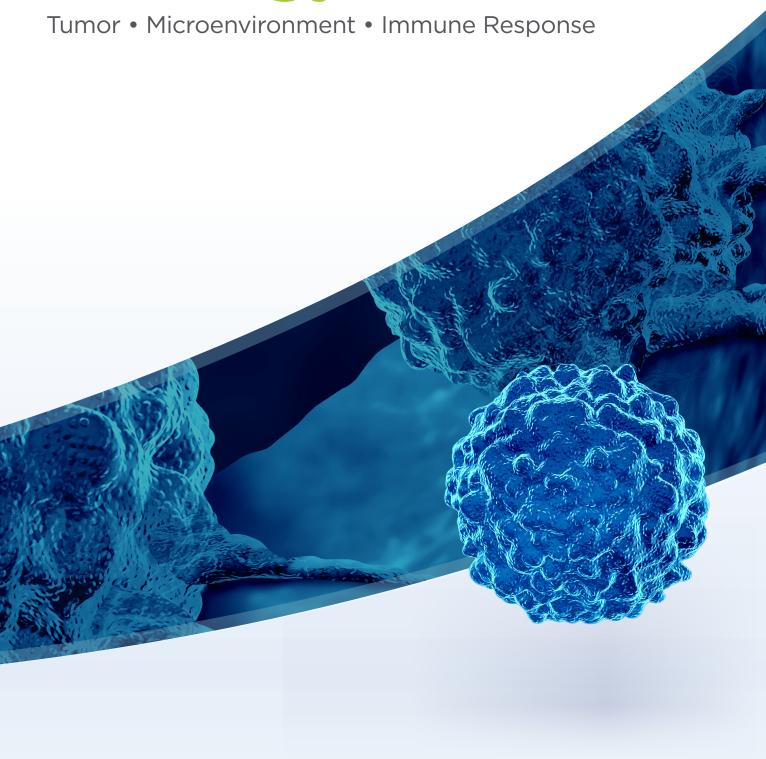
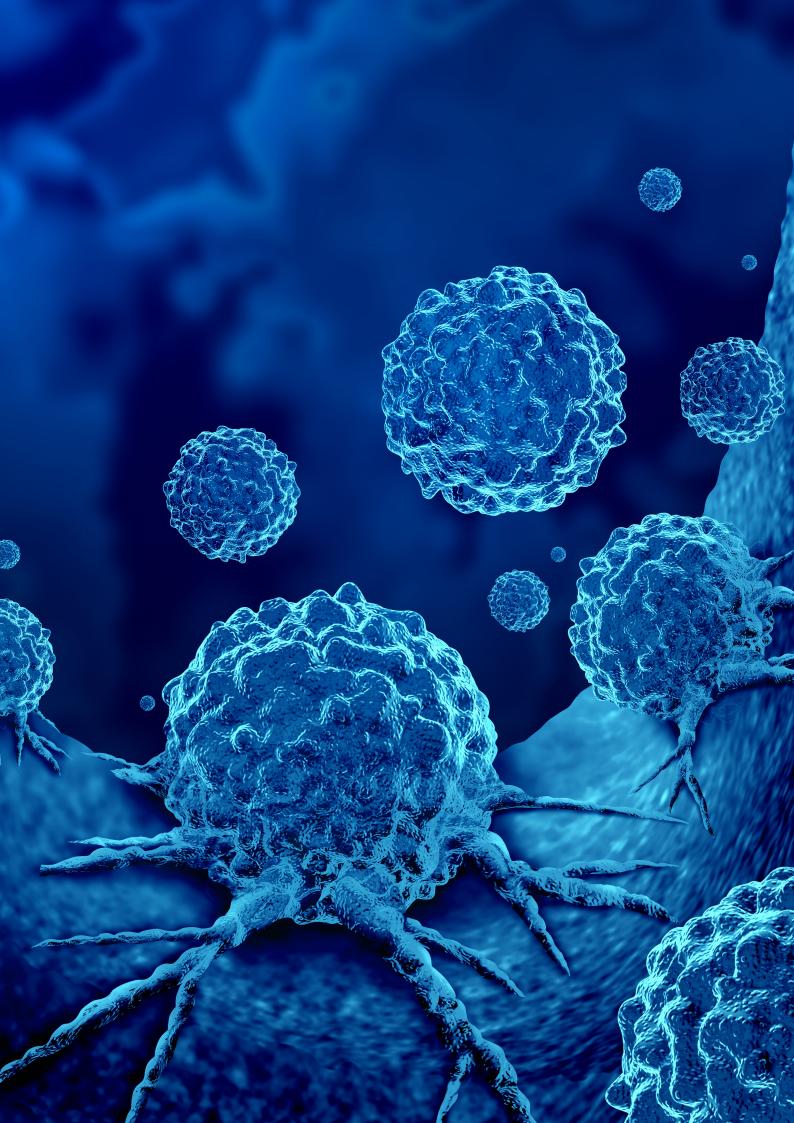
Oncology Solutions





Challenges in Oncology Research

20 years of progress: finding the answers to cancer together

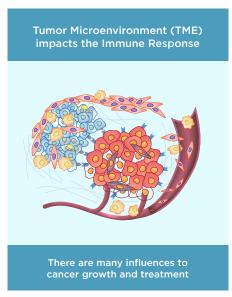
Cancer is a constellation of highly heterogenous diseases that share a common origin in mutations that drive key cellular functions like proliferation and cell death. Each cell in a tumor can bear its own genomic alterations and expression patterns which may also be caused by tissue and microenvironmental 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.

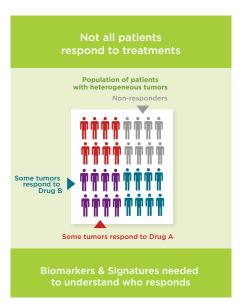
Our integrated research tools empower you to better understand the tumor, tumor microenvironment (TME), and immune response in single cells, multicellular tissue compartments, and across patient cohorts.

- 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)

With over 20 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, NanoString can take you there.





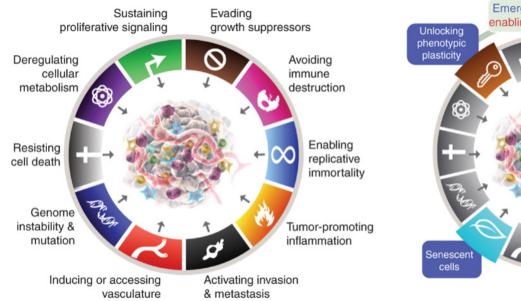




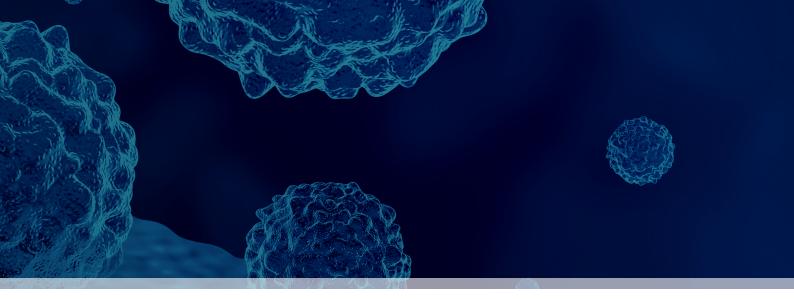
Addressing Biological Needs Through Disease 'Hallmarks'

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 NanoString's 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 and CosMx SMI, 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.









A Holistic View of Cancer that Goes Beyond Hallmarks

NanoString 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 three 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.



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, NanoString has you covered.



nCounter®

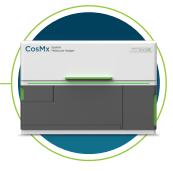
Analysis System

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



GeoMx[®] Digital Spatial Profiler

Spatial profile the wholde transcriptome and 100+ protein targets from FFPE and fresh frozen tissue



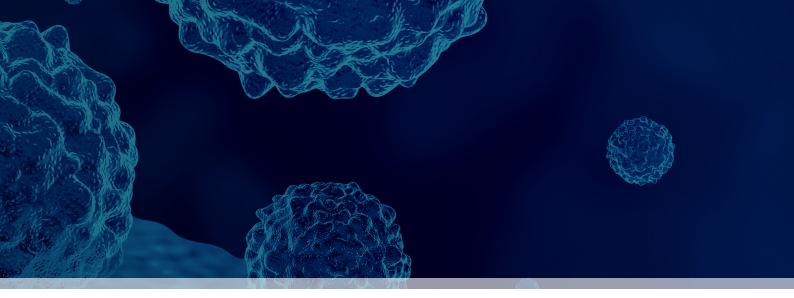
CosMx

Spatial Molecular Imager

Single-cell profiling of RNA and Proteins with subcellular resolution from a single slide.

- 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
- · Understand tumor heterogeneity
- Understand impact of the tumor microenvironment on the immune response
- Measure treatment response in clinical trials
- Characterize the microenvironment along the tumor invasive margin
- Discover and validate spatial biomarkers

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



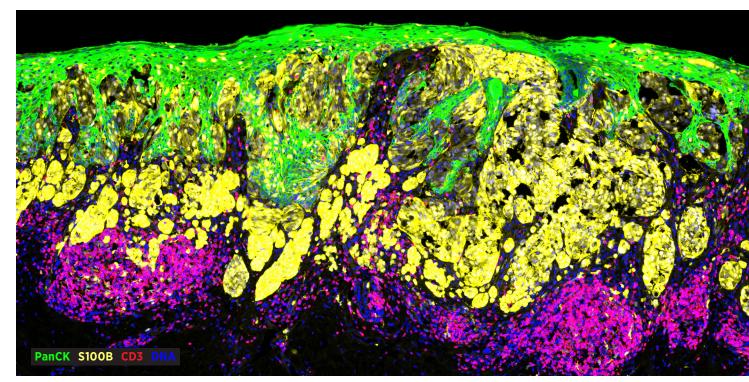


SPOTLIGHT ON SUCCESS

"The nCounter Analysis System, GeoMx DSP and CosMx SMI are highly complementary for oncology research, especially for biomarker discovery. This powerful instrument combo provides an unprecedented view of molecular tissue architecture that can be applied to basic and translational research, especially in cases where tissues samples are scarce and precious."

Nina Radosevic, Investigative Pathologist
Centre Jean Perrin, INSERM U 1240, Clermont-Ferrand, France

Melanoma stained for PanCK, S100B, CD3 and DNA





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

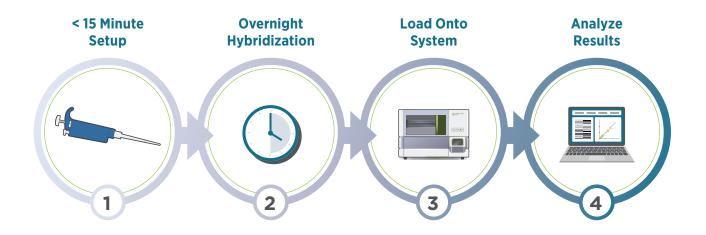
Flexible Assays

- 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



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.

SIGNATURES PARTIES PARTIES SUBTY PE SUBTY

The PanCancer IO 360[™] Panel

Examen 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.

MERSCHED STANDARD

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.	

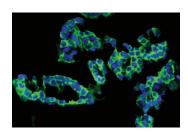


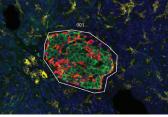
Resolve tumor heterogeneity. Accelerate translational discoveries with spatial multiomics at scale

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.

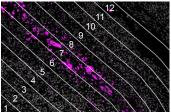
Biology-Driven Profiling

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 or mouse transcriptome or select RNA and protein targets either separately or simultaneously.









Segmentation

Geometric Profiling

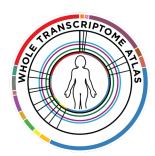
Cell Type Specific

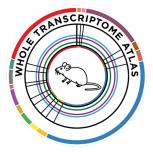
Contour

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.



Immuno-Oncology Protein Panels

- Take advantage of curated content that includes protein targets for immuno-oncology research such as immune checkpoints and proteins involved in the MAPK and PI3K/ AKT signaling pathways.
- Use a universal human or mouse core module and pick and choose to add up to 10 modules containing 6-10 targets each.
- Choose from readout using the nCounter Analysis System (96 targets) or an Illumina NGS system (150+ targets).



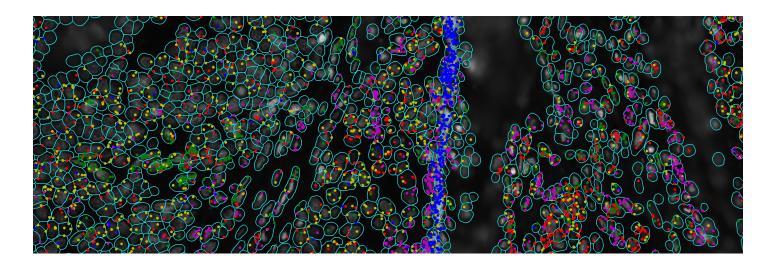
Highest-plex, single-cell and subcellular spatial multiomics

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 1000s of 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 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 level, CosMx SMI helps you understand how treatment impacts the TME and identify potential resistance mechanisms.

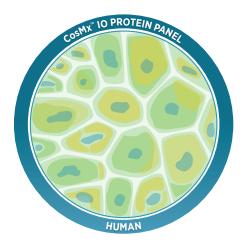


CosMx Assays for Oncology Research



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 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 biomarkers and therapeutic targets.

Integrating Platforms Across the Cancer Research Continuum

By offering a portfolio of complementary solutions that span the entire cancer research continuum, NanoString 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 trials.

	Discovery	Pre-Clinical Development & Translational Research	Manufacturing/ Biomanufacturing	Clinical Development	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 non-responders 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	nCounter	nCounter, GeoMx	nCounter, GeoMx



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.



Rosalind

- Cloud-based analysis tool
- Available at no-charge with some fee-based modules
- 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
- 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 NanoString scientist inclusive of a consultative reportout.

Spatial Data Analysis Service (sDAS):

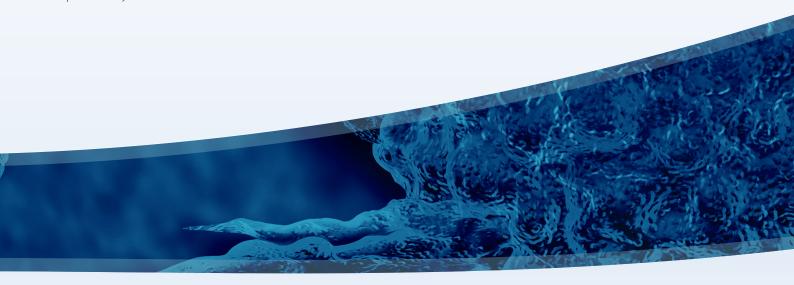
- Work one-on-one with NanoString computational biologists
- Fully interpreted GeoMx data to answer biological questions.



The CosMx[™] SMI and decoder probes are not offered and/or delivered to the following UPC member states* for use in these countries for the detection of RNA in a method used for the detection of a plurality of analytes in a cell or tissue sample without the consent of the President and Fellows of Harvard College (Harvard Corporation) as owner of the Unitary Patent EP 4 108 782 B1. The use for the detection of RNA is prohibited without the consent of the President and Fellows of Harvard College (Harvard Corporation).

*Austria, Belgium, Bulgaria, Denmark, Estonia, Finland, France, Germany, Italy, Latvia, Lithuania, Luxembourg, Malta, Netherlands, Portugal, Slovenia, Sweden

The CosMx™ SMI and decoder probes are not offered and/or delivered to the Federal Republic of Germany for use in the Federal Republic of Germany for the detection of cellular RNA, messenger RNA, microRNA, ribosomal RNA and any combinations thereof in a method used in fluorescence in situ hybridization for detecting a plurality of analytes in a sample without the consent of the President and Fellows of Harvard College (Harvard Corporation) as owner of the German part of EP 2 794 928 B1. The use for the detection of cellular RNA, messenger RNA, microRNA, ribosomal RNA and any combinations thereof is prohibited without the consent of the President and Fellows of Harvard College (Harvard Corporation).



For more information, please visit nanostring.com/oncology

NanoString Technologies, Inc.

530 Fairview Avenue North Seattle, Washington 98109 T (888) 358-6266 F (206) 378-6288 nanostring.com info@nanostring.com Sales Contacts

United States us.sales@nanostring.com EMEA: europe.sales@nanostring.com

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

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