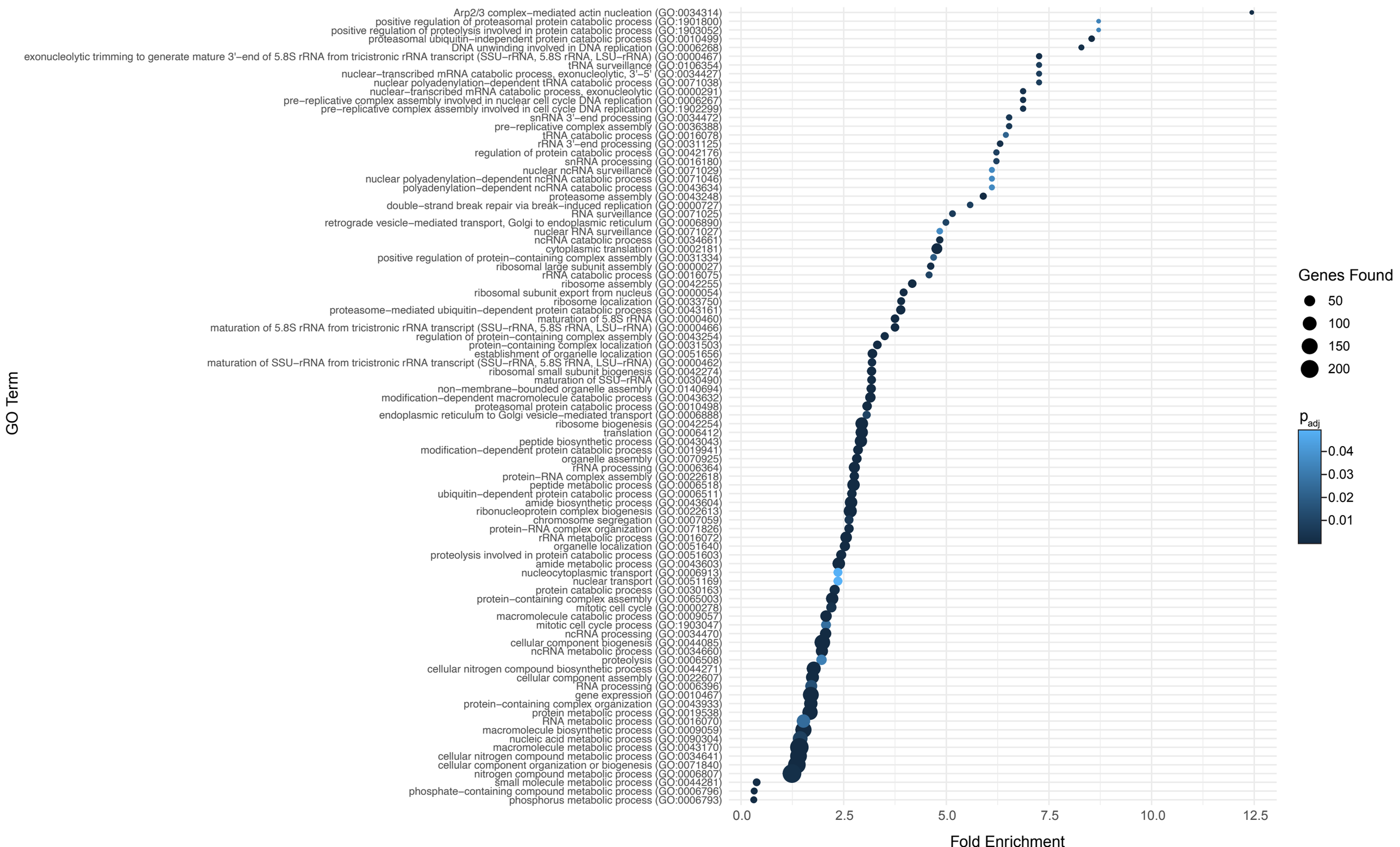
Arp2/3 complex−mediated actin nucleation (GO:0034314)
positive regulation of proteasomal protein catabolic process (GO:1901800)
positive regulation of proteolysis involved in protein catabolic process (GO:1903052)
proteasomal ubiquitin−independent protein catabolic process (GO:0010499)
DNA unwinding involved in DNA replication (GO:0006268)
exonucleolytic trimming to generate mature 3'−end of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA) (GO:0000467)
tRNA surveillance (GO:0106354)
nuclear−transcribed mRNA catabolic process, exonucleolytic, 3'−5' (GO:0034427)
nuclear polyadenylation−dependent tRNA catabolic process (GO:0071038)
nuclear−transcribed mRNA catabolic process, exonucleolytic (GO:0000291)
pre−replicative complex assembly involved in nuclear cell cycle DNA replication (GO:0006267)
pre−replicative complex assembly involved in cell cycle DNA replication (GO:1902299)
snRNA 3'−end processing (GO:0034472)
pre−replicative complex assembly (GO:0036388)
tRNA catabolic process (GO:0016078)
rRNA 3'−end processing (GO:0031125)
regulation of protein catabolic process (GO:0042176)
snRNA processing (GO:0016180)
nuclear ncRNA surveillance (GO:0071029)
nuclear polyadenylation−dependent ncRNA catabolic process (GO:0071046)
polyadenylation−dependent ncRNA catabolic process (GO:0043634)
proteasome assembly (GO:0043248)
double−strand break repair via break−induced replication (GO:0000727)
RNA surveillance (GO:0071025)
retrograde vesicle−mediated transport, Golgi to endoplasmic reticulum (GO:0006890)
nuclear RNA surveillance (GO:0071027)
ncRNA catabolic process (GO:0034661)
cytoplasmic translation (GO:0002181)
positive regulation of protein−containing complex assembly (GO:0031334)
ribosomal large subunit assembly (GO:0000027)
rRNA catabolic process (GO:0016075)
ribosome assembly (GO:0042255)
ribosomal subunit export from nucleus (GO:0000054)
ribosome localization (GO:0033750)
proteasome−mediated ubiquitin−dependent protein catabolic process (GO:0043161)
maturation of 5.8S rRNA (GO:0000460)
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA) (GO:0000466)
regulation of protein−containing complex assembly (GO:0043254)
protein−containing complex localization (GO:0031503)
establishment of organelle localization (GO:0051656)
