



Ovary

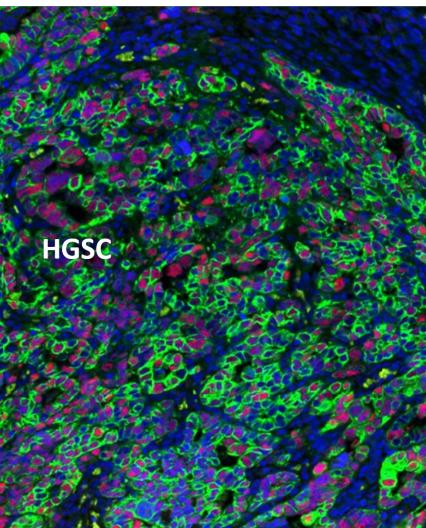
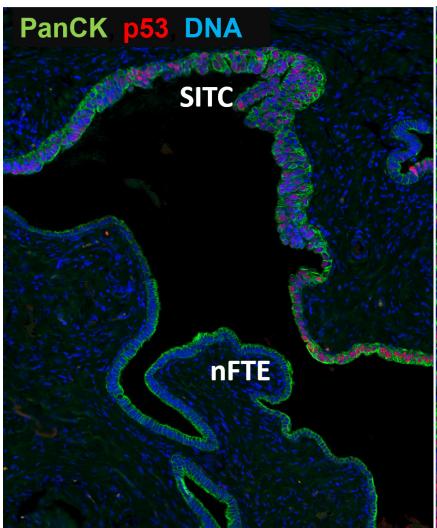
Ovarian Cancer

Study Purpose

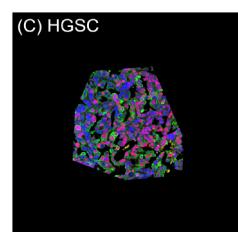
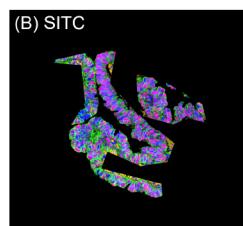
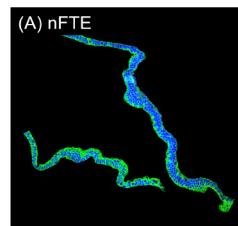
Human ovarian tissue with different malignant stages were profiled using the GeoMx Human Whole Transcriptome Atlas. Regions of interest (ROIs) were placed on normal fallopian tube epithelium (nFTE), and p53 positive lesion areas associated with serous tubal intraepithelial carcinoma (STIC) and high-grade serous carcinoma (HGSC). The epithelial and stromal compartments were segmented and profiled respectively. Differential gene expression analysis and pathway analysis were conducted to understand transcriptomic changes among these regions.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Geometric
Assay	Human Whole Transcriptome Atlas
Morphology Markers	PanCK, p53, DNA
Targets Detected	17,648 targets
Application	Biomarker discovery

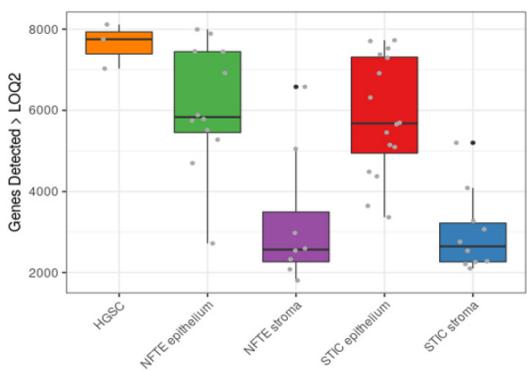


Segmentation Strategy



Legend

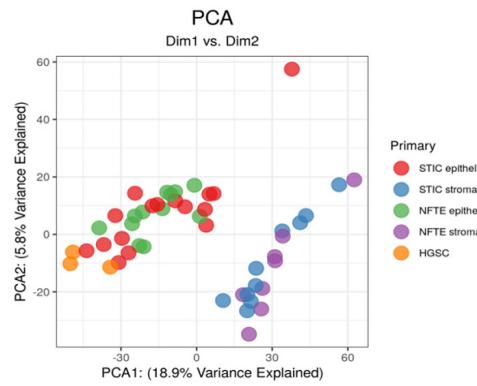
Pan-cytokeratin (PanCK) staining was used to separate the epithelial (A-C) and stromal (not shown) compartments in normal fallopian tube epithelium (nFTE, A), serous tubal intraepithelial carcinoma with p53 (STIC, B), and high-grade serous carcinoma (HGSC, C).



Legend

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

Right:
Principal component analysis (PCA) plot.



*AOI = Area of Illumination; LOQ=Limit of Quantitation

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Reference: Y Wang, P Huang, BG Wang, et al. Cancer Res. 2022 <https://doi.org/10.1158/0008-5472.CAN-22-1620>

For more information, please visit

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

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