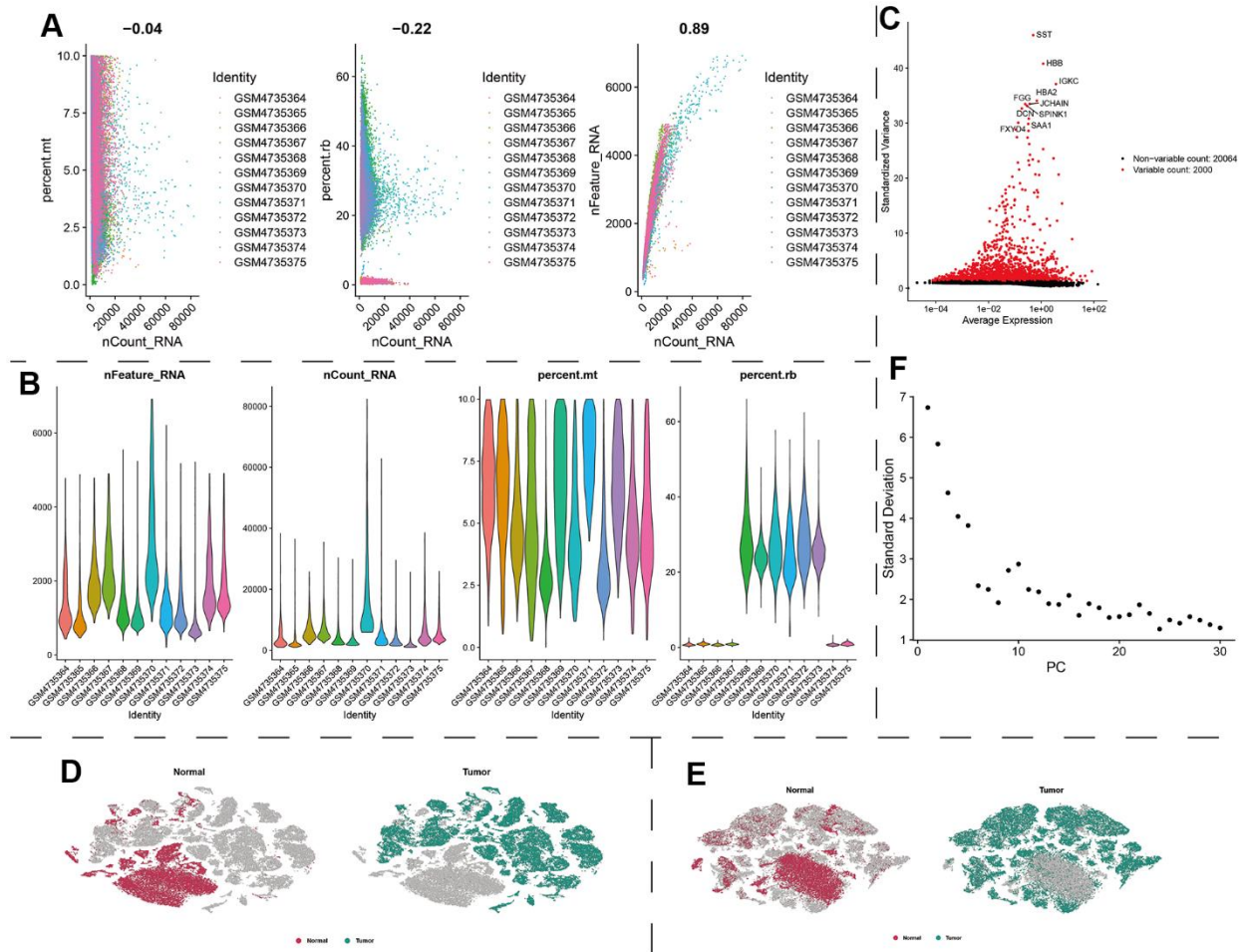
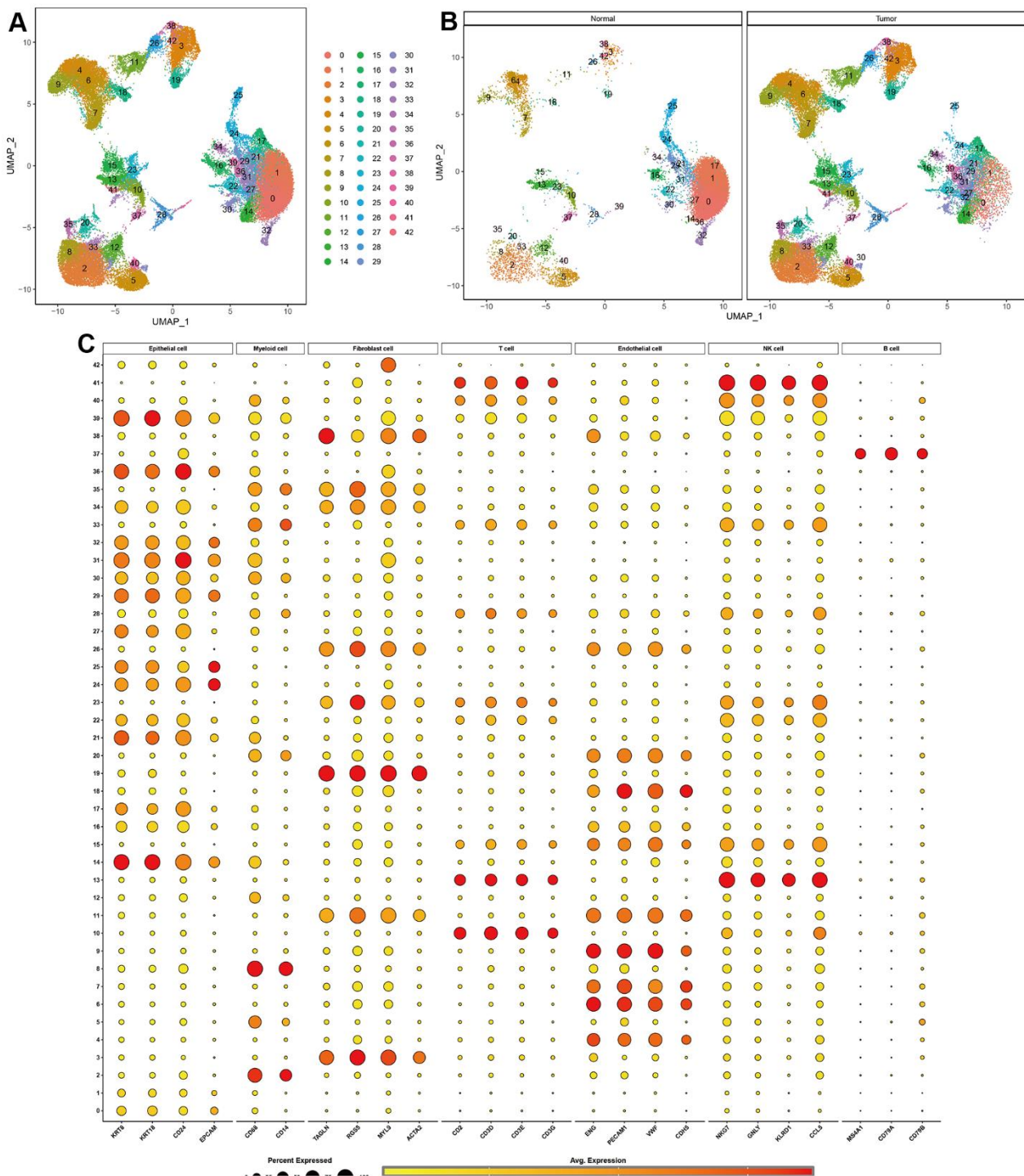


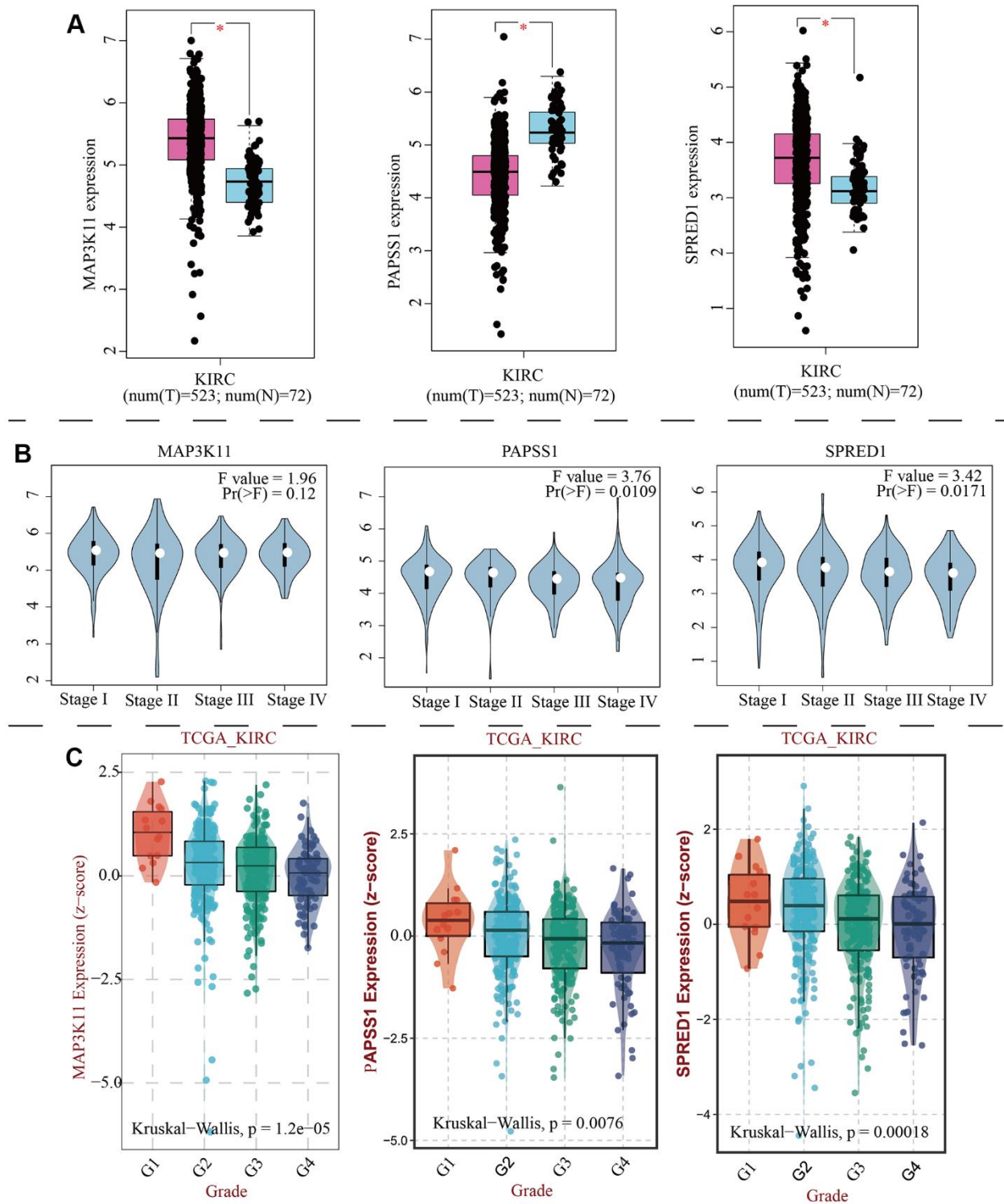
SUPPLEMENTARY FIGURES



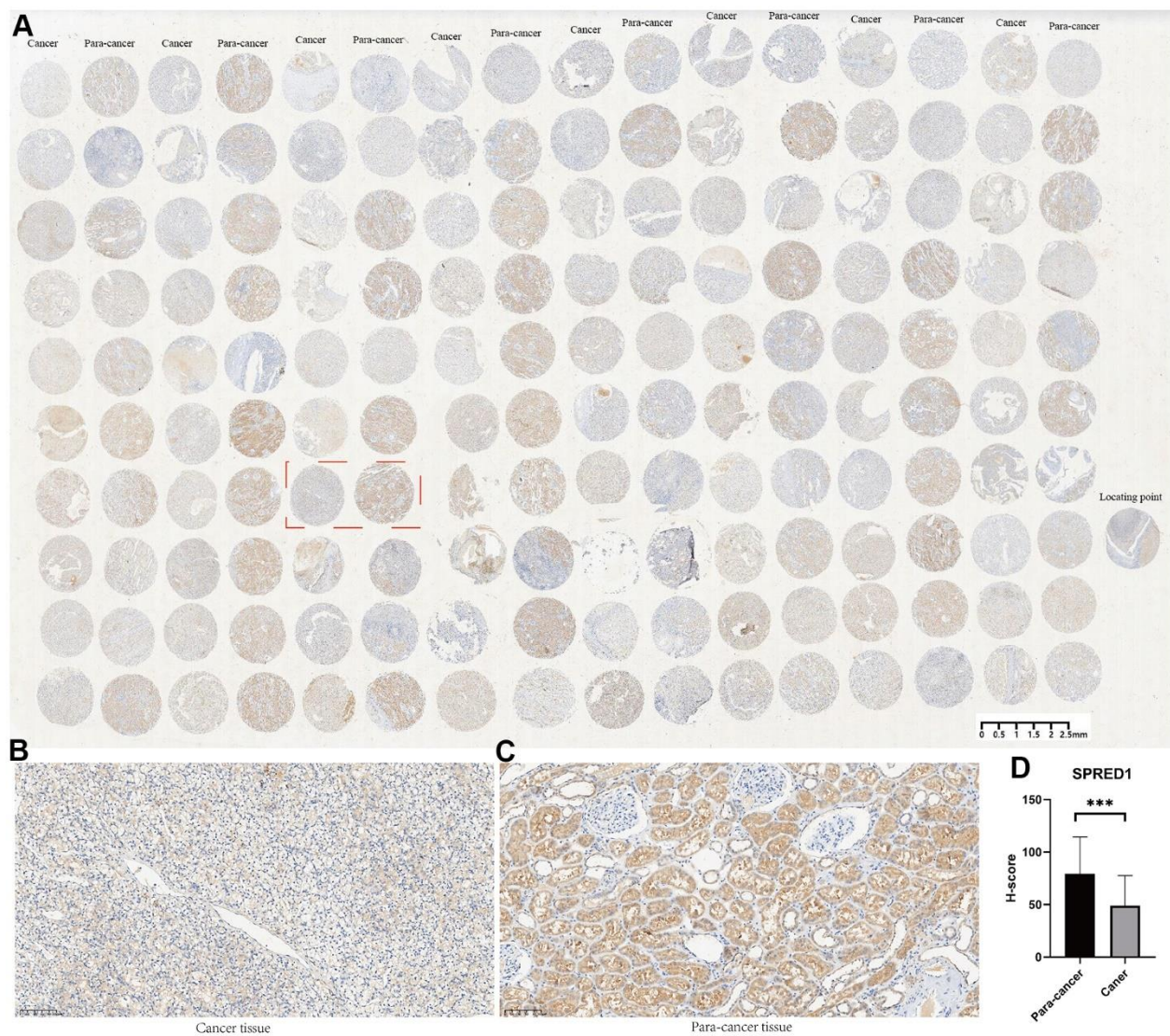
Supplementary Figure 1. Single-cell data processing. (A, B) Data quality control of sc-RNA data. (C) Highly variable genes of the data. (D, E) Cell distribution before and after removing the batch effect by Harmony. (F) ElbowPlot for identifying suitable PC number.



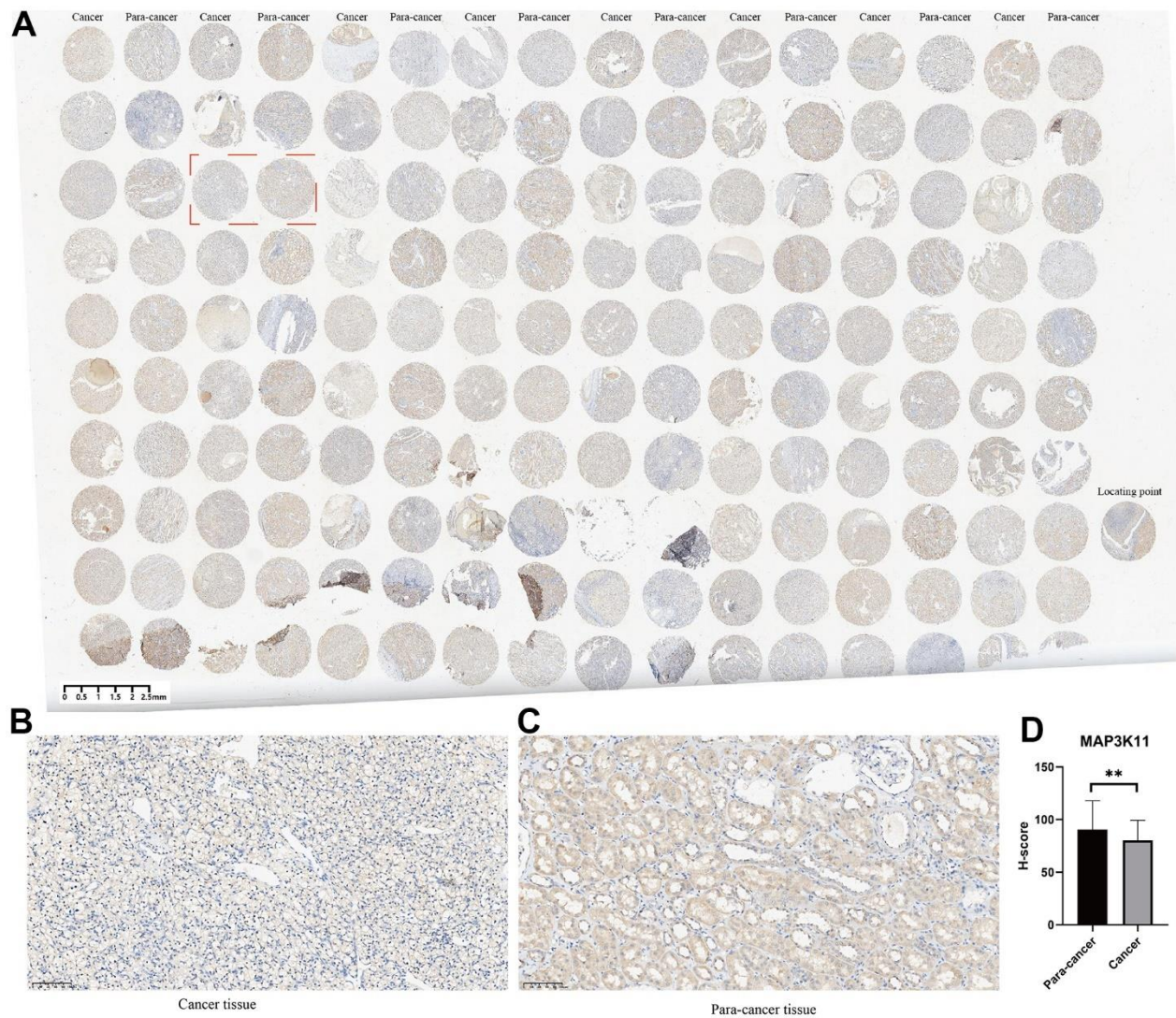
Supplementary Figure 2. Single-cell dimension reduction and annotation process. (A) UMAP dimension reduction plots for all samples. (B) UMAP dimension reduction plots for normal and tumor groups. (C) Single-cell annotation process.



Supplementary Figure 3. Identification of hub genes in the occurrence of KIRC. (A) The mRNA expression of hub genes. (B) The relationship between the expression of each hub gene and tumor stage in KIRC. (C) The relationship between the expression of each hub gene and tumor grade in KIRC.



Supplementary Figure 4. The tissue microarray and immunohistochemistry (IHC) of SPRED1. (A) Immunohistochemical maps for all samples. (B) Immunohistochemical maps of typical cancer samples. (C) Immunohistochemical maps of typical para-cancer samples. (D) Immunohistochemical statistical analysis results.



Supplementary Figure 5. The tissue microarray and immunohistochemistry (IHC) of MAP3K11. (A) Immunohistochemical maps for all samples. (B) Immunohistochemical maps of typical cancer samples. (C) Immunohistochemical maps of typical para-cancer samples. (D) Immunohistochemical statistical analysis results.