Supplementary Material

1 Supplementary Figures

Supplementary Fig.S1 The epithelial cells subsets highly associated with EMT

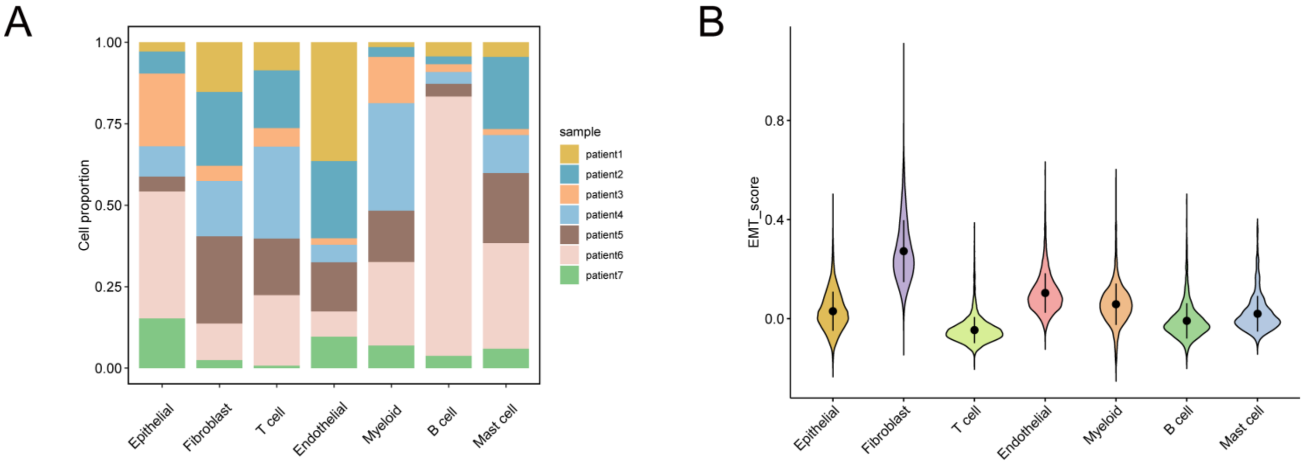
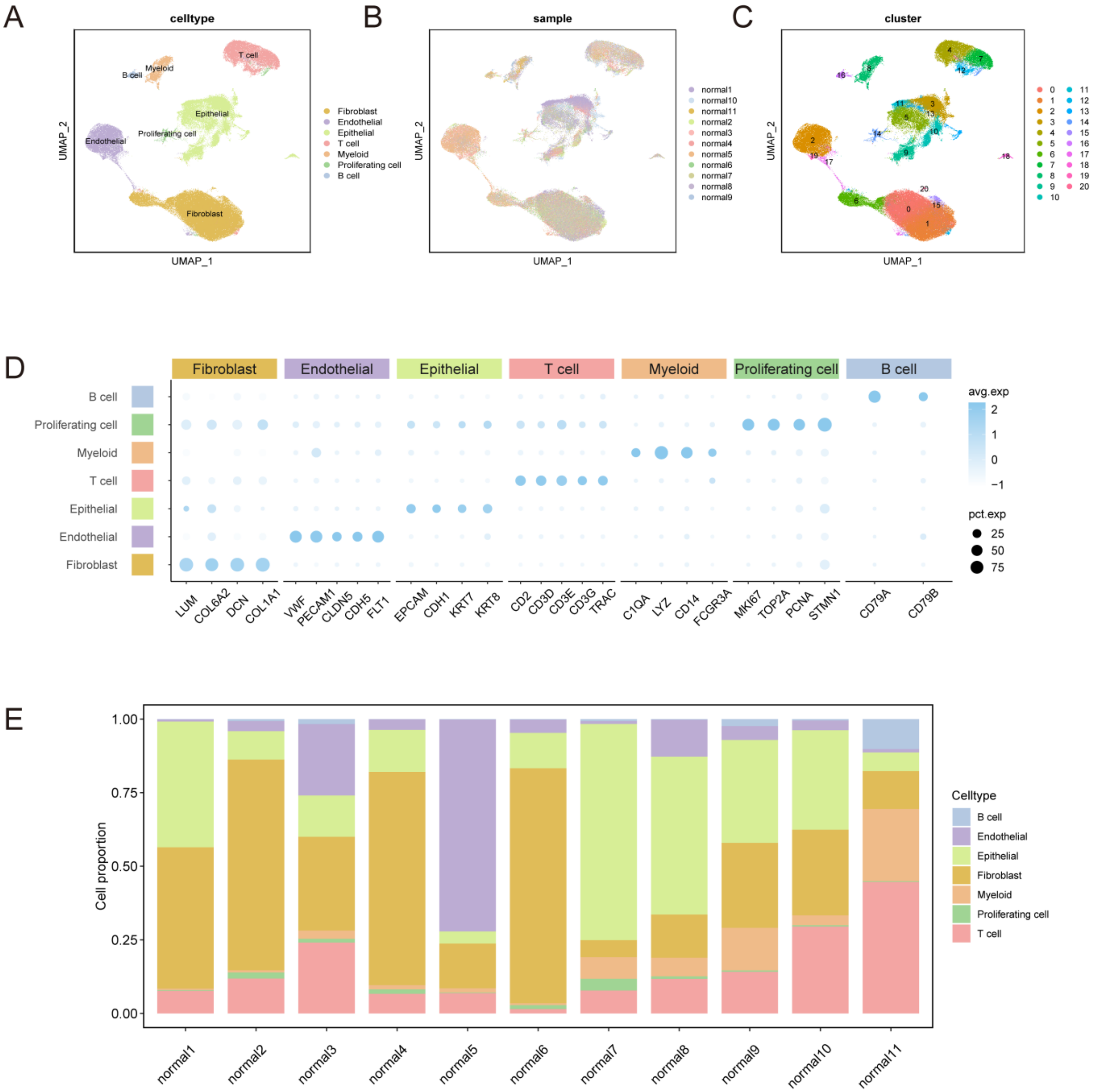


Fig.S2 The epithelial cells subsets highly associated with EMT **A** Stacked bar plot showing the proportional distribution of 7 individual patients across 7 major cell types. **B** Violin plot showing the EMT score level of 7 major cell type.

Supplementary Fig. S2 The GO enrichment analysis of biological processes

Supplementary Fig. S3 Single-cell landscape of 11 normal endometrial samples



Supplementary Fig. S3 Single-cell landscape of 11 normal endometrial samples **A-C** UMAP plot of single-cell transcriptomes: **A** coded by annotated cell types. B, ratified by patient origin. **C** segregated by unsupervised clustering. **D** The dot plot of the representative marker genes for the cell types. **E** Stacked bar plot showing the proportional distribution of major cell types across individual patients.

Supplementary Tables

Supplementary TableS1 The detailed information for 7 ScRNAseq EC sample and 11 ScRNAseq normal endometrial samples

Supplementary TableS2 The 200 EMT_related genes used to EMT score

Supplementary TableS3 The top500 genes of trajectory analysis

Supplementary TableS4 The cNMF anlysis outcome of MP1

Supplementary TableS5 The 47 EMT related genes

Supplementary TableS6 The genes highly expressed in tumor epithelial cells (8403) and in tumor fibroblasts (3974)

Supplementary TableS7 The detailed information for siRNAs sequence and RT-qPCR Primers of INHBA and POSTN and related Antibody