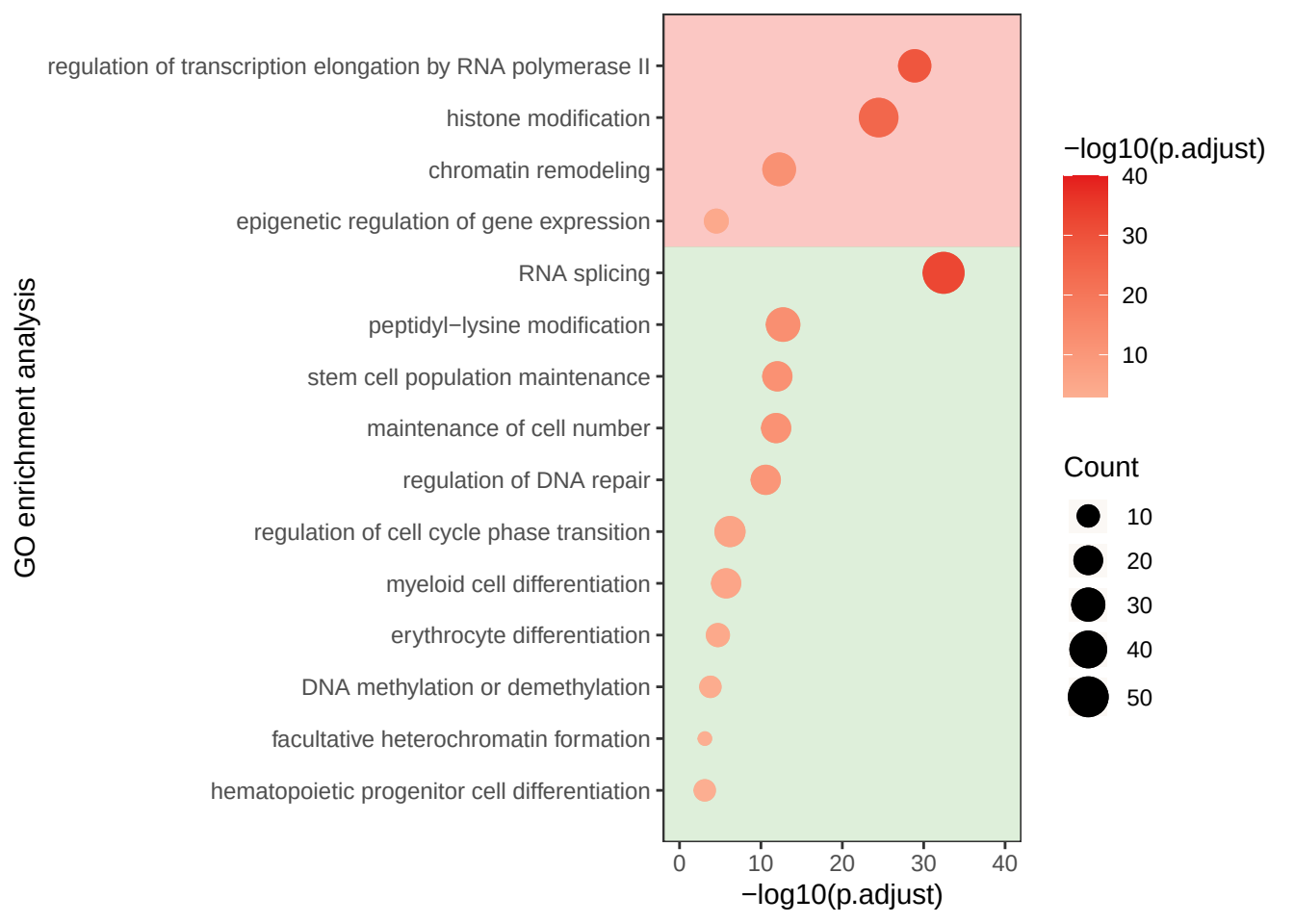
regulation of transcription elongation by RNA polymerase II
histone modification
chromatin remodeling
epigenetic regulation of gene expression
RNA splicing
peptidyl−lysine modification
stem cell population maintenance
maintenance of cell number
regulation of DNA repair
regulation of cell cycle phase transition
myeloid cell differentiation
erythrocyte differentiation
DNA methylation or demethylation
facultative heterochromatin formation
hematopoietic progenitor cell differentiation
GO enrichment analysis
0
10
20
30
40
−log10(p.adjust)
−log10(p.adjust)
40
30
20
10
Count
10
20
30
40
50