Beyond the Cell
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Supplementary information

Democratizing the spatial view: STAMP technology from an analytical perspective

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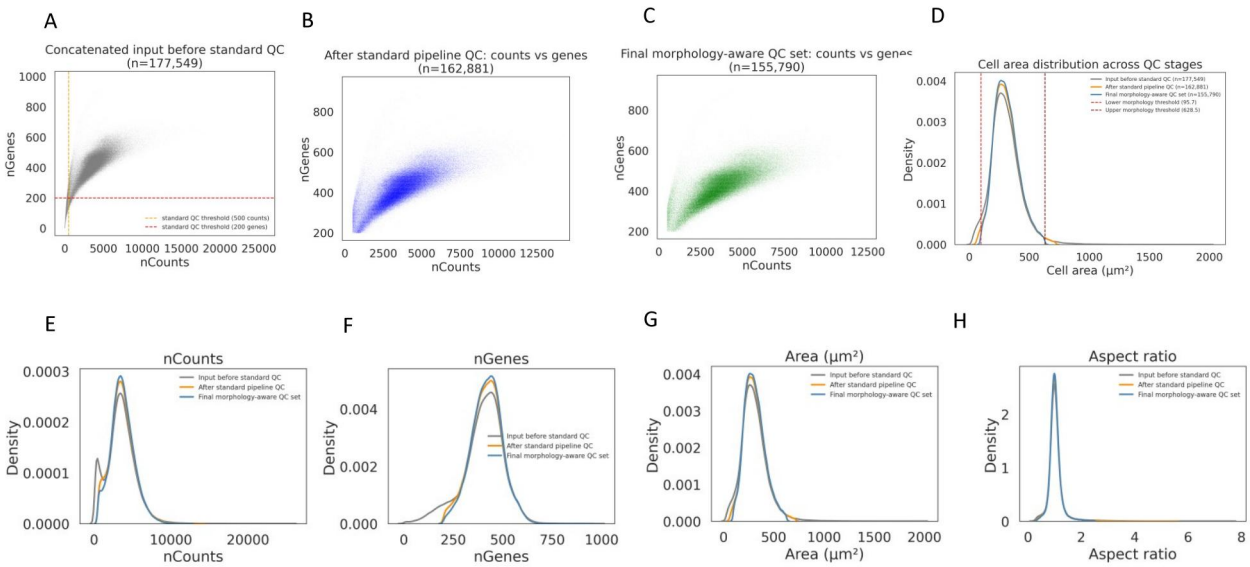

Figure S1. Standard and morphology-aware QC for STAMP data. (A) Counts-versus-genes distribution for the concatenated input before standard QC; dashed lines denote the standard pipeline thresholds (500 counts and 200 genes); (B) Counts-versus-genes distribution after standard pipeline QC; (C) Final morphology-aware QC set used for downstream morpho-transcriptomic analysis; (D) Cell-area distributions across QC stages, with dashed lines indicating the morphology-based area thresholds (95.7 and 628.5 µm²); (E–H) Density plots of total counts, detected genes, cell area, and aspect ratio across QC stages, showing the effect of sequential filtering on molecular and morphometric features.

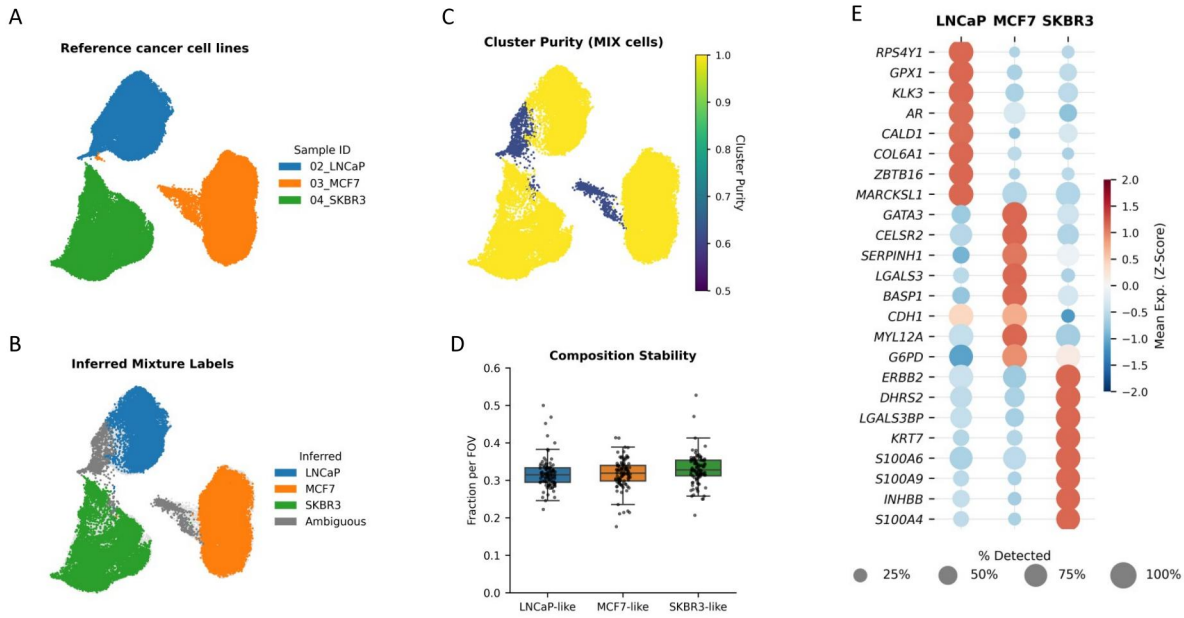

Figure S2. Unsupervised Leiden analysis of the pooled STAMP dataset. (A) UMAP of the pure reference STAMP samples colored by sample identity; (B) MIX cells projected on the same embedding and colored by identities inferred from pure-reference cluster enrichment; ambiguous cells are shown in gray; (C) MIX cells colored by cluster purity, defined as the fraction of pure-reference cells within each Leiden cluster belonging to the dominant reference lineage; (D) Per-field-of-view distribution of inferred LNCaP-like, MCF7-like, and SKBR3-like fractions in the MIX sample; (E) Compact dotplot of top differentially expressed genes across Leiden-inferred MIX identities, with dot size indicating the fraction of cells expressing each gene and color indicating gene-wise z-scored mean expression.