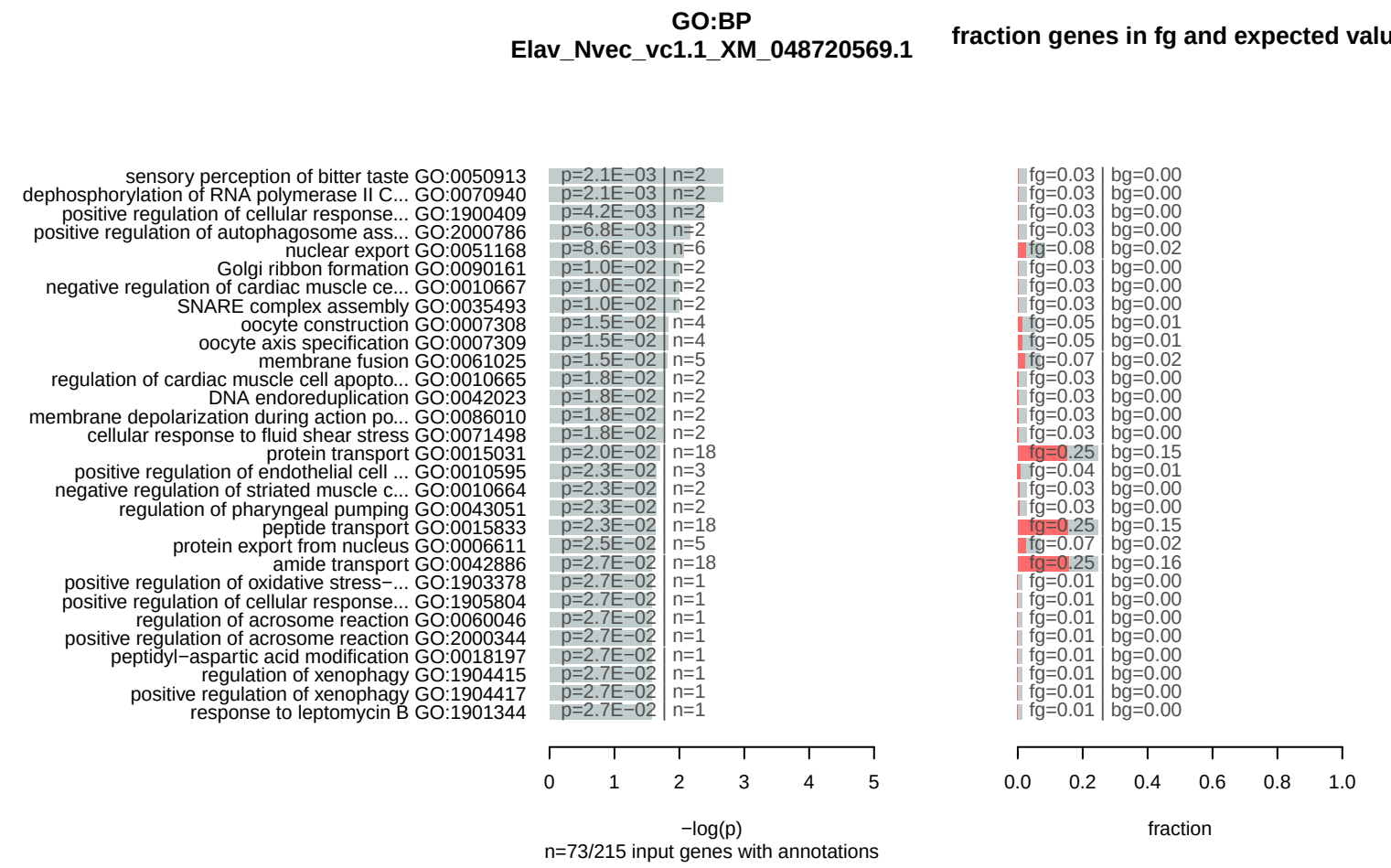
GO:BP
Elav_Nvec_vc1.1_XM_048720569.1
fraction genes in fg and expected valu
sensory perception of bitter taste GO:0050913 p=2.1E−03 n=2 fg=0.03 bg=0.00
dephosphorylation of RNA polymerase II C... GO:0070940 p=2.1E−03 n=2 fg=0.03 bg=0.00
positive regulation of cellular response... GO:1900409 p=4.2E−03 n=2 fg=0.03 bg=0.00
positive regulation of autophagosome ass... GO:2000786 p=6.8E−03 n=2 fg=0.03 bg=0.00
nuclear export GO:0051168 p=8.6E−03 n=6 fg=0.08 bg=0.02
Golgi ribbon formation GO:0090161 p=1.0E−02 n=2 fg=0.03 bg=0.00
negative regulation of cardiac muscle ce... GO:0010667 p=1.0E−02 n=2 fg=0.03 bg=0.00
SNARE complex assembly GO:0035493 p=1.0E−02 n=2 fg=0.03 bg=0.00
oocyte construction GO:0007308 p=1.5E−02 n=4 fg=0.05 bg=0.01
oocyte axis specification GO:0007309 p=1.5E−02 n=4 fg=0.05 bg=0.01
membrane fusion GO:0061025 p=1.5E−02 n=5 fg=0.07 bg=0.02
regulation of cardiac muscle cell apopto... GO:0010665 p=1.8E−02 n=2 fg=0.03 bg=0.00
DNA endoreduplication GO:0042023 p=1.8E−02 n=2 fg=0.03 bg=0.00
membrane depolarization during action po... GO:0086010 p=1.8E−02 n=2 fg=0.03 bg=0.00
cellular response to fluid shear stress GO:0071498 p=1.8E−02 n=2 fg=0.03 bg=0.00
protein transport GO:0015031 p=2.0E−02 n=18 fg=0.25 bg=0.15
positive regulation of endothelial cell ... GO:0010595 p=2.3E−02 n=3 fg=0.04 bg=0.01
negative regulation of striated muscle c... GO:0010664 p=2.3E−02 n=2 fg=0.03 bg=0.00
regulation of pharyngeal pumping GO:0043051 p=2.3E−02 n=2 fg=0.03 bg=0.00
peptide transport GO:0015833 p=2.3E−02 n=18 fg=0.25 bg=0.15
protein export from nucleus GO:0006611 p=2.5E−02 n=5 fg=0.07 bg=0.02
amide transport GO:0042886 p=2.7E−02 n=18 fg=0.25 bg=0.16
positive regulation of oxidative stress−... GO:1903378 p=2.7E−02 n=1 fg=0.01 bg=0.00
positive regulation of cellular response... GO:1905804 p=2.7E−02 n=1 fg=0.01 bg=0.00
regulation of acrosome reaction GO:0060046 p=2.7E−02 n=1 fg=0.01 bg=0.00
positive regulation of acrosome reaction GO:2000344 p=2.7E−02 n=1 fg=0.01 bg=0.00
peptidyl−aspartic acid modification GO:0018197 p=2.7E−02 n=1 fg=0.01 bg=0.00
regulation of xenophagy GO:1904415 p=2.7E−02 n=1 fg=0.01 bg=0.00
positive regulation of xenophagy GO:1904417 p=2.7E−02 n=1 fg=0.01 bg=0.00
response to leptomycin B GO:1901344 p=2.7E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=73/215 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048720569.1
fraction genes in fg and expected valu
GDP−dissociation inhibitor activity GO:0005092 p=2.1E−03 n=2 fg=0.03 bg=0.00
SNAP receptor activity GO:0005484 p=4.2E−03 n=3 fg=0.05 bg=0.01
metal cluster binding GO:0051540 p=1.3E−02 n=2 fg=0.03 bg=0.00
iron−sulfur cluster binding GO:0051536 p=1.3E−02 n=2 fg=0.03 bg=0.00
ATP hydrolysis activity GO:0016887 p=2.4E−02 n=7 fg=0.11 bg=0.05
macrophage migration inhibitory factor b... GO:0035718 p=2.7E−02 n=1 fg=0.02 bg=0.00
oxidized pyrimidine DNA binding GO:0032358 p=2.7E−02 n=1 fg=0.02 bg=0.00
aminomethyltransferase activity GO:0004047 p=2.7E−02 n=1 fg=0.02 bg=0.00
phosphatidylinositol phosphate kinase ac... GO:0016307 p=2.7E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−4−phosphate 5−kin... GO:0016308 p=2.7E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−5−phosphate 4−kin... GO:0016309 p=2.7E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=2.7E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=2.7E−02 n=1 fg=0.02 bg=0.00
1−phosphatidylinositol−3−phosphate 4−kin... GO:0052811 p=2.7E−02 n=1 fg=0.02 bg=0.00
N6−methyladenosine−containing RNA bindin... GO:1990247 p=2.7E−02 n=1 fg=0.02 bg=0.00
riboflavin binding GO:1902444 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein−L−isoaspartate (D−aspartate) O−m... GO:0004719 p=2.7E−02 n=1 fg=0.02 bg=0.00
ADP−ribose diphosphatase activity GO:0047631 p=2.7E−02 n=1 fg=0.02 bg=0.00
DNA clamp loader activity GO:0003689 p=2.7E−02 n=1 fg=0.02 bg=0.00
UDP−sugar diphosphatase activity GO:0008768 p=2.7E−02 n=1 fg=0.02 bg=0.00
carboxyl−O−methyltransferase activity GO:0010340 p=2.7E−02 n=1 fg=0.02 bg=0.00
3'−5' RNA helicase activity GO:0034458 p=2.7E−02 n=1 fg=0.02 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=2.7E−02 n=1 fg=0.02 bg=0.00
hedgehog receptor activity GO:0008158 p=2.7E−02 n=1 fg=0.02 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=2.7E−02 n=1 fg=0.02 bg=0.00
supercoiled DNA binding GO:0097100 p=2.7E−02 n=1 fg=0.02 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein carboxyl O−methyltransferase act... GO:0051998 p=2.7E−02 n=1 fg=0.02 bg=0.00
protein phosphatase 5 binding GO:1990634 p=2.7E−02 n=1 fg=0.02 bg=0.00
ATP−dependent activity GO:0140657 p=3.9E−02 n=7 fg=0.11 bg=0.05
0 1 2 3 4 5
−log(p)
n=63/215 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048720569.1
fraction genes in fg and expected valu
integral component of synaptic vesicle m... GO:0030285 p=4.3E−03 n=3 fg=0.04 bg=0.00
SNARE complex GO:0031201 p=7.9E−03 n=3 fg=0.04 bg=0.01
CAF−1 complex GO:0033186 p=2.7E−02 n=1 fg=0.01 bg=0.00
UTP−C complex GO:0034456 p=2.7E−02 n=1 fg=0.01 bg=0.00
CURI complex GO:0032545 p=2.7E−02 n=1 fg=0.01 bg=0.00
NF−kappaB complex GO:0071159 p=2.7E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=2.7E−02 n=1 fg=0.01 bg=0.00
voltage−gated potassium channel complex GO:0008076 p=2.8E−02 n=2 fg=0.03 bg=0.00
potassium channel complex GO:0034705 p=2.8E−02 n=2 fg=0.03 bg=0.00
phagocytic vesicle GO:0045335 p=3.0E−02 n=3 fg=0.04 bg=0.01
cation channel complex GO:0034703 p=3.0E−02 n=3 fg=0.04 bg=0.01
cytosolic ribosome GO:0022626 p=3.3E−02 n=4 fg=0.06 bg=0.02
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=3.5E−02 n=4 fg=0.06 bg=0.02
DNA−directed RNA polymerase complex GO:0000428 p=3.7E−02 n=4 fg=0.06 bg=0.02
Golgi trans cisterna GO:0000138 p=3.9E−02 n=2 fg=0.03 bg=0.00
RNA polymerase complex GO:0030880 p=4.3E−02 n=4 fg=0.06 bg=0.02
ion channel complex GO:0034702 p=4.4E−02 n=3 fg=0.04 bg=0.01
PcG protein complex GO:0031519 p=4.5E−02 n=2 fg=0.03 bg=0.00
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.3E−02 n=1 fg=0.01 bg=0.00
Sin3 complex GO:0016580 p=5.3E−02 n=1 fg=0.01 bg=0.00
THO complex part of transcription export... GO:0000445 p=5.3E−02 n=1 fg=0.01 bg=0.00
THO complex GO:0000347 p=5.3E−02 n=1 fg=0.01 bg=0.00
Elg1 RFC−like complex GO:0031391 p=5.3E−02 n=1 fg=0.01 bg=0.00
DRM complex GO:0070176 p=5.3E−02 n=1 fg=0.01 bg=0.00
extrinsic component of Golgi membrane GO:0090498 p=5.3E−02 n=1 fg=0.01 bg=0.00
glycine cleavage complex GO:0005960 p=5.3E−02 n=1 fg=0.01 bg=0.00
COP9 signalosome GO:0008180 p=5.3E−02 n=1 fg=0.01 bg=0.00
protein−containing complex GO:0032991 p=5.7E−02 n=39 fg=0.54 bg=0.42
endocytic vesicle GO:0030139 p=5.7E−02 n=4 fg=0.06 bg=0.02
microtubule cytoskeleton GO:0015630 p=5.9E−02 n=12 fg=0.17 bg=0.10
0 1 2 3 4 5
−log(p)
n=72/215 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction