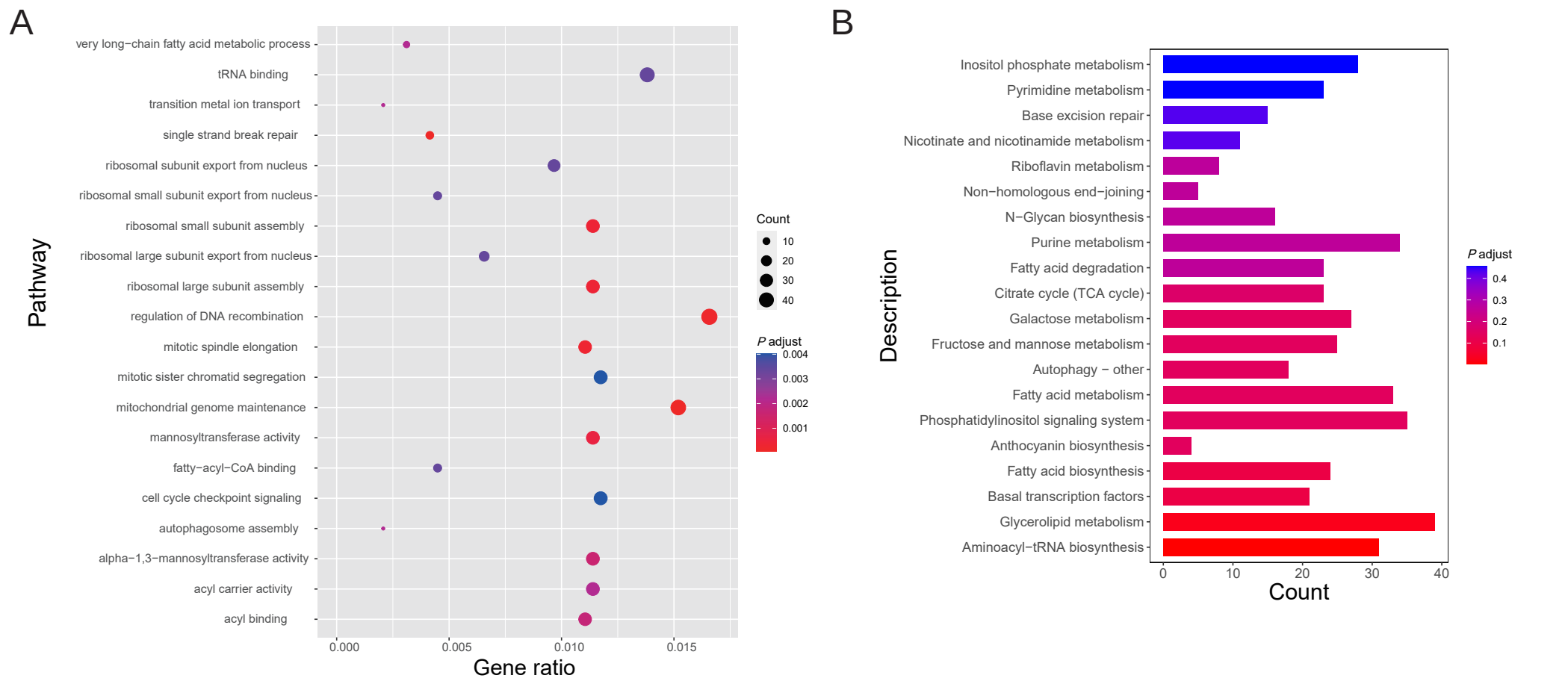
A
very long−chain fatty acid metabolic process
tRNA binding
transition metal ion transport
single strand break repair
ribosomal subunit export from nucleus
ribosomal small subunit export from nucleus
ribosomal small subunit assembly
ribosomal large subunit export from nucleus
ribosomal large subunit assembly
regulation of DNA recombination
mitotic spindle elongation
mitotic sister chromatid segregation
mitochondrial genome maintenance
mannosyltransferase activity
fatty−acyl−CoA binding
cell cycle checkpoint signaling
autophagosome assembly
alpha−1,3−mannosyltransferase activity
acyl carrier activity
acyl binding
Pathway
0.000
0.005
0.010
0.015
Gene ratio
Count
10
20
30
40
P adjust
0.004
0.003
0.002
0.001
B
Inositol phosphate metabolism
Pyrimidine metabolism
Base excision repair
Nicotinate and nicotinamide metabolism
Riboflavin metabolism
Non−homologous end−joining
N−Glycan biosynthesis
Purine metabolism
Fatty acid degradation
Citrate cycle (TCA cycle)
Galactose metabolism
Fructose and mannose metabolism
Autophagy − other
Fatty acid metabolism
Phosphatidylinositol signaling system
Anthocyanin biosynthesis
Fatty acid biosynthesis
Basal transcription factors
Glycerolipid metabolism
Aminoacyl−tRNA biosynthesis
Description
0
10
20
30
40
Count
P adjust
0.4
0.3
0.2
0.1