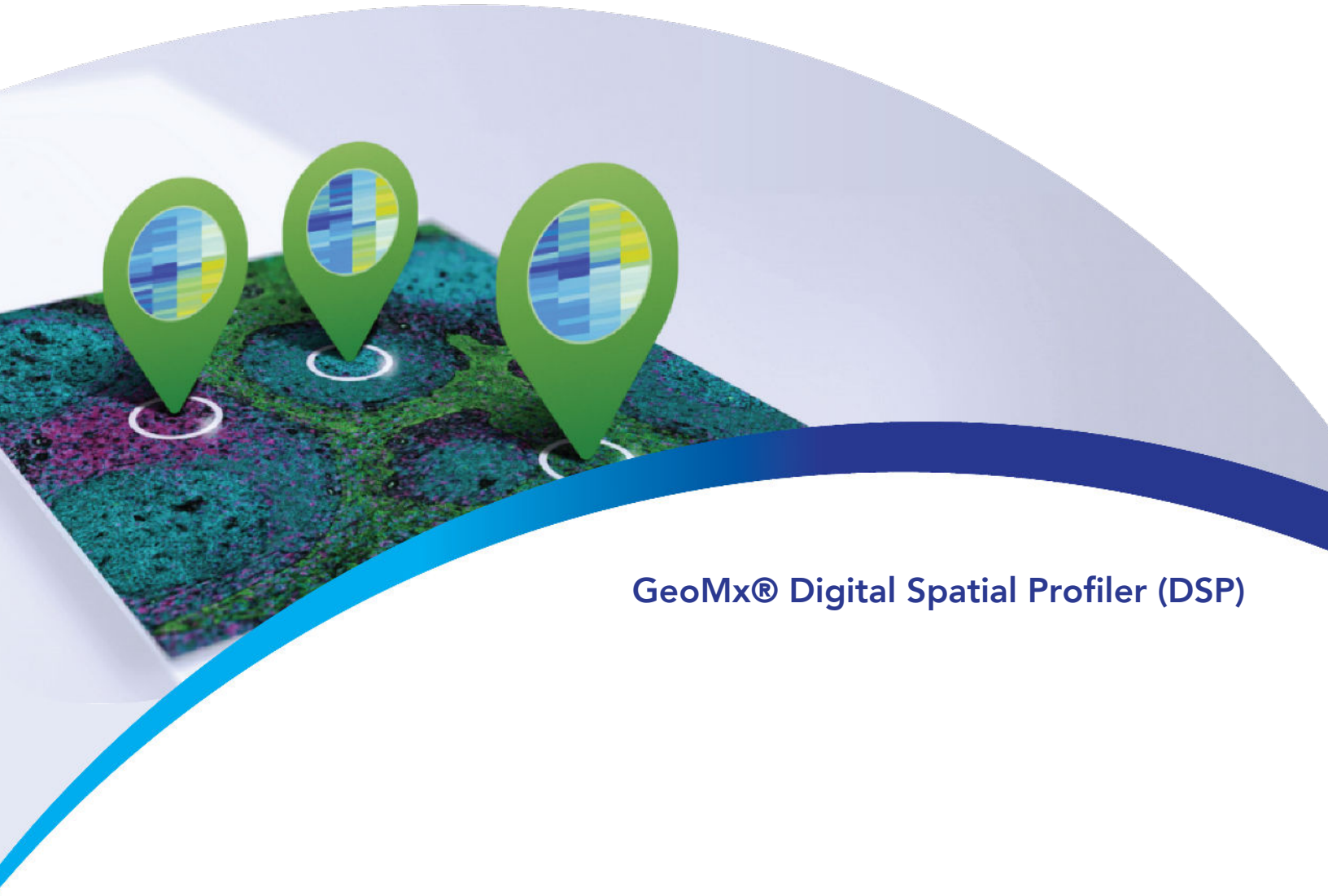
canopy BIOSCIENCES® A BRUKER COMPANY

CRO Services for Spatial Transcriptomics

Pre-Validated RNA Panels



GeoMx® Digital Spatial Profiler (DSP)

Table of Contents

Our Trusted CRO Services

GeoMx® Digital Spatial Profiler RNA Assays from NanoString® are now widely available for critical service projects with Canopy Biosciences® CRO services. Canopy Biosciences® has been named a Center of Excellence and offers:

- Excellent spatial transcriptomics services to profile the tumor microenvironment
- Expertise in histopathology to guide development of custom morphology markers to optimize ROI selection
- Comprehensive data review with our scientists and walk-through of analysis software

GeoMx® RNA Assays		
Product and Description	**Species**	**Number of Targets**
Immune Pathways Panel Designed for comprehensive profiling of tumor biology, the tumor microenvironment, and the immune response	Human	84
Cancer Transcriptome Atlas Designed for comprehensive profiling of tumor biology, the tumor microenvironment, and the immune response	Human	1834
Whole Transcriptome Atlas Designed for comprehensive profiling of spatial biology in human samples	Human	18,000+
Whole Transcriptome Atlas Designed for comprehensive profiling of spatial biology in mouse samples	Mouse	21,000+

1

Send us your samples

Ship us your FFPE slides or tissue blocks and tell us which morphology markers to stain with.

2

Select your ROIs

Work with our scientists to select up to 12 ROIs for each sample based on morphology images.

3

Review your data

Receive your data and participate in a one-on-one session to review the data and the analysis software.

GeoMx® RNA Assays

The GeoMx® Digital Spatial Profiler combines high-plex and high-throughput spatial analysis of RNA and protein expression data. Conduct morphologically-guided gene expression profiling of tissue using predesigned panels. Use our expertise in histopathology to guide development of custom morphology markers.

Product Highlights

- Comprehensive RNA coverage for immunology, cancer biology, and other research applications
- Superior sensitivity to detect 1000s unique genes in <50 µm regions
- Robust performance across sample types including FFPE with high concordance with RNA-Seq and RNAscope®
- Map single cell RNA-Seq populations to their tissue location
- Integrated Illumina® library prep protocols and streamlined NGS analysis pipelines
- Flexibility to customize with up to 60 additional targets to assay non-coding RNA, synthetic DNA or exogenous genes
- Visualization and statistical analysis using GeoMx® Data Suite and bioinformatics toolset

Discover a new way to look at biology

GeoMx® RNA Assays deliver the maximum amount of sensitivity and confidence in each transcript through unique probe architecture. Each assay contains between hundreds and thousands of protein-coding genes. Along with a high specificity for their target molecules, DSP RNA probes are screened for a myriad of factors including melting temperature, GC content, off target hits, and repetitive sequences. Each probe is assigned a unique DSP barcode for downstream molecular counting on an Illumina sequencer. With GeoMx® RNA Assays, researchers can explore pathways across the whole transcriptome or immune pathways or cancer biology in user defined regions of interest.

Key Features of GeoMx® RNA Assays

Explore the biology that matters

Traditional gene expression technologies are unable to capture heterogeneity of the transcriptome with spatial context. Bulk RNA sequencing and single cell RNA-Seq have delivered interesting clinical and cell type signatures but localizing these signatures has proven challenges with protein based IHC. Other, more precise, technologies like fluorescently-labeled in situ hybridization lack the plex to truly make new discoveries. GeoMx® RNA Assays deliver both spatial precision and high plex. Furthermore, assays compare favorable RNA sequencing and RNAscope® and confidently detect transcripts in small regions.

Map the location of your cell populations

Spatial analysis of a non-small cell carcinoma sample using the GeoMx® Spatial Decon algorithm reveals cell type abundance in each region of interest (ROI) (Figure 1). Researchers can use the pre-defined cell definitions or their single cell RNA-Seq data to assess cell type abundance throughout the tissue.

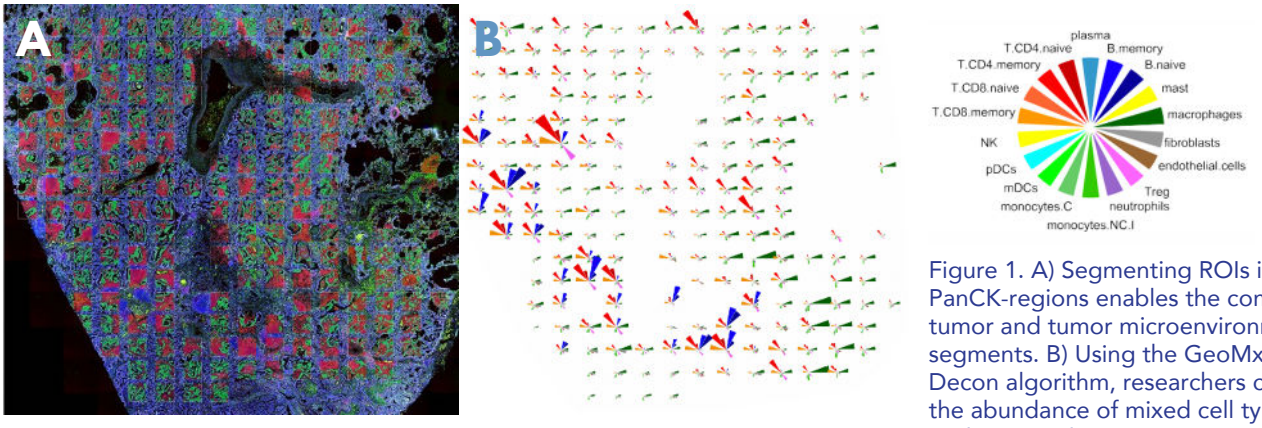


Figure 1. A) Segmenting ROIs in PanCK+ and PanCK-regions enables the comparison of tumor and tumor microenvironment segments. B) Using the GeoMx® Spatial Decon algorithm, researchers can estimate the abundance of mixed cell types within each ROI and segment. Legend to right indicates cell type.

GeoMx® WTA Workflow

GeoMx® RNA Assays contain in situ hybridization (ISH) probes conjugated to unique DNA indexing-oligonucleotides (DSP barcodes) via a UV-photocleavable linker. After selecting regions of interest (ROIs) on the GeoMx® DSP, the DSP barcodes are UV cleaved and collected (Figure 2). During library preparation, the DSP barcodes are tagged with their ROI location then sequenced on an Illumina sequencer. DNA oligonucleotide sequences contain ROI indices mapping them back to their tissue location, an RNA target identification sequence matching them to their ISH probes, and a unique molecular identifier (UMI) to

deduplicate reads. Sequenced oligonucleotides are processed then imported back into the GeoMx® DSP platform for integration with the slide images and ROI selections for spatially-resolved RNA expression.

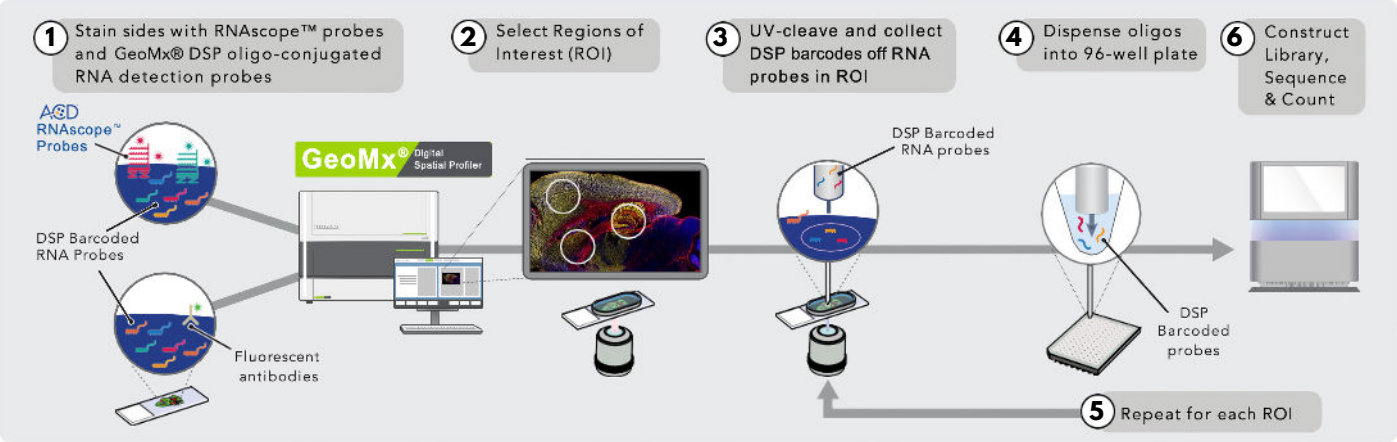


Figure 2. GeoMx® DSP workflow enables the analysis of whole transcriptome data from user-defined regions.

GeoMx® Data Analysis

GeoMx® software uniquely combines whole tissue visualization at single cell resolution with advanced ROI selection to enable comprehensive spatial profiling of tissue sections. The fully integrated workflow tracks image data to corresponding profiling data, allowing users to easily go from data collection to data analysis and to interact with either data type in real time. The data analysis suite provides multiple options to assess the quality of the raw data and various methods to normalize data sets. Moreover, multiple analysis methods are available, including statistical methods, and cluster and pathway analysis. Multiple data visualizations are available to enable data exploration and are then exportable as publication-quality figures. Visualization plots include: heatmap, dendograms, bar graph, box plot, scatter plot, line/trend plot, volcano plot, and PCA.

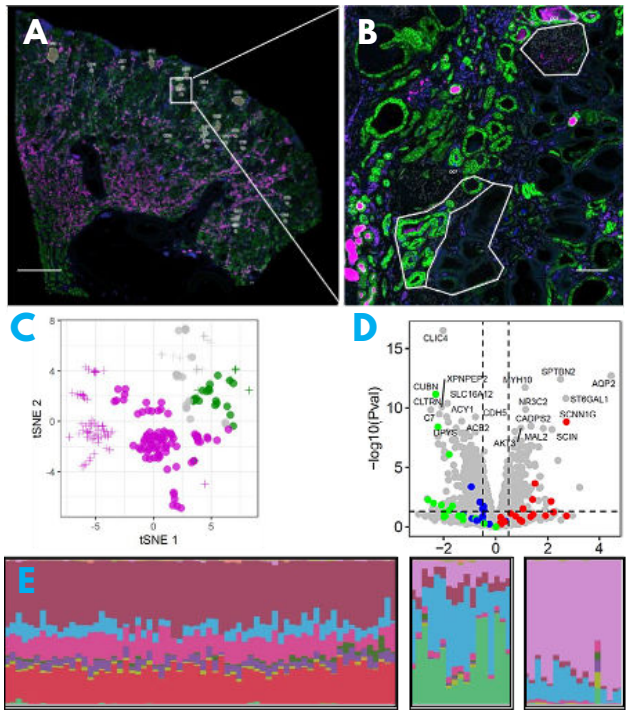


Figure 3. A-B) ROI selection strategy in kidney to study normal and diseased (DKD) kidney C) tSNE representation of glomerulus (magenta), proximal (green) and distal (gray) tubules D) Differential expression showing genes from scRNA-Seq expressed in podocytes (blue), proximal (green) or distal (red) tubules. E) Cell type abundance estimates based on scRNA Seq from kidney samples.

Ordering Information

Canopy Biosciences' Center of Excellence offers CRO services for projects requiring comprehensive RNA coverage for immunology, cancer biology, and other research applications using GeoMx® RNA Assays. Refer to the table below for pricing and project minimums.

GeoMx® RNA Assays			
Product	**Species**	**Sample Price**	**Project Minimum**
Immune Pathways Panel	Human	$2,350	6 samples
Cancer Transcriptome Atlas	Human	$4,675	6 samples
Whole Transcriptome Atlas	Human	$5,693	4 samples
Whole Transcriptome Atlas	Mouse	$5,693	4 samples

Terms & Conditions

Additional fees may be included for project management and additional services, including histopathology services. All assays are validated by NanoString®.

Contact your Canopy Biosciences® Business Development Representative for more information or to receive a quote.

To learn more, visit canopybiosciences.com/geomx
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