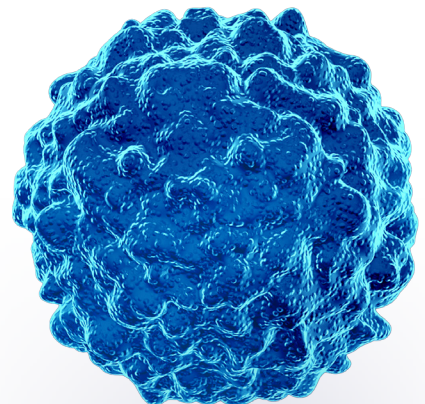


BRUKER SPATIAL BIOLOGY

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 heterogeneous 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 platforms are designed to work together as a cohesive multiomic ecosystem, delivering high fidelity resolution and information depth across every layer of biology and accelerating insights from discovery through translational research. These integrated 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 up to 800 gene expression targets along with over 500 protein targets using the nCounter® Analysis System, including pre-designed panels for tumor signaling, immune pathways, breast cancer, and more
- Spatially profile the whole transcriptome and 1200+ protein targets, including 130 post-translational modifications, within distinct tissue compartments and cell populations with the GeoMx® Digital Spatial Profiler (DSP)
- Obtain unmatched same-cell whole transcriptome multiomics for complete pathway-level spatial insights 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™ XR 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.

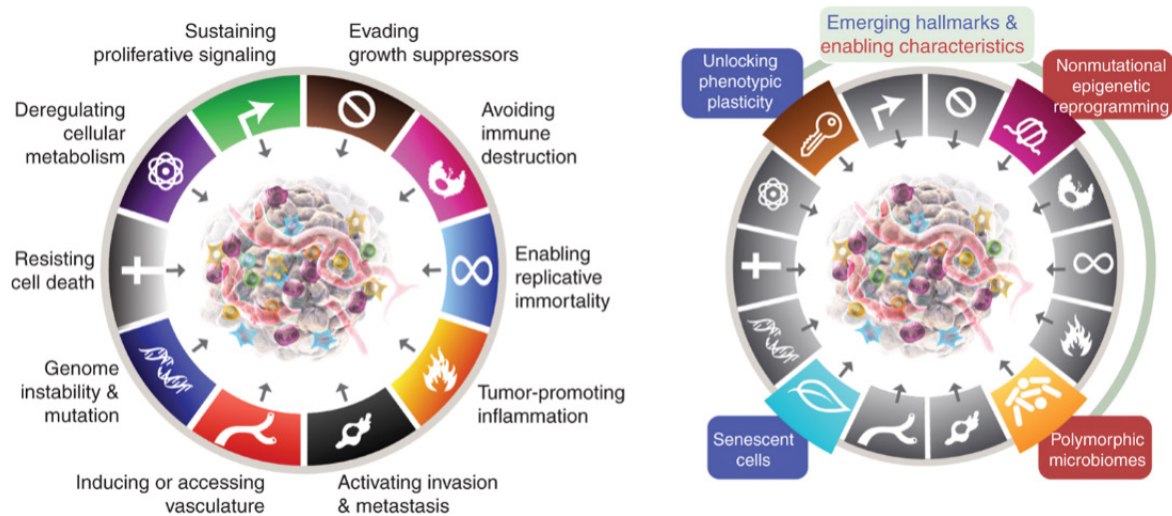


Addressing Needs

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.

Complete, High-Fidelity Solutions

Knit together the full complexity of cancer biology.

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



Highly robust single or multiomic bulk analysis for rapid biomarker discovery and development

- 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

CellScope[™] XR Precise Spatial Proteomics Platform



Flexible spatial proteomics for rapid and quantitative spatial phenotyping

- Validate biomarkers and confirm spatial phenotypes at subcellular resolution in intact tissue
- Identify cancerous tissue with subcellular resolution
- Detect tumor immune infiltration patterns and discover rare cell types
- Design custom assays to validate biomarkers and translate discoveries into reproducible workflows

CosMx[®] Spatial Molecular Imager



High sensitivity, subcellular imaging of the whole transcriptome for complete pathway-level spatial insights

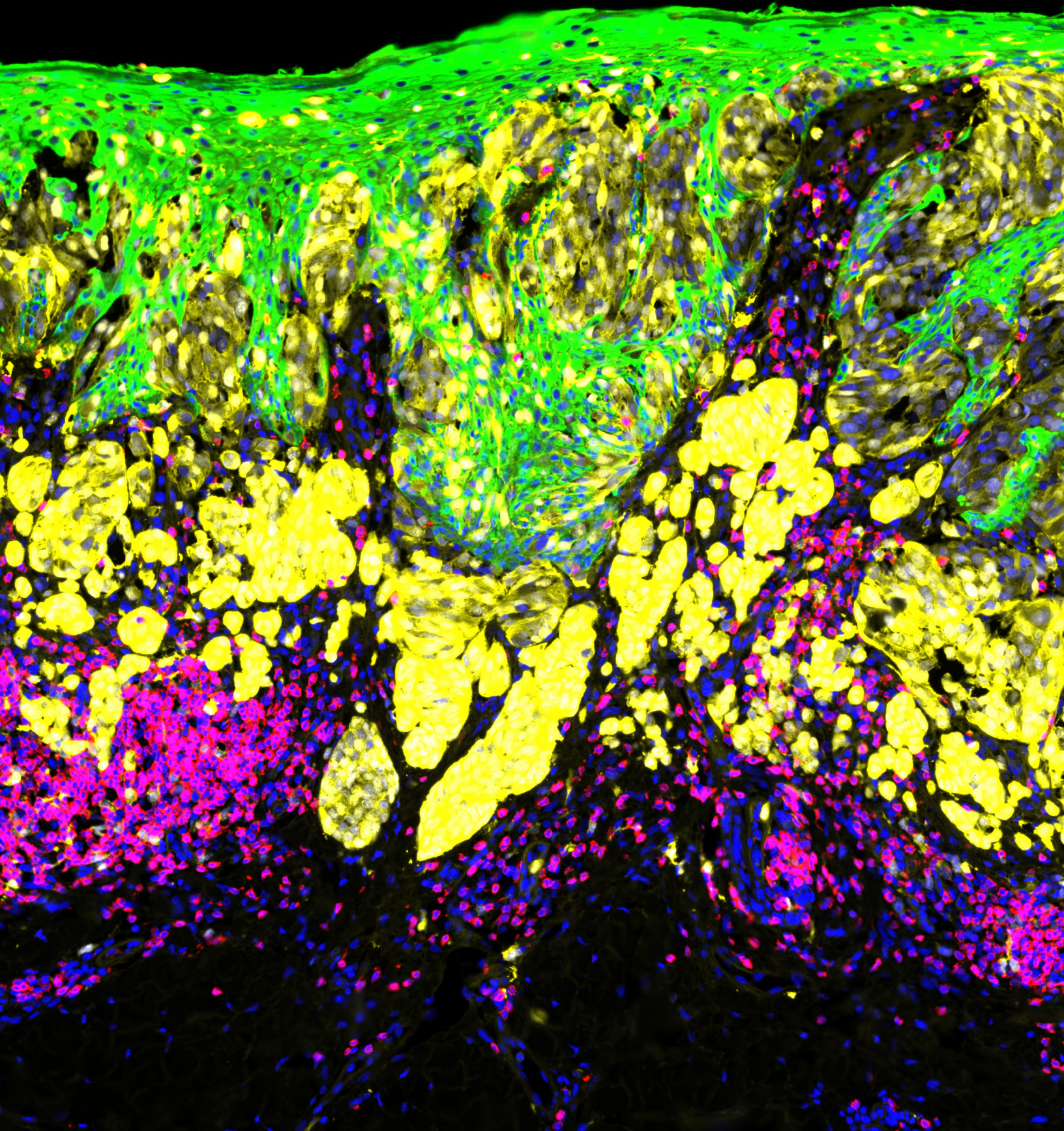
- Identify cellular neighborhoods that reveal tumor heterogeneity
- Reveal functional changes within a tumor at single cell resolution
- Integrate high-plex RNA and protein data to generate comprehensive spatial profiles that inform precision oncology and patient stratification

GeoMx[®] Digital Spatial Profiler



Mechanistic spatial multiomics for biomarker discovery at scale

- Distinguish active vs. inactive biological pathways driving tumor heterogeneity
- Reveal mechanisms of treatment response by resolving RNA-protein discordance
- Identify spatially resolved drivers of tumor-microenvironment interactions
- Discover mechanistically grounded biomarkers for downstream validation



Melanoma | GeoMx DSP

PanCK S100B CD3 DNA

nCounter Analysis System



Highly robust single or multiomic bulk analysis for rapid biomarker discovery and development

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

Robust Performance

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

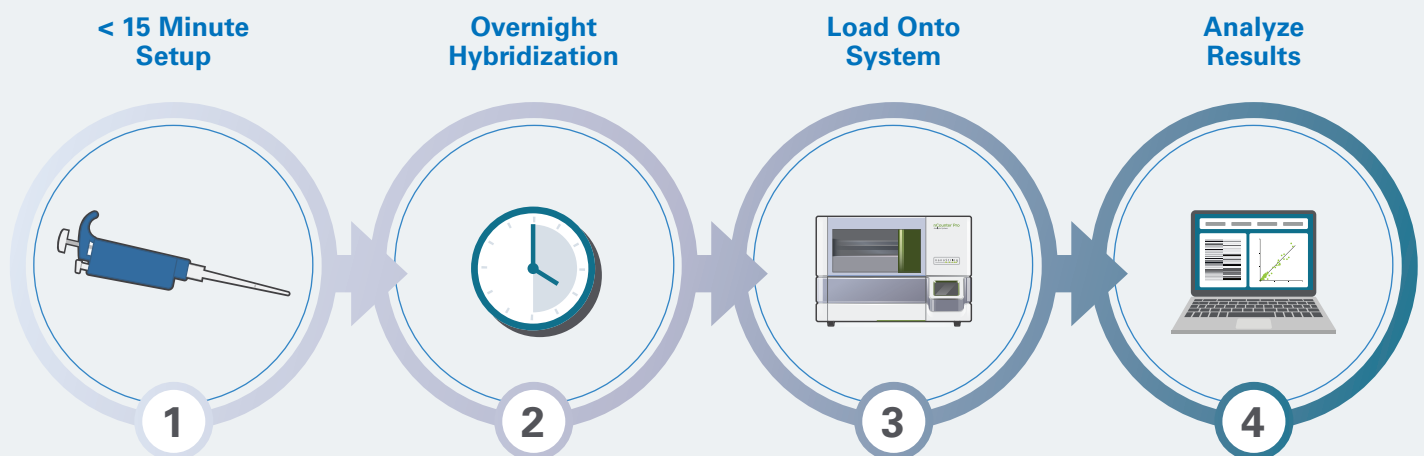
Flexible Assays

- Extensive, ready-to-ship gene and protein panels
- 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



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.

Gene Expression Panels



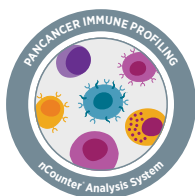
The PanCancer IO 360™ Panel

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.



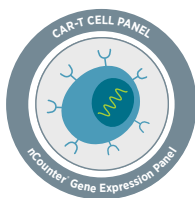
The Breast Cancer 360™ Panel

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.

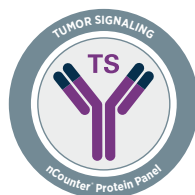


The CAR-T Characterization Panel

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.

Protein Panels

Measure RNA and protein together from the same FFPE sample for multiomics analysis by combining nCounter Protein Panels with any nCounter Gene Expression Panel.



Tumor Signaling Panel

This 325-plex panel enables analysis of proteins focused on tumor signaling. Coverage includes key cellular processes in cancer such as apoptosis and autophagy, as well as metabolism and more than 25 tumor signaling pathways.



Immune Pathways Panel

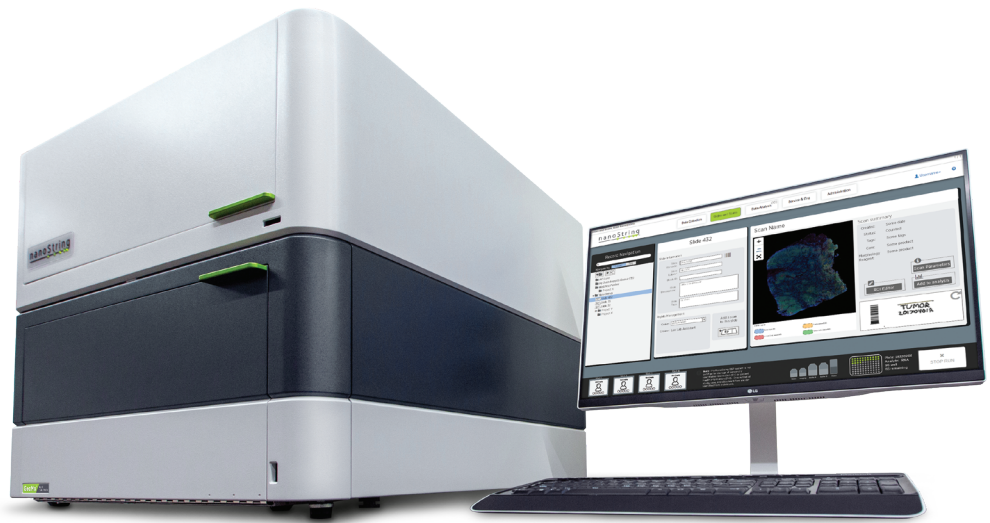
This 204-plex panel enables analysis of proteins focused on immune pathway content. Targets cover adaptive and innate immunity, as well as immune signaling and trafficking.

nCounter 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

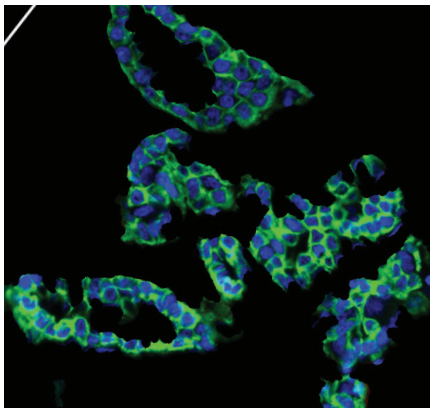


Resolve tumor heterogeneity. Accelerate translational discoveries with mechanistic spatial multiomics at scale

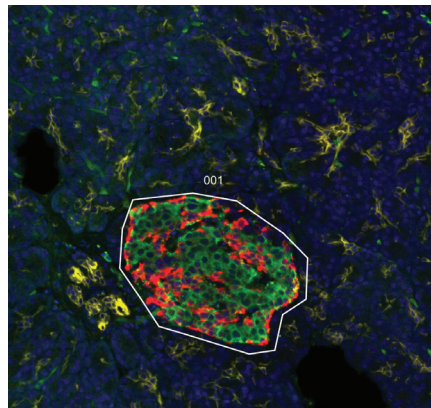
As the discovery anchor for spatial biology workflows, the GeoMx® Digital Spatial Profiler (DSP) unlocks novel biological insights in morphologically distinct tissue compartments by distinguishing active biology from inferred expression to reveal true disease drivers. Detect new biomarkers and add spatial 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

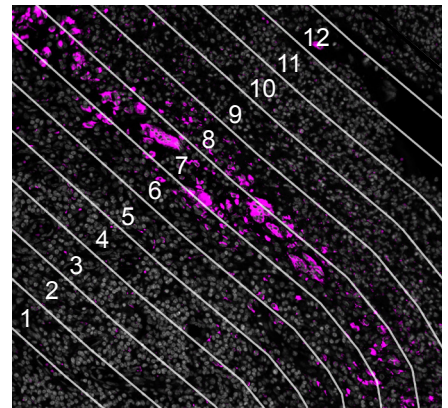
Spatially resolve gene and protein expression with flexible profiling strategies that focus on the biology and areas of the tissue that are most relevant to your research questions, enabling direct measurement of pathway activity within biologically defined regions. Using immunofluorescent (IF) or *in 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



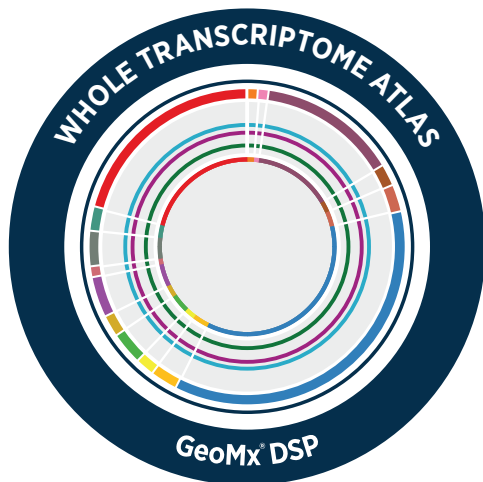
Geometric Profiling



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.
- Generate high-throughput, cost-effective transcriptomic insights across cohorts
- Spike in up to 400 custom RNA targets including noncoding RNAs, exogenous sequences, and/or viral/bacterial transcripts.
- Extend into protein and PTM analysis for mechanistic validation by combining with GeoMx Discovery Proteome Atlas (DPA)



Discovery Proteome Atlas

- Directly measure spatial protein expression and pathway activity to move beyond inferred biology.
- Utilize IHC compatible antibodies in Abcam's catalog to spatially profile the expression of over 1200 human proteins involved in the immune response to cancer and beyond
- Leverage mechanistic interpretation of biological pathways rather than inference from RNA alone.

CellScape™ XR

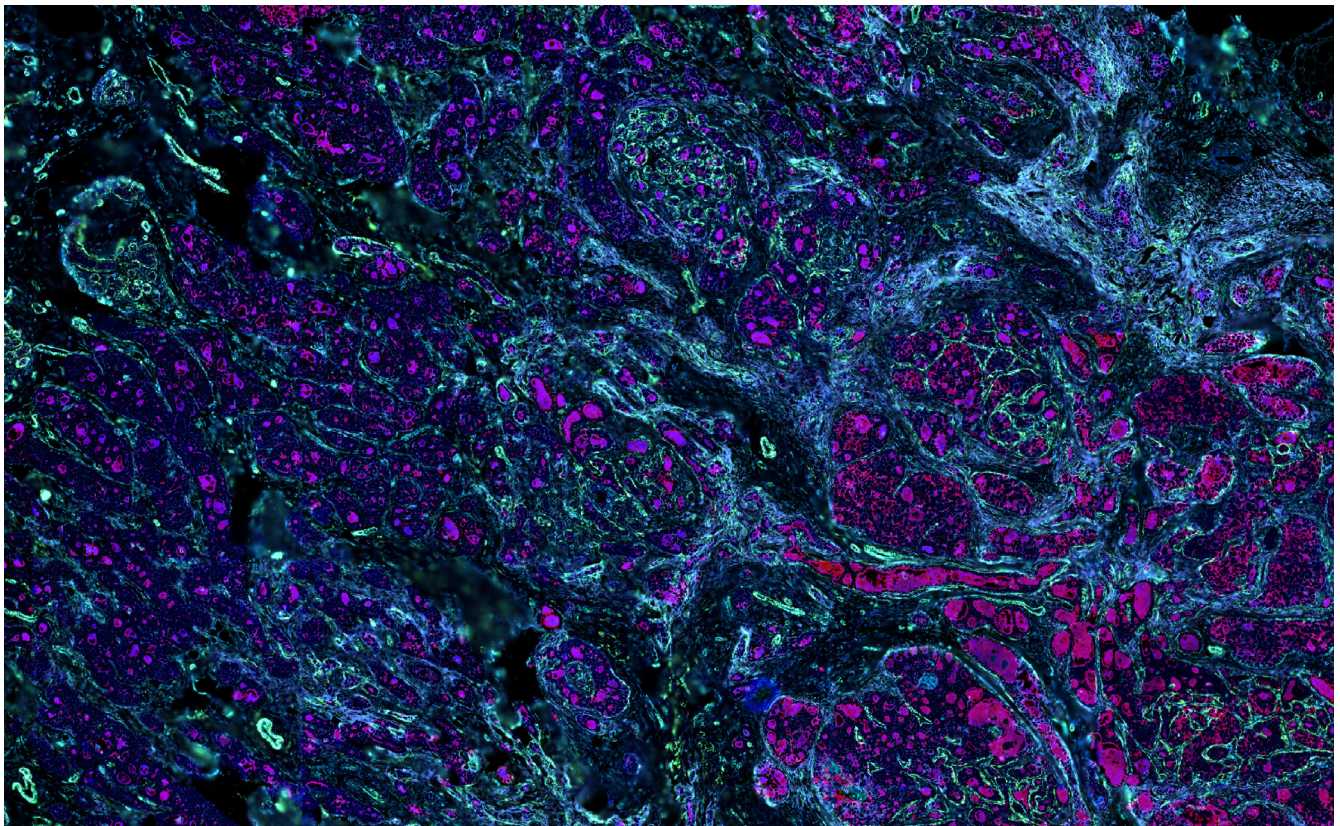
Precise Spatial
Proteomics
Platform



Flexible subcellular proteomics for rapid and quantitative spatial phenotyping

The CellScape XR Precise Spatial Proteomics platform delivers reproducible, high-quality quantitative phenotyping at subcellular resolution across whole-slide tumor microenvironments. With best-in-class quantitative performance, extended dynamic range, and flexible, scalable workflows, it accurately detects both low- and high-expressing biomarkers within the same tissue section, enabling robust validation of spatial phenotypes and maximizing biological insight from every sample.

Sample preparation is simple: the CellScape Whole-Slide Imaging Chamber converts a standard microscope slide into a microfluidic device for automated staining, imaging, and safe sample storage. Built on direct immunofluorescence and EpiclF™ signal removal technology, the platform supports iterative imaging with virtually any dye-conjugated primary antibody, enabling flexible panel design and efficient analysis of large cohorts without compromising quantitative performance.



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.

Standardized and customizable assays to support reproducible, translation-ready spatial phenotyping workflows

Spatial Immune Profiling Assay Kit

Available for Human FFPE, Human Fresh Frozen, Mouse FFPE, and Mouse Fresh Frozen tissue samples

The Spatial Immune Profiling Kit enables detection of phenotypic biomarkers that define key immune cell populations and subpopulations within the tissue microenvironment. This panel is optimized for ease of use and throughput in immuno-oncology research, supporting characterization of major lymphoid and myeloid cell types, immune activation states, and regulatory populations while preserving spatial context.

Tissue Architecture Assay Kit

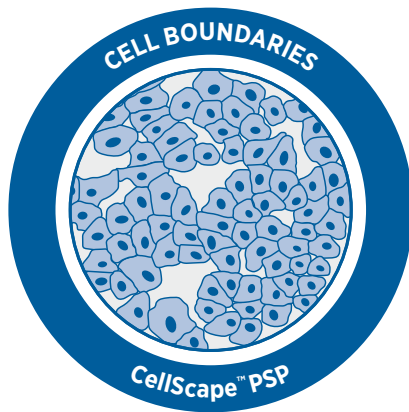
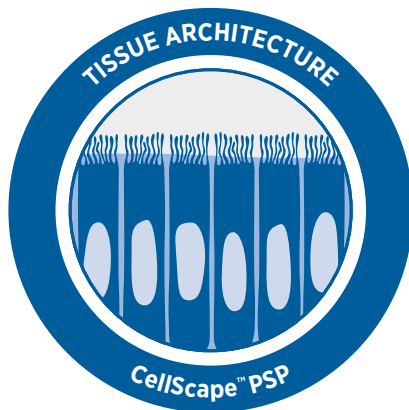
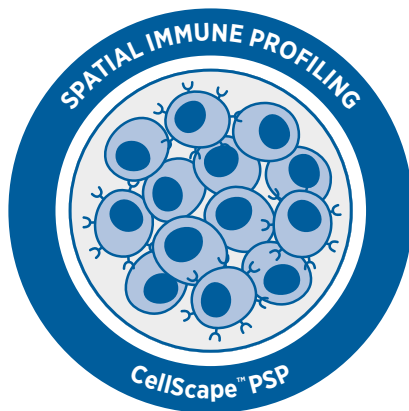
Available for Human FFPE tissue samples

The Tissue Architecture Kit enables visualization of key structural components of the tissue microenvironment, including epithelial, stromal, and vascular compartments. This panel supports spatial mapping of tissue organization and microenvironmental context to guide interpretation of cellular phenotypes and disease-associated remodeling.

Cell Boundaries Assay Kit

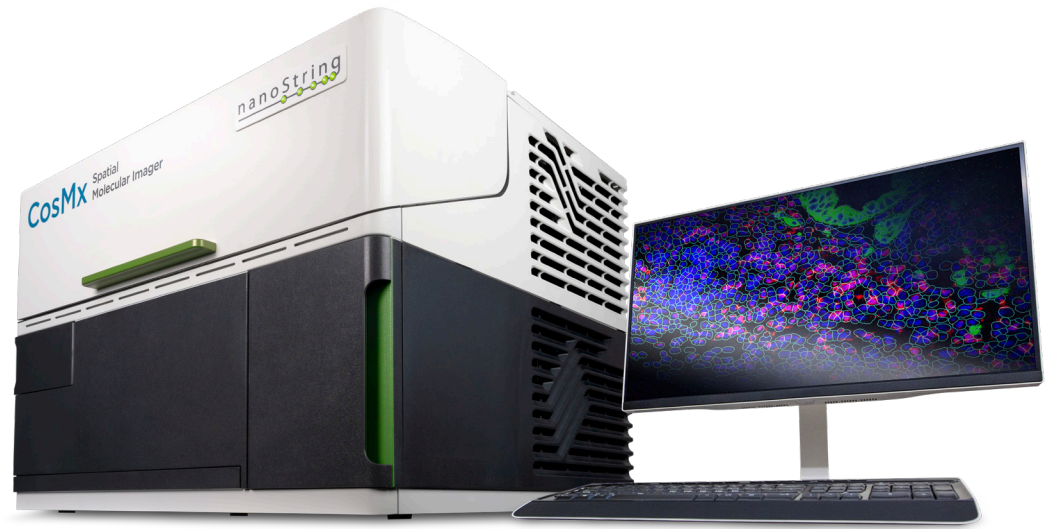
Available for Human FFPE, Human Fresh Frozen, Mouse FFPE, and Mouse Fresh Frozen tissue samples

Achieve robust identification of nuclear and plasma membrane structures to support accurate cell segmentation in spatial imaging experiments with the Cell Boundaries Assay Kit. This panel provides reliable delineation of individual cells across diverse tissue regions to enable precise single-cell analysis and spatial quantification.



CosMx

Spatial Molecular Imager



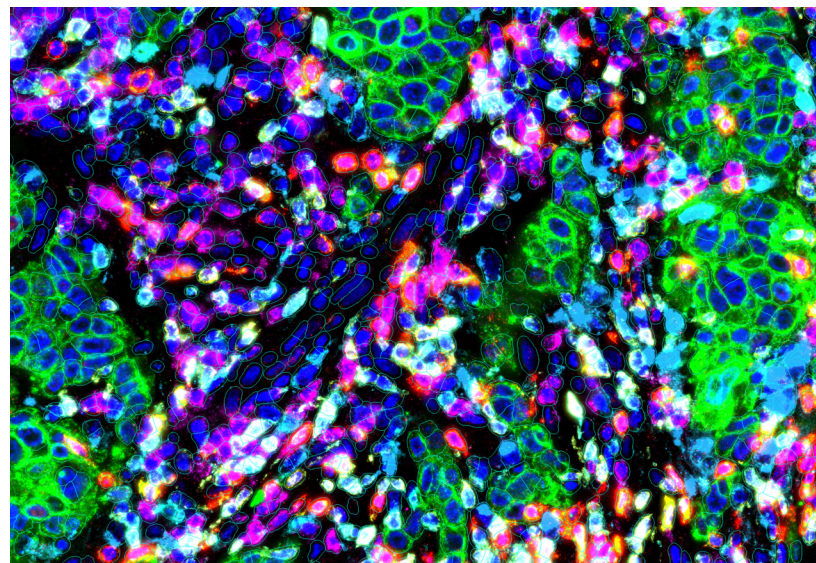
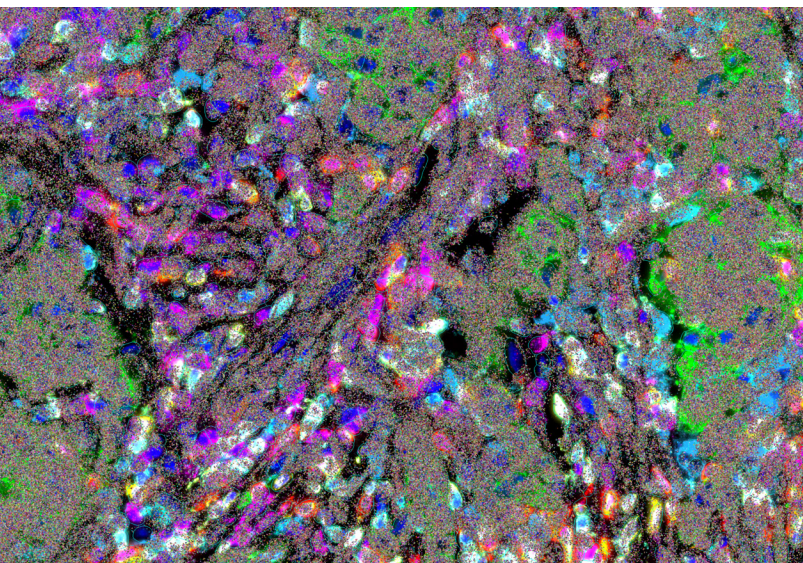
High sensitivity, subcellular imaging of the whole transcriptome for complete pathway-level spatial insights

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 19,000 RNAs and 64+ 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 best-in-class 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.



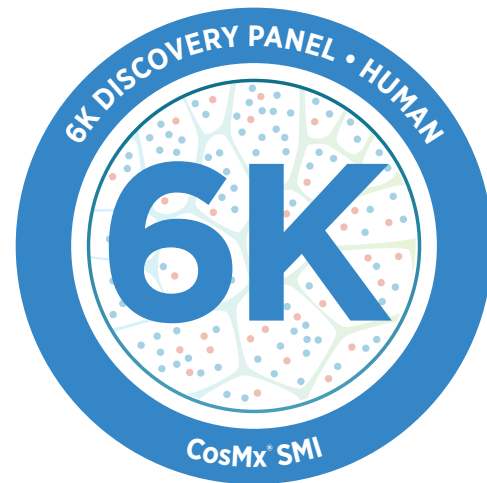
Same-cell subcellular multiomic imaging of the human whole transcriptome (WTX) and 64+ proteins from human breast cancer FFPE tissue.

