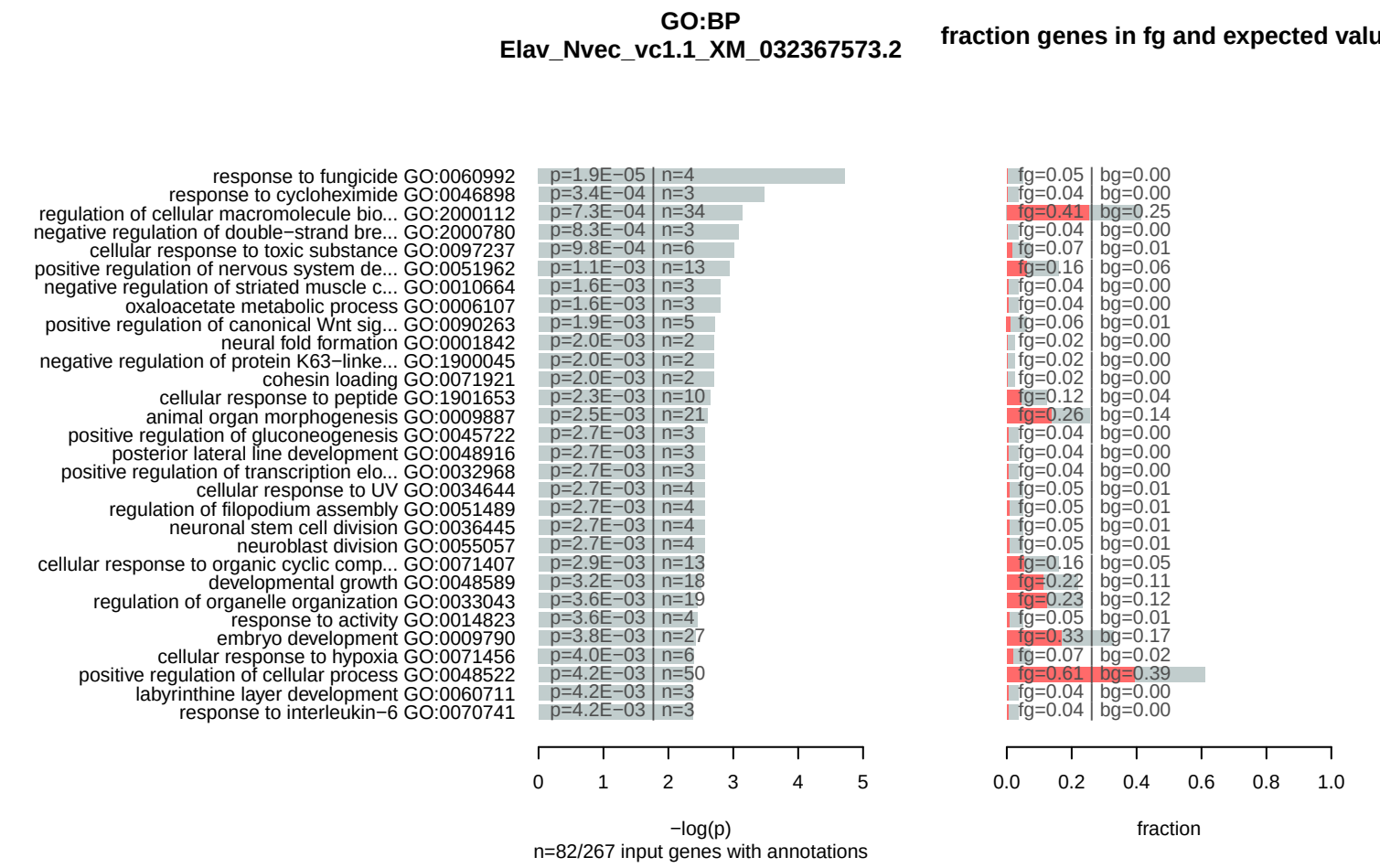
GO:BP
Elav_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
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response to cycloheximide GO:0046898 p=3.4E−04 n=3 fg=0.04 bg=0.00
regulation of cellular macromolecule bio... GO:2000112 p=7.3E−04 n=34 fg=0.41 bg=0.25
negative regulation of double−strand bre... GO:2000780 p=8.3E−04 n=3 fg=0.04 bg=0.00
cellular response to toxic substance GO:0097237 p=9.8E−04 n=6 fg=0.07 bg=0.01
positive regulation of nervous system de... GO:0051962 p=1.1E−03 n=13 fg=0.16 bg=0.06
negative regulation of striated muscle c... GO:0010664 p=1.6E−03 n=3 fg=0.04 bg=0.00
oxaloacetate metabolic process GO:0006107 p=1.6E−03 n=3 fg=0.04 bg=0.00
positive regulation of canonical Wnt sig... GO:0090263 p=1.9E−03 n=5 fg=0.06 bg=0.01
neural fold formation GO:0001842 p=2.0E−03 n=2 fg=0.02 bg=0.00
negative regulation of protein K63−linke... GO:1900045 p=2.0E−03 n=2 fg=0.02 bg=0.00
cohesin loading GO:0071921 p=2.0E−03 n=2 fg=0.02 bg=0.00
cellular response to peptide GO:1901653 p=2.3E−03 n=10 fg=0.12 bg=0.04
animal organ morphogenesis GO:0009887 p=2.5E−03 n=21 fg=0.26 bg=0.14
positive regulation of gluconeogenesis GO:0045722 p=2.7E−03 n=3 fg=0.04 bg=0.00
posterior lateral line development GO:0048916 p=2.7E−03 n=3 fg=0.04 bg=0.00
positive regulation of transcription elo... GO:0032968 p=2.7E−03 n=3 fg=0.04 bg=0.00
cellular response to UV GO:0034644 p=2.7E−03 n=4 fg=0.05 bg=0.01
regulation of filopodium assembly GO:0051489 p=2.7E−03 n=4 fg=0.05 bg=0.01
neuronal stem cell division GO:0036445 p=2.7E−03 n=4 fg=0.05 bg=0.01
neuroblast division GO:0055057 p=2.7E−03 n=4 fg=0.05 bg=0.01
cellular response to organic cyclic comp... GO:0071407 p=2.9E−03 n=13 fg=0.16 bg=0.05
developmental growth GO:0048589 p=3.2E−03 n=18 fg=0.22 bg=0.11
regulation of organelle organization GO:0033043 p=3.6E−03 n=19 fg=0.23 bg=0.12
response to activity GO:0014823 p=3.6E−03 n=4 fg=0.05 bg=0.01
embryo development GO:0009790 p=3.8E−03 n=27 fg=0.33 bg=0.17
cellular response to hypoxia GO:0071456 p=4.0E−03 n=6 fg=0.07 bg=0.02
positive regulation of cellular process GO:0048522 p=4.2E−03 n=50 fg=0.61 bg=0.39
labyrinthine layer development GO:0060711 p=4.2E−03 n=3 fg=0.04 bg=0.00