maturation of SSU−rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA) (GO:0000462)
ribosomal small subunit biogenesis (GO:0042274)
maturation of SSU−rRNA (GO:0030490)
non−membrane−bounded organelle assembly (GO:0140694)
modification−dependent macromolecule catabolic process (GO:0043632)
proteasomal protein catabolic process (GO:0010498)
endoplasmic reticulum to Golgi vesicle−mediated transport (GO:0006888)
ribosome biogenesis (GO:0042254)
translation (GO:0006412)
peptide biosynthetic process (GO:0043043)
modification−dependent protein catabolic process (GO:0019941)
organelle assembly (GO:0070925)
rRNA processing (GO:0006364)
protein−RNA complex assembly (GO:0022618)
peptide metabolic process (GO:0006518)
ubiquitin−dependent protein catabolic process (GO:0006511)
amide biosynthetic process (GO:0043604)
ribonucleoprotein complex biogenesis (GO:0022613)
chromosome segregation (GO:0007059)
protein−RNA complex organization (GO:0071826)
rRNA metabolic process (GO:0016072)
organelle localization (GO:0051640)
proteolysis involved in protein catabolic process (GO:0051603)
amide metabolic process (GO:0043603)
nucleocytoplasmic transport (GO:0006913)
nuclear transport (GO:0051169)
protein catabolic process (GO:0030163)
protein−containing complex assembly (GO:0065003)
mitotic cell cycle (GO:0000278)
macromolecule catabolic process (GO:0009057)
mitotic cell cycle process (GO:1903047)
ncRNA processing (GO:0034470)
cellular component biogenesis (GO:0044085)
ncRNA metabolic process (GO:0034660)
proteolysis (GO:0006508)
cellular nitrogen compound biosynthetic process (GO:0044271)
cellular component assembly (GO:0022607)
RNA processing (GO:0006396)
gene expression (GO:0010467)
protein−containing complex organization (GO:0043933)
protein metabolic process (GO:0019538)
RNA metabolic process (GO:0016070)
macromolecule biosynthetic process (GO:0009059)
nucleic acid metabolic process (GO:0090304)
macromolecule metabolic process (GO:0043170)
cellular nitrogen compound metabolic process (GO:0034641)
cellular component organization or biogenesis (GO:0071840)
nitrogen compound metabolic process (GO:0006807)
small molecule metabolic process (GO:0044281)
phosphate−containing compound metabolic process (GO:0006796)
phosphorus metabolic process (GO:0006793)
GO Term
0.0
2.5
5.0
7.5
10.0
12.5
Fold Enrichment
Genes Found
50
100
150
200
p_{adj}
0.04
0.03
0.02
0.01