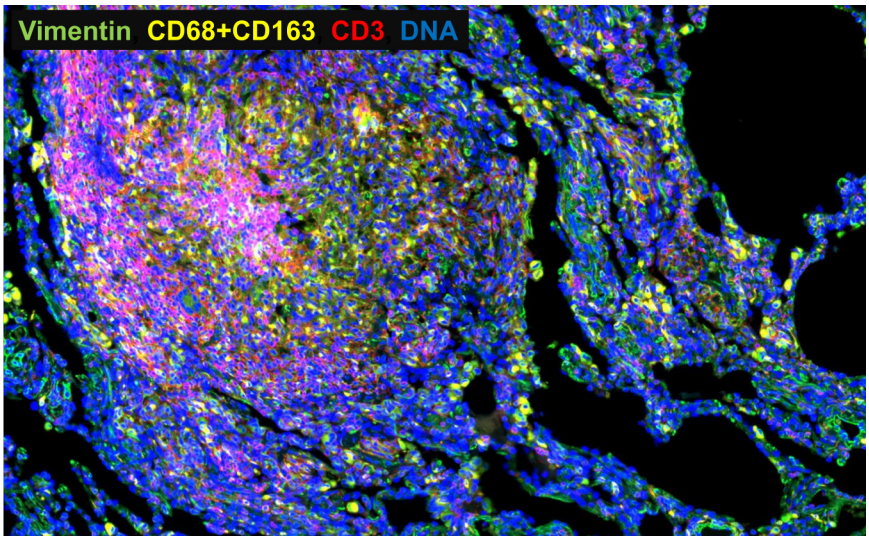
Lung
Tuberculosis

Study Purpose

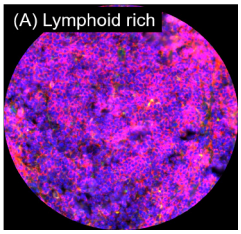
Myeloid-derived suppressor cells (MDSC) have been shown to increase in the peripheral blood of active tuberculosis (TB) patients. To explore the role of MDSC in cell-cell associations, localization, and phenotype of tuberculosis lesions, the transcriptional spatial landscape of macrophage populations in uninvolved lung or granulomatous lesions were profiled using the GeoMx Human Whole Transcriptome Atlas. Spatial heterogeneity of gene expression was also studied across multiple lymphoid-rich regions.

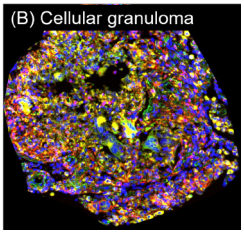
Study Summary

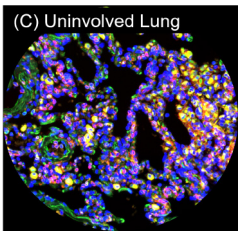
Sample Type	FFPE
Species	Human
AOI* Strategy	Geometric
Assay	Human Whole Transcriptome Atlas
Morphology Markers	Vimentin, CD68+CD163, CD3, DNA
Targets Detected	12,236 targets
Application	Pathway analysis



Segmentation Strategy

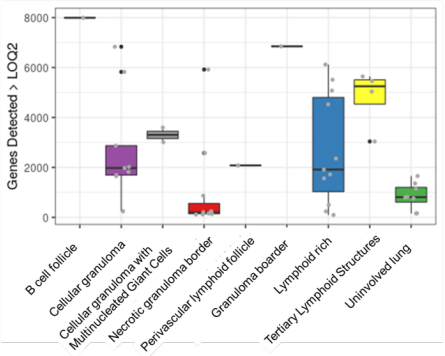






Legend

Regions of interest were placed on lymphoid-rich areas (A), granulomatous lesions (B) and uninvolved lung (C) based on fluorescent staining.



Legend

The number of targets detected above the background (LOQ2*) by AOI groups.

*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Amanda Martinot from Tufts University for sharing these images.

For more information, please visit https://nanostring.com/geomx-morphology-markers/

NanoString Technologies, Inc.
530 Fairview Avenue North
Seattle, Washington 98109
T (888) 358-6266
F (206) 378-6288
nanostring.com
info@nanostring.com

Sales Contacts
United States us.sales@nanostring.com
EMEA: europe.sales@nanostring.com
Asia Pacific & Japan apac.sales@nanostring.com
Other Regions info@nanostring.com