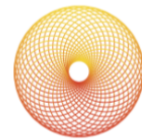


BRUKER SPATIAL BIOLOGY

Industry-leading spatial solutions for high-plex multiomic tissue exploration and discovery

Westley Heydeck, PhD
Senior Field Application Scientist

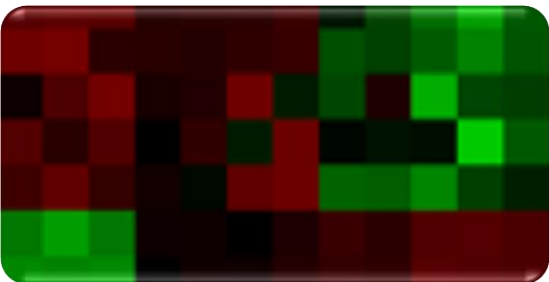
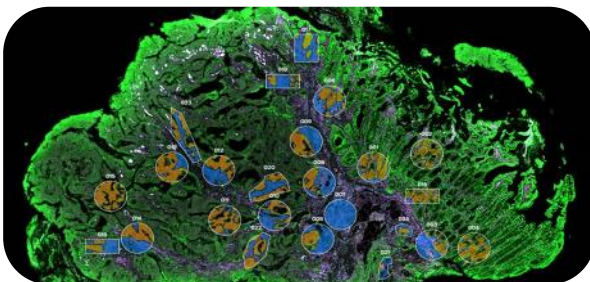
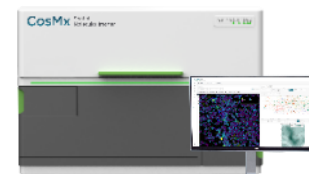
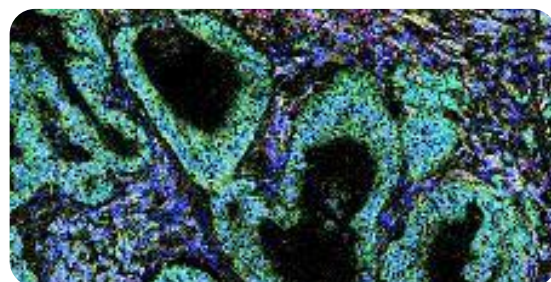
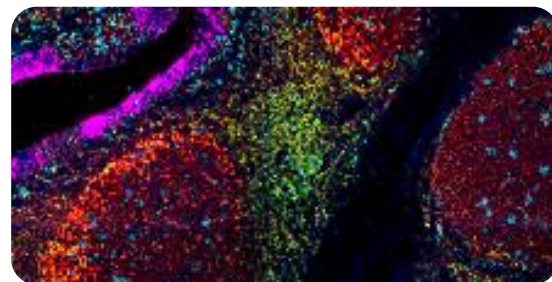
Calgary Spatial Omics Seminar
November 7th, 2024



Applied Spatial Omics Centre

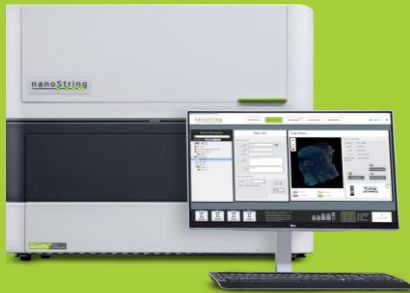
Platforms optimized to deliver industry-leading performance for your application objective

Platforms excel with FFPE tissues and diverse sample or disease types

		Spatial biology	
Bulk	Regional	Single Cell and Sub-Cellular	
2008  nCounter®  • Robust, direct molecule detection • Rapid turnaround, minimal hands-on time • Flexible assays (up to 800-Plex) • Simplified data analytics	2019  GeoMx® DSP  • High-plex, whole transcriptome RNA, 570+ protein (multiomics) • Fast and flexible platform • High sensitivity with user-defined tissue sampling • <i>ex situ</i> sequencing readout	2022  CosMx™ SMI  • High Plex detection 6K→18K RNA, 72 proteins • Accurate cell segmentation • Comprehensive data analysis with AtoMx™ SIP • <i>In situ</i> imager	2022  CellScope™  • Best in class resolution • Highest dynamic range • Flexible assays, high-plex ~100 proteins • Cyclic, highly multiplexed IF

Spatial Biology Demands Multiple Levels of Plex, Resolution, and Throughput

TISSUE EXPLORATION



GeoMx[®]
Digital Spatial Profiler

**Whole Transcriptome (WTA) (18,000+ plex)
> 570-plex Proteins (IPA)**

Gain insights into complex **tissue microenvironments**

Simultaneously co-detect RNA and protein

Discover and develop biomarkers

Run multi-omic cohort studies

How do multicellular areas of interest (AOIs) compare?

**Both platforms
available
through ASOC**

CELLULAR EXPLORATION



CosMx
Spatial Molecular Imager

**Up to 6375-Plex RNA;
72-plex Protein
Human WTx in 2025**

Map tissue cellular composition

Discover cell-cell interactions (niches)

Identify mechanisms of cell behavior and response

Discover biomarkers

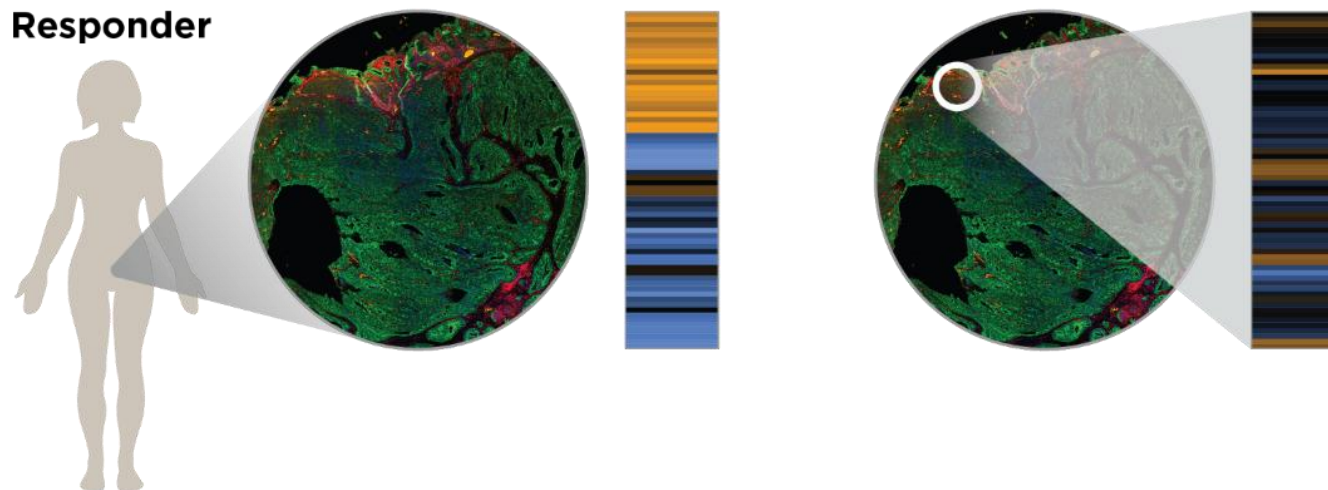
How do single cells compare?

nanoString

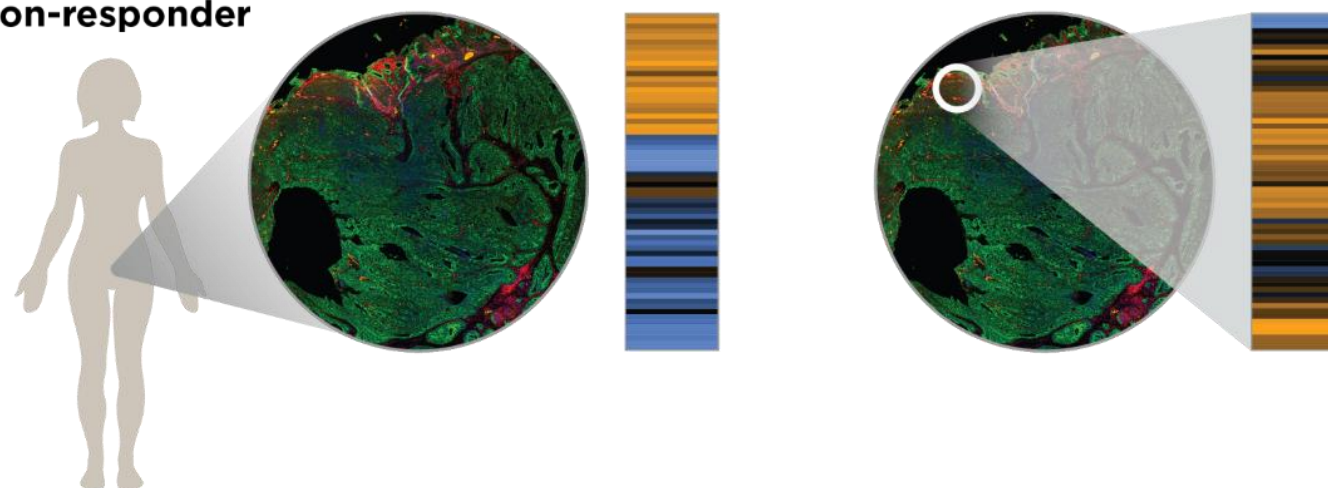
The Challenge of Heterogeneous Tissue

Spatial profiling has the potential to reveal actionable differences in biology

Responder

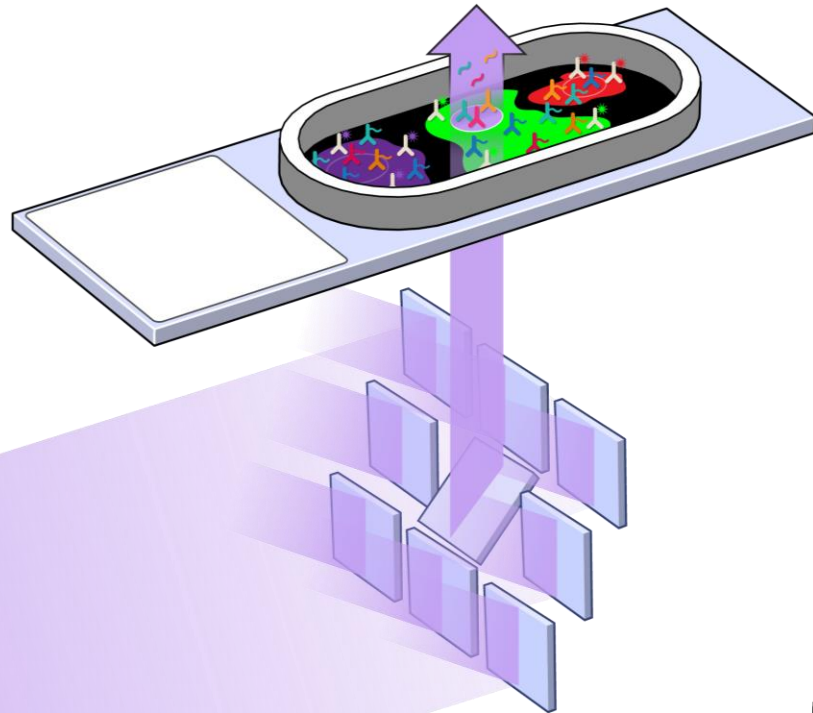


Non-responder



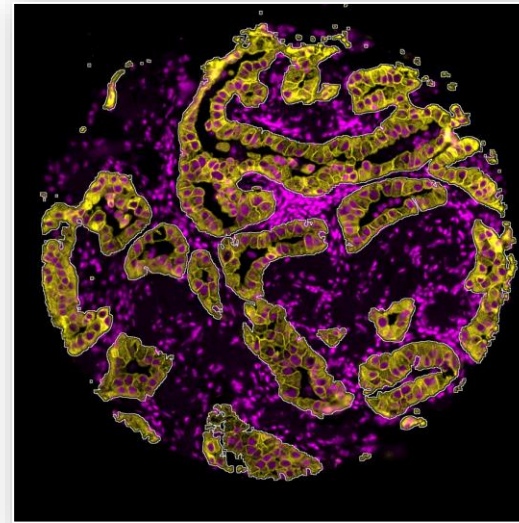
FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

GeoMx DSP Adaptive Optics



Digital micromirror chip (DMD)
~ 1 million 1um² mirrors

Stain



Whole Transcriptome



Expression Level

Tumor Cells Only



Tumor Mask

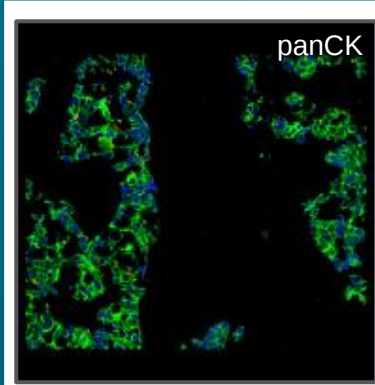


Tumor
Microenvironment
Mask

Only Microenvironment

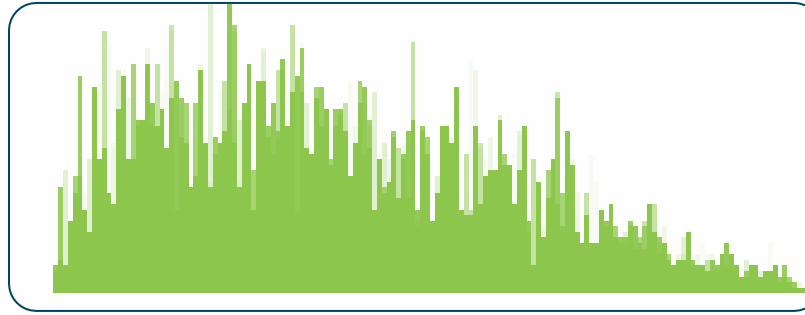
GeoMx Delivers High Sensitivity to Detect Low, Medium, and High Expressors with 5+ Logs of Dynamic Range

Tissue Masking

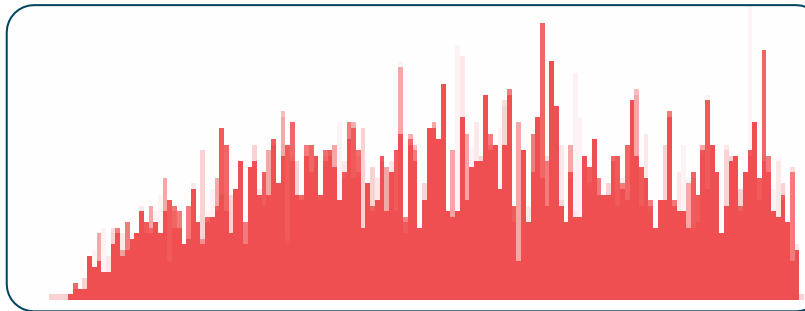


Biologically Relevant Result

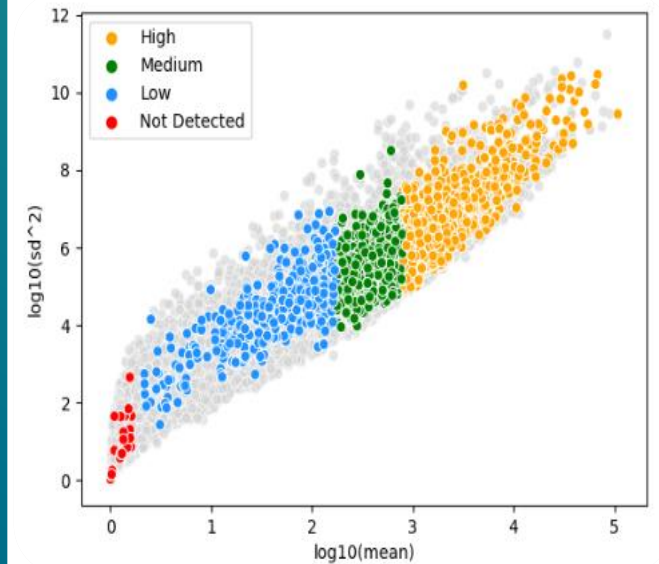
Tumor Profile



Immune Profile



Dynamic Expression Range

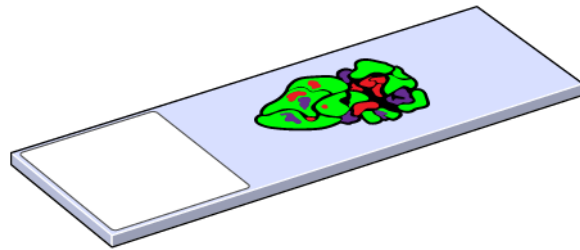


Expression bins defined
using TCGA data

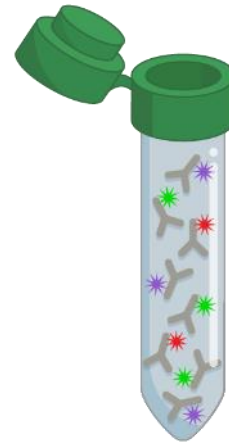
nanoString®

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

GeoMx Digital Spatial Profiler – How it works



Histology slide stained with GeoMx reagents (FFPE, FF, TMA, etc.)



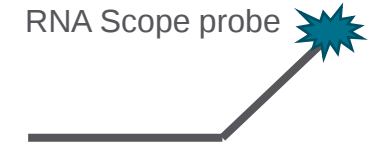
Imaging Reagents



Profiling Reagents

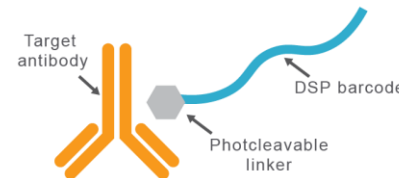
Morphology marker (visible)

Fluorescent labeled Ab

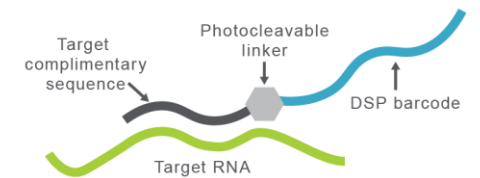


Profiling Reagents (invisible)

Protein reagents
(UV cleavable linker)



RNA reagents
(UV cleavable linker)

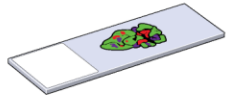


nanoString

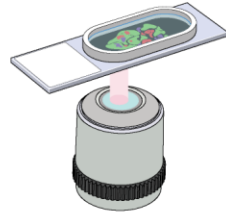
GeoMx Workflow

illumina

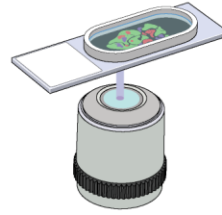
① Stain



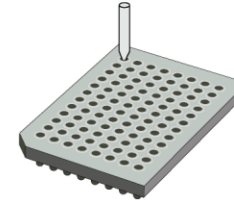
② Select ROI



③ UV-Cleave



④ Collect & Dispense



⑥ Count



Rich data sets of biology, region by region.

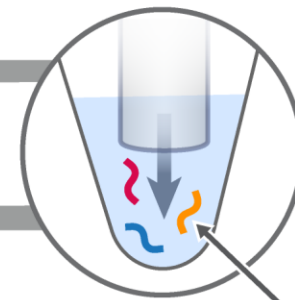
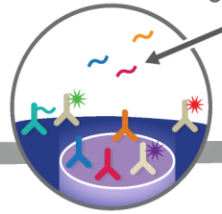
UV-photocleavable oligos

Fluorescent antibodies

Customize your regions of interest.

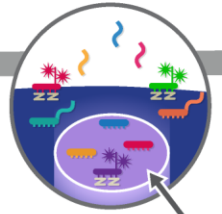


photocleaved oligos ready for collection

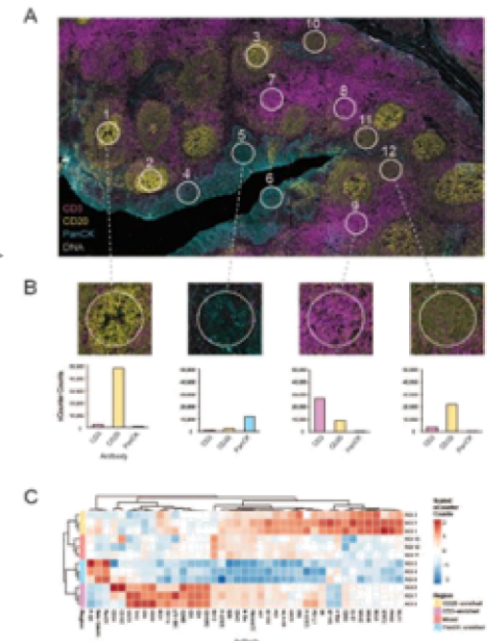


photocleaved oligos

UV light projected onto ROI from below



⑤ Repeat for each ROI



nanoString

GeoMx Region of Interest (ROI) Selection and Segmentation

GeoMx DSP Control Center
Version 2.5.0.144

Records ROI demo CRC Slide 1 CRC Slide 1 (Scanned)

Render Settings

- Enable or disable the display of each channel with the check boxes.
- Change the display intensity and colors with the sliders and dropdown.
- Undo and redo adjustments you've made with ctrl-z and ctrl-y or the buttons in the lower right.
- Revert to the default settings with the Revert button.
- Your settings will be saved automatically.

☒ **FITC/525 nm Channel - DNA**

Intensity:

Color Mapping:

☒ **Cy3/568 nm Channel - PanCK**

Intensity:

Color Mapping:

☒ **Texas Red/615 nm Channel - CD45**

Intensity:

Color Mapping:

Undo Redo Revert

Slot 1 Inactive Slot 2 Inactive Slot 3 Inactive Slot 4 Inactive

ROI Selection tools

Render settings

Protein reagents
Oligo-labeled antibodies

Target antibody DSP barcode Photocleavable linker

RNA reagents
Oligo-labeled probe

Target complementary sequence Photocleavable linker DSP barcode Target RNA

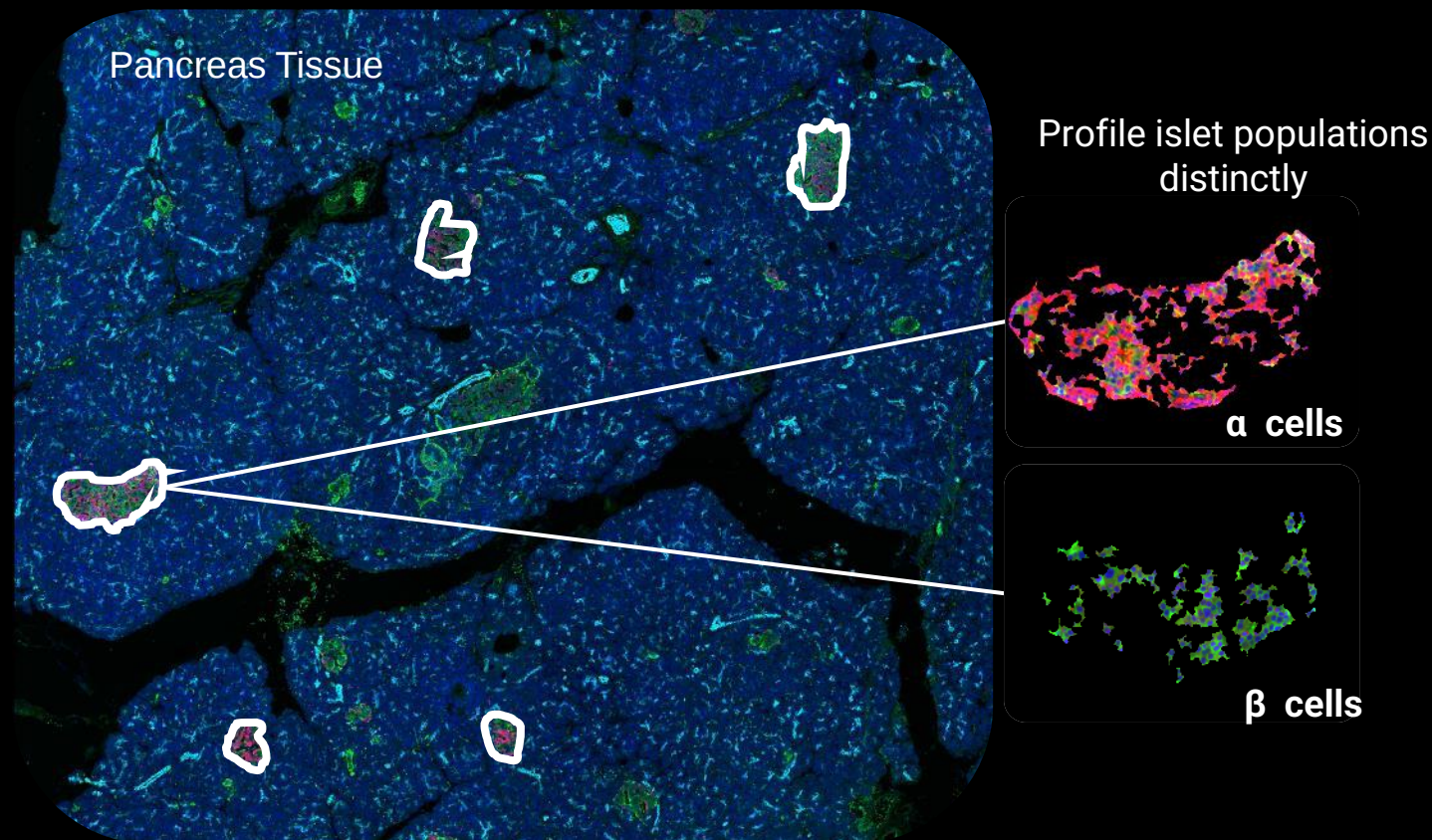
Geometric Segmentation Cell Type Specific Contour Gridded

Minimize Dashboard

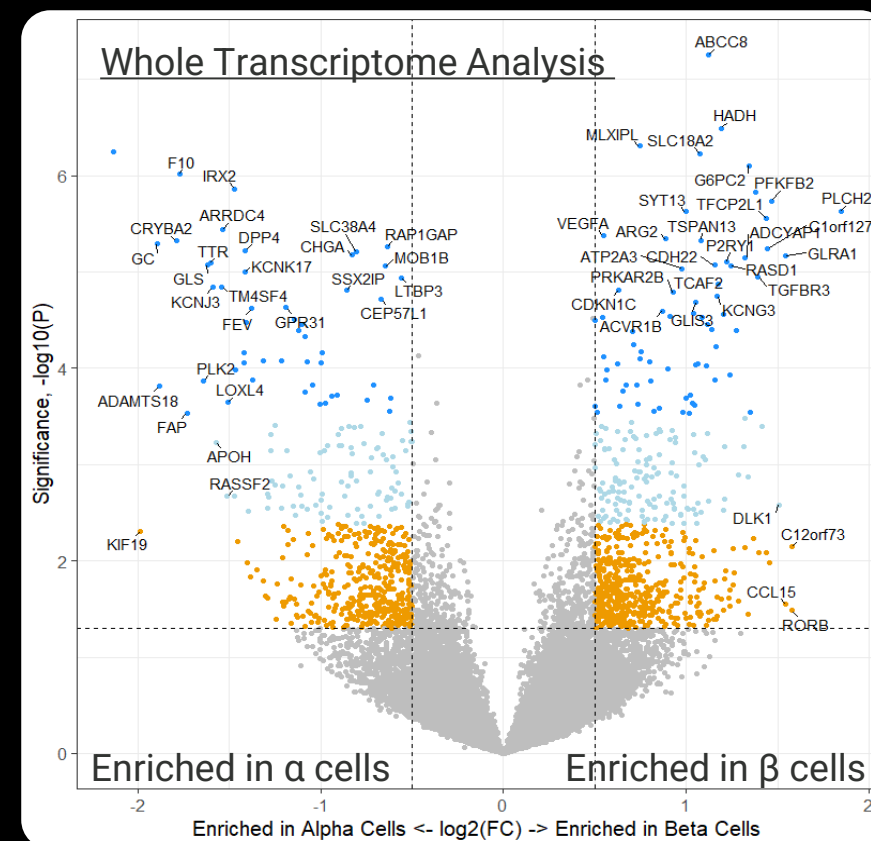
Note: The GeoMx DSP Control Center ensures that all recorded data is accurate and reliable.

Focus on the biology of interest and maximize discovery with whole transcriptome exploration (WTA Assay)

What genes are differentially expressed in alpha and beta cell populations in the Islets of Langerhans?



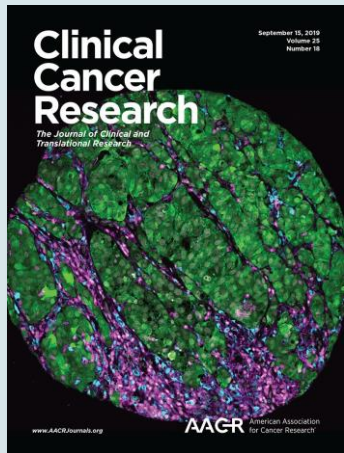
Biology Driven ROI Selection of Pancreatic Islets



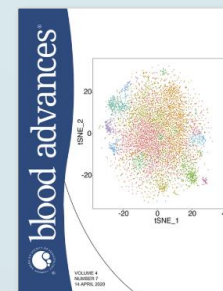
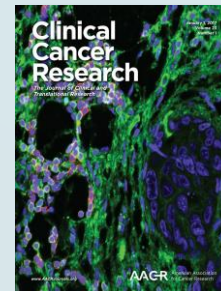
>8000 genes detected

GeoMx® Validated in 400+ Peer-Reviewed Publications

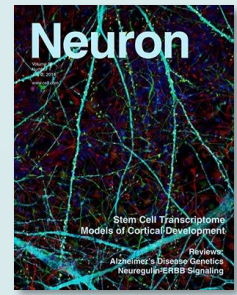
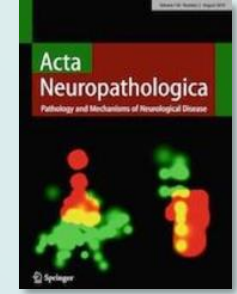
GeoMx Covers



Immuno-oncology



Neurology



Infectious Dis.



Introducing the GeoMx[®] IO Proteome Atlas (IPA)

The most comprehensive spatial proteomics panel



- Covers virtually every IO protein target in the world's largest IHC-compatible antibody catalog – Abcam ***clone list available***
- 570+ protein targets across cancer, metabolism, infectious disease, organ transplant, epigenetics, autoimmunity, and post-translational modifications
- Curated by IO subject matter experts
- Comprehensive coverage of the Hallmarks of Cancer, across 77 functional pathways
- Ability to add up to 40 of your own protein targets

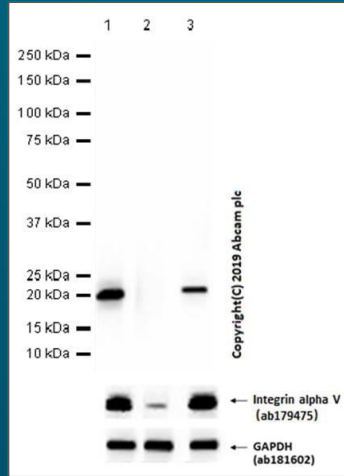
nanoString

GeoMx® IPA delivers results you can trust

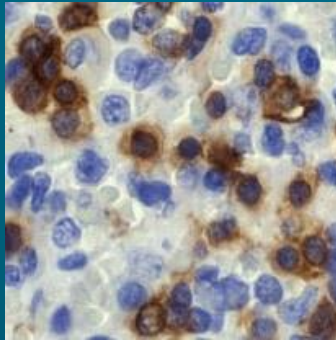
Independent functional validation of reagents using orthogonal methods

Single-plex IHC validation by Abcam

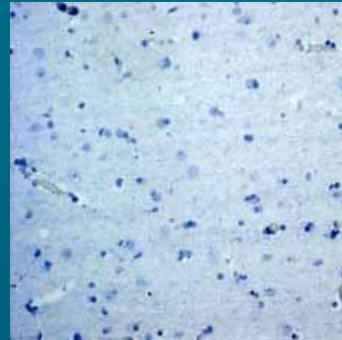
CD3e (Clone ID: EP449E)



Western Blot



Positive IHC staining in Normal spleen tissue



Negative IHC staining in Normal brain tissue

Multiplex validation by NSTG

Measured on 90 pellet CPA and an FDA-approved screening array (TMA) with tumor and normal tissues.

Assessed:

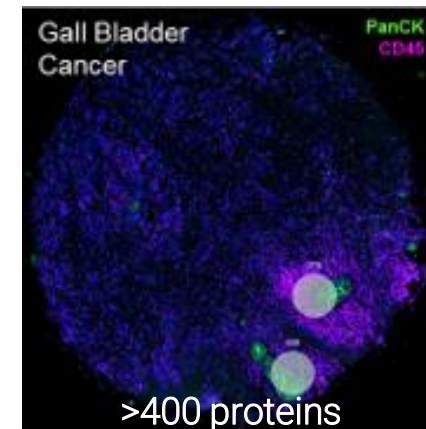
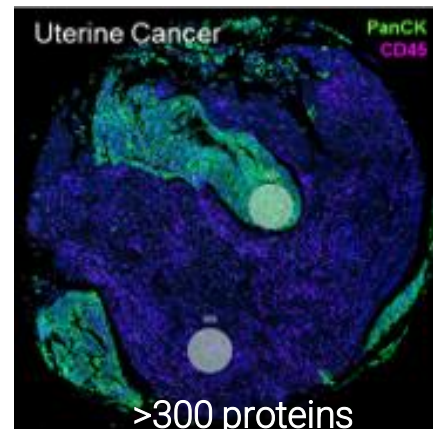
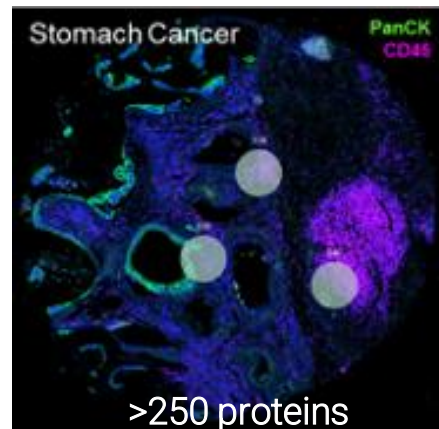
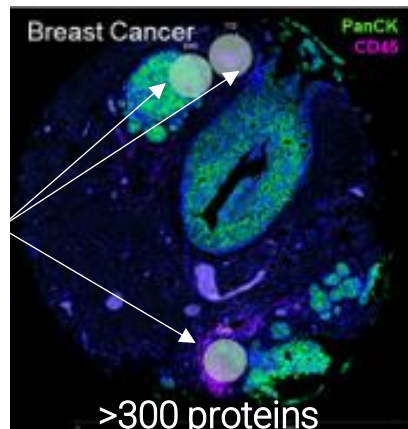
- Clear positive signal in positive control cells & tissues
- Clear negative signal in negative control cells & tissues
- Phospho-specific antibodies also validated using established models, including phosphatase inhibitor treatment prior to fixation



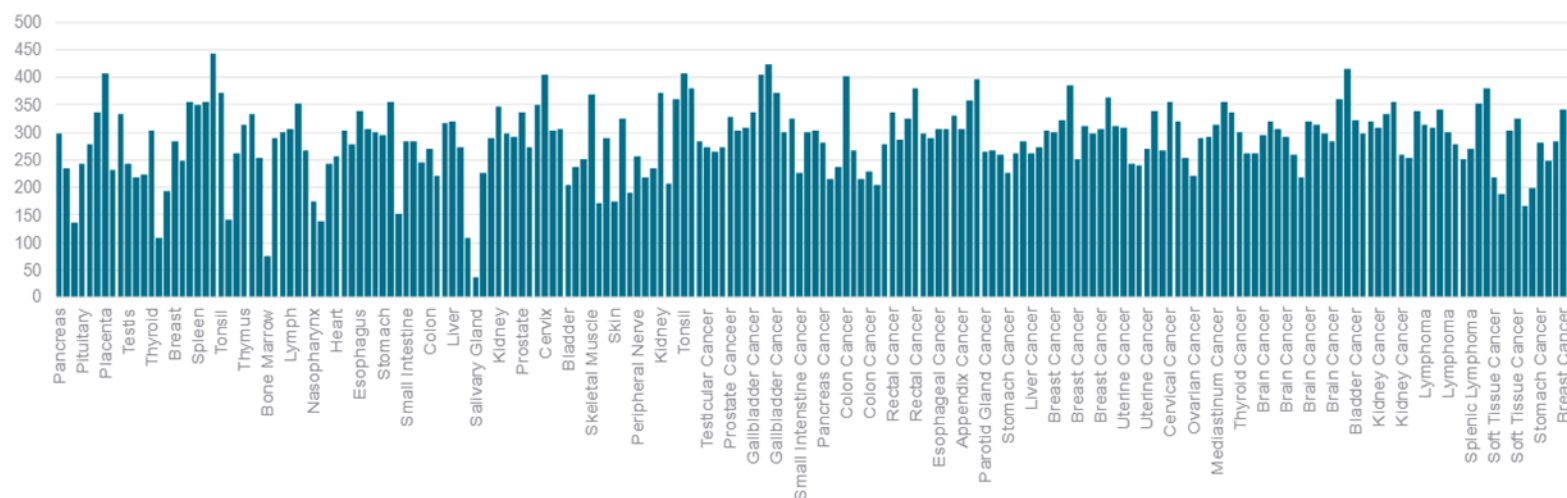
GeoMx DSP has the highest plex spatial protein assay in the world to discover previously unexplored biology across any tissue and disease

Profile 570+ protein targets from each tissue section: *Discover the next PD-L1 biomarker*

Regions of interest



Proteins detected
per AOI per Tissue Type



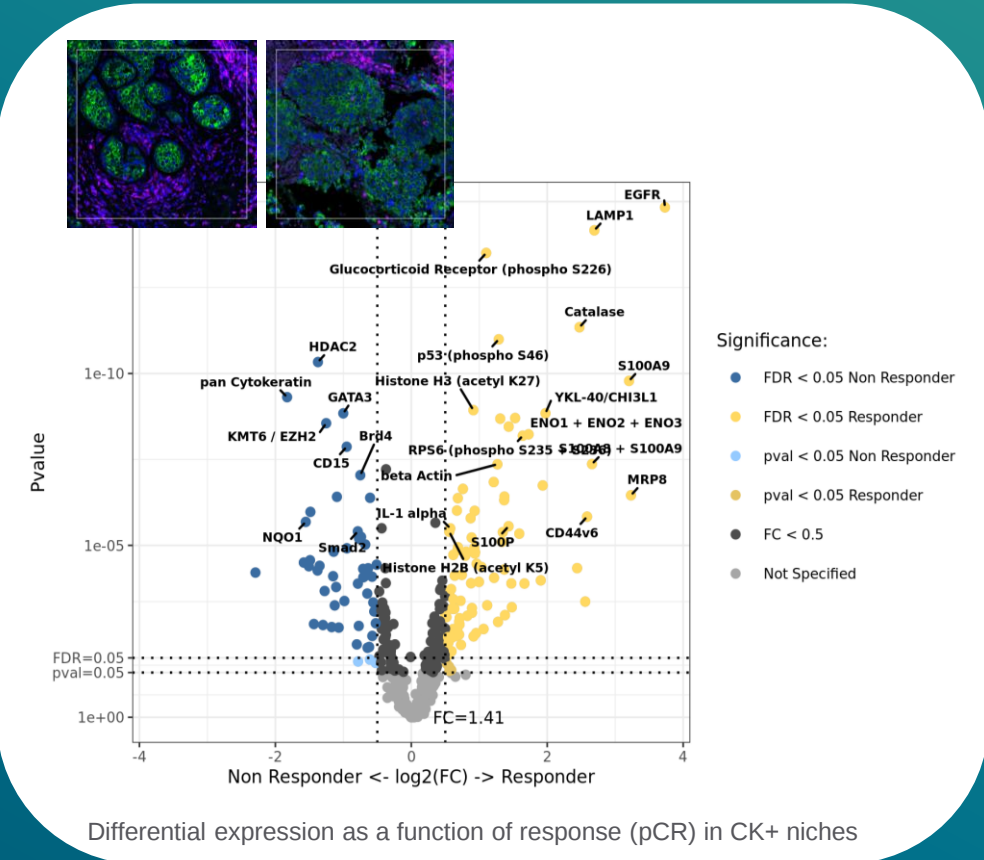
GeoMx IPA Reveals Novel Protein Markers with Implications for Patient Stratification

Clinical early stage HER2+ breast cancer tumor biopsies for responders and non-responders to neoadjuvant (TCHP)-treatment were analyzed using the GeoMx IPA.

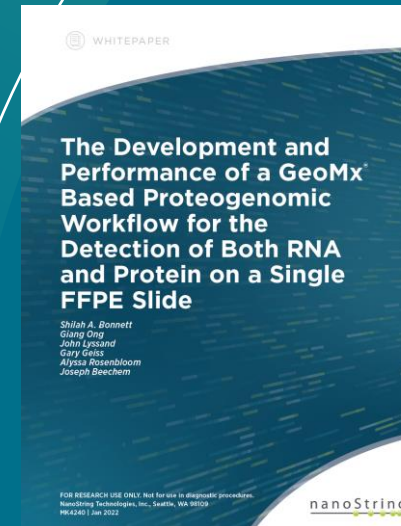
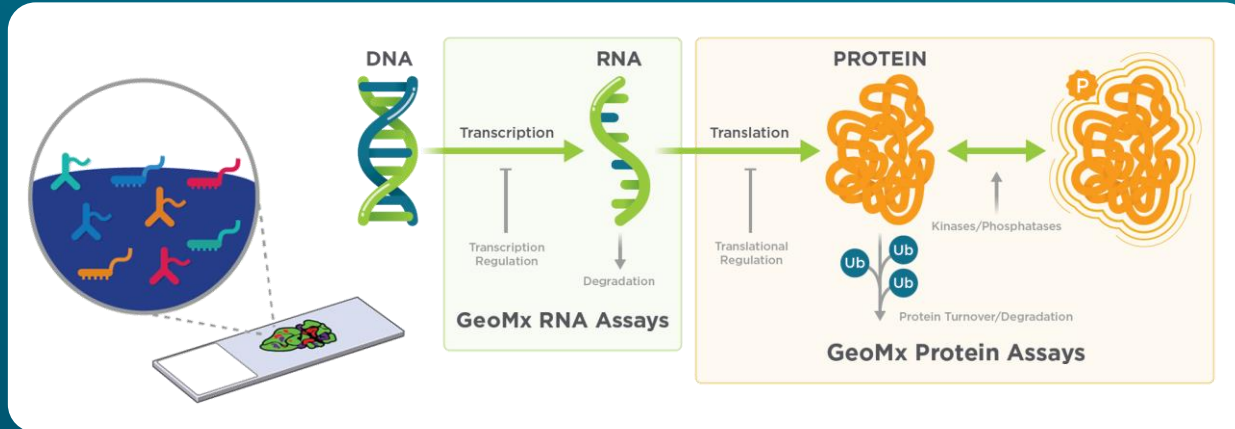
- GeoMx IPA data revealed:
 - New and "provocative" protein biomarkers with potential implications for patient stratification.
 - Clear differences in the phospho-protein profiles of responders vs non-responders.
 - Enrichment of proteins associated with the ERBB signaling pathway in responders.
- GeoMx® IPA data showed concordance with CosMx 1K-plex RNA data.



