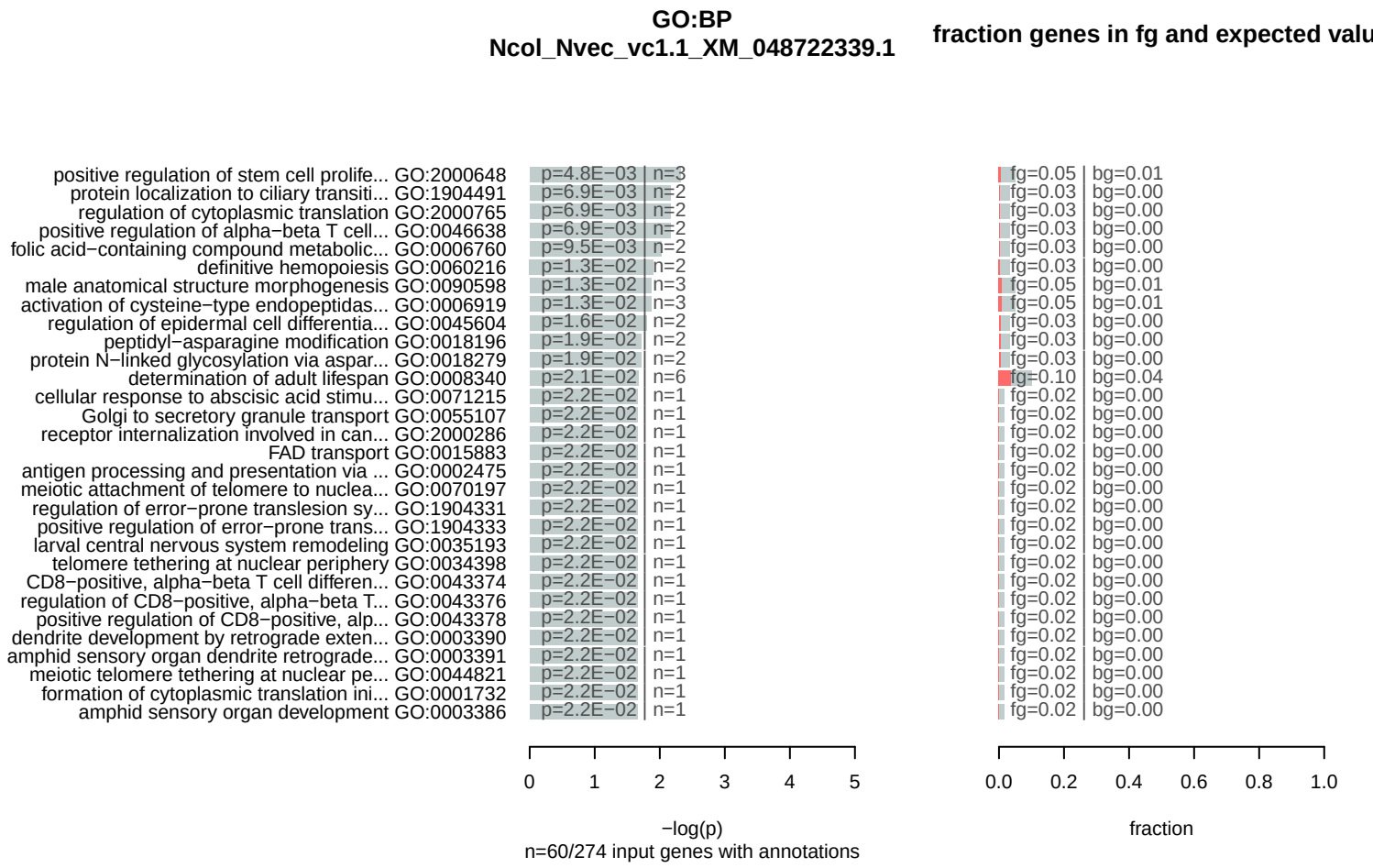
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Ncol_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
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protein localization to ciliary transiti... GO:1904491 p=6.9E−03 n=2 fg=0.03 bg=0.00
regulation of cytoplasmic translation GO:2000765 p=6.9E−03 n=2 fg=0.03 bg=0.00
positive regulation of alpha−beta T cell... GO:0046638 p=6.9E−03 n=2 fg=0.03 bg=0.00
folic acid−containing compound metabolic... GO:0006760 p=9.5E−03 n=2 fg=0.03 bg=0.00
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male anatomical structure morphogenesis GO:0090598 p=1.3E−02 n=3 fg=0.05 bg=0.01
activation of cysteine−type endopeptidas... GO:0006919 p=1.3E−02 n=3 fg=0.05 bg=0.01
regulation of epidermal cell differentia... GO:0045604 p=1.6E−02 n=2 fg=0.03 bg=0.00
peptidyl−asparagine modification GO:0018196 p=1.9E−02 n=2 fg=0.03 bg=0.00
protein N−linked glycosylation via aspar... GO:0018279 p=1.9E−02 n=2 fg=0.03 bg=0.00
determination of adult lifespan GO:0008340 p=2.1E−02 n=6 fg=0.10 bg=0.04
cellular response to abscisic acid stimu... GO:0071215 p=2.2E−02 n=1 fg=0.02 bg=0.00
Golgi to secretory granule transport GO:0055107 p=2.2E−02 n=1 fg=0.02 bg=0.00
receptor internalization involved in can... GO:2000286 p=2.2E−02 n=1 fg=0.02 bg=0.00
FAD transport GO:0015883 p=2.2E−02 n=1 fg=0.02 bg=0.00
antigen processing and presentation via ... GO:0002475 p=2.2E−02 n=1 fg=0.02 bg=0.00
meiotic attachment of telomere to nuclea... GO:0070197 p=2.2E−02 n=1 fg=0.02 bg=0.00
regulation of error−prone translesion sy... GO:1904331 p=2.2E−02 n=1 fg=0.02 bg=0.00
positive regulation of error−prone trans... GO:1904333 p=2.2E−02 n=1 fg=0.02 bg=0.00
larval central nervous system remodeling GO:0035193 p=2.2E−02 n=1 fg=0.02 bg=0.00
telomere tethering at nuclear periphery GO:0034398 p=2.2E−02 n=1 fg=0.02 bg=0.00
CD8−positive, alpha−beta T cell differen... GO:0043374 p=2.2E−02 n=1 fg=0.02 bg=0.00
regulation of CD8−positive, alpha−beta T... GO:0043376 p=2.2E−02 n=1 fg=0.02 bg=0.00
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dendrite development by retrograde exten... GO:0003390 p=2.2E−02 n=1 fg=0.02 bg=0.00
amphid sensory organ dendrite retrograde... GO:0003391 p=2.2E−02 n=1 fg=0.02 bg=0.00
meiotic telomere tethering at nuclear pe... GO:0044821 p=2.2E−02 n=1 fg=0.02 bg=0.00
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n=60/274 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
translation repressor activity GO:0030371 p=3.1E−03 n=2 fg=0.04 bg=0.00
3−phosphoinositide−dependent protein kin... GO:0004676 p=2.3E−02 n=1 fg=0.02 bg=0.00
oxidoreductase activity, acting on the C... GO:0046997 p=2.3E−02 n=1 fg=0.02 bg=0.00
dimethylglycine dehydrogenase activity GO:0047865 p=2.3E−02 n=1 fg=0.02 bg=0.00
ubiquitin−like protein−specific endopept... GO:0070137 p=2.3E−02 n=1 fg=0.02 bg=0.00
SUMO−specific endopeptidase activity GO:0070139 p=2.3E−02 n=1 fg=0.02 bg=0.00
JUN kinase kinase activity GO:0008545 p=2.3E−02 n=1 fg=0.02 bg=0.00
alpha−1,6−mannosylglycoprotein 2−beta−N−... GO:0008455 p=2.3E−02 n=1 fg=0.02 bg=0.00
hedgehog receptor activity GO:0008158 p=2.3E−02 n=1 fg=0.02 bg=0.00
steryl−sulfatase activity GO:0004773 p=2.3E−02 n=1 fg=0.02 bg=0.00
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FAD transmembrane transporter activity GO:0015230 p=2.3E−02 n=1 fg=0.02 bg=0.00
translation factor activity, RNA binding GO:0008135 p=2.6E−02 n=3 fg=0.05 bg=0.01
amide transmembrane transporter activity GO:0042887 p=3.0E−02 n=2 fg=0.04 bg=0.01
translation regulator activity, nucleic ... GO:0090079 p=3.1E−02 n=3 fg=0.05 bg=0.01
BH3 domain binding GO:0051434 p=4.6E−02 n=1 fg=0.02 bg=0.00
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pre−mRNA 3'−splice site binding GO:0030628 p=6.8E−02 n=1 fg=0.02 bg=0.00
tRNA (uracil) methyltransferase activity GO:0016300 p=6.8E−02 n=1 fg=0.02 bg=0.00
UDP−glucosyltransferase activity GO:0035251 p=6.8E−02 n=1 fg=0.02 bg=0.00
caspase binding GO:0089720 p=6.8E−02 n=1 fg=0.02 bg=0.00
death domain binding GO:0070513 p=6.8E−02 n=1 fg=0.02 bg=0.00
lamin binding GO:0005521 p=6.8E−02 n=1 fg=0.02 bg=0.00
mRNA regulatory element binding translat... GO:0000900 p=6.8E−02 n=1 fg=0.02 bg=0.00
