

Human Breast Invasive Ductal Carcinoma

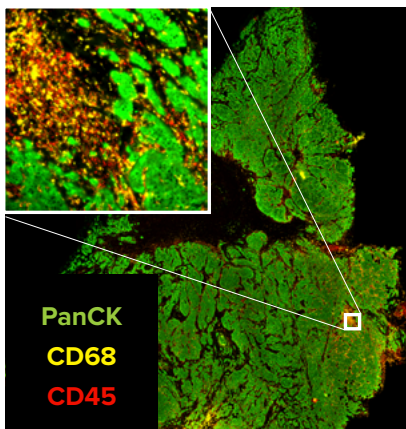
Study Purpose

In this breast cancer study, the whole tissue area of a 5 µm section from an archived FFPE human breast invasive ductal carcinoma was profiled with CosMx Human Universal Cell Characterization RNA panel. 3 protein markers (PanCK, CD68 and CD45) along with nuclei DAPI were co-detected on the same section. RNA profile from CosMx SMI was compared to the publicly available bulk RNAseq profile of breast cancer from TCGA, indicating a high correlation between the two platforms. Outliers in the correlation plots are likely due to differences in sample sources. Cell types were identified with the spatial location of every single cell, showing heavy immune infiltration in some specific areas of the tissue. The CosMx RNA profile indicates that this is a triple-positive (HER2+, ER+, PR+) breast cancer, which agrees with patient's metadata. CosMx cell typing algorithm was able to identify two populations of ERBB2+ cells (high vs. low TOP2A, NUSAP1, MIK167, CENPF, and BIRC5 expression) close to each other, demonstrating the power of this high-plex RNA panel in granular cell typing with spatial information at a single-cell resolution.

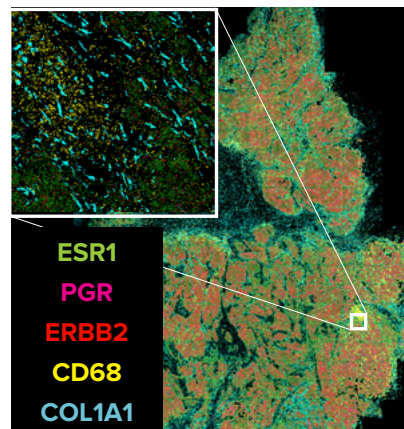
Study Summary

Tissue Type	FFPE Breast Cancer
Panel	1000-plex Human RNA Universal Cell Characterization
Segmentation Markers	PanCK, CD68, CD45, DAPI
Total tissue area analyzed	~91 mm ²
Cells analyzed	542,874
% Cells passed QC	96 %
Number of Genes detected above background	785
% of transcripts assigned a cell	90 %
Mean total transcripts/cell	389
Maximum transcripts/ cell	4,900

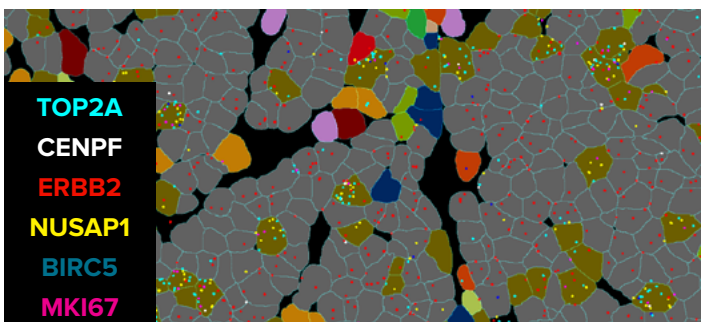
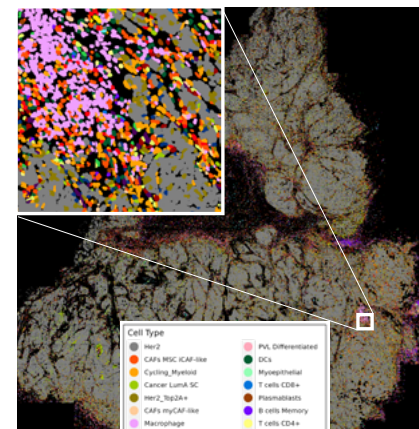
Upfront segmentation marker staining



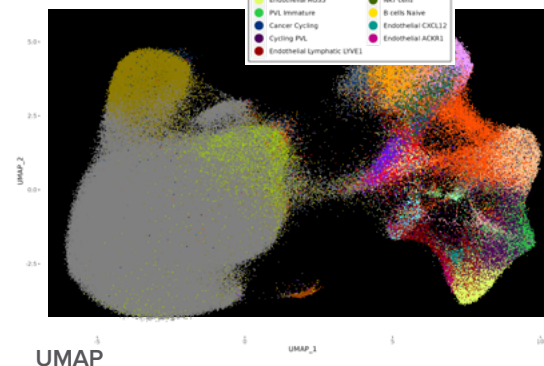
CosMx detection of genes of interest in breast cancer



Cell typing correlates with PanCK, CD45, CD68 staining



Differential gene expression observed between ERBB2+ cell types



For more information, please visit nanosttring.com/CosMx

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