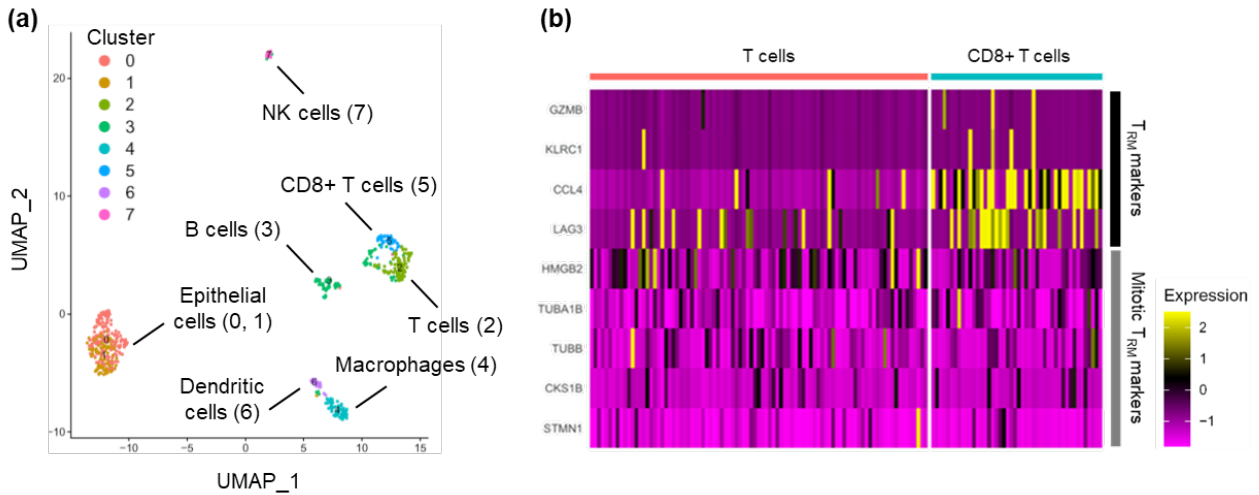


SUPPLEMENTARY FIGURES

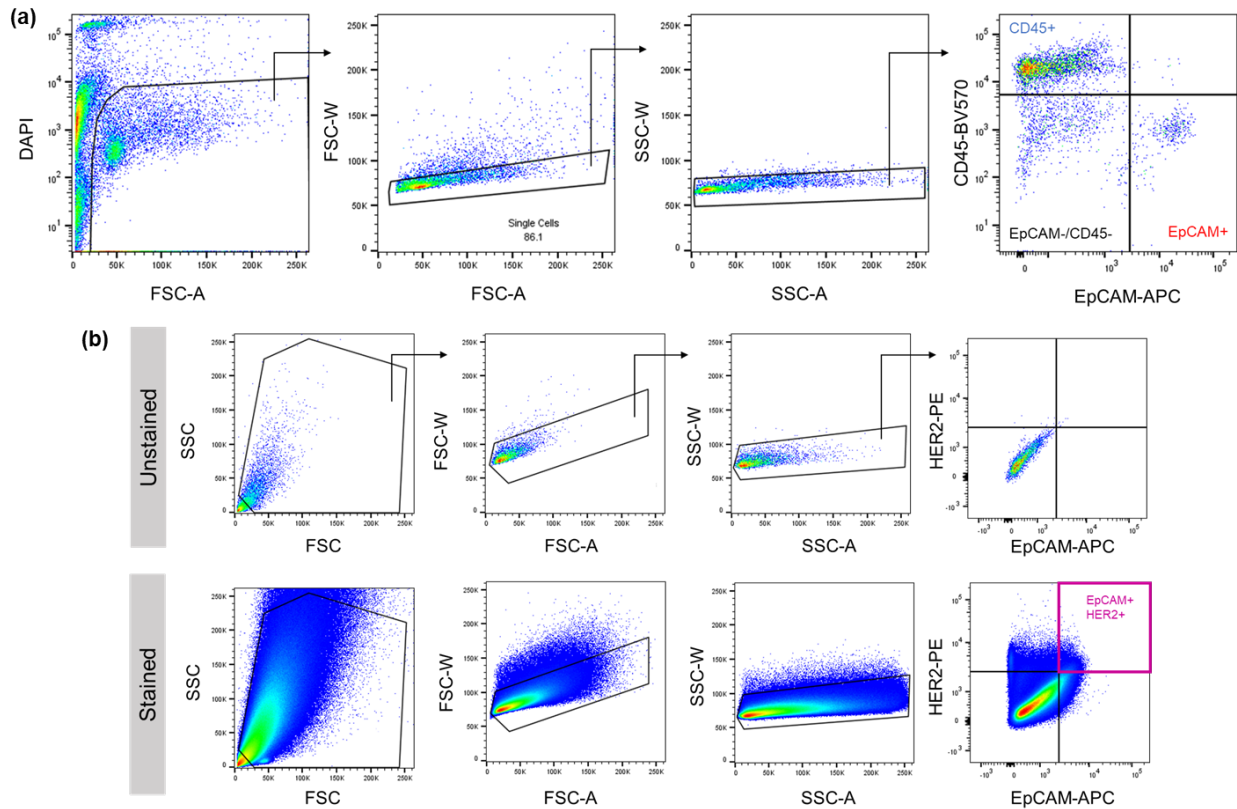


Supplementary Figure 1. Single-cell transcriptomic analysis shows cellular diversity in a research core biopsy specimen.

(a) High-dimensional uniform manifold approximation and projection (UMAP) clustering of single-cell transcriptomic data from a triple-negative breast core biopsy specimen shows a diverse composition of epithelial, lymphoid and myeloid cells.

(b) Heatmap of single-cell transcriptome of all T cells identified in the triple-negative breast core biopsy specimen. T cells positive for non-mitotic T_{RM} markers (top) were enriched in the CD8+ T cell cluster, while few or none of them were positive for mitotic T_{RM} markers (bottom). T_{RM} markers were derived from a previous publication (Savas P et al., 2018).

See also Figure 3C.



Supplementary Figure 2. Gating strategies were used to define specific cell populations in research core biopsy specimens.

(a) Gating strategy used to identify viable (DAPI-negative) EpCAM-positive, CD45-positive or double-negative cells. See also Figure 2c.

(b) Gating strategy used to identify formalin-fixed EpCAM/HER2-positive cells. See also Figure 3b.

SUPPLEMENTARY TABLE

Specimen -Clinical specimen -Research specimen	Primary pathologic diagnosis	Grade	Cellularity
1	IDC IDC	1 1	< 5% < 5%
2	IDC IDC	1 1	10% < 1%
3	Fibroadenoma Fibroadenoma	N/A N/A	N/A N/A
4	IDC IDC	2-3 2	20% 20%
5	ILC ILC	2-3 2	30% 30%
6	IDC IDC	3 3	20% 30%
7	IDC IDC	3 3	60% 10%
8	ILC ILC	2 2	30% 30%
9	IDC Non-diagnostic, debris	2 N/A	50% N/A
10	IDC IDC	2 2	40% 40%

Legend: IDC, invasive ductal carcinoma; ILC, invasive lobular carcinoma.

Supplementary Table 1. Concordance between clinical and research biopsy specimens.