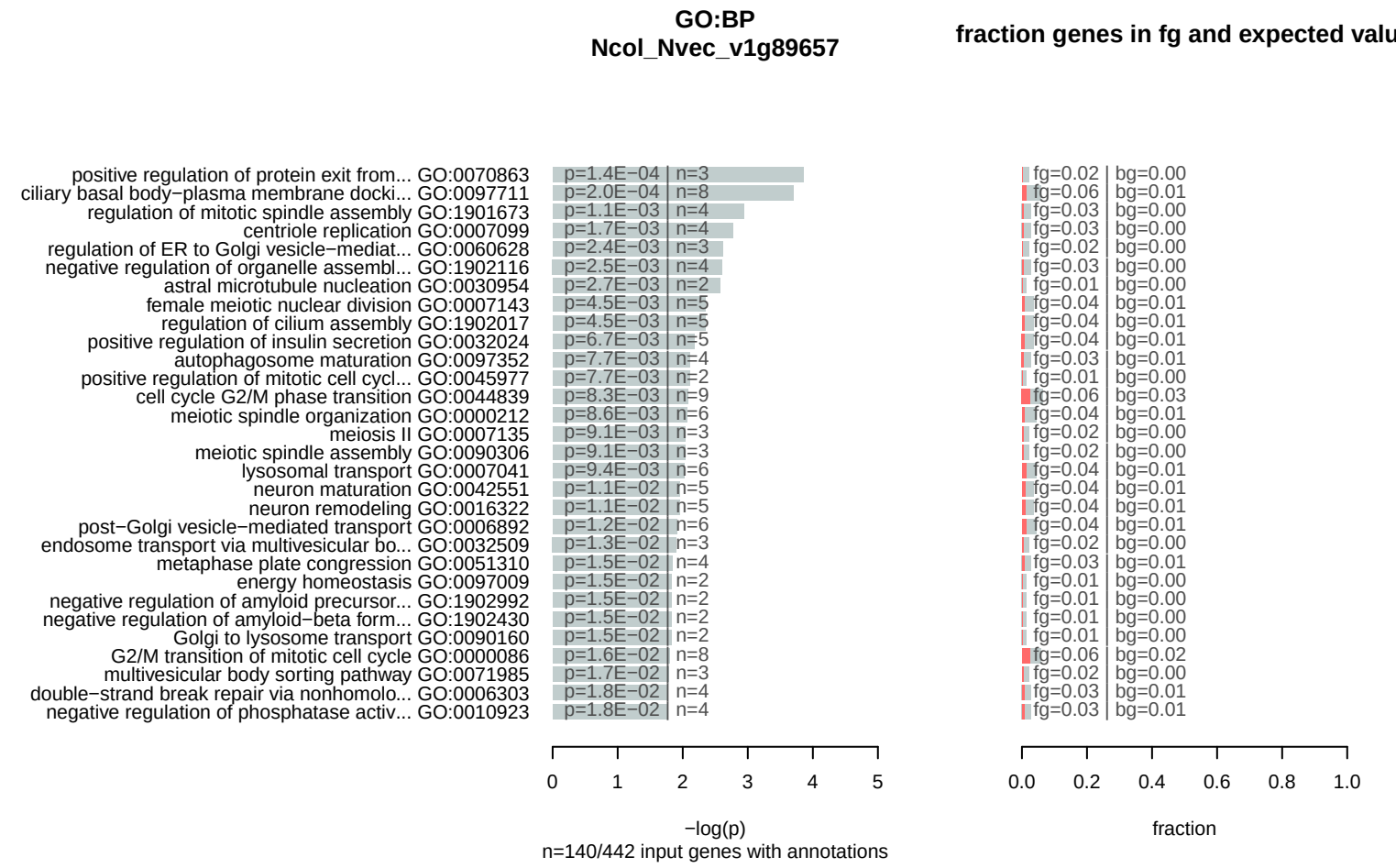
GO:BP
Ncol_Nvec_v1g89657
fraction genes in fg and expected valu
positive regulation of protein exit from... GO:0070863 p=1.4E−04 n=3 fg=0.02 bg=0.00
ciliary basal body−plasma membrane docki... GO:0097711 p=2.0E−04 n=8 fg=0.06 bg=0.01
regulation of mitotic spindle assembly GO:1901673 p=1.1E−03 n=4 fg=0.03 bg=0.00
centriole replication GO:0007099 p=1.7E−03 n=4 fg=0.03 bg=0.00
regulation of ER to Golgi vesicle−mediat... GO:0060628 p=2.4E−03 n=3 fg=0.02 bg=0.00
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astral microtubule nucleation GO:0030954 p=2.7E−03 n=2 fg=0.01 bg=0.00
female meiotic nuclear division GO:0007143 p=4.5E−03 n=5 fg=0.04 bg=0.01
regulation of cilium assembly GO:1902017 p=4.5E−03 n=5 fg=0.04 bg=0.01
positive regulation of insulin secretion GO:0032024 p=6.7E−03 n=5 fg=0.04 bg=0.01
autophagosome maturation GO:0097352 p=7.7E−03 n=4 fg=0.03 bg=0.01
positive regulation of mitotic cell cycl... GO:0045977 p=7.7E−03 n=2 fg=0.01 bg=0.00
cell cycle G2/M phase transition GO:0044839 p=8.3E−03 n=9 fg=0.06 bg=0.03
meiotic spindle organization GO:0000212 p=8.6E−03 n=6 fg=0.04 bg=0.01
meiosis II GO:0007135 p=9.1E−03 n=3 fg=0.02 bg=0.00
meiotic spindle assembly GO:0090306 p=9.1E−03 n=3 fg=0.02 bg=0.00
lysosomal transport GO:0007041 p=9.4E−03 n=6 fg=0.04 bg=0.01
neuron maturation GO:0042551 p=1.1E−02 n=5 fg=0.04 bg=0.01
neuron remodeling GO:0016322 p=1.1E−02 n=5 fg=0.04 bg=0.01
post−Golgi vesicle−mediated transport GO:0006892 p=1.2E−02 n=6 fg=0.04 bg=0.01
endosome transport via multivesicular bo... GO:0032509 p=1.3E−02 n=3 fg=0.02 bg=0.00
metaphase plate congression GO:0051310 p=1.5E−02 n=4 fg=0.03 bg=0.01
energy homeostasis GO:0097009 p=1.5E−02 n=2 fg=0.01 bg=0.00
negative regulation of amyloid precursor... GO:1902992 p=1.5E−02 n=2 fg=0.01 bg=0.00
negative regulation of amyloid−beta form... GO:1902430 p=1.5E−02 n=2 fg=0.01 bg=0.00
Golgi to lysosome transport GO:0090160 p=1.5E−02 n=2 fg=0.01 bg=0.00
G2/M transition of mitotic cell cycle GO:0000086 p=1.6E−02 n=8 fg=0.06 bg=0.02
multivesicular body sorting pathway GO:0071985 p=1.7E−02 n=3 fg=0.02 bg=0.00
double−strand break repair via nonhomolo... GO:0006303 p=1.8E−02 n=4 fg=0.03 bg=0.01
negative regulation of phosphatase activ... GO:0010923 p=1.8E−02 n=4 fg=0.03 bg=0.01
