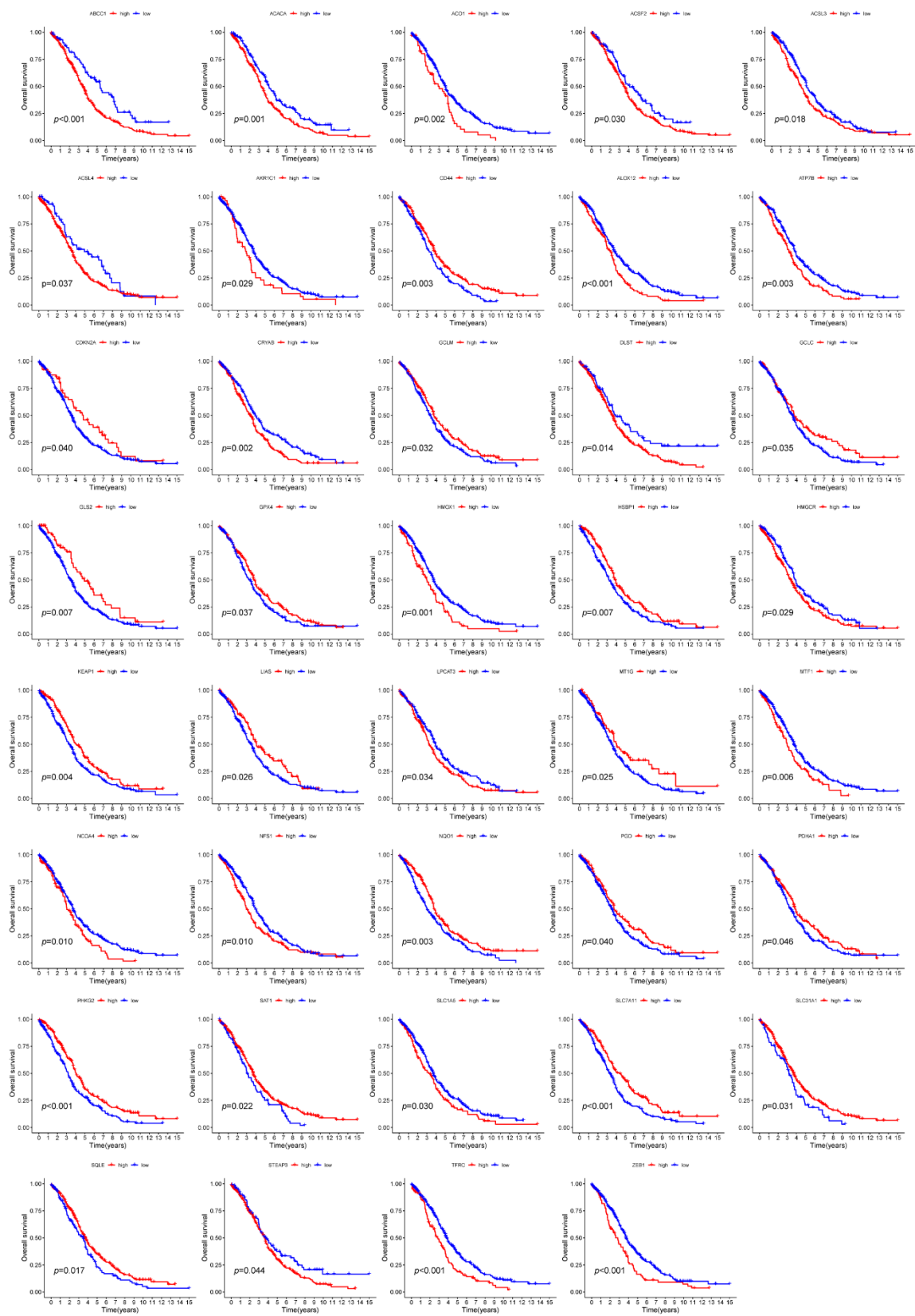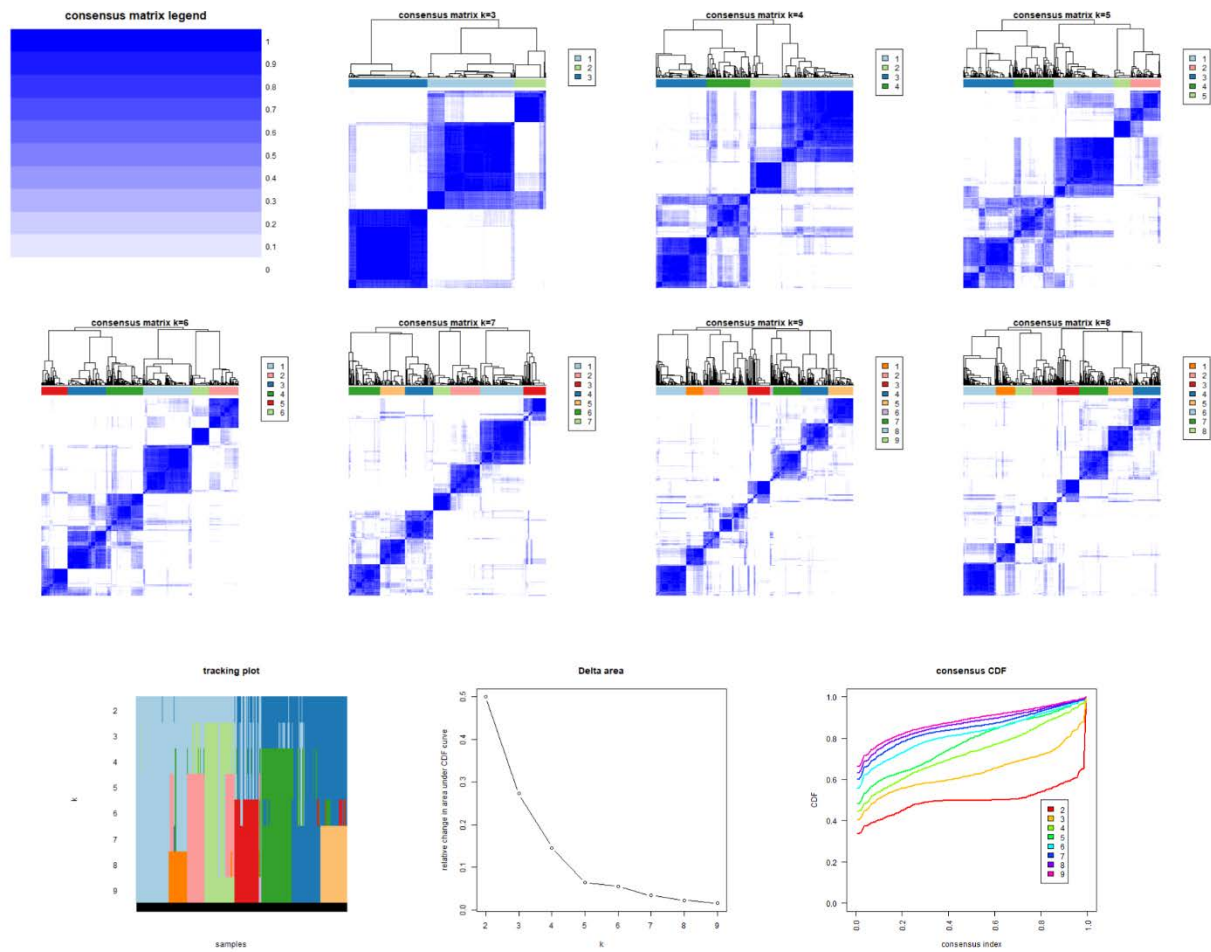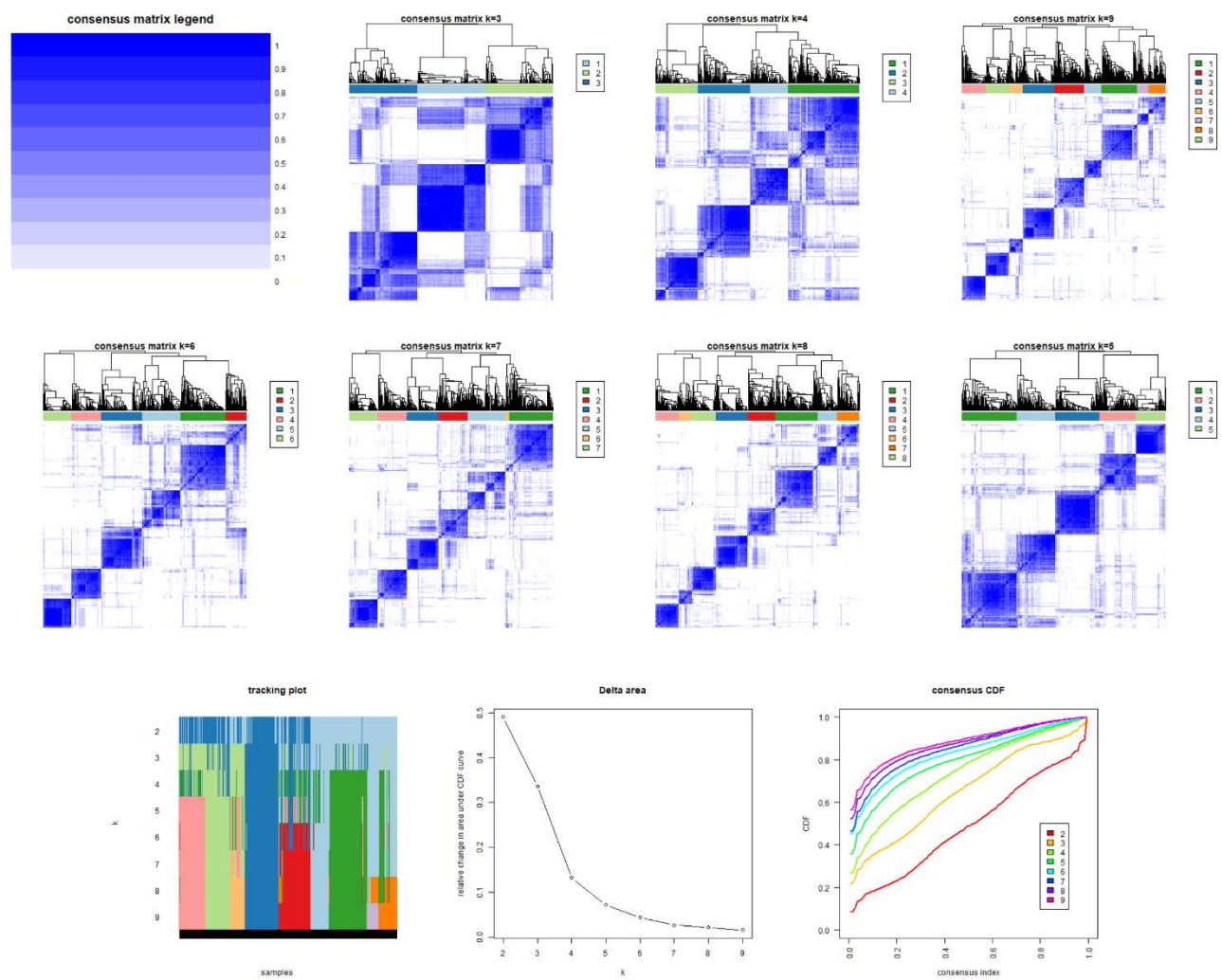**Supplementary Figure S1.** Based on TCGA-OV and GTEx-ovary, 57 differentially expressed ferroptosis-related genes were identified.
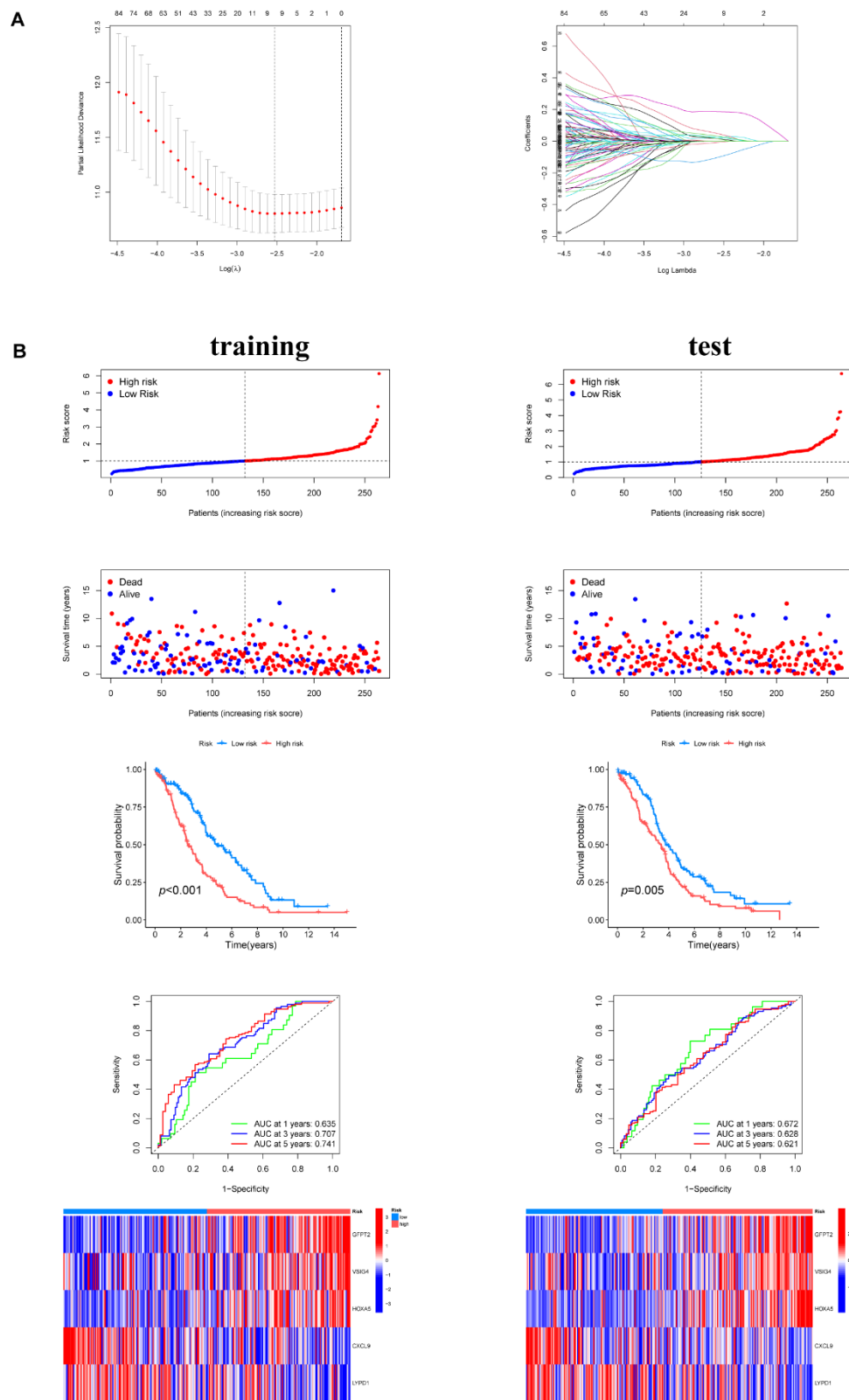
Supplementary Figure S2. 39 prognosis-related genes (*PRGs*) were identified for our subsequent analysis.
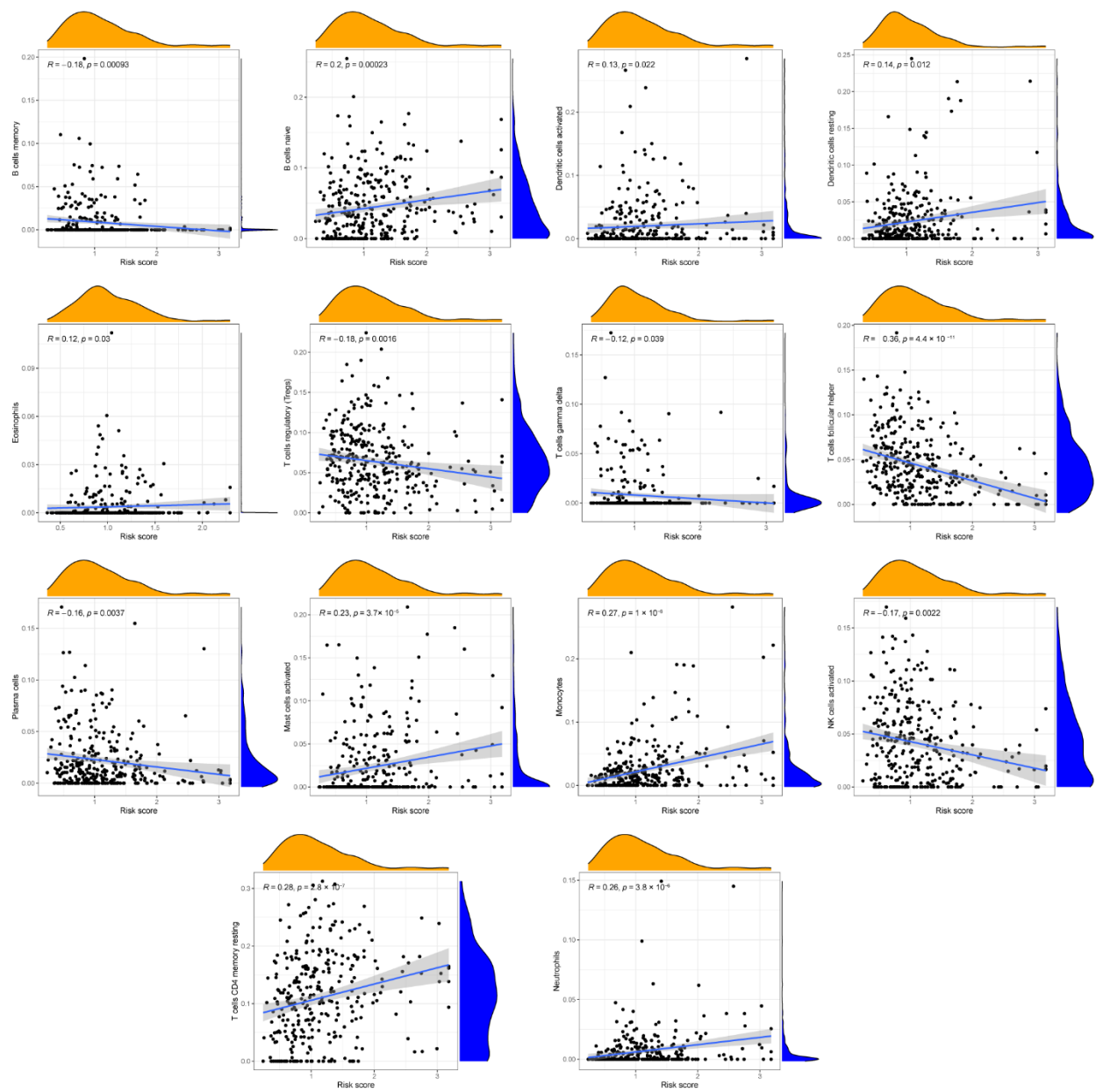
Supplementary Figure S3. Consensus matrixes for all samples were clustered into an appropriate number of prognosis-related clusters (k=1-9).

Supplementary Figure S4: Consensus matrix identifies different gene clusters (k = 1–9).

Supplementary Figure S5: Construction of risk model. (**A**) Minimal crossover validation points show the number of hub genes and the trajectory of each independent variable based on the training set. (**B**) Risk model identification in training and test cohorts.

Supplementary Figure S6: The association between risk score and immune cells.