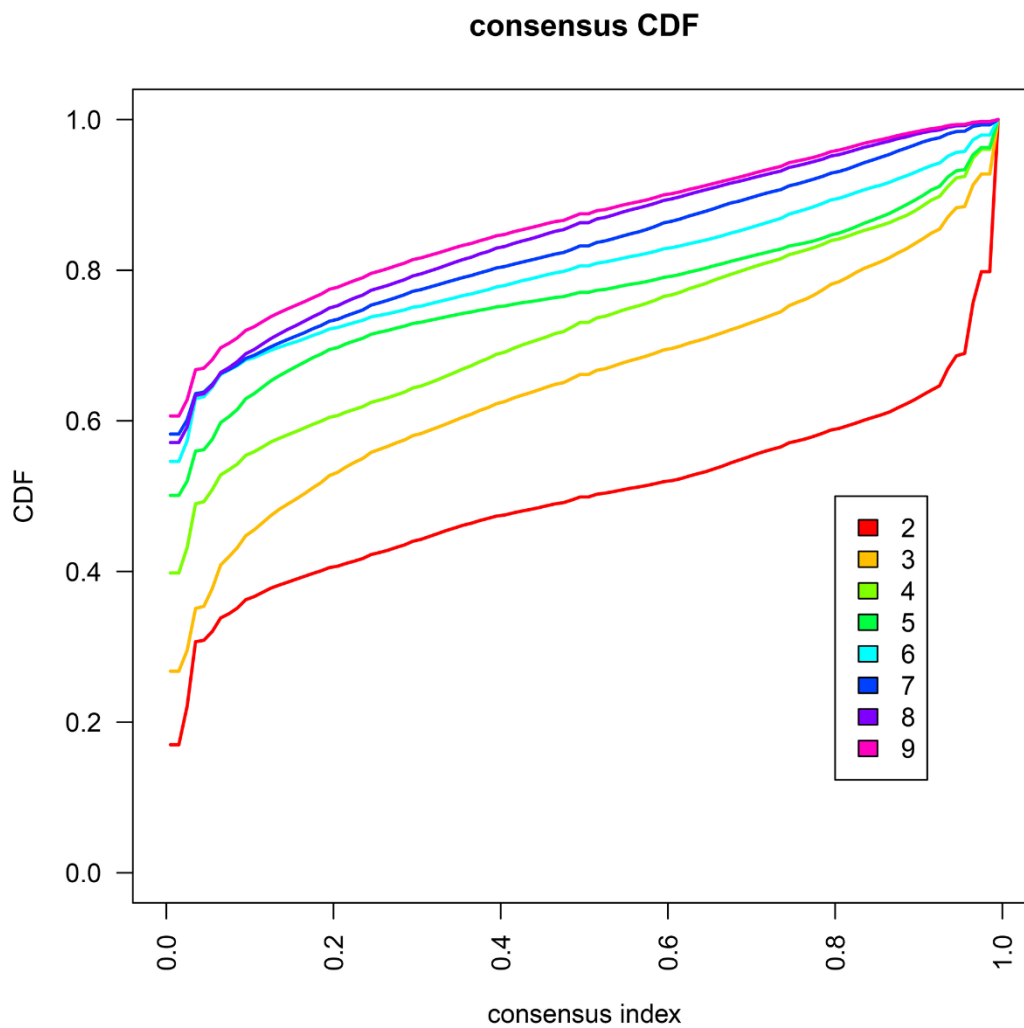
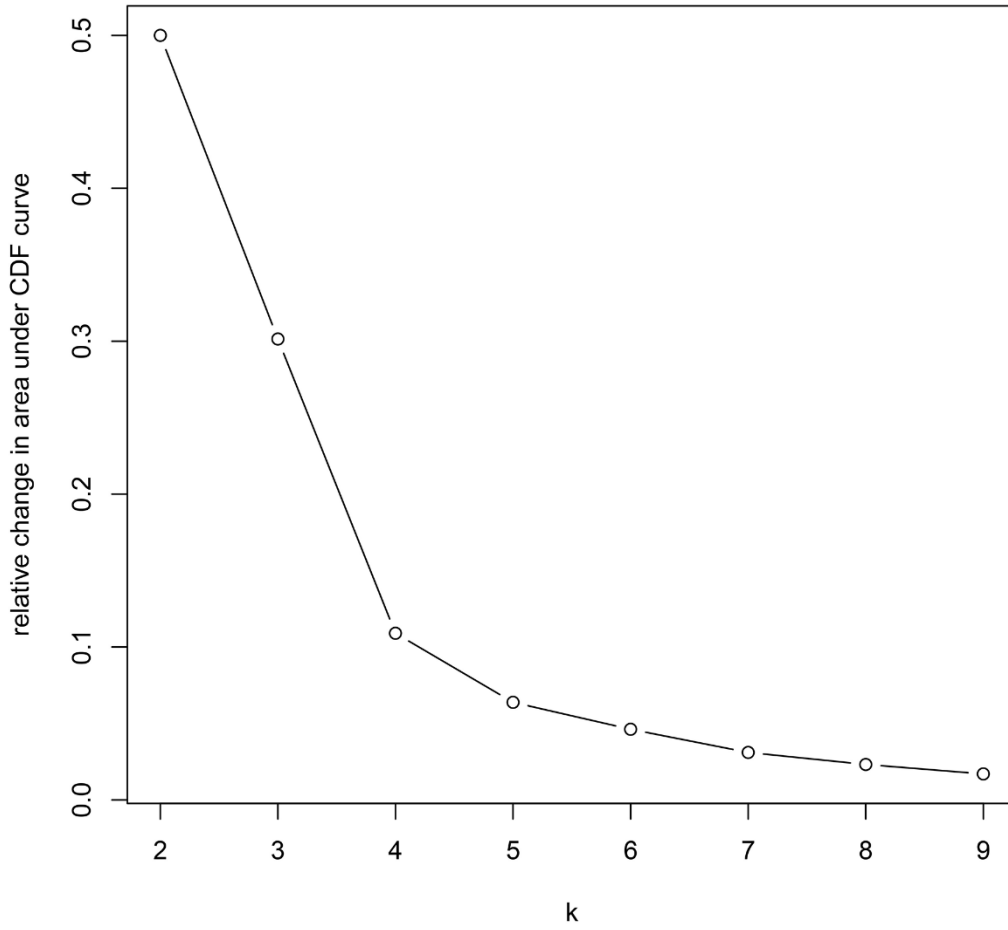


SUPPLEMENTARY FIGURES

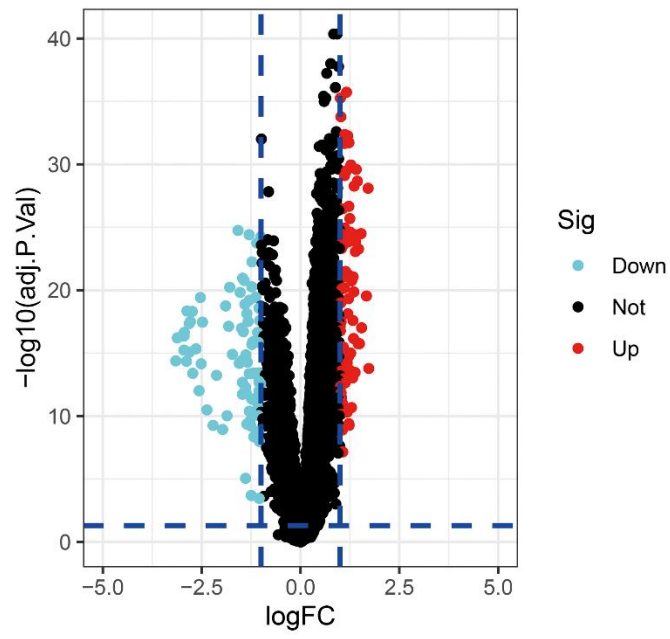


Supplementary Figure 1. Cumulative distribution function curve when cluster number $k = 2-9$.

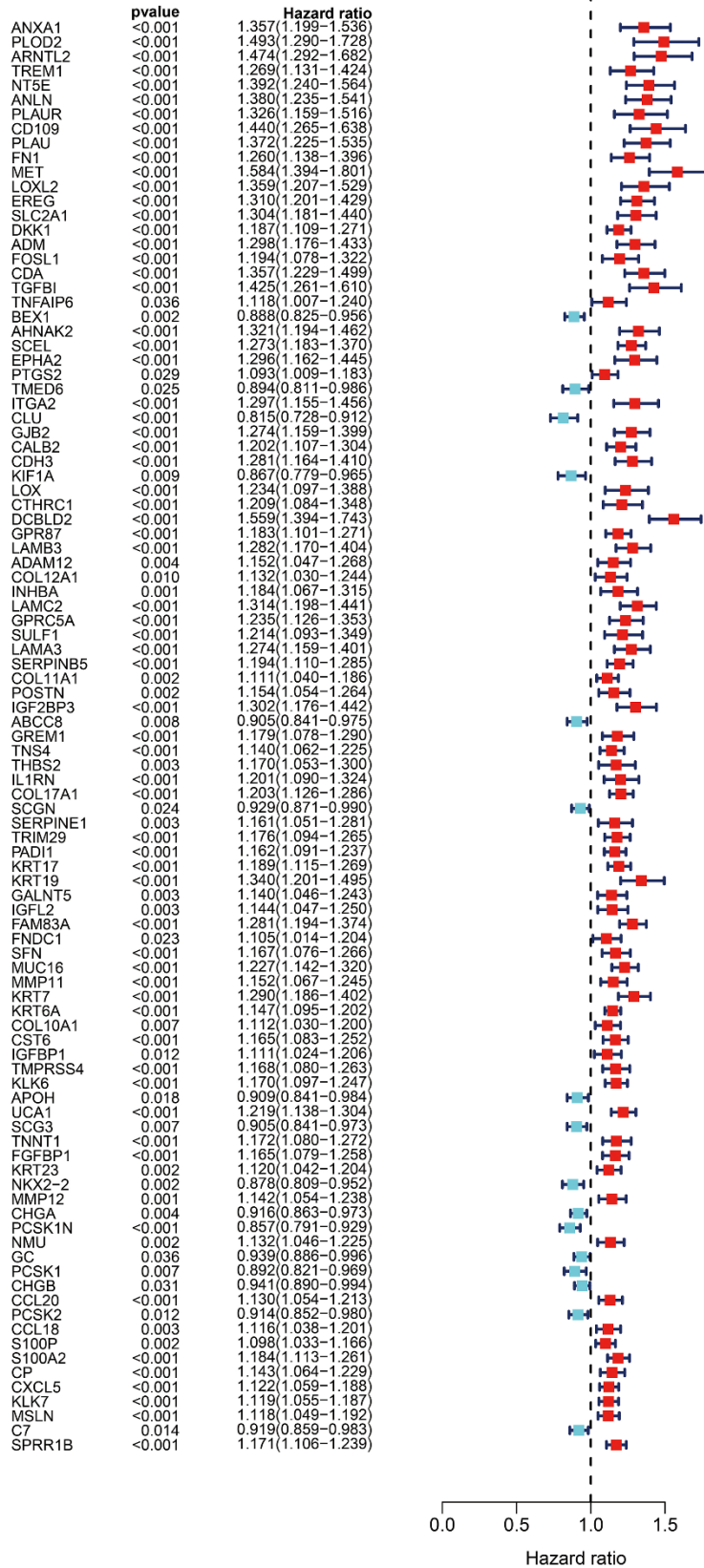
Delta area



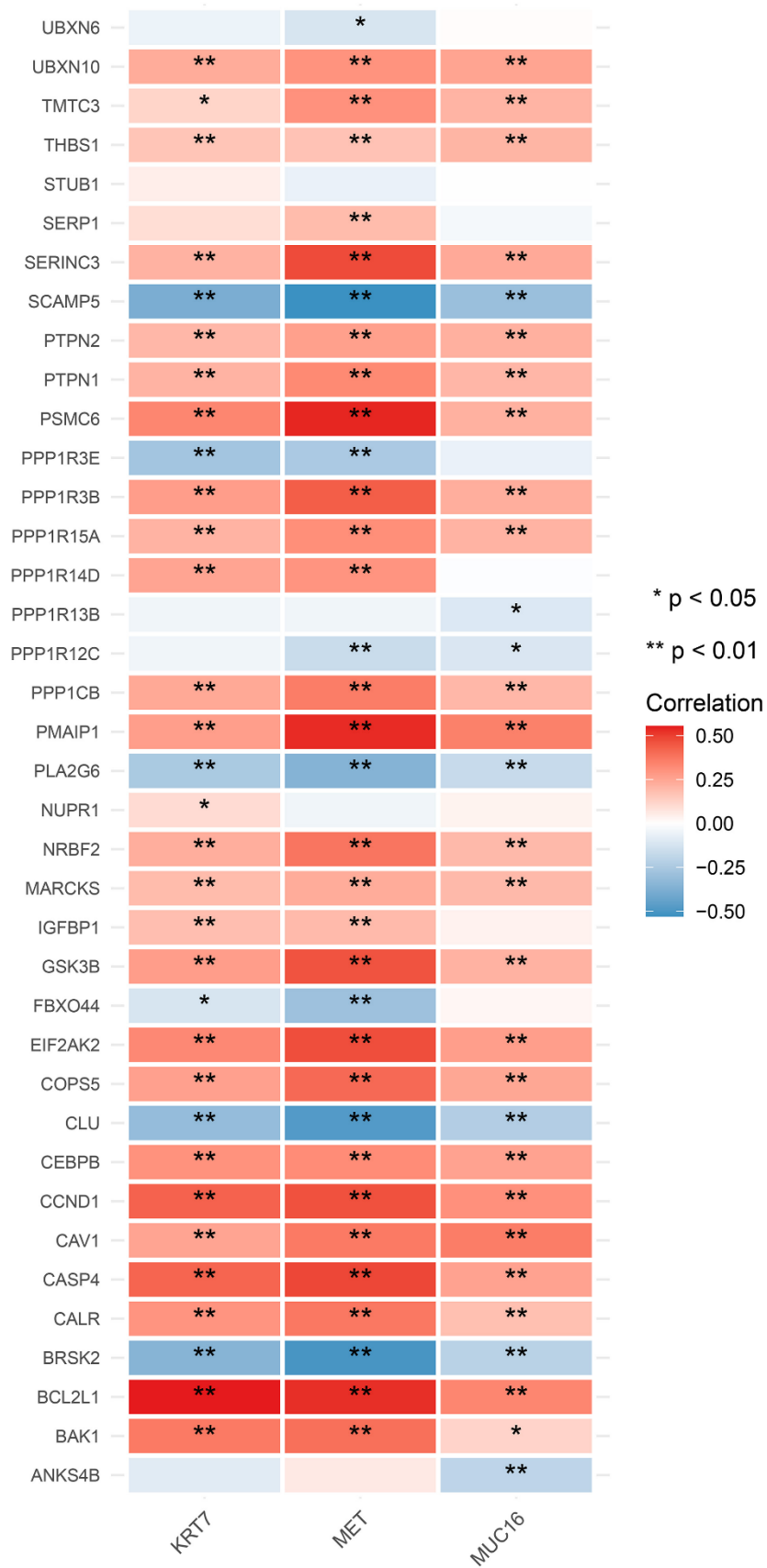
Supplementary Figure 2. Relative change of the area under the cumulative distribution function curve.



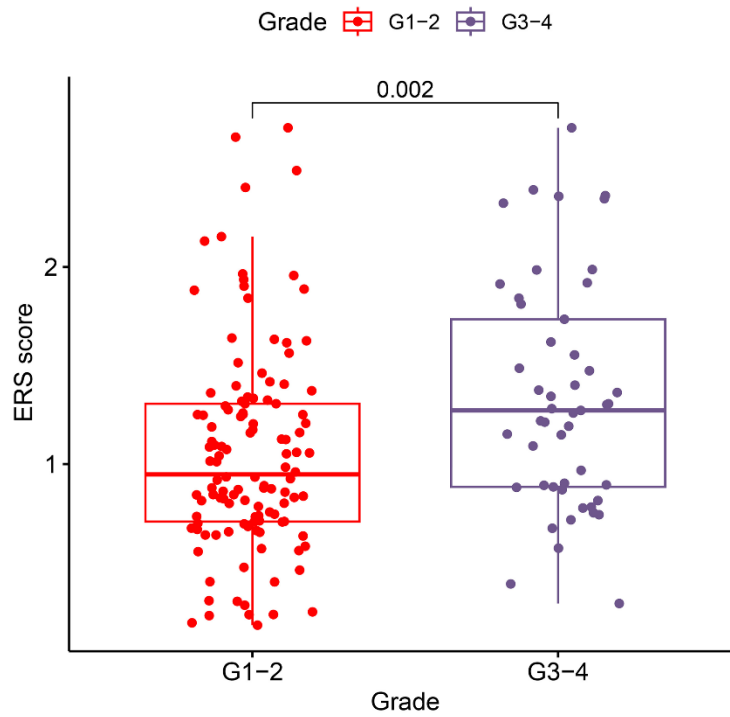
Supplementary Figure 3. The differentially expressed genes between ERGcluster A and B.



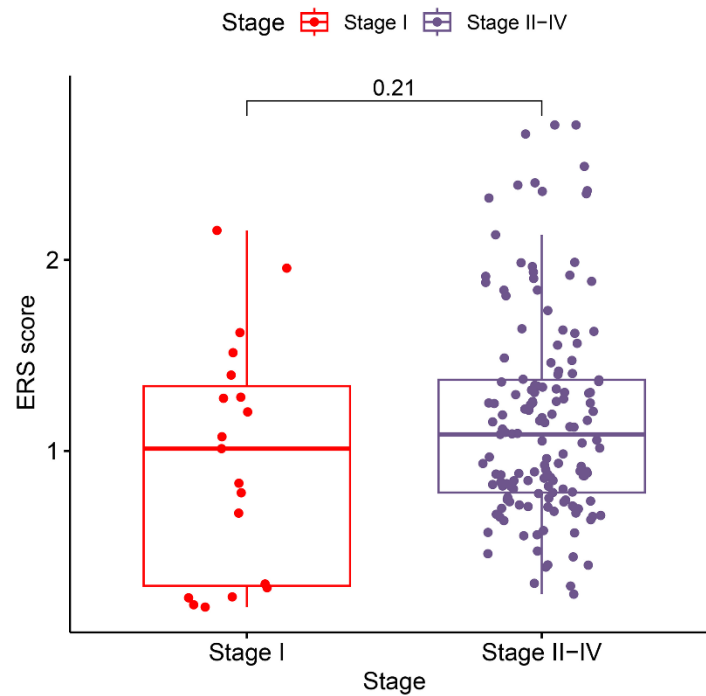
Supplementary Figure 4. Univariate Cox regression analysis using the differentially expressed genes between ERGcluster A and B.



Supplementary Figure 5. The correlation of model genes and ERGs.

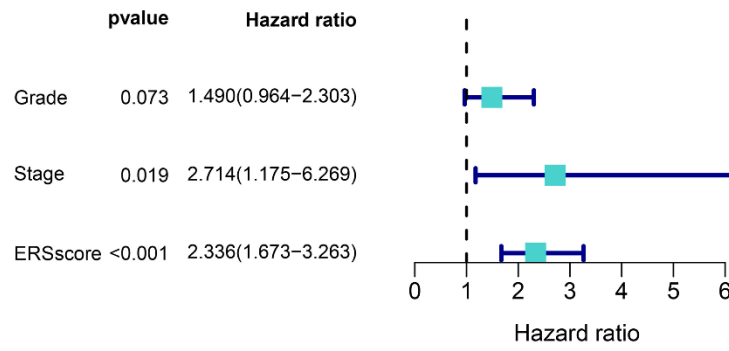


Supplementary Figure 6. The comparison of ERS score between the high and low pathological grade.

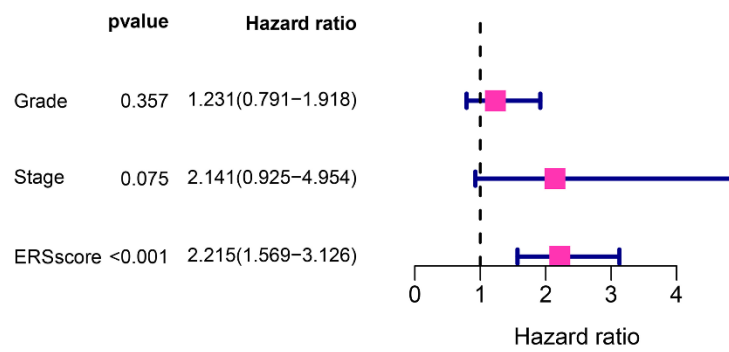


Supplementary Figure 7. The comparison of ERS score between the high and low TNM stage.

Univariate Cox regression



Multivariate Cox regression



Supplementary Figure 8. Forest maps of univariate and multivariate Cox regression.