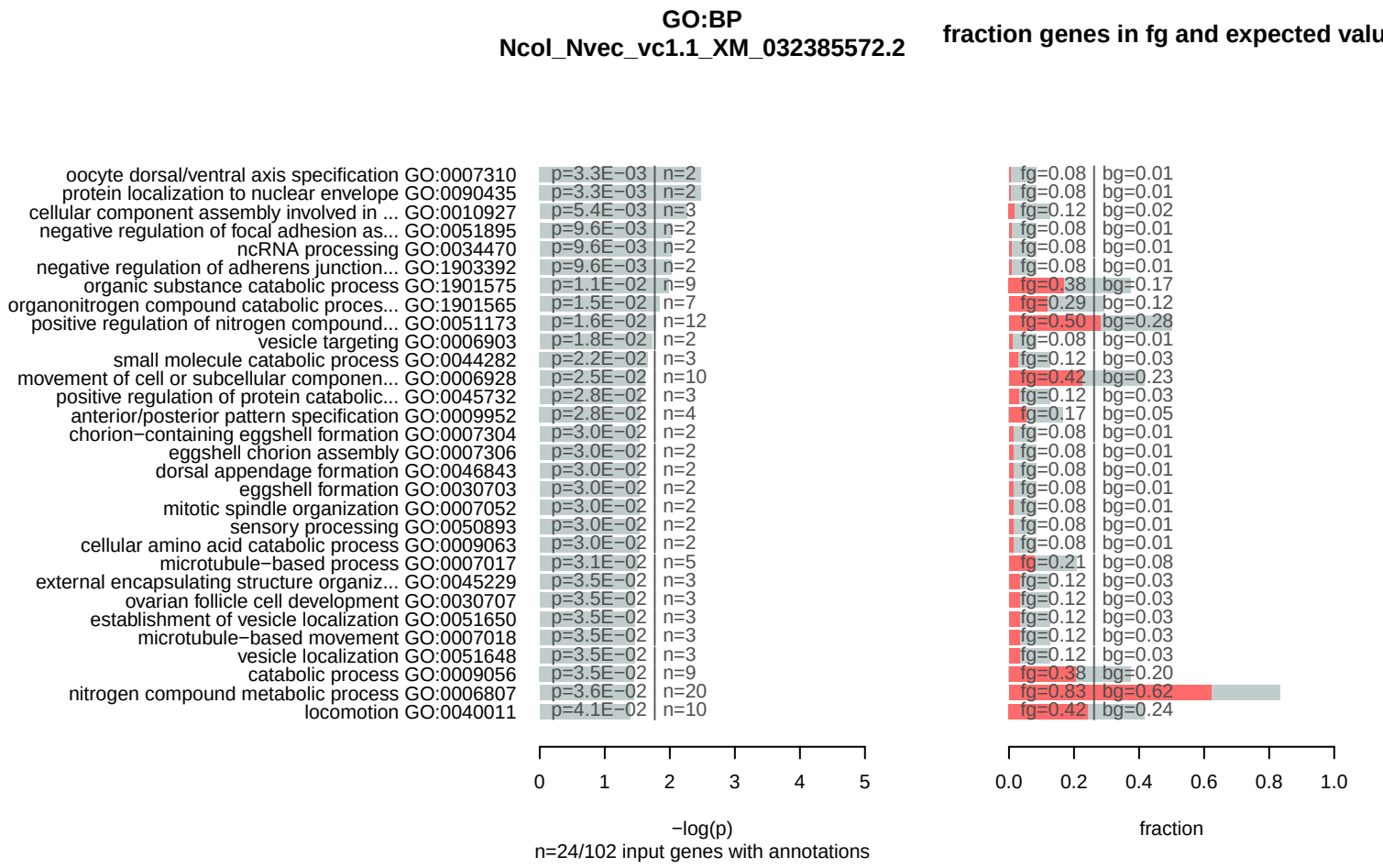
GO:BP
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
oocyte dorsal/ventral axis specification GO:0007310 p=3.3E−03 n=2 fg=0.08 bg=0.01
protein localization to nuclear envelope GO:0090435 p=3.3E−03 n=2 fg=0.08 bg=0.01
cellular component assembly involved in ... GO:0010927 p=5.4E−03 n=3 fg=0.12 bg=0.02
negative regulation of focal adhesion as... GO:0051895 p=9.6E−03 n=2 fg=0.08 bg=0.01
ncRNA processing GO:0034470 p=9.6E−03 n=2 fg=0.08 bg=0.01
negative regulation of adherens junction... GO:1903392 p=9.6E−03 n=2 fg=0.08 bg=0.01
organic substance catabolic process GO:1901575 p=1.1E−02 n=9 fg=0.38 bg=0.17
organonitrogen compound catabolic proces... GO:1901565 p=1.5E−02 n=7 fg=0.29 bg=0.12
positive regulation of nitrogen compound... GO:0051173 p=1.6E−02 n=12 fg=0.50 bg=0.28
vesicle targeting GO:0006903 p=1.8E−02 n=2 fg=0.08 bg=0.01
small molecule catabolic process GO:0044282 p=2.2E−02 n=3 fg=0.12 bg=0.03
movement of cell or subcellular componen... GO:0006928 p=2.5E−02 n=10 fg=0.42 bg=0.23
positive regulation of protein catabolic... GO:0045732 p=2.8E−02 n=3 fg=0.12 bg=0.03
anterior/posterior pattern specification GO:0009952 p=2.8E−02 n=4 fg=0.17 bg=0.05
chorion−containing eggshell formation GO:0007304 p=3.0E−02 n=2 fg=0.08 bg=0.01
eggshell chorion assembly GO:0007306 p=3.0E−02 n=2 fg=0.08 bg=0.01
dorsal appendage formation GO:0046843 p=3.0E−02 n=2 fg=0.08 bg=0.01
eggshell formation GO:0030703 p=3.0E−02 n=2 fg=0.08 bg=0.01
mitotic spindle organization GO:0007052 p=3.0E−02 n=2 fg=0.08 bg=0.01
sensory processing GO:0050893 p=3.0E−02 n=2 fg=0.08 bg=0.01
cellular amino acid catabolic process GO:0009063 p=3.0E−02 n=2 fg=0.08 bg=0.01
microtubule−based process GO:0007017 p=3.1E−02 n=5 fg=0.21 bg=0.08
external encapsulating structure organiz... GO:0045229 p=3.5E−02 n=3 fg=0.12 bg=0.03
ovarian follicle cell development GO:0030707 p=3.5E−02 n=3 fg=0.12 bg=0.03
establishment of vesicle localization GO:0051650 p=3.5E−02 n=3 fg=0.12 bg=0.03
microtubule−based movement GO:0007018 p=3.5E−02 n=3 fg=0.12 bg=0.03
vesicle localization GO:0051648 p=3.5E−02 n=3 fg=0.12 bg=0.03
catabolic process GO:0009056 p=3.5E−02 n=9 fg=0.38 bg=0.20
nitrogen compound metabolic process GO:0006807 p=3.6E−02 n=20 fg=0.83 bg=0.62
locomotion GO:0040011 p=4.1E−02 n=10 fg=0.42 bg=0.24
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−log(p)
n=24/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
excitatory extracellular ligand−gated io... GO:0005231 p=3.4E−02 n=2 fg=0.09 bg=0.01
ammonium ion binding GO:0070405 p=4.9E−02 n=2 fg=0.09 bg=0.02
dystroglycan binding GO:0002162 p=6.3E+02 n=1 fg=0.04 bg=0.00
phosphofructokinase activity GO:0008443 p=6.3E+02 n=1 fg=0.04 bg=0.00
glucosylceramidase activity GO:0004348 p=6.3E+02 n=1 fg=0.04 bg=0.00
fructose−6−phosphate binding GO:0070095 p=6.3E+02 n=1 fg=0.04 bg=0.00
fructose−2,6−bisphosphate 2−phosphatase ... GO:0004331 p=6.3E+02 n=1 fg=0.04 bg=0.00
threonine−type peptidase activity GO:0070003 p=6.3E+02 n=1 fg=0.04 bg=0.00
phosphatidylserine binding GO:0001786 p=6.3E+02 n=1 fg=0.04 bg=0.00
modified amino acid binding GO:0072341 p=6.3E+02 n=1 fg=0.04 bg=0.00
beta−aspartyl−peptidase activity GO:0008798 p=6.3E+02 n=1 fg=0.04 bg=0.00
peptidyl−prolyl cis−trans isomerase acti... GO:0003755 p=6.3E+02 n=1 fg=0.04 bg=0.00
phosphatidylinositol−4−phosphate binding GO:0070273 p=6.3E+02 n=1 fg=0.04 bg=0.00
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cis−trans isomerase activity GO:0016859 p=6.3E+02 n=1 fg=0.04 bg=0.00
sugar−phosphatase activity GO:0050308 p=6.3E+02 n=1 fg=0.04 bg=0.00
acetylcholine−gated cation−selective cha... GO:0022848 p=6.3E+02 n=1 fg=0.04 bg=0.00
acetyltransferase activator activity GO:0010698 p=6.3E+02 n=1 fg=0.04 bg=0.00
postsynaptic neurotransmitter receptor a... GO:0098960 p=6.3E+02 n=1 fg=0.04 bg=0.00
acetylcholine receptor activity GO:0015464 p=6.3E+02 n=1 fg=0.04 bg=0.00
carbohydrate kinase activity GO:0019200 p=6.3E+02 n=1 fg=0.04 bg=0.00
carbohydrate phosphatase activity GO:0019203 p=6.3E+02 n=1 fg=0.04 bg=0.00
neurotransmitter receptor activity invol... GO:0099529 p=6.3E+02 n=1 fg=0.04 bg=0.00
omega peptidase activity GO:0008242 p=6.3E+02 n=1 fg=0.04 bg=0.00
transmitter−gated ion channel activity i... GO:1904315 p=6.3E+02 n=1 fg=0.04 bg=0.00
6−phosphofructo−2−kinase activity GO:0003873 p=6.3E+02 n=1 fg=0.04 bg=0.00
chloride channel regulator activity GO:0017081 p=6.3E+02 n=1 fg=0.04 bg=0.00
acetylcholine binding GO:0042166 p=6.3E+02 n=1 fg=0.04 bg=0.00
toxic substance binding GO:0015643 p=6.3E+02 n=1 fg=0.04 bg=0.00
structural constituent of ribosome GO:0003735 p=6.3E+02 n=1 fg=0.04 bg=0.00
0 1 2 3 4 5
−log(p)
n=23/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
cytoplasmic microtubule GO:0005881 p=1.8E−02 n=2 fg=0.09 bg=0.01
smooth endoplasmic reticulum GO:0005790 p=4.1E−02 n=2 fg=0.09 bg=0.01
transferase complex, transferring phosph... GO:0061695 p=5.5E+02 n=2 fg=0.09 bg=0.02
chromosomal region GO:0098687 p=5.5E+02 n=2 fg=0.09 bg=0.02
6−phosphofructo−2−kinase/fructose−2,6−bi... GO:0043540 p=5.7E+02 n=1 fg=0.04 bg=0.00
cortical microtubule plus−end GO:1903754 p=5.7E+02 n=1 fg=0.04 bg=0.00
ribosomal subunit GO:0044391 p=5.7E+02 n=1 fg=0.04 bg=0.00
microtubule plus−end GO:0035371 p=5.7E+02 n=1 fg=0.04 bg=0.00
spindle microtubule GO:0005876 p=5.7E+02 n=1 fg=0.04 bg=0.00
chromosome, telomeric region GO:0000781 p=5.7E+02 n=1 fg=0.04 bg=0.00
kinetochore microtubule GO:0005828 p=5.7E+02 n=1 fg=0.04 bg=0.00
cortical microtubule cytoskeleton GO:0030981 p=5.7E+02 n=1 fg=0.04 bg=0.00
organellar ribosome GO:0000313 p=5.7E+02 n=1 fg=0.04 bg=0.00
kinetochore GO:0000776 p=5.7E+02 n=1 fg=0.04 bg=0.00
organellar small ribosomal subunit GO:0000314 p=5.7E+02 n=1 fg=0.04 bg=0.00
cytoplasmic microtubule plus−end GO:1904511 p=5.7E+02 n=1 fg=0.04 bg=0.00
integrator complex GO:0032039 p=5.7E+02 n=1 fg=0.04 bg=0.00
cortical microtubule GO:0055028 p=5.7E+02 n=1 fg=0.04 bg=0.00
mitochondrial ribosome GO:0005761 p=5.7E+02 n=1 fg=0.04 bg=0.00
mitochondrial small ribosomal subunit GO:0005763 p=5.7E+02 n=1 fg=0.04 bg=0.00
small ribosomal subunit GO:0015935 p=5.7E+02 n=1 fg=0.04 bg=0.00
ER to Golgi transport vesicle membrane GO:0012507 p=5.7E+02 n=1 fg=0.04 bg=0.00
U2−type spliceosomal complex GO:0005684 p=5.7E+02 n=1 fg=0.04 bg=0.00
centrosomal corona GO:0031592 p=5.7E+02 n=1 fg=0.04 bg=0.00
U2 snRNP GO:0005686 p=5.7E+02 n=1 fg=0.04 bg=0.00
acetylcholine−gated channel complex GO:0005892 p=5.7E+02 n=1 fg=0.04 bg=0.00
perinuclear endoplasmic reticulum GO:0097038 p=5.7E+02 n=1 fg=0.04 bg=0.00
microtubule GO:0005874 p=7.1E−02 n=2 fg=0.09 bg=0.02
chromosome GO:0005694 p=7.4E−02 n=4 fg=0.17 bg=0.07
mitochondrial matrix GO:0005759 p=8.8E−02 n=2 fg=0.09 bg=0.02
0 1 2 3 4 5
−log(p)
n=23/102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction