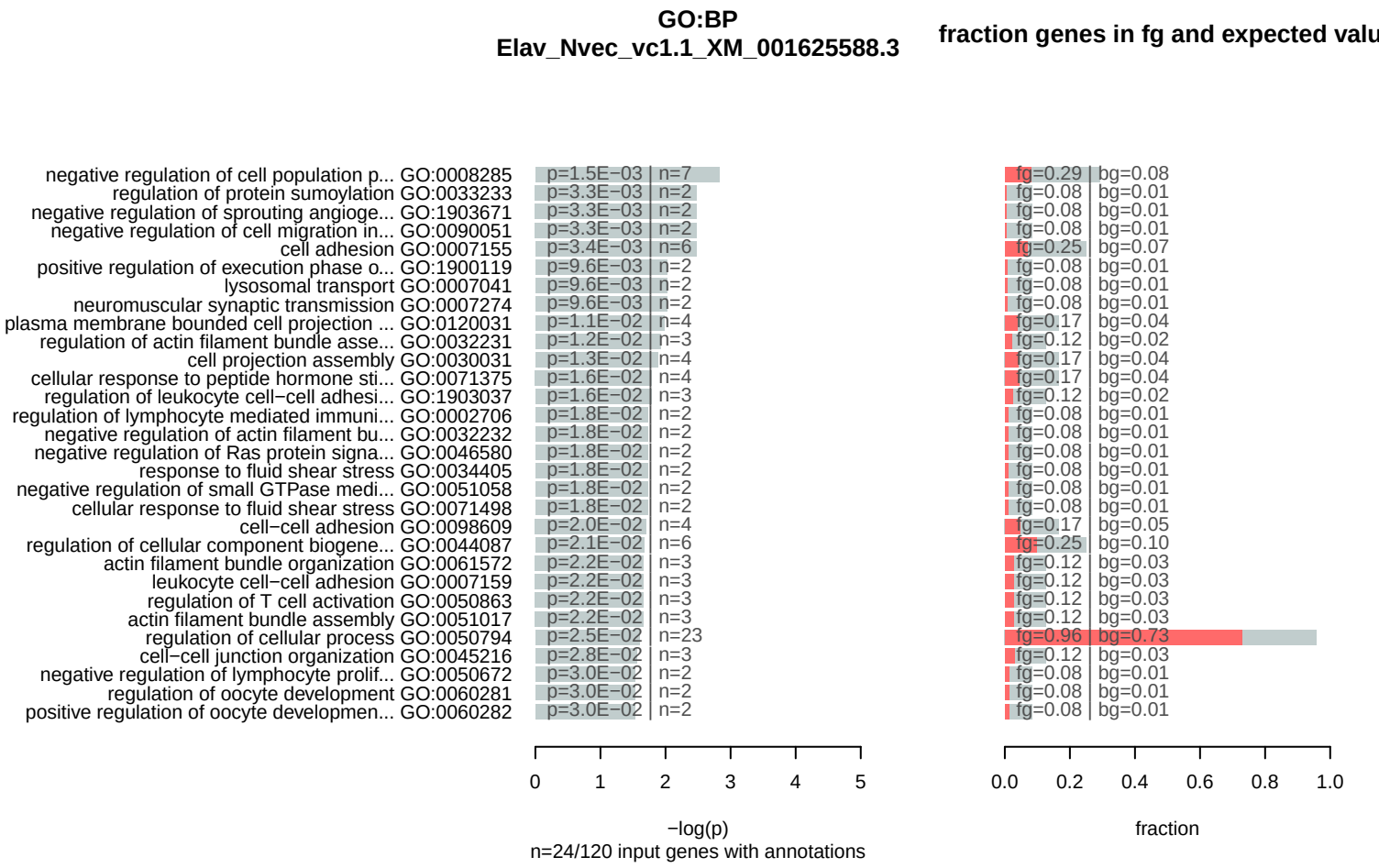
GO:BP
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fraction genes in fg and expected valu
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regulation of protein sumoylation GO:0033233 p=3.3E−03 n=2 fg=0.08 bg=0.01
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cell adhesion GO:0007155 p=3.4E−03 n=6 fg=0.25 bg=0.07
positive regulation of execution phase o... GO:1900119 p=9.6E−03 n=2 fg=0.08 bg=0.01
lysosomal transport GO:0007041 p=9.6E−03 n=2 fg=0.08 bg=0.01
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regulation of actin filament bundle asse... GO:0032231 p=1.2E−02 n=3 fg=0.12 bg=0.02
cell projection assembly GO:0030031 p=1.3E−02 n=4 fg=0.17 bg=0.04
cellular response to peptide hormone sti... GO:0071375 p=1.6E−02 n=4 fg=0.17 bg=0.04
regulation of leukocyte cell−cell adhesi... GO:1903037 p=1.6E−02 n=3 fg=0.12 bg=0.02
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negative regulation of actin filament bu... GO:0032232 p=1.8E−02 n=2 fg=0.08 bg=0.01
negative regulation of Ras protein signa... GO:0046580 p=1.8E−02 n=2 fg=0.08 bg=0.01
response to fluid shear stress GO:0034405 p=1.8E−02 n=2 fg=0.08 bg=0.01
negative regulation of small GTPase medi... GO:0051058 p=1.8E−02 n=2 fg=0.08 bg=0.01
cellular response to fluid shear stress GO:0071498 p=1.8E−02 n=2 fg=0.08 bg=0.01
cell−cell adhesion GO:0098609 p=2.0E−02 n=4 fg=0.17 bg=0.05
regulation of cellular component biogene... GO:0044087 p=2.1E−02 n=6 fg=0.25 bg=0.10
actin filament bundle organization GO:0061572 p=2.2E−02 n=3 fg=0.12 bg=0.03
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actin filament bundle assembly GO:0051017 p=2.2E−02 n=3 fg=0.12 bg=0.03
regulation of cellular process GO:0050794 p=2.5E−02 n=23 fg=0.96 bg=0.73
cell−cell junction organization GO:0045216 p=2.8E−02 n=3 fg=0.12 bg=0.03
negative regulation of lymphocyte prolif... GO:0050672 p=3.0E−02 n=2 fg=0.08 bg=0.01
regulation of oocyte development GO:0060281 p=3.0E−02 n=2 fg=0.08 bg=0.01
positive regulation of oocyte developmen... GO:0060282 p=3.0E−02 n=2 fg=0.08 bg=0.01
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−log(p)
n=24/120 input genes with annotations
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fraction
GO:MF
Elav_Nvec_vc1.1_XM_001625588.3
fraction genes in fg and expected valu
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kinase inhibitor activity GO:0019210 p=1.1E−02 n=2 fg=0.09 bg=0.01
cyclic nucleotide binding GO:0030551 p=2.1E−02 n=2 fg=0.09 bg=0.01
protein kinase regulator activity GO:0019887 p=2.1E−02 n=2 fg=0.09 bg=0.01
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protein serine/threonine kinase inhibito... GO:0030291 p=6.3E+02 n=1 fg=0.04 bg=0.00
exogenous protein binding GO:0140272 p=6.3E+02 n=1 fg=0.04 bg=0.00
vinculin binding GO:0017166 p=6.3E+02 n=1 fg=0.04 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=6.3E+02 n=1 fg=0.04 bg=0.00
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protein lysine deacetylase activity GO:0033558 p=6.3E+02 n=1 fg=0.04 bg=0.00
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potassium ion binding GO:0030955 p=6.3E+02 n=1 fg=0.04 bg=0.00
virus receptor activity GO:0001618 p=6.3E+02 n=1 fg=0.04 bg=0.00
WW domain binding GO:0050699 p=6.3E+02 n=1 fg=0.04 bg=0.00
N−acetylglucosamine−1−phosphodiester alp... GO:0003944 p=6.3E+02 n=1 fg=0.04 bg=0.00
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small molecule sensor activity GO:0140299 p=6.3E+02 n=1 fg=0.04 bg=0.00
serine−type endopeptidase activity GO:0004252 p=6.3E+02 n=1 fg=0.04 bg=0.00
JUN kinase kinase kinase activity GO:0004706 p=6.3E+02 n=1 fg=0.04 bg=0.00
oxygen binding GO:0019825 p=6.3E+02 n=1 fg=0.04 bg=0.00
oxygen sensor activity GO:0019826 p=6.3E+02 n=1 fg=0.04 bg=0.00
carbon monoxide binding GO:0070025 p=6.3E+02 n=1 fg=0.04 bg=0.00
nitric oxide binding GO:0070026 p=6.3E+02 n=1 fg=0.04 bg=0.00
polyubiquitin modification−dependent pro... GO:0031593 p=6.3E+02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_001625588.3
fraction genes in fg and expected valu
ruffle GO:0001726 p=4.9E−03 n=3 fg=0.13 bg=0.02
actin cytoskeleton GO:0015629 p=5.6E−03 n=4 fg=0.17 bg=0.03
ruffle membrane GO:0032587 p=1.8E−02 n=2 fg=0.09 bg=0.01
cell−cell junction GO:0005911 p=2.5E−02 n=4 fg=0.17 bg=0.05
anchoring junction GO:0070161 p=2.5E−02 n=4 fg=0.17 bg=0.05
cell junction GO:0030054 p=4.5E−02 n=8 fg=0.35 bg=0.19
cation channel complex GO:0034703 p=4.7E−02 n=3 fg=0.13 bg=0.04
transporter complex GO:1990351 p=5.6E+02 n=3 fg=0.13 bg=0.04
transmembrane transporter complex GO:1902495 p=5.6E+02 n=3 fg=0.13 bg=0.04
ion channel complex GO:0034702 p=5.6E+02 n=3 fg=0.13 bg=0.04
filamentous actin GO:0031941 p=5.7E+02 n=1 fg=0.04 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=5.7E+02 n=1 fg=0.04 bg=0.00
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actin filament GO:0005884 p=5.7E+02 n=1 fg=0.04 bg=0.00
transferase complex GO:1990234 p=6.6E−02 n=4 fg=0.17 bg=0.07
voltage−gated potassium channel complex GO:0008076 p=7.1E−02 n=2 fg=0.09 bg=0.02
potassium channel complex GO:0034705 p=7.1E−02 n=2 fg=0.09 bg=0.02
membrane protein complex GO:0098796 p=7.4E−02 n=4 fg=0.17 bg=0.07
plasma membrane raft GO:0044853 p=1.1E−01 n=2 fg=0.09 bg=0.02
adherens junction GO:0005912 p=1.1E−01 n=2 fg=0.09 bg=0.02
endocytic vesicle GO:0030139 p=1.1E−01 n=2 fg=0.09 bg=0.02
Derlin−1 retrotranslocation complex GO:0036513 p=1.1E−01 n=1 fg=0.04 bg=0.00
cAMP−dependent protein kinase complex GO:0005952 p=1.1E−01 n=1 fg=0.04 bg=0.00
cytoplasmic ubiquitin ligase complex GO:0000153 p=1.1E−01 n=1 fg=0.04 bg=0.00
germinal vesicle GO:0042585 p=1.1E−01 n=1 fg=0.04 bg=0.00
transcription elongation factor complex GO:0008023 p=1.1E−01 n=1 fg=0.04 bg=0.00
female germ cell nucleus GO:0001674 p=1.1E−01 n=1 fg=0.04 bg=0.00
ER ubiquitin ligase complex GO:0000835 p=1.1E−01 n=1 fg=0.04 bg=0.00
Hrd1p ubiquitin ligase complex GO:0000836 p=1.1E−01 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/120 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction