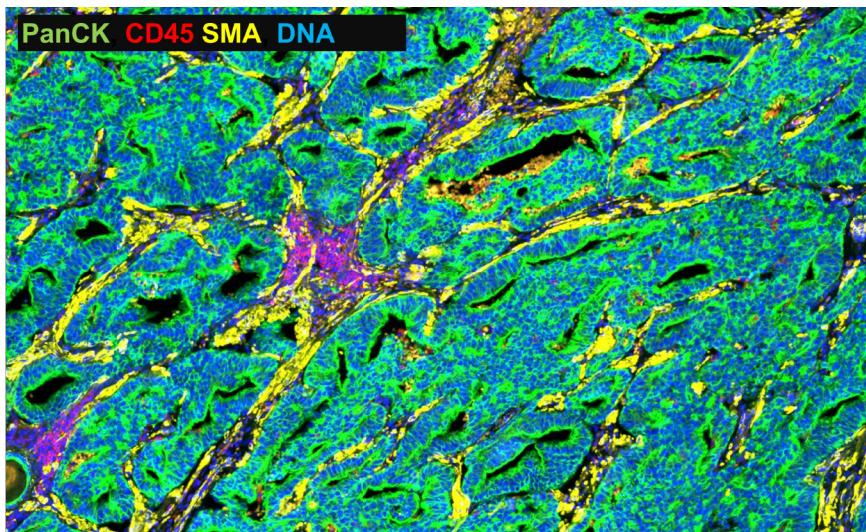nanoString®

Prostate
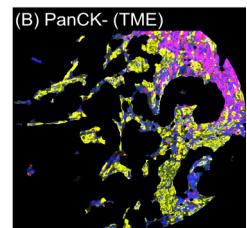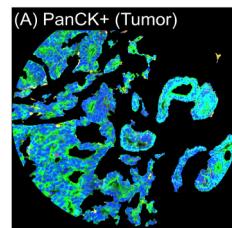## Prostate Cancer

Study Purpose

Prostate cancer samples with peripheral zone and transitional zone tumors were profiled using the GeoMx Human Whole Transcriptome Atlas. Pan-Cytokeratin (PanCK) was used to segment the tissue into the tumor and tumor microenvironment (TME) areas. Differential gene expression analysis and pathway analysis were conducted to understand transcriptomic changes that occur in the tumor compared to the transitional and peripheral tumor zones in the surrounding microenvironment.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Segmentation
Assay	Human Whole Transcriptome Atlas
Morphology Markers	Pan-Cytokeratin (PanCK), CD45, SMA, DNA
Targets Detected	17,117 targets
Application	Biomarker discovery

PanCK CD45 SMA DNA

Segmentation Strategy

(A) PanCK+ (Tumor)   (B) PanCK- (TME)
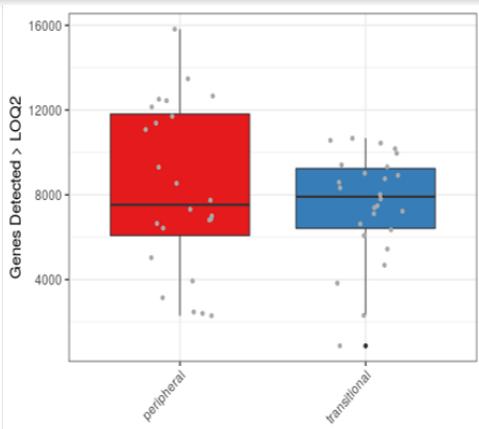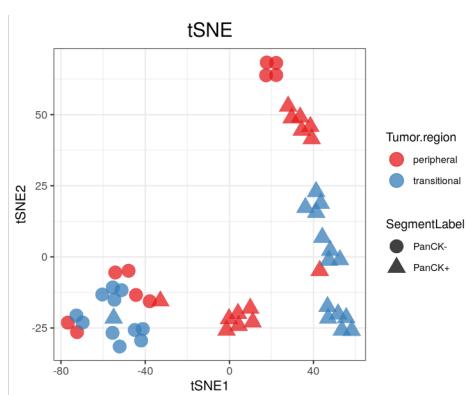
Legend

Tumor (A) and the tumor environment (TME) (B) were segmented based on PanCK staining.

Legend

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

Right:
T-distributed stochastic neighbor embedding (tSNE) plot.

*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Simpa Salami from the University of Michigan for sharing these images.

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