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n=140/442 input genes with annotations
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fraction
GO:MF
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fraction genes in fg and expected valu
protein self−association GO:0043621 p=5.5E−03 n=4 fg=0.03 bg=0.01
toxic substance binding GO:0015643 p=2.3E−02 n=2 fg=0.02 bg=0.00
extracellular ligand−gated ion channel a... GO:0005230 p=2.5E−02 n=3 fg=0.03 bg=0.01
cysteine−type endopeptidase activity GO:0004197 p=3.1E−02 n=3 fg=0.03 bg=0.01
poly−purine tract binding GO:0070717 p=3.3E−02 n=2 fg=0.02 bg=0.00
dynein intermediate chain binding GO:0045505 p=3.3E−02 n=2 fg=0.02 bg=0.00
small GTPase binding GO:0031267 p=3.9E−02 n=10 fg=0.08 bg=0.04
protein heterodimerization activity GO:0046982 p=3.9E−02 n=12 fg=0.10 bg=0.06
calmodulin binding GO:0005516 p=3.9E−02 n=4 fg=0.03 bg=0.01
enzyme binding GO:0019899 p=4.0E−02 n=35 fg=0.29 bg=0.22
protein folding chaperone GO:0044183 p=4.5E−02 n=2 fg=0.02 bg=0.00
transmitter−gated ion channel activity GO:0022824 p=4.5E−02 n=2 fg=0.02 bg=0.00
transmitter−gated channel activity GO:0022835 p=4.5E−02 n=2 fg=0.02 bg=0.00
insulin−like growth factor II binding GO:0031995 p=5.1E−02 n=1 fg=0.01 bg=0.00
heteroduplex DNA loop binding GO:0000404 p=5.1E−02 n=1 fg=0.01 bg=0.00
double−strand/single−strand DNA junction... GO:0000406 p=5.1E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease activity GO:0000213 p=5.1E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=5.1E−02 n=1 fg=0.01 bg=0.00
mannose binding GO:0005537 p=5.1E−02 n=1 fg=0.01 bg=0.00
poly(G) binding GO:0034046 p=5.1E−02 n=1 fg=0.01 bg=0.00
endoribonuclease activity, producing 3'−... GO:0016892 p=5.1E−02 n=1 fg=0.01 bg=0.00
RNA guanylyltransferase activity GO:0008192 p=5.1E−02 n=1 fg=0.01 bg=0.00
tRNA guanylyltransferase activity GO:0008193 p=5.1E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=5.1E−02 n=1 fg=0.01 bg=0.00
anaphase−promoting complex binding GO:0010997 p=5.1E−02 n=1 fg=0.01 bg=0.00
branched−chain−amino−acid transaminase a... GO:0004084 p=5.1E−02 n=1 fg=0.01 bg=0.00
butyryl−CoA dehydrogenase activity GO:0004085 p=5.1E−02 n=1 fg=0.01 bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946 p=5.1E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on the C... GO:0052890 p=5.1E−02 n=1 fg=0.01 bg=0.00
