BRUKER

BRUKER SPATIAL BIOLOGY

Oncology Solutions

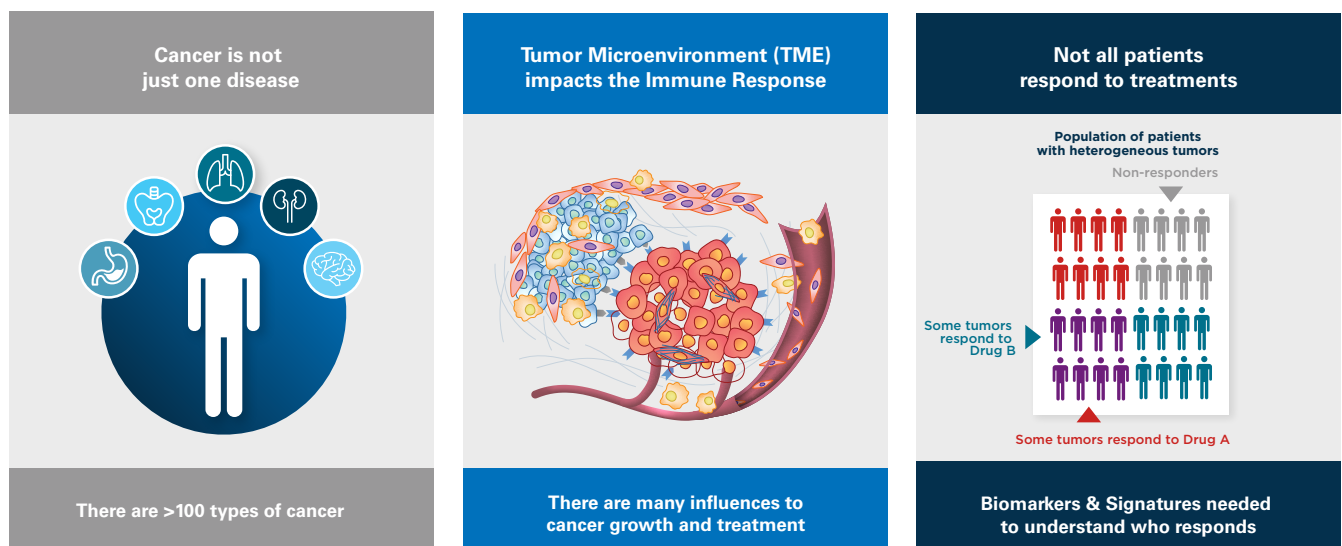Tumor • Microenvironment • Immune Response
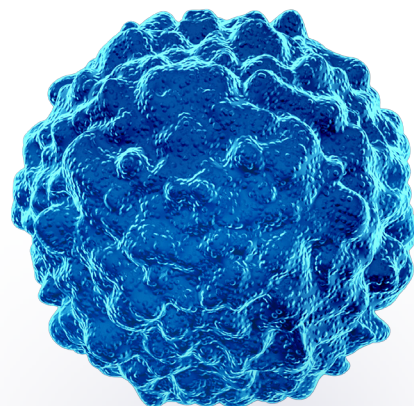
Challenges of Oncology Research
20 years of progress: finding the answers to cancer together

Cancer is a constellation of highly heterogenous diseases that share a common origin in mutations that drive key cellular functions like proliferation and cell death. Each cell in a tumor can bear its own genomic alterations and expression patterns which may also be caused by tissue and microenvironmental pressures. Additionally, patients may respond differently to treatment due to their genetics and microbiome, creating challenges when translating insight from model organisms to humans. Lastly, immune response adds an additional axis of complexity in cancer research and treatment.

Our integrated research tools empower you to better understand the tumor, tumor microenvironment (TME), and immune response in single cells, multicellular tissue compartments, and across cohorts.

- Profile the expression of 800+ genes from a single sample with the nCounter® Analysis System, including validated gene signatures such as TIS, PAM50 and LST

- Spatially profile the whole transcriptome and select protein targets within distinct tissue compartments and cell populations with the GeoMx® Digital Spatial Profiler (DSP)

- Obtain the highest plex single-cell and subcellular spatial multiomics data with the CosMx® Spatial Molecular Imager (SMI)

- Explore tissue biomarker expression with high dynamic range and characterize the interactions of tumors, immune cells, and surrounding healthy tissues with CellScape™ Precise Spatial Proteomics.

With over 20 combined years of experience developing cancer research tools, we believe in partnering with you to enable your oncology work. So, wherever you are headed with your oncology research, Bruker Spatial Biology can take you there.


Cancer is not just one disease

There are >100 types of cancer

Tumor Microenvironment (TME) impacts the Immune Response

There are many influences to cancer growth and treatment

Not all patients respond to treatments

Population of patients with heterogeneous tumors

Non-responders

Some tumors respond to Drug B

Some tumors respond to Drug A

Biomarkers & Signatures needed to understand who responds

Addressing Needs

Addressing Biological Needs Through Disease 'Hallmarks'

The Hallmarks of Cancer, first introduced in 2000 by authors Douglas Hanahan and Robert Weinberg, is one of the most widely recognized principles for the holistic study of cancer. This framework, represented in the now famous Hallmarks of Cancer wheel, is often the first roadmap researchers use to study all types of cancer. Hallmarks help explain the complexities of cancer by describing a common set of processes that, if unstopped, allow cancer cells to thrive and proliferate in the unique tumor microenvironment they create.

From our beginnings with the creation of the first PanCancer Gene Expression Panel for nCounter, to the more recent development of spatial gene and protein expression assays for GeoMx DSP, CosMx SMI, and CellScape, the Hallmarks of Cancer have acted as an important foundation for the biology behind our products, ensuring that our assays are up to date with the latest and most comprehensive insight behind cancer biology.
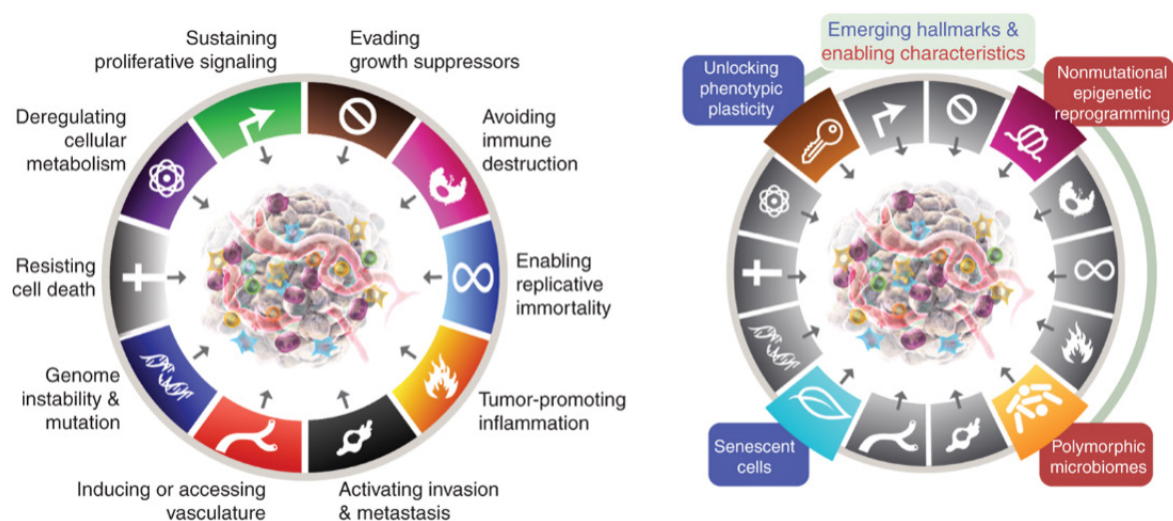
Reprinted from Cancer Discovery, 2022 Jan; 12(1):31-46, Hanahan D. Hallmarks of Cancer: New Dimensions, with permission from AACR.

A Holistic View of Cancer that Goes Beyond Hallmarks

Bruker Spatial Biology has gone beyond the Hallmarks of Cancer to incorporate key markers of the immune response and other cells within the tumor microenvironment in our assays to provide a holistic, 360-degree view of cancer biology. Our collection of assays across all of our platforms delivers a family of multiplex gene and protein expression assays that support basic and translational studies that enable a better understanding of how cancer arises, how the immune system responds, and how the microenvironment affects tumor growth and metastasis.

Creating Novel Solutions

One Suite of Tools. Unlimited Potential.

Whether you are looking to discover biomarkers using gene expression profiles to understand disease onset, progression, localized immune response or treatment response or characterize tumor heterogeneity at single-cell resolution, Bruker Spatial Biology has you covered.

nCounter®
Analysis System

800+ plex pathway-based gene expression profiling in a single tube. Compatible with full spectrum of sample types.

- Discover predictive and prognostic biomarkers
- Evaluate mechanisms of treatment response
- Monitor disease biomarkers in clinical trials
- Stratify patients using validated TIS, PAM50 and LST gene signatures

CosMx®
Spatial Molecular Imager
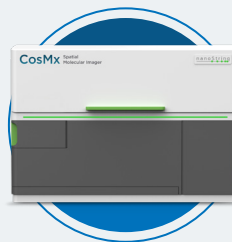
High-plex single-cell profiling of RNA with subcellular resolution.

- Identify cellular neighborhoods that reveal tumor heterogeneity
- Reveal functional changes within a tumor at single cell resolution
- Characterize up to 100 oncology specific ligand receptor pairs (including major drug targets) between interacting cells

CellScape
Precise Spatial Proteomics Platform

Highly multiplexed whole-slide immunofluorescence imaging and quantitative spatial phenotyping.

- Identify cancerous tissue with sub-cellular resolution
- Detect tumor immune infiltration patterns and discover rare cell types
- Leverage versatile assay design and create bespoke targeted panels to monitor novel biomarkers

GeoMx®
Digital Spatial Profiler

Spatially profile the whole transcriptome and 570+ protein targets from FFPE and fresh frozen tissue.

- Understand tumor heterogeneity
- Measure treatment response in clinical trials
- Characterize the microenvironment along the tumor invasive margin
- Discover and validate spatial biomarkers
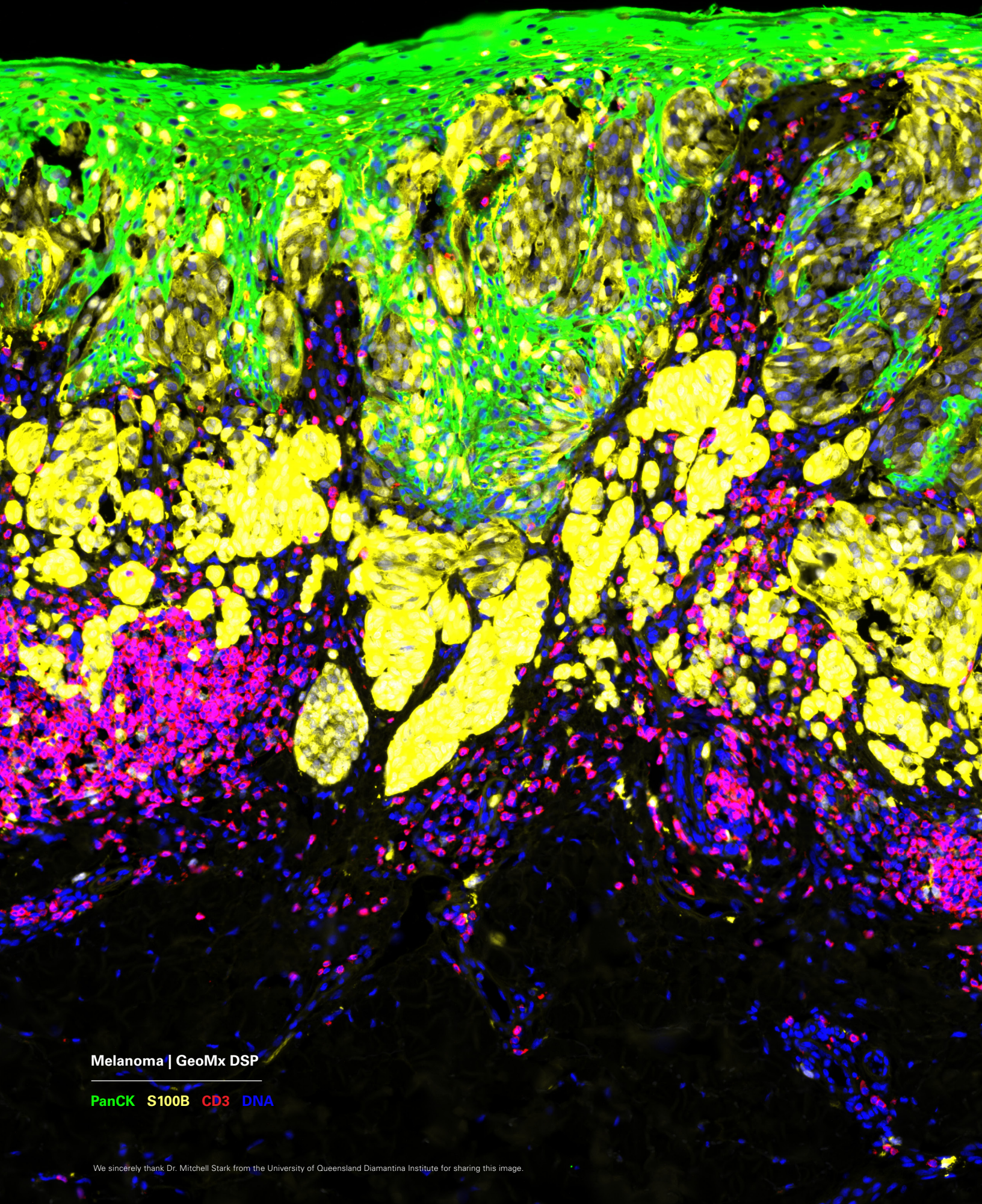
Melanoma | GeoMx DSP

PanCK S100B CD3 DNA

nCounter
Analysis System

Gene Expression You Can Count On: Accelerate your biomarker discovery and development with confidence and peace of mind with the nCounter Analysis System. With robust performance on even the most difficult sample types and unparalleled flexibility in content and throughput, you can rapidly translate discoveries into actionable clinical insights.

Robust Performance

- Gold standard performance on FFPE
- No technical replicates required
- Five logs of dynamic range
- Broad sample compatibility
- No RT or enzymatic steps

Flexible Assays

- Extensive ready-to-ship panel menu
- Guided by industry experts and the latest peer-reviewed literature
- Bioinformatics support for custom designs
- Customization of ready-to-ship panels with up to 55 targets

Efficient Workflow

- Less than 15 minutes hands-on-time
- Go from sample to answer in less than 24 hours
- Highly scalable set-up
- Simplified data analysis
- Minimal data storage required

Four Simple Steps Produce a Huge Amount of Data

< 15 Minute Setup	Overnight Hybridization	Load Onto System	Analyze Results
1	2	3	4
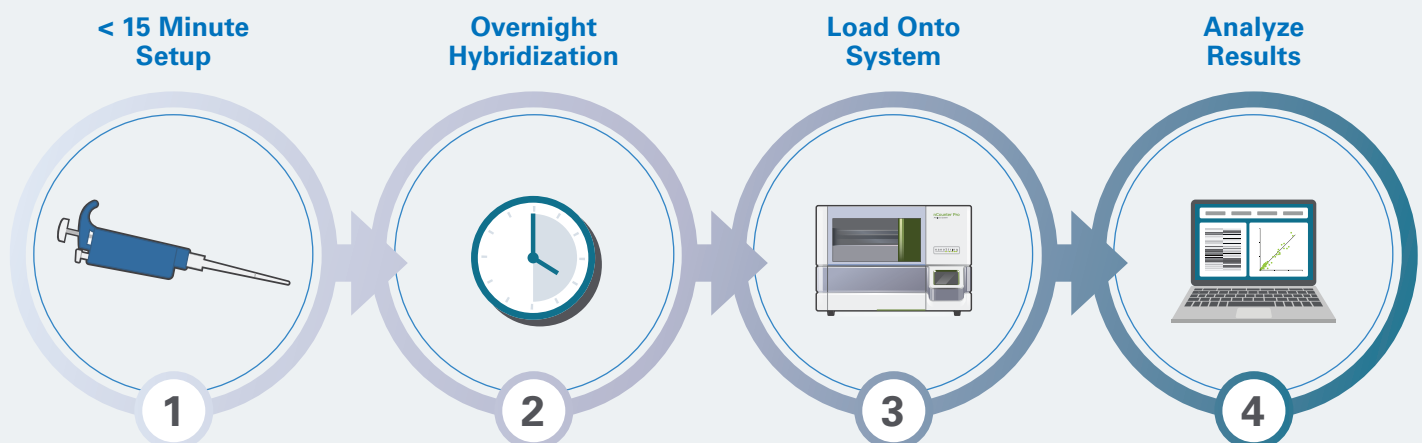
nCounter Oncology Panels & Signatures

A large portfolio of expression panels with carefully curated content delivers views into the biology of the tumor, TME, immune response, and beyond.

**Select nCounter Oncology Panels**

The PanCancer IO 360™ Panel

Examine the complex interplay between the tumor, microenvironment, and immune response in cancer, allowing for a multifaceted characterization of disease biology and interrogation of mechanisms of immune evasion. Includes TIS.

The Breast Cancer 360™ Panel

Quickly decode the complexities of breast cancer biology, develop novel breast cancer gene signatures, and categorize heterogeneity. Includes PAM50 and TIS.
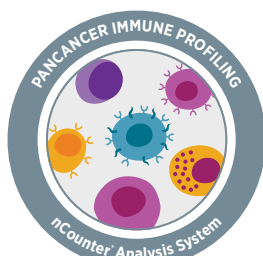
The PanCancer Immune Profiling Panel

Profile different immune cell types, common checkpoint inhibitors, CT antigens, and genes covering both the adaptive and innate immune response.
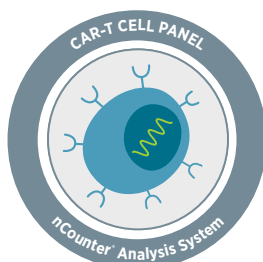
The CAR-T Characterization Panel

Use this panel throughout CAR-T development and manufacturing as a standardized panel of genes for optimizing methods, developing manufacturing acceptance criteria and understanding the host influences beyond manufacturing.

NanoString Signatures

Tumor Inflammation Signature (TIS)	PAM50	Lymphoma Subtyping Test (LST)
An 18-gene signature that measures a pre-existing but suppressed adaptive immune response within the tumor.	An 50 gene signature that distinguishes between breast cancer intrinsic subtypes— Luminal A, Luminal B, HER2-enriched and Basal-like.	An 20 gene signature that determines the Cell-of-Origin (COO) molecular subtypes in diffuse large B-cell lymphomas, activated B-Cells and germinal center B-Cells.

GeoMx
Digital Spatial
Profiler

Resolve tumor heterogeneity. Accelerate translational discoveries with spatial multiomics at scale.

Bridging the gap between tissue imaging and molecular profiling technologies such as single cell analysis, the GeoMx® Digital Spatial Profiler (DSP) allows you to unlock novel biological insights with spatial multiomics in morphologically distinct tissue compartments. Detect new biomarkers and add spatial context to gene signatures discovered with RNA-seq, spatially profile the immune contexture across a tumor sample, and spatially map the expression profiles of different tumor types.

Biology-Driven Profiling

Spatially resolve gene and protein expression with flexible profiling strategies that focus on the biology and areas of the tissue that are most relevant to your research questions. Using immunofluorescent (IF) or *in situ* hybridization (ISH) staining as a guide, select specific biologically-relevant regions and areas of interest, and spatially profile the whole human transcriptome, whole mouse transcriptome, or select RNA targets and protein targets.
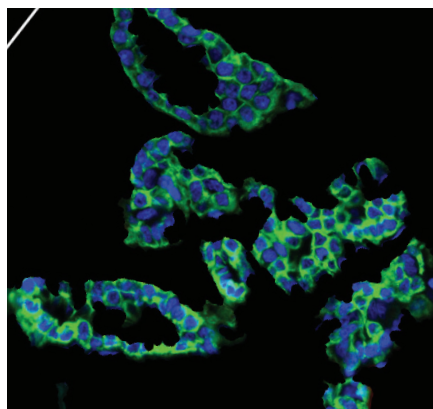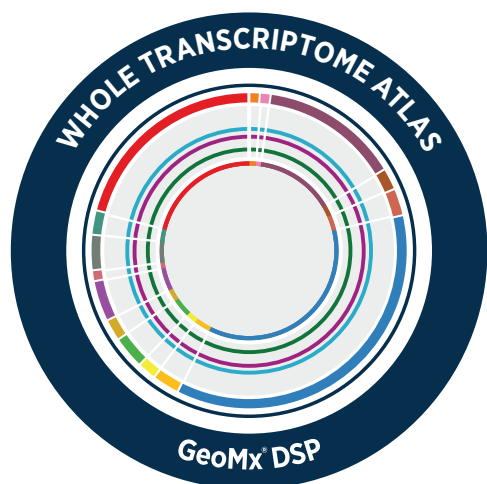

Segmentation
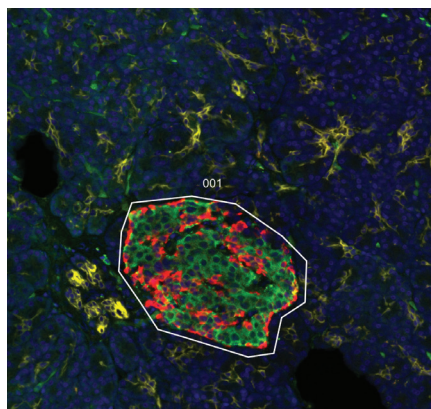

Geometric Profiling
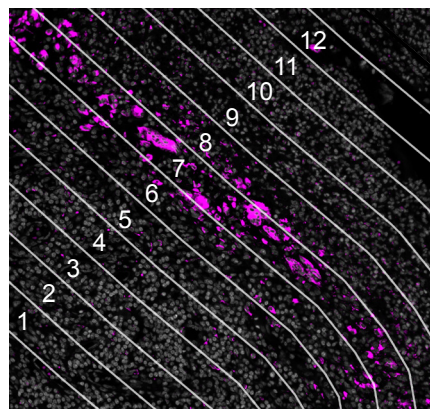
Contour

GeoMx Assays for Oncology Research

Flexible, pre-validated content for spatial multiomics: GeoMx RNA and protein assays can be performed separately or together on the same tissue section and include content curated for oncology research.

Human and Mouse Whole Transcriptome Atlas

- Comprehensively spatially profile all protein-coding genes from human or mouse samples.

- Spike in up to 400 custom RNA targets including noncoding RNAs, exogenous sequences, and/or viral/bacterial transcripts.

- Superior sensitivity: not reliant on poly-A pulldown.

- Uses an Illumina NGS platform for readout.
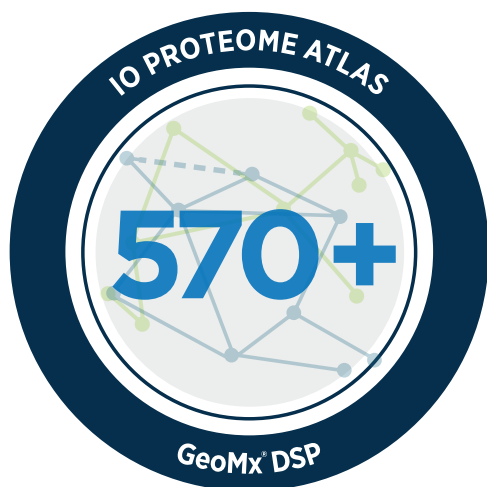
IO Proteome Atlas

- Utilize nearly all IHC compatible antibodies in Abcam's catalog to spatially profile the expression of over 570 human proteins involved in the immune response to cancer.

- Customize with up to 40 targets of your choice.

- Run as a standalone assay or in conjunction with the GeoMx Human Whole Transcriptome Atlas using the spatial multiomics workflow for GeoMx DSP.
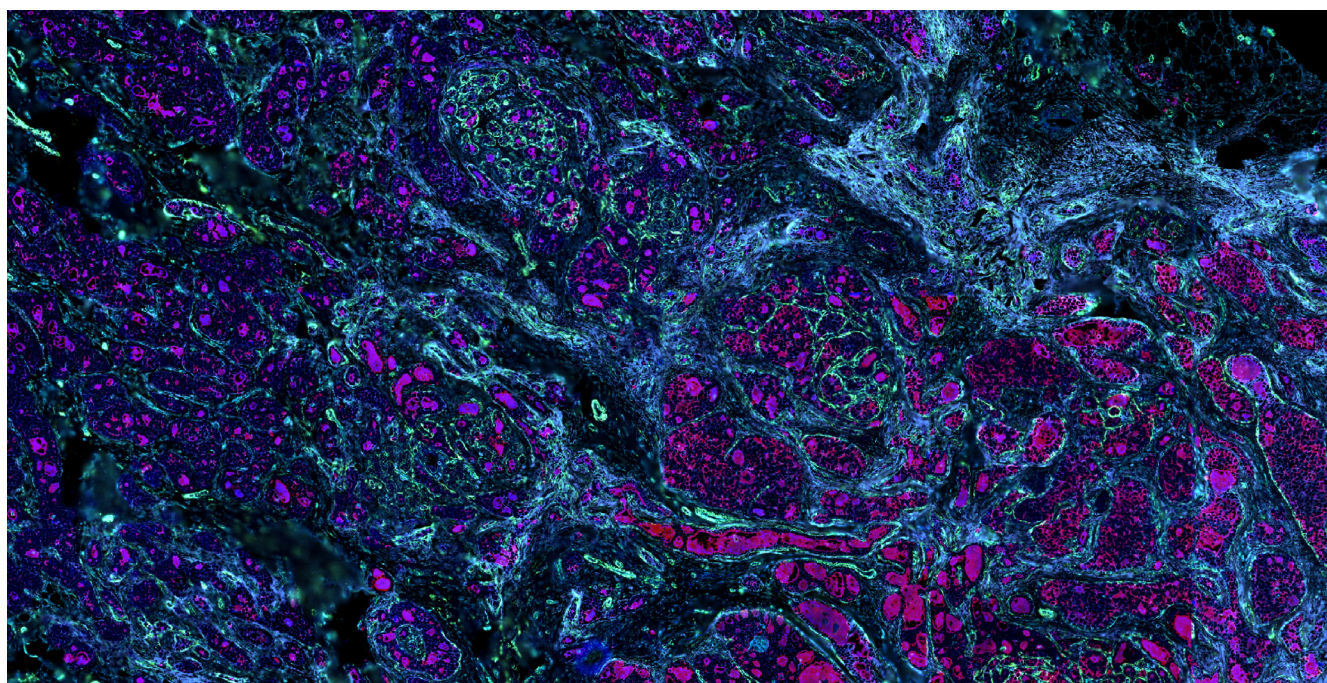
CellScape
Precise Spatial Proteomics Platform

The CellScape™ Precise Spatial Proteomics platform is a cutting-edge imaging solution for quantitative in situ spatial phenotyping. CellScape enables high-plex targeted spatial proteomics with single-cell resolution for whole-slide analyses of tumor microenvironments.

CellScape features high-quality optical performance, integrated fluidics for walk-away automation, and flexibility in assay design. Supported by high dynamic range imaging, the CellScape platform can detect both high- and low-expressing biomarker targets simultaneously.

Sample preparation is simple: the CellScape™ Whole-Slide Imaging Chamber converts a standard microscope slide into a microfluidic device for staining, imaging, and safe sample storage. The CellScape staining and imaging technology is compatible with commercially available fluorescently labeled antibodies, circumventing the need for proprietary antibody conjugation and complex assay validation.

Learn more about CellScape at www.brukerspatialbiology.com/cellscape

CellScape Panels for Oncology Research

Biomarker detection can be jumpstarted using VistaPlex™ Multiplex Assay Kits: modular antibody panels with optimized protocols. Combine the assay kits together or add your own antibodies to conveniently investigate your sample with the right biomarkers for your oncology research needs.
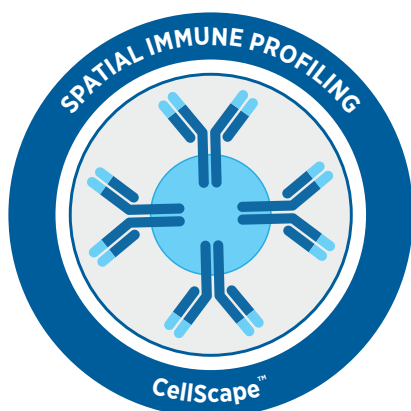
Spatial Immune Profiling Assay Kit

The Spatial Immune Profiling Kit enables detection of 14 phenotypic biomarkers that define key immune cell populations and subpopulations in human FFPE samples. This panel is optimized for ease of use and throughput in immuno-oncology research. This assay kit consists of antibodies targeting CD3, CD27, Ki-67, CD45, CD4, CD45RA, FoxP3, CD68, EpCAM, PD-1, CD8, PD-L1, Granzyme B, and nuclear counterstains.
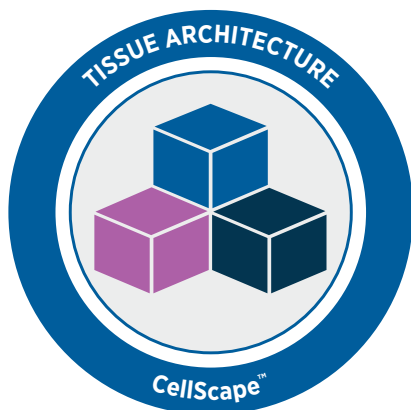
Tissue Architecture Assay Kit

Providing a modular building block for identification of key structural features of human FFPE samples, the Tissue Architecture Assay Kit includes a panel of antibodies targeting epithelial, lymphatic, lamina, vasculature and connective tissue biomarkers and can be expanded by pairing with additional VistaPlex assay kits. This panel consists of antibodies targeting CD138, SMA, CD31, Collagen IV, Podoplanin, Beta-catenin, CD34, E-Cadherin, Vimentin, MUC1, and nuclear stain.

Fresh Frozen Immune Profiling Assay Kit

Achieve fundamental spatial immunophenotyping of the tumor microenvironment in human fresh frozen tissue sample using the Fresh Frozen Immune Profiling Assay Kit. This panel consists of antibodies targeting HLA-DR, CD56, CD45RA, CD8, CD123, CD14, CD20, CD4, CD27, CD45, Pan-cytokeratin, CD11c, CD3, and nuclear counterstain.

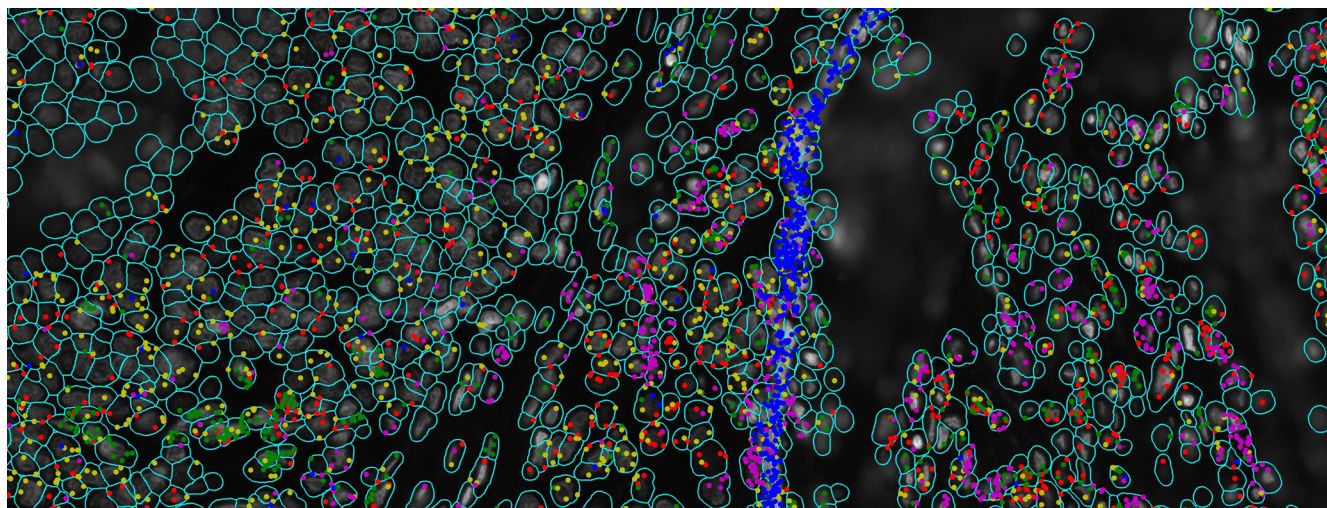# CosMx

Spatial Molecular Imager

Highest-plex, single-cell and subcellular spatial multiomics

Understanding tissue composition, cell phenotype, cell-cell interactions, and cellular function enhances our ability to interpret the onset and progression of cancer. The CosMx SMI allows researchers to comprehensively map the expression of over 6000 RNAs and 50+ proteins to individual cells in their native environment to extract deeper biological insights into the cell and tissue changes that occur in cancer.

Uncover Single-cell and Subcellular Insights

With superior single-cell segmentation that utilizes multi-analyte markers and a machine learning algorithm, CosMx SMI can visualize the immune infiltrate within the tumor and profile expression changes that lead to immune evasion. With CosMx SMI, cell state, cellular function, ligand-receptor interaction, and cell signaling can be resolved in FFPE or fresh frozen tissue.

By analyzing the spatial distribution of specific cell receptors and their downstream signaling pathways at both the RNA and protein levels, CosMx SMI helps you understand how treatment impacts the TME and identify potential resistance mechanisms.

CosMx Assays for Oncology Research

CosMx Human Universal Cell Characterization Panel

Get robust cell typing data and analyze cell-cell interactions with the CosMx Human Universal Cell Characterization Panel. Spatially profile the expression of 1000 highly curated targets at subcellular resolution and customize with up to 50 custom targets. Identify up to 100 unique ligand-receptor pairs that contribute to all aspects of tumorigenesis.
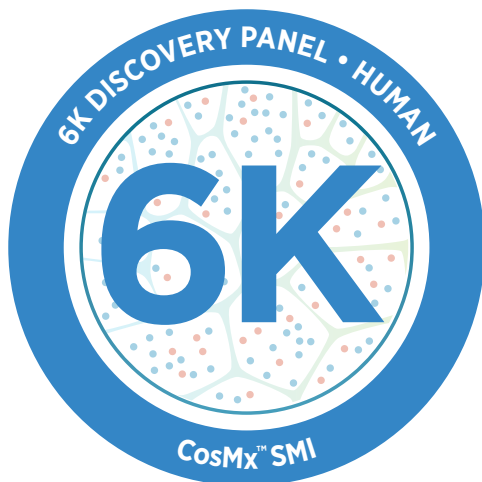
CosMx 6K Human Discovery Panel

Accelerate your single cell spatial transcriptomics with this fully validated, 6K plex RNA panel, with simple sample preparation, an easy-to-use and reliable spatial multiomics platform and streamlined data analysis.
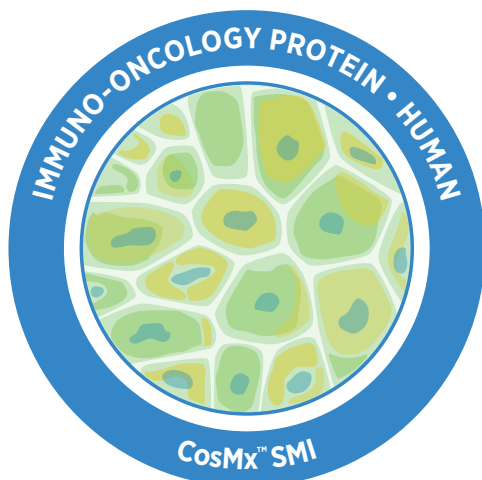
CosMx Protein Assays

Get a complete picture of the expression changes that occur in cancer with the CosMx Protein Assays and single cell, high-plex analysis of up to 68 proteins from a single FFPE slide. Gain a deeper understanding of the proteomic landscape of tumor biopsies and identify new disease indicators and therapeutic targets.

Integrating Platforms
Across the Cancer Research Continuum

By offering a portfolio of complementary solutions that span the entire cancer research continuum, Bruker Spatial Biology provides innovative tools that enable a multiomic, holistic view of cancer. This deeper understanding of cancer heterogeneity and the impact of the TME and immune response can be applied to multiple stages of oncology research, from discovery to pre-clinical work, translational research, and clinical study monitoring.

	Discovery	Pre-Clinical Development	Manufacturing	Translational Research	Clinical Study Monitoring
Key Applications	▪ Cell and tissue atlasing ▪ Cell phenotyping ▪ Understanding heterogeneity of cancer onset and progression ▪ Exploring cell-cell interactions, ligand-receptor pairs	▪ Discovering and developing biomarkers ▪ Understanding tumor heterogeneity ▪ Characterizing treatment response, identifying spatial explanations for nonresponders ▪ Exploring mechanisms of disease ▪ Determining drug MOA	▪ Developing robust and reproducible therapeutics ▪ Perform analytical tests for cell quality, contamination, potency, dosing, characterizing T-cell response	▪ Examining drug treatment safety, efficacy and response ▪ Characterizing innate & adaptive immune response ▪ Generating multiomic data across Clinical Trials	▪ Performing pharmacovigilance ▪ Monitoring for adverse events, response durability and toxicity
Key Platforms	CosMx, GeoMx	nCounter, GeoMx, CosMx, CellScape	nCounter	nCounter, GeoMx, CellScape	nCounter GeoMx, CellScape

Data Analysis
Options for Discovery and Decision Making

Having access to a comprehensive range of analysis tools and services transforms your valuable data to bring test hypotheses, and deliver publication-quality results. Expedite analysis and accelerate discoveries with on-system data analysis tools, secure cloud-based platforms, expert bioinformatics support, and data analysis services.

| nCounter Analysis Solutions | GeoMx DSP Data Analysis Tools | AtoMx™ Spatial Informatics Platform | Analysis Services |

ROSALIND

- Cloud-based analysis tool
- Secure platform with flexibility for internal or external collaboration
- T Cell Receptor (TCR) Diversity Analysis

nSolver Analysis Software

- On-premises analysis tool
- Available at no charge
- Advanced Analysis Module for additional statistics

GeoMx DSP Data Analysis suite (DSPDA)

- On-instrument
- Data visualization and analysis

GeoScript Hub Open-Source Software

- Developed by NanoString R&D
- Supplements capabilities of DSPDA

- A cloud-based, integrated informatics platform for spatial biology on CosMx SMI
- Analyze and visualize large amounts of spatial multiomics data
- Preset analysis modules and pipelines
- Advanced analytics support global data sharing and collaboration

Data Analysis Service

- nCounter differential gene expression data fully analyzed
- Interpreted by a Buker scientist inclusive of a consultative reportout.

Spatial Data Analysis Service (sDAS):

- Work one-on-one with Bruker Spatial Biology computational biologists
- Fully interpreted GeoMx data to answer biological questions.
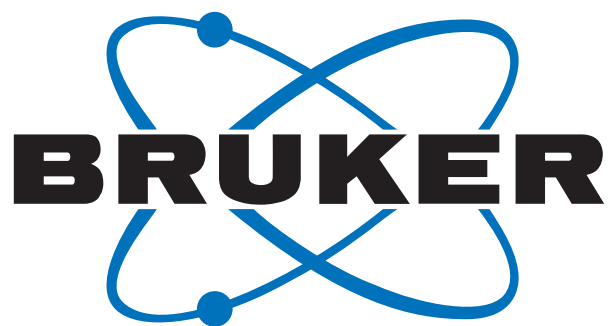
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