

Supplementary Data 1: Single-cell quality control. (a) Before: nFeature_RNA, nCount_RNA, and percent.Mt; (b) After : nFeature_RNA, nCount_RNA, and percent.Mt.

Supplementary Data 2: Cell communication. (a) Cellular communication between single cell types and other cells. (b) Ligand-receptor interactions between different cell types.

Supplementary Data 8. Differential expression analysis of key genes and construction of nomogram. (a) Differential expression of key genes in the training set GSE22491. *: $P < 0.05$; **: $P < 0.01$; ns: no significance. (b) Construction of nomogram. (c) The calibration curve of the nomogram. (d) The decision curve analysis of the nomogram. (e) The receiver operating characteristic (ROC) curve of the nomogram

Supplementary Data 9. GSEA enrichment results of four biomarkers. The ordinate represents the enrichment fraction, and enrichment score (ES) is positive, indicating that a certain functional gene set is enriched in front of the sequencing sequence, indicating that it is positively correlated with gene enrichment. ES is negative, indicating that a certain functional gene set is enriched behind the sequencing sequence, indicating that it is negatively correlated with gene enrichment. The horizontal coordinates represent genes, and each little vertical line represents a gene. (a) SLC11a1. (b) DDX17. (c) MRAS. (d) PDIA3. (e) Protein co-expression network of four biomarkers.