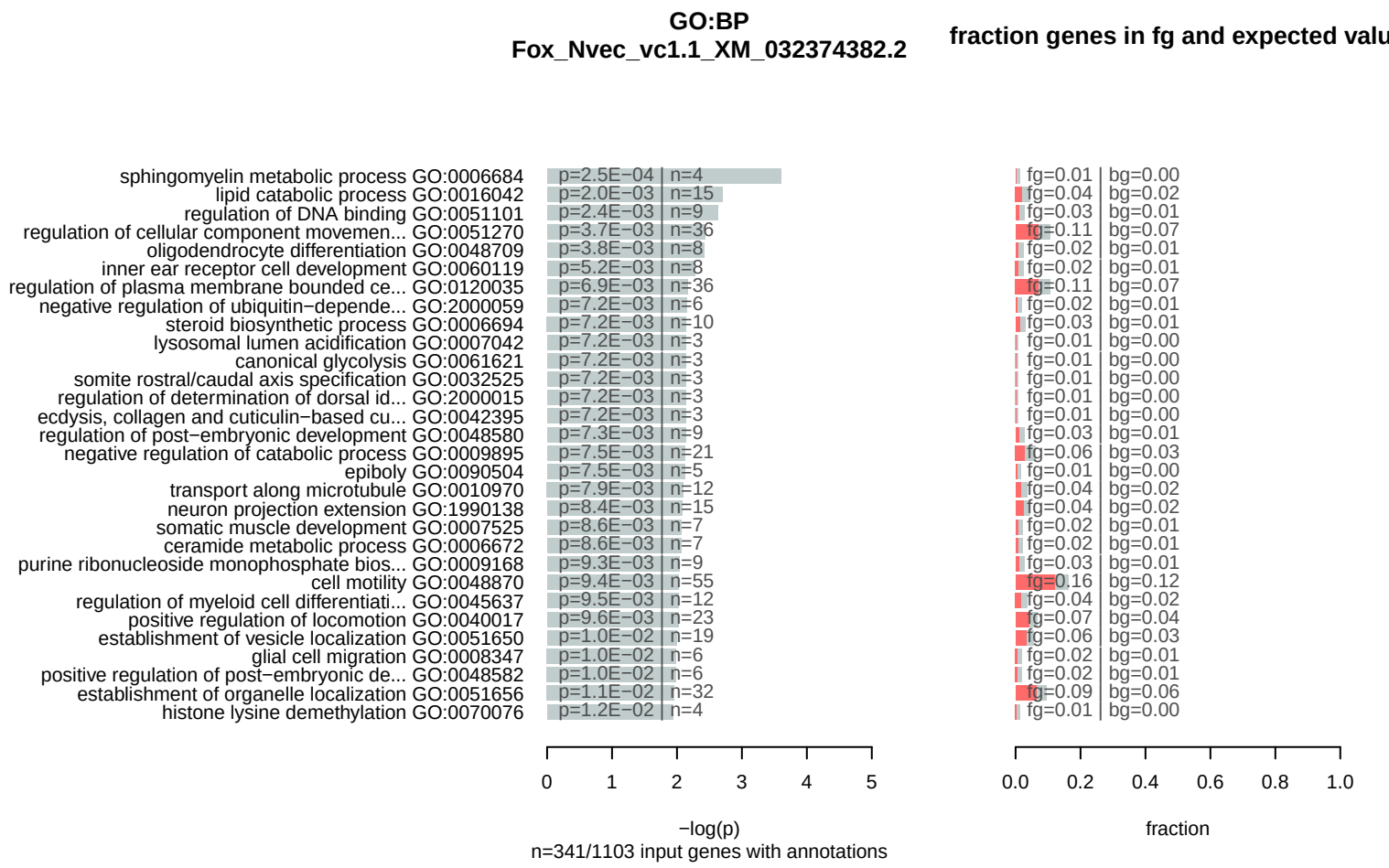
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fraction genes in fg and expected valu
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lipid catabolic process GO:0016042 p=2.0E−03 n=15 fg=0.04 bg=0.02
regulation of DNA binding GO:0051101 p=2.4E−03 n=9 fg=0.03 bg=0.01
regulation of cellular component movemen... GO:0051270 p=3.7E−03 n=36 fg=0.11 bg=0.07
oligodendrocyte differentiation GO:0048709 p=3.8E−03 n=8 fg=0.02 bg=0.01
inner ear receptor cell development GO:0060119 p=5.2E−03 n=8 fg=0.02 bg=0.01
regulation of plasma membrane bounded ce... GO:0120035 p=6.9E−03 n=36 fg=0.11 bg=0.07
negative regulation of ubiquitin−depende... GO:2000059 p=7.2E−03 n=6 fg=0.02 bg=0.01
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somite rostral/caudal axis specification GO:0032525 p=7.2E−03 n=3 fg=0.01 bg=0.00
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ecdysis, collagen and cuticulin−based cu... GO:0042395 p=7.2E−03 n=3 fg=0.01 bg=0.00
regulation of post−embryonic development GO:0048580 p=7.3E−03 n=9 fg=0.03 bg=0.01
negative regulation of catabolic process GO:0009895 p=7.5E−03 n=21 fg=0.06 bg=0.03
epiboly GO:0090504 p=7.5E−03 n=5 fg=0.01 bg=0.00
transport along microtubule GO:0010970 p=7.9E−03 n=12 fg=0.04 bg=0.02
neuron projection extension GO:1990138 p=8.4E−03 n=15 fg=0.04 bg=0.02
somatic muscle development GO:0007525 p=8.6E−03 n=7 fg=0.02 bg=0.01
ceramide metabolic process GO:0006672 p=8.6E−03 n=7 fg=0.02 bg=0.01
purine ribonucleoside monophosphate bios... GO:0009168 p=9.3E−03 n=9 fg=0.03 bg=0.01
cell motility GO:0048870 p=9.4E−03 n=55 fg=0.16 bg=0.12
regulation of myeloid cell differentiati... GO:0045637 p=9.5E−03 n=12 fg=0.04 bg=0.02
positive regulation of locomotion GO:0040017 p=9.6E−03 n=23 fg=0.07 bg=0.04
establishment of vesicle localization GO:0051650 p=1.0E−02 n=19 fg=0.06 bg=0.03
glial cell migration GO:0008347 p=1.0E−02 n=6 fg=0.02 bg=0.01
positive regulation of post−embryonic de... GO:0048582 p=1.0E−02 n=6 fg=0.02 bg=0.01
establishment of organelle localization GO:0051656 p=1.1E−02 n=32 fg=0.09 bg=0.06
histone lysine demethylation GO:0070076 p=1.2E−02 n=4 fg=0.01 bg=0.00
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n=341/1103 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
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dynein intermediate chain binding GO:0045505 p=3.3E−03 n=4 fg=0.01 bg=0.00
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protein demethylase activity GO:0140457 p=1.3E−02 n=4 fg=0.01 bg=0.00
lipid transporter activity GO:0005319 p=1.3E−02 n=8 fg=0.03 bg=0.01
ATP−dependent protein binding GO:0043008 p=1.7E−02 n=2 fg=0.01 bg=0.00
oxidoreductase activity, acting on NAD(P... GO:0016652 p=1.7E−02 n=2 fg=0.01 bg=0.00
mitogen−activated protein kinase p38 bin... GO:0048273 p=1.7E−02 n=2 fg=0.01 bg=0.00
NAD(P)+ transhydrogenase activity GO:0008746 p=1.7E−02 n=2 fg=0.01 bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019 p=1.7E−02 n=2 fg=0.01 bg=0.00
calcium channel inhibitor activity GO:0019855 p=1.7E−02 n=2 fg=0.01 bg=0.00
sphingomyelin phosphodiesterase activity GO:0004767 p=1.7E−02 n=2 fg=0.01 bg=0.00
oxysterol binding GO:0008142 p=1.7E−02 n=2 fg=0.01 bg=0.00
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5'−3' RNA polymerase activity GO:0034062 p=2.0E−02 n=4 fg=0.01 bg=0.00
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N−acyltransferase activity GO:0016410 p=2.6E−02 n=5 fg=0.02 bg=0.01
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metallochaperone activity GO:0016530 p=4.6E−02 n=2 fg=0.01 bg=0.00
neurexin family protein binding GO:0042043 p=4.6E−02 n=2 fg=0.01 bg=0.00
galactosidase activity GO:0015925 p=4.6E−02 n=2 fg=0.01 bg=0.00
Arp2/3 complex binding GO:0071933 p=4.6E−02 n=2 fg=0.01 bg=0.00
acylglycerol lipase activity GO:0047372 p=4.6E−02 n=2 fg=0.01 bg=0.00
U2 snRNA binding GO:0030620 p=4.6E−02 n=2 fg=0.01 bg=0.00
MHC protein binding GO:0042287 p=4.6E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=306/1103 input genes with annotations
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fraction
GO:CC
Fox_Nvec_vc1.1_XM_032374382.2
fraction genes in fg and expected valu
cytoplasmic dynein complex GO:0005868 p=1.3E−03 n=5 fg=0.01 bg=0.00
proton−transporting two−sector ATPase co... GO:0016469 p=4.6E−03 n=5 fg=0.01 bg=0.00
vesicle GO:0031982 p=5.5E−03 n=73 fg=0.21 bg=0.16
lysosome GO:0005764 p=5.9E−03 n=25 fg=0.07 bg=0.04
Cul2−RING ubiquitin ligase complex GO:0031462 p=6.4E−03 n=4 fg=0.01 bg=0.00
microvillus membrane GO:0031528 p=6.4E−03 n=4 fg=0.01 bg=0.00
neuron projection GO:0043005 p=7.2E−03 n=55 fg=0.16 bg=0.12
cortical endoplasmic reticulum GO:0032541 p=7.2E−03 n=3 fg=0.01 bg=0.00
membrane raft GO:0045121 p=7.7E−03 n=17 fg=0.05 bg=0.03
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secretory granule GO:0030141 p=1.5E−02 n=27 fg=0.08 bg=0.05
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intracellular vesicle GO:0097708 p=1.6E−02 n=67 fg=0.20 bg=0.15
Elg1 RFC−like complex GO:0031391 p=1.6E−02 n=2 fg=0.01 bg=0.00
stereocilium tip GO:0032426 p=1.6E−02 n=2 fg=0.01 bg=0.00
collagen and cuticulin−based cuticle ext... GO:0060102 p=1.6E−02 n=2 fg=0.01 bg=0.00
secretory vesicle GO:0099503 p=1.6E−02 n=34 fg=0.10 bg=0.07
large ribosomal subunit GO:0015934 p=1.6E−02 n=10 fg=0.03 bg=0.01
somatodendritic compartment GO:0036477 p=1.9E−02 n=40 fg=0.12 bg=0.09
caveola GO:0005901 p=1.9E−02 n=7 fg=0.02 bg=0.01
nuclear membrane GO:0031965 p=1.9E−02 n=14 fg=0.04 bg=0.02
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organelle membrane contact site GO:0044232 p=3.0E−02 n=3 fg=0.01 bg=0.00
axon cytoplasm GO:1904115 p=3.0E−02 n=3 fg=0.01 bg=0.00
lysosomal membrane GO:0005765 p=3.3E−02 n=11 fg=0.03 bg=0.02
neuron projection cytoplasm GO:0120111 p=4.0E−02 n=4 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=341/1103 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction