Appendix PDF

Appendix Figure S1
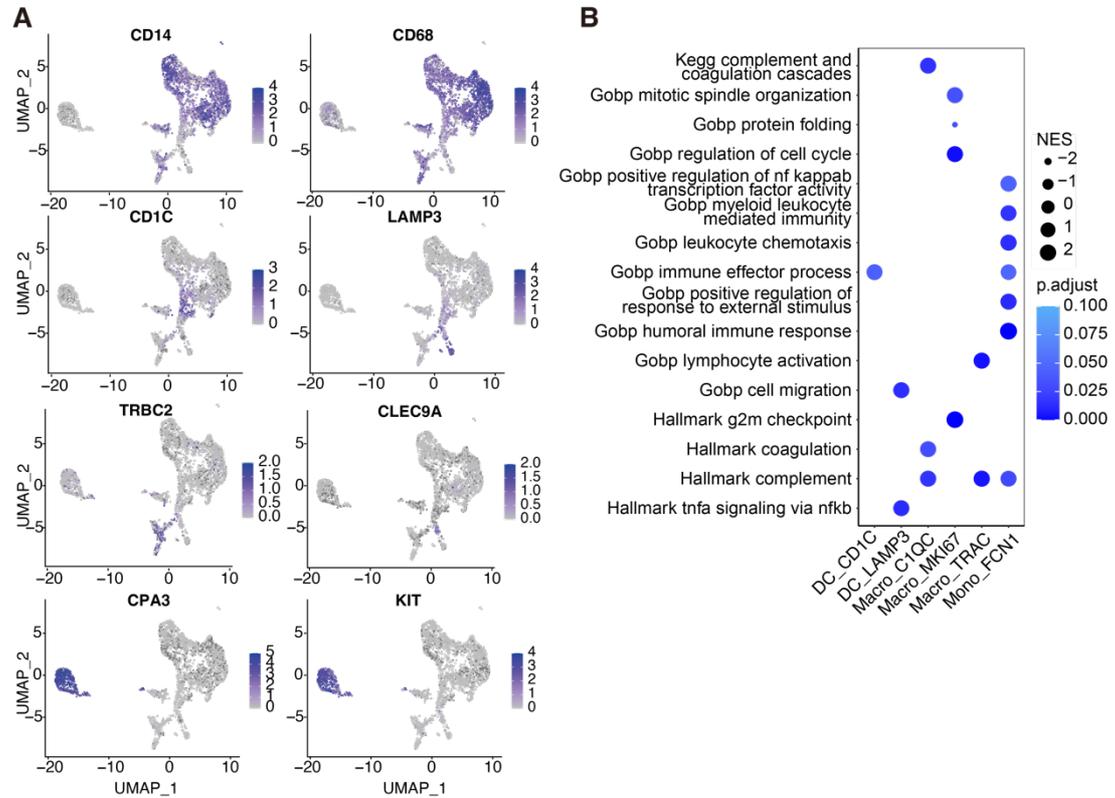
Appendix Figure S1. Additional analysis of myeloid cells

A UMAP plot showing the expression distribution of marker genes in myeloid cells;

B Dot plot showing the selected signaling pathways (rows) with significant enrichment of GO, KEGG, and Hallmark terms for myeloid cell clusters.

(related to Figure 5)

Appendix Figure S2

Novel Findings of Tumor Microenvironment in Cervical Cancer
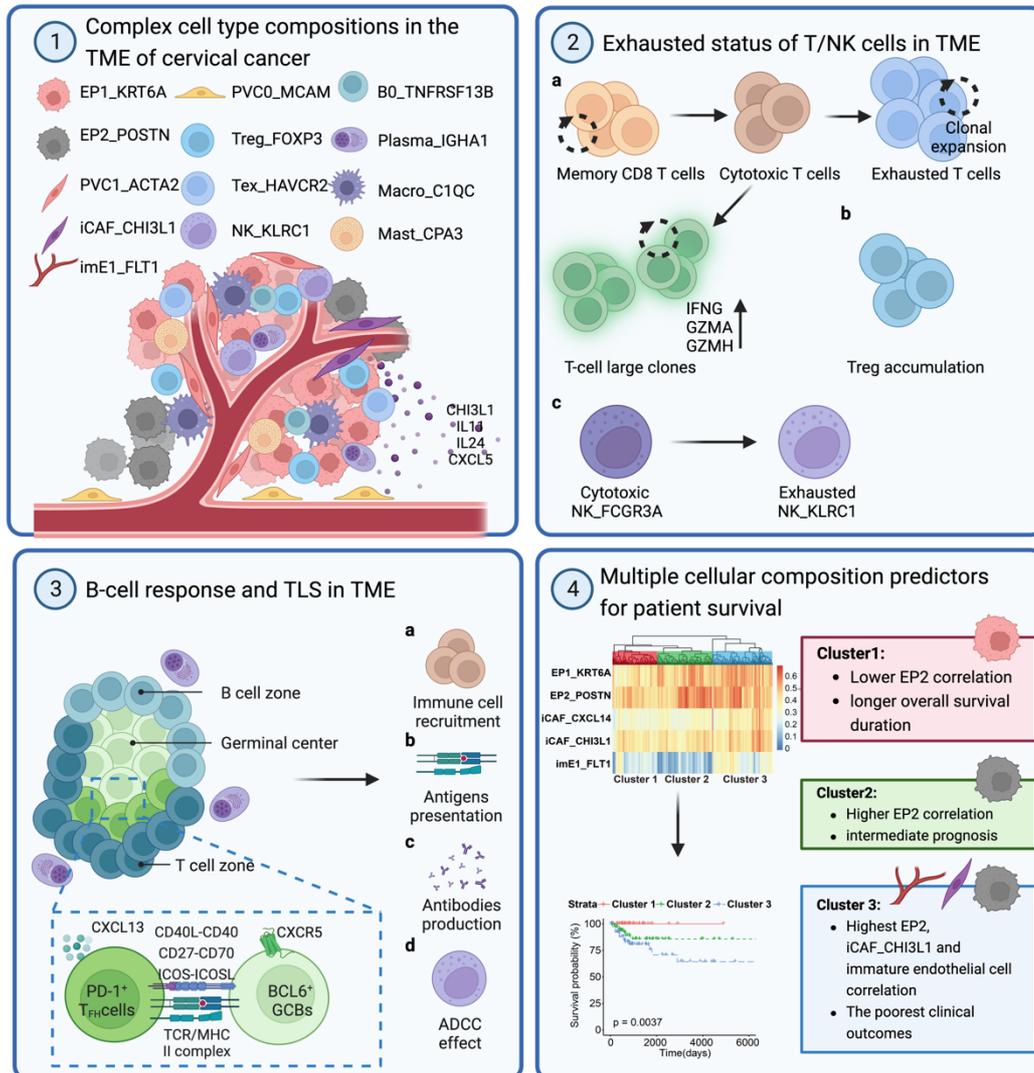
Appendix Figure S2. Schematic diagram of novel findings in the TME of CC. Created with BioRender.com.

Appendix Figure S3
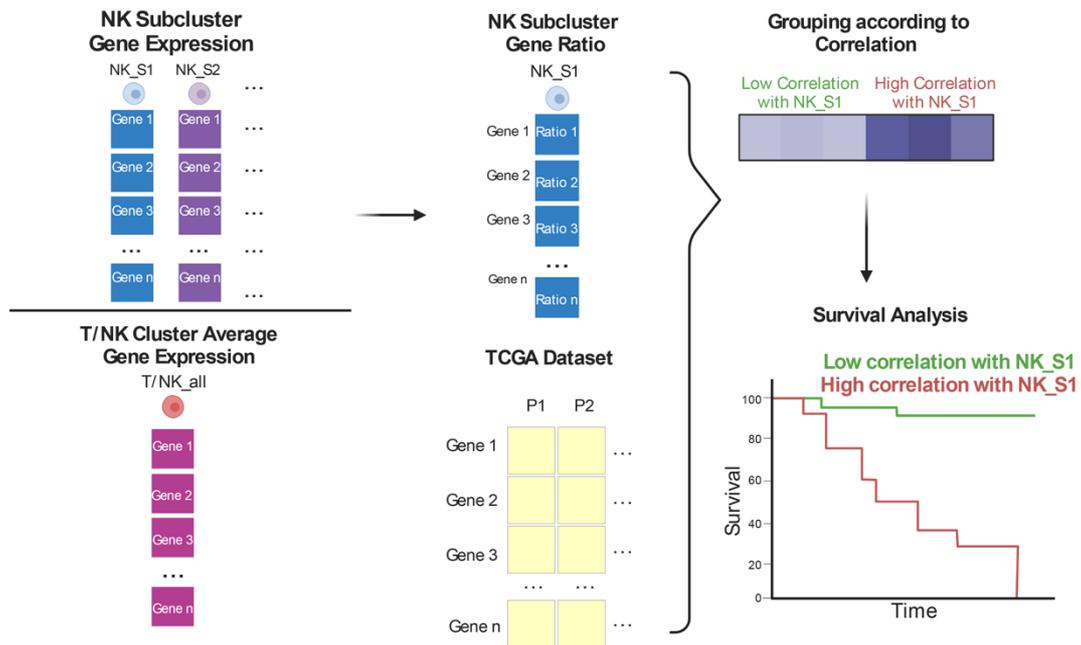
Appendix Figure S3. Schematic diagram of survival analysis with the NK subset as an example. Created with BioRender.com.

For example, for each cell type subset, such as NK_FCGR3A , we generated the averaged gene expression for all of the genes for that subset; for each gene, we divided the gene expression by the corresponding averaged gene expression of all T and NK cells, which generated a list of ratios for all genes. These ratios represented the specificity of each gene for the NK_FCGR3A cell subset. Then, for each patient in the TCGA cohort (TCGA, CESC-squamous cell neoplasms), we calculated the overlapping genes between all TCGA patient genes and NK_FCGR3A signature genes and the Spearman correlation using the expression of overlapped genes from that patient with ratios of overlapped genes from scRNA-seq data. Patients will be classified into a higher correlation group and a lower correlation group by 55th and 45th quantile values, for which higher correlation indicates that the patient might have higher infiltration of NK_FCGR3A, and lower correlation, and vice versa.