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Fig. S9

Fig. S9. Mapping the breast cancer TME

a t-SNE showing marker gene expressions in breast cancer. **b** Heatmaps comparing marker gene expression of unaligned (left, only BC) and CCA-aligned (right, BC aligned to LC, CRC and OvC) subclusters. **c** t-SNE showing subclusters of ECs, fibroblasts, myeloid cells and B-cells by alignment of 3' and 5'scRNAseq datasets with CCA. **d-h** Heatmaps of conserved marker gene expressions for subclusters of ECs (**d**), fibroblasts (**e**), myeloid cells (**f**), B-cells (**g**), T-/NK-cells (**h**) across different cancer types. **i** Fraction of cells in each cancer type per subcluster. **j** Per cell type, the fraction of cells (grey bars) and cell subclusters (coloured bars) within the tumour is given for each cancer type. BC was enriched for C4_LILRA4_ (FDR = 9.6×10^{-8}), but had few C5_PROX1 (FDR = 3.4×10^{-5}).