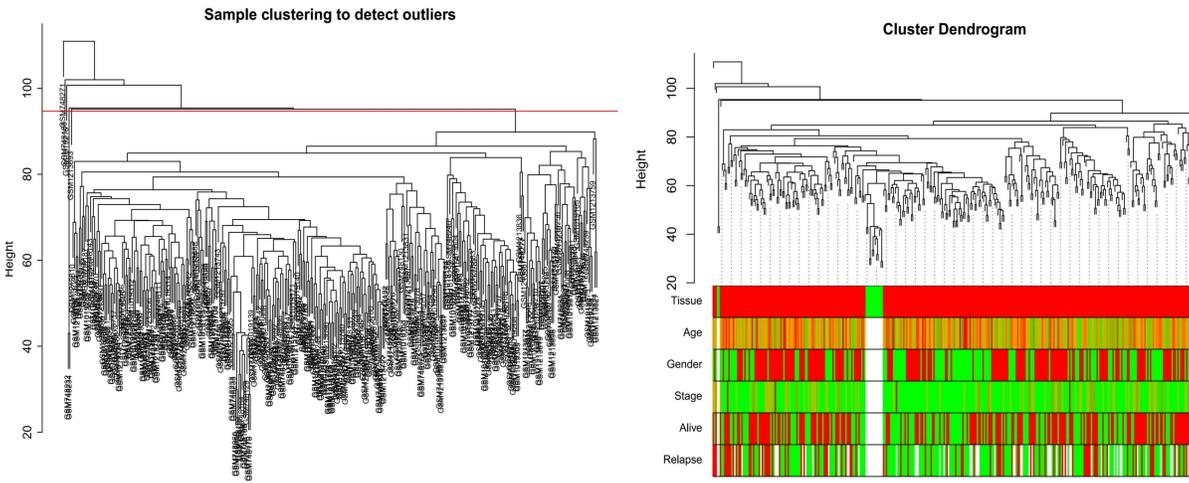
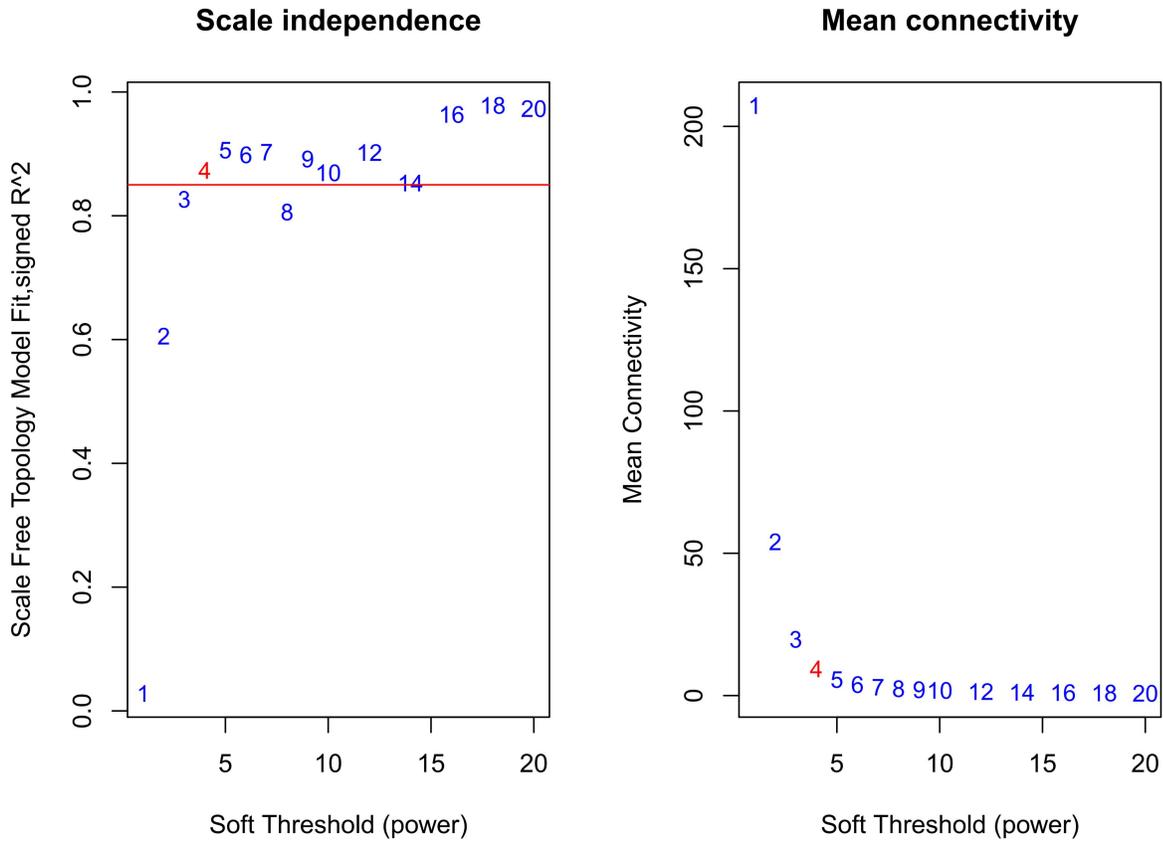


# Supplemental figures

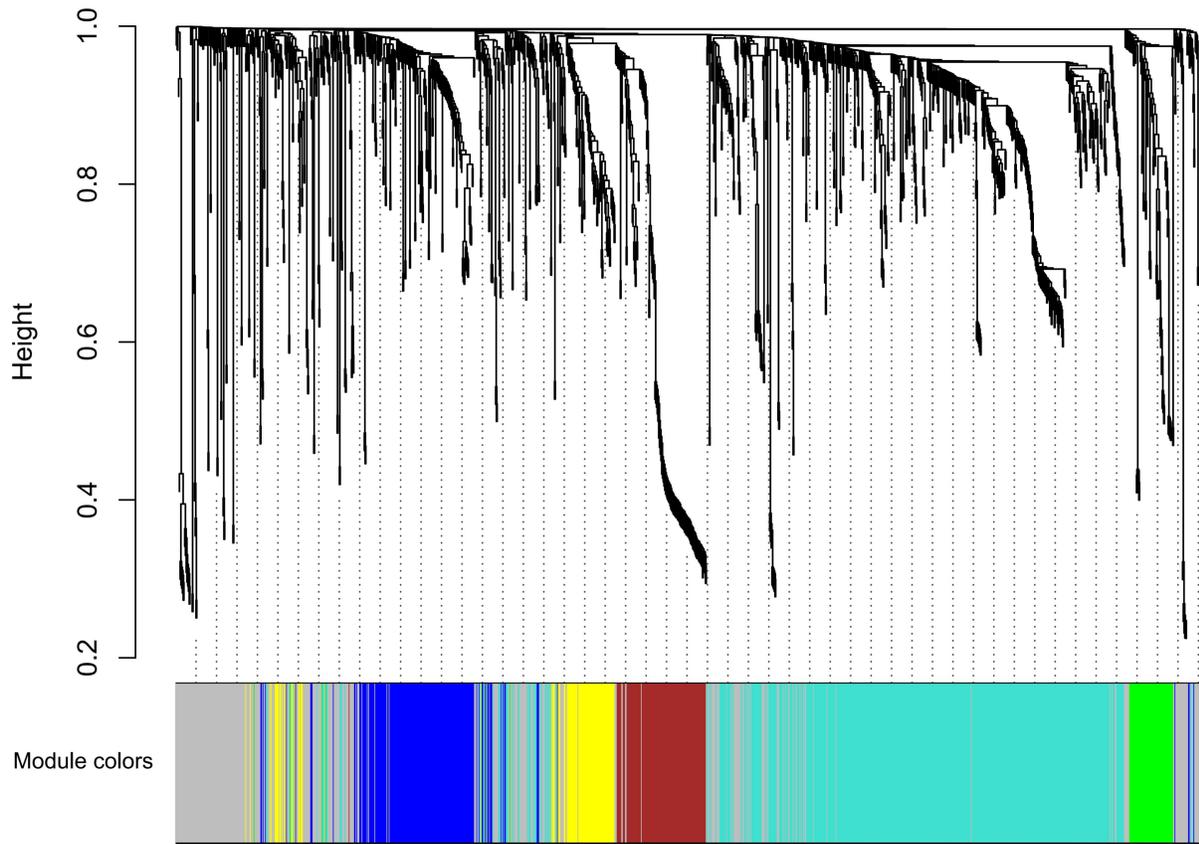


Supplementary Figure S1. Sample clustering to detect outliers

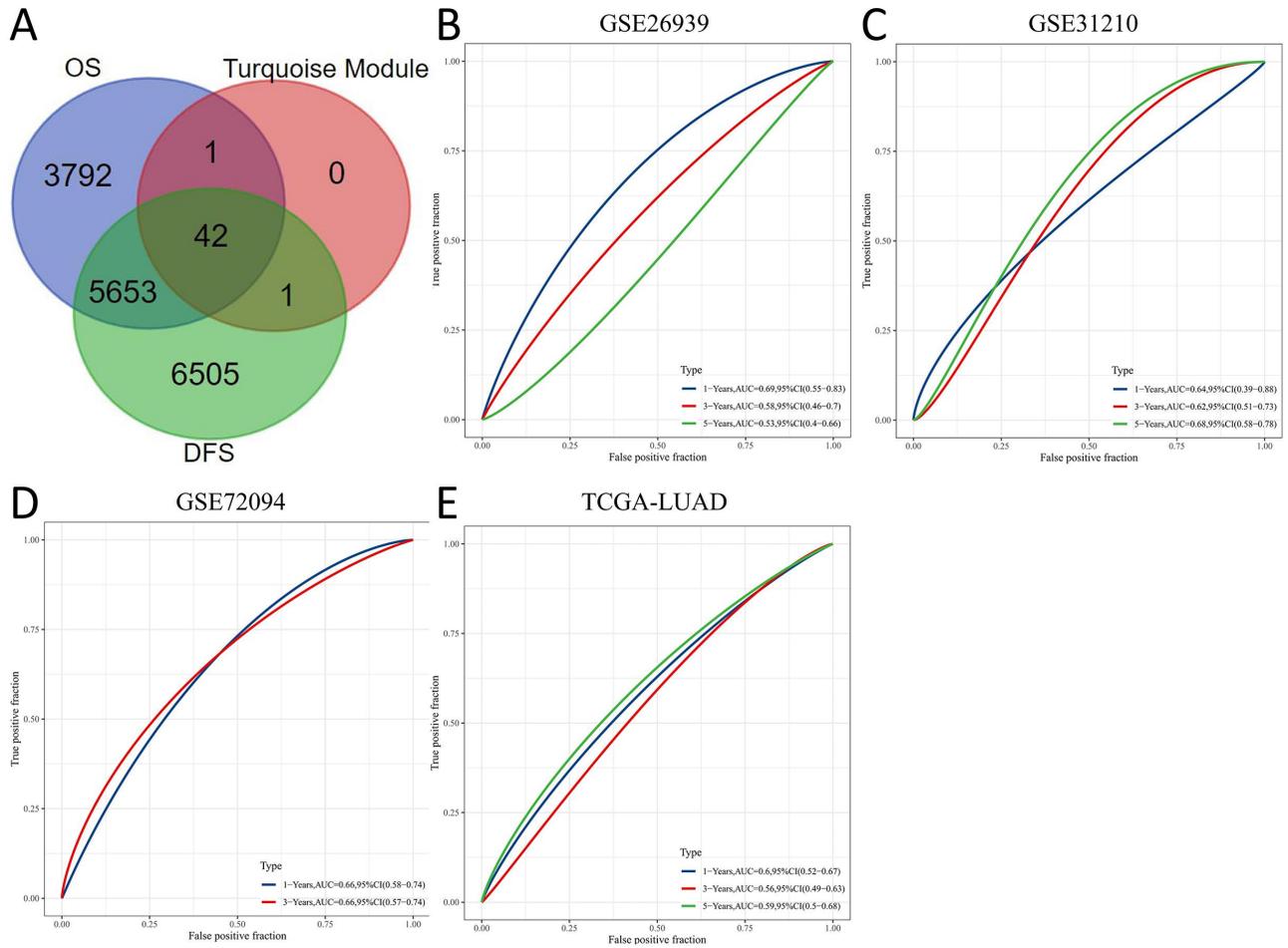


Supplementary Figure S2. Determination of soft-thresholding power in the weighted gene co-expression network analysis (WGCNA)

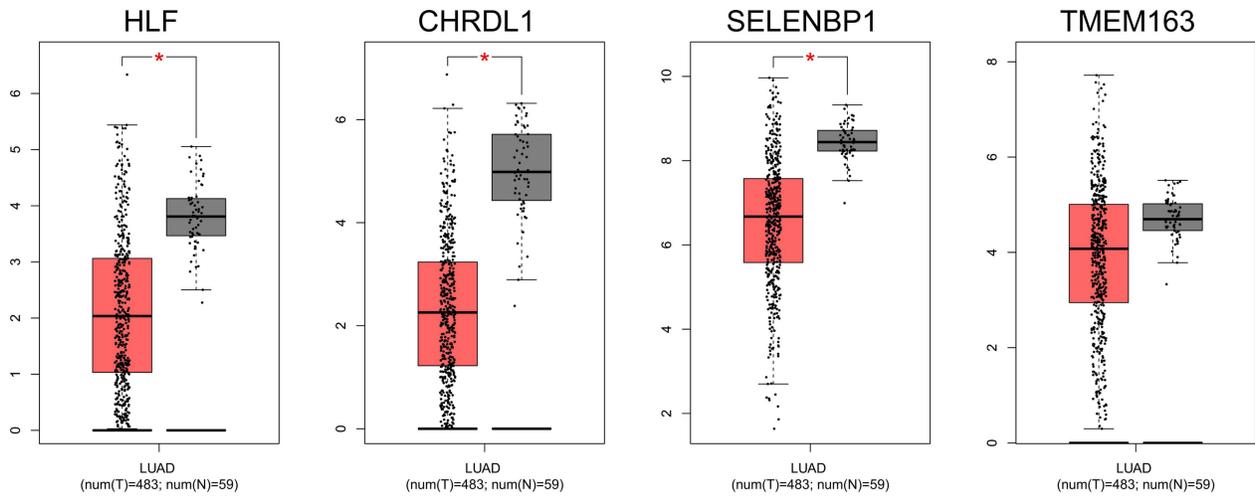
### Cluster Dendrogram



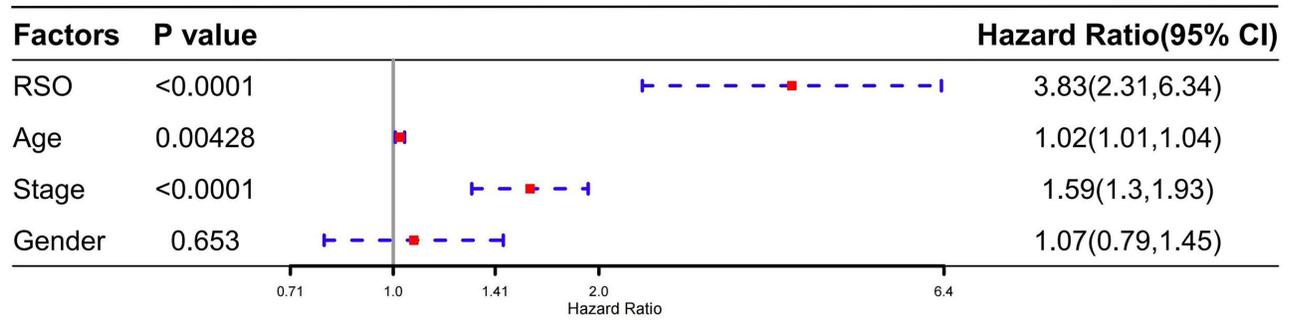
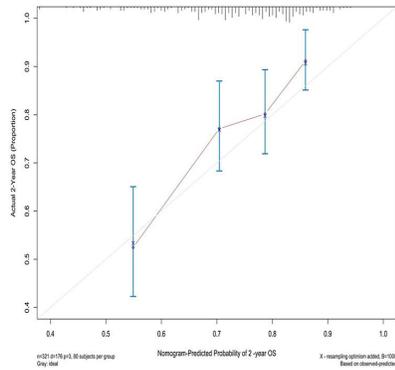
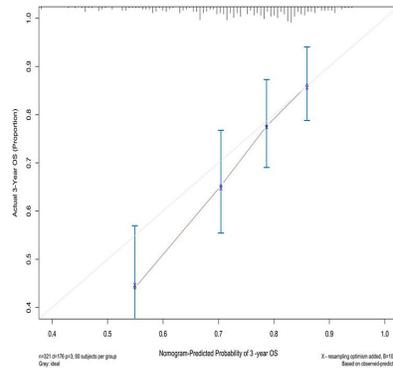
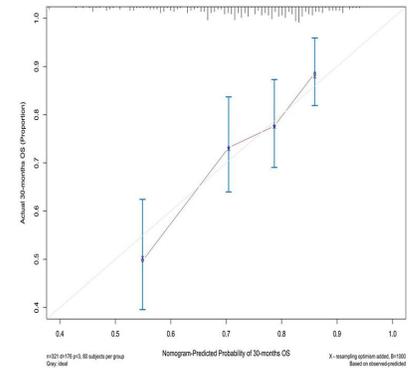
**Supplementary Figure S3.** Dendrogram of all genes clustered based on a dissimilarity measure



**Supplementary Figure S4.** (A) Venn plots of overlapping genes in the turquoise module with genes affecting OS and DFS; (B) ROC curves of 1-year, 3-year, 5-year OS in GSE26939; (C) ROC curves of 1-year, 3-year, 5-year OS in GSE31210; (D) ROC curves of 1-year, 3-year, 5-year OS in GSE72094; (E) ROC curves of 1-year, 3-year, 5-year OS in TCGA-LUAD;



**Supplementary Figure S5** The analysis of the differences in the expression of HLF, CHRDL1, SELENBP1 and TMEM163 between cancer and normal tissues via GEPIA database. Red indicates the expression of tumor tissue (num T = 438), gray indicates the expression of normal tissue (num N = 59), and each point represents a tissue. Log<sub>2</sub>(TPM + 1) were used for log-scale. \* P < 0.05

**A****B****C****D**

**Supplementary Figure S6.** (A) Univariate regression analysis: The four-gene signature RSO, age, stage and gender; (B) Nomogram: predicting probability 2-year OS; (C) Nomogram: predicting probability 3-year OS; (D) Nomogram: predicting probability 30-months OS.