sulfuric ester hydrolase activity GO:0008484 p=6.8E−02 n=1 fg=0.02 bg=0.00
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−log(p)
n=55/274 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_048722339.1
fraction genes in fg and expected valu
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polytene chromosome interband GO:0005705 p=2.3E−02 n=2 fg=0.03 bg=0.00
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core−binding factor complex GO:0016513 p=2.4E−02 n=1 fg=0.02 bg=0.00
AP−3 adaptor complex GO:0030123 p=2.4E−02 n=1 fg=0.02 bg=0.00
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box H/ACA scaRNP complex GO:0072589 p=4.8E−02 n=1 fg=0.02 bg=0.00
box H/ACA telomerase RNP complex GO:0090661 p=4.8E−02 n=1 fg=0.02 bg=0.00
DRM complex GO:0070176 p=4.8E−02 n=1 fg=0.02 bg=0.00
TORC2 complex GO:0031932 p=4.8E−02 n=1 fg=0.02 bg=0.00
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centrosome GO:0005813 p=4.9E−02 n=7 fg=0.11 bg=0.05
transcription repressor complex GO:0017053 p=6.8E−02 n=2 fg=0.03 bg=0.01
TORC1 complex GO:0031931 p=7.0E−02 n=1 fg=0.02 bg=0.00
Bcl−2 family protein complex GO:0097136 p=7.0E−02 n=1 fg=0.02 bg=0.00
intrinsic component of nuclear inner mem... GO:0031229 p=7.0E−02 n=1 fg=0.02 bg=0.00
multi−eIF complex GO:0043614 p=7.0E−02 n=1 fg=0.02 bg=0.00
TOR complex GO:0038201 p=7.0E−02 n=1 fg=0.02 bg=0.00
integral component of nuclear inner memb... GO:0005639 p=7.0E−02 n=1 fg=0.02 bg=0.00
intraciliary transport particle A GO:0030991 p=7.0E−02 n=1 fg=0.02 bg=0.00
prefoldin complex GO:0016272 p=7.0E−02 n=1 fg=0.02 bg=0.00
nuclear envelope GO:0005635 p=7.3E−02 n=6 fg=0.09 bg=0.05
organelle envelope GO:0031967 p=7.5E−02 n=11 fg=0.17 bg=0.11
envelope GO:0031975 p=7.5E−02 n=11 fg=0.17 bg=0.11
ciliary basal body GO:0036064 p=7.9E−02 n=3 fg=0.05 bg=0.02
eukaryotic translation initiation factor... GO:0071541 p=9.3E−02 n=1 fg=0.02 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=9.3E−02 n=1 fg=0.02 bg=0.00
0 1 2 3 4 5
−log(p)
n=65/274 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction