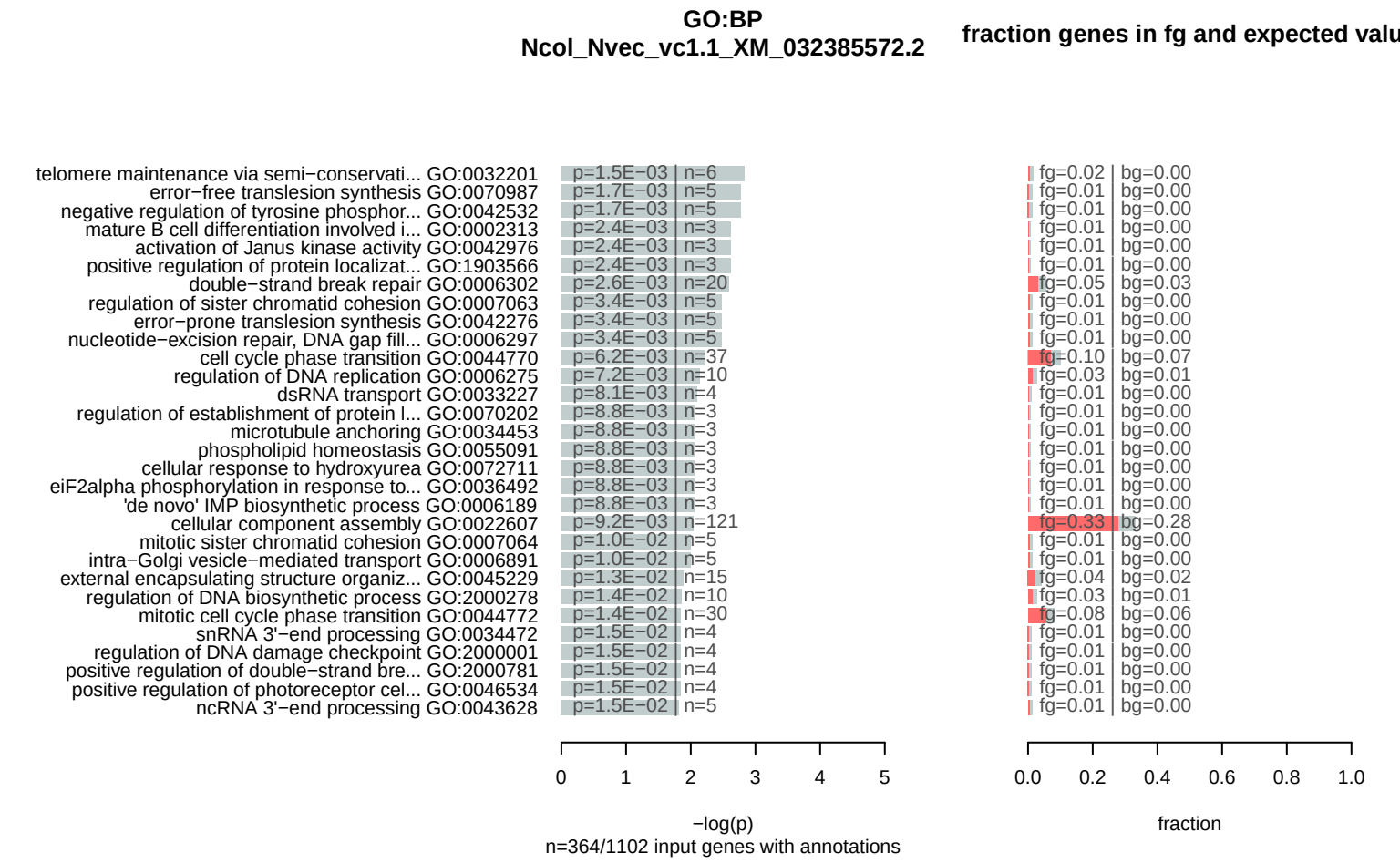
GO:BP
Ncol_Nvec_vc1.1_XM_032385572.2
fraction genes in fg and expected valu
telomere maintenance via semi−conservati... GO:0032201 p=1.5E−03 n=6 fg=0.02 bg=0.00
error−free translesion synthesis GO:0070987 p=1.7E−03 n=5 fg=0.01 bg=0.00
negative regulation of tyrosine phosphor... GO:0042532 p=1.7E−03 n=5 fg=0.01 bg=0.00
mature B cell differentiation involved i... GO:0002313 p=2.4E−03 n=3 fg=0.01 bg=0.00
activation of Janus kinase activity GO:0042976 p=2.4E−03 n=3 fg=0.01 bg=0.00
positive regulation of protein localizat... GO:1903566 p=2.4E−03 n=3 fg=0.01 bg=0.00
double−strand break repair GO:0006302 p=2.6E−03 n=20 fg=0.05 bg=0.03
regulation of sister chromatid cohesion GO:0007063 p=3.4E−03 n=5 fg=0.01 bg=0.00
error−prone translesion synthesis GO:0042276 p=3.4E−03 n=5 fg=0.01 bg=0.00
nucleotide−excision repair, DNA gap fill... GO:0006297 p=3.4E−03 n=5 fg=0.01 bg=0.00
cell cycle phase transition GO:0044770 p=6.2E−03 n=37 fg=0.10 bg=0.07
regulation of DNA replication GO:0006275 p=7.2E−03 n=10 fg=0.03 bg=0.01
dsRNA transport GO:0033227 p=8.1E−03 n=4 fg=0.01 bg=0.00
regulation of establishment of protein l... GO:0070202 p=8.8E−03 n=3 fg=0.01 bg=0.00
microtubule anchoring GO:0034453 p=8.8E−03 n=3 fg=0.01 bg=0.00
phospholipid homeostasis GO:0055091 p=8.8E−03 n=3 fg=0.01 bg=0.00
cellular response to hydroxyurea GO:0072711 p=8.8E−03 n=3 fg=0.01 bg=0.00
eiF2alpha phosphorylation in response to... GO:0036492 p=8.8E−03 n=3 fg=0.01 bg=0.00
'de novo' IMP biosynthetic process GO:0006189 p=8.8E−03 n=3 fg=0.01 bg=0.00
cellular component assembly GO:0022607 p=9.2E−03 n=121 fg=0.33 bg=0.28
mitotic sister chromatid cohesion GO:0007064 p=1.0E−02 n=5 fg=0.01 bg=0.00
intra−Golgi vesicle−mediated transport GO:0006891 p=1.0E−02 n=5 fg=0.01 bg=0.00
external encapsulating structure organiz... GO:0045229 p=1.3E−02 n=15 fg=0.04 bg=0.02
regulation of DNA biosynthetic process GO:2000278 p=1.4E−02 n=10 fg=0.03 bg=0.01
mitotic cell cycle phase transition GO:0044772 p=1.4E−02 n=30 fg=0.08 bg=0.06
snRNA 3'−end processing GO:0034472 p=1.5E−02 n=4 fg=0.01 bg=0.00
regulation of DNA damage checkpoint GO:2000001 p=1.5E−02 n=4 fg=0.01 bg=0.00
positive regulation of double−strand bre... GO:2000781 p=1.5E−02 n=4 fg=0.01 bg=0.00
positive regulation of photoreceptor cel... GO:0046534 p=1.5E−02 n=4 fg=0.01 bg=0.00
ncRNA 3'−end processing GO:0043628 p=1.5E−02 n=5 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=364/1102 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
single−stranded DNA binding GO:0003697 p=2.2E−03 n=10 fg=0.03 bg=0.01
nucleotidyltransferase activity GO:0016779 p=7.6E−03 n=11 fg=0.04 bg=0.02
armadillo repeat domain binding GO:0070016 p=1.6E−02 n=2 fg=0.01 bg=0.00
inositol monophosphate 4−phosphatase act... GO:0052833 p=1.6E−02 n=2 fg=0.01 bg=0.00
inositol monophosphate phosphatase activ... GO:0052834 p=1.6E−02 n=2 fg=0.01 bg=0.00
5S rDNA binding GO:0080084 p=1.6E−02 n=2 fg=0.01 bg=0.00
eukaryotic translation initiation factor... GO:0004694 p=1.6E−02 n=2 fg=0.01 bg=0.00
RNA 2'−O−methyltransferase activity GO:0062105 p=1.6E−02 n=2 fg=0.01 bg=0.00
calcium−independent phospholipase A2 act... GO:0047499 p=1.6E−02 n=2 fg=0.01 bg=0.00
citrate transmembrane transporter activi... GO:0015137 p=1.6E−02 n=2 fg=0.01 bg=0.00
microtubule motor activity GO:0003777 p=1.8E−02 n=5 fg=0.02 bg=0.01
unfolded protein binding GO:0051082 p=2.1E−02 n=10 fg=0.03 bg=0.02
DNA−directed DNA polymerase activity GO:0003887 p=2.5E−02 n=5 fg=0.02 bg=0.01
DNA polymerase activity GO:0034061 p=2.5E−02 n=5 fg=0.02 bg=0.01
translation initiation factor binding GO:0031369 p=2.5E−02 n=5 fg=0.02 bg=0.01
peptide antigen binding GO:0042605 p=3.1E−02 n=3 fg=0.01 bg=0.00
L−cystine transmembrane transporter acti... GO:0015184 p=3.1E−02 n=3 fg=0.01 bg=0.00
snRNP binding GO:0070990 p=3.1E−02 n=3 fg=0.01 bg=0.00
protein phosphatase regulator activity GO:0019888 p=3.4E−02 n=5 fg=0.02 bg=0.01
adenylyltransferase activity GO:0070566 p=4.2E−02 n=4 fg=0.01 bg=0.00
active transmembrane transporter activit... GO:0022804 p=4.2E−02 n=16 fg=0.05 bg=0.03
manganese ion binding GO:0030145 p=4.2E−02 n=6 fg=0.02 bg=0.01
catalytic activity, acting on DNA GO:0140097 p=4.5E−02 n=14 fg=0.05 bg=0.03
annealing activity GO:0140666 p=4.5E−02 n=2 fg=0.01 bg=0.00
RNA polymerase III transcription regulat... GO:0001016 p=4.5E−02 n=2 fg=0.01 bg=0.00
minus−end−directed microtubule motor act... GO:0008569 p=4.5E−02 n=2 fg=0.01 bg=0.00
tricarboxylic acid transmembrane transpo... GO:0015142 p=4.5E−02 n=2 fg=0.01 bg=0.00
protein folding chaperone GO:0044183 p=4.9E−02 n=3 fg=0.01 bg=0.00
rRNA methyltransferase activity GO:0008649 p=4.9E−02 n=3 fg=0.01 bg=0.00
polynucleotide adenylyltransferase activ... GO:0004652 p=4.9E−02 n=3 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=303/1102 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
centrosome GO:0005813 p=1.9E−03 n=31 fg=0.09 bg=0.05
nuclear DNA−directed RNA polymerase comp... GO:0055029 p=2.1E−03 n=14 fg=0.04 bg=0.02
DNA replication factor A complex GO:0005662 p=2.3E−03 n=3 fg=0.01 bg=0.00
precatalytic spliceosome GO:0071011 p=2.3E−03 n=6 fg=0.02 bg=0.00
U2 snRNP GO:0005686 p=7.6E−03 n=4 fg=0.01 bg=0.00
replication fork GO:0005657 p=1.2E−02 n=9 fg=0.03 bg=0.01
cyclin−dependent protein kinase holoenzy... GO:0000307 p=1.4E−02 n=4 fg=0.01 bg=0.00
U12−type spliceosomal complex GO:0005689 p=1.4E−02 n=4 fg=0.01 bg=0.00
cytoplasmic cyclin−dependent protein kin... GO:0000308 p=1.7E−02 n=2 fg=0.01 bg=0.00
chaperonin−containing T−complex GO:0005832 p=1.9E−02 n=3 fg=0.01 bg=0.00
DNA packaging complex GO:0044815 p=2.0E−02 n=8 fg=0.02 bg=0.01
centriolar satellite GO:0034451 p=2.2E−02 n=4 fg=0.01 bg=0.00
RNA polymerase II, holoenzyme GO:0016591 p=2.2E−02 n=10 fg=0.03 bg=0.01
chromosome GO:0005694 p=2.4E−02 n=45 fg=0.13 bg=0.09
integrator complex GO:0032039 p=3.3E−02 n=4 fg=0.01 bg=0.00
nuclear replisome GO:0043601 p=3.3E−02 n=6 fg=0.02 bg=0.00
replisome GO:0030894 p=3.3E−02 n=6 fg=0.02 bg=0.00
sperm midpiece GO:0097225 p=3.4E−02 n=3 fg=0.01 bg=0.00
dendrite terminus GO:0044292 p=3.4E−02 n=3 fg=0.01 bg=0.00
transcription factor TFTC complex GO:0033276 p=3.4E−02 n=3 fg=0.01 bg=0.00
MCM complex GO:0042555 p=3.4E−02 n=3 fg=0.01 bg=0.00
photoreceptor connecting cilium GO:0032391 p=3.8E−02 n=5 fg=0.01 bg=0.01
Golgi medial cisterna GO:0005797 p=3.8E−02 n=5 fg=0.01 bg=0.01
specific granule membrane GO:0035579 p=3.9E−02 n=6 fg=0.02 bg=0.01
chromatin GO:0000785 p=4.4E−02 n=24 fg=0.07 bg=0.05
pronucleus GO:0045120 p=4.6E−02 n=4 fg=0.01 bg=0.00
cohesin complex GO:0008278 p=4.8E−02 n=2 fg=0.01 bg=0.00
integral component of nuclear inner memb... GO:0005639 p=4.8E−02 n=2 fg=0.01 bg=0.00
Ctf18 RFC−like complex GO:0031390 p=4.8E−02 n=2 fg=0.01 bg=0.00
zona pellucida receptor complex GO:0002199 p=4.8E−02 n=2 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=357/1102 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction