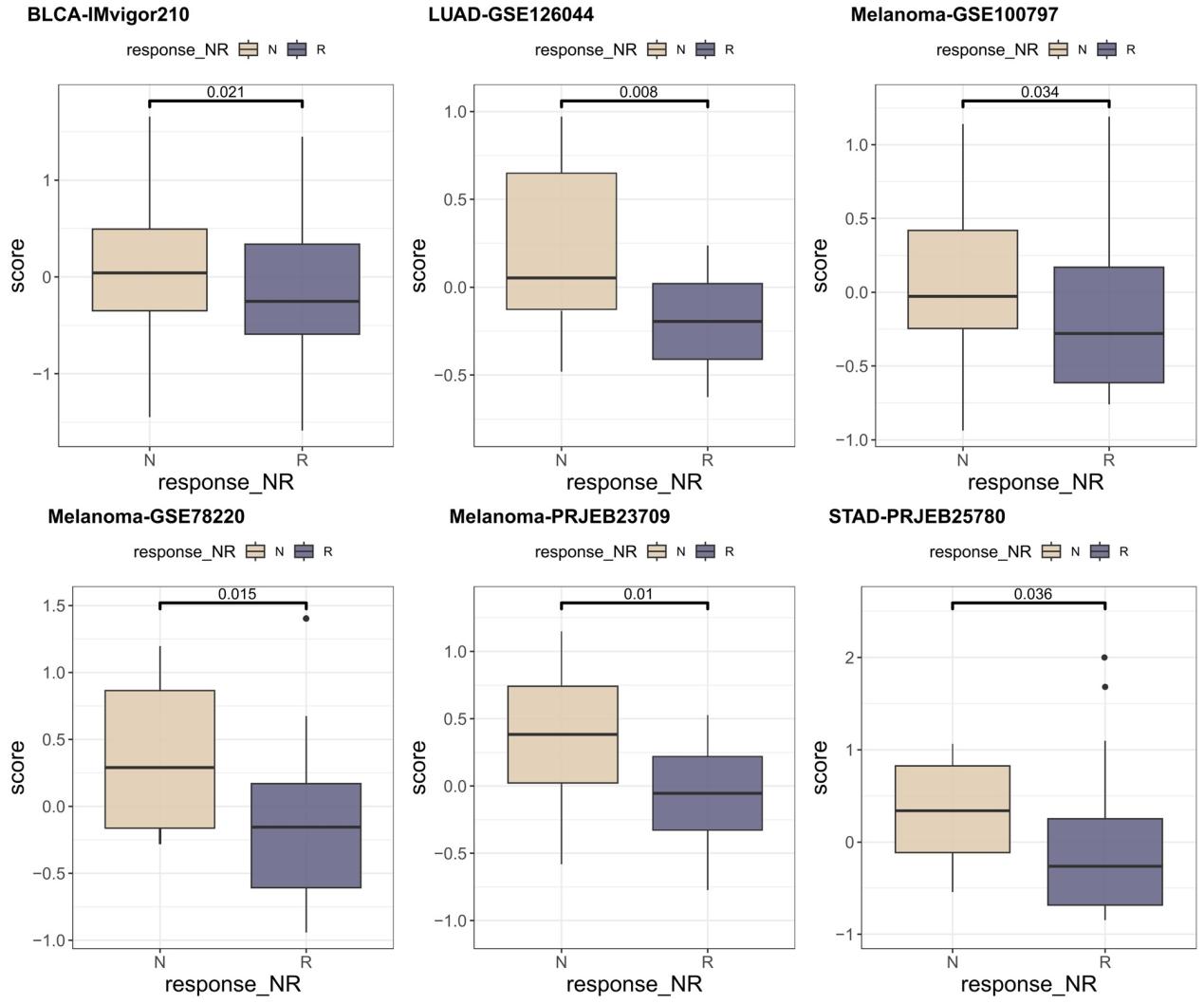
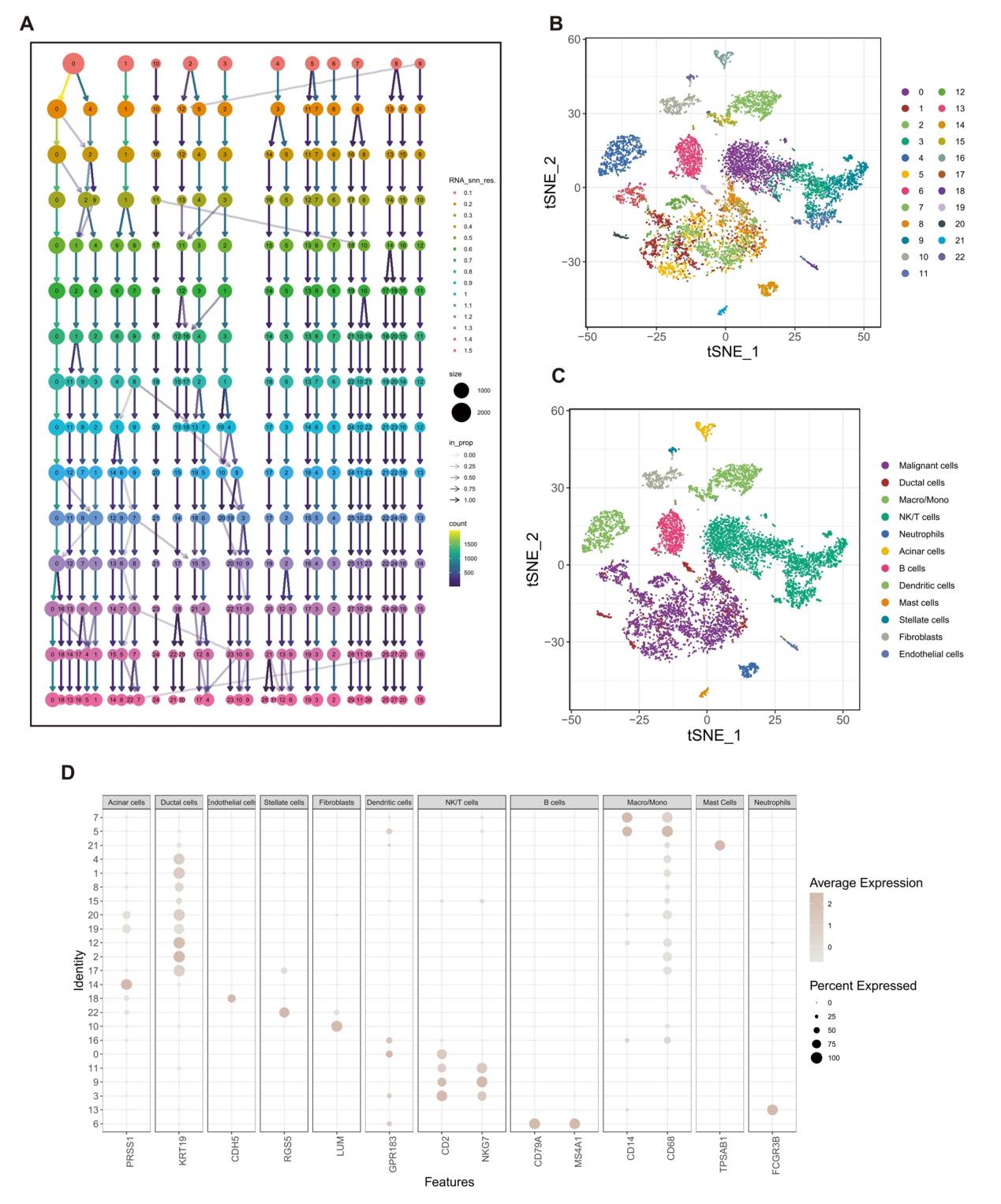
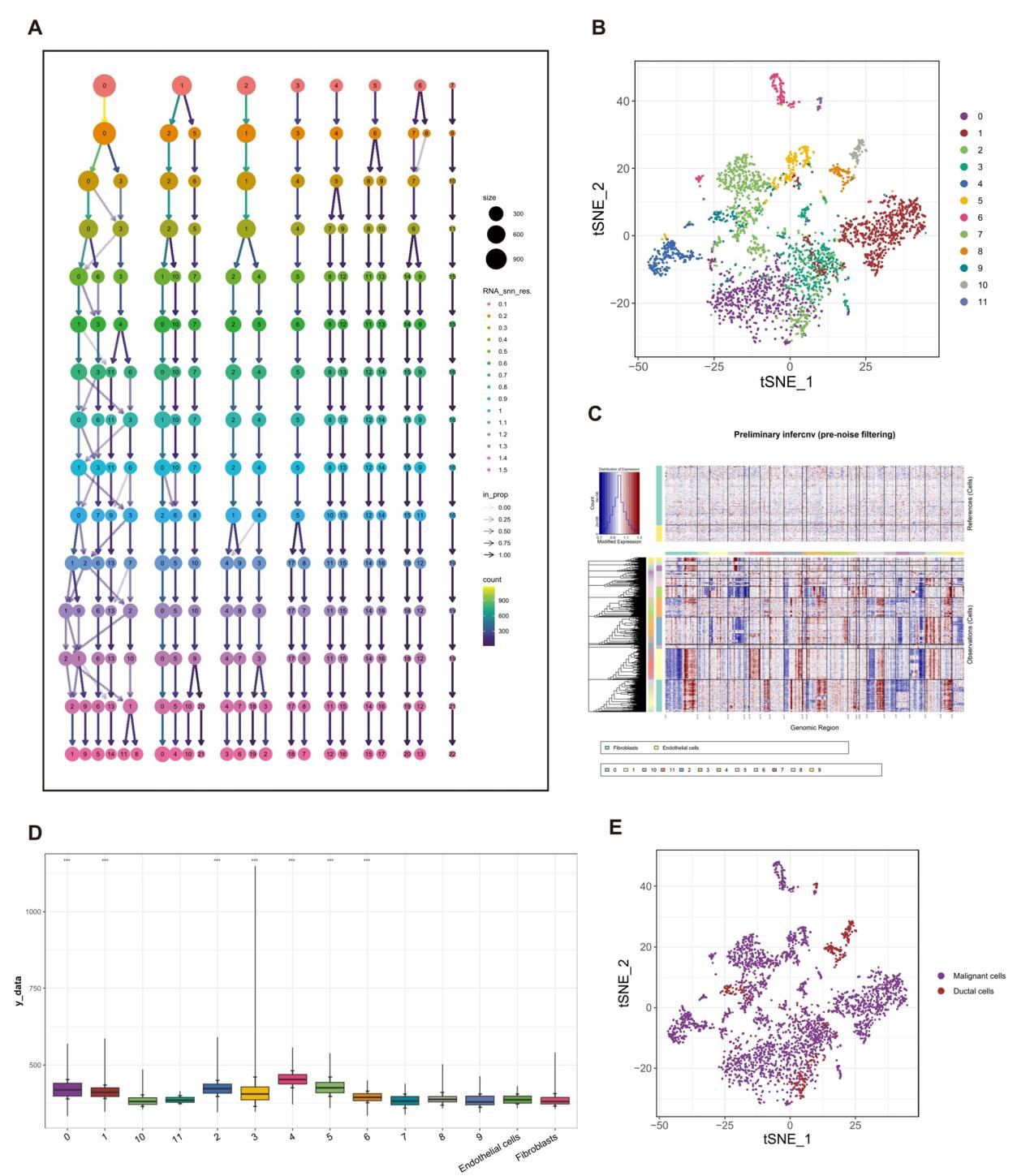
**SFigure 1 Box plot displaying the correlation between the RCDS signature and immunotherapy response in the immunotherapy cohorts.**



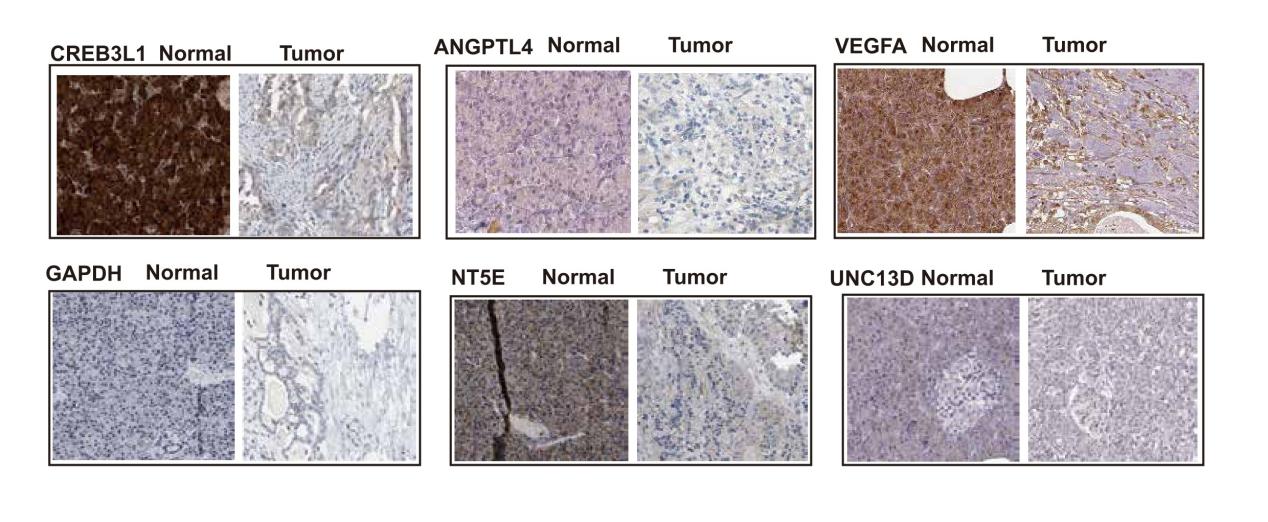
**SFigure 2 Annotation of scRNA-seq mate data**

1. The clustering tree displaying total scRNA-seq mate data analyzed at different resolutions. **(B)** The t-SNE plot displaying the cell clusters in the microenvironment of PACA. **(C)** The t-SNE plot displaying the composition of cells in the microenvironment of PACA. **(D)** Dot plot displaying expression of cell-type markers across cell clusters. Dot size indicates the percentage of expressed cells, colored by their relative expression levels

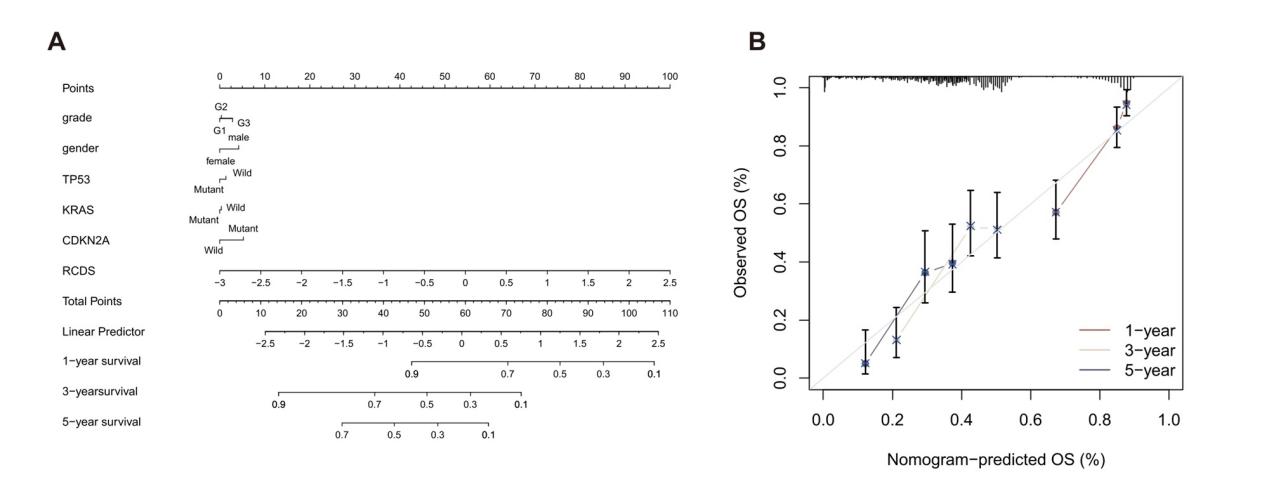


**SFigure 3 Distinguishing between malignant and normal cells in ductal cells**

1. The clustering tree displaying total scRNA-seq mate data analyzed at different resolutions. **(B)** The t-SNE plot displaying the ductal cell clusters in the microenvironment of PACA. **(C)**Infercnv plotidentified malignant cells in duct cells.**(D)**The boxplot displaying the levels of CNV scores for each cluster of ductal cells and the reference cells.**(E)** The t-SNE plot displaying the composition of cells in the microenvironment of PACA.



**SFigure 4 The immunohistochemistry (IHC) staining images of RCDS genes from GC and healthy stomach tissue in the HPA database.**



**SFigure 5** Theestablishment of nomogram.

1. Nomogram was established to predict the prognostic of PACA patients. **(B)** The Calibration curves for overall survival (OS) at 1-year ,3-year and 5-year in PACA patients.