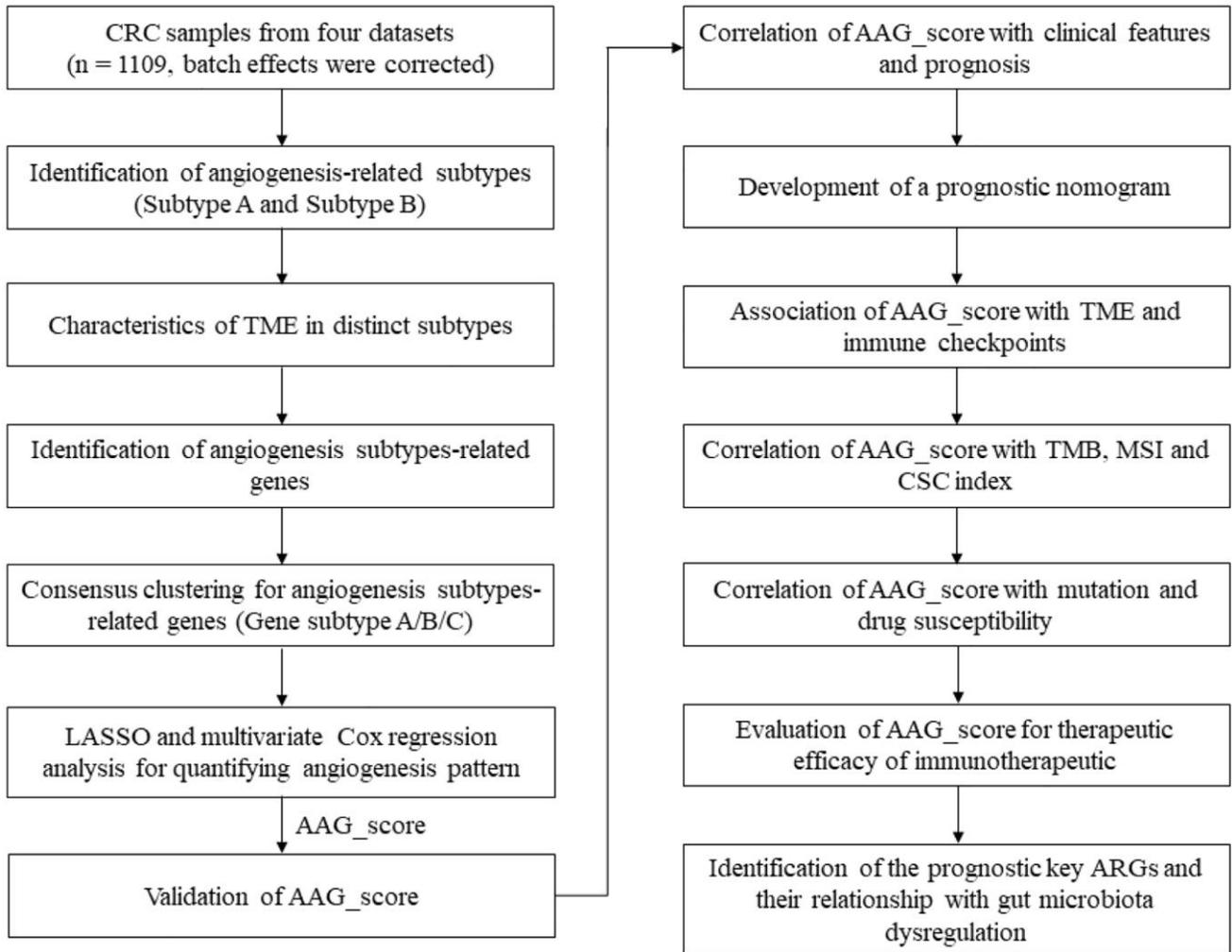
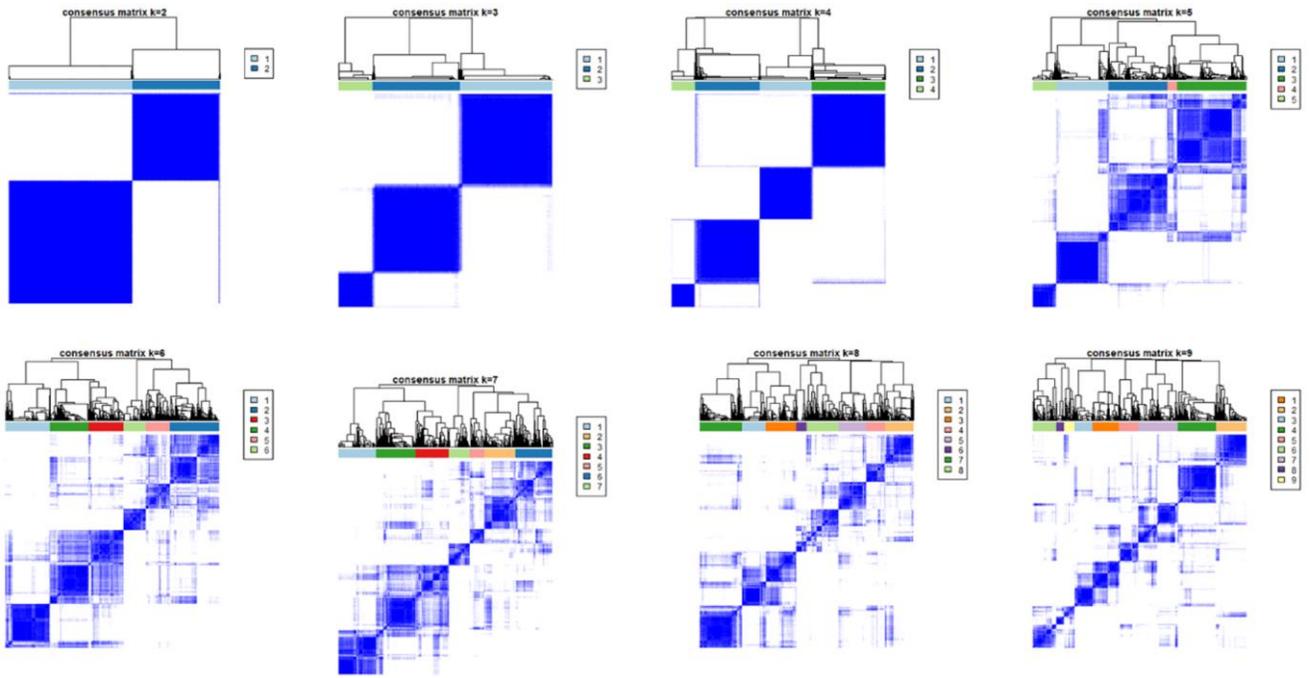


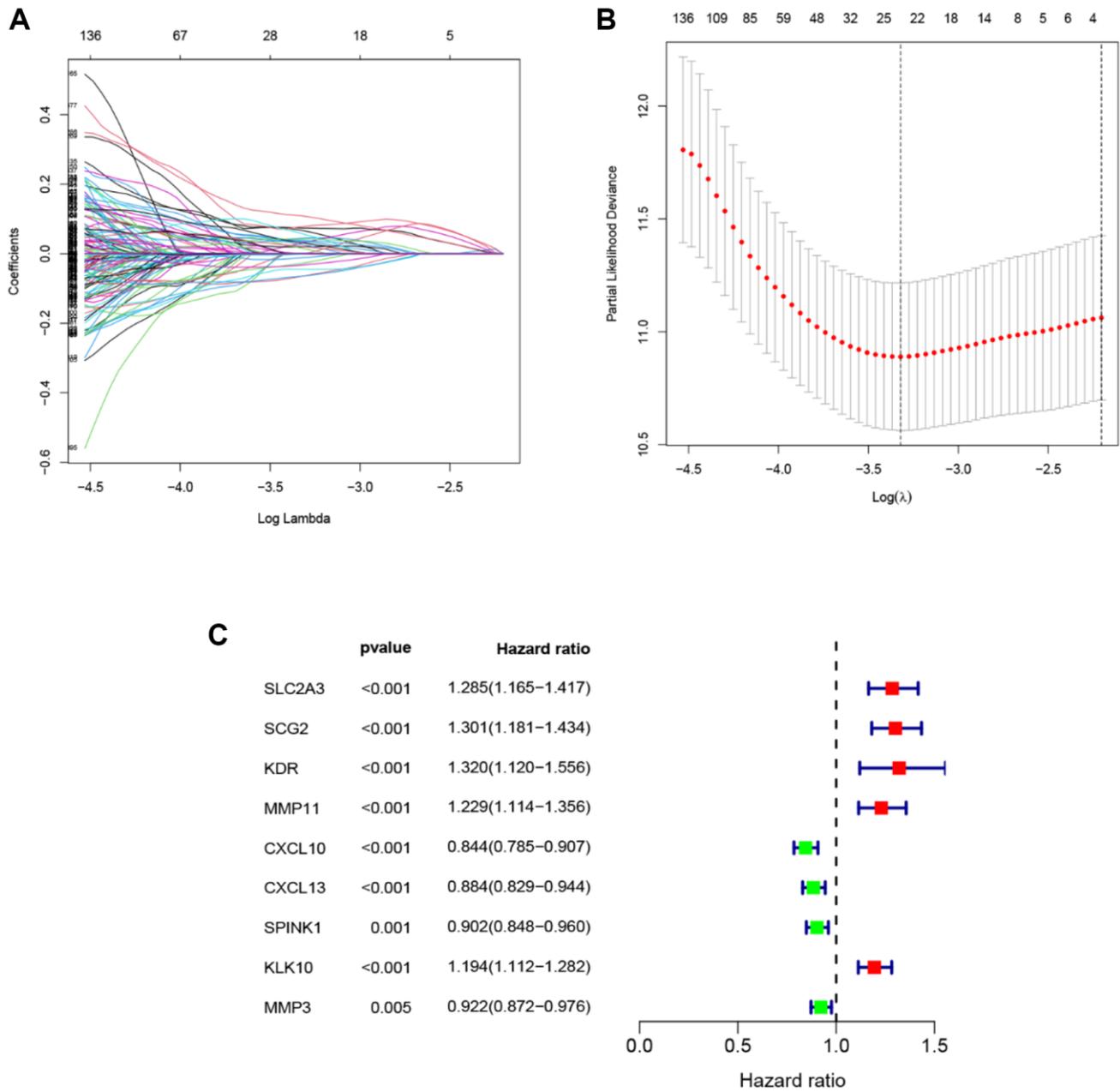
SUPPLEMENTARY FIGURES



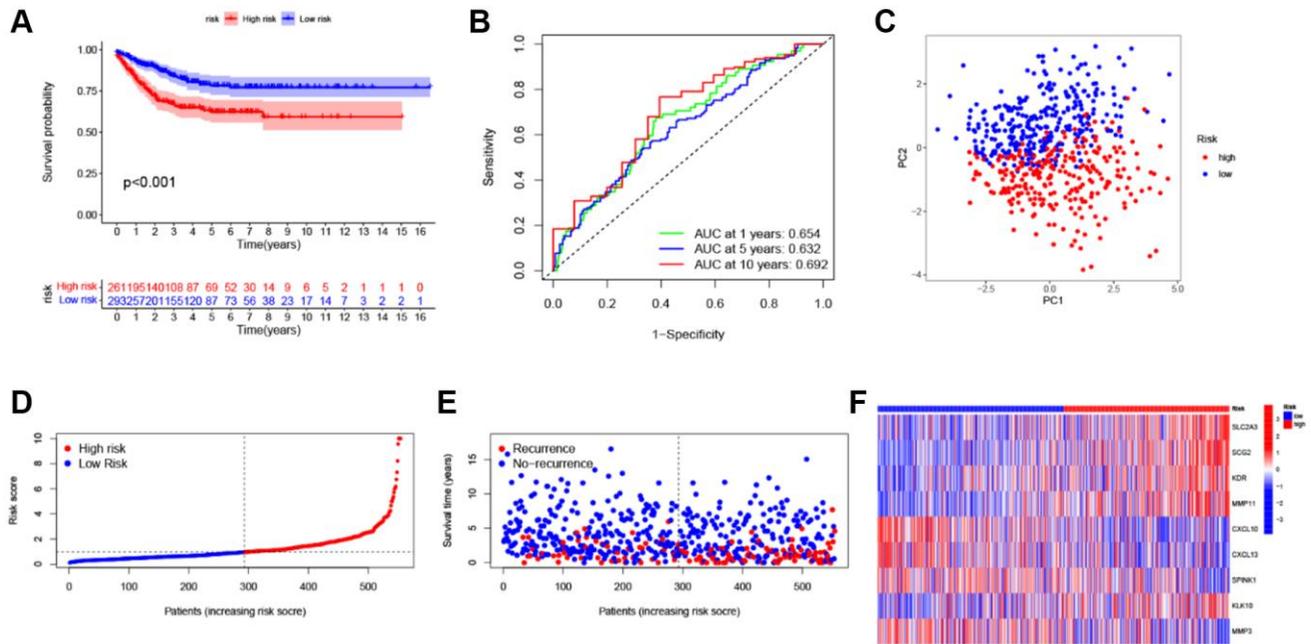
Supplementary Figure 1. The specific workflow graph of data analysis.



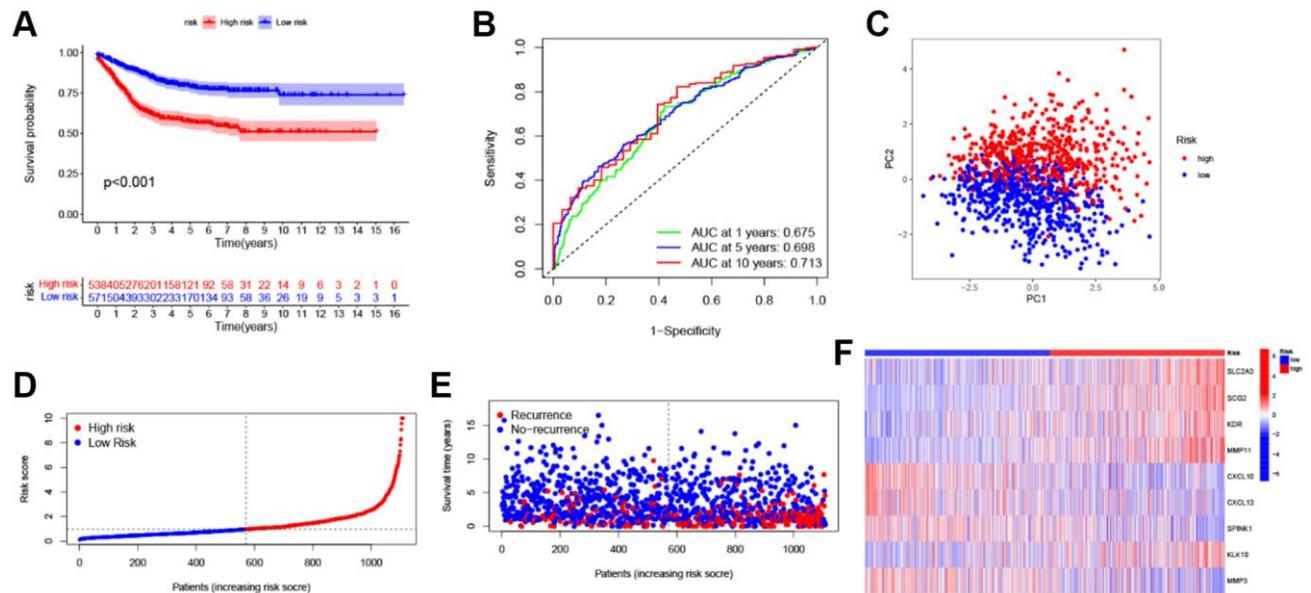
Supplementary Figure 2. Unsupervised clustering of gene subtypes based on DEGs and Consensus matrix heatmaps for k = 2–9.



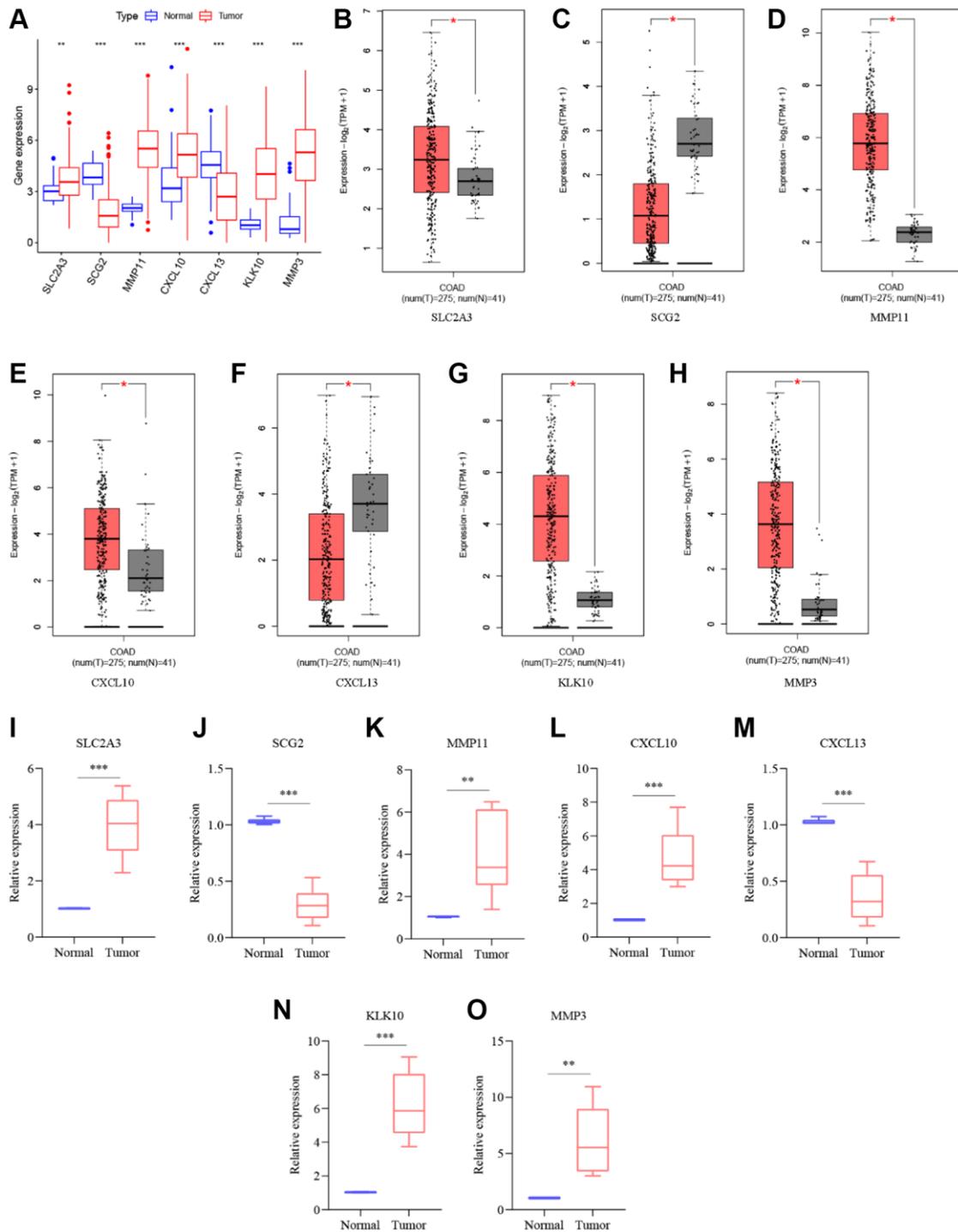
Supplementary Figure 3. Identifying representative candidate prognostic genes. (A, B) The LASSO regression analysis and partial likelihood deviance on the prognostic genes. (C) Forest plot of multivariate cox regression analysis for prognostic genes.



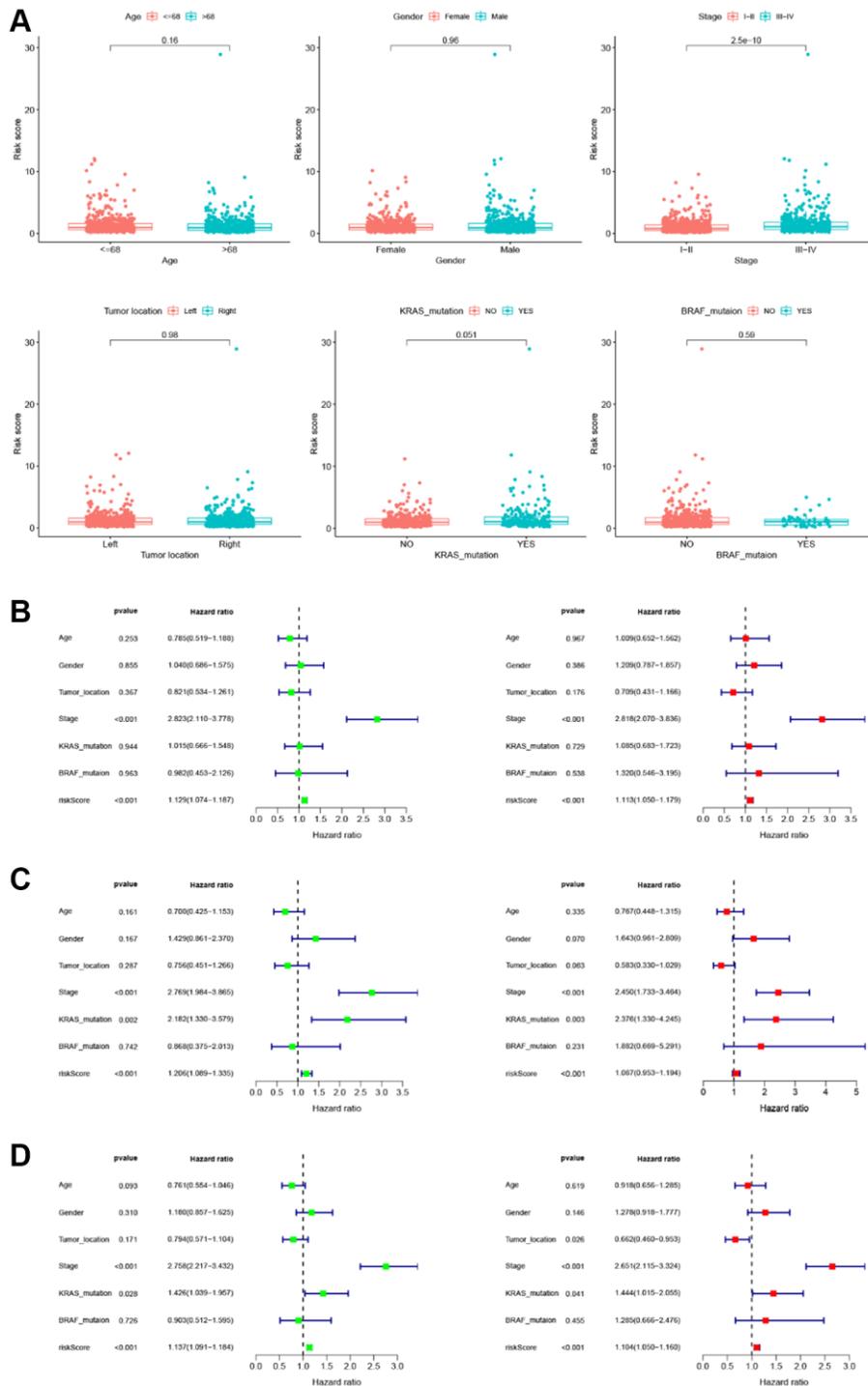
Supplementary Figure 4. Validation of ARG_score in testing cohort. (A) K-M analysis of the RFS between the two ARG_score groups. (B) ROC curves to predict the sensitivity and specificity of 1-, 5-, and 10-year survival according to the ARG_score. (C) The PCA analysis demonstrated that the patients in the different ARG_score groups were distributed in two directions. (D, E) The ranked dot plot indicates the ARG_score distribution and scatter plot presenting the patients' survival status. (F) Expression patterns of 9 selected prognostic genes in high- and low-ARG_score groups.



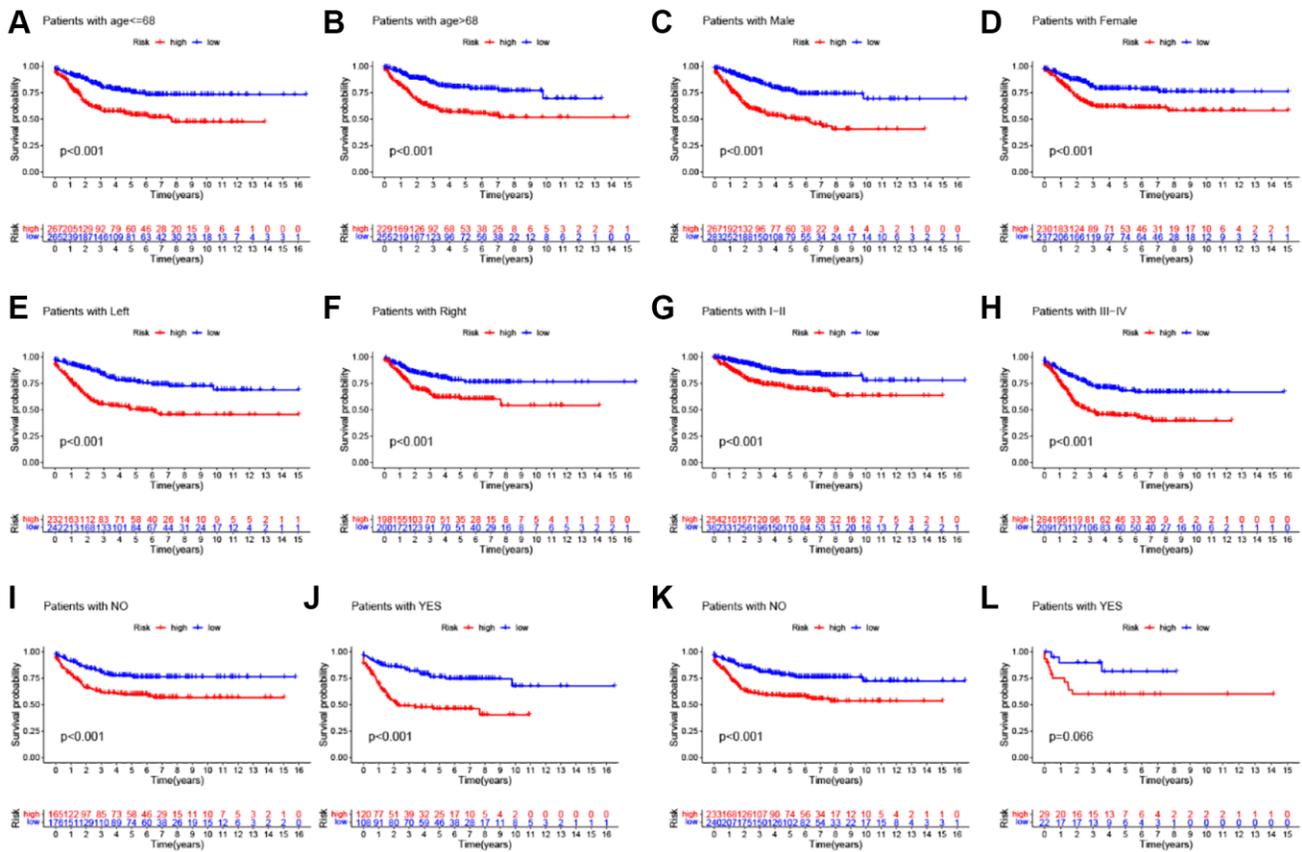
Supplementary Figure 5. Validation of ARG_score in entire cohort. (A) K-M analysis of the RFS between the two ARG_score groups. (B) ROC curves to predict the sensitivity and specificity of 1-, 5-, and 10-year survival according to the ARG_score. (C) The PCA analysis demonstrated that the patients in the different ARG_score groups were distributed in two directions. (D, E) The ranked dot plot indicates the ARG_score distribution and scatter plot presenting the patients' survival status. (F) Expression patterns of 9 selected prognostic genes in high- and low-ARG_score groups.



Supplementary Figure 6. Expression levels of 9 selected angiogenesis-related prognostic genes in CRC tissues and corresponding normal tissues. (A–H) Expression of 9 prognostic genes in CRC tissues and normal human colon tissues (TCGA cohort). **(B–H)** Expression of 9 prognostic genes in CRC tissues and normal human colon tissues (GEPIA 2 cohort). **(I–O)** Expression levels of 9 prognostic genes in CRC tissues and corresponding normal tissues by RT-PCR. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.



Supplementary Figure 7. The correlation and independent prognosis analysis of ARG_score and clinicopathological variables in CRC. (A) The correlation between the ARG_score and clinical characteristics, including age, gender, TNM stage, tumor location, KRAS mutation status, and BRAF mutation status. **(B)** Univariate and multivariate analyses showed the prognostic value of the ARG_score in the training cohort. **(C)** Univariate and multivariate analyses showed the prognostic value of the ARG_score in the testing cohort. **(D)** Univariate and multivariate analyses showed the prognostic value of the ARG_score in the entire cohort.



Supplementary Figure 8. Stratification analysis of the ARG_score in CRC. (A, B) Age (age ≤ 68 and age > 68 years old). (C, D) Gender (female and male). (E, F) Tumor location (left-side or right-side). (G, H) Tumor stage (I-II or III-IV). (I, J) KRAS mutation (yes and no). (K, L) BRAF mutation (yes and no).