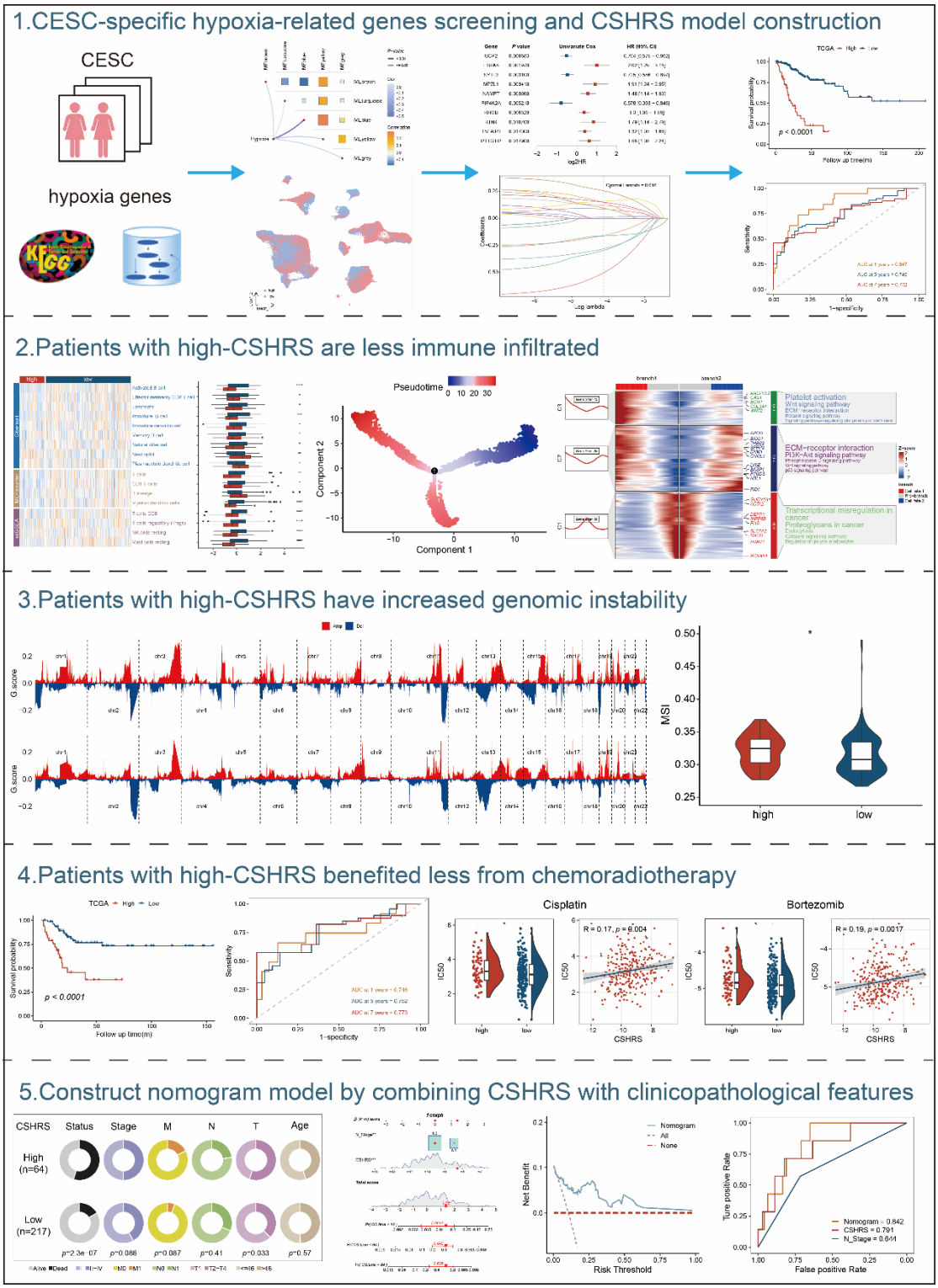
Supplementary Figure S1 Research Process Flowchart



Supplementary Figure S1 Research Process Flowchart. Firstly, the CESC-specific hypoxia gene sets shared between scRNA-seq, and bulk data were identified using WGCNA and FindMarkers. A CSHRS risk model was constructed using LASSO and Cox regression analyses based on these genes. The prognostic differences were explored from immune infiltration, mutations, and drug

resistance perspectives. Finally, a nomogram model was constructed by integrating clinicopathological features to facilitate precision treatment for CESC.

Supplementary Table: Supplementary table on tumor marker levels. Table S1: Table of tumor marker genes. Table S2: Table of tumor marker levels.