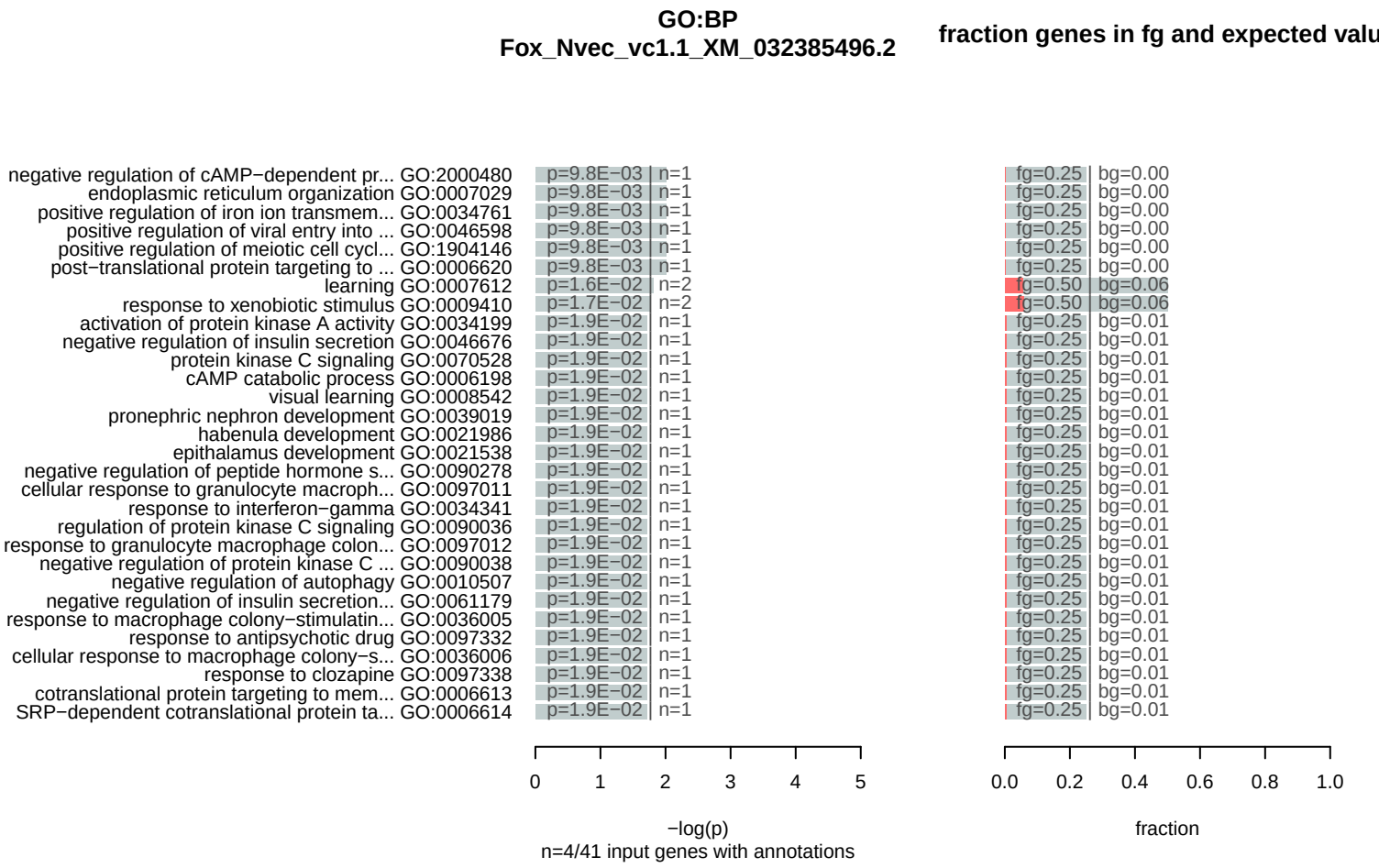
GO:BP
Fox_Nvec_vc1.1_XM_032385496.2
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endoplasmic reticulum organization GO:0007029 p=9.8E−03 n=1 fg=0.25 bg=0.00
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positive regulation of viral entry into ... GO:0046598 p=9.8E−03 n=1 fg=0.25 bg=0.00
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learning GO:0007612 p=1.6E−02 n=2 fg=0.50 bg=0.06
response to xenobiotic stimulus GO:0009410 p=1.7E−02 n=2 fg=0.50 bg=0.06
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epithalamus development GO:0021538 p=1.9E−02 n=1 fg=0.25 bg=0.01
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cellular response to granulocyte macroph... GO:0097011 p=1.9E−02 n=1 fg=0.25 bg=0.01
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regulation of protein kinase C signaling GO:0090036 p=1.9E−02 n=1 fg=0.25 bg=0.01
response to granulocyte macrophage colon... GO:0097012 p=1.9E−02 n=1 fg=0.25 bg=0.01
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response to macrophage colony−stimulatin... GO:0036005 p=1.9E−02 n=1 fg=0.25 bg=0.01
response to antipsychotic drug GO:0097332 p=1.9E−02 n=1 fg=0.25 bg=0.01
cellular response to macrophage colony−s... GO:0036006 p=1.9E−02 n=1 fg=0.25 bg=0.01
response to clozapine GO:0097338 p=1.9E−02 n=1 fg=0.25 bg=0.01
cotranslational protein targeting to mem... GO:0006613 p=1.9E−02 n=1 fg=0.25 bg=0.01
SRP−dependent cotranslational protein ta... GO:0006614 p=1.9E−02 n=1 fg=0.25 bg=0.01
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n=4/41 input genes with annotations
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fraction
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protein kinase A catalytic subunit bindi... GO:0034236 p=8.2E−03 n=1 fg=0.33 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=8.2E−03 n=1 fg=0.33 bg=0.00
beta−2 adrenergic receptor binding GO:0031698 p=8.2E−03 n=1 fg=0.33 bg=0.00
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ribosome binding GO:0043022 p=1.6E−02 n=1 fg=0.33 bg=0.01
ribonucleoprotein complex binding GO:0043021 p=2.5E−02 n=1 fg=0.33 bg=0.01
cGMP binding GO:0030553 p=2.5E−02 n=1 fg=0.33 bg=0.01
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ubiquitin−like protein ligase binding GO:0044389 p=1.0E−01 n=1 fg=0.33 bg=0.04
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protein binding GO:0005515 p=8.4E−01 n=2 fg=0.67 bg=0.60
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phosphoric diester hydrolase activity GO:0008081 p=1.0E+00 n=1 fg=0.33 bg=0.03
nucleoside phosphate binding GO:1901265 p=1.0E+00 n=2 fg=0.67 bg=0.07
ribonucleotide binding GO:0032553 p=1.0E+00 n=2 fg=0.67 bg=0.06
catalytic activity GO:0003824 p=1.0E+00 n=1 fg=0.33 bg=0.40
signaling receptor binding GO:0005102 p=1.0E+00 n=1 fg=0.33 bg=0.13
purine ribonucleotide binding GO:0032555 p=1.0E+00 n=2 fg=0.67 bg=0.06
0 1 2 3 4 5
−log(p)
n=3/41 input genes with annotations
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fraction
GO:CC
Fox_Nvec_vc1.1_XM_032385496.2
fraction genes in fg and expected valu
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phagocytic vesicle membrane GO:0030670 p=2.0E−02 n=1 fg=0.25 bg=0.01
cAMP−dependent protein kinase complex GO:0005952 p=2.0E−02 n=1 fg=0.25 bg=0.01
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germinal vesicle GO:0042585 p=2.0E−02 n=1 fg=0.25 bg=0.01
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fusome GO:0045169 p=2.0E−02 n=1 fg=0.25 bg=0.01
germ cell nucleus GO:0043073 p=3.0E−02 n=1 fg=0.25 bg=0.01
protein kinase complex GO:1902911 p=3.0E−02 n=1 fg=0.25 bg=0.01
rough endoplasmic reticulum GO:0005791 p=3.0E−02 n=1 fg=0.25 bg=0.01
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neuronal cell body GO:0043025 p=6.4E−02 n=2 fg=0.50 bg=0.11
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cell body GO:0044297 p=7.4E−02 n=2 fg=0.50 bg=0.12
mitochondrial inner membrane GO:0005743 p=7.8E−02 n=1 fg=0.25 bg=0.02
dendritic shaft GO:0043198 p=8.7E−02 n=1 fg=0.25 bg=0.02
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endocytic vesicle GO:0030139 p=9.6E−02 n=1 fg=0.25 bg=0.03
plasma membrane raft GO:0044853 p=9.6E−02 n=1 fg=0.25 bg=0.03
integral component of endoplasmic reticu... GO:0030176 p=1.0E−01 n=1 fg=0.25 bg=0.03
intrinsic component of endoplasmic retic... GO:0031227 p=1.0E−01 n=1 fg=0.25 bg=0.03
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centrosome GO:0005813 p=1.2E−01 n=1 fg=0.25 bg=0.03
cytosol GO:0005829 p=1.3E−01 n=3 fg=0.75 bg=0.35
mitochondrial membrane GO:0031966 p=1.3E−01 n=1 fg=0.25 bg=0.04
0 1 2 3 4 5
−log(p)
n=4/41 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction