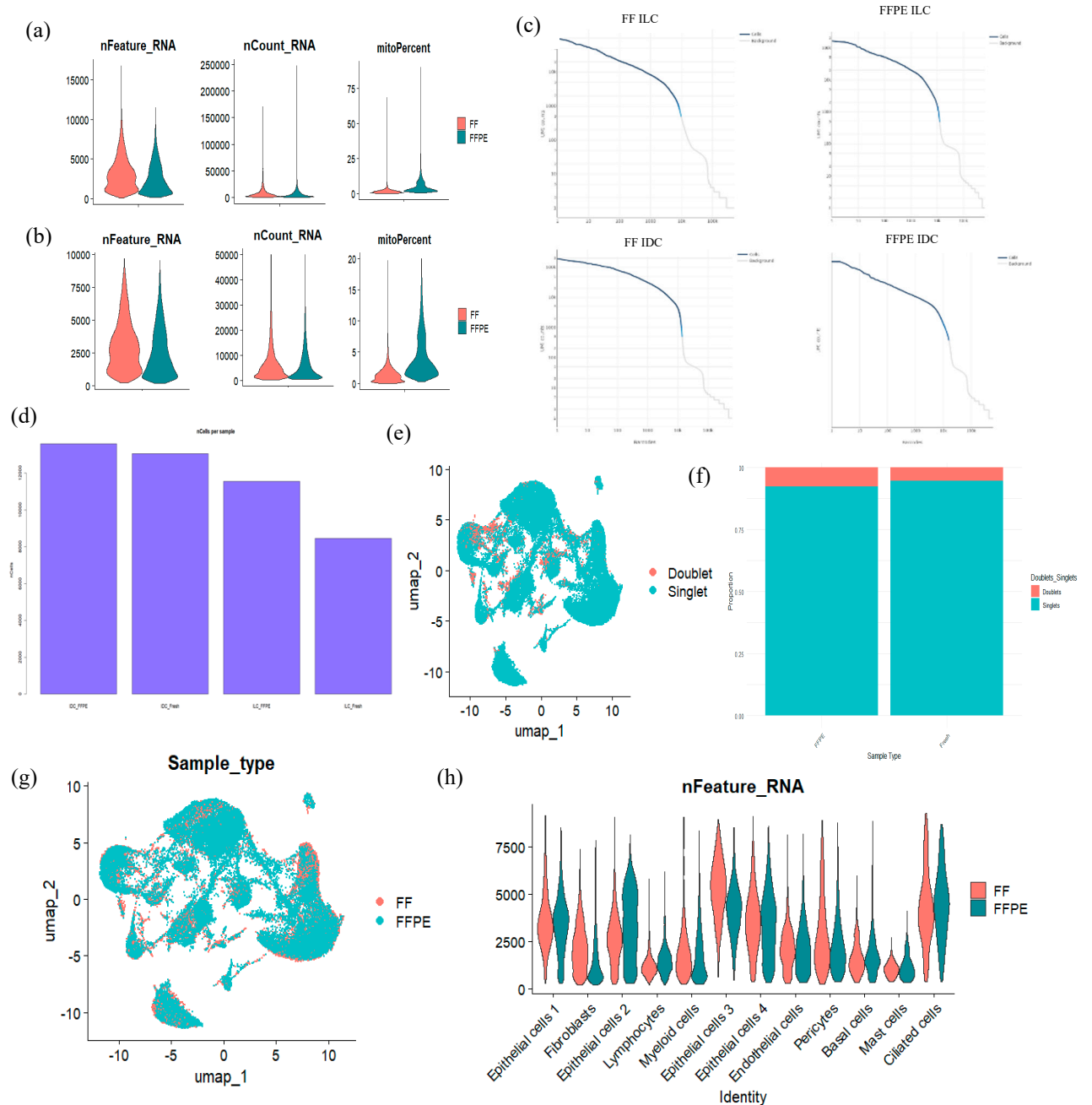
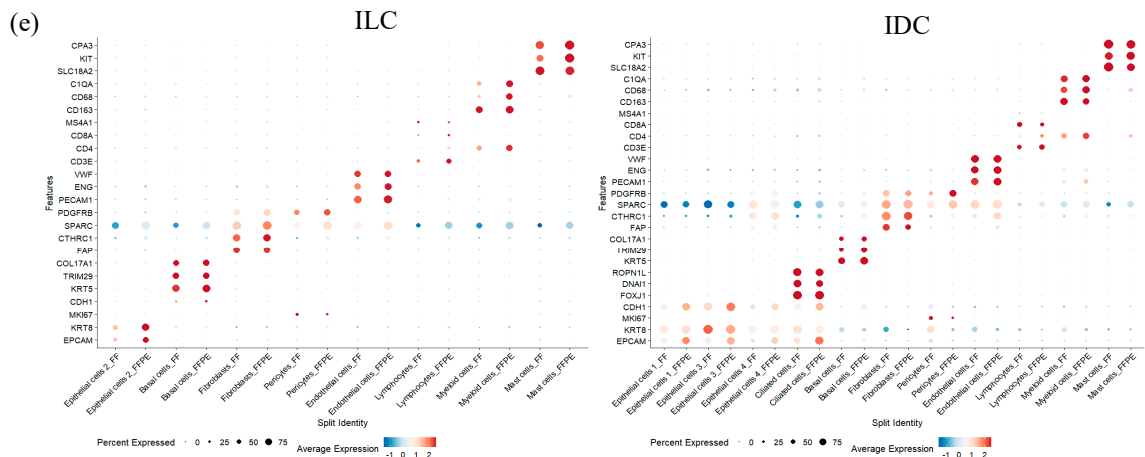
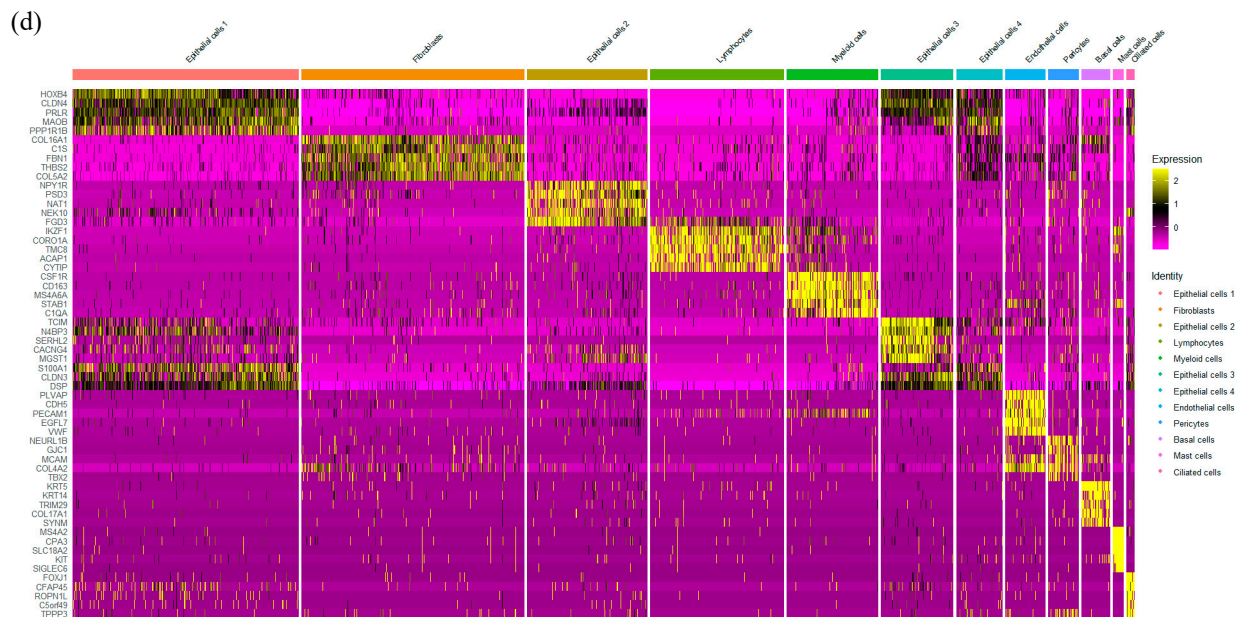
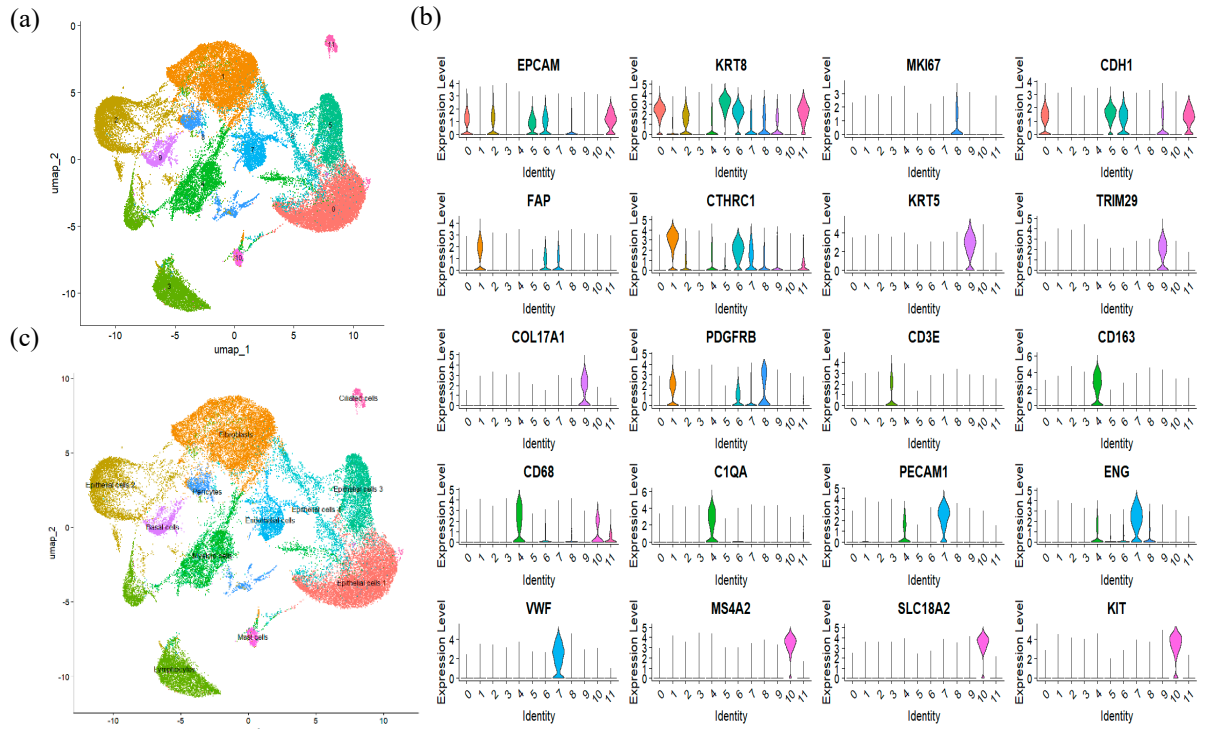


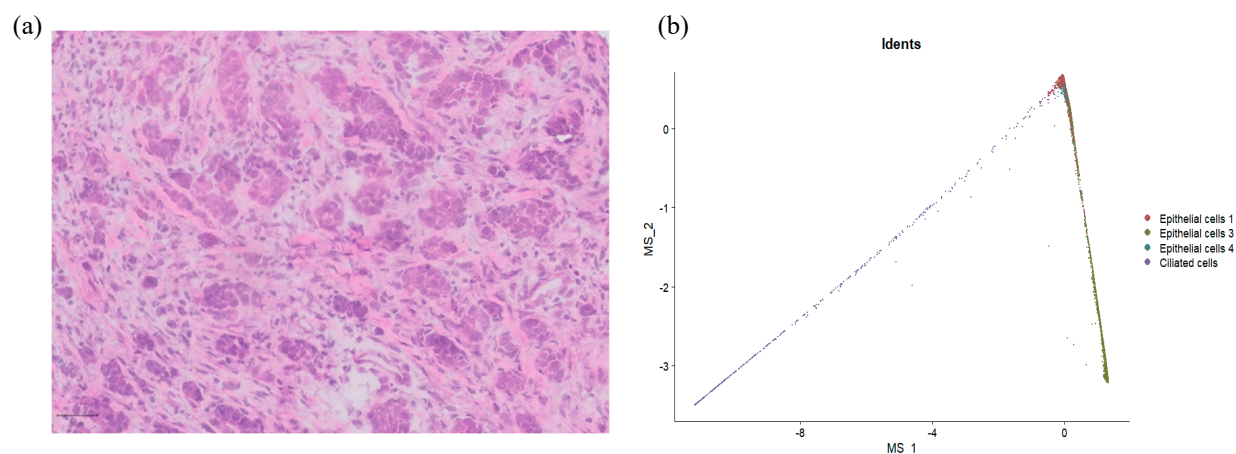
## Supplementary Figures



**Figure S1.** Quality control parameters. (a) Gene expression data, numbers of UMIs and fractions of mitochondrial reads per cell merged before filtering and colored by sample origin. (b) Gene expression data, numbers of UMIs and fractions of mitochondrial reads per cell merged after filtering for the quality parameters: >200 and <10,000 genes per cell, >250 and <5,000 UMIs per cell, fraction of mitochondrial reads lower than 20%. (c) Barcode Rank Plots showing the count of filtered UMIs mapped to each barcode. The color of the graph represents the local density of barcodes that are cell-associated. The plots demonstrated a high quality based on their profiles, all showing a distinctive "cliff and knee" shape. (d) Bar chart showing the number of cells per case after filtering. (e) UMAP plot of 43,599 individual cells from 4 samples generated from the top 15 principal components of all single-cell transcriptomes post-filtering, doublets removing and data integration, colored by singlets and doublets. (f) Bar plot showing singlets and doublets proportions in FFPE and fresh samples. (g) UMAP plot of 43,599 individual cells after doublet removal, colored by tissue origin. (h) Number of genes detected per cell in each cellular population in FFPE and fresh samples.



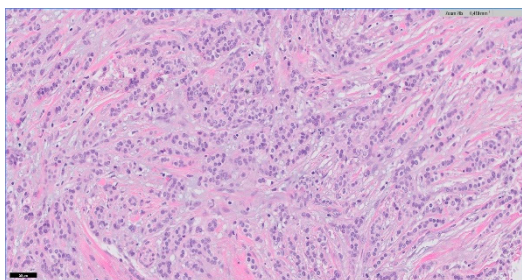
**Figure S2.** scRNAseq annotation. (a) Clustered UMAP plot generated from the top 15 principal components of all single-cell transcriptomes post-filtering and data integration. (b) Markers for cell type annotation. (c) UMAP plot annotated according to the cell markers identified in Figure c. (d) Heatmap representing the top 10 most overexpressed genes ( $\text{avg\_log2FC} > 1$ ) in each cell population. (e) Dot plots showing the percentage of cells and the average gene expression levels of canonical markers for each cluster, analyzed separately in FF and FFPE samples for each histological type.



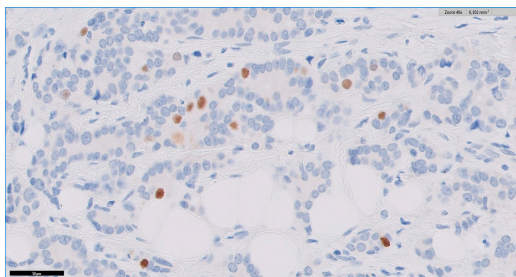
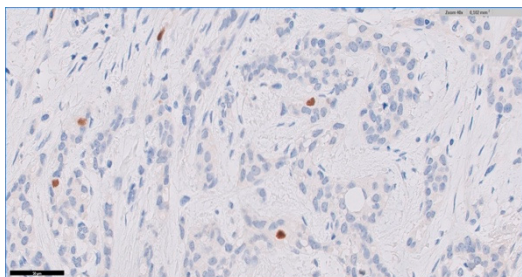
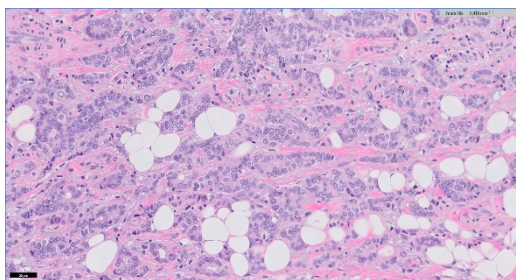
**Figure S3.** IDC cells. (a) IDC H&E staining (scale bar 50  $\mu\text{m}$ ). (b) Cell trajectory analysis of epithelial cells from IDC case.



ILC luminal series



IDC luminal series



**Figure S5.** H&E staining, and FOXJ1 expression evaluation in one ILC and one IDC of the luminal breast carcinomas series (scale bar 50  $\mu$ m).