoside triphosphate bindi... GO:0035639 p=2.6E−02 n=6 fg=0.15 bg=0.06
phosphatidylinositol binding GO:0035091 p=2.6E−02 n=4 fg=0.10 bg=0.03
0 1 2 3 4 5
−log(p)
n=40/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001631673.3
fraction genes in fg and expected valu
Set1C/COMPASS complex GO:0048188 p=3.8E−03 n=2 fg=0.04 bg=0.00
organelle membrane GO:0031090 p=2.0E−02 n=19 fg=0.40 bg=0.26
clathrin−coated pit GO:0005905 p=2.1E−02 n=2 fg=0.04 bg=0.00
THO complex part of transcription export... GO:0000445 p=2.6E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic activ... GO:0098891 p=2.6E−02 n=1 fg=0.02 bg=0.00
transcription export complex GO:0000346 p=2.6E−02 n=1 fg=0.02 bg=0.00
THO complex GO:0000347 p=2.6E−02 n=1 fg=0.02 bg=0.00
extrinsic component of synaptic membrane GO:0099243 p=2.6E−02 n=1 fg=0.02 bg=0.00
CHRAC GO:0008623 p=2.6E−02 n=1 fg=0.02 bg=0.00
extrinsic component of presynaptic membr... GO:0098888 p=2.6E−02 n=1 fg=0.02 bg=0.00
anchored component of synaptic vesicle m... GO:0098993 p=2.6E−02 n=1 fg=0.02 bg=0.00
ACF complex GO:0016590 p=2.6E−02 n=1 fg=0.02 bg=0.00
methionine adenosyltransferase complex GO:0048269 p=2.6E−02 n=1 fg=0.02 bg=0.00
polycystin complex GO:0002133 p=2.6E−02 n=1 fg=0.02 bg=0.00
synaptic membrane GO:0097060 p=2.7E−02 n=4 fg=0.09 bg=0.02
mitochondrial inner membrane GO:0005743 p=2.8E−02 n=5 fg=0.11 bg=0.04
endocytic vesicle GO:0030139 p=3.2E−02 n=4 fg=0.09 bg=0.03
plasma membrane region GO:0098590 p=3.3E−02 n=9 fg=0.19 bg=0.10
P granule GO:0043186 p=3.7E−02 n=2 fg=0.04 bg=0.01
organelle inner membrane GO:0019866 p=4.0E−02 n=5 fg=0.11 bg=0.04
germ plasm GO:0060293 p=4.3E−02 n=2 fg=0.04 bg=0.01
pole plasm GO:0045495 p=4.3E−02 n=2 fg=0.04 bg=0.01
myelin sheath GO:0043209 p=4.4E−02 n=3 fg=0.06 bg=0.02
NURF complex GO:0016589 p=5.1E−02 n=1 fg=0.02 bg=0.00
PTW/PP1 phosphatase complex GO:0072357 p=5.1E−02 n=1 fg=0.02 bg=0.00
mitochondrial crista GO:0030061 p=5.1E−02 n=1 fg=0.02 bg=0.00
RSF complex GO:0031213 p=5.1E−02 n=1 fg=0.02 bg=0.00
pyruvate dehydrogenase (lipoamide) phosp... GO:0045253 p=5.1E−02 n=1 fg=0.02 bg=0.00
mitochondrial pyruvate dehydrogenase (li... GO:0019910 p=5.1E−02 n=1 fg=0.02 bg=0.00
organelle subcompartment GO:0031984 p=6.2E−02 n=11 fg=0.23 bg=0.14
0 1 2 3 4 5
−log(p)
n=47/153 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction