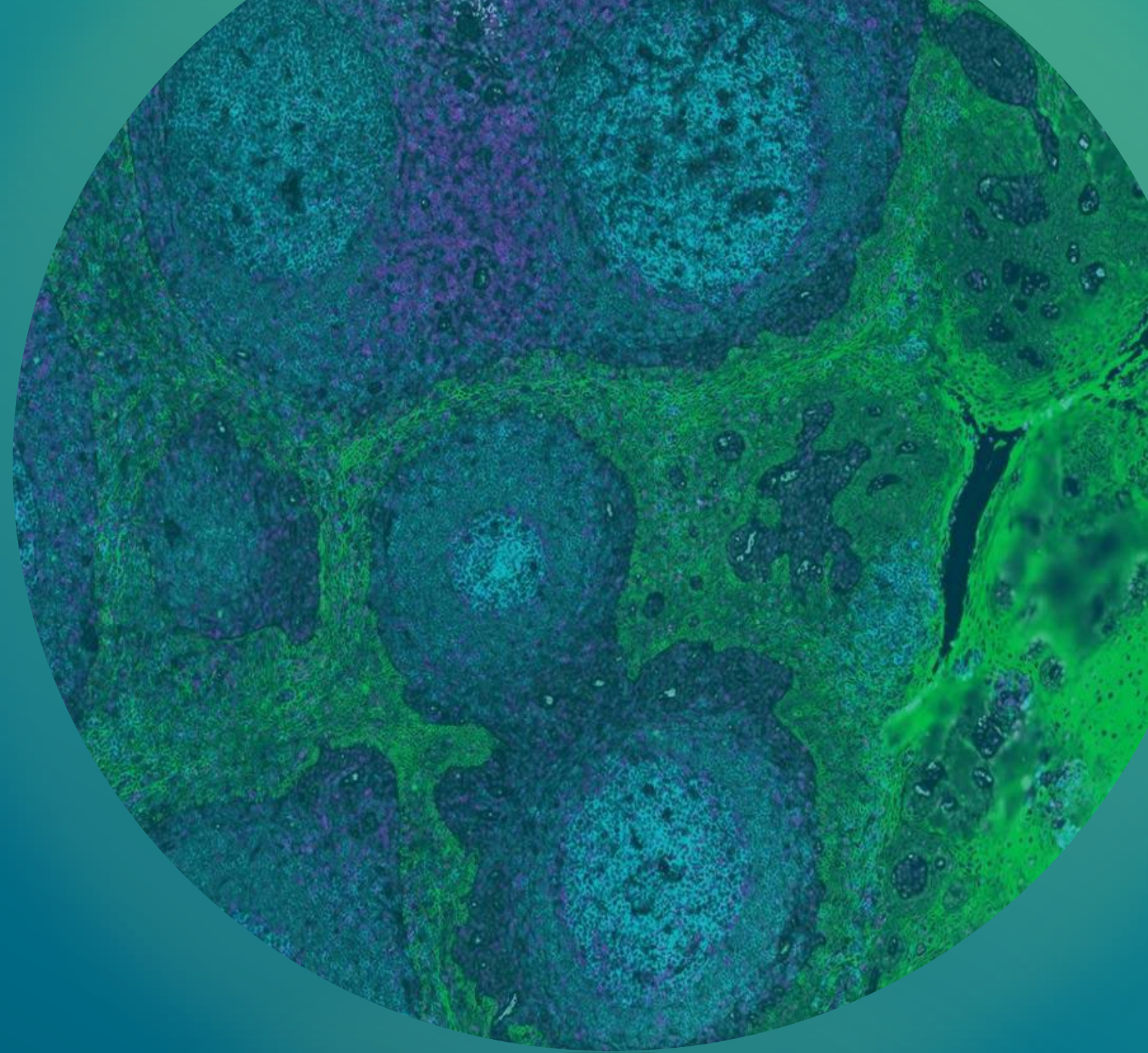


Spatial Molecular Imaging of FFPE Cancer Samples at Unlimited Multi-Omic Spatial Plex allows True Systems Biology Understanding

Joseph Beechem, PhD.
SVP and CSO
NanoString Technologies
Seattle, Washington

Spatial Multi-Omics For Cancer Systems Biology
Feb 12, 2024



nanoString®

Notice

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 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 of the President and Fellows of Harvard College (Harvard Corporation).

Spatial Biology is the Next Life Sciences Revolution



Bulk



Single Cell



Spatial

2006

2012

2019

2022



Genome Analyzer

Next Generation Sequencing
2009 Method of the Year



Chromium

Single Cell Genomics
2013 Method of the Year



GeoMx[®] DSP



CosMx[®] SMI

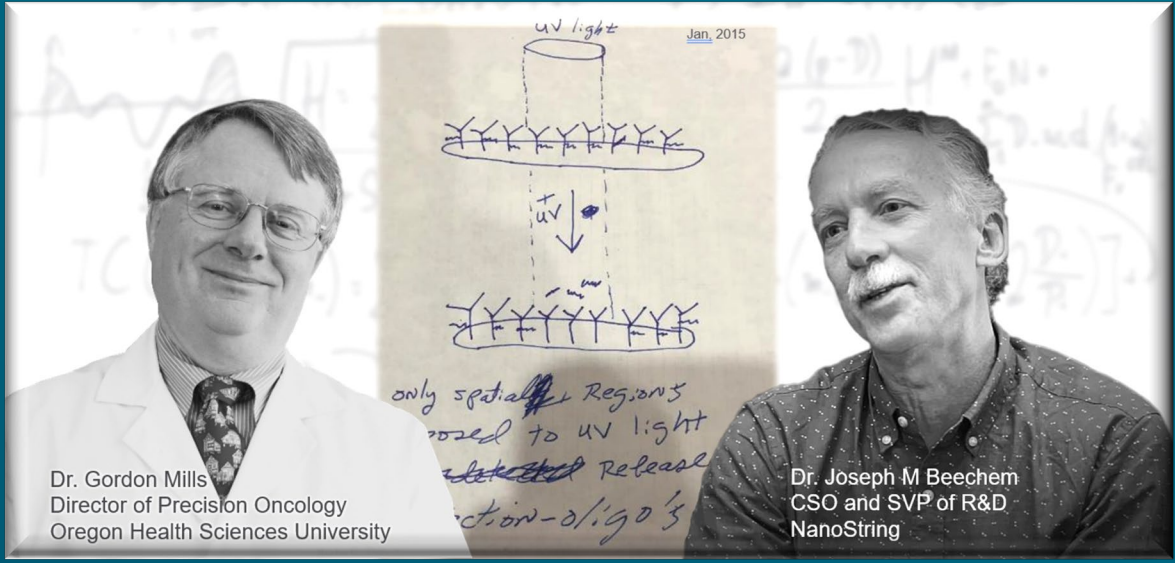
Spatially-resolved Transcriptomics
2020 Method of the Year

Adapted from concept and images by Dr. Aviv Regev of The Broad Institute; *Nature Methods*



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From very first AGBT Spatial Summit (2019) to Spatial Single-Cell Whole Transcriptome Imaging (2024), pushing multi-omic plex to the absolute maximum, for true systems-biology interrogation of tissue



Adding a “same-slide” > 570-plex protein assay (Immune-Oncology Proteome Atlas) in 2023

CosMx 6,000 genes

CosMx* Whole Transcriptome >18,000 genes

CosMx 1,000 genes

GeoMx Whole Transcriptome 18,000 genes

GeoMx 1,800+ genes

GeoMx 84 genes

NanoString’s CosMx SMI Achieves Whole Transcriptome Imaging at Single-Cell Resolution

Major milestone marked by first public dataset released for CosMx Whole Transcriptome Panel with additional data forthcoming at the AGBT Meeting

January 7, 2024

SEATTLE--(BUSINESS WIRE)--NanoString Technologies, Inc. (NASDAQ: NSTG), a leading provider of life science tools for discovery and translational research, today announced the release of the first public dataset of the whole transcriptome obtained at true single-cell resolution on the CosMx™ Spatial Molecular Imager (SMI). The data will be highlighted at the 42nd annual J.P. Morgan Healthcare Conference 2024 in San Francisco during NanoString’s corporate presentation on Wednesday, January 10, 2024, at 5:15 pm ET.

“Using the CosMx Whole Transcriptome Panel Achieves Scientific Moonshot”

“born” as a sequencing chemistry, and applied to spatial-sequencing



*Estimated Commercial Launch Year

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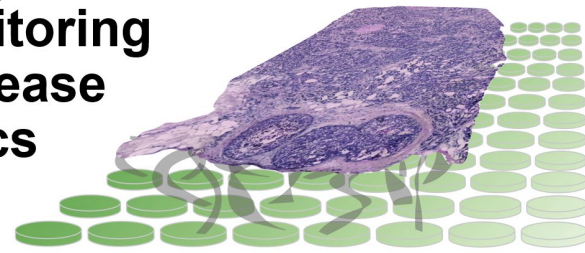


Marco Island, Feb 27 2019: AGBT's very first Spatial Biology Event was NSTG-proposed & Sponsored. NSTG invited all of the spatial technologies to our event, in order to be inclusive and work together to advance the science...



Spatial transcriptomics for monitoring ALS disease dynamics

Sanja Vickovic,
Wallenberg Fellow,
Regev lab
Feb 27, 2019
Marco Island FL



BROAD
INSTITUTE

Digital Spatial Profiling: Delivering on the Promise of Spatial Genomics & Proteomics

Joseph M. Beechem, PhD
SVP of Research and Development

27-Feb-2019
Spatial Genomics Summit --- AGBT
Marco Island FL

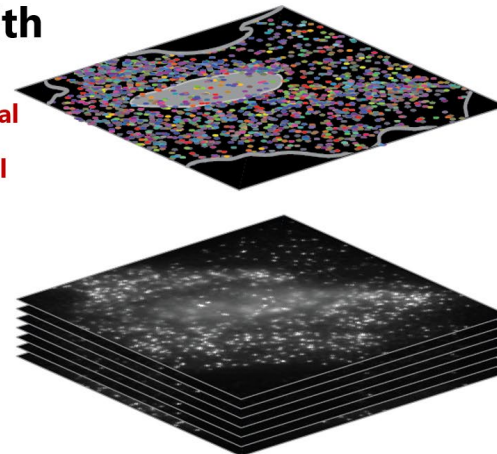
Mapping the brain with MERFISH

The molecular, spatial, and functional organization of the hypothalamic preoptic region via in situ single-cell transcriptomics

Jeffrey R. Moffitt

Program in Cellular and Molecular Medicine
Boston Children's Hospital

Department of Microbiology
Harvard Medical School



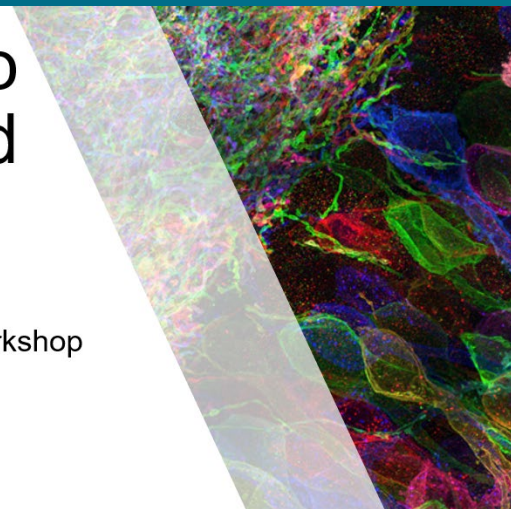
Spatial Genomics Summit | February 27, 2019

From tissues to single cells and back again...

Fei Chen

Nanostring *In Situ* Genomics Workshop

Feb 27, 2019



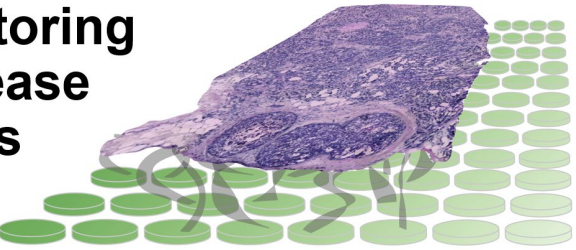
nanoString
®

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NSTG Not Going Anywhere. Accomplished \$47.5M new funding for 2024.

Purchase - Visium

Spatial transcriptomics for monitoring ALS disease dynamics



Sanja Vickovic, Wallenberg Fellow, Regev lab
Feb 27, 2019
Marco Island FL

BROAD INSTITUTE



Lawsuit – CosMx, Lawsuit – GeoMx

Digital Spatial Profiling: Delivering on the Promise of Spatial Genomics & Proteomics

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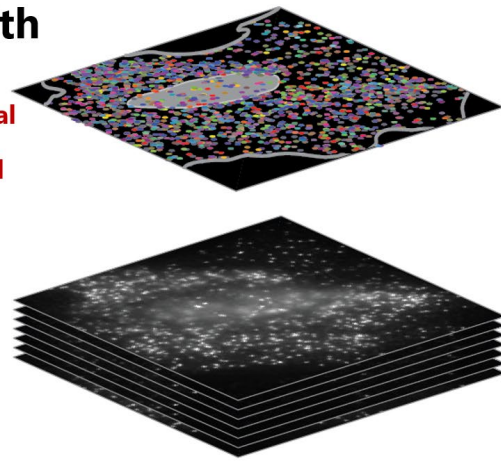
Lawsuit - Vizgen

Lawsuit - Curio

Mapping the brain with MERFISH

The molecular, spatial, and functional organization of the hypothalamic preoptic region via in situ single-cell transcriptomics

Jeffrey R. Moffitt
Program in Cellular and Molecular Medicine
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Spatial Genomics Summit | February 27, 2019

From tissues to single cells and back again...

Fei Chen
Nanostring *In Situ* Genomics Workshop
Feb 27, 2019



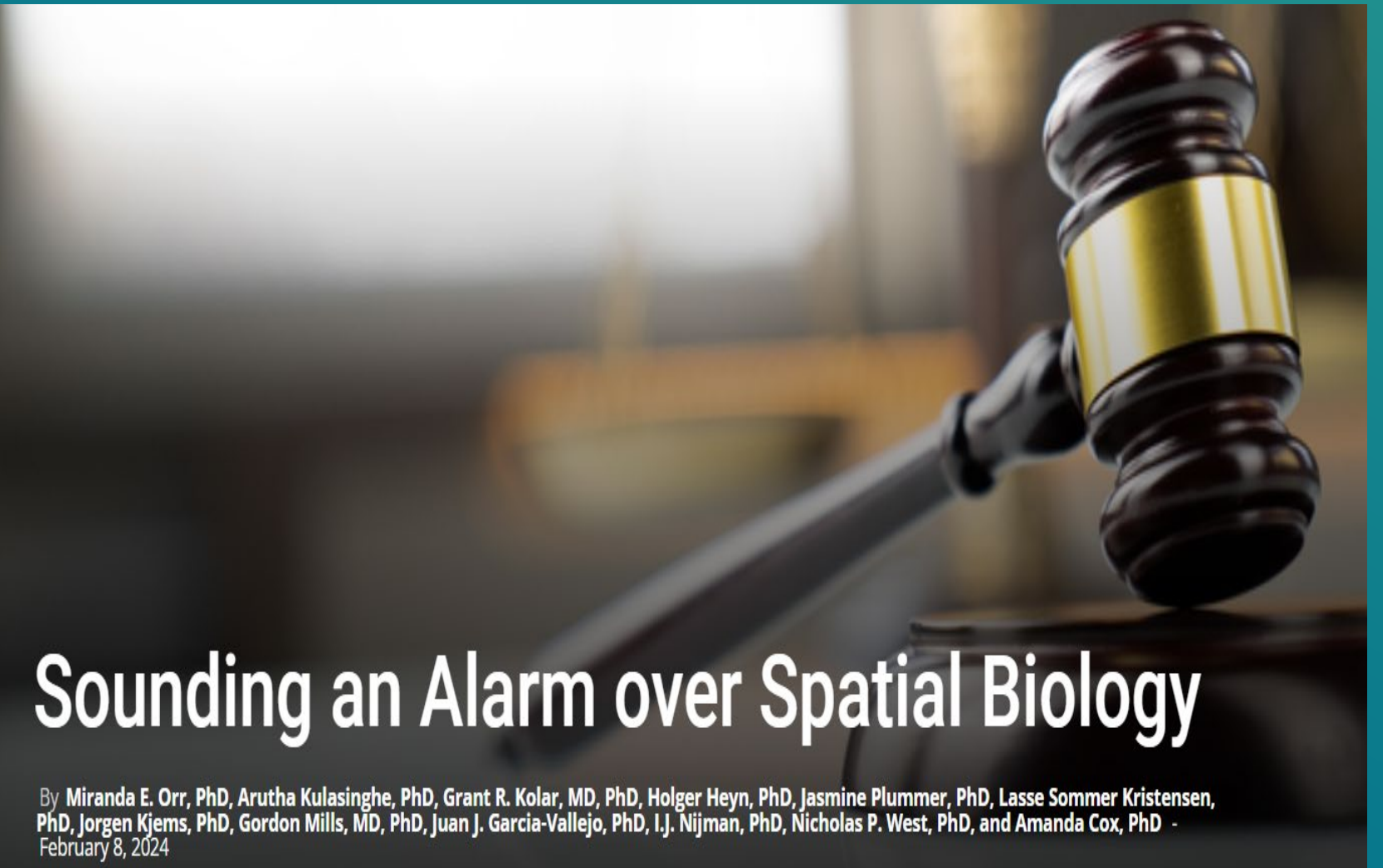

Feb 8, 2024: GEN publishes two articles on the problem of the attempt to Monopolize all Spatial Biology Approaches



NanoString CSO Joe Beechem Insists the Company "Not Going Anywhere"

GEN talks to Joe Beechem about the decision to file Chapter 11, where the company goes from here, and the future of innovation in the spatial biology field

By Julianna LeMieux, PhD - February 8, 2024



Sounding an Alarm over Spatial Biology

By Miranda E. Orr, PhD, Arutha Kulasinghe, PhD, Grant R. Kolar, MD, PhD, Holger Heyn, PhD, Jasmine Plummer, PhD, Lasse Sommer Kristensen, PhD, Jorgen Kjems, PhD, Gordon Mills, MD, PhD, Juan J. Garcia-Vallejo, PhD, I.J. Nijman, PhD, Nicholas P. West, PhD, and Amanda Cox, PhD - February 8, 2024

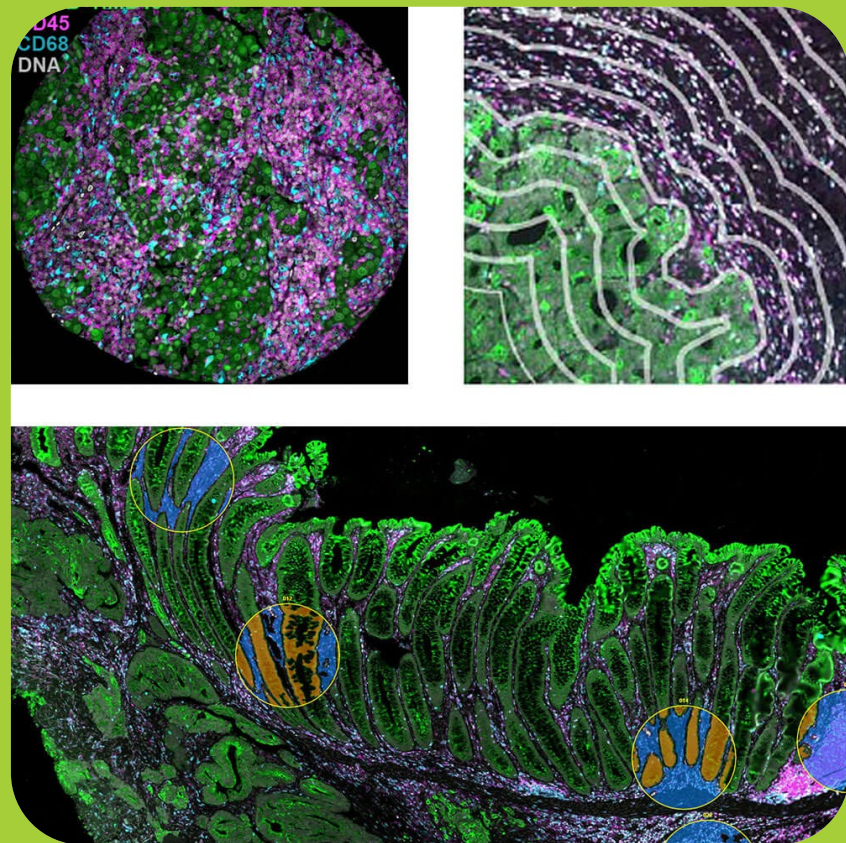
nanoString®

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

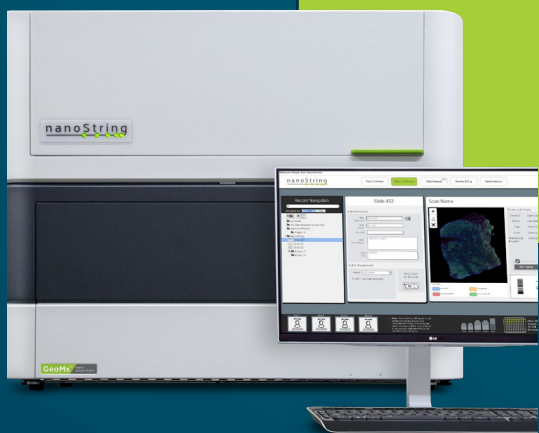
Profilers

TISSUE STRUCTURES
~ 100 μm



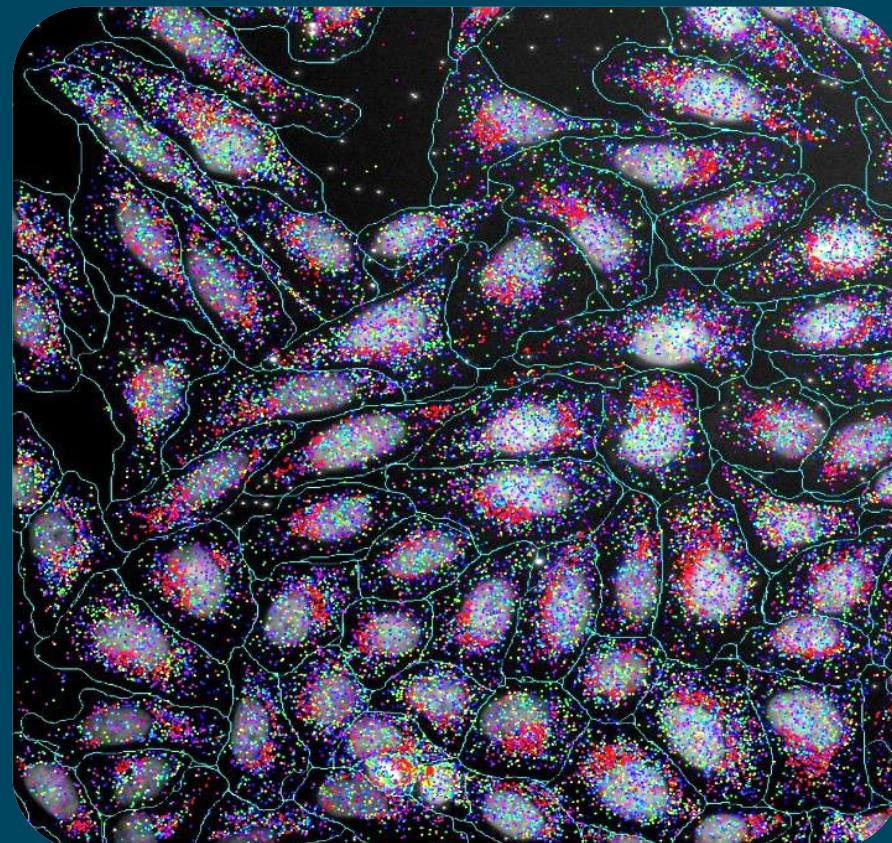
GeoMx[®]
Digital Spatial Profiler

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

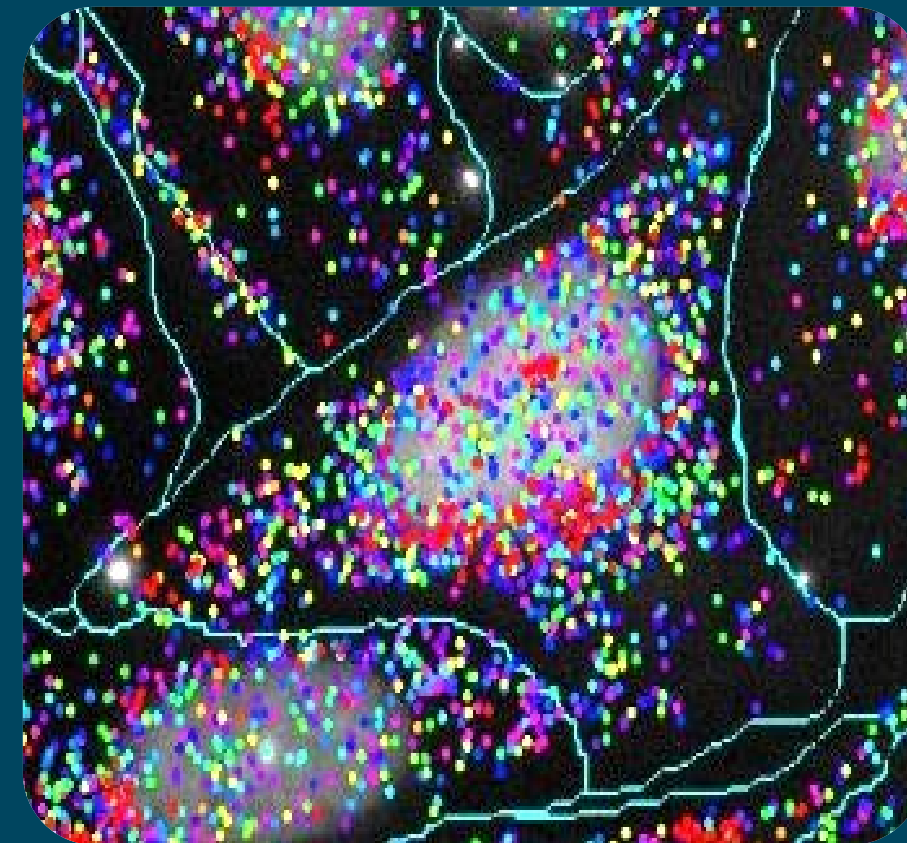


Imagers

SINGLE CELL
~ 10 μm



SUB-CELLULAR
~ 1 μm



CosMx[™]
Spatial Molecular Imager

**Up to Whole Transcriptome (>18,000-plex) RNA
76-plex Proteins**



nanoString[®]

GeoMx[®] IO Proteome Atlas

Discover the Next Immuno-Oncology Biomarker

REQUEST A QUOTE



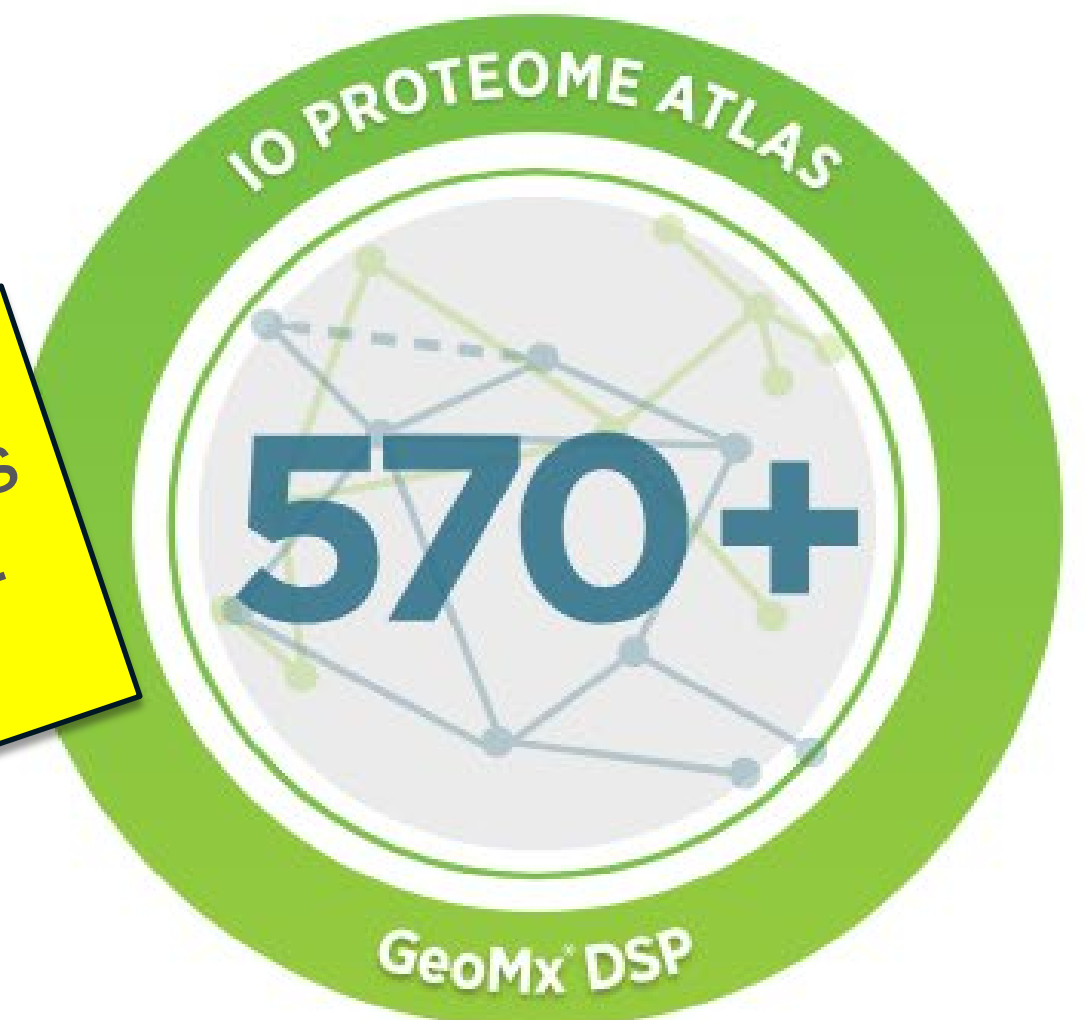
Launched Nov 2023

Home » Products » GeoMx Digital Spatial Profiler » GeoMx Protein Assays » GeoMx[®] IO Proteome Atlas

Spatial Proteomics Redefined

Comprising nearly all Abcam's IHC-validated human antibodies for immuno-oncology (IO), the GeoMx IO Proteome Atlas (IPA) is the highest-plex spatial proteomics panel available for FFPE and fresh frozen tissue sections, and enables broad biomarker discovery for translational research. Rapidly discover new protein biomarkers and drug targets by multiplexed spatial profiling over 570 proteins in different tissue compartments such as the tumor core, tumor microenvironment, and the immune infiltrate. Get more comprehensive data than any traditional immunohistochemistry (IHC) or immunofluorescence assay yet seamlessly integrate GeoMx IPA into your lab with a histology compatible workflow.

You can add 40- custom targets to this panel, to yield 610-plex screening

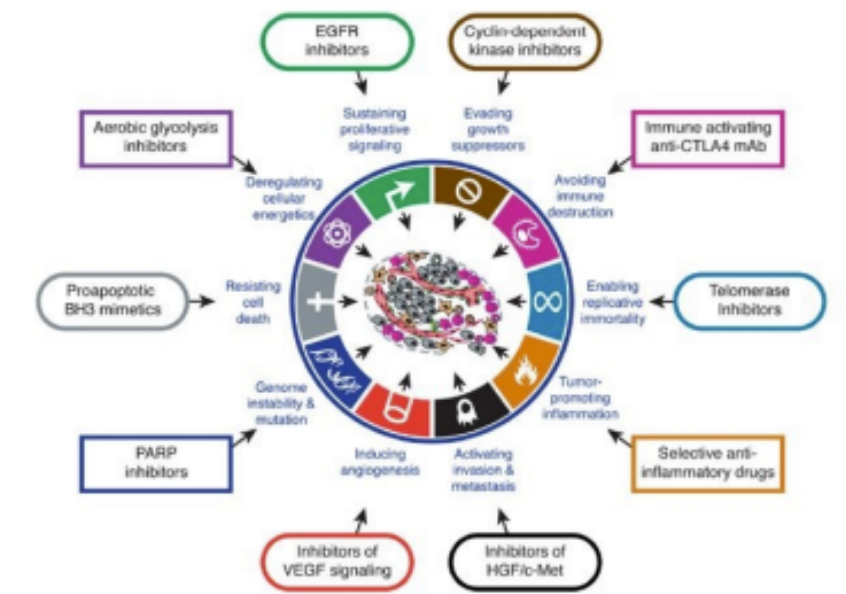
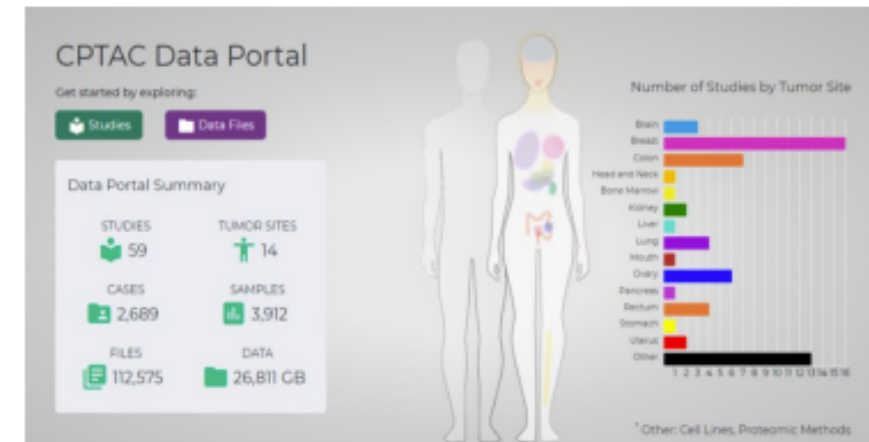


Highest-Plex Systems-Biology Approach, Spatially-Resolved, Cancer-Focused Panel Ever Developed (by far)

Designing an Immuno Oncology Proteome Atlas

Curated and validated IO Content

- Use Clinical Proteomic Tumor Analysis Consortium (CPTAC) data
- Focus on post-translational modifications
- Use high quality abcam antibodies
- Employ Immuno Oncology subject matter experts
- Human Specific
- 570+ Proteins, Mapped to 556 Unique Genes
- 77 Functional Annotations
- All Hallmarks of Cancer

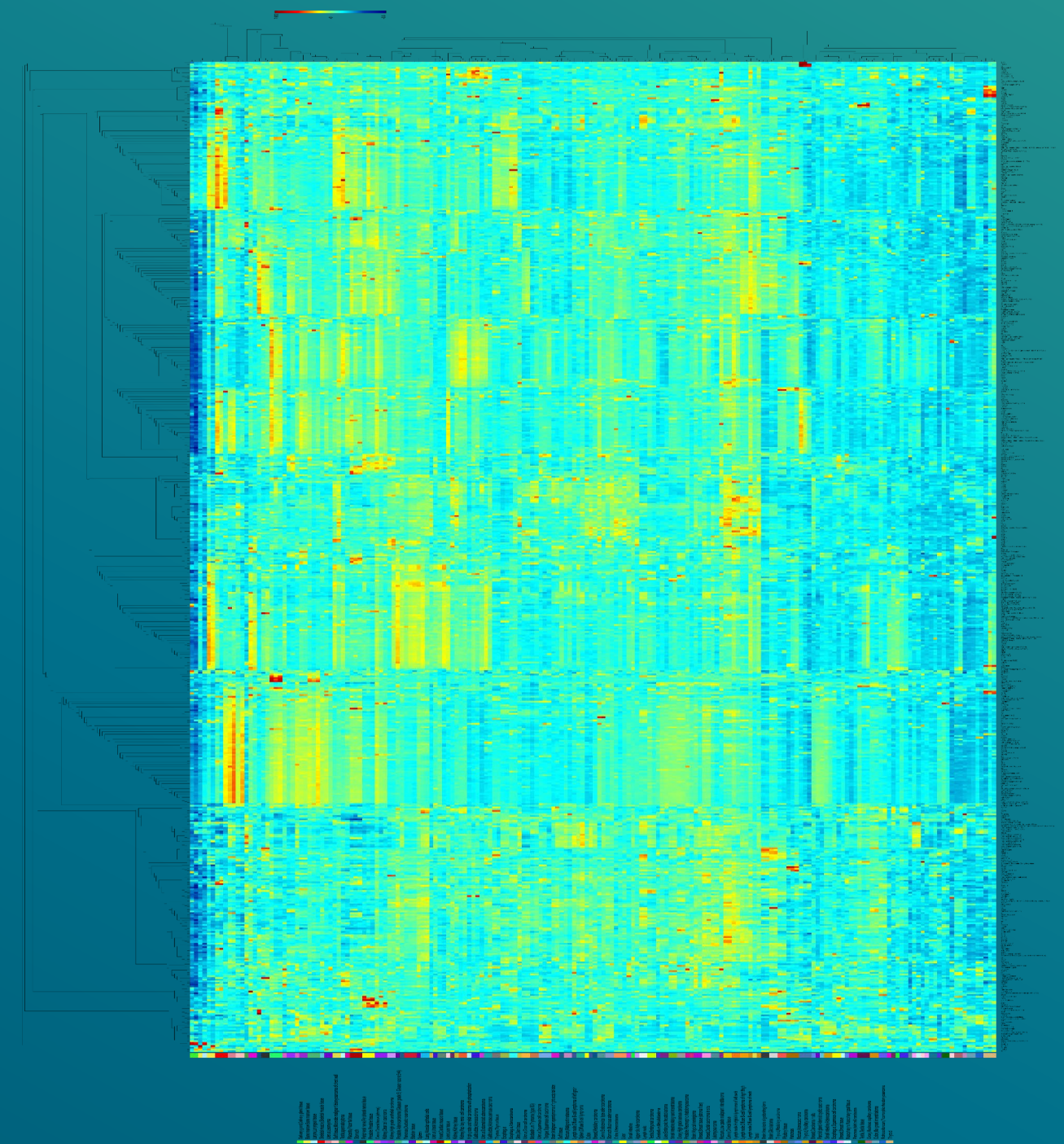
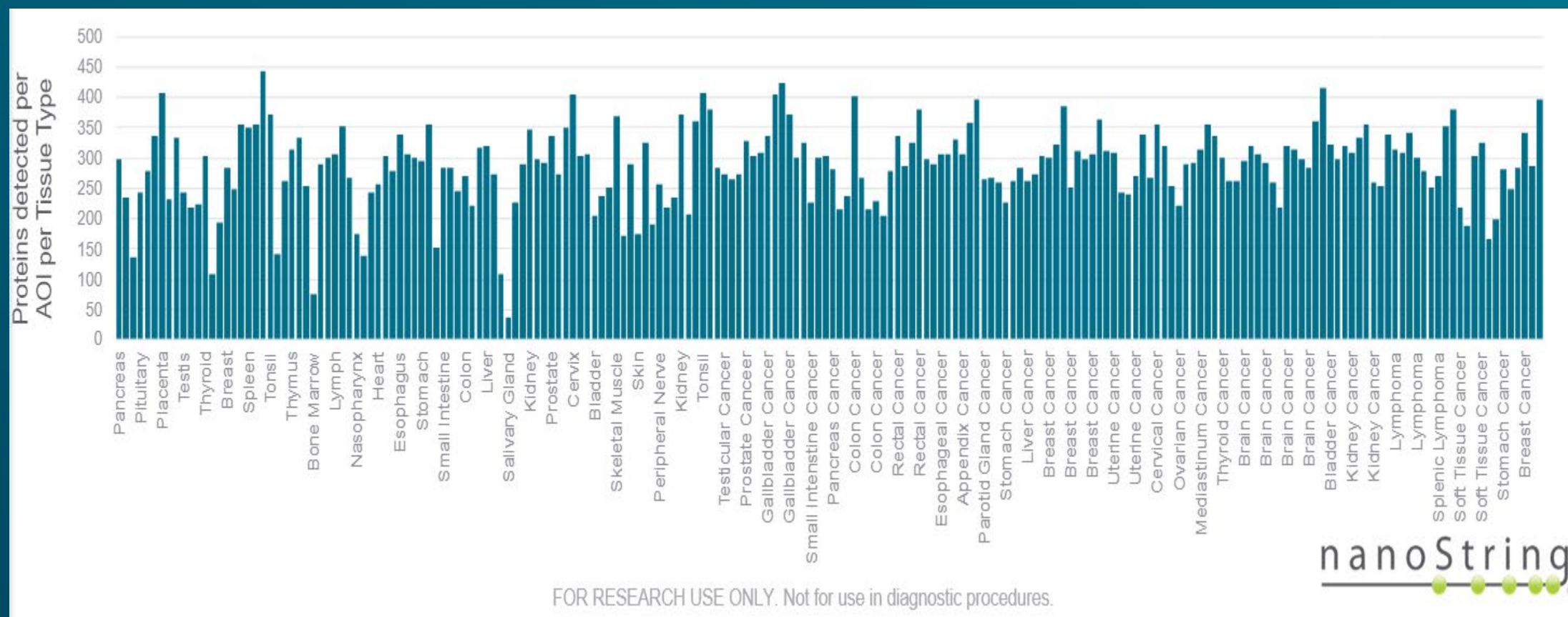
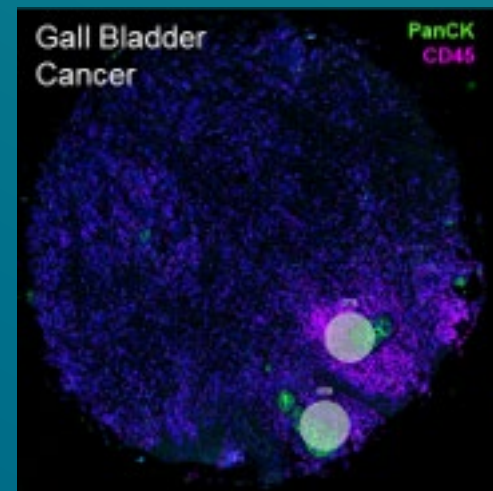
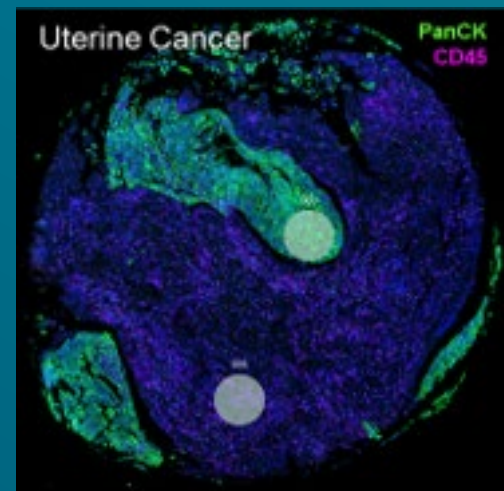
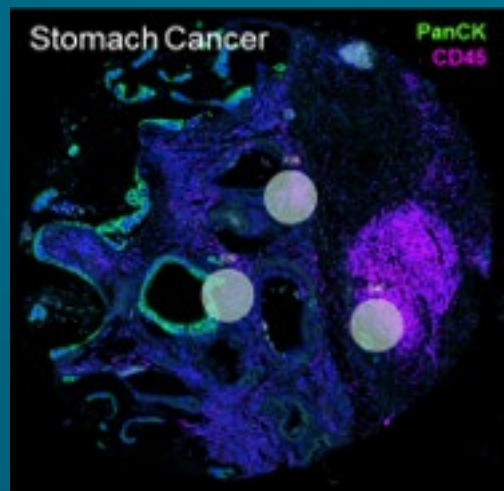
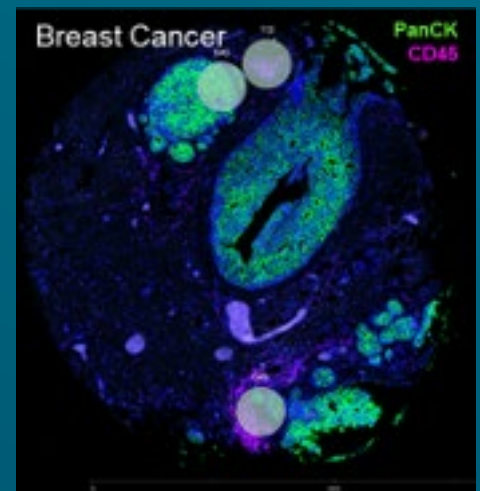


AMPK Signaling	Epigenetic Modifications	Lipid Metabolism	Proteotoxic Stress	Complement System	HIF1 Signaling	NO Signaling	TH1 Differentiation
Androgen Signaling	ERBB2 Signaling	MET Signaling	Purinergic Signaling	Cytotoxicity	Hippo Signaling	Notch Signaling	TH17 Differentiation
Apoptosis	Estrogen Signaling	MHC I/II	RAGE Signaling	Differentiation	IDH1/2	NRF2 Signaling	TH2 Differentiation
Autophagy	FGFR Signaling	Mitochondrial Metabolism	Senescence	DNA Damage Repair	IL Signaling	Oxidative Stress	TLR Signaling
Cancer	FoxO Signaling	mTor Signalling	T Cell Exhaustion	Drug Resistance	Immortality & Stemness	P53 Signaling	TNF Signaling
Cell Adhesion	Glutamine Metabolism	Myc	T-Cell Checkpoints	EGFR Signaling	Insulin Signaling	P13-Akt Signaling	Treg Differentiation
Cell Cycle	Glycolysis-Glucose Transport	Myeloid Inflammation	TCR Signaling	EMT	Interferon Response	PDGF Signaling	Type 1 & 2 Interferon Signalling
Chemokine Signaling	Hedgehog Signaling	NF-kB Signaling	TGF-Beta Signaling	Endocytosis	JAK-STAT Signaling	Prostaglandin Inflammation	VEGF Signaling
							Wnt Signaling

GeoMx Immuno Oncology Proteome Atlas Functional Pathways

Also, can be "same-slide" combined with GeoMx Whole Transcriptome Atlas (> 18,000 plex) RNA

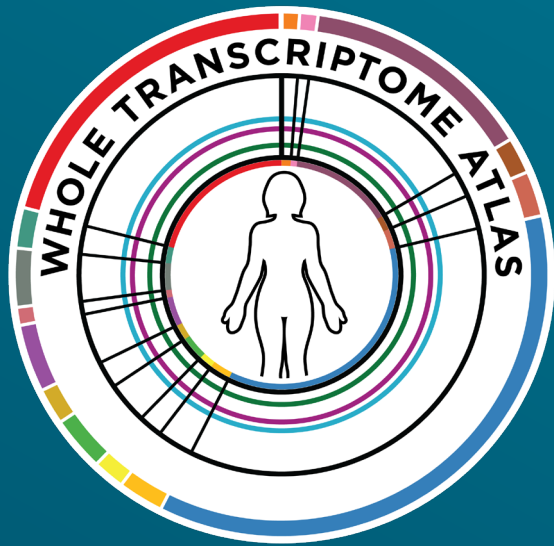
GeoMx 570-plex Immune-Proteome Atlas Resolves hundreds of proteins on nearly every tissue of the body (normal & cancerous)



Same-Slide, 570-plex Protein (up to 610-plex with Custom) plus 18,000+ RNA in Tissue: Finally a Protein-Plex to get excited about!



CRC FFPE sample



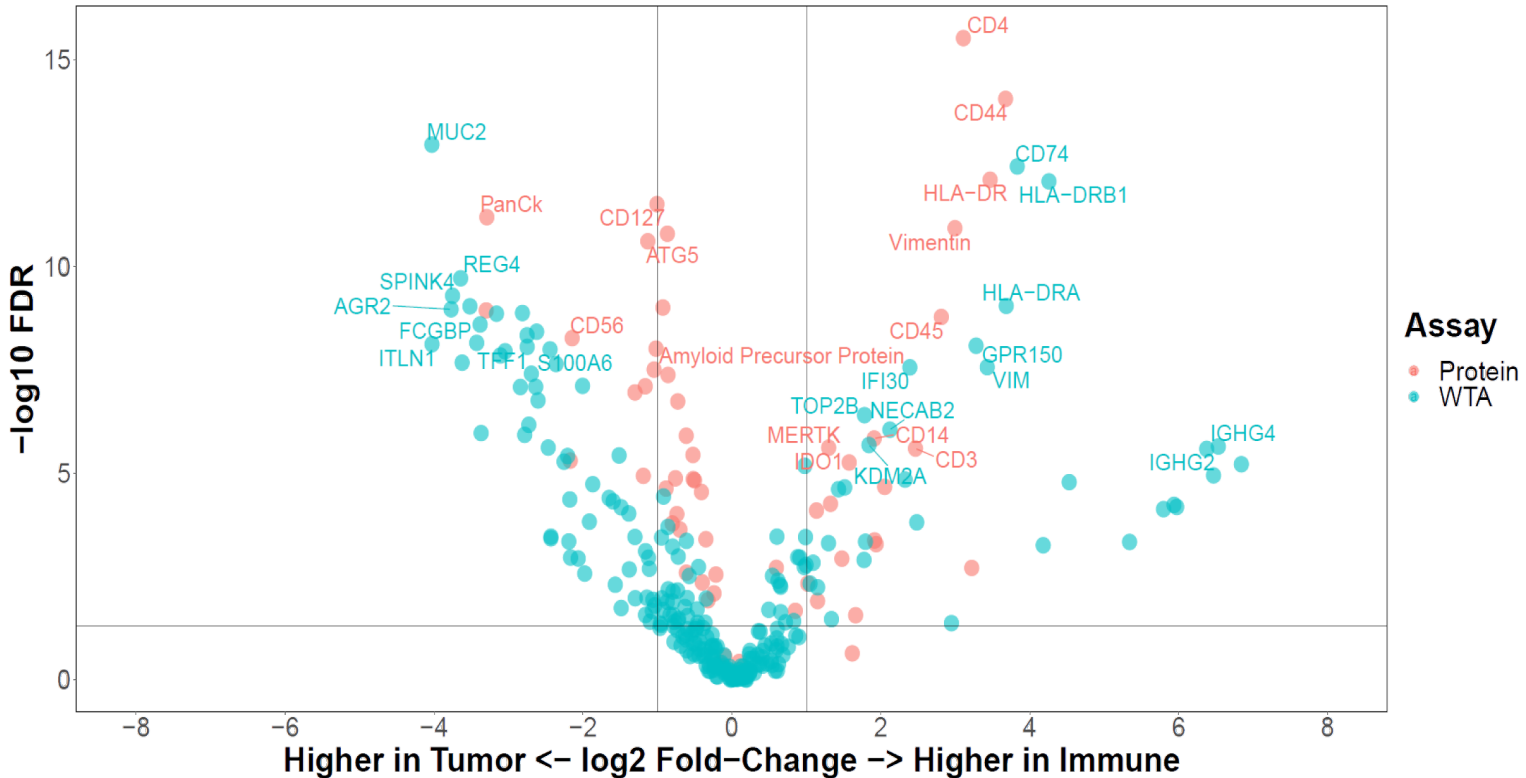
Information on cellular mechanisms and regulation

+

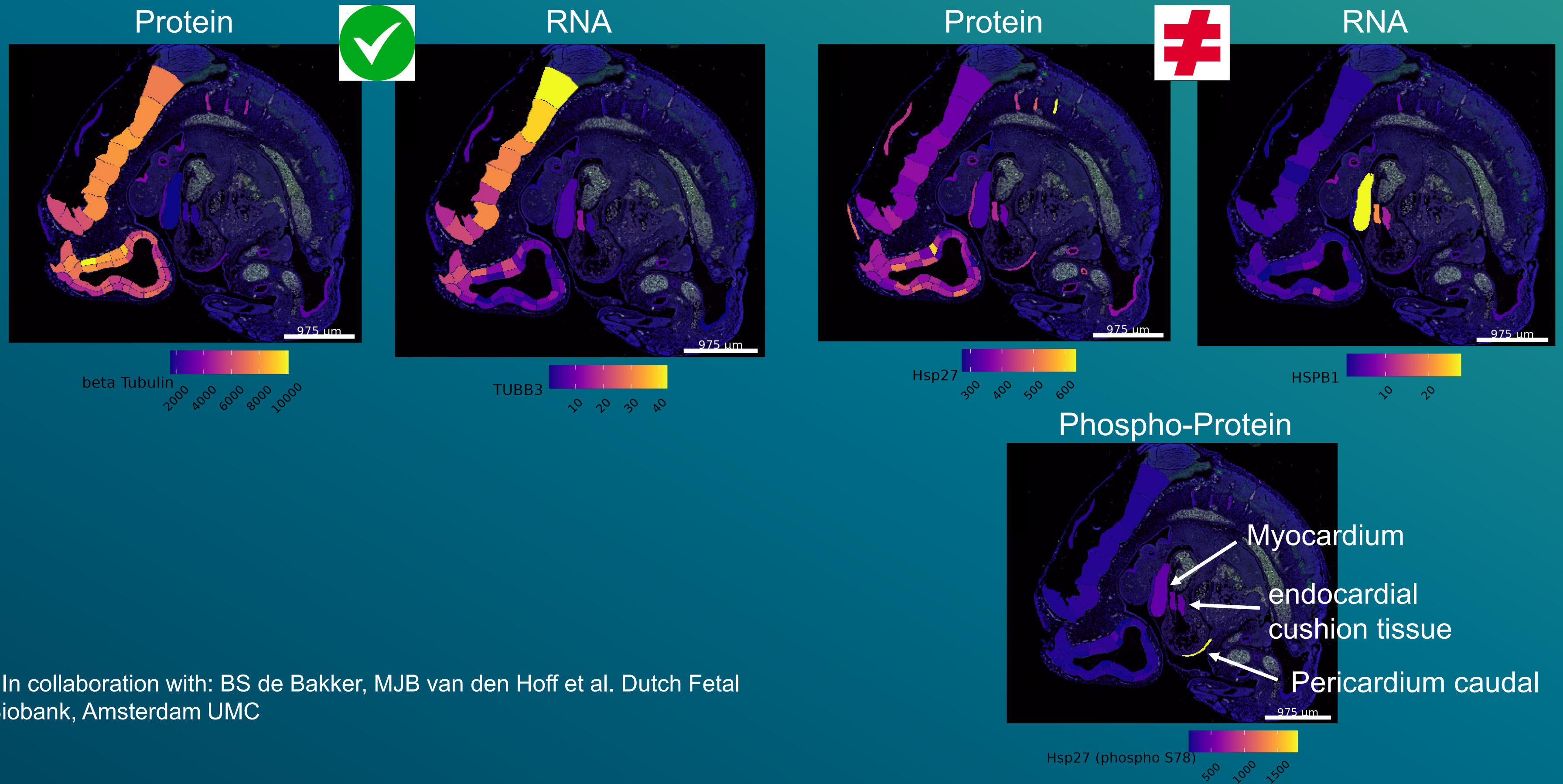


Information on cellular function and phenotypes

DE between Immune and Tumor Segments

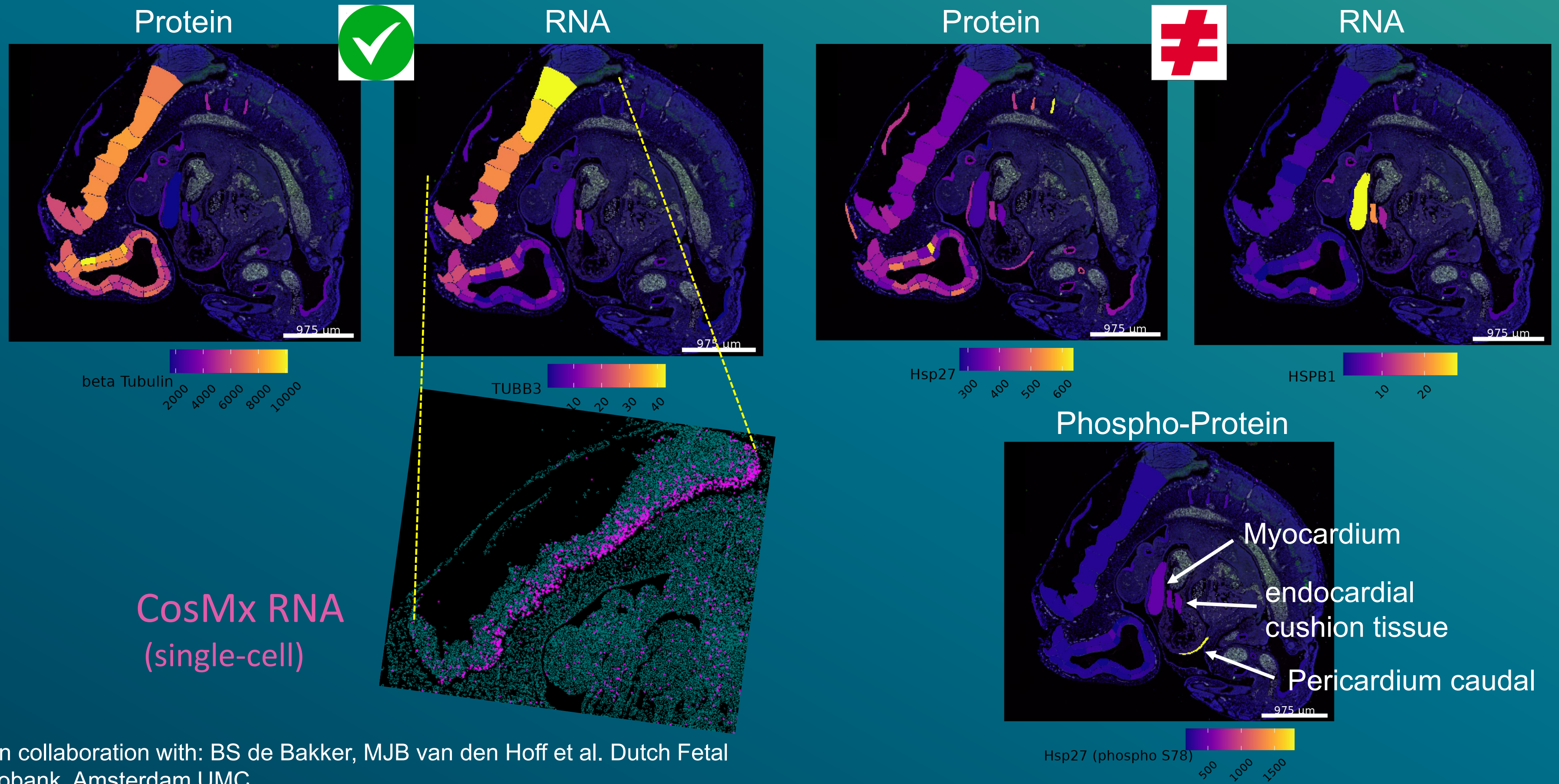


Example of same slide 570-plex protein, 18,000-plex RNA in an 8-week (post-gestation) whole human embryo*



* In collaboration with: BS de Bakker, MJB van den Hoff et al. Dutch Fetal Biobank, Amsterdam UMC

Example of same slide 570-plex protein, 18,000-plex RNA in an 8-week (post-gestation) whole human embryo*

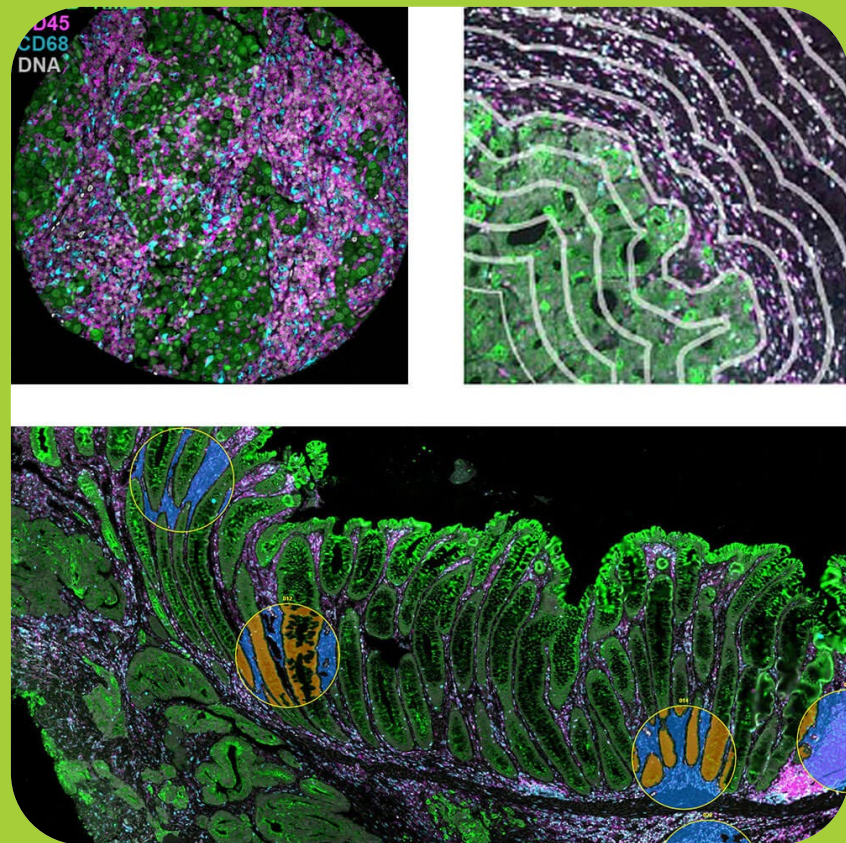


* In collaboration with: BS de Bakker, MJB van den Hoff et al. Dutch Fetal Biobank, Amsterdam UMC

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

Profilers

TISSUE STRUCTURES
~ 100 μm



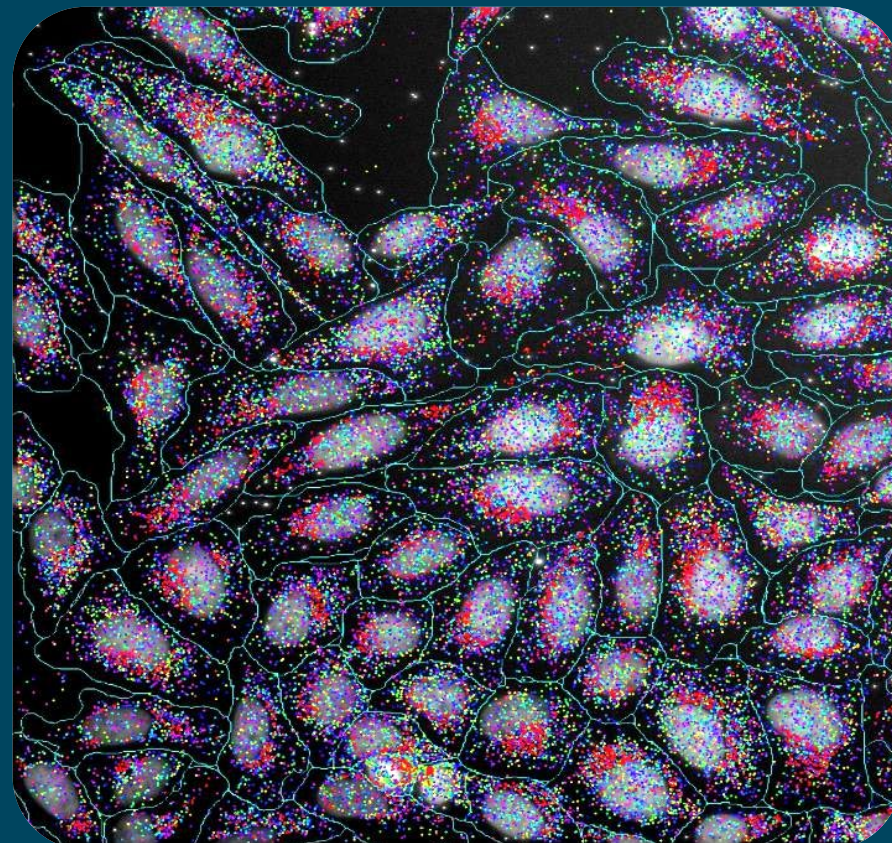
GeoMx[®]
Digital Spatial Profiler

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

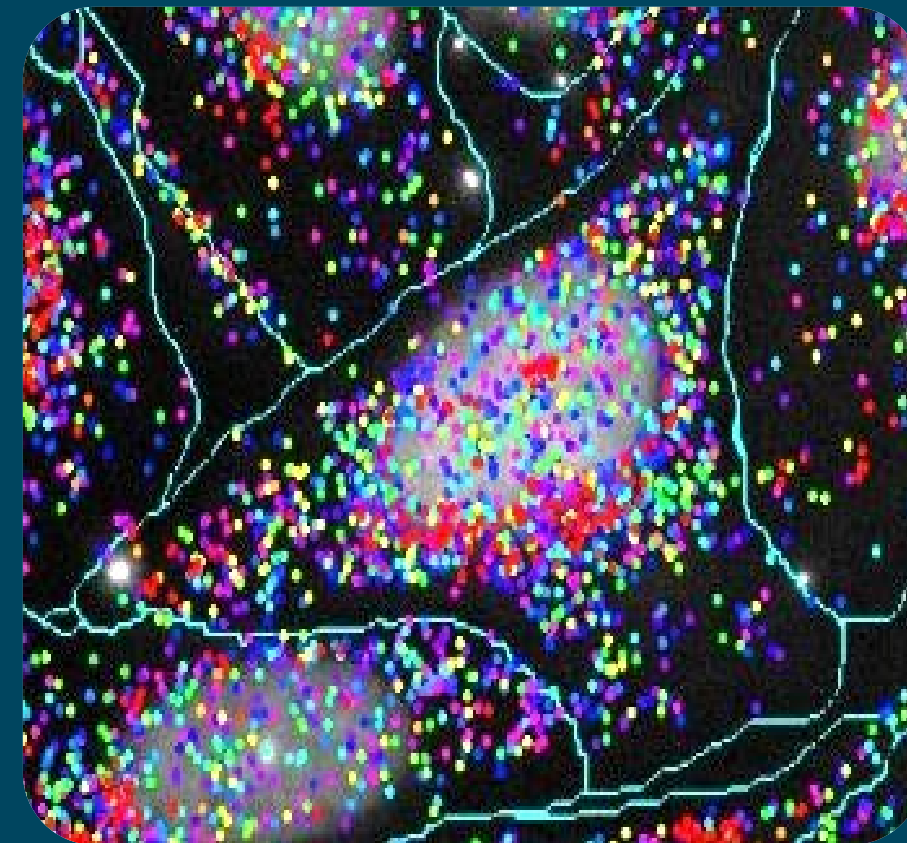


Imagers

SINGLE CELL
~ 10 μm



SUB-CELLULAR
~ 1 μm



CosMx[™]
Spatial Molecular Imager

**Up to Whole Transcriptome (>18,000-plex) RNA
76-plex Proteins**



nanoString[®]

CosMx Whole Transcriptome Key Performance Characteristics

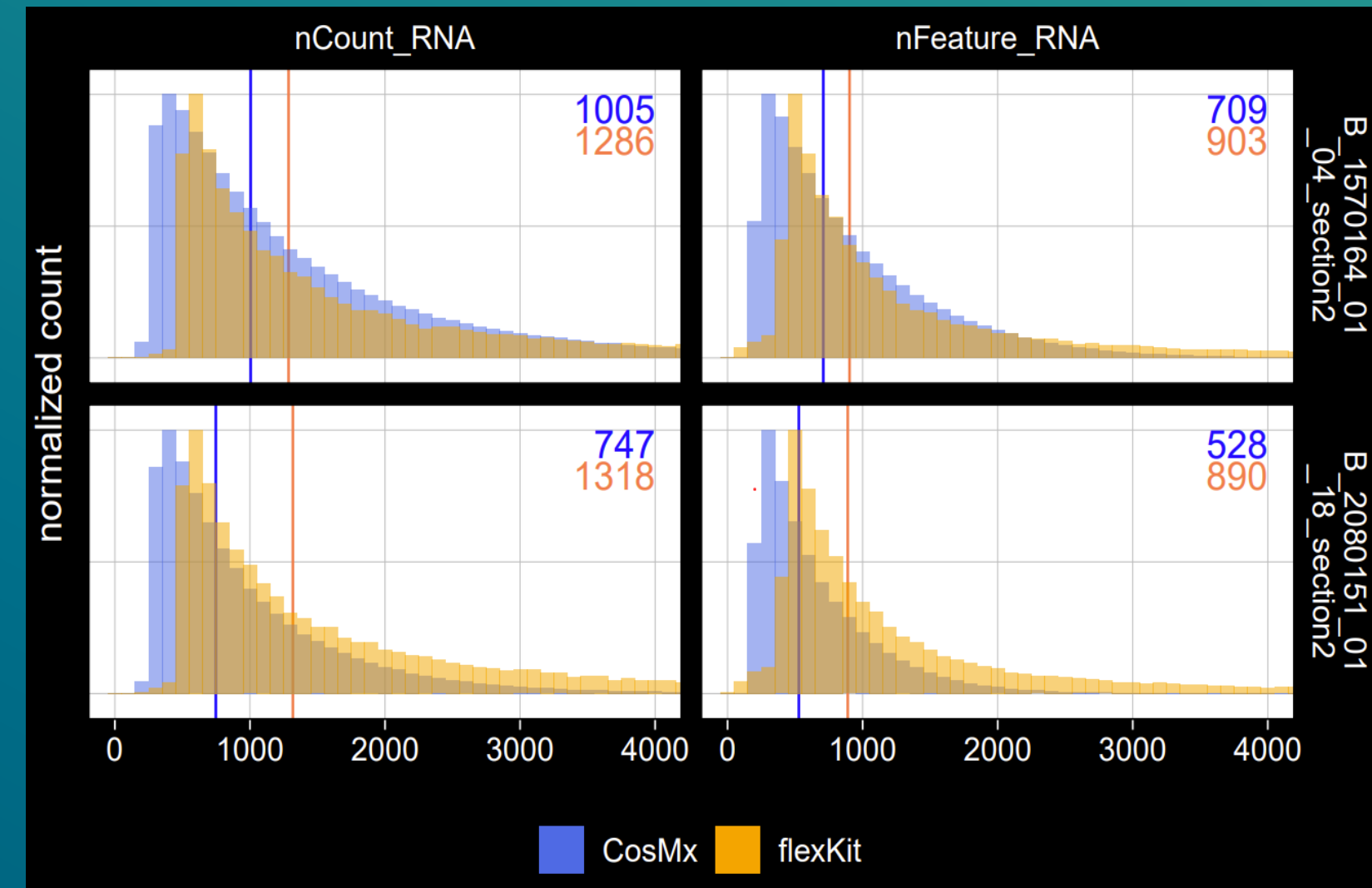
From the very beginning of CosMx design, we had one overriding goal:

Recapitulate ALL of the capabilities of scRNA-seq, but with sub-cellular spatial resolution

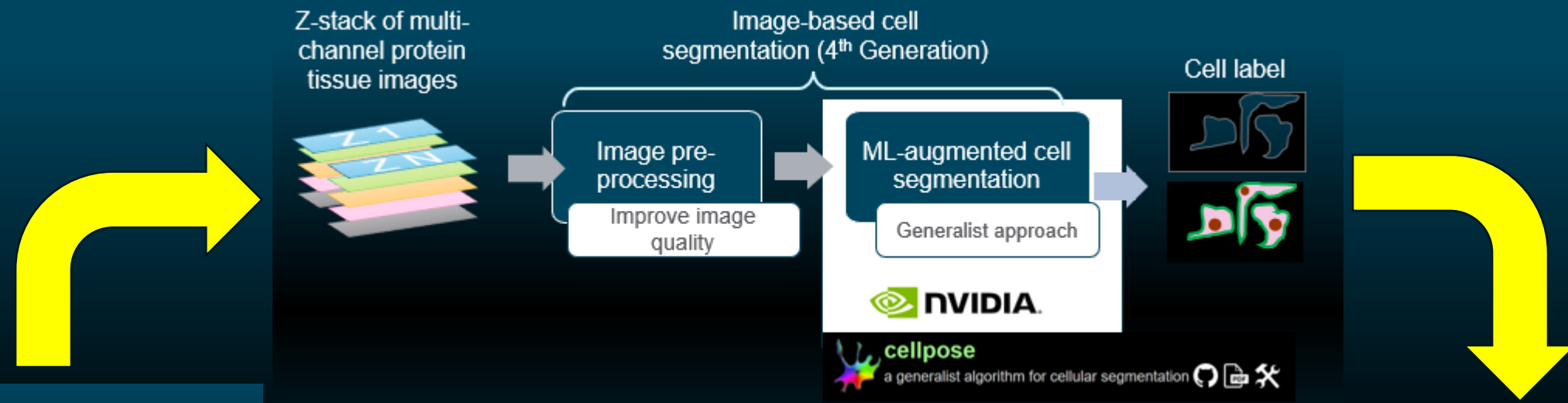
The Performance Specifications that count should be identical to how scRNA-seq is measured

- Sensitivity = maximum number of transcripts per cell =
CosMx clearly wins here...
- Sensitivity = largest diversity of transcripts per cell =
CosMx clearly wins here...
- For above specifications to be real, best-in-class segmentation required
CosMx clearly wins here...

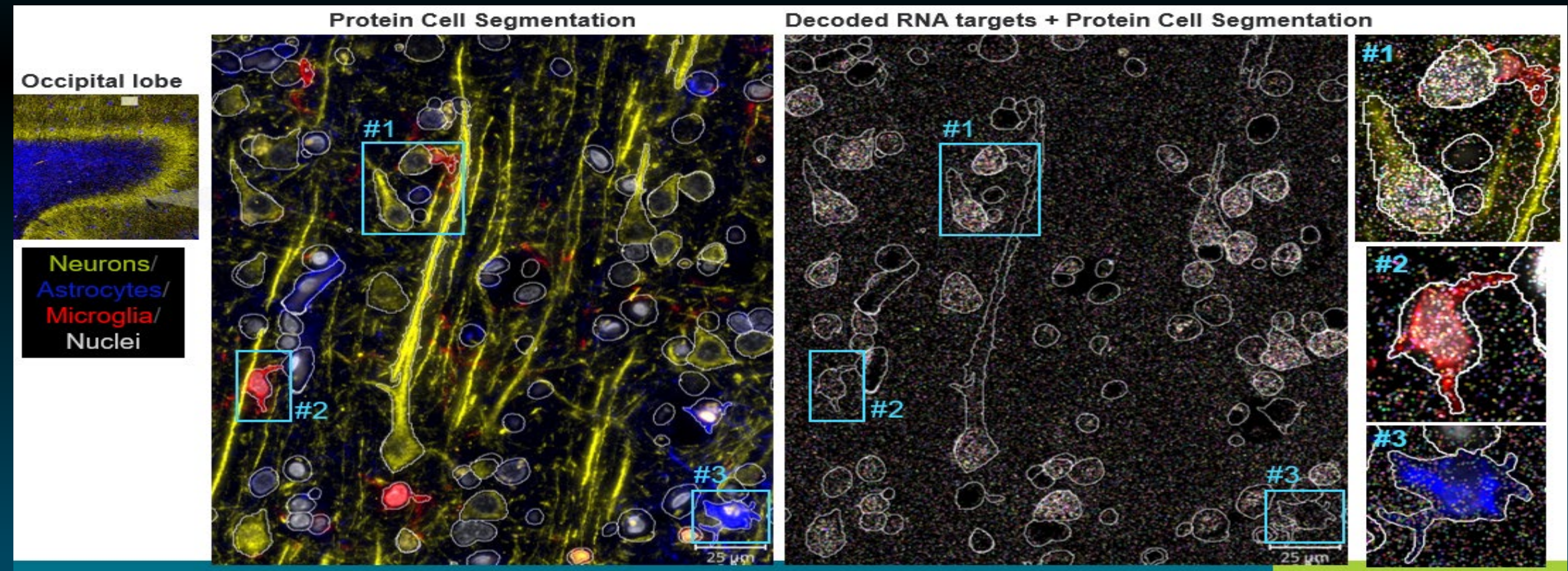
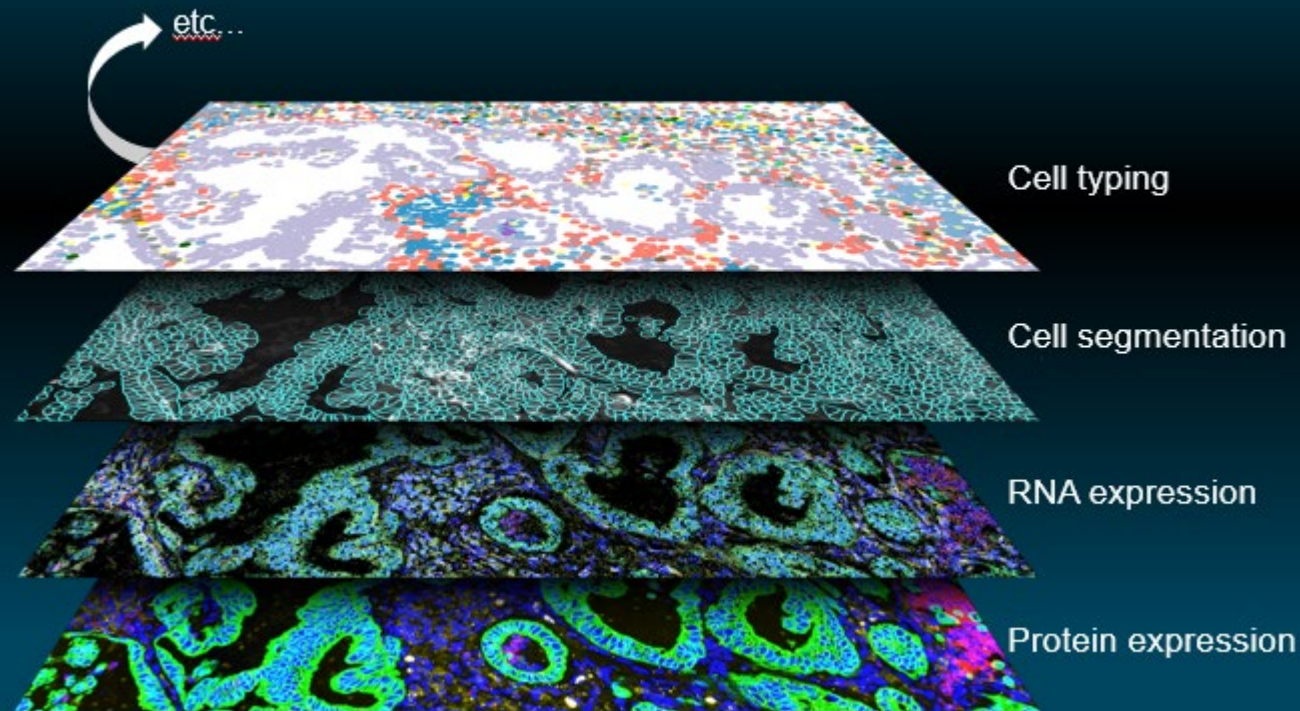
(in collaboration with Dr. Holger Heyn, CNAG)



CosMx Cell-Segmentation: High-Plex Protein Driven, nVIDIA Accelerated, AI-ML trained, and with 4th Generation Release



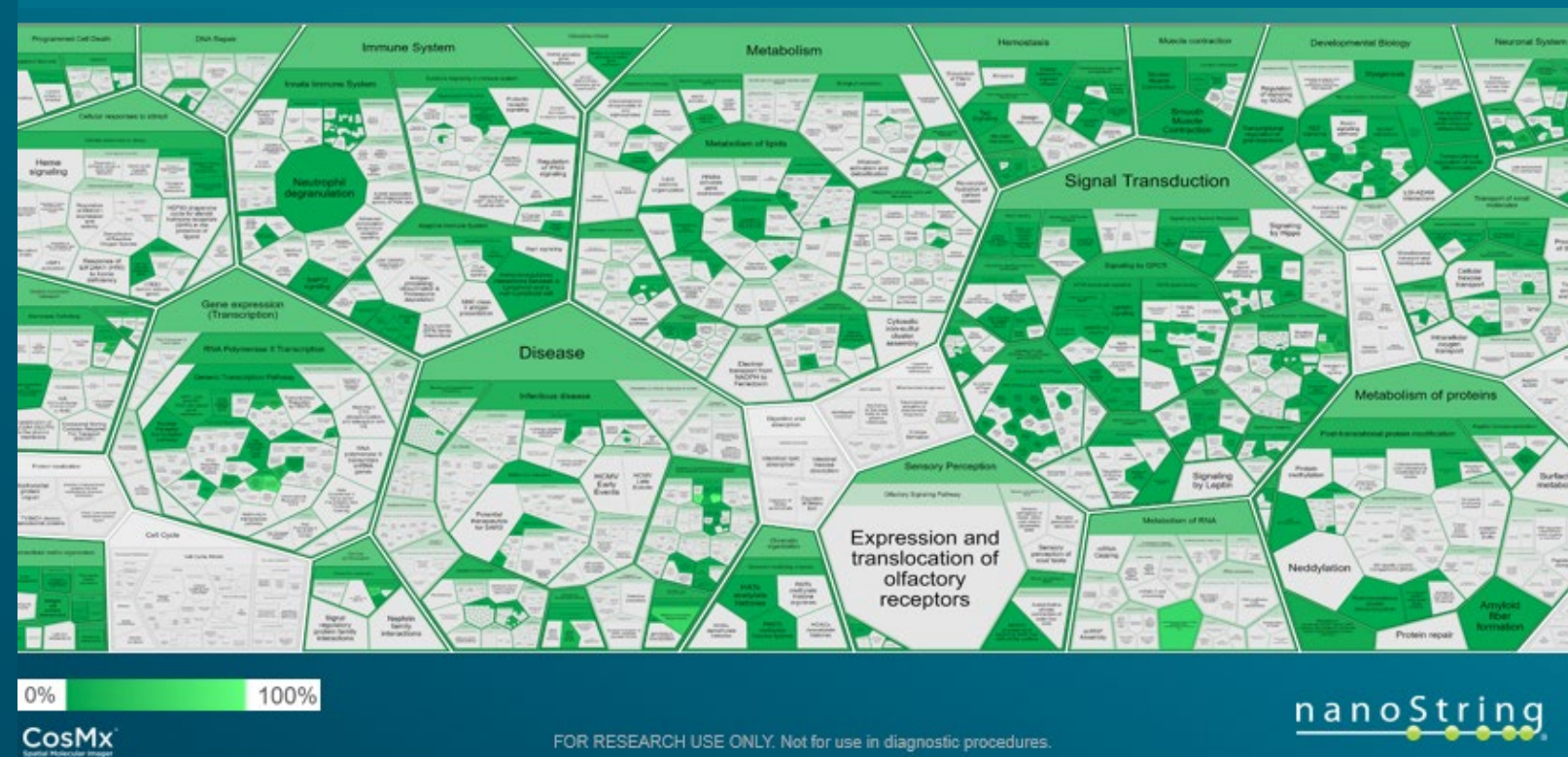
Delivers multiple-layer information



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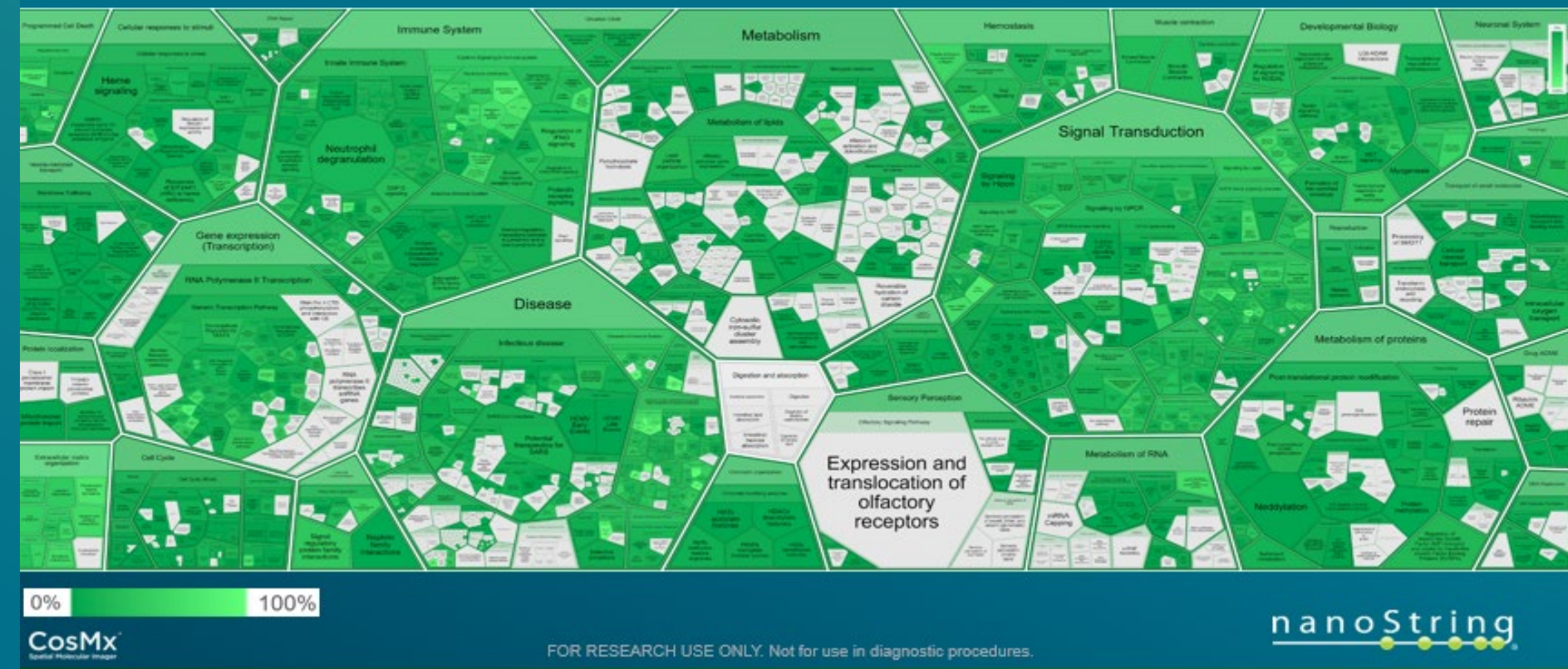
High-Plex Panels can be organ/disease agnostic. 200 Million single-cells and 60 publications later now proves this point

Example: Commercial 247-plex Panel



Organ-specific panel coverage of reactome

CosMx 1,000-plex Panel: Covers Single Cell Biology



CosMx SMI 1000-plex Delivered 60+ Publications and Preprints

Tissue Encyclopedia

Cell Reports
Stomach encyclopedia: Combined single-cell and spatial transcriptomics reveal cell diversity and homeostatic regulation of human stomach

Authors: Aydin Talebiani, Dinkar Kumar, Mehdi Kahrizi, ...

Patient-to-Patient Heterogeneity

nature communications
Macrophage and neutrophil heterogeneity at single-cell spatial resolution in human inflammatory bowel disease

Authors: Alisa Santilli-Trig, ...

Drug Mechanism of Action

CLINICAL CANCER RESEARCH | TRANSLATIONAL CANCER MECHANISMS AND THERAPY
Trackable intratumor microdosing and spatial profiling provide early insights into activity of investigational agents in the intact tumor microenvironment

Authors: Jonathan M. J. Derry, ...

Disease Characterization

bioRxiv
Resolving high-resolution spatial transcriptomics to characterize the amyloid disease cell niche in Alzheimer's Disease

Authors: Anna Malach, ...

3D Cell Atlas

bioRxiv
High-resolution molecular atlas of a lung tumor in 3D

Authors: Tarek Mounir Permal, ...

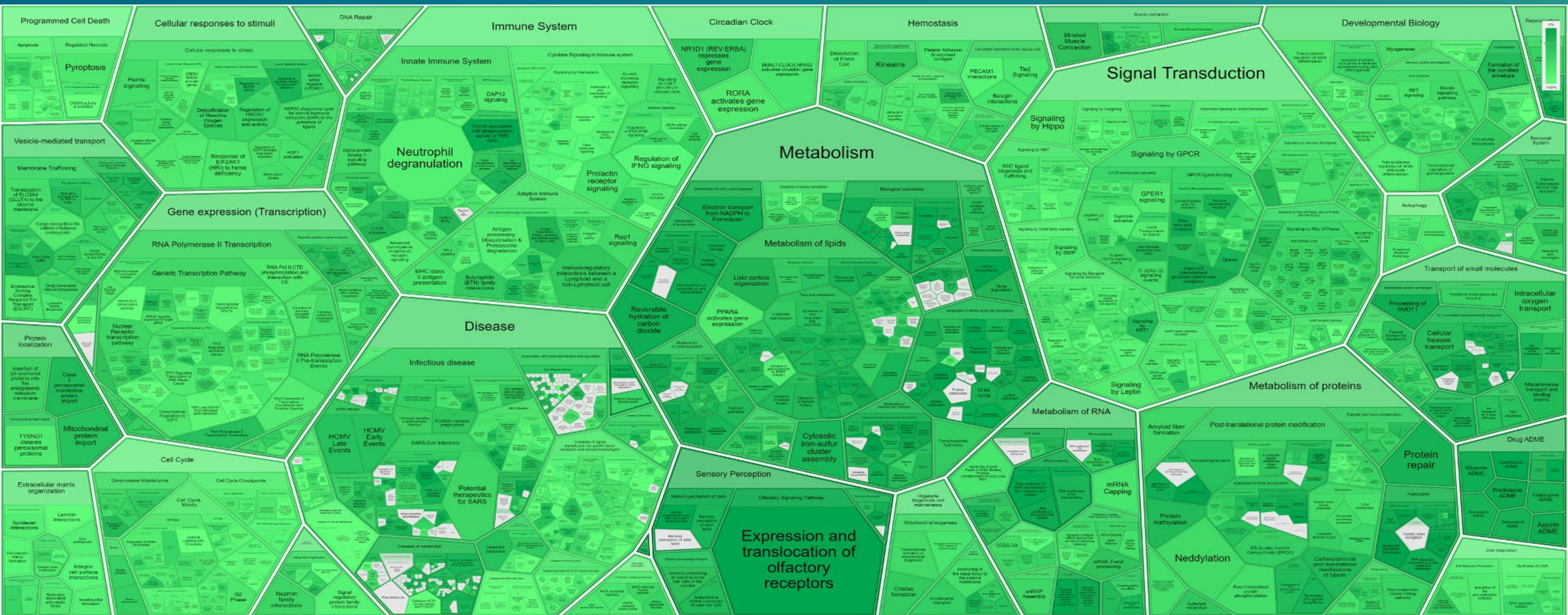
-- Selected Publications --

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CosMx 6,000-plex Panel: Now Shipping Commercially

scRNA-seq NOT required, measure all the sample biology in a single slide



0% 100%

CosMx
Spatial Molecular Imager

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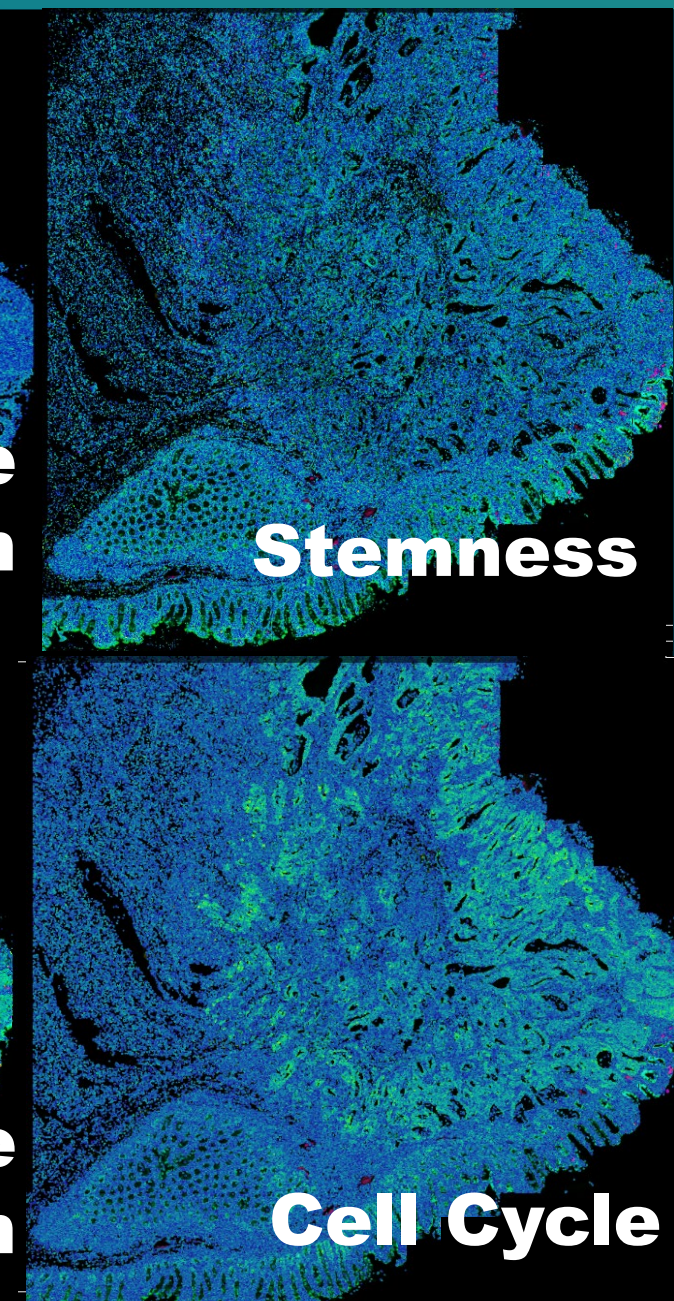
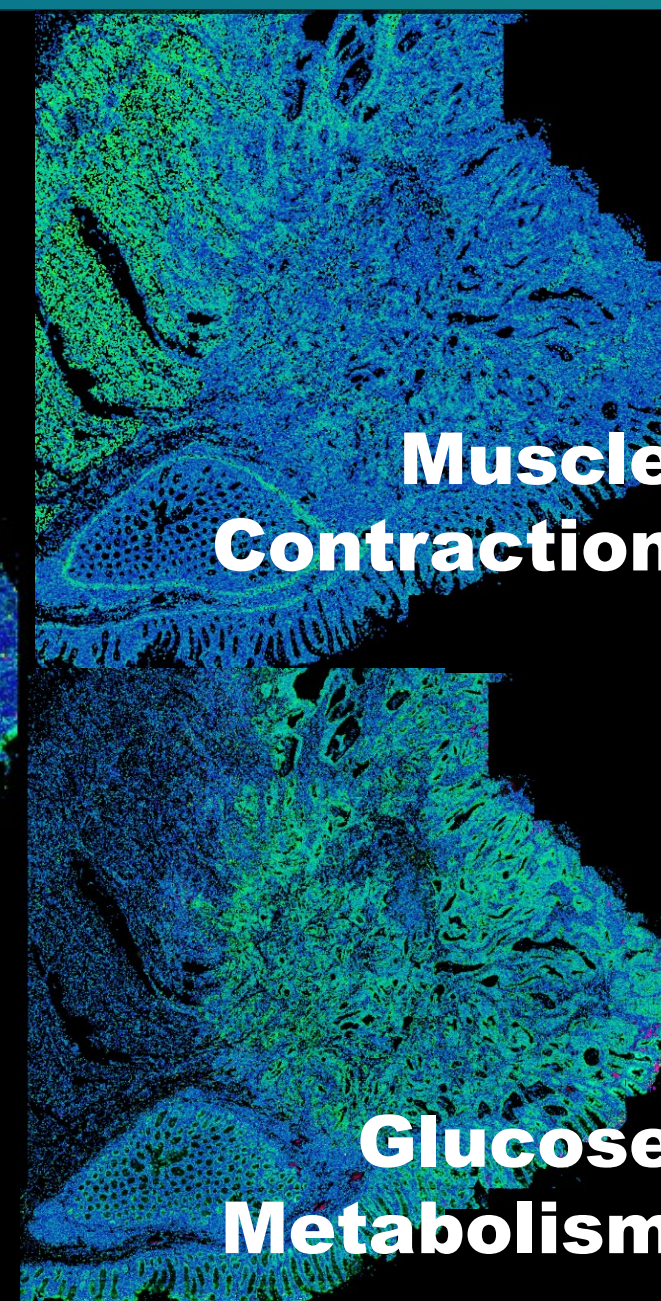
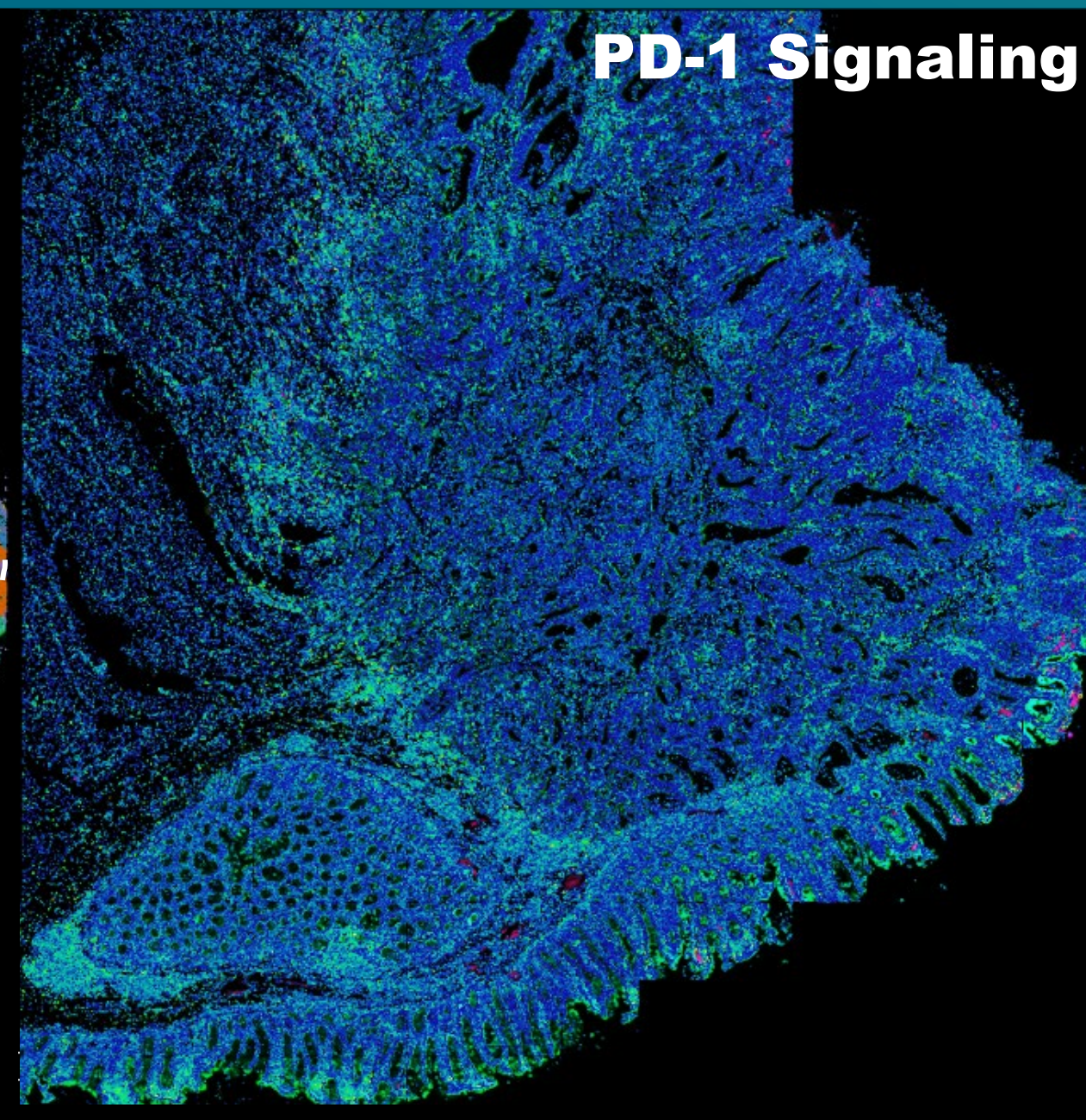
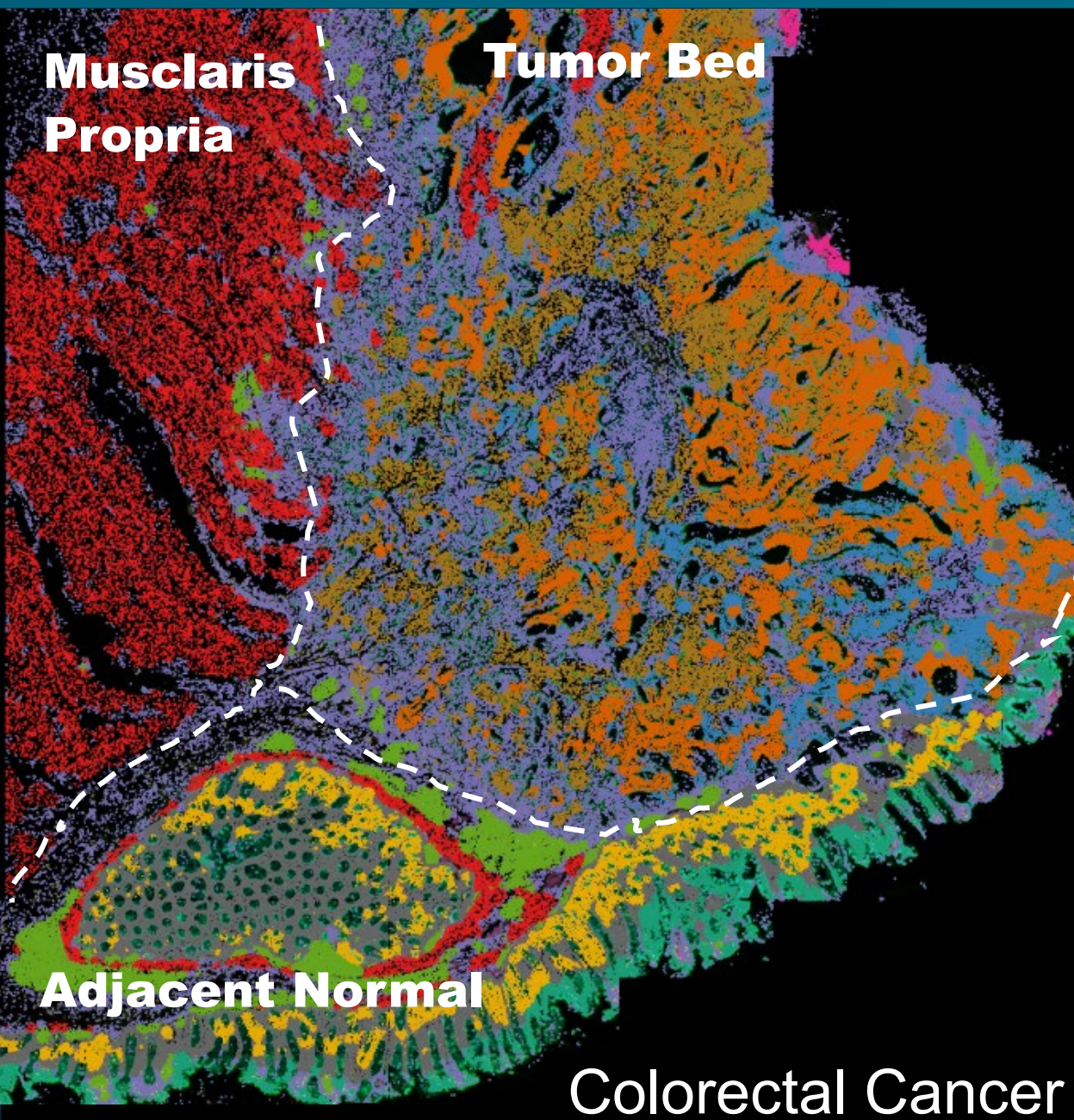
nanoString

Move beyond “marker-gene” and “individual-gene” analysis with 6,000-plex, directly “project” the full-biology of the reactome onto the tissue



CosMx 6,000-plex public dataset

Directly “view” in the tissue, >90% of the Reactome (~ 400 pathways-of-biology)



Does CosMx 6000-plex work on real-world FFPE samples? ABSOLUTELY, Extended the work that made the cover of *Nature Genetics*



Single-nucleus and spatial transcriptome profiling of pancreatic cancer identifies multicellular dynamics associated with neoadjuvant treatment. (Aug 2022)

William L. Hwang, MD, PhD

Assistant Professor, Harvard Medical School

Principal Investigator, Center for Systems Biology/

Department of Radiation Oncology/Center for Cancer Research, Massachusetts General Hospital

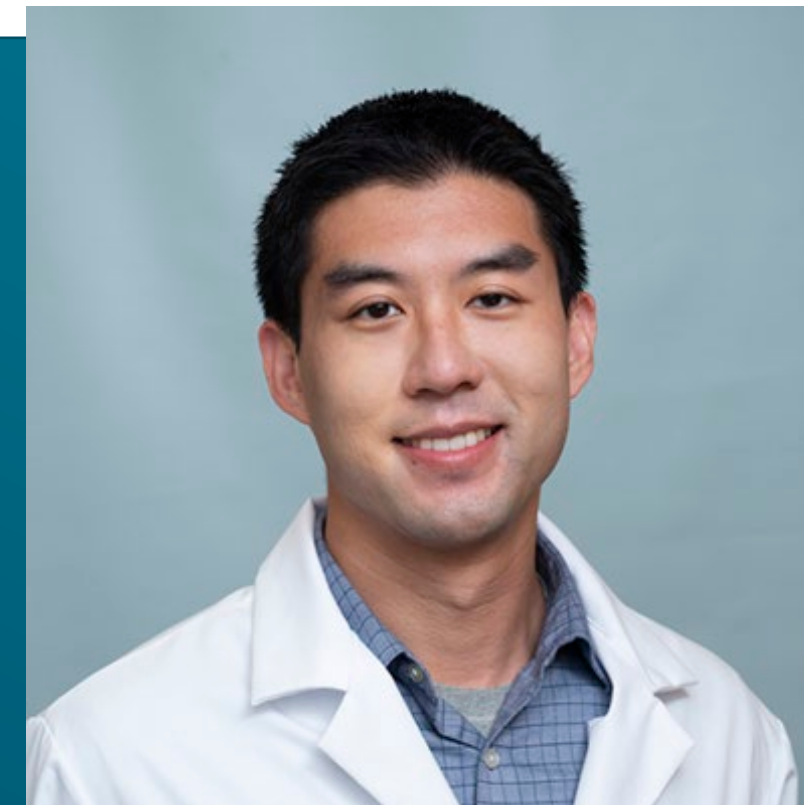
Associate Member, Broad Institute of MIT and Harvard



HARVARD
MEDICAL SCHOOL



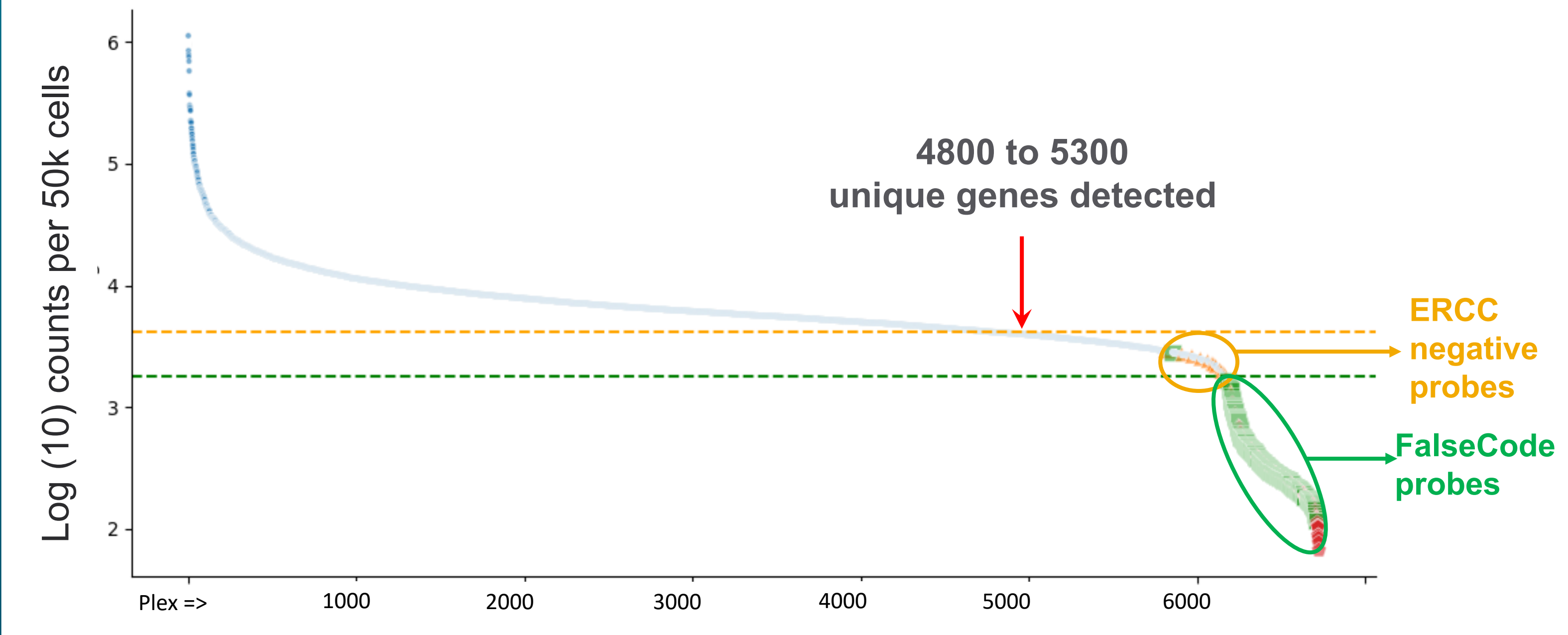
MASSACHUSETTS
GENERAL HOSPITAL



nanoString®

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CosMx 6000-plex: Amazing Diversity of Transcripts with Real-world FFPE Cancer Tissues



99.5% confidence above both ERCC and FalseCodes

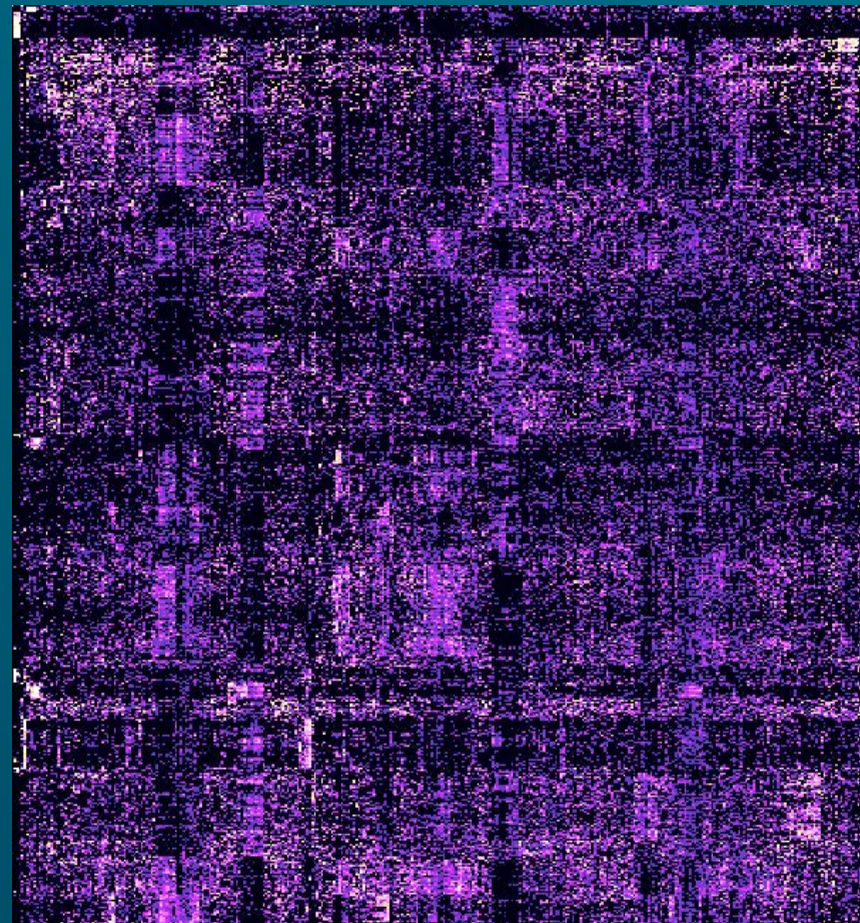
Spatial Cell-Signaling Ligand Exploration, Spatially *Co-expressed* Ligands.

Discovered a clear participation of NERVE-cells in the tumor microenvironment directly effecting tumor-immune interactions...

One cluster:
CCL5, CCL8, CXCL9, CXCL10, CD48, SEMA4D, SIGLEC1
Immune cell chemoattractants and activators.
Expressed in sporadic hotspots.

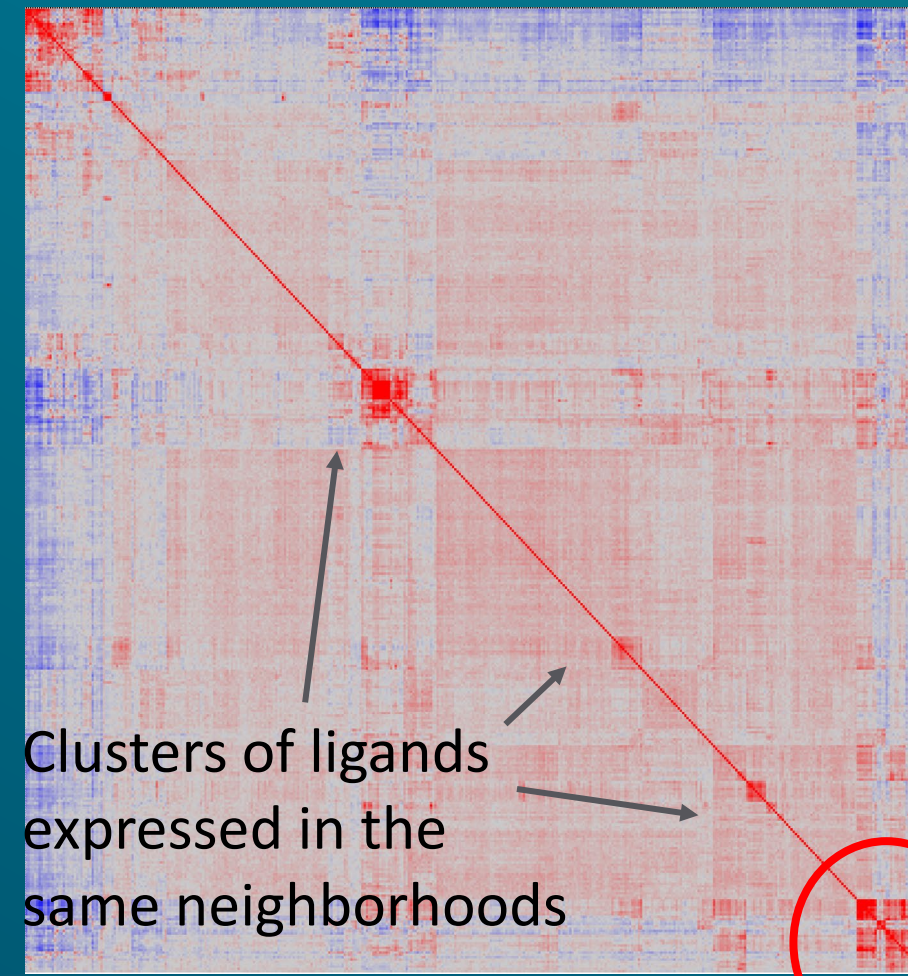
Profiles of cells' "ligand environments"

Correlation matrix of neighborhood expression from 407 x 407 ligands



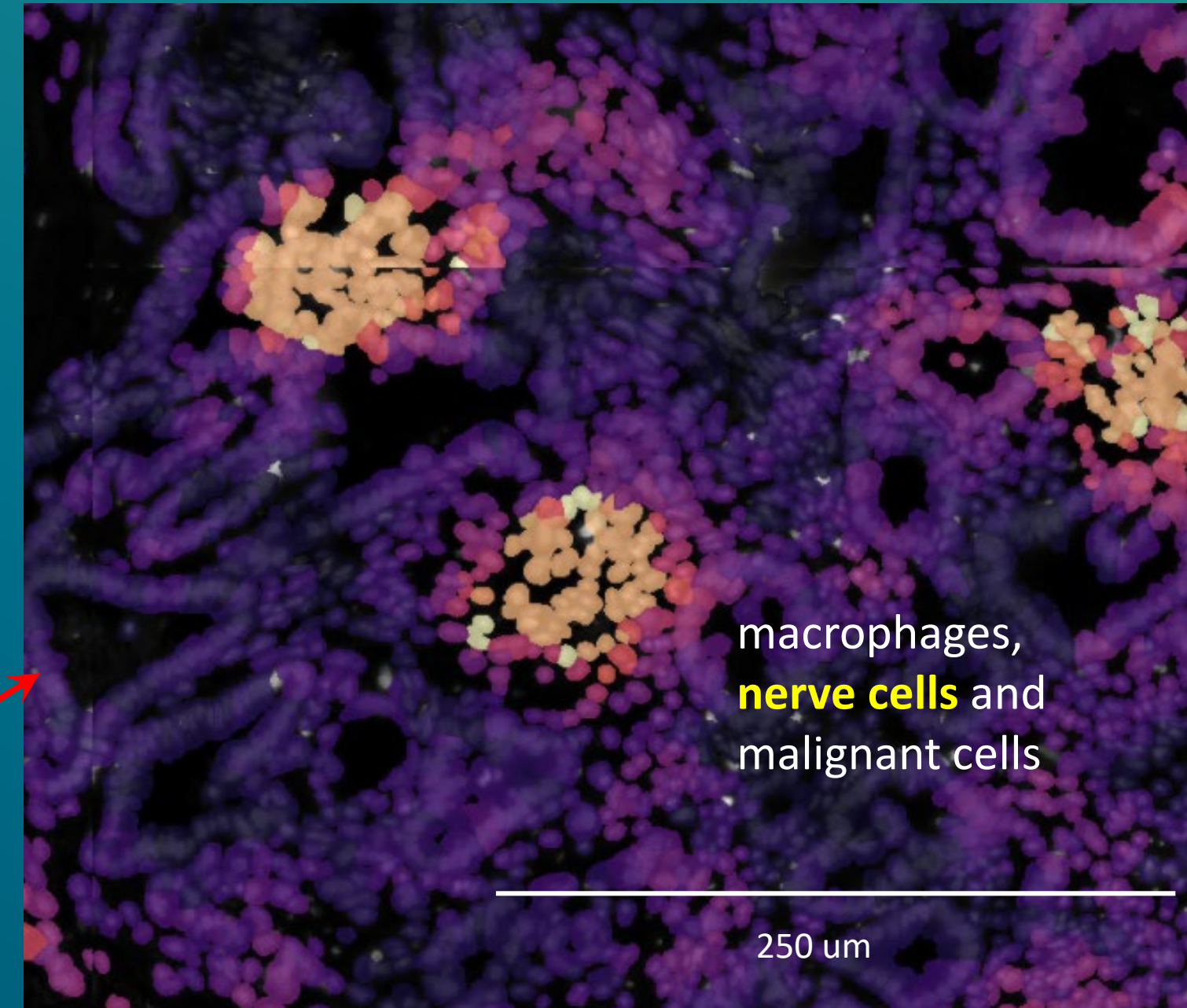
Ligands

407 Ligands



Clusters of ligands expressed in the same neighborhoods

Ligands



macrophages, **nerve cells** and malignant cells

250 um

(NOTE: can perform this analysis on 6000 X 6000 genes (36 Million spatial correlations))

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nanostRING

New Results

Follow this preprint

InSituCor: a toolkit for discovering non-trivial spatial correlations in spatial transcriptomics

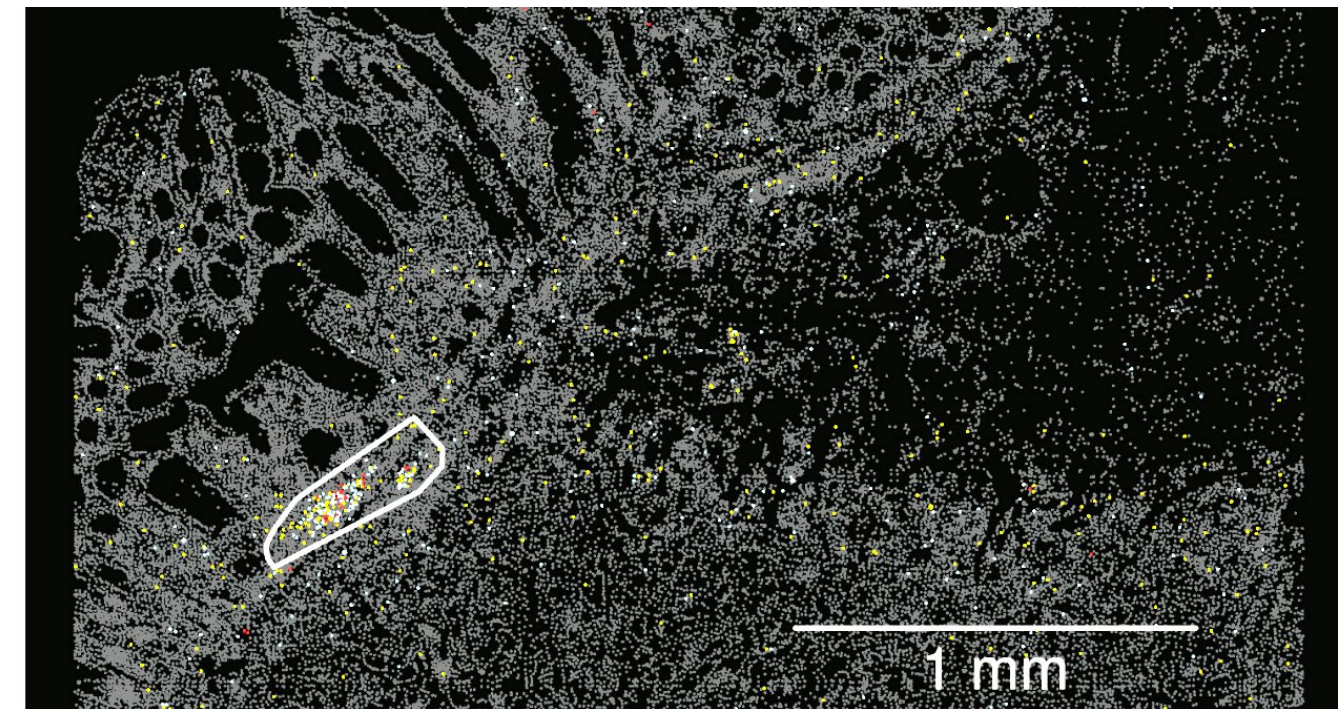
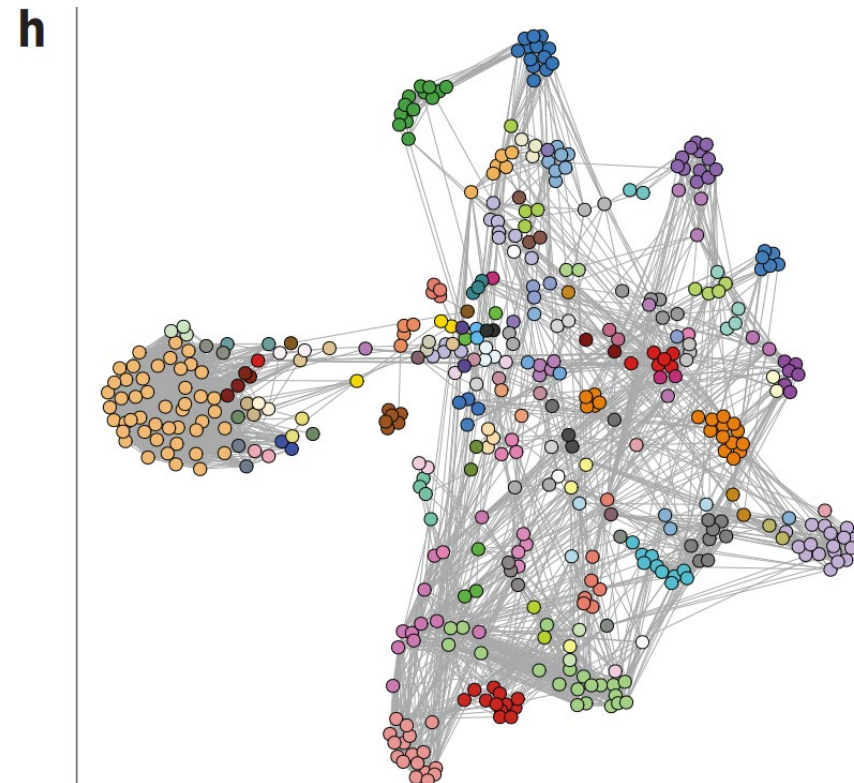
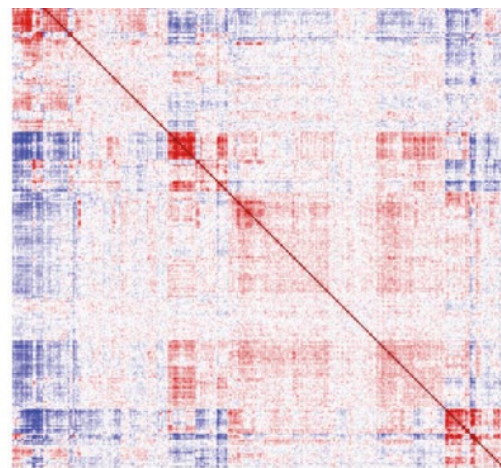
