



## **NanoString Highlights Groundbreaking Spatial Genomics Research Using Expanding Portfolio of GeoMx High-Plex RNA Atlas Products at 2020 Advances in Genome Biology and Technology (AGBT) Conference**

February 20, 2020

*Presenting Ten Research Studies using the Cancer Transcriptome Atlas to Discover Novel Biomarkers and First Data from Forthcoming Whole Transcriptome Atlas*

*Unveiling GeoMx DSP Roadmap at 2<sup>nd</sup> Annual Spatial Genomics Summit on Sun February 23<sup>rd</sup>*

SEATTLE--(BUSINESS WIRE)--Feb. 20, 2020-- NanoString Technologies, Inc. (NASDAQ:NSTG), a leading provider of life science tools for discovery and translational research, today announced ten scientific studies utilizing the GeoMx™ Digital Spatial Profiler (DSP) that will be showcased at the 2020 Advances in the Genome Biology and Technology (AGBT) conference being held at the JW Marriott in Marco Island, Florida. These studies span cancer translational research to neuroscience discovery applications, illustrating the platform's flexibility and opportunity to spatially map distinct cell types and quantitate biological activity. NanoString will also be hosting the 2<sup>nd</sup> Annual Spatial Genomics Summit on Sunday, February 23<sup>rd</sup> from 12 – 4pm ET. Attendees do not need to be registered for AGBT to attend the Summit.

The GeoMx Digital Spatial Profiler provides researchers high throughput, high multi-plex, spatial profiling of RNA and protein targets in a variety of sample types, including both fresh frozen and formalin-fixed, paraffin-embedded (FFPE) tissue sections. GeoMx DSP is currently available for read-out using NanoString's nCounter Analysis System, allowing analysis of up to 96 proteins and 96 RNA targets. Beginning mid-2020, GeoMx DSP will be enabled to read-out on Illumina's Next Generation Sequencers (NGS), which will increase the number of RNA targets that can be analyzed by approximately twenty-fold. First NGS-enabled assay will be Cancer Transcriptome Atlas for human samples, which profiles more than 1,800 genes within oncology and immune pathways. This will be followed in 2021 with launch of the Whole Transcriptome Atlases for human and mouse.

"As one of the first labs in the world to have acquired the GeoMx DSP platform, we are enthusiastic about the potential to discover novel biology with the system," said Alex Swarbrick Ph.D., Garvan Institute of Medical Research, Sydney, Australia. "We used the GeoMx Whole Transcriptome Atlas to spatially characterize distinct cell types in triple negative breast cancer. These data allowed us to track the spatial heterogeneity of cancer signaling pathways and of T cell subsets, leading to insights inaccessible to bulk or single-cell RNA sequencing."

"2020 is shaping up to be the breakthrough year for spatial biology," said Brad Gray, president and CEO of NanoString. "At the AGBT conference, researchers will highlight the powerful new capabilities that will be unlocked using NGS read-out, including our Cancer Transcriptome and Whole Transcriptome Atlases. I'd like to thank all of our customers and collaborators that have worked so diligently to make such groundbreaking research a reality."

At AGBT 2020, studies performed by leading academic researcher centers demonstrate three major applications for GeoMx DSP:

### **1. Discovering novel spatial biomarkers that are not readily detectable by traditional bulk profiling**

#### ***Spatial landscape of the immune microenvironment in metastatic prostate cancer using GeoMx™ Digital Spatial Profiler***

**Pete Nelson, MD, et al., Fred Hutchinson Cancer Research Center, Seattle, WA USA**

Used GeoMx DSP Cancer Transcriptome Atlas to interrogate tissue microarrays of metastatic prostate cancer samples and characterize immune responses. Spatial analysis revealed intra-patient heterogeneity that would not have been readily apparent from bulk RNA profiling experiments.

#### ***Spatial proteomic characterization of the tumor and immune microenvironment reveals features associated with response to neoadjuvant HER2-targeted therapy***

**Katherine McNamara et al., Stanford University, Palo Alto, CA, USA**

Used spatial proteomic analysis of biopsies from on-treatment HER2+ breast cancer patients to stratify responders v. non-responders early during a course of neoadjuvant HER2-targeted therapy. GeoMx analysis allowed unique segmentation of cell populations to provide insight into the effect of innate immune markers, ER status, and PAM50 subtype on treatment response.

#### ***Identification of cell type-specific RNA biomarker candidates in melanocytic tumors using GeoMx Digital Spatial Profiling***

**Maija Kiuru, MD, Ph.D., University of California, Davis, CA, USA**

GeoMx Cancer Transcriptome Atlas analysis revealed microenvironment-specific expression of a novel cell-type specific biomarker, DAMP, in response to early melanoma development. This marker may allow for more sensitive detection of melanoma via patch biopsy.

***Single-nucleus RNA-seq reveals distinct intratumoral transcriptomic heterogeneity in treatment-naïve and chemoradiotherapy-treated primary pancreatic ductal adenocarcinoma***

**William Hwang, MD, Ph.D., et al. et al., Broad Institute, Cambridge, MA, USA**

GeoMx Cancer Transcriptome Atlas and Whole Transcriptome Atlas applications were used to profile tumor, fibroblast, and immune compartments in Pancreatic ductal adenocarcinoma (PDAC) samples from twelve patients. Differential gene expression was measured in tumor and fibroblast compartments between treatment groups and by levels of immune infiltration.

