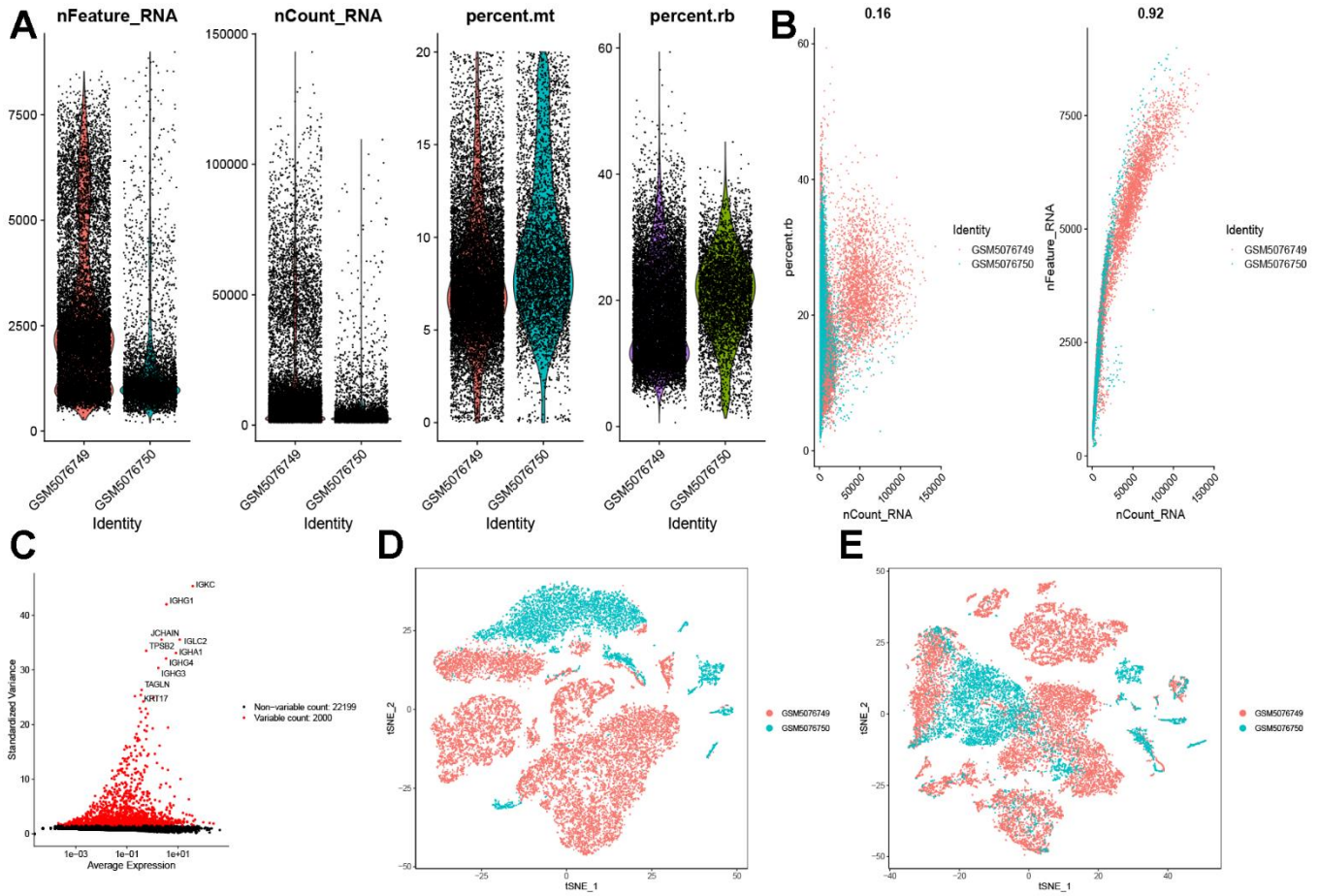
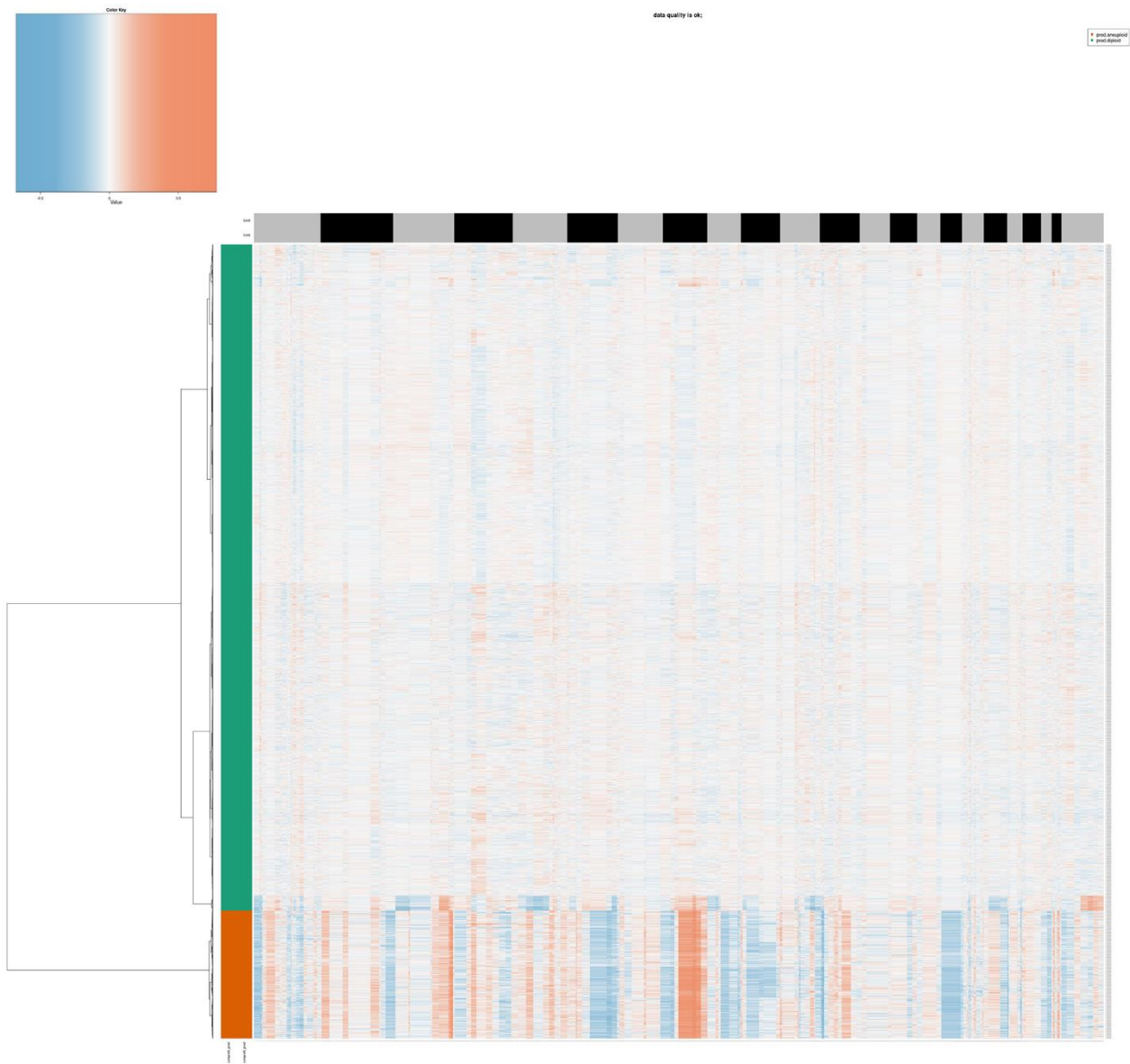


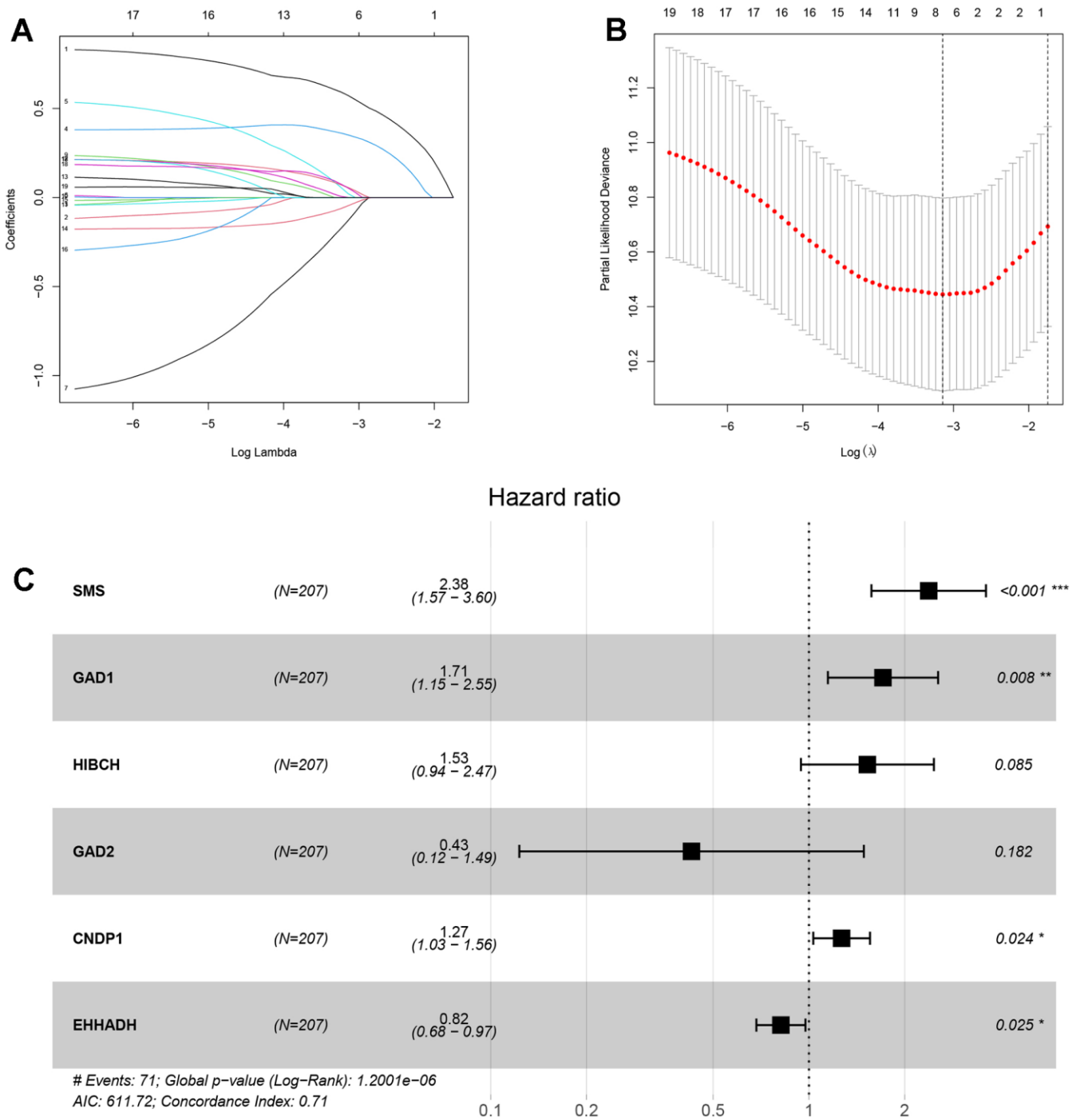
SUPPLEMENTARY FIGURES



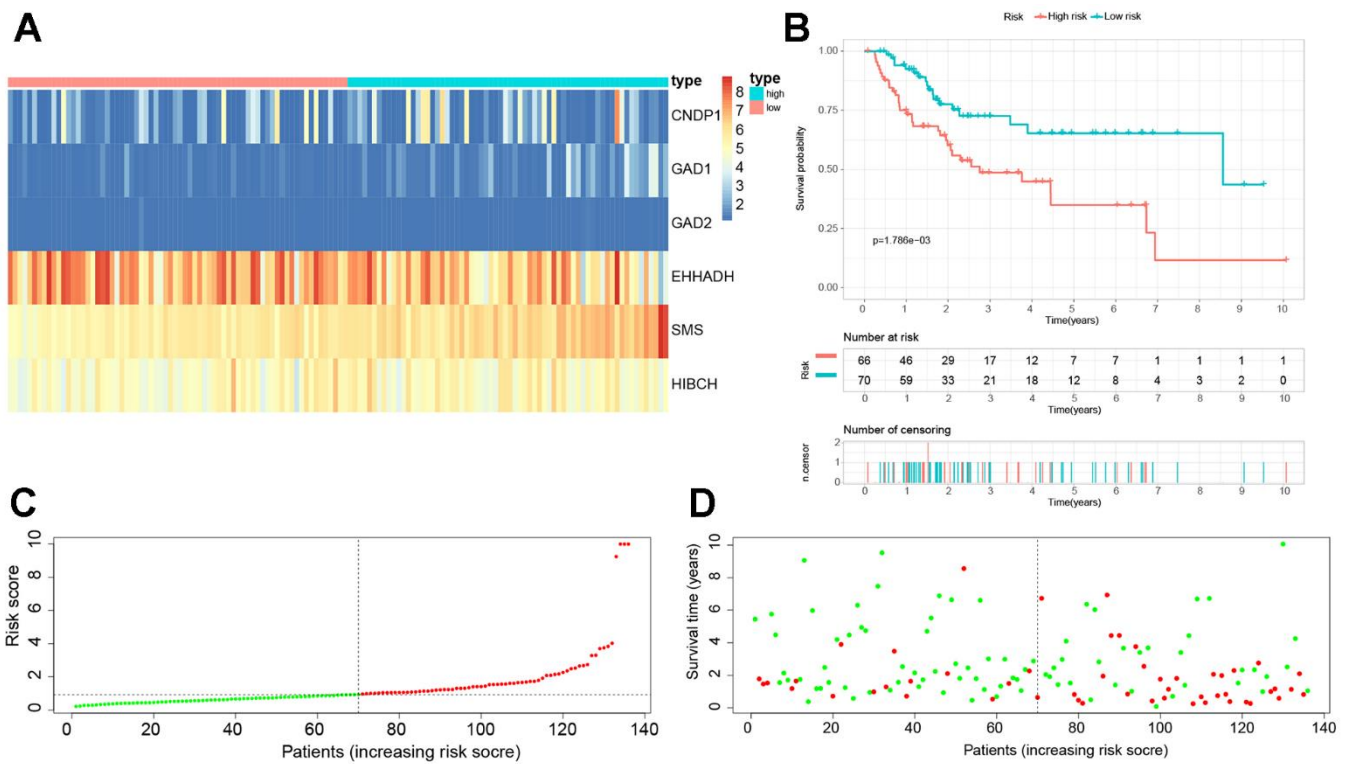
**Supplementary Figure 1. Single-cell data processing steps.** (A) By controlling the sequencing depth, number of genes, mitochondrial content and ribosome content, the unqualified cells are filtered out; (B) Correlation between above indicators; (C) Identification of highly variable genes; Batch correction and dimensionality reduction using Harmony before (D) and after (E) analysis.



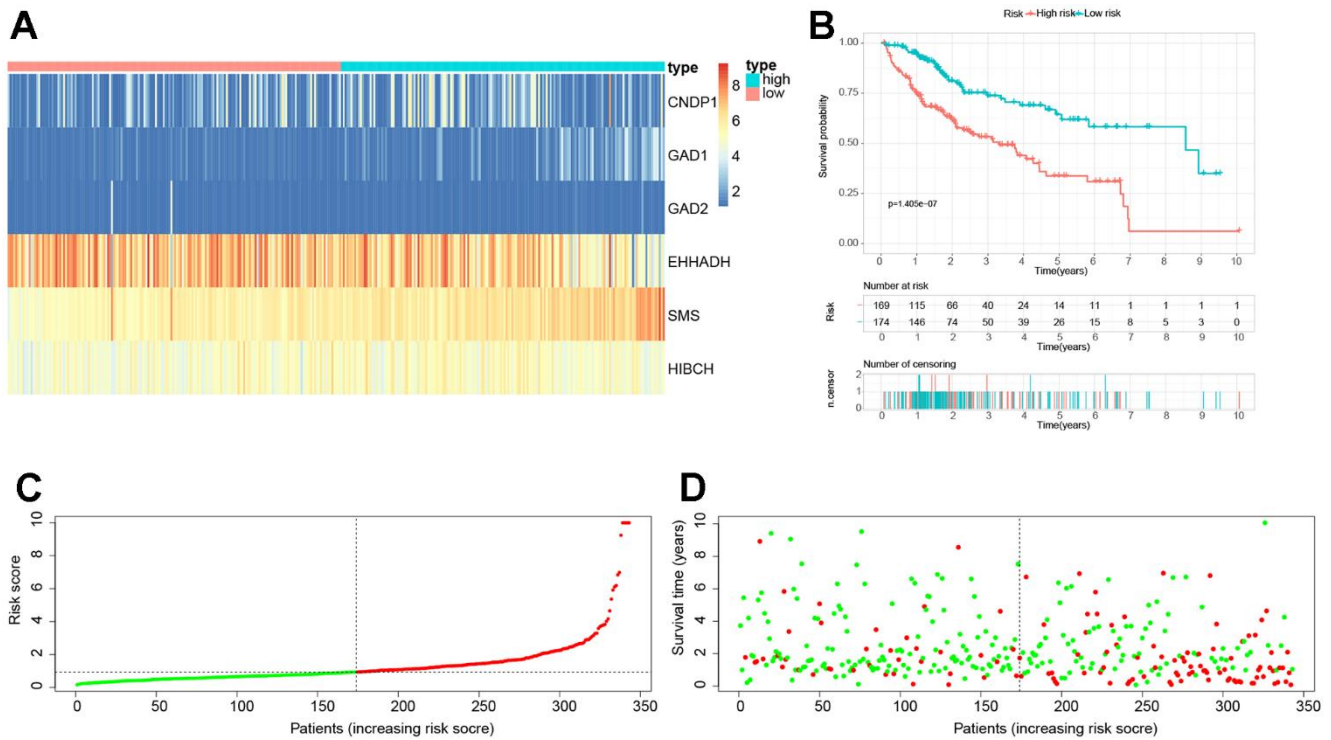
Supplementary Figure 2. The results of CopyKat algorithms.



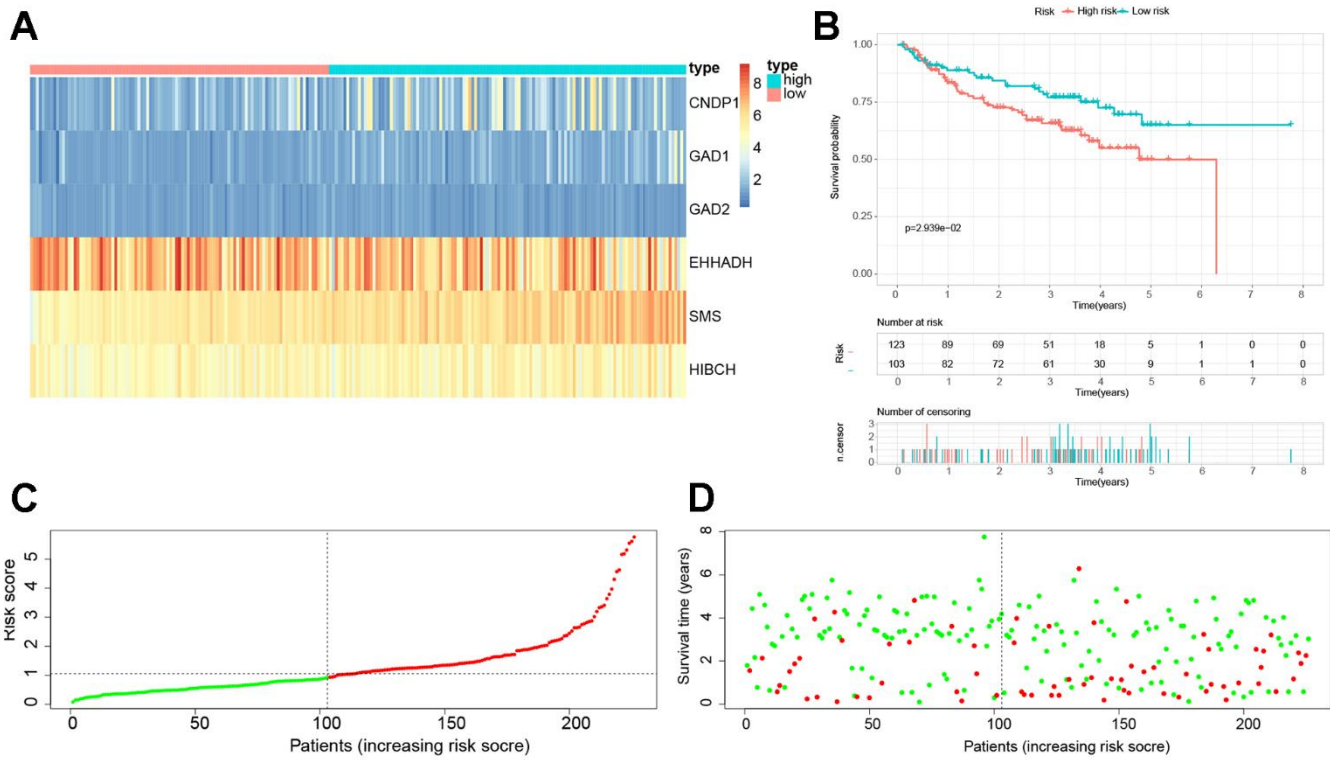
**Supplementary Figure 3. Screening of the hub genes of  $\beta$ AMRGs-RPS.** (A) LASSO coefficient profiles of  $\beta$ AMRGs mRNA in HCC. (B) Cross-validation results of the model construction. A total of six genes were selected using LASSO Cox regression analysis. (C) Analysis of multivariate Cox regression of  $\beta$ AMRGs mRNA.



**Supplementary Figure 4. Internal validation of the robust  $\beta$ AMRGs-RPS in the test1 cohort. (A)** Heatmap illustrating the expression levels of six genes between subgroups with high and low risk scores. **(B)** Prognostic prediction depicted by the Kaplan-Meier survival curve comparing subgroups with high and low risk scores. **(C)** Risk score curve plot exhibiting the distribution of individual risk scores, with the patients categorized into low-risk (green) and high-risk (red) groups. **(D)** Risk score scatter plot, where red dots indicate deceased patients and green dots indicate surviving patients.



**Supplementary Figure 5. Internal validation of the robust  $\beta$ AMRGs-RPS in the test2 cohort.** (A) Heatmap illustrating the expression levels of six genes between subgroups with high and low risk scores. (B) Prognostic prediction depicted by the Kaplan-Meier survival curve comparing subgroups with high and low risk scores. (C) Risk score curve plot exhibiting the distribution of individual risk scores, with the patients categorized into low-risk (green) and high-risk (red) groups. (D) Risk score scatter plot, where red dots indicate deceased patients and green dots indicate surviving patients.



**Supplementary Figure 6. External validation of the robust  $\beta$ AMRGs-RPS in the test3 cohort.** (A) Heatmap illustrating the expression levels of six genes between subgroups with high and low risk scores. (B) Prognostic prediction depicted by the Kaplan-Meier survival curve comparing subgroups with high and low risk scores. (C) Risk score curve plot exhibiting the distribution of individual risk scores, with the patients categorized into low-risk (green) and high-risk (red) groups. (D) Risk score scatter plot, where red dots indicate deceased patients and green dots indicate surviving patients.