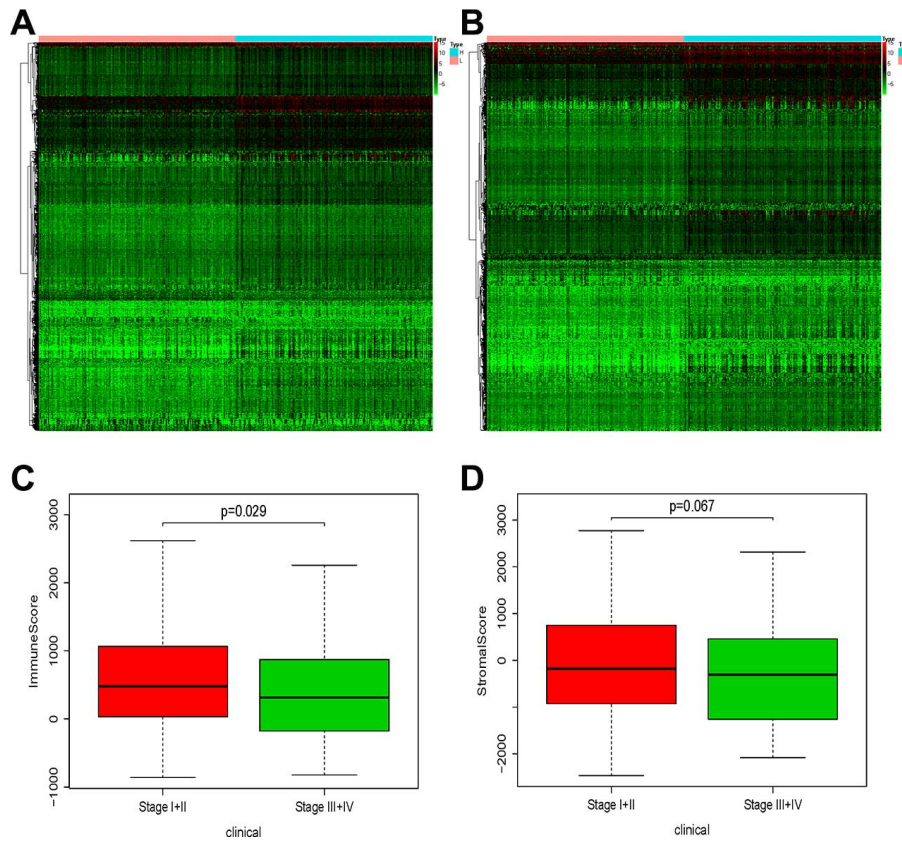
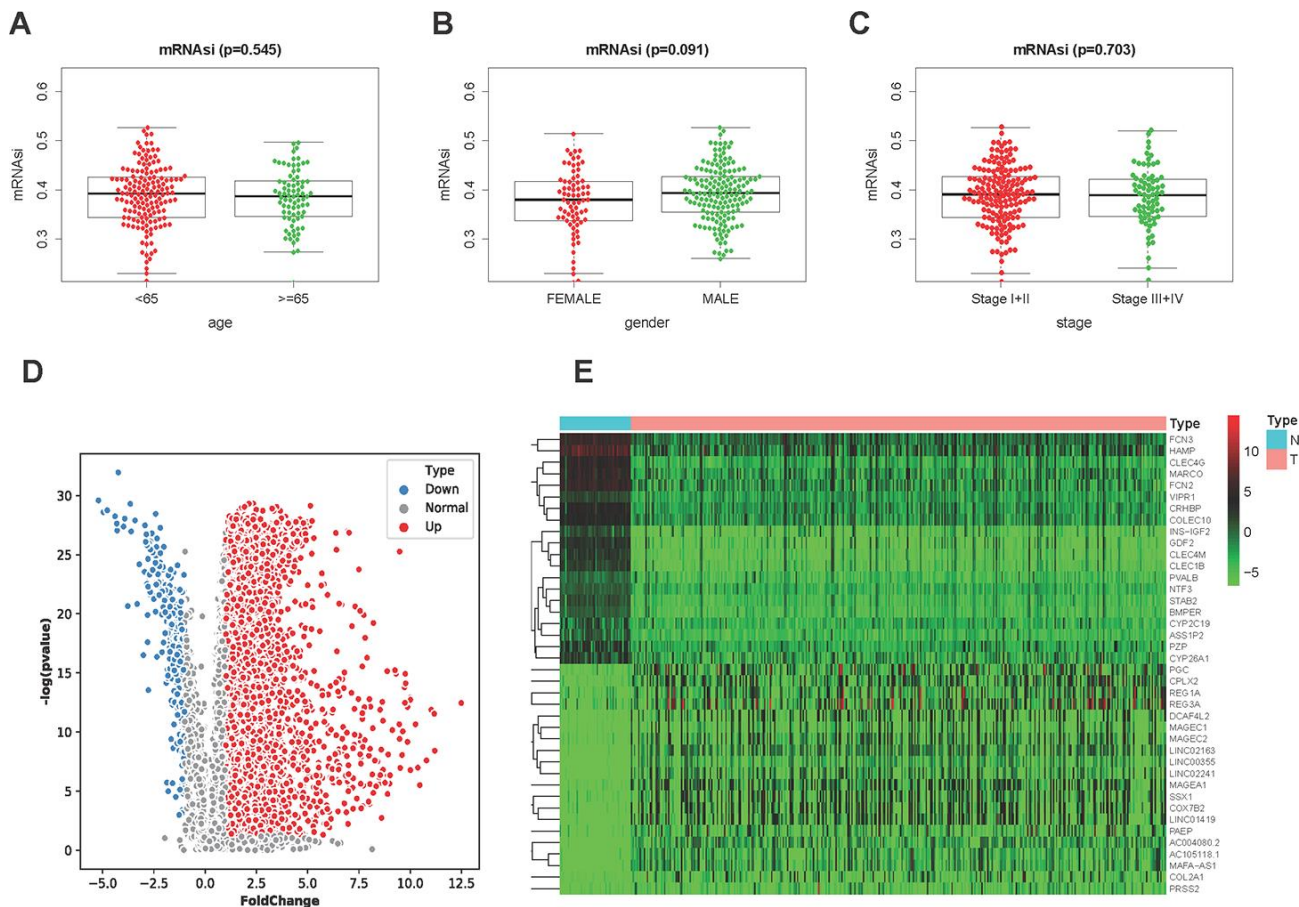


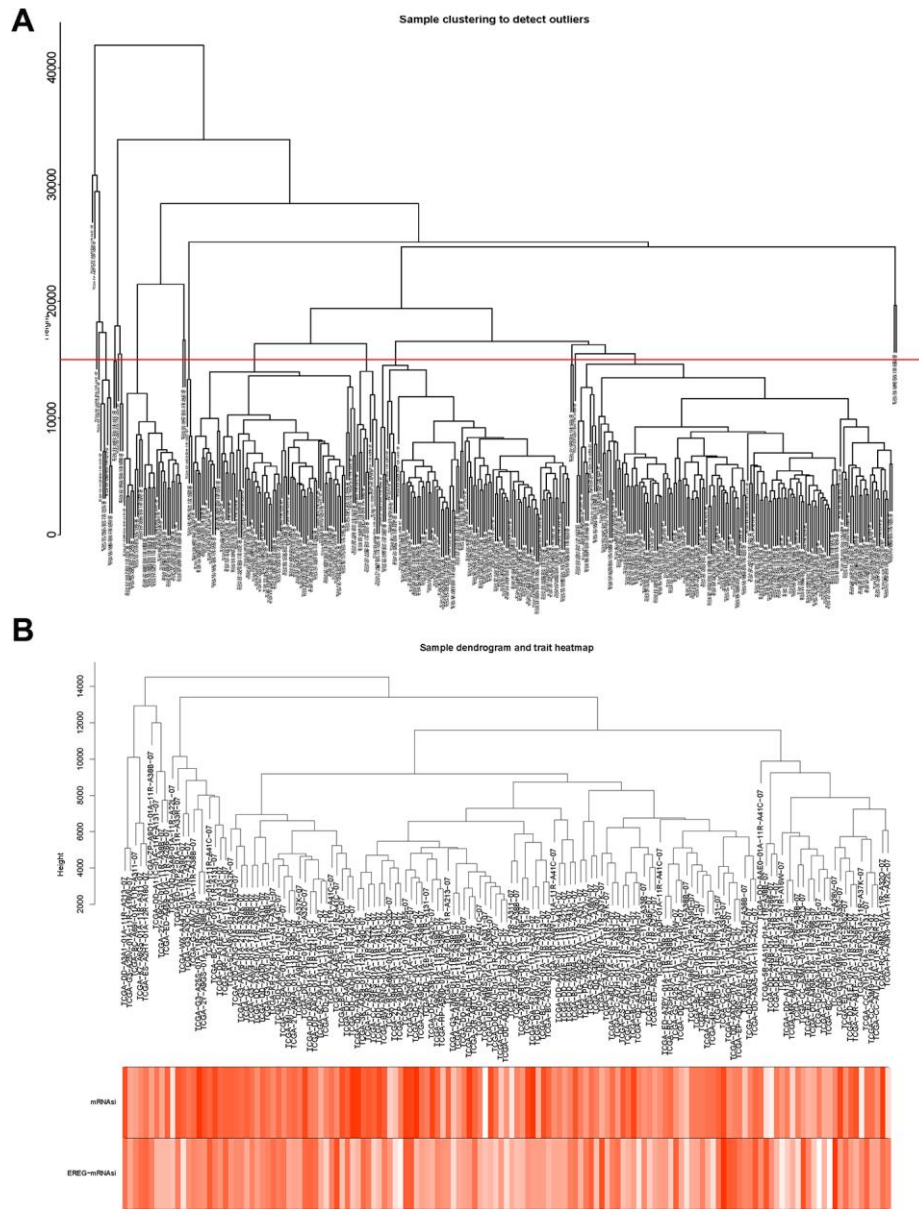
## SUPPLEMENTARY FIGURES



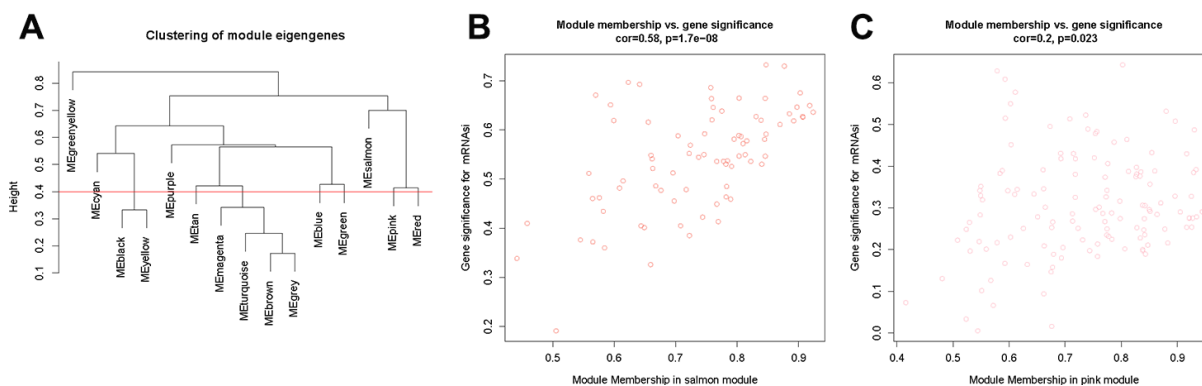
**Supplementary Figure 1. Results of the ESTIMATE method.** (A) Heatmap of DEGs for ImmuneScore. In the "Type," Cyan (H) denotes the high-score group and pink (L) denotes the low-score group. (B) Heatmap of DEGs for StromalScore. In the "Type," Cyan (H) denotes the high-score group and pink (L) denotes the low-score group. (C) The relationship between ImmuneScore and tumor stage was tested using the Wilcoxon test. (D) The relationship between StromalScore and tumor stage was tested using the Wilcoxon test.



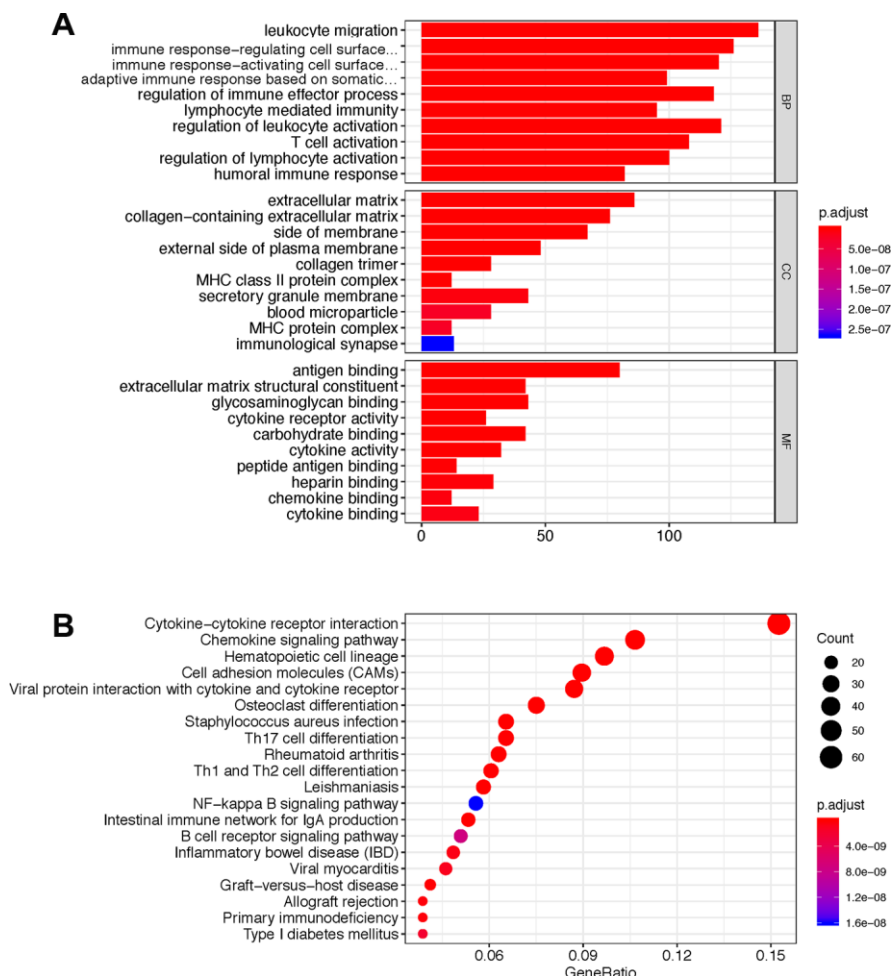
**Supplementary Figure 2. The relationship between mRNAsi and clinical traits and DEGs in patients with LIHC and normal samples. (A)** The relationship between mRNAsi and age. The Wilcoxon test was used. **(B)** Relationship between mRNAsi and sex. The Wilcoxon test was used. **(C)** Relationship between mRNAsi and stage. The Wilcoxon test was used. **(D)** Volcano figure of DEGs from patients with LIHC and normal samples. **(E)** Heat map of DEGs. The figure shows the expression of the top 40 genes in  $|\log FC|$ . In the "Type," cyan denotes normal samples and pink denotes the tumor samples.



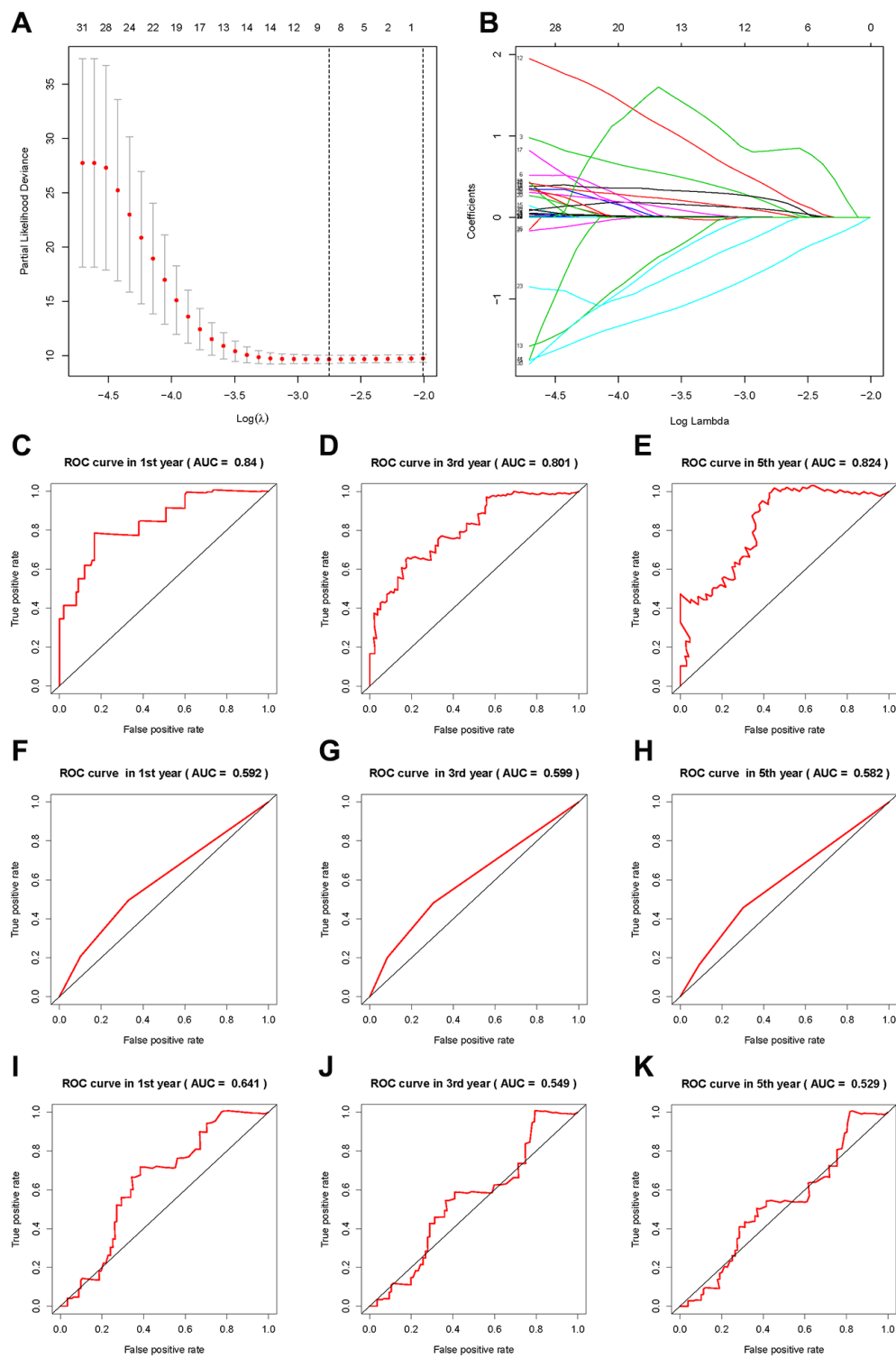
**Supplementary Figure 3. Pretreatment of samples before WGCNA.** (A) The result of hierarchical clustering before excluding samples. Criteria for excluding samples: the red line is 15,000. (B) Results of hierarchical clustering after excluding samples. The heatmap shows the mRNAsi score and EREG-mRNAsi score.



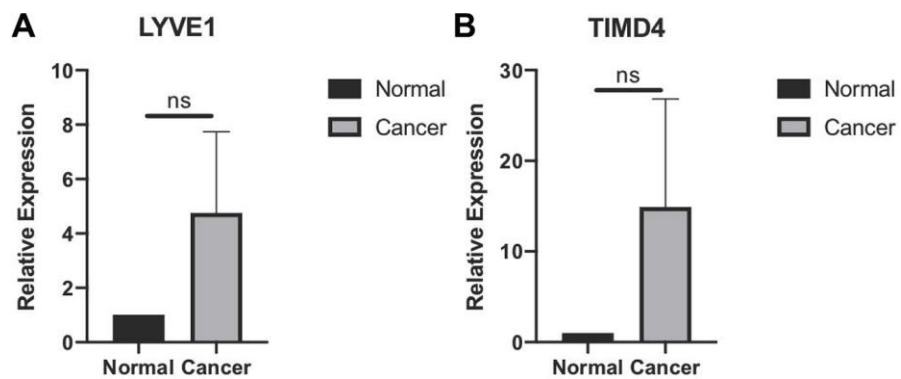
**Supplementary Figure 4. Results of WGCNA analysis.** (A) Gene module clustering results. Modules with height less than 0.4 (red line) were merged. (B) Scatter plot of gene importance in the salmon module. The x-axis is the Pearson correlation coefficient of gene expression and the first principal component of the salmon module. The y-axis is the correlation coefficient of gene expression and mRNA<sub>si</sub> of the sample. Genes in the upper right are generally thought to be involved in this module. (C) Scatter plot of gene importance in the pink module.



**Supplementary Figure 5. GO and KEGG analyses of DEGs from ESTIMATE algorithm.** (A) GO analysis; (B) KEGG analysis.



**Supplementary Figure 6. Results of lasso regression and ROC curves during prognosis.** (A) The result of cross-validation. The y-axis is partial likelihood deviance. The x-axis (bottom) is  $\log(\lambda)$ , and the x-axis (up) is the number of remaining variables. The dashed line gives the  $\lambda$  value when the partial likelihood deviance is minimum. (B) The y-axis is the coefficient of the variables in the lasso regression equation. (C–E) ROC curve of the ICRP score forecast result after 1, 3, and 5 years in the training set. (F–H) ROC curve of AJCC stage forecast result after 1, 3, and 5 years in the training set. (I–K) ROC curve of ALBI score prediction results after 1, 3, and 5 years in the training set.



**Supplementary Figure 7.** (A, B) QPCR analysis of LYVE1 and TIMD4 in the normal liver cell line and LHC cell line ( $n = 3$ ). No significance, paired-sample  $t$  test.