

NSCLC Cancer research

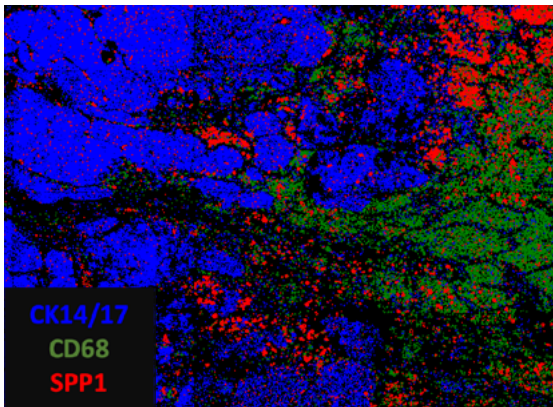
Study Purpose

This study was performed in a cohort of 8 NSCLC samples. Segmentation markers CD298 and B2M, along with PanCK, CD68 and CD45 were co-detected with the CosMx Human Universal Cell Characterization RNA panel on a ~150 mm² of tissue area. Semi-supervised clustering was used to identify and map immune cell types in the tumors. Marker expression, UMAP, and physical representation of a sample is shown below. Tumor cell nests were classified based on cell proportions within a given radius. By classifying both the tumor and stromal neighborhoods, differential gene expression near or far from the tumor was analyzed in unique immune subsets. SPP1 was found to be significantly (FDR < 0.01) enriched near the tumor while SPP1-macrophages were farther from the tumor itself.

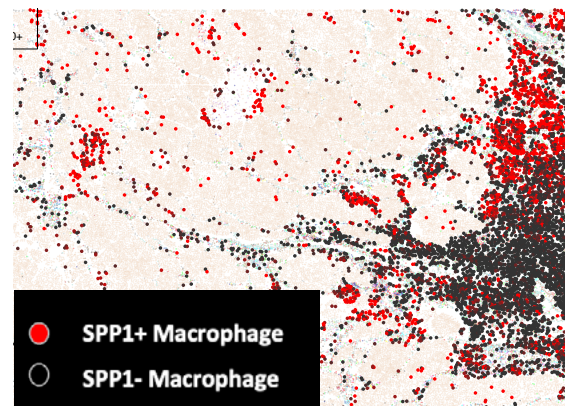
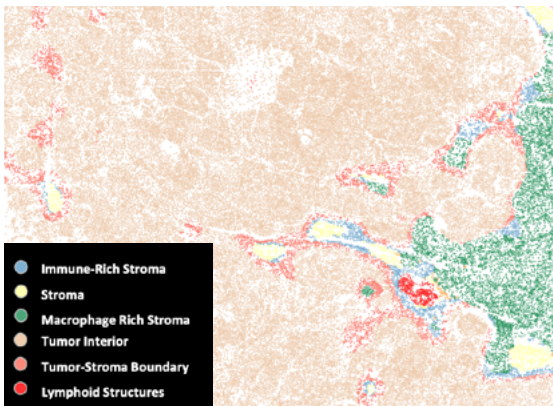
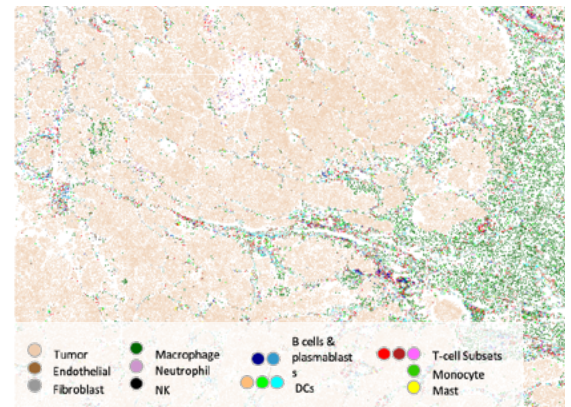
Study Summary

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|---|--|
| Tissue Type | FFPE Lung Cancer |
| Panel | 1000-plex Human RNA Universal Cell Characterization |
| Segmentation Markers | CD68, CD45, DAPI |
| Total tissue area analyzed | ~150 mm ² |
| Cells analyzed | 766,313 |
| % Cells passed QC | 96 % |
| Number of Genes detected above background | 79% |
| % of transcripts assigned a cell | 265 |

RNA marker expression



UMAP



Tumor microenvironment niche classification

SPP1 +/- Macrophage distribution

For more information, please visit nanosttring.com/CosMx

NanoString Technologies, Inc.

530 Fairview Avenue North
Seattle, Washington 98109

T (888) 358-6266
F (206) 378-6288

nanosttring.com
info@nanosttring.com

Sales Contacts

United States us.sales@nanosttring.com
EMEA: europe.sales@nanosttring.com

Asia Pacific & Japan apac.sales@nanosttring.com
Other Regions info@nanosttring.com