



# Spatial Transcriptomics Profiling Service on the GeoMx® Platform

## Profile Patterns of Gene Expression in Selected Regions of Tumor Sections

**Collecta's Digital Spatial Profiling Service** combines genome-wide gene expression profiling with the spatial resolution of immunohistochemistry to identify gene or pathway activation differences.

Spatial gene expression profiling of particular regions and cells in complex tissues provides information about the active genes that produce the unique biology of those selected regions or cells of interest. Characterizing these spatial differences in complex tissues enables investigators to disentangle complex biology and perform studies like the following:

- Investigate heterogeneity and microenvironments of tumors
- Identify genes associated with lymphocyte tumor infiltration
- Characterize markers of immune response
- Profile normal and diseased tissues in the same sample, and much more

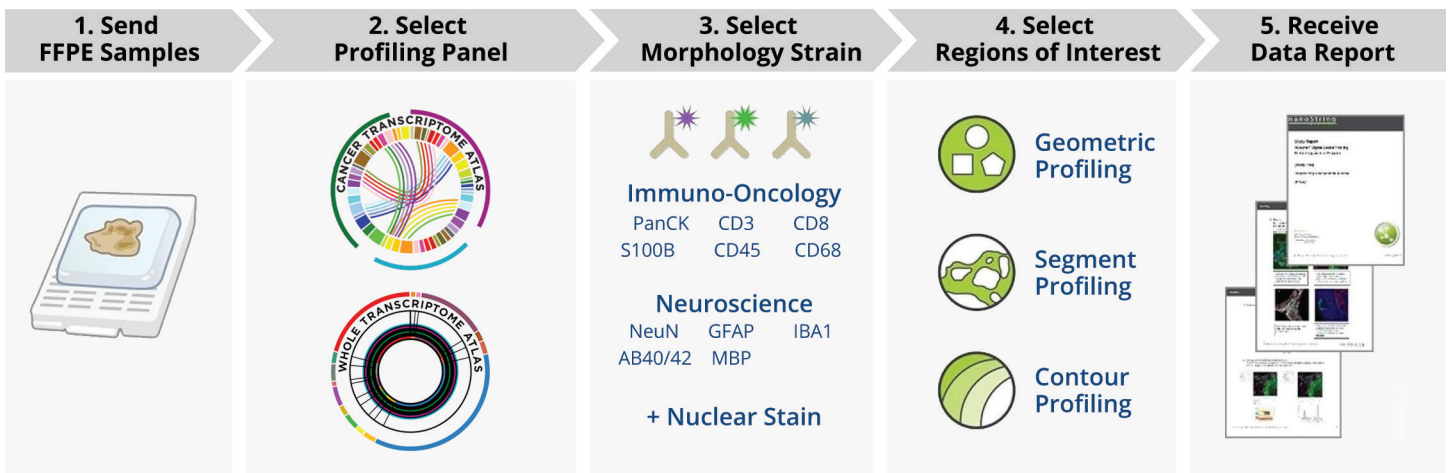
These types of analyses provide insight into disease pathology, a basis to explain therapeutic responses, and markers and targets for diagnostic and treatment purposes.

## Collecta Spatial Transcriptomics Profiling Service

The investigator provides Collecta with FFPE tissue sections that have the morphology to be analyzed. After discussing the details of the project with the investigator, Collecta will label the tissue, select regions of interest that meet the project requirements, and quantify gene expression levels of the selected regions.

Collecta's team works collaboratively with the researcher and has the expertise and in-house technical capabilities to carry out the project to the highest standards, providing:

- Board-certified anatomic pathologist
- Immunohistochemistry staining experience
- Nanostring GeoMx® Digital Spatial Profiler
- Illumina Next-Generation Sequencing (NGS) instrument
- Molecular Biology expertise
- Bioinformatics and data analysis with a summary report



**Figure 1** Spatial Transcriptomics Workflow on the Nanostring GeoMx Platform.

**How Is Spatial Profiling Done?**

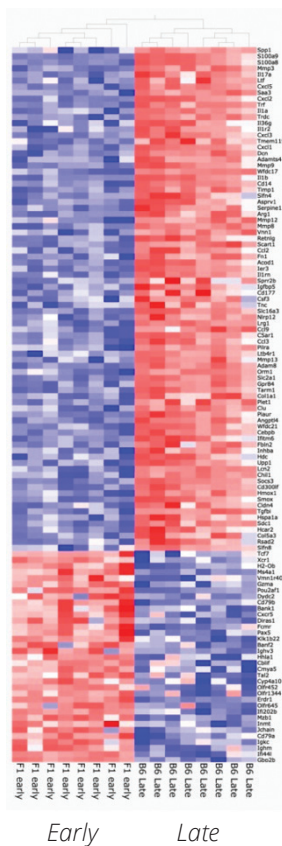
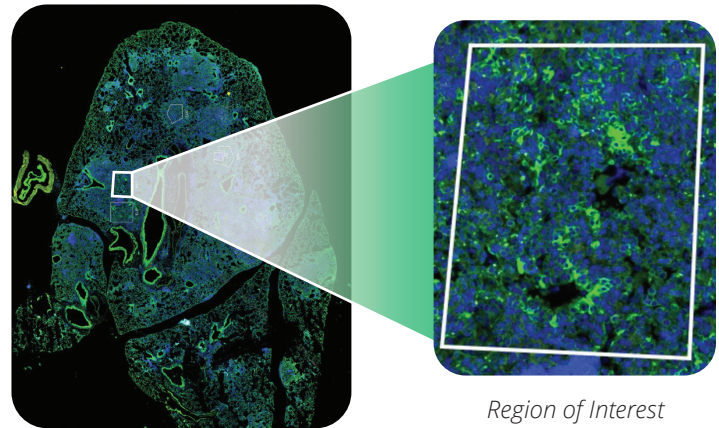
The Nanostring® GeoMx® Digital Spatial Profiling Instrument furnishes the core platform to measure patterns of gene expression in specific targeted areas of interest in tumor or other tissue sections. However, there are preparative steps (Fig. 1) required to set up the analysis and data readout using NGS after collecting probes from the regions of interest, as described below:

- Label tissue sections or fixed cells with fluorescently tagged antibodies to visualize structures and cells of interest
- Select cells or regions of interest
- Hybridize selected regions to RNA transcript probes with UV-cleavable barcodes
- Cleave and collect barcoded labels from hybridized RNA probes in the defined regions
- Use NGS to quantify the number of barcodes collected from each region
- Assess expression of each gene target based on the probe-barcode NGS reads

Researchers can analyze and compare gene activity in selected areas of the section, such as the center of tumor, near tumor/normal tissue interface, areas of immune cell infiltration, structures, cells with receptors/antigens of interest, etc. (Fig. 2) The GeoMx platform provides numerous modes to select almost any cells and areas of the tissue that can be visualized with fluorescently labeled antibodies

**If you are interested in RNA Profiling, please contact us.**

Cellecta is a GeoMx Premier Access site and offers a comprehensive Spatial Transcriptomics Profiling service. This service complements **Cellecta’s DriverMap™ Targeted RNA Sequencing service** which provides comprehensive and quantitative gene expression analysis from as little as 10 pg of total RNA.



**Figure 2**

Heat map corresponding to regions of interest (ROI) analyzed.

For more information visit [cellecta.com/dsp](http://cellecta.com/dsp) or email [info@cellecta.com](mailto:info@cellecta.com)