

Kidney

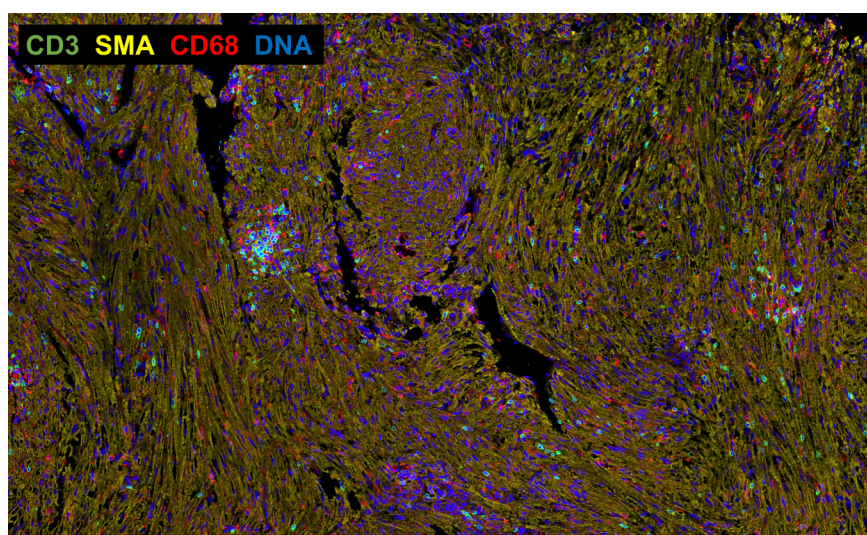
Kidney Cancer

Study Purpose

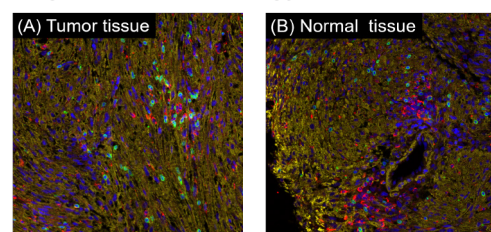
To investigate transcriptomic changes that occur in kidney carcinogenesis, tumor tissue taken from the kidney and normal control tissues were profiled using the GeoMx Human Whole Transcriptome Atlas. Geometric regions of interest (ROIs) were selected in different places on the tumor tissue sample and on the normal control tissue sample and differentially expressed genes were assessed as potential biomarkers.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Geometric
Assay	Human Whole Transcriptome Atlas
Morphology Markers	CD3, SMA, CD68, DNA
Targets Detected	12,099 targets
Application	Biomarker discovery

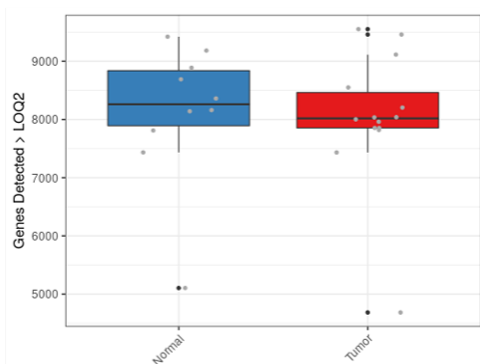


Segmentation Strategy



Legend

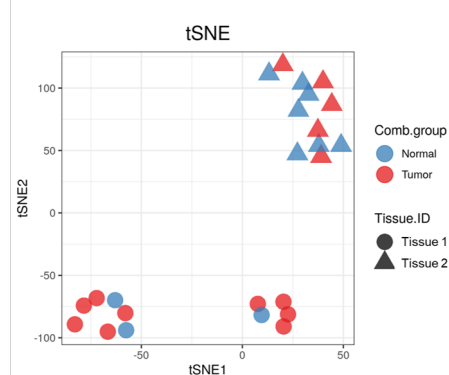
ROIs were placed on the tumor (A) and normal areas (B) associated with different levels of macrophages (CD68+ cells) or T cells (CD3+ cells).



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 Drs. Elizabeth Henske and Yan Tang from Physician at Brigham and Women's Hospital for sharing these images.

For more information, please visit

<https://nanosttring.com/geomx-morphology-markers/>

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