CosMx Assays for Oncology Research



CosMx Human and Mouse Whole Transcriptome Panels

Project complete pathway biology in space, map every cell-to-cell interaction at the individual transcript level, and discover the unknown and unexpected all with best-in-class sensitivity and genomic breadth within a single intact FFPE tissue section. CosMx WTX delivers disruptive discoveries at subcellular resolution so every single cell contributes to your tissue's full story.



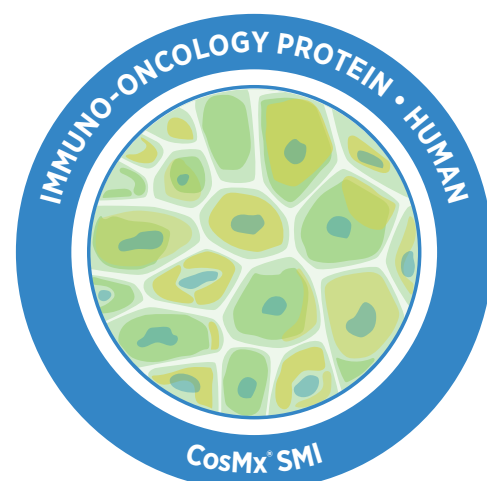
CosMx 6K Human Discovery Panel

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 Human and Mouse Universal Cell Characterization Panels

Get robust cell typing data and analyze cell-cell interactions with the CosMx Human and Mouse Universal Cell Characterization Panels. 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 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	<ul style="list-style-type: none"> Cell and tissue atlasing Cell phenotyping Understanding heterogeneity of cancer onset and progression Exploring cell-cell interactions, ligand-receptor pairs Identify mechanistically relevant biomarkers and active biological pathways 	<ul style="list-style-type: none"> Discovering and developing biomarkers Understanding tumor heterogeneity Characterizing treatment response, identifying spatial explanations for nonresponders Exploring mechanisms of disease Determining drug MOA 	<ul style="list-style-type: none"> Developing robust and reproducible therapeutics Perform analytical tests for cell quality, contamination, potency, dosing, characterizing T-cell response 	<ul style="list-style-type: none"> Examining drug treatment safety, efficacy and response Characterizing innate & adaptive immune response Generating multiomic data across Clinical Trials Validate spatial phenotypes and biomarkers at subcellular resolution in intact tissue 	<ul style="list-style-type: none"> 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 Data Analysis Platform (DAP)

- Open-access, on-premises analysis platform for all your nCounter data analysis needs
- Ability to run quality control, normalization, and statistical analysis, and produce publication-quality figures without the need for bioinformatics expertise

EuropaXp Omics Cloud

- Cloud-based system that enables scientists to analyze and interpret differential gene expression data without the need for bioinformatics or programming skills.
- OmicsCloud makes analysis of nCounter data easy with no-code support

GeoMx DSP Data Analysis suite (DSPDA)

- On-instrument
- Data visualization and analysis

GeoScript Hub Open-Source Software

- Developed by Bruker Spatial Biology R&D
- Supplements capabilities of DSPDA

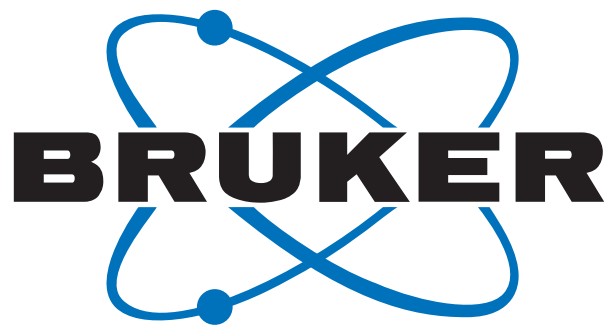
- A cloud-based interactive spatial analytics platform for CosMx data
- Analyze and visualize large amounts of spatial multiomics data
- Preset analysis modules and pipelines to accelerate study-level insights from CosMx SMI data
- Advanced analytics support global data sharing and collaboration
- Spatial Discovery Mode for rapid image-based exploration of subcellular and single cell whole transcriptome data with precomputed insights and LLM ready exports for deeper AI driven biological discovery.

Data Analysis Service

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

Spatial Data Analysis Service (sDAS):

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



Bruker Spatial Biology | For more information, visit brukerspatialbiology.com/oncology

Bruker Spatial Biology, Inc.

530 Fairview Avenue North
Seattle, Washington 98109

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

brukerspatialbiology.com
customerservice.spatial@bruker.com

Sales Contacts

North America
EMEA

nasales.bsb@bruker.com
emeasales.bsb@bruker.com

Asia Pacific & Japan
Other Regions

apacsales.bsb@bruker.com
globalsales.bsb@bruker.com

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