***Spatial Profiling of the Immune Landscape of Solid Tumors Treated with Low Dose Radiation and Immunotherapy Using High Plex RNA Profiling with the GeoMx™ Platform***

**Krisztian Homicsko, MD, Ph.D., et al., Ludwig Institute for Cancer Research, Lausanne, Switzerland**

This project interrogated gene expression changes associated with low-dose radiation immunogenic induction therapy in ovarian cancer. GeoMx Cancer Transcriptome Atlas analysis revealed a pretreatment microenvironment associated with favorable response to therapy, and allowed in depth analysis of needle core biopsies, providing important spatial information in samples that would not have been ideal for bulk transcriptomic assays.

***Localizing and quantifying the immune contexture of human glioma with GeoMx™ high -plex RNA profiling***

**Troy McEachron, MD, et al., University of Southern California, Los Angeles, CA, USA**

Combined single cell RNA sequencing with GeoMx Cancer Transcriptome Atlas analysis to characterize immune cell distribution in glioma samples. GeoMx DSP demonstrates that synchronizing digital pathology and bioinformatics provides layers of insight that conventional methods couldn't.

## **2. Spatial mapping of the whole transcriptome in FFPE tissue**

***Neural stem cell differentiation trajectories in the developing human brain revealed by whole-transcriptome in situ spatial profiling***

**Kenny Roberts, MD, Ph.D., et al. et al., Sanger Institute, Cambridge, UK**

GeoMx DSP Whole Transcriptome Atlas was used to distinguish the transcriptomic profiles of neural stem cells, intermediate progenitors and neurons in the fetal human cerebral cortex at 14 and 19 post-conception weeks. This study examined cell type specific gene expression programs throughout the cortical germinal zones, subplate and the maturing cortical plate and identified spatiotemporal gene expression correlated with neural stem cell self-renewal and differentiation.

***Single Cell Programs of Immune Activation in Human MSI vs MSS Colorectal Carcinoma***

**Jonathan Chen, MD, Ph.D., et al. et al., Broad Institute, Cambridge, MA, USA**

GeoMx DSP Cancer Transcriptome Atlas and Whole Transcriptome Atlas were used to interrogate how tumor and microenvironment interactions vary spatially within colorectal cancers, allowing spatial mapping of signatures linked to single cell RNA sequencing. This study highlights the capacity of GeoMx to identify locations of specific cell populations distributed across tissues.

***Measuring the Spatial Whole Transcriptome and High-Plex Proteins on FFPE samples from Glioblastoma Multiforme Immunotherapy Clinical Trials Using Digital Spatial Profiling***

**Yue Lu Ph.D., et al., Institute Systems Biology, Seattle, WA, USA**

GeoMx Cancer Transcriptome Atlas analysis of glioblastoma multiforme (GBM) samples generated a high-resolution spatial map of the tumor microenvironment and provided the framework for creating a GBM tumor atlas. Use of whole transcriptome sequencing combined with spatial analysis provides the potential to discover the biology underpinning response to new immunotherapy treatment for glioblastoma.

## **3. Phenotyping of single cells through spatial profiling algorithms**

***Mapping intratumoural heterogeneity of triple negative breast cancer through integrated single cell RNA-Sequencing and whole transcriptome Digital Spatial Profiling***

**Alex Swarbrick Ph.D. et al., Garvan Institute of Medical Research, Sydney, Australia**

Primary, untreated, triple negative breast cancer (TNBC) was profiled using GeoMx DSP whole transcriptome. Segmentation was performed based on visual markers characterize immune and stromal cells in the invasive edge, tumor core, and distant stromal regions with the goal of discovering novel therapeutic targets in TNBC.

***Updating immune cell deconvolution for the spatial genomics era***

**Danaher Ph.D. et al., NanoString Technologies, Seattle, WA USA**

GeoMx DSP Cancer Transcriptome Atlas was used to estimate abundance of different immune cell types using novel computational methods. This allows researchers to study how immune cells interact spatially in different regions of a tissue.

***Enabling pathway analysis of RNA expression in formalin-fixed paraffin embedded tissues with the GeoMx™ DSP Platform.***

**Boykin et al., NanoString Technologies, Seattle, WA USA**

GeoMx Cancer Transcriptome Atlas, bulk RNA sequencing, and NanoString nCounter analysis was used to profile the same samples. This project demonstrates how GeoMx analysis can be expanded beyond single gene analysis to understand how biological pathways vary spatially in different regions of a tissue.

NanoString is currently accepting applications to a Technology Access Program for its Cancer Transcriptome Atlas using the DSP technology at [TAP@nanosttring.com](mailto:TAP@nanosttring.com).

To learn more about GeoMx DSP, please visit <https://www.nanosttring.com/scientific-content/technology-overview/digital-spatial-profiling-technology>.

**About NanoString Technologies, Inc.**

NanoString Technologies is a leading provider of life science tools for discovery and translational research. The company's nCounter® Analysis System is used in life sciences research and has been cited in more than 3,200 peer-reviewed publications. The nCounter Analysis System offers a cost-effective way to easily profile the expression of hundreds of genes, proteins, miRNAs, or copy number variations, simultaneously with high sensitivity and precision, facilitating a wide variety of basic research and translational medicine applications, including biomarker discovery and validation. The company's GeoMx™ Digital Spatial Profiler enables highly-multiplexed spatial profiling of RNA and protein targets in a variety of sample types, including FFPE tissue sections.

For more information, please visit [www.nanosttring.com](http://www.nanosttring.com).

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