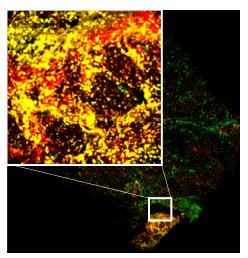


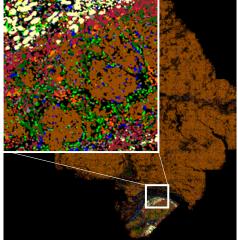
Human Hepatocellular Carcinoma

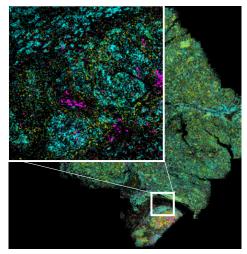
Study Purpose

This study was done on a 5 μ m FFPE liver tissue section from a 65-year-old female who was diagnosed with stage II hepatocellular carcinoma without metastasis. The whole primary tumor region bearing 99% tumor content was profiled with CosMx Human Universal Cell Characterization RNA panel. The sample contained a sub-population of large, abnormally-shaped cancer cells. High-quality staining of cell segmentation markers combined with machine learning-powered cell segmentation ensured that transcripts were properly assigned, leading to highly accurate cell typing. There are 16 cell types identified using SMI RNA profile on this tissue section. Some regions of the tissue have remarkable immune infiltration as evidenced by protein co-detection on the same slides using CD68 and CD45 antibodies. High expression of IGHM gene identified in some macrophage cells (CD68+ cells) indicates an immune response in the tumor microenvironment. High expression of MT2A gene in tumor cells might have contributed to metastasis prevention.

Study Summary	
Tissue Type	FFPE Liver cancer
Panel	1000-plex Human RNA Universal Cell Characterization
Segmentation Markers	PanCK, CD68, CD45, DAPI
Total tissue area analyzed	100 mm ²
Cells analyzed	464,126
% Cells passed QC	99 %
Number of Genes detected above background	622
% of transcripts assigned a cell	89 %
Mean total transcripts/cell	1,150
Maximum transcripts/ cell	27,491



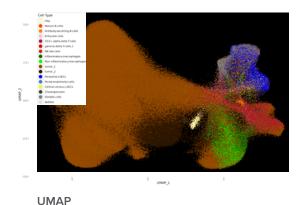


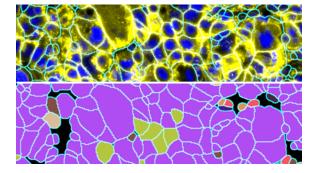


Upfront segmentation marker staining

Cell typing correlates with immunostaining

CosMx detection of genes of interest in liver cancer





Segmentation markers aid in accurate cell segmentation and cell typing

For more information, please visit nanostring.com/CosMx

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