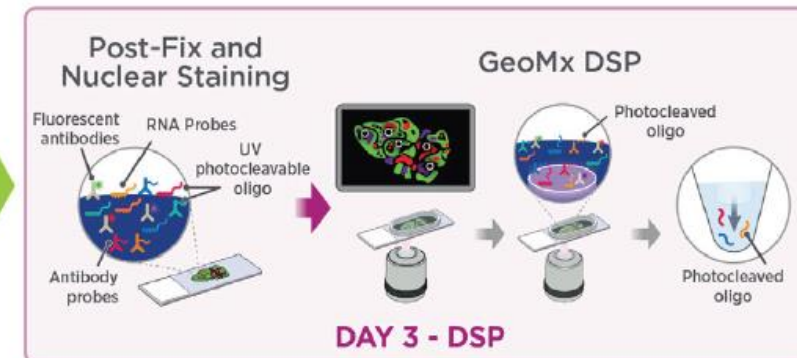
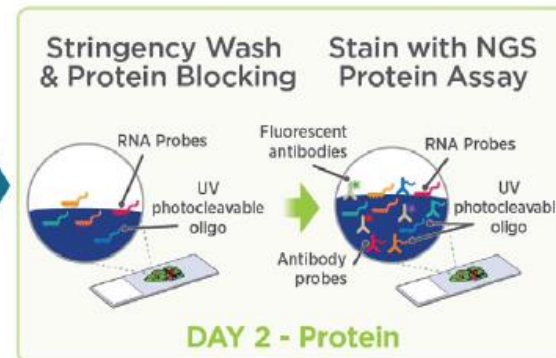
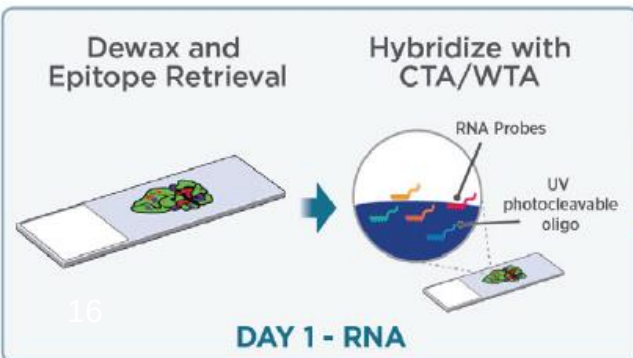
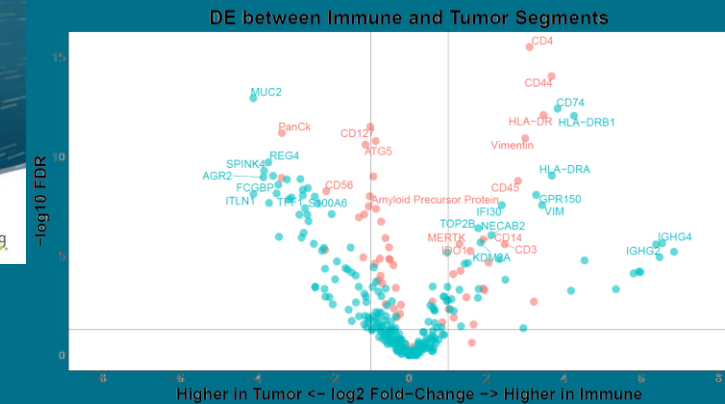
E. Aubrey Thompson, PhD
Professor
Mayo Clinic



GeoMx Spatial Proteogenomics: Assay RNA and Protein on same slide!



White Paper Showcases Highest Ever Protein and RNA Detection From a Single FFPE Section (WTA + IPA)

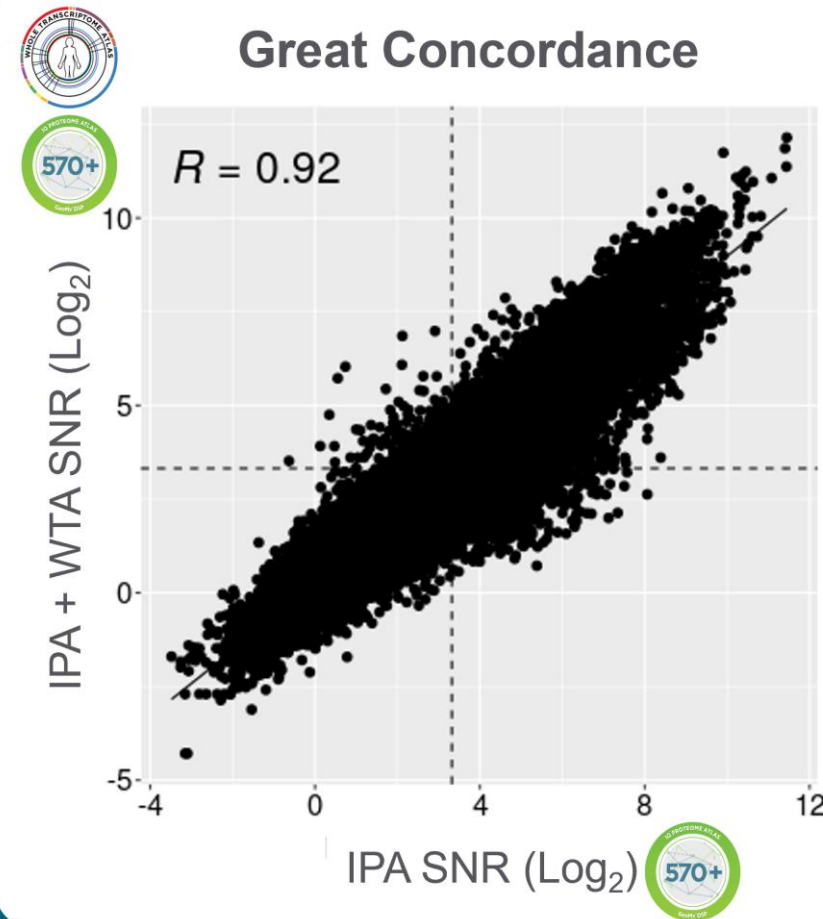


IPA assay performance remains consistent for IPA *alone* and IPA + WTA

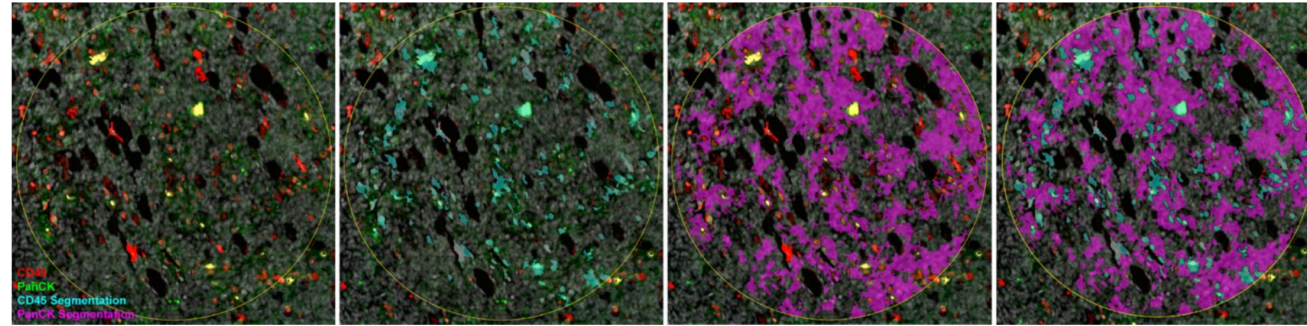
Similar SNR Distribution Pattern



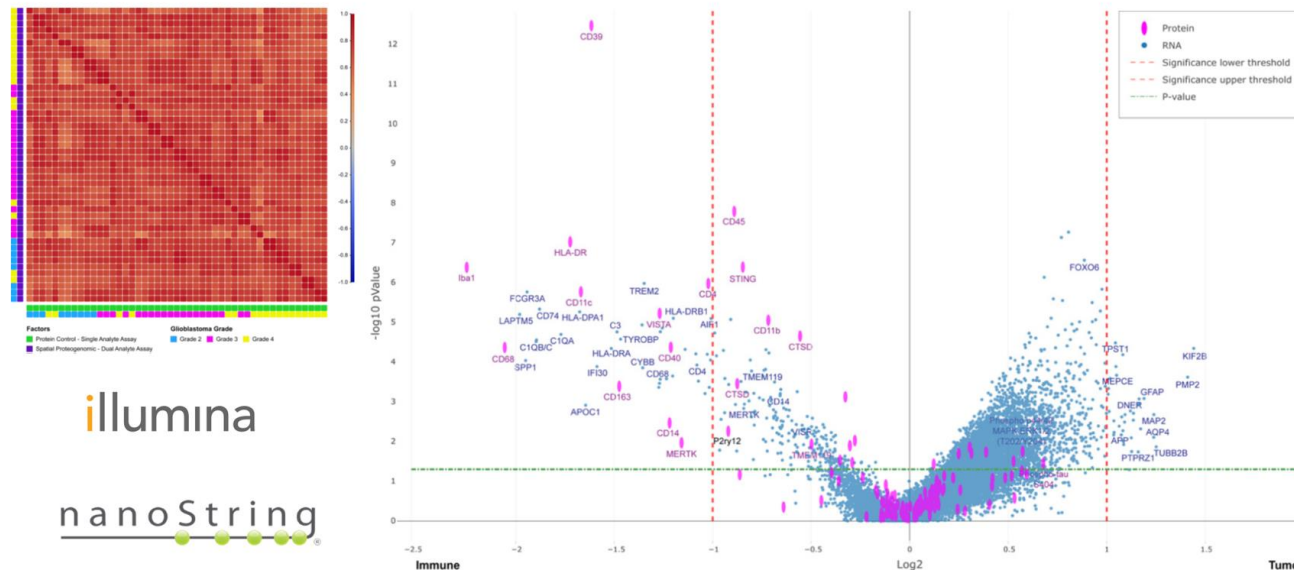
Great Concordance



Spatial Proteogenomics: Co-detection of whole transcriptome and 570 proteins



Human Grade 2-3 astrocytoma (n=12, n=20) and Grade 4 glioblastoma (n=16)



illumina
nanoString

Highest Ever Protein and RNA Detection From a Single FFPE Section

- Detection of Cell Composition and Function

Spatial Proteogenomics Drives Research Further

- Novel workflow saves precious samples and enables researchers to study the relationship between RNA and Protein

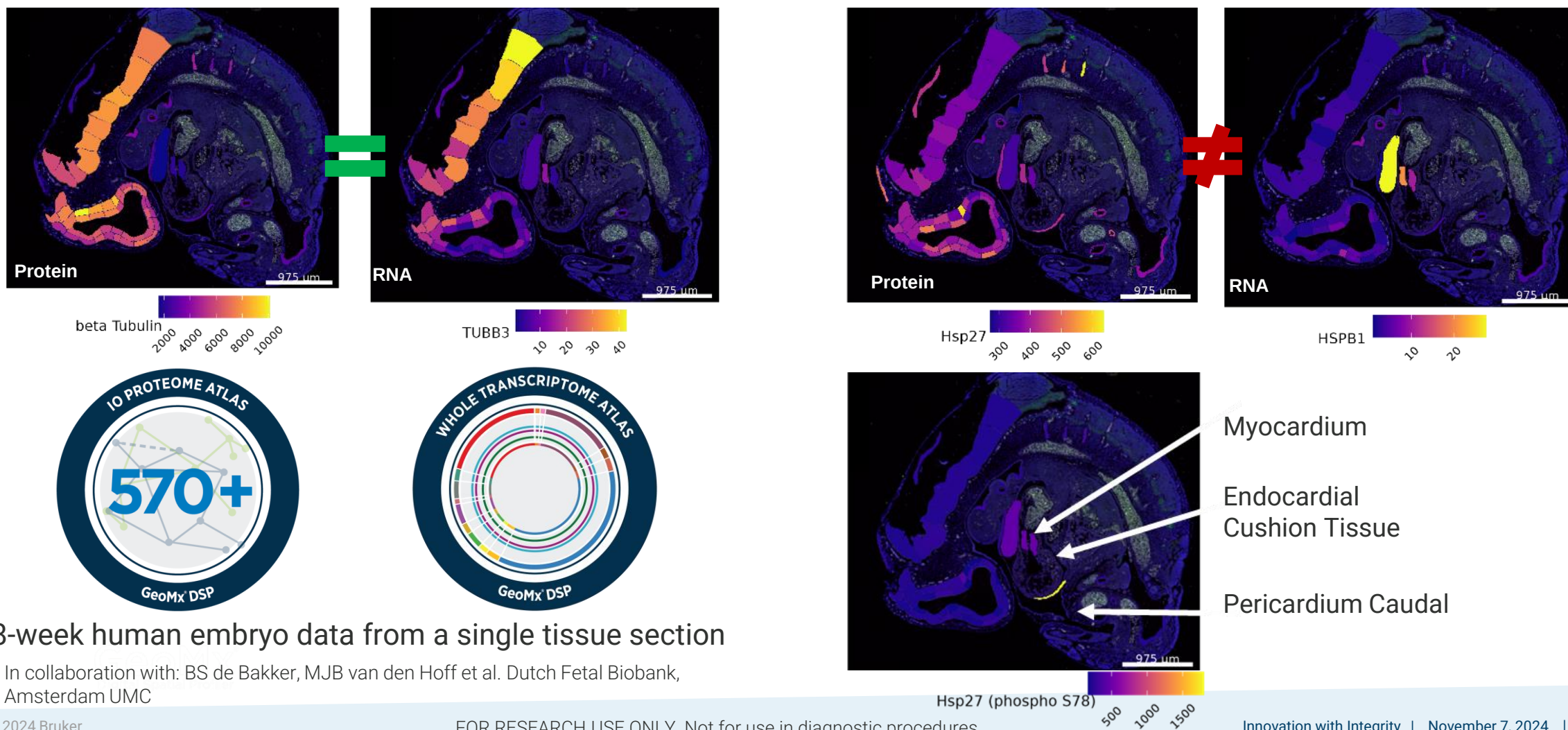
RESEARCH ARTICLE <https://doi.org/10.1158/2767-9764.CRC-22-0396> OPEN ACCESS

Ultra High-plex Spatial Proteogenomic Investigation of Giant Cell Glioblastoma Multiforme Immune Infiltrates Reveals Distinct Protein and RNA Expression Profiles

Shilah A. Bonnett¹, Alyssa B. Rosenbloom¹, Giang T. Ong¹, Mark Conner¹, Aric B.E. Rininger¹, Daniel Newhouse¹, Felicia New¹, Chi Q. Phan¹, Saskia Ilcisin¹, Hiromi Sato¹, John S. Lyssand¹, Gary Geiss¹, and Joseph M. Beechem¹

The only spatial platform to interrogate the whole transcriptome and high-plex protein discovery from the same slide simultaneously

Interrogate correlative and post-translational dynamics all from a single precious section



FFPE Tissue from the Influenza Epidemic of 1918 (>100 years old!)



Uncoupling pathways involved in immunotherapy resistance: insights from deep tissue profiling

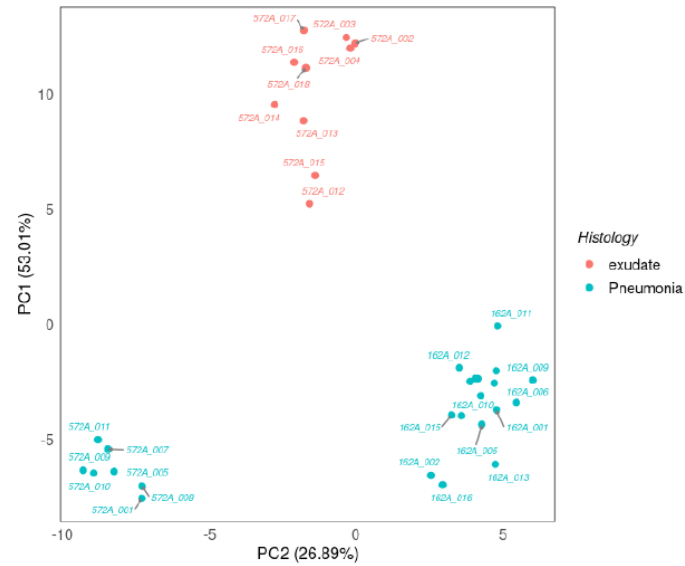
Arutha Kulasinghe, Ph.D.
Queensland University

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

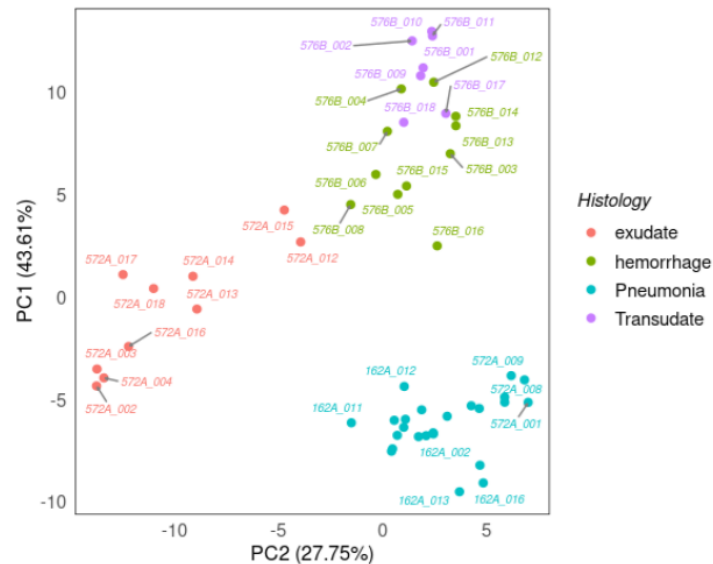
nanoString

IPA (570-plex protein), WTA (18,000-plex RNA)

PCA of genes in regions of 1918 influenza virus-infected lungs

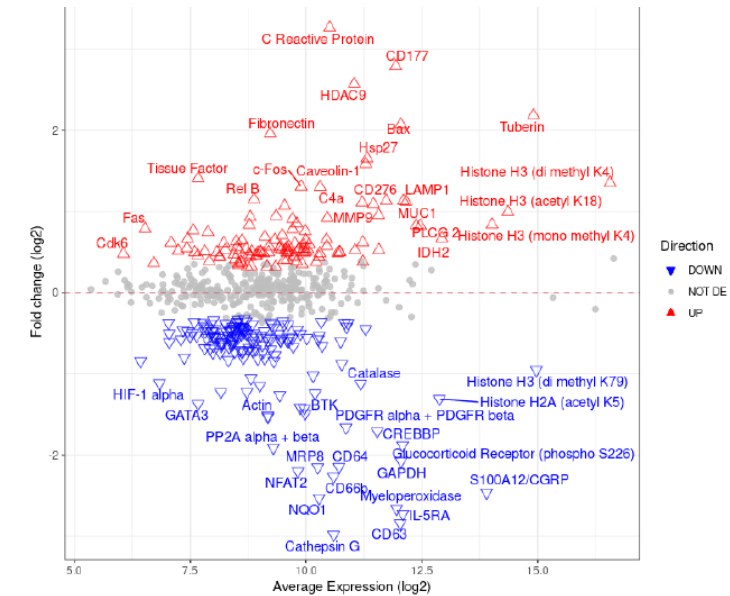


PCA of proteins in regions of 1918 influenza virus-infected lungs



Uncoupling pathways involved in immunotherapy resistance: insights from deep tissue profiling

