

Lung

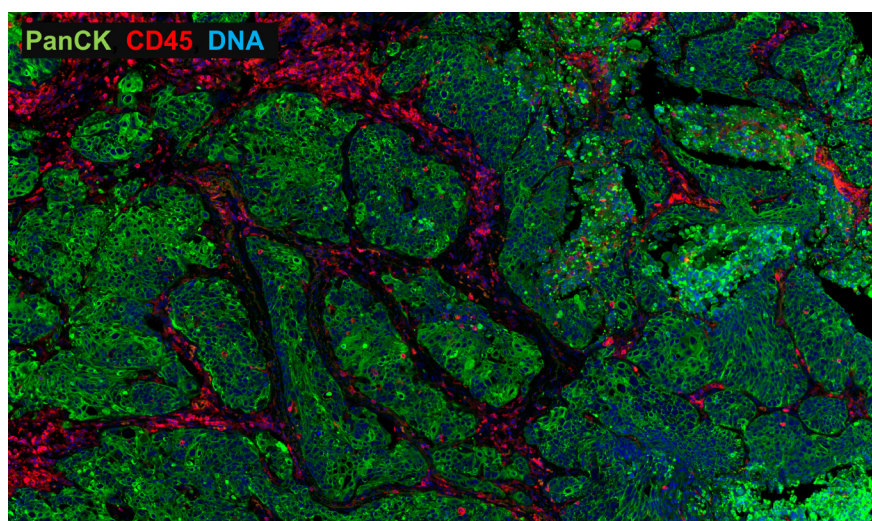
Non-Small Cell Lung Cancer

Study Purpose

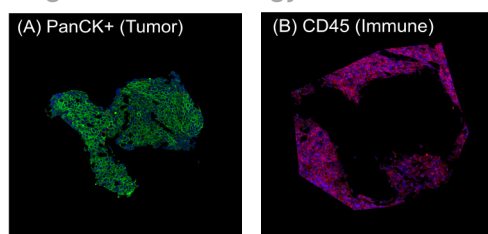
The GeoMx Human Whole Transcriptome Atlas was used to discover potential biomarkers for immuno-oncology therapy responders and non-responders in Non-Small Cell Lung Cancer (NSCLC) formalin-fixed, paraffin-embedded (FFPE) tissues. Tumor and immune cells were segmented based on morphology marker staining. Differentially expressed genes between responders and non-responders were used to conduct pathway analysis.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Segmentation, Cell-type specific
Assay	Human Whole Transcriptome Atlas
Morphology Markers	Pan-Cytokeratin (PanCK), CD45, DNA
Targets Detected	17,010 targets
Application	Biomarker discovery

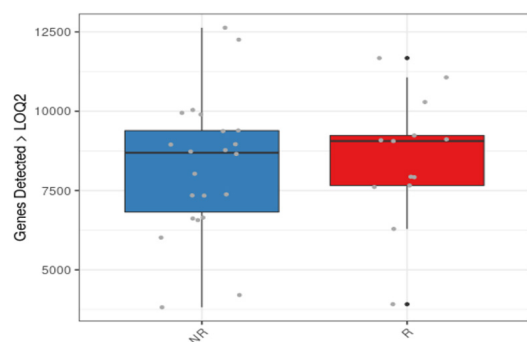


Segmentation Strategy



Legend

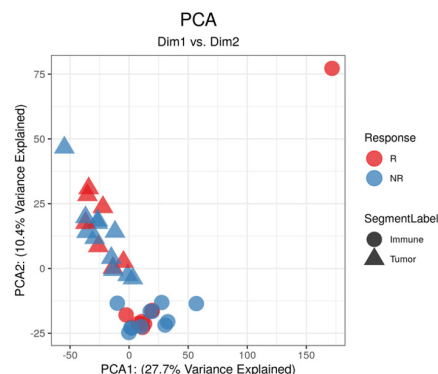
Tumor (A) and immune (B) cells were segmented and enriched using PanCK and CD45 staining, respectively.



Legend

Left:
The number of targets detected above the background (LOG2*) by AOI groups.

Right:
Principal component analysis (PCA) plot.



*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Sehui Kim from Severance Hospital for sharing these images.

For more information, please visit

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

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