mediator complex binding GO:0036033 p=5.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=120/442 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_v1g89657
fraction genes in fg and expected valu
mitotic spindle pole GO:0097431 p=1.8E−03 n=4 fg=0.03 bg=0.00
centrosome GO:0005813 p=5.3E−03 n=15 fg=0.11 bg=0.05
CHRAC GO:0008623 p=7.8E−03 n=2 fg=0.01 bg=0.00
mitochondrial intermembrane space protei... GO:0042719 p=1.5E−02 n=2 fg=0.01 bg=0.00
centriole GO:0005814 p=2.1E−02 n=5 fg=0.04 bg=0.01
mediator complex GO:0016592 p=2.2E−02 n=3 fg=0.02 bg=0.00
kinetochore GO:0000776 p=2.3E−02 n=5 fg=0.04 bg=0.01
ESCRT complex GO:0036452 p=2.7E−02 n=3 fg=0.02 bg=0.00
multivesicular body GO:0005771 p=2.7E−02 n=3 fg=0.02 bg=0.00
chromosome, centromeric region GO:0000775 p=3.3E−02 n=6 fg=0.04 bg=0.02
ESCRT III complex GO:0000815 p=3.5E−02 n=2 fg=0.01 bg=0.00
meiotic spindle GO:0072687 p=3.5E−02 n=2 fg=0.01 bg=0.00
TIM23 mitochondrial import inner membran... GO:0005744 p=3.5E−02 n=2 fg=0.01 bg=0.00
condensed chromosome, centromeric region GO:0000779 p=4.5E−02 n=5 fg=0.04 bg=0.01
protein serine/threonine phosphatase com... GO:0008287 p=4.7E−02 n=3 fg=0.02 bg=0.01
endosome membrane GO:0010008 p=5.1E−02 n=8 fg=0.06 bg=0.03
rhabdomere microvillus GO:0035996 p=5.2E−02 n=1 fg=0.01 bg=0.00
rhabdomere microvillus membrane GO:0035997 p=5.2E−02 n=1 fg=0.01 bg=0.00
tRNA−intron endonuclease complex GO:0000214 p=5.2E−02 n=1 fg=0.01 bg=0.00
phagolysosome GO:0032010 p=5.2E−02 n=1 fg=0.01 bg=0.00
FHF complex GO:0070695 p=5.2E−02 n=1 fg=0.01 bg=0.00
alveolar lamellar body GO:0097208 p=5.2E−02 n=1 fg=0.01 bg=0.00
MutSbeta complex GO:0032302 p=5.2E−02 n=1 fg=0.01 bg=0.00
TIM22 mitochondrial import inner membran... GO:0042721 p=5.2E−02 n=1 fg=0.01 bg=0.00
DNA topoisomerase type II (double strand... GO:0009330 p=5.2E−02 n=1 fg=0.01 bg=0.00
rhabdomere membrane GO:0033583 p=5.2E−02 n=1 fg=0.01 bg=0.00
meiotic cohesin complex GO:0030893 p=5.2E−02 n=1 fg=0.01 bg=0.00
mRNA cap methyltransferase complex GO:0031533 p=5.2E−02 n=1 fg=0.01 bg=0.00
phagolysosome membrane GO:0061474 p=5.2E−02 n=1 fg=0.01 bg=0.00
RES complex GO:0070274 p=5.2E−02 n=1 fg=0.01 bg=0.00
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n=141/442 input genes with annotations
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fraction