Arutha Kulasinghe, Ph.D.
Queensland University



GeoMx[®] DSP for robust tissue exploration

UNBIASED PLEX MULTIOMICS

Measure whole transcriptome and 570+ proteins on the same slide

BIOLOGY-DRIVEN

Profile meaningful regions to minimize noise and simplify analysis

HIGH SENSITIVITY

Detect low, medium, and high expressors with 5 logs of dynamic range

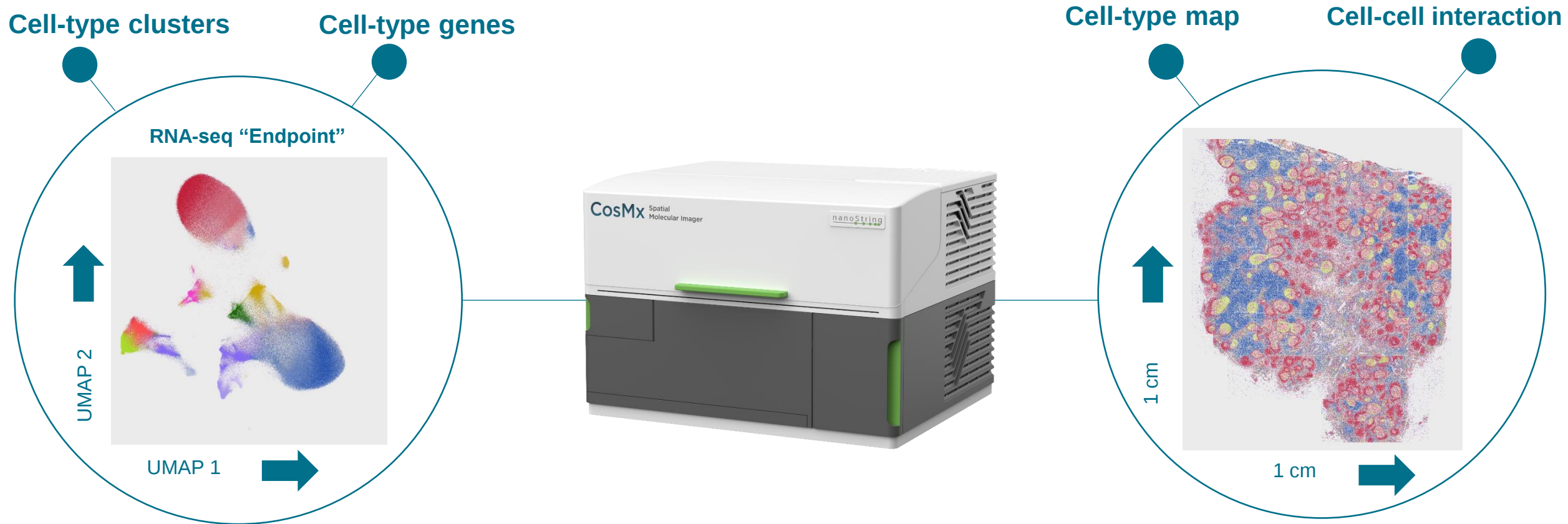
SCALABLE THROUGHPUT

Process up to 4 slides at a time and scale with automated workflows

ANY SAMPLE

Analyze FFPE, FF, Whole Mount, TMA, organoid

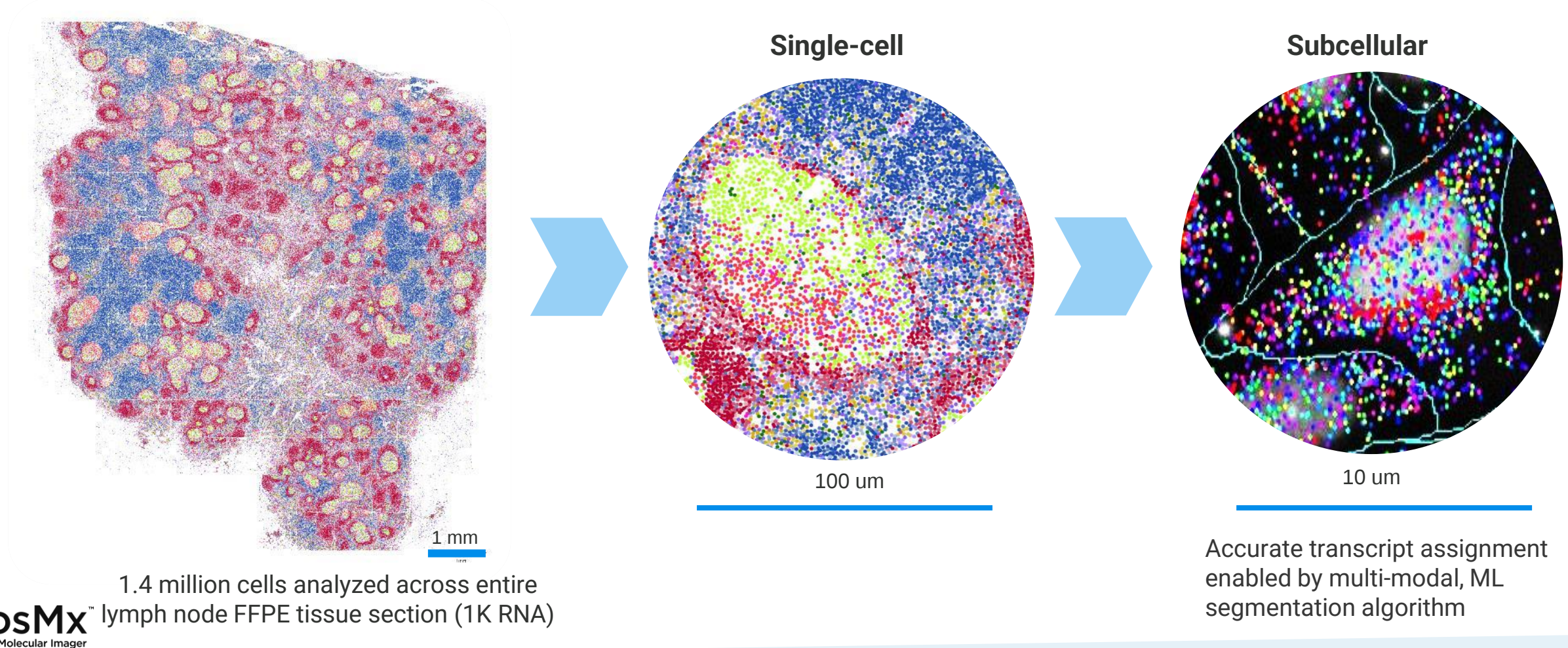
Advancing from scRNA-Seq to Spatially-Resolved Single-Cell (CosMx™ SMI)



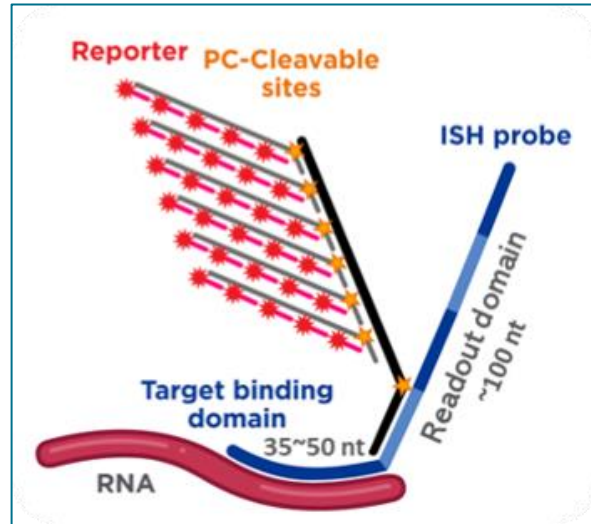
CosMx SMI: the highest-plex (6000+ plex) single-cell spatial platform

Capture the story of every cell-to-cell interaction from an entire tissue section

Resolve millions of cells and billions of transcripts at single-cell and subcellular resolution

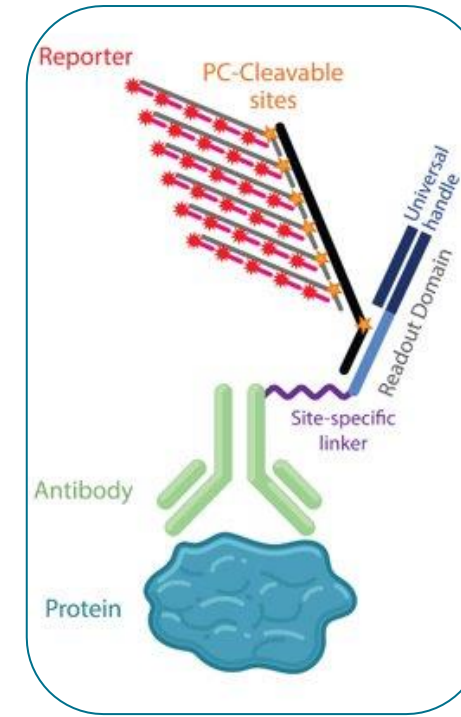


High-Plex CosMx™ RNA and Protein Panels



RNA Panels Consist of Pooled ISH Probes

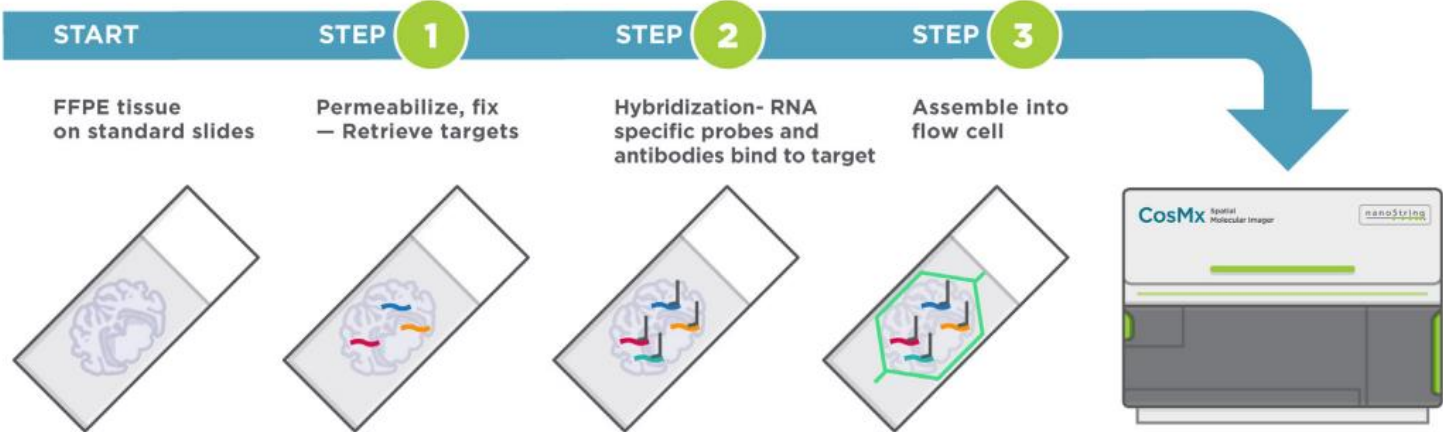
- Five ISH probes per target
- Panels include ERCC Negative Probe controls, non-target-binding
- Currently up to a commercial 6175-Plex + 200 custom targets (whole transcriptome in 2025)



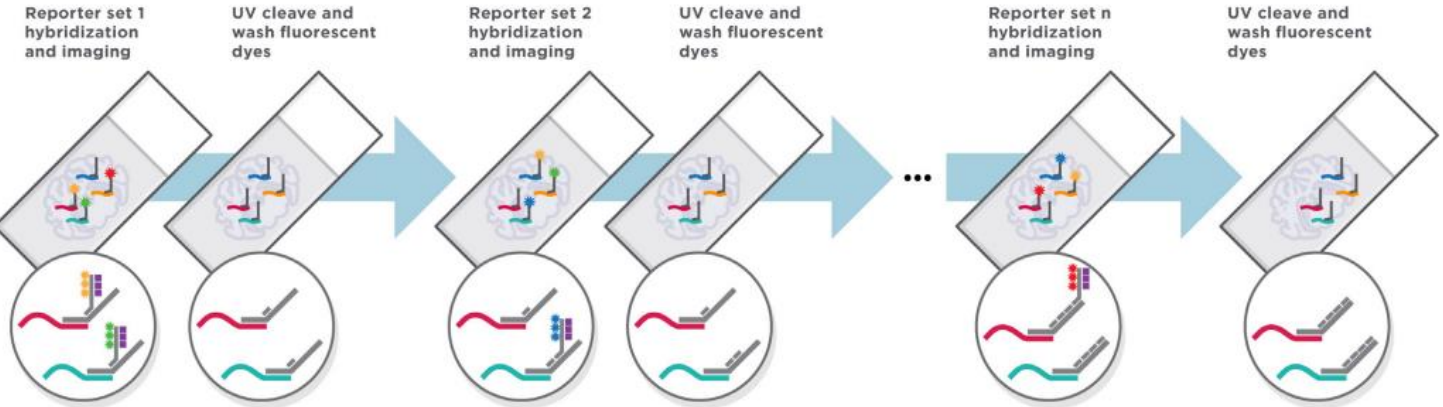
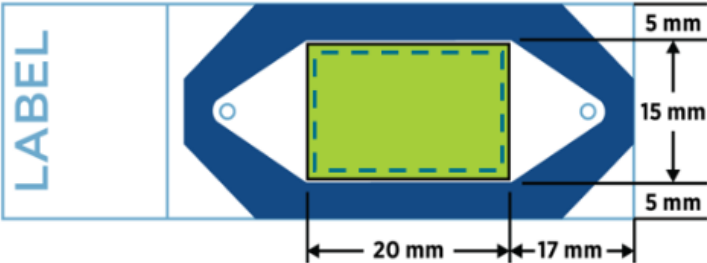
Protein Panels Consist of Pooled Antibodies

- Monoclonal antibodies w/ site-specific conjugation
- IgG controls, non-target-binding
- Currently up to 64-Plex + 8 custom targets

CosMx™ Uses Single Molecule In Situ Hybridization Chemistry with Cyclic Imaging and Optical Barcodes



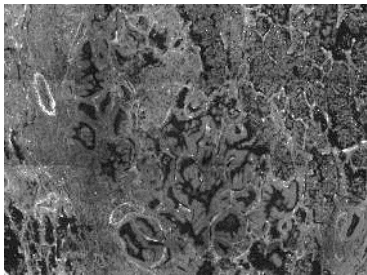
Simple and streamlined sample prep workflow.



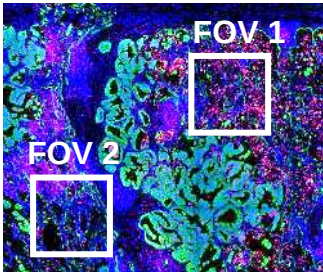
CosMx™ Spatially Resolves Molecules (*in situ* Imaging)



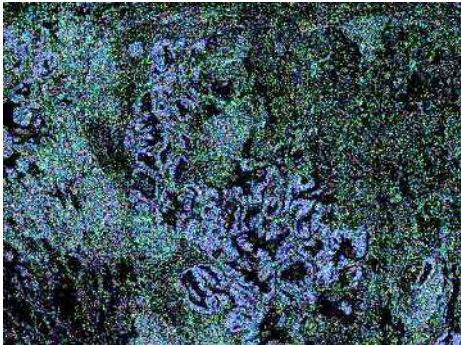
Step 0: Sample preparation and flow cell assembly



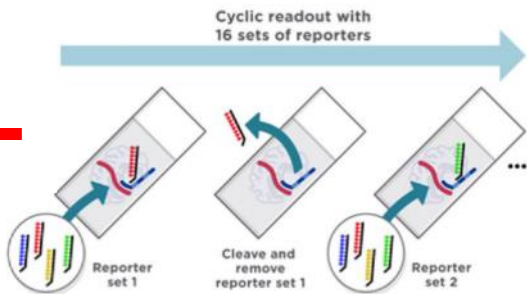
Step 1: Rapid low-resolution scan of entire tissue section



Step 2: Select Fields of View (morphology markers + nuclear stain)



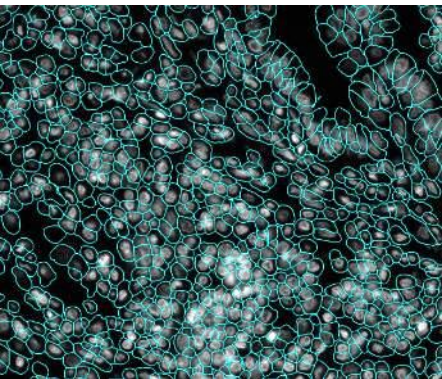
Step 3: Cyclic readout to image and quantify transcripts (up to 1000 genes)



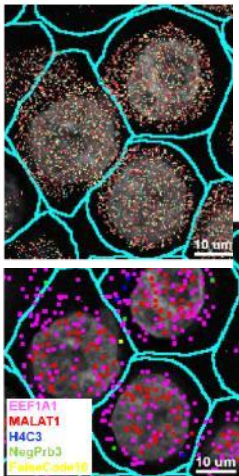
Pre-instrument

On-instrument

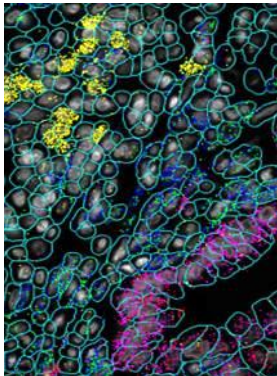
Post-instrument



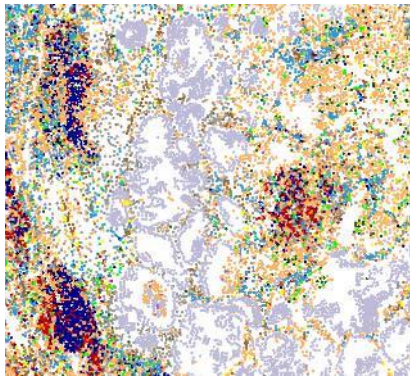
Step 4: Cell Segmentation



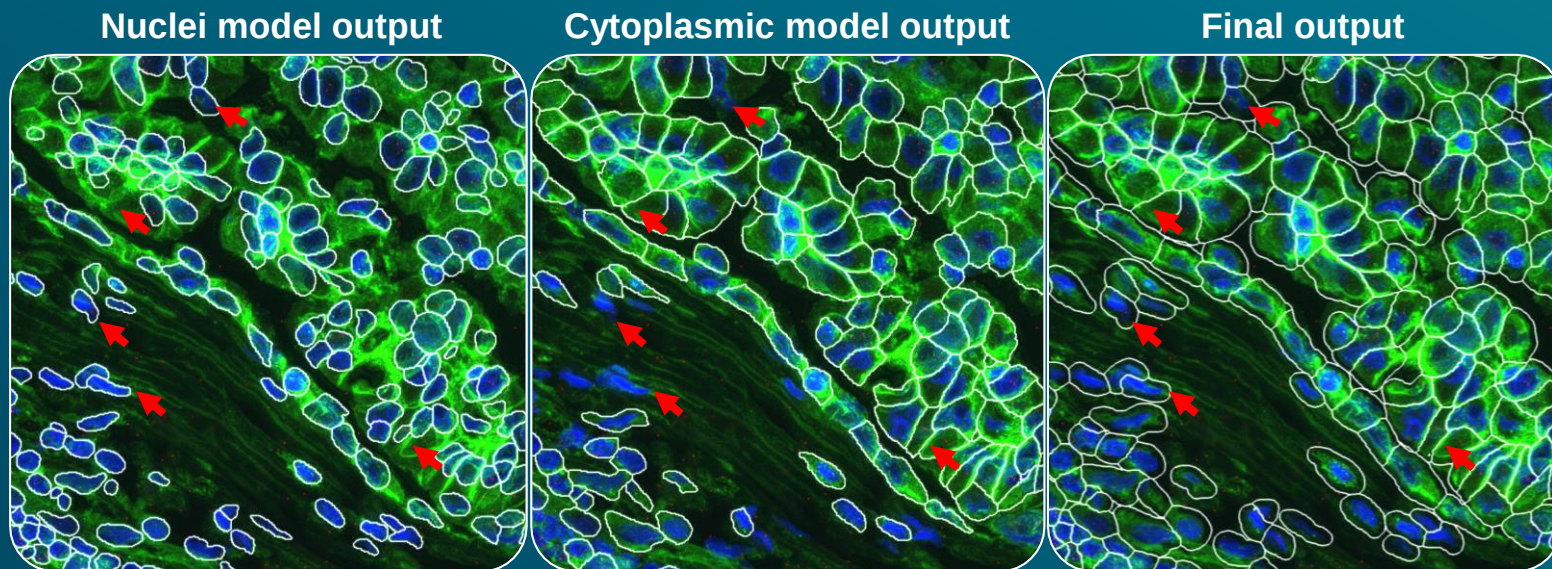
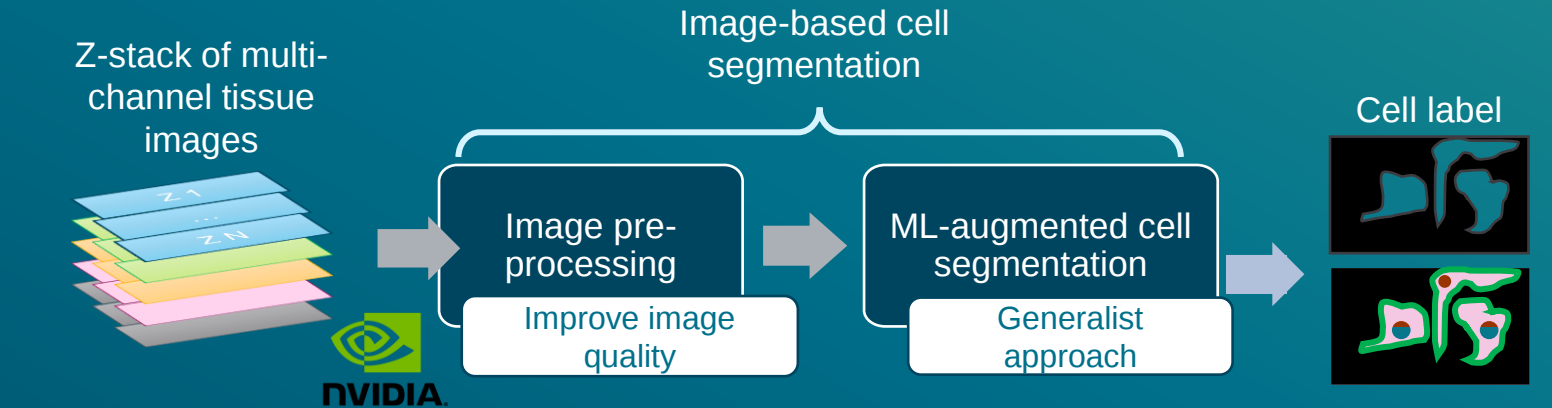
Step 5: Allocate transcripts to single cells



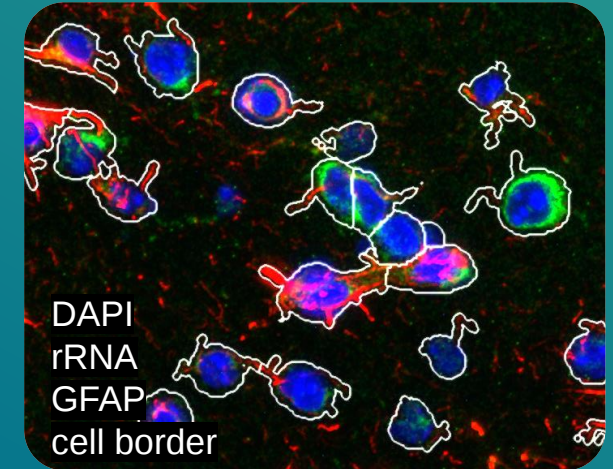
Step 6: Cell Typing and mapping



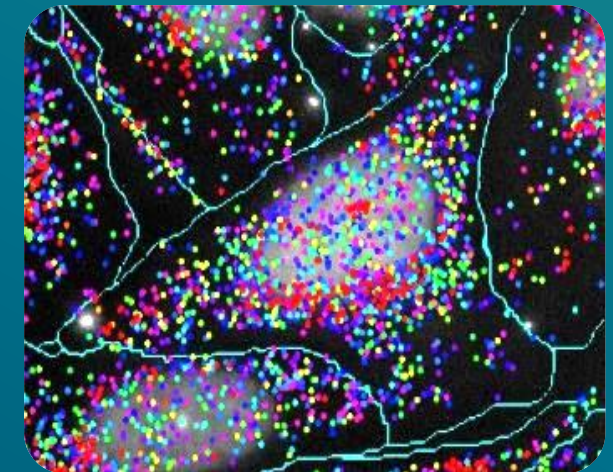
Robust segmentation of cell boundaries and compartments



FFPE renal cell carcinoma



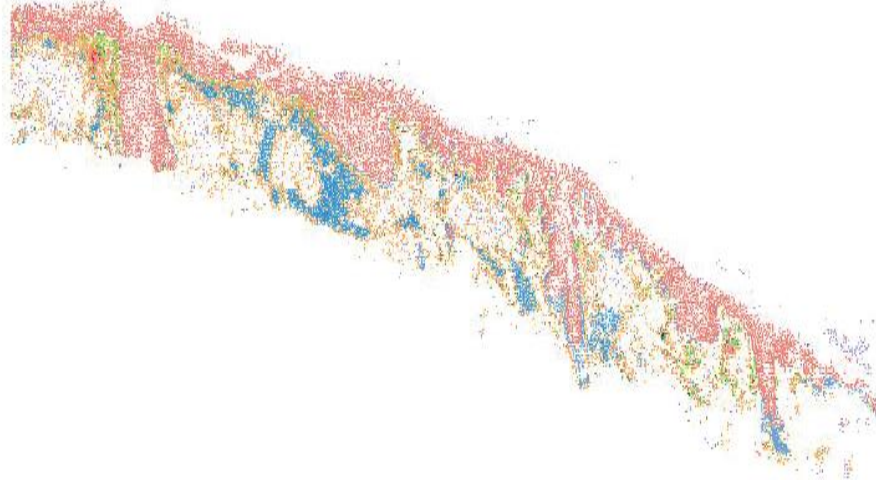
Fibroblasts



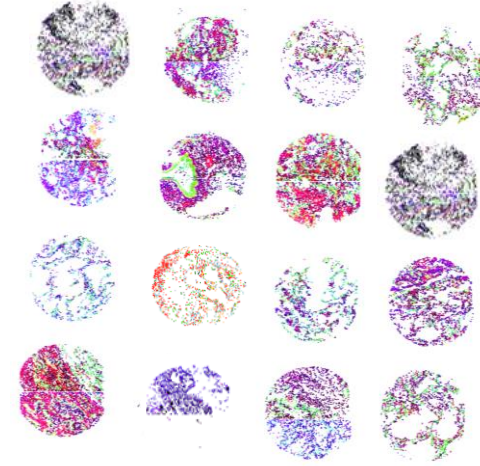
nanoString®

Generates Robust Data with All Samples: FFPE to Fresh Frozen

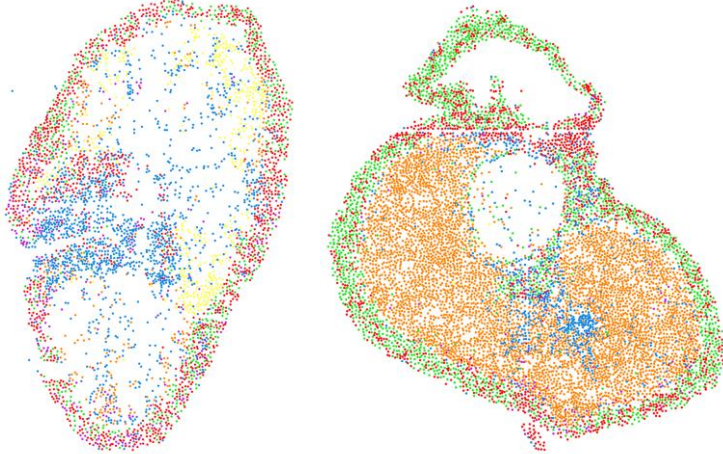
FFPE Tissue (Skin)



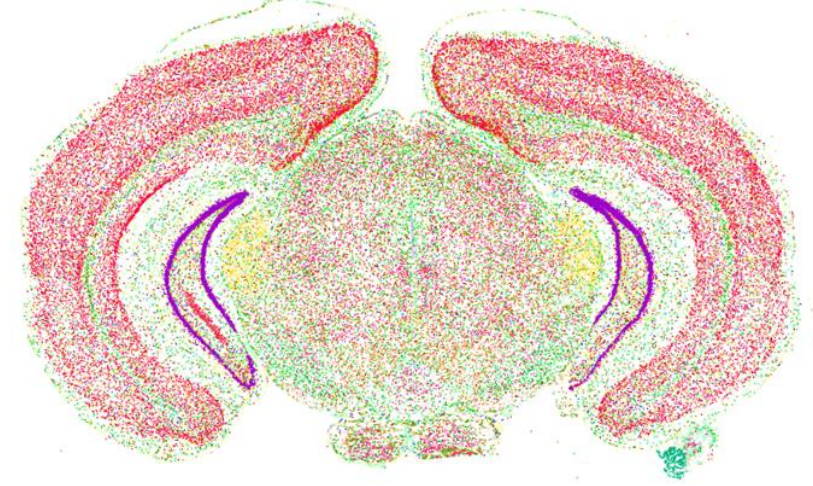
Tissue Microarray (Lung)



Organoids (Human Brain)



Fresh Frozen (Mouse Brain)

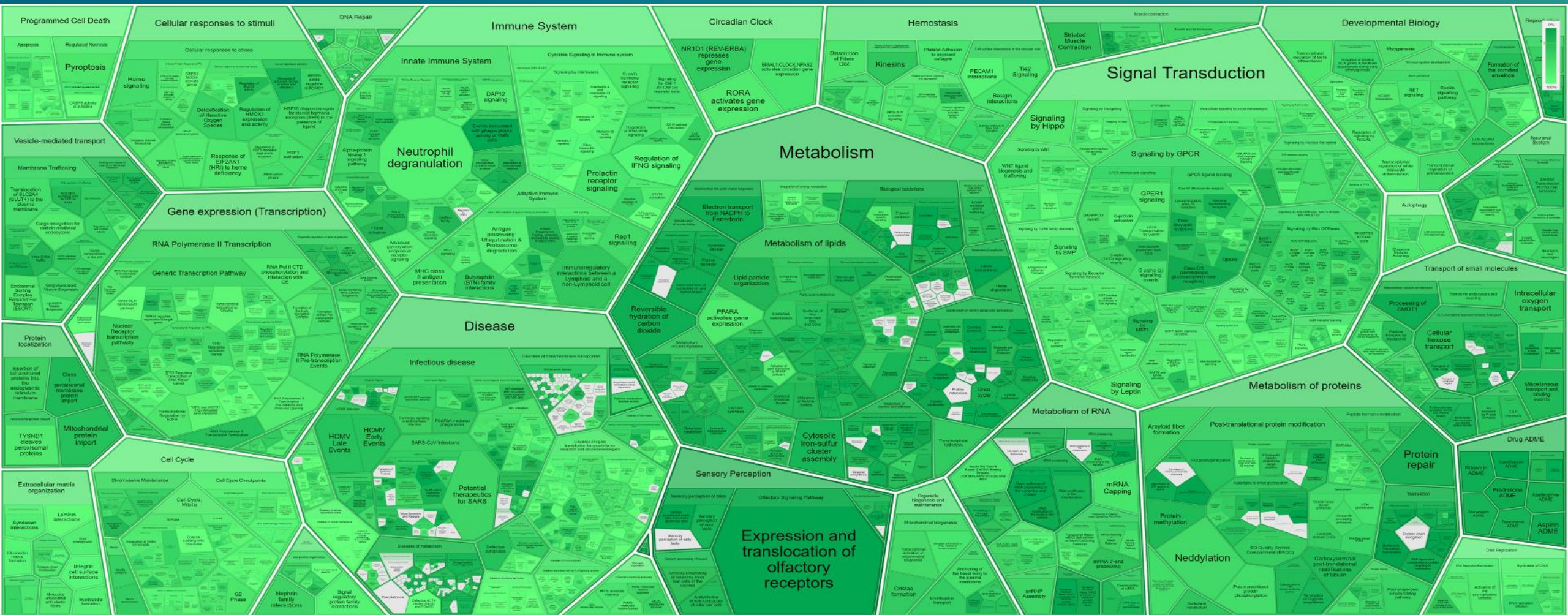


CosMx™ 6K Discovery RNA Panel



- 6175 curated RNA targets
- Customizable with up to 200 targets
- Accurate, multi-modal cell segmentation
- Compatible with wide range of tissues
- Profile nearly the entire human reactome
- Available for human tissue
- Human Neuro coverage

CosMx 6000-plex Panel: Virtually the Entire Reactome



0% 100%

CosMx
Spatial Molecular Imager

nanoString

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

CosMx™ 6K Discovery Public Dataset

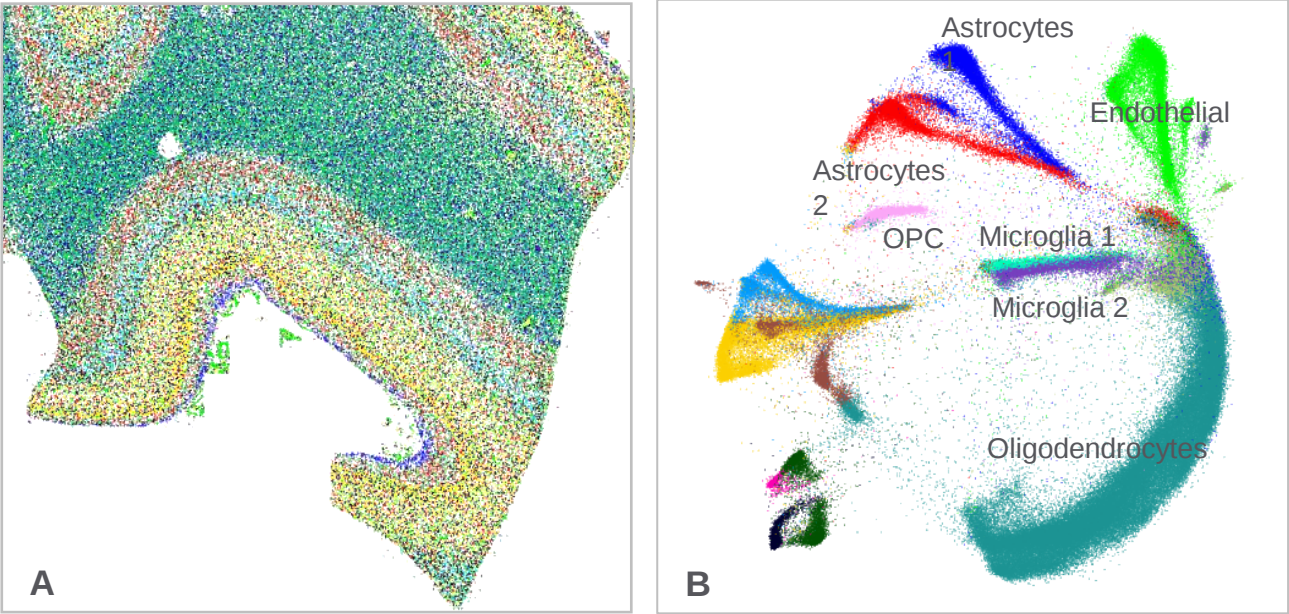
Tissue type	Human frontal cortex
Plex	6078 gene targets (Pre-commercial)
Scan area	102.7 mm ²
Total cells	194,065
% cells pass QC	97.2%
Total transcripts detected	331,132,591
% of Transcripts Assigned to a Cell	49%
Sensitivity (Mean Transcripts per cell)	839
Sensitivity (Mean transcripts/um3)	1.29
Genomic Breadth (Mean unique genes per cell)	544
Genomic Breadth (Unique genes detected above LOD)	3364
False Positives (Mean negatives/target/cell)	0.027



QR code to download 6K dataset

FOR RESEARCH USE ONLY. Not for use in diagnostic procedures.

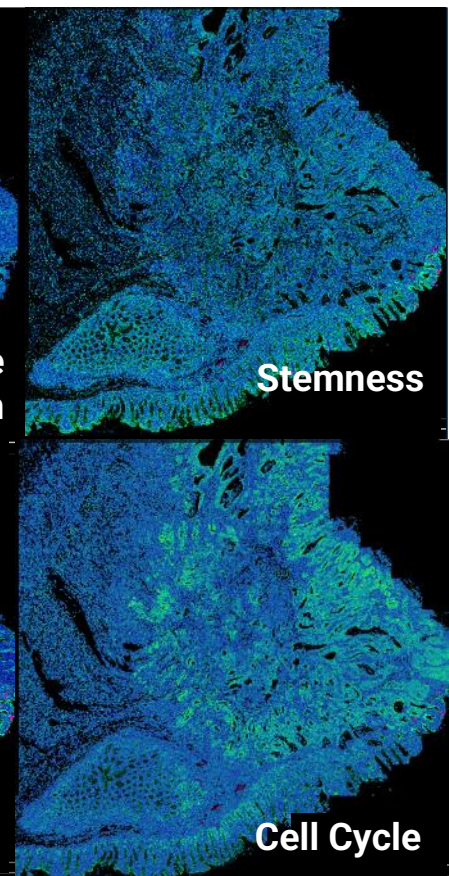
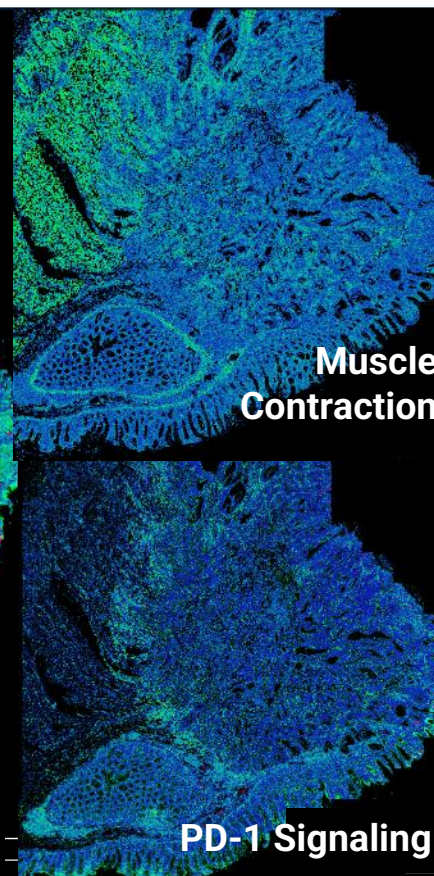
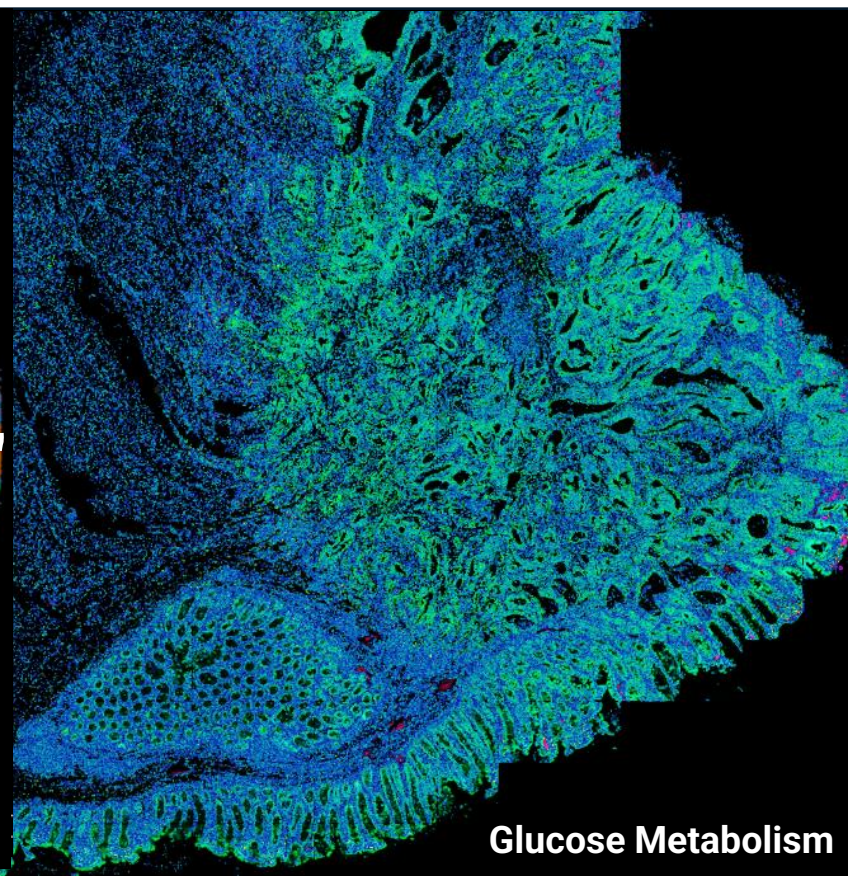
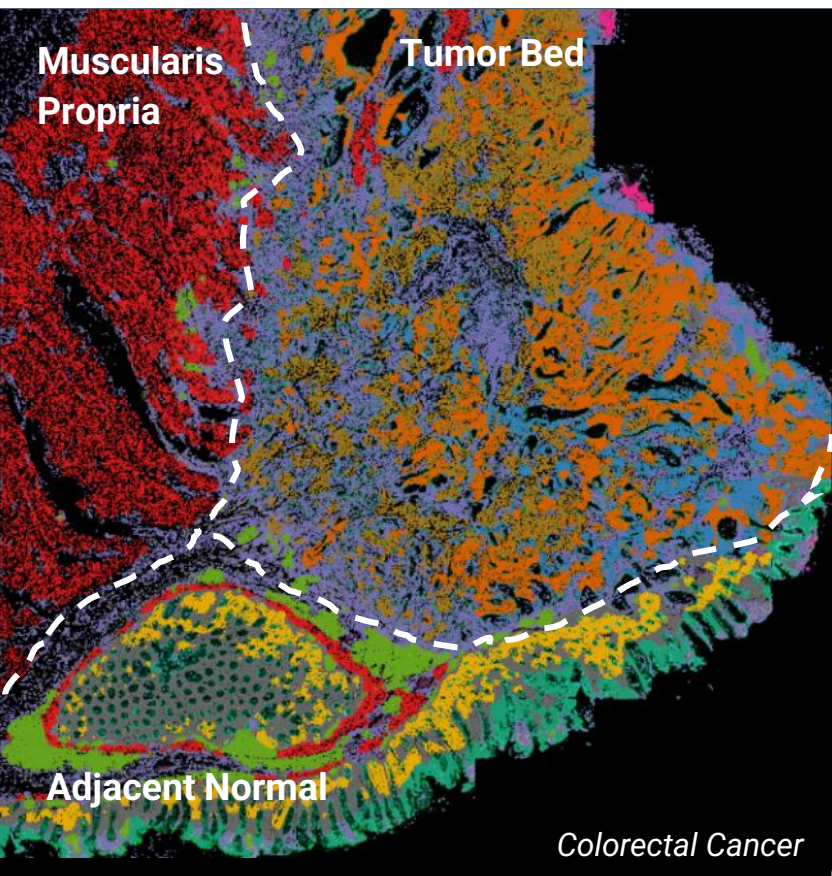
First Single-Cell Spatial Dataset with over 6000 Genes



Cell type map of human frontal cortex tissue. (A) Spatially resolved cell type map of entire tissue section. (B) UMAP projection of cell type clusters.

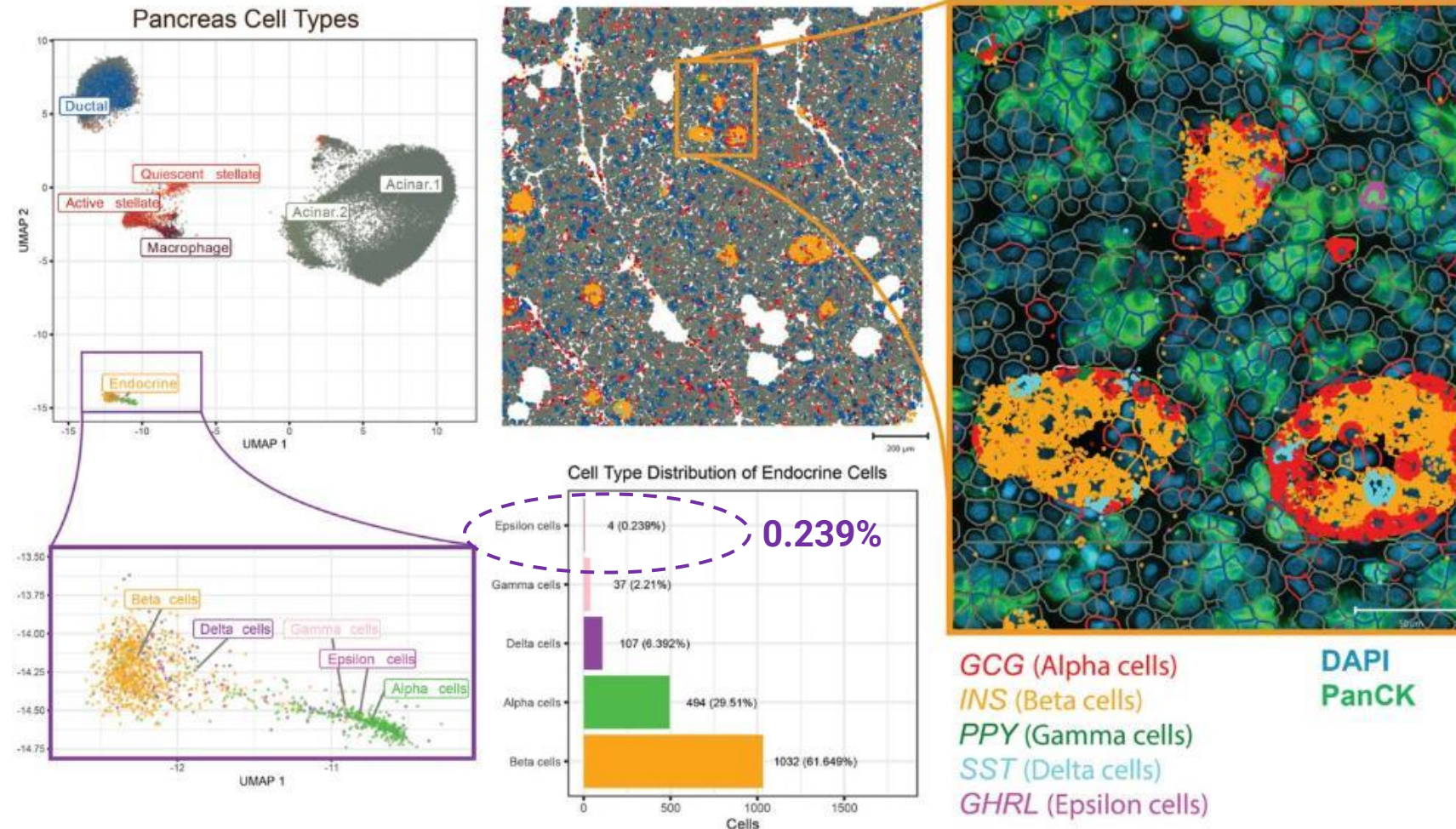
Move beyond individual gene analysis to understand functional pathways of biology at single-cell resolution

Project the Reactome directly onto tissue with CosMx 6K Discovery



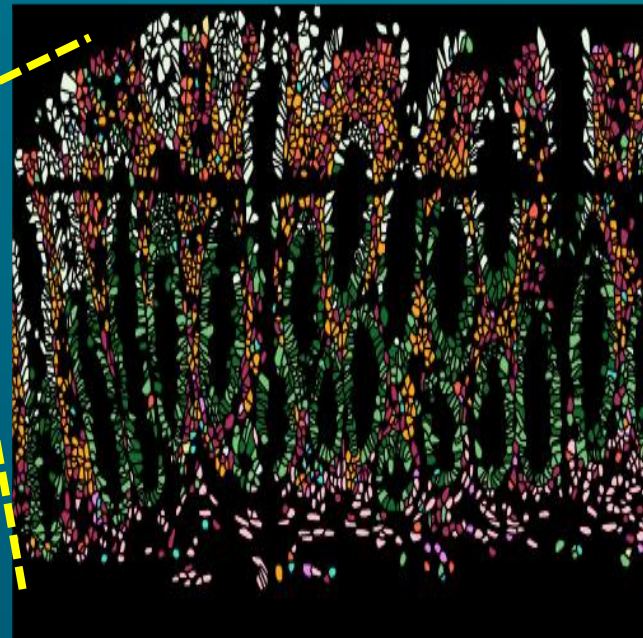
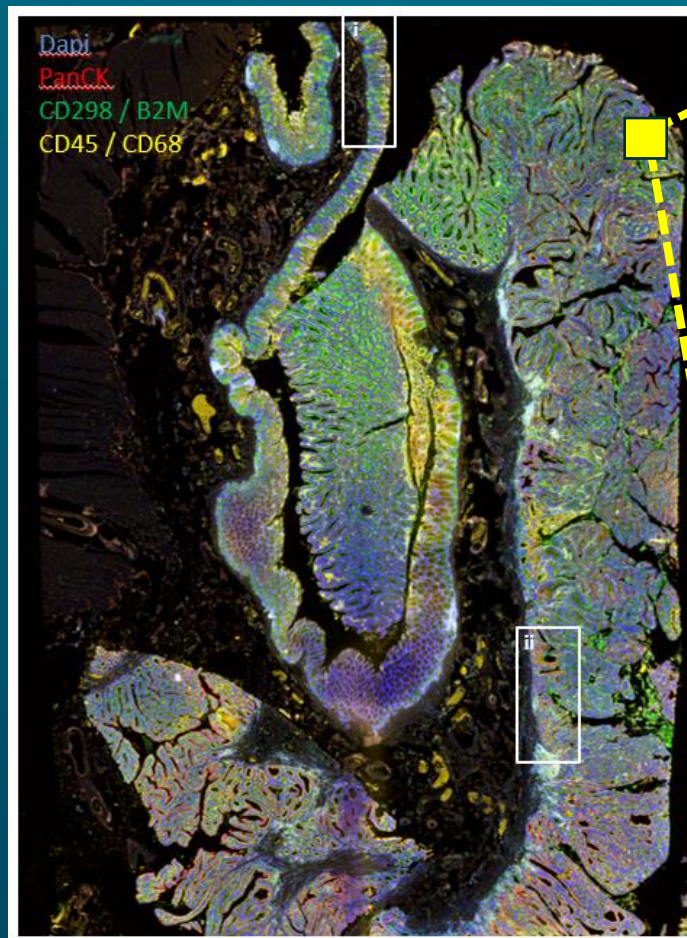
The only single-cell spatial platform to demonstrate whole transcriptome biology: FFPE public dataset available

Commercially available for the CosMx SMI in 2025



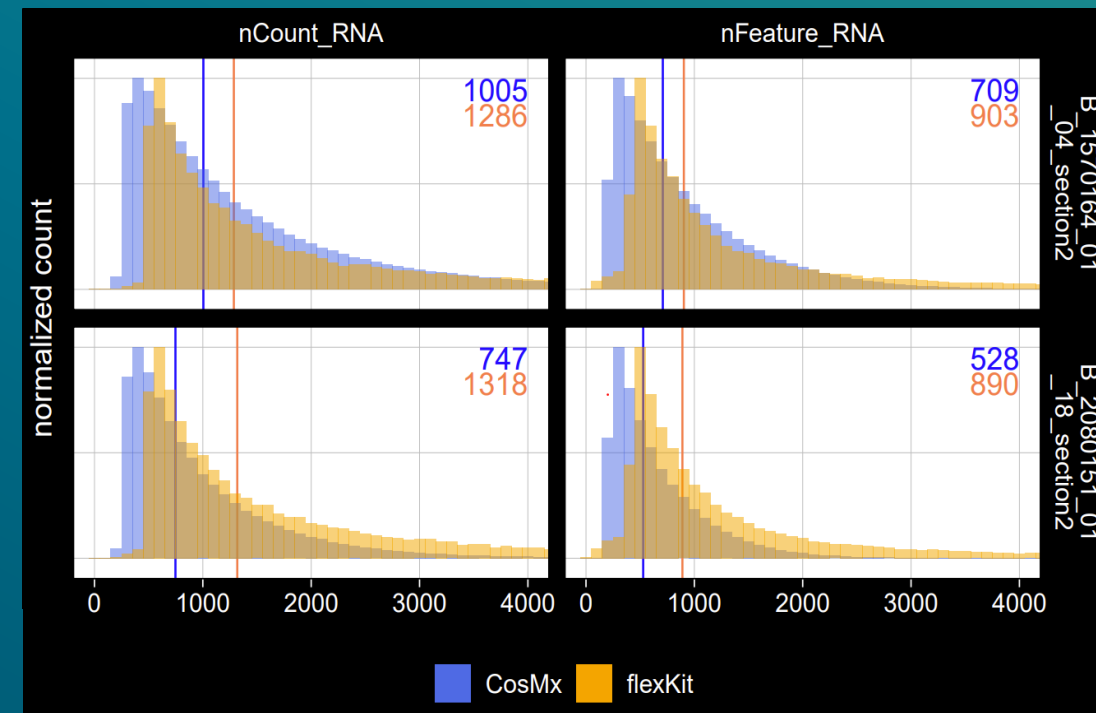
Resolve rare cell types with subcellular spatial context (healthy human pancreas)

CosMx WTx Panel: True Single-Cell Spatially-resolved Whole Transcriptome with Dr. Holger Heyn (CNAG, Barcelona)



Tubulovillous adenomas
(early CRC)

- Total single cells = 1.4 Million cells
- Transcripts = over 1.4 Billion
- Transcripts per cell > 1,000
- Close to snRNA-seq on all key metrics
- Less than 1-cent per transcriptome

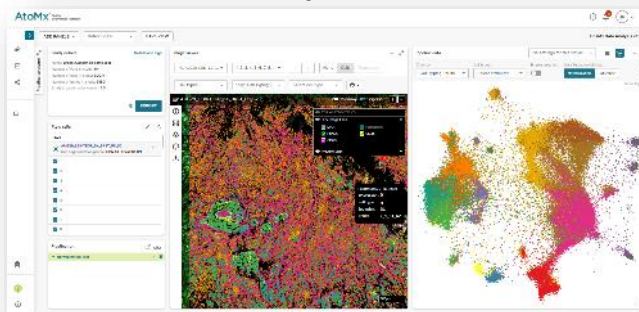


First comprehensive cloud platform for single-cell spatial informatics that scales to any plex and throughput

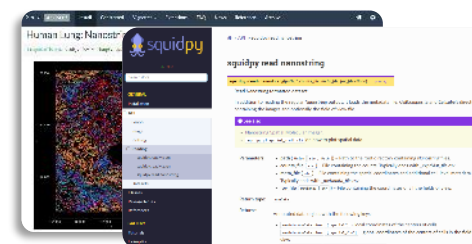
Cloud platform fully integrated with CosMx from sample to data for analysis

Demo of AtoMx
this afternoon!

Multi-sample and Iterative Analytics Suite



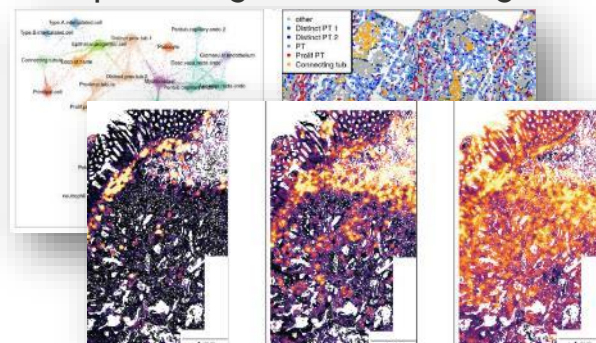
Opensource Portable and Flexible Data formats



Tunable Machine-learning Cell Segmentation Toolkit



New Spatial Algorithms for Single-cell



AtoMxTM
Spatial Informatics Platform

CosMx™ SMI for high fidelity gene expression

HIGHEST SINGLE-CELL PLEX

Broader biological insights with 6,000+ plex

ACCURATE CELL SEGMENTATION

Advanced multi-modal precision

MULTIOMICS

RNA and Protein Assays

DEVELOPED FOR FFPE

FF, TMA and organoids

EASY-TO-USE WORKFLOWS

Standard IHC with automation options

CellScape™ Precise Spatial Proteomics

Optimized for high-throughput, high-plex, spatial protein detection and quantitative phenotyping



Integrated fluidics

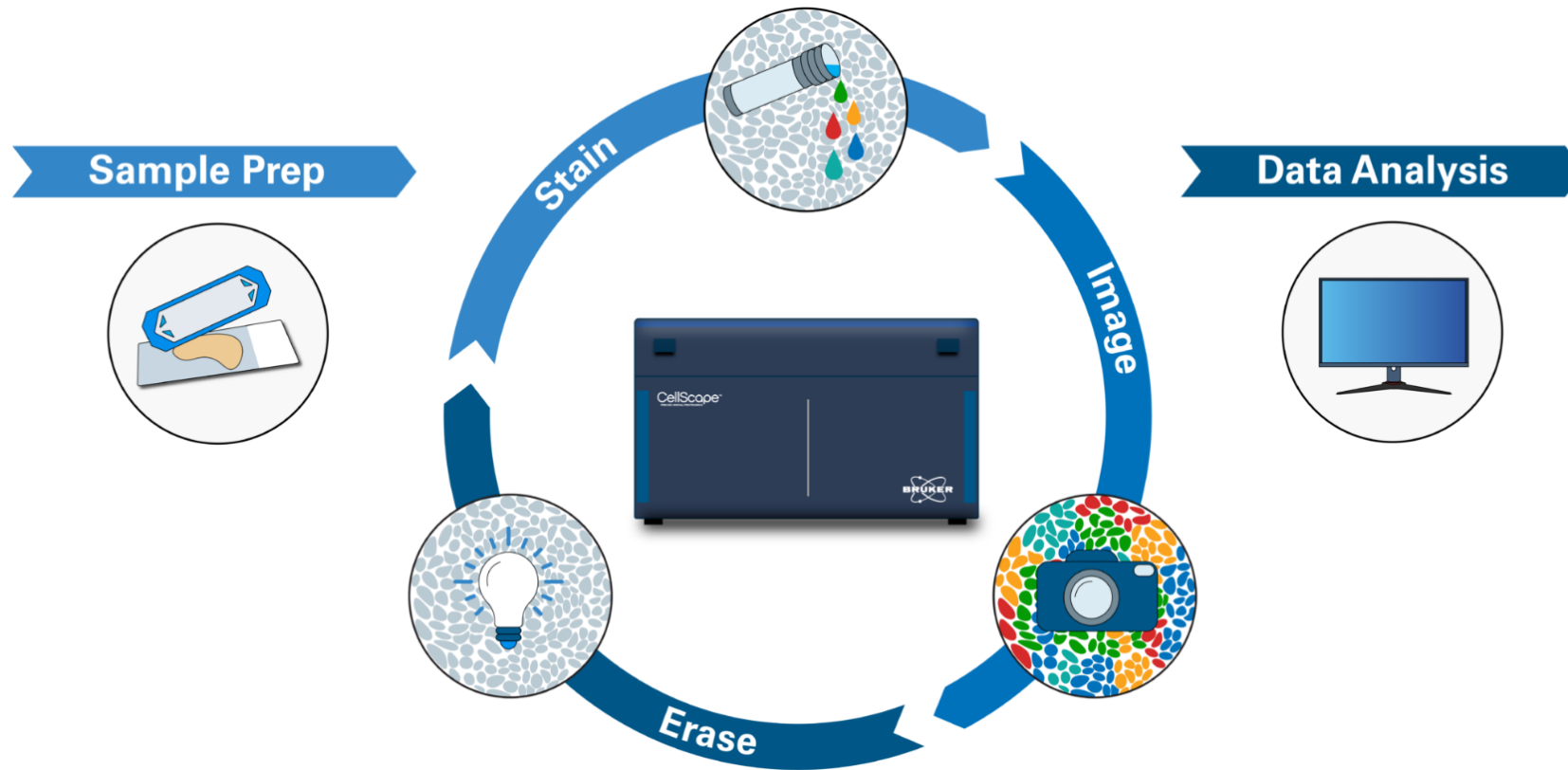
Enclosed imaging system

4-sample holder



Connected software

Stain. Image. Repeat.

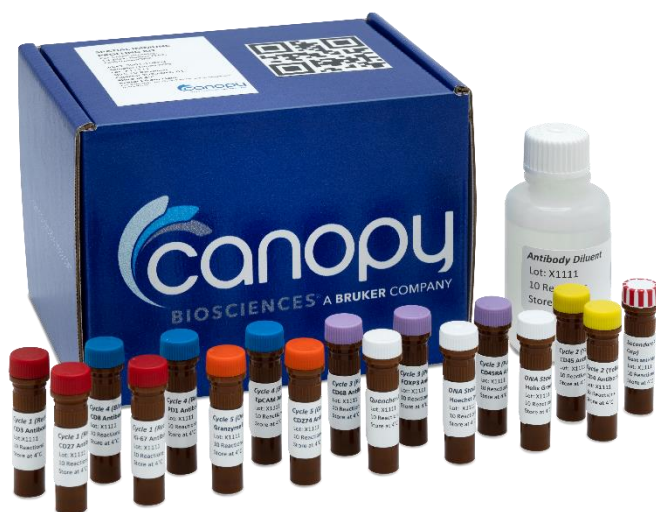


Samples are prepared with CellScope™ Whole-Slide Imaging Chambers. Cycles of staining, imaging, and signal removal are automatically completed by the instrument. Images are digitally overlaid to achieve high-plex spatial proteomic datasets.

Straightforward, reliable technique with open-source antibodies

Rigorously validated panels and open-source antibodies **get you productive sooner, at less cost**

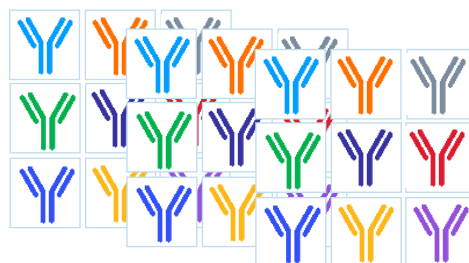
Use Our Antibodies



Reliable, modular, and robustly validated **VistaPlex™ Assay kits** for core applications:

- Immune profiling
- Tissue architecture
- Immune cell subtyping

Beyond our panels, leverage our database of **over 350 CellScape-compatible antibodies**



Use Your Antibodies

- Capture the advantage of biomarker flexibility and customization — **Use the clones you know**
- Primary monoclonal antibodies for **high specificity**
- **Faster and more straightforward** antibody validation - no custom conjugation needed
- **Directly conjugated antibodies**

The most comprehensive and customizable off-the-shelf modular antibody panels . . . Build and expand your high-plex assay at any time

Mix and match pre-validated panels can be applied today, tomorrow, or next month

Tissue Architecture

(Myo-) Epithelia: *Beta catenin, CD138, E-cadherin, podoplanin, SMA*

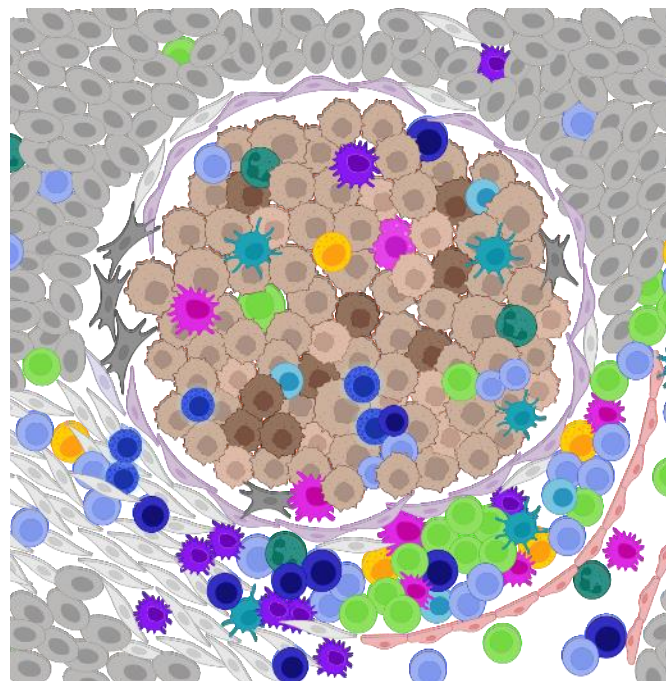
Endothelia: *CD31, CD34, Podoplanin*

Other: *Vimentin, CollagenIV*

Myeloid

Macrophages: *CD11b, CD11c, CD14, CD163, iNOS, CD206*

Dendritic Cells: *HLA-DR, CD123, DC-SIGN, CD80, CD86*



Immune Profiling

Lymphocytes: *CD45, CD45RA, CD27*

T-cells: *CD3, CD4, CD8, FoxP3*

B-cells, Macs: *CD20, CD68,*

Cell States: *GrnB, PD-1, PD-L1, Ki67*

Tumor: *PanCK*

NK Cells

CD56, NKG2D, CD161, CD57, NCR1

Checkpoints

LAG-3, OX40, TIM-3, CTLA-4, TIGIT

Activation / Proliferation

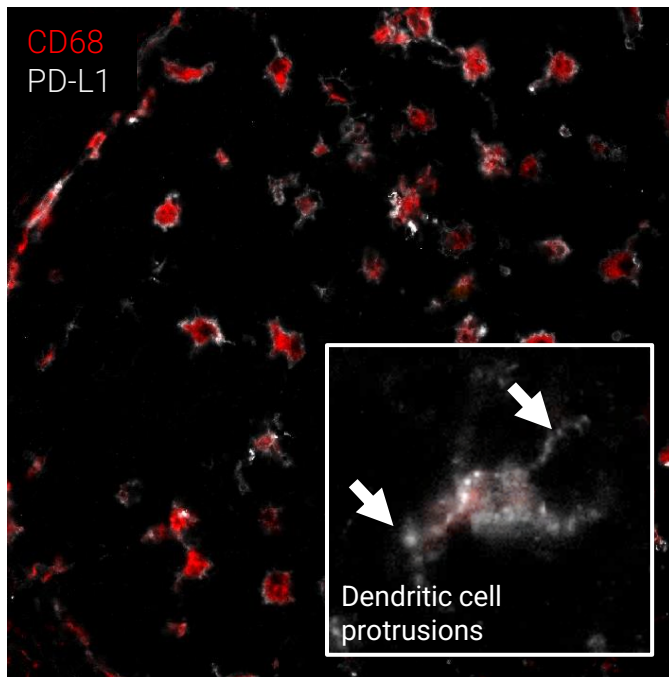
ICOS, CD40, CD40L, IL2RA, IDO1, VISTA, IFNG, PCNA



What is quantitative spatial phenotyping?

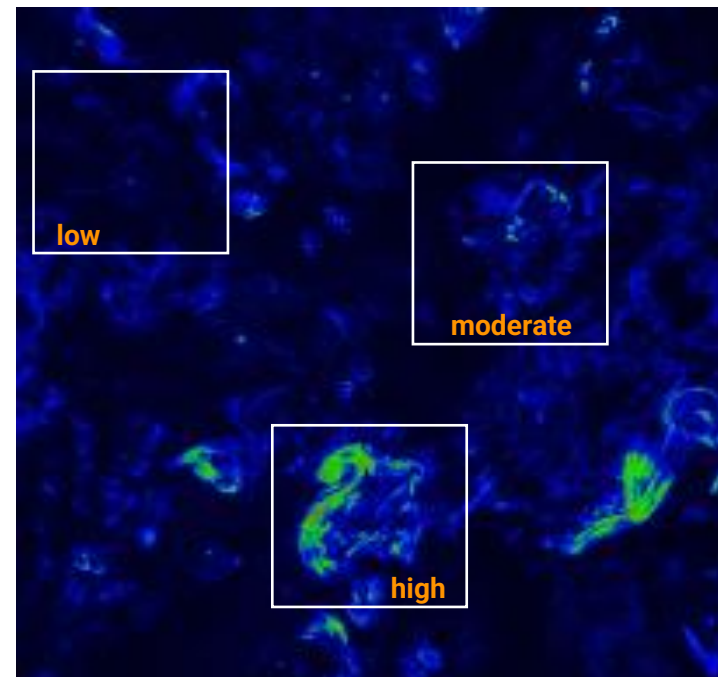
See the whole spatial neighborhood...

... At high resolution



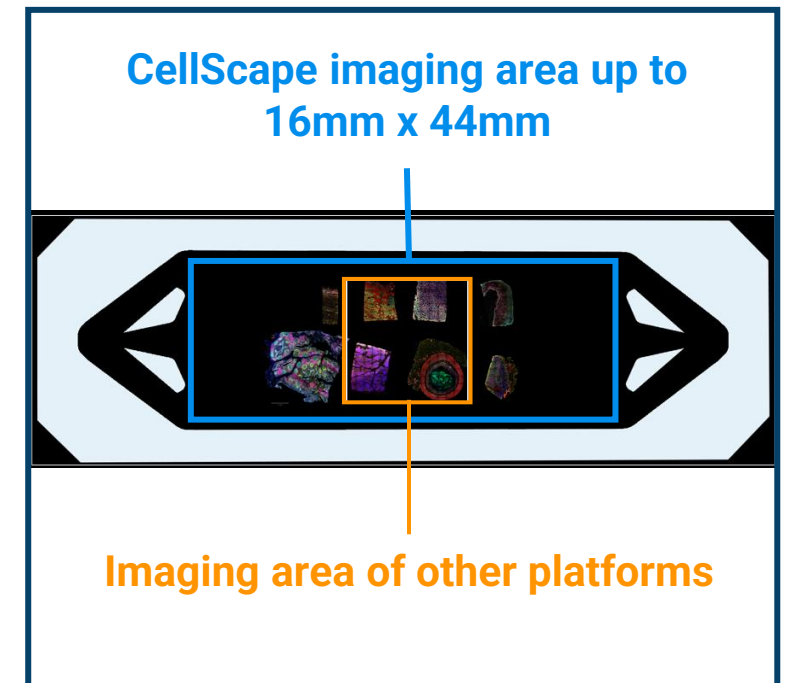
True single cell and subcellular detail (182 nm/pixel)

... Over a high dynamic range



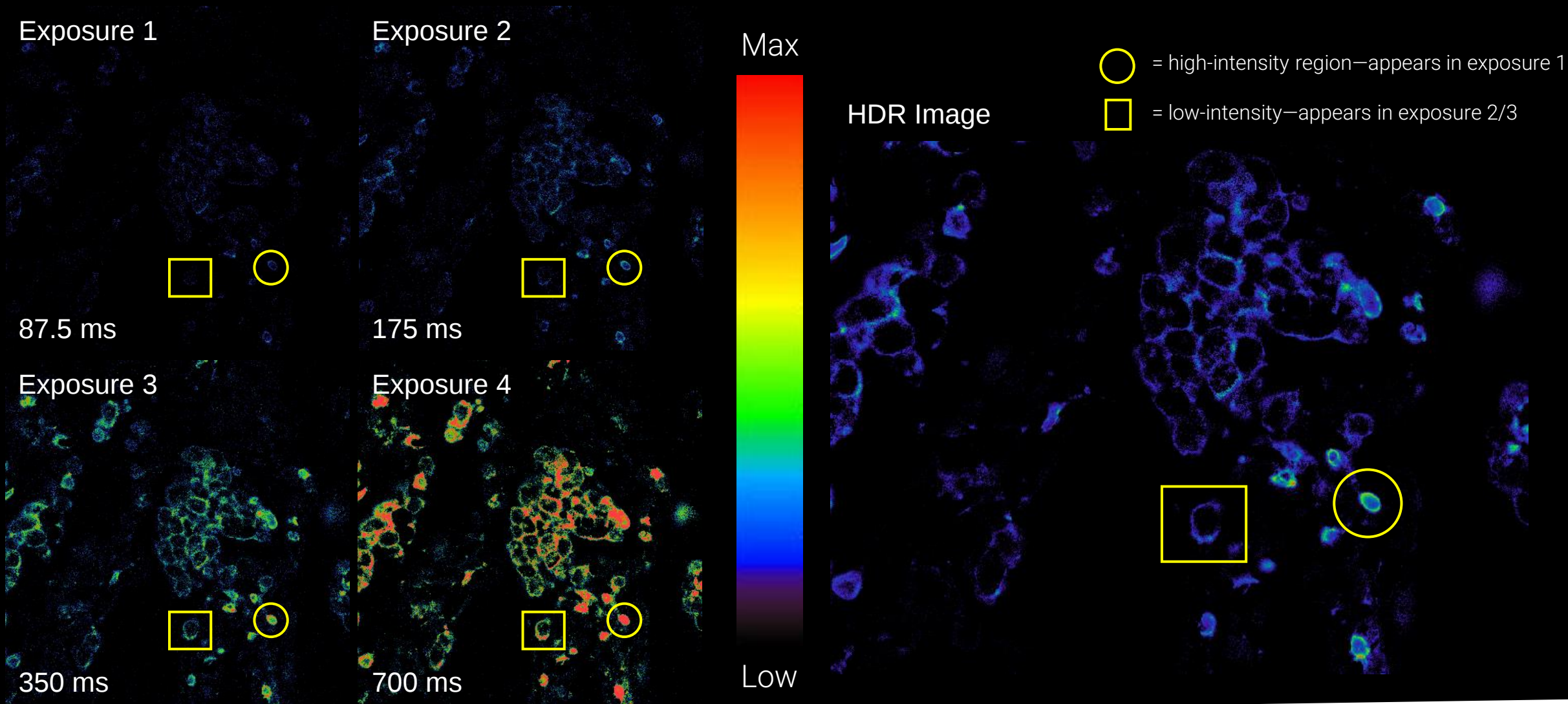
Quantify relative abundance and identify low expressors (automated high dynamic range imaging)

... Across the whole slide

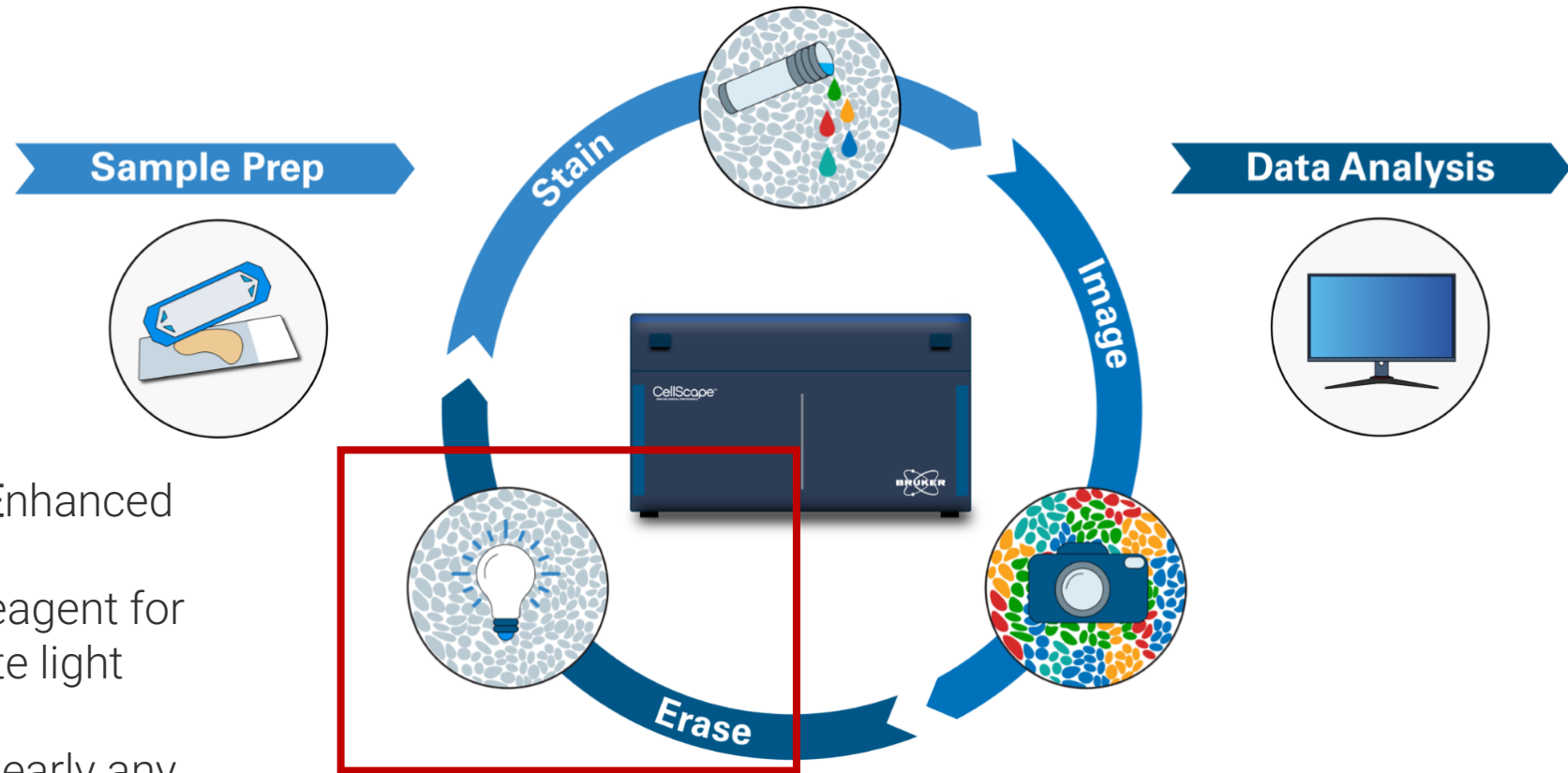


Increase throughput and reproducibility

Our High Dynamic Range technology deploys multiple exposures to enable quantification of the full range of protein expression present in biology



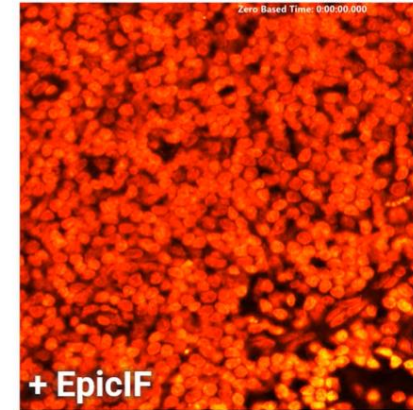
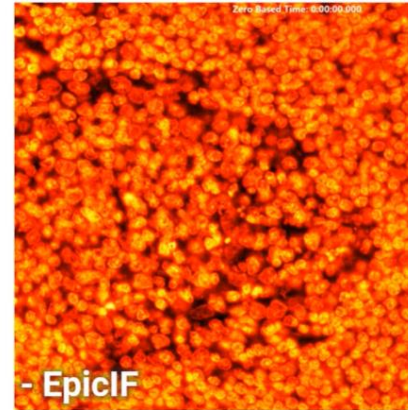
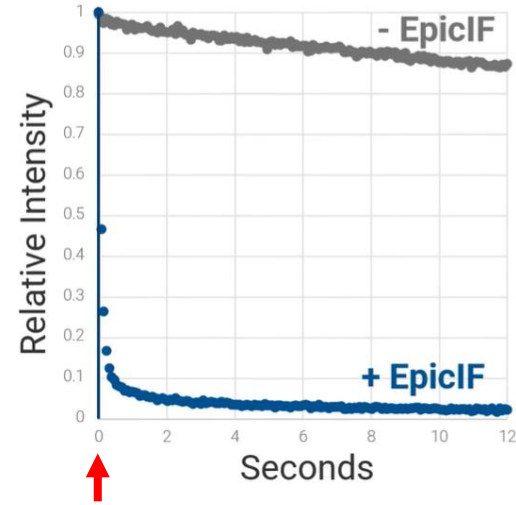
Stain. Image. Repeat.



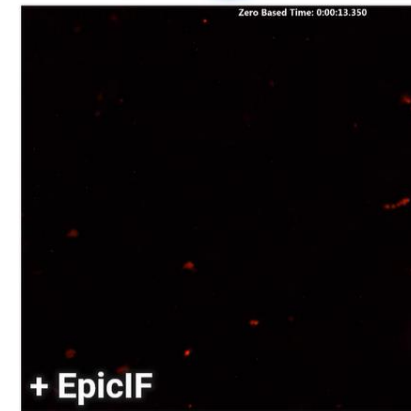
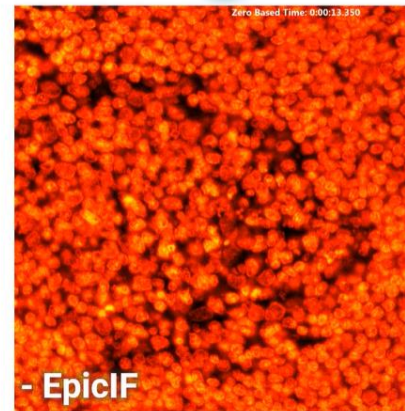
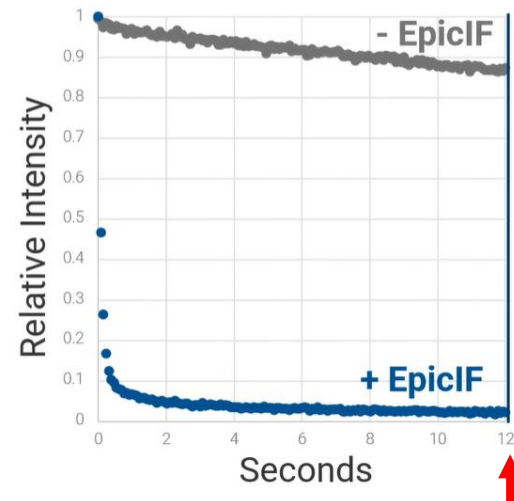
Newly launched **EpicIF** (Enhanced Photobleaching In Cyclic ImmunoFluorescence) reagent for photobleaching with white light

- Announced Oct 2024
- Signal removal from nearly any photostable fluorophore
- Non-destructive to tissue or epitopes
- <https://www.brukerspatialbiology.com/EpicIF>

Sytox Orange (DNA)

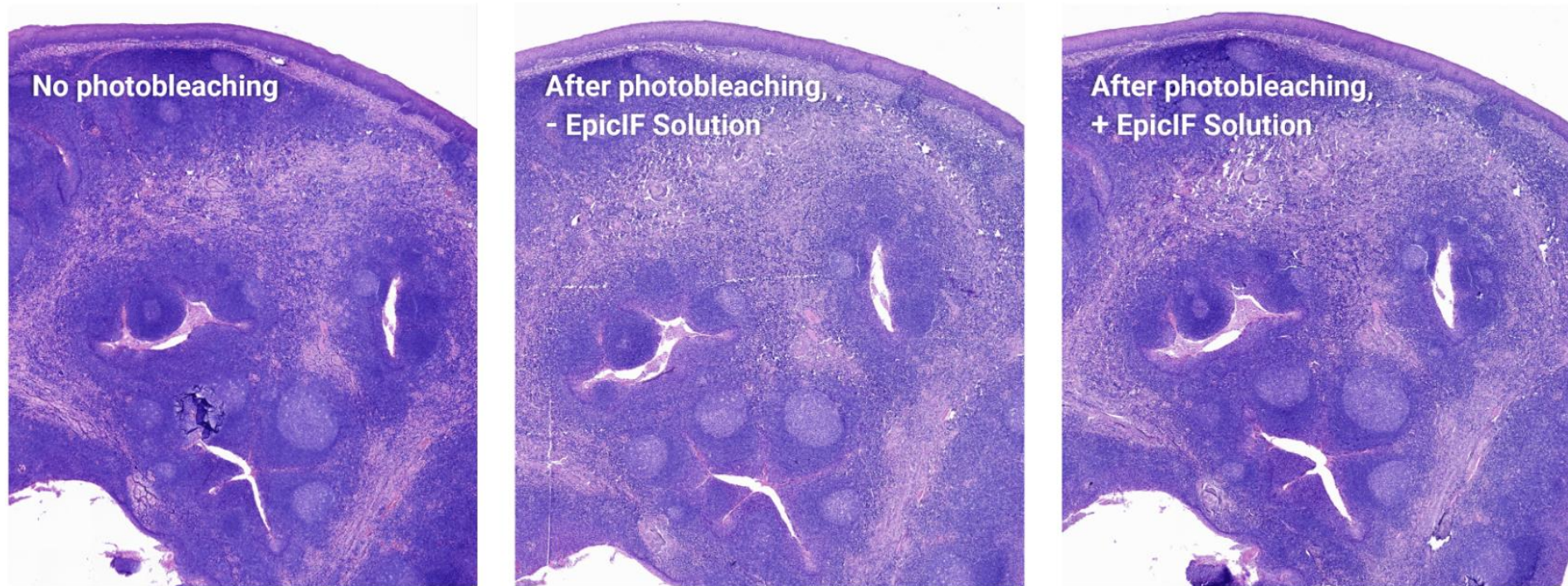


Sytox Orange (DNA)



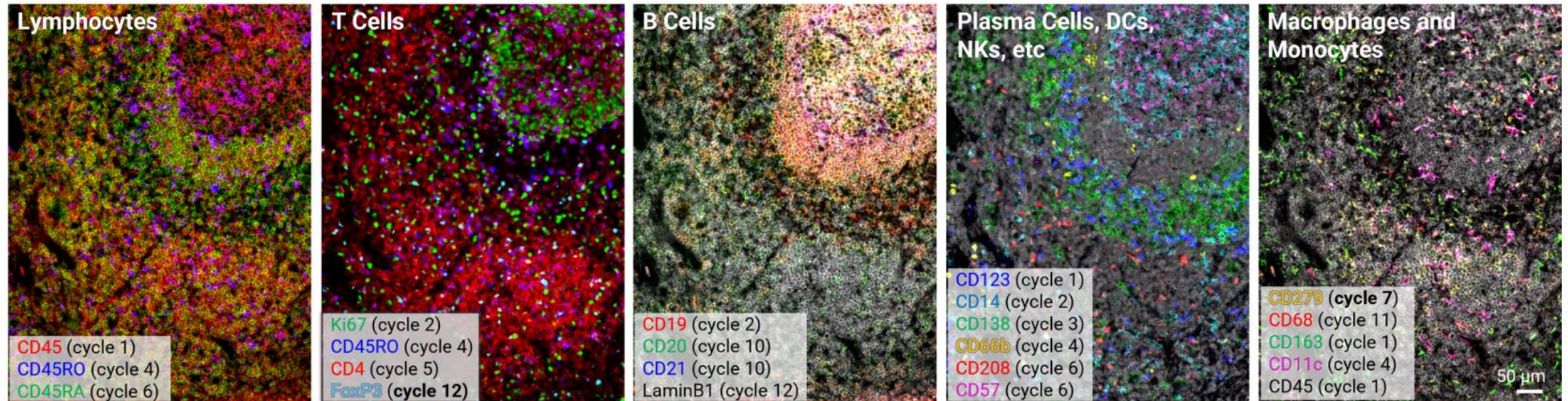
Modular sample re-examination is enabled by non-destructive and robust cyclic multiplexing

Photobleaching Preserves Epitope Stability and Tissue Integrity



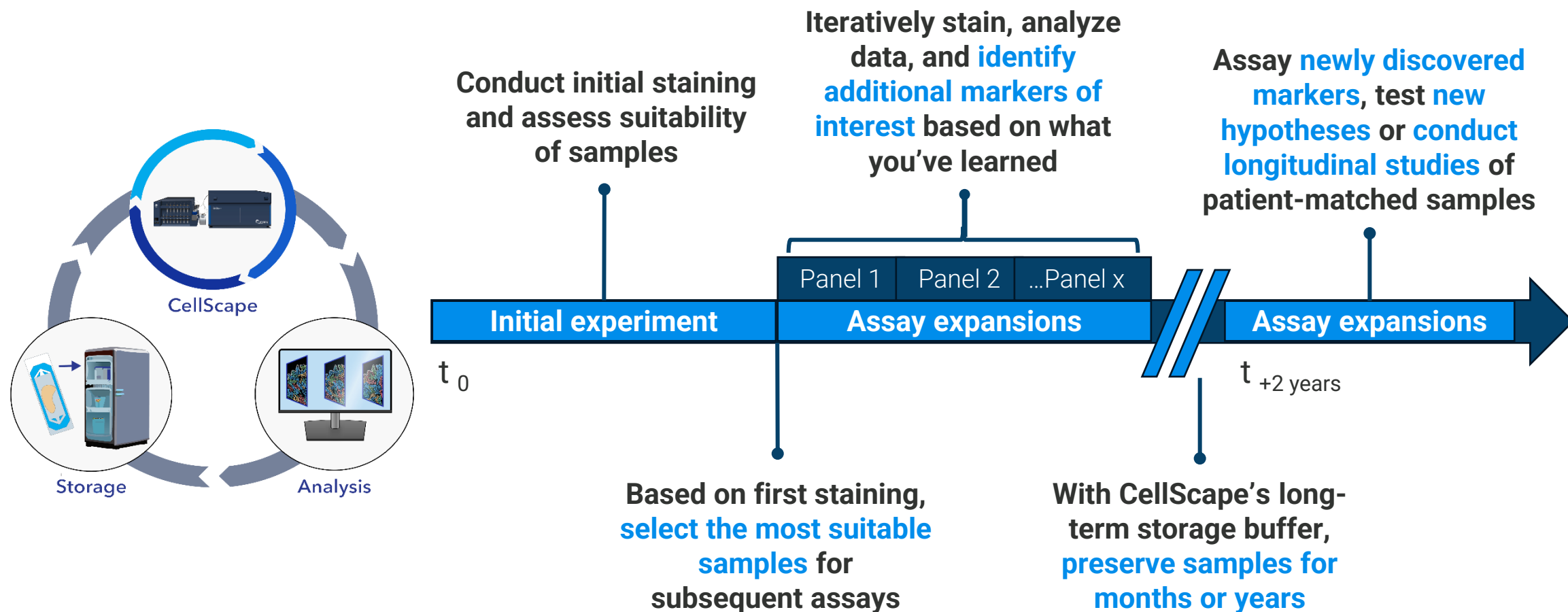
H&E staining of serial tonsil sections treated with (left to right) no photobleaching, 10 rounds of photobleaching without EpicIF solution, and 10 rounds of photobleaching with EpicIF solution. A pathologist concluded that the sections are the same with respect to integrity and preservation of cellular architecture.

Stain. Image. Repeat.



48-plex image acquisition of an FFPE tonsil sample completed in 12 EpicIF cycles using fluorophores AF488, AF532, AF594, and AF647, with key markers indicated in legends.

What hypothesis-driven spatial biology looks like



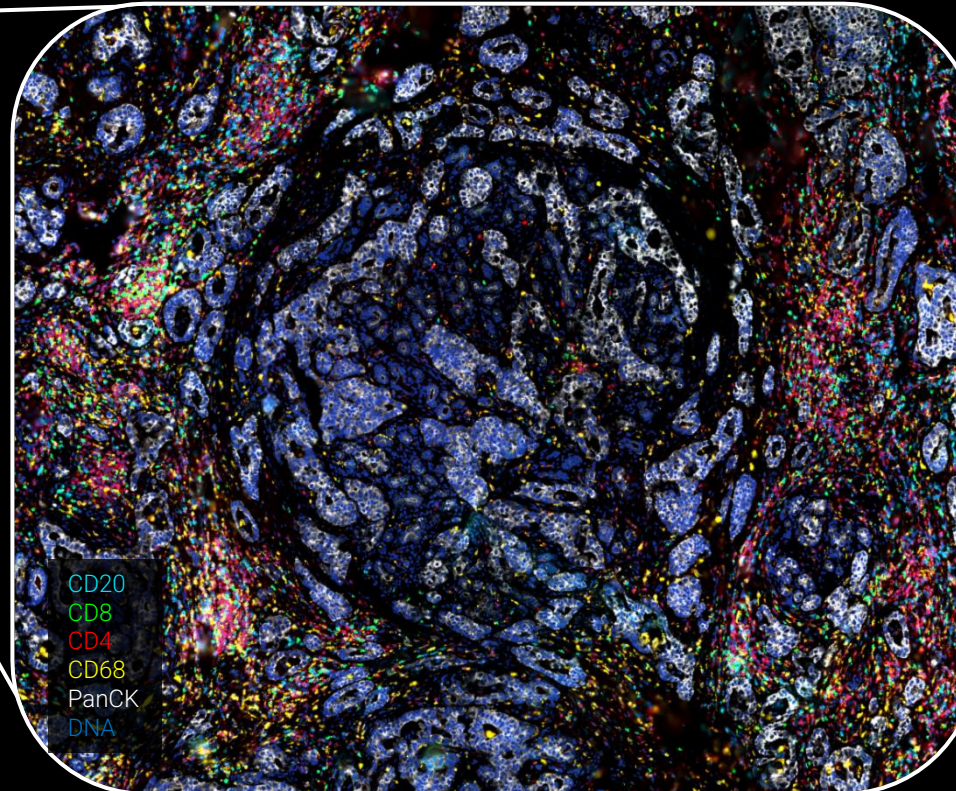
Initial Assay: Immune Profiling

Initial experiment

Assay expansions

Grade II invasive
ductal carcinoma
(breast)

CD3
CD45
CD68
PanCK
CD4
DNA



Observation:

Exceptionally strong
immune infiltrate is
accompanied by
regional immune
exclusion.

Follow-Up Question:

What is the mechanism
of immune exclusion?

**Assay Expansion
with CellScape**

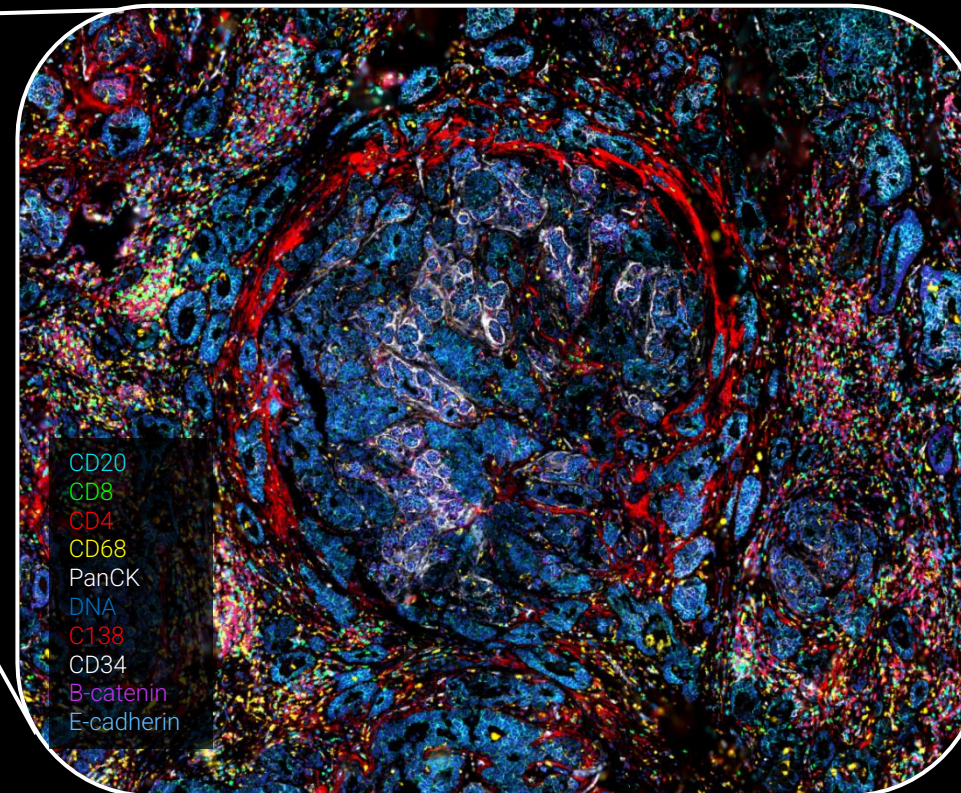
Assay 2: Tissue Architecture Profiling

Initial experiment

Assay expansions

Grade II invasive
ductal carcinoma
(breast)

CD3
CD45
CD68
PanCK
CD4
DNA
C138
CD31
B-catenin
E-cadherin
MUC1



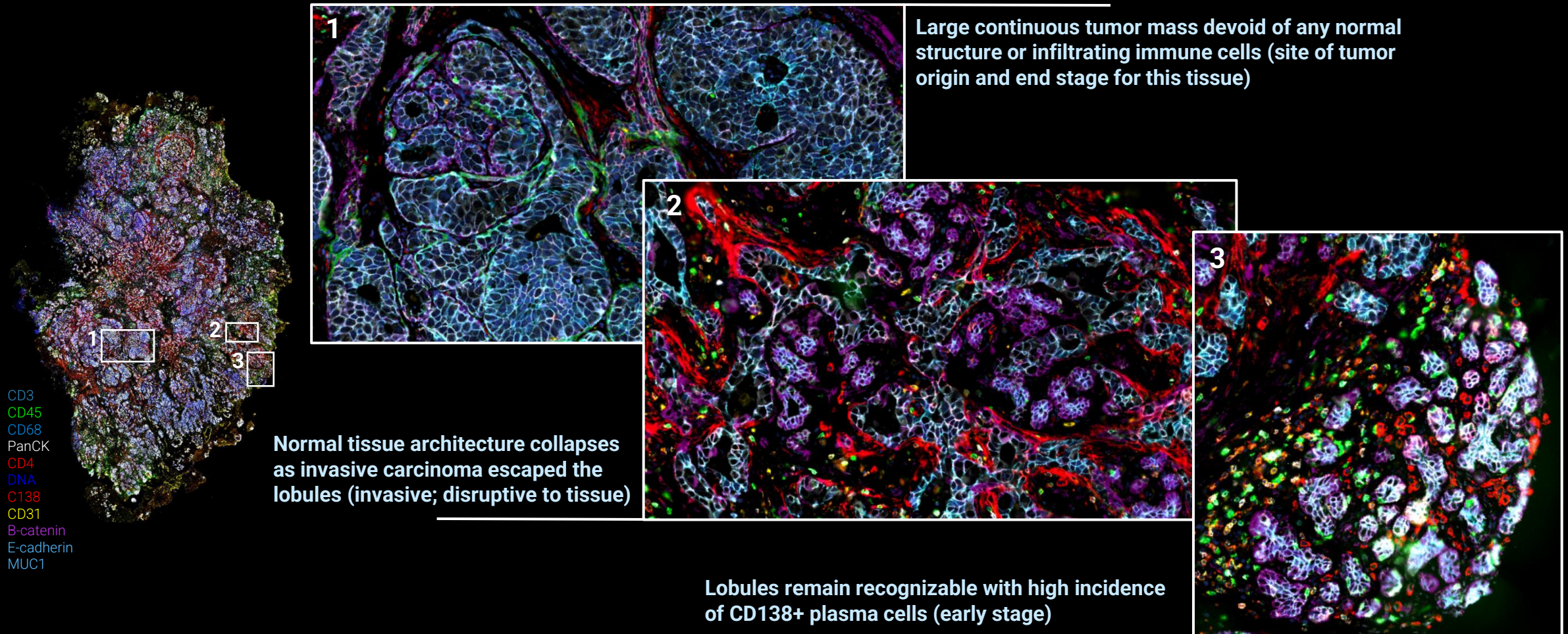
Observation:

Immune infiltrate is compartmentalized by **CD138+ plasma cells / epithelia**, which may act as an immune barrier.

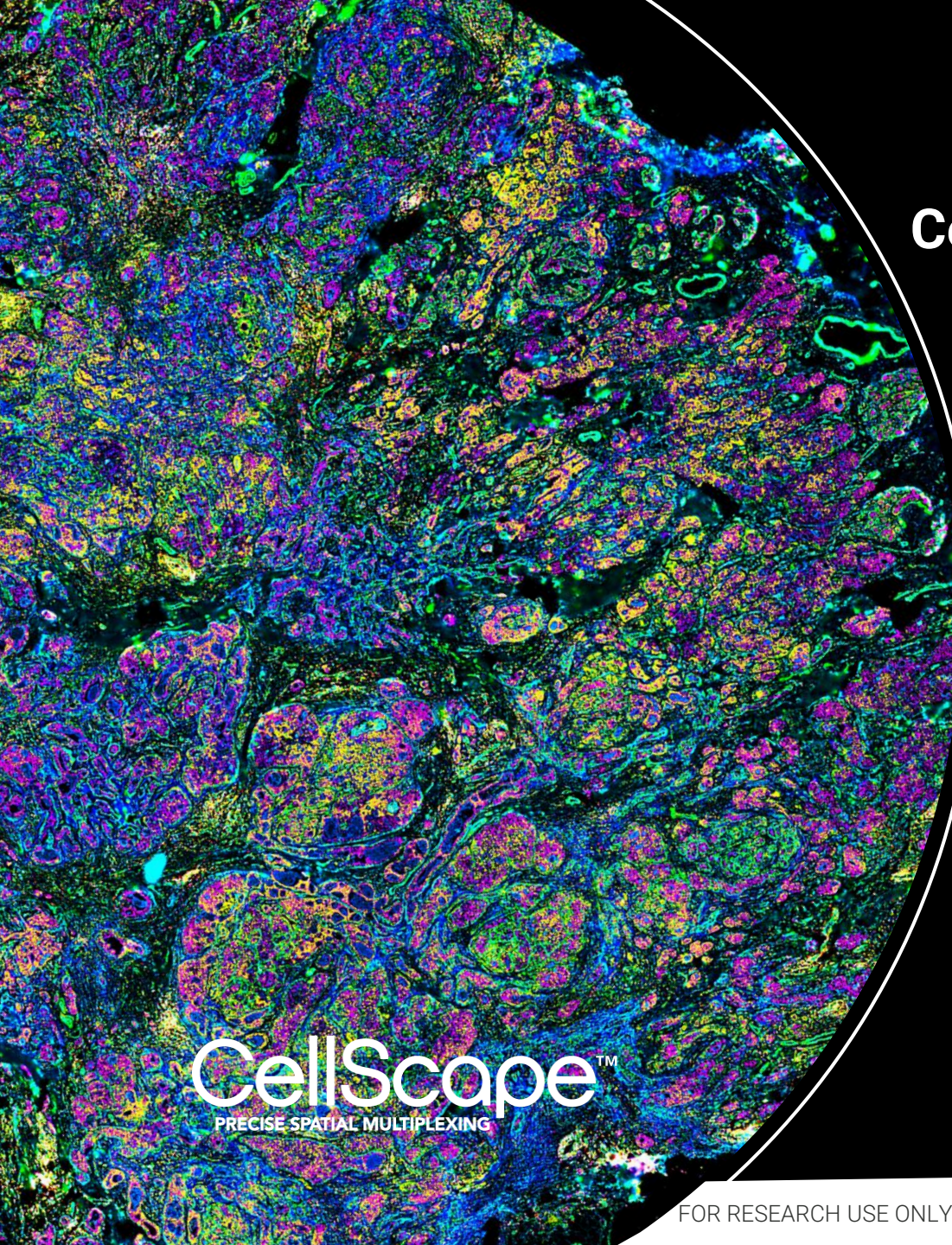
Conclusion:

This spatial arrangement within the tumor may determine the course of development for treatment.

Additional Assays: Immune-Architectural Profiling Illustrates Tumor Progression



Get the whole story for every sample

A large, circular inset image on the left side of the slide showing a highly detailed, multi-colored fluorescence microscopy image of a tissue section. The colors represent different protein markers, creating a complex, textured pattern of purple, blue, green, and yellow. The tissue structure is clearly visible, with various cellular and extracellular components highlighted by the different colors.

CellScape™ Precise Spatial Proteomics

QUANTITATIVE PERFORMANCE

High resolution & high dynamic range (HDR)

STRAIGHTFORWARD & RELIABLE TECHNIQUE

Robust Assay Performance

STREAMLINED ASSAY DEVELOPMENT

Flexible marker selection and plex at scalable cost & throughput

EXPANDABLE ASSAYS

Re-examination enabled through gentle chemistry

LARGEST IMAGING AREA

Whole tissues on standard slides

CellScape™
PRECISE SPATIAL MULTIPLEXING

Comprehensive platforms to solve any spatial problem

Excel with FFPE tissues mounted on **standard** microscope slides

Tissue Exploration

Tumor Profile

Immune Profile

Cellular Exploration

Cellular Exploration

Proteomic
phenotyping

Transcriptomic
phenotyping

GeoMx
Digital Spatial Profiler

CosMx
Spatial Molecular Imager

CellScape
PRECISE SPATIAL MULTIPLEXING

Non-Small Cell Lung Cancer

• AtoMx SIP: Streamlined, Scalable, Flexible

Instruments

CosMx™



GeoMx®



Standardized
Data Formats

Seurat
OME-TIFF

3rd Party & Open-Source Tools

Open-Source
Analytics

Digital Pathology Analysis

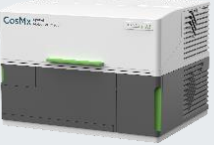
ROI Selection
AI Algorithms

Benefits:

- Application can scale to needs of end user
- Ease of use (Chrome on client computer)
- More streamlined data sharing and AWS security
- Automated file transfer from CosMx to AtoMx

CosMx + AtoMx Integrated Workflow

CosMx Workflow

	Run Setup	Reporter Cycling	Data Transfer to AtoMx	Flow Cell(s) in AtoMx Gallery	Study Creation and Data Analysis	Data Export
						
						

- Data is automatically transferred from CosMx to AtoMx
- Computationally-intensive processing in AtoMx (XYZ positions of fluor. spots decoded to transcripts)
- Data can be analyzed immediately after instrument completes

BRUKER SPATIAL BIOLOGY

Please see NanoString University and our website for more information. Thank you!



NanoString University

<https://university.nanosttring.com/>

Please reach out to us for project discussions and pricing options.

Wes Heydeck

Sr. FAS

westley.heydeck@bruker.com

Amir Farooqui

Account Manager

amir.farooqui@bruker.com