response to interleukin−6 GO:0070741 p=4.2E−03 n=3 fg=0.04 bg=0.00
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−log(p)
n=82/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
protein phosphatase 1 binding GO:0008157 p=5.1E−03 n=3 fg=0.04 bg=0.01
core promoter sequence−specific DNA bind... GO:0001046 p=5.9E−03 n=4 fg=0.05 bg=0.01
transcription coactivator activity GO:0003713 p=6.2E−03 n=8 fg=0.10 bg=0.04
profilin binding GO:0005522 p=6.7E−03 n=2 fg=0.03 bg=0.00
oxidoreductase activity, acting on the C... GO:0016899 p=6.7E−03 n=2 fg=0.03 bg=0.00
DNA binding domain binding GO:0050692 p=6.7E−03 n=2 fg=0.03 bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613 p=6.7E−03 n=2 fg=0.03 bg=0.00
lactate dehydrogenase activity GO:0004457 p=6.7E−03 n=2 fg=0.03 bg=0.00
inosine kinase activity GO:0008906 p=6.7E−03 n=2 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate ph... GO:0106019 p=6.7E−03 n=2 fg=0.03 bg=0.00
GTP binding GO:0005525 p=1.1E−02 n=5 fg=0.06 bg=0.02
purine ribonucleoside binding GO:0032550 p=1.1E−02 n=5 fg=0.06 bg=0.02
ribonucleoside binding GO:0032549 p=1.1E−02 n=5 fg=0.06 bg=0.02
nucleoside diphosphate kinase activity GO:0004550 p=1.3E−02 n=2 fg=0.03 bg=0.00
nucleoside binding GO:0001882 p=1.5E−02 n=5 fg=0.06 bg=0.02
purine nucleoside binding GO:0001883 p=1.5E−02 n=5 fg=0.06 bg=0.02
nucleic acid binding GO:0003676 p=1.7E−02 n=25 fg=0.32 bg=0.19
guanyl ribonucleotide binding GO:0032561 p=1.7E−02 n=5 fg=0.06 bg=0.02
guanyl nucleotide binding GO:0019001 p=1.7E−02 n=5 fg=0.06 bg=0.02
phosphatidylinositol kinase activity GO:0052742 p=2.1E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 p=2.1E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol 3−kinase activity GO:0035004 p=2.1E−02 n=2 fg=0.03 bg=0.00
epinephrine binding GO:0051379 p=2.1E−02 n=2 fg=0.03 bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303 p=2.1E−02 n=2 fg=0.03 bg=0.00
phosphatidylinositol bisphosphate kinase... GO:0052813 p=2.1E−02 n=2 fg=0.03 bg=0.00
catecholamine binding GO:1901338 p=2.1E−02 n=2 fg=0.03 bg=0.00
protein phosphatase regulator activity GO:0019888 p=2.2E−02 n=3 fg=0.04 bg=0.01
GTPase binding GO:0051020 p=2.8E−02 n=10 fg=0.13 bg=0.07
phosphatase regulator activity GO:0019208 p=3.3E−02 n=3 fg=0.04 bg=0.01
RNA polymerase II transcription regulato... GO:0000977 p=3.3E−02 n=8 fg=0.10 bg=0.05
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−log(p)
n=77/267 input genes with annotations
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fraction
GO:CC
Elav_Nvec_vc1.1_XM_032367573.2
fraction genes in fg and expected valu
cytosol GO:0005829 p=4.1E−04 n=47 fg=0.57 bg=0.39
transcription elongation factor complex GO:0008023 p=1.5E−03 n=4 fg=0.05 bg=0.01
transcription repressor complex GO:0017053 p=2.1E−03 n=4 fg=0.05 bg=0.01
nucleoplasm GO:0005654 p=7.4E−03 n=35 fg=0.43 bg=0.27
ruffle membrane GO:0032587 p=8.6E−03 n=3 fg=0.04 bg=0.01
growth cone GO:0030426 p=9.1E−03 n=6 fg=0.07 bg=0.02
specific granule GO:0042581 p=1.1E−02 n=4 fg=0.05 bg=0.01
cell cortex GO:0005938 p=1.7E−02 n=8 fg=0.10 bg=0.04
cytoskeleton GO:0005856 p=1.7E−02 n=19 fg=0.23 bg=0.14
protein phosphatase type 1 complex GO:0000164 p=1.9E−02 n=2 fg=0.02 bg=0.00
specific granule membrane GO:0035579 p=2.3E−02 n=3 fg=0.04 bg=0.01
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ficolin−1−rich granule membrane GO:0101003 p=2.7E−02 n=2 fg=0.02 bg=0.00
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protein serine/threonine phosphatase com... GO:0008287 p=2.8E−02 n=3 fg=0.04 bg=0.01
nuclear body GO:0016604 p=3.2E−02 n=10 fg=0.12 bg=0.06
PML body GO:0016605 p=3.7E−02 n=2 fg=0.02 bg=0.00
cytoplasmic side of plasma membrane GO:0009898 p=3.9E−02 n=5 fg=0.06 bg=0.02
phosphatase complex GO:1903293 p=3.9E−02 n=3 fg=0.04 bg=0.01
mitotic spindle GO:0072686 p=3.9E−02 n=3 fg=0.04 bg=0.01
tertiary granule GO:0070820 p=4.5E−02 n=3 fg=0.04 bg=0.01
internode region of axon GO:0033269 p=4.5E−02 n=1 fg=0.01 bg=0.00
elongin complex GO:0070449 p=4.5E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=4.5E−02 n=1 fg=0.01 bg=0.00
proteasome storage granule GO:0034515 p=4.5E−02 n=1 fg=0.01 bg=0.00
dendritic growth cone GO:0044294 p=4.5E−02 n=1 fg=0.01 bg=0.00
Scc2−Scc4 cohesin loading complex GO:0090694 p=4.5E−02 n=1 fg=0.01 bg=0.00
Rb−E2F complex GO:0035189 p=4.5E−02 n=1 fg=0.01 bg=0.00
SMC loading complex GO:0032116 p=4.5E−02 n=1 fg=0.01 bg=0.00
RES complex GO:0070274 p=4.5E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=82/267 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction