

Esophagus

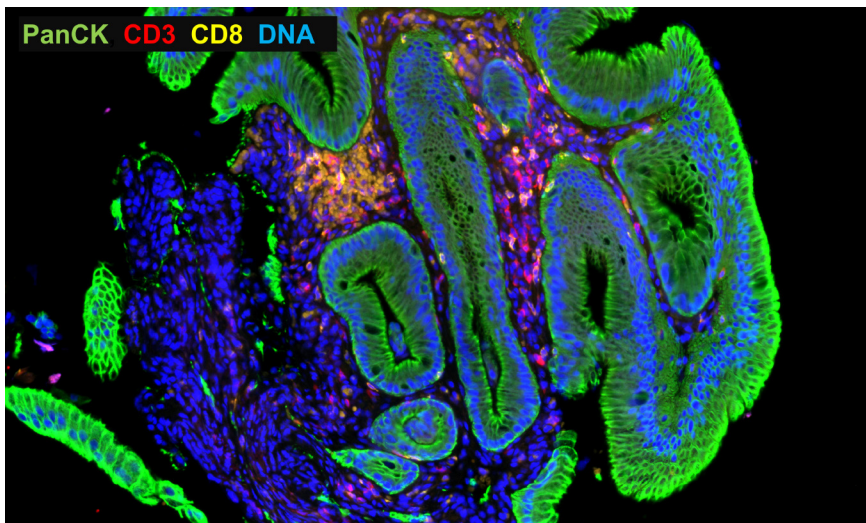
Barrett's Mucosa

Study Purpose

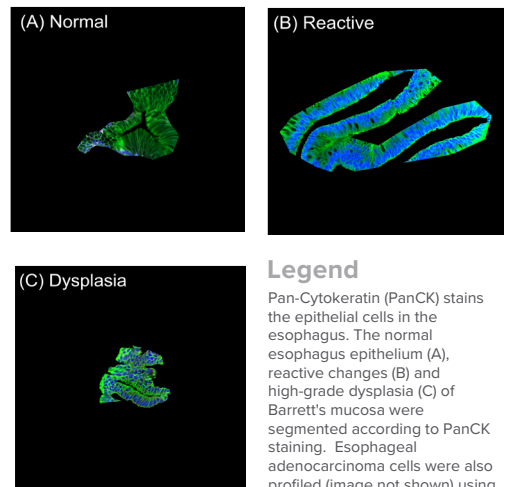
The GeoMx Human Whole Transcriptome Atlas was used to profile transcriptomic changes during the onset and progression of Barrett's Mucosa. Differential expression changes across normal esophageal epithelium, reactive epithelium, and epithelium characterized by high-grade dysplasia were analyzed for potential biomarkers and the data set was used for pathway analysis.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Segmentation
Assay	Human Whole Transcriptome Atlas
Morphology Markers	Pan-Cytokeratin (PanCK), CD3, CD8, DNA
Targets Detected	15,565 targets
Application	Biomarker discovery

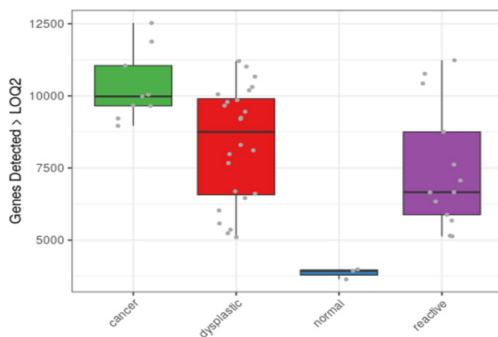


Segmentation Strategy



Legend

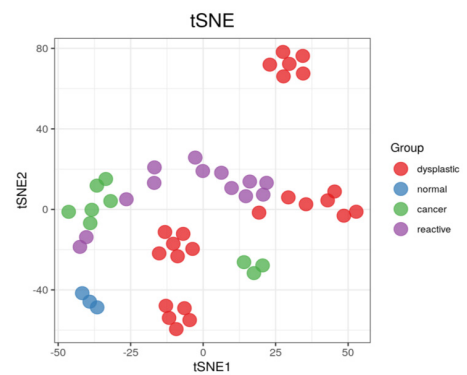
Pan-Cytokeratin (PanCK) stains the epithelial cells in the esophagus. The normal esophagus epithelium (A), reactive changes (B) and high-grade dysplasia (C) of Barrett's mucosa were segmented according to PanCK staining. Esophageal adenocarcinoma cells were also profiled (image not shown) using PanCK staining for segmentation.



Legend

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

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



*AOI = Area of Illumination

Acknowledgement: We sincerely thank Drs. Bruno Maerkl, Bianca Grosser, and Sebastian Dintner from the University Augsburg for sharing these images.

For more information, please visit

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

NanoString Technologies, Inc.
530 Fairview Avenue North
Seattle, Washington 98109

T (888) 358-6266
F (206) 378-6288

nanosttring.com
info@nanosttring.com

Sales Contacts
United States us.sales@nanosttring.com
EMEA: europe.sales@nanosttring.com

Asia Pacific & Japan apac.sales@nanosttring.com
Other Regions info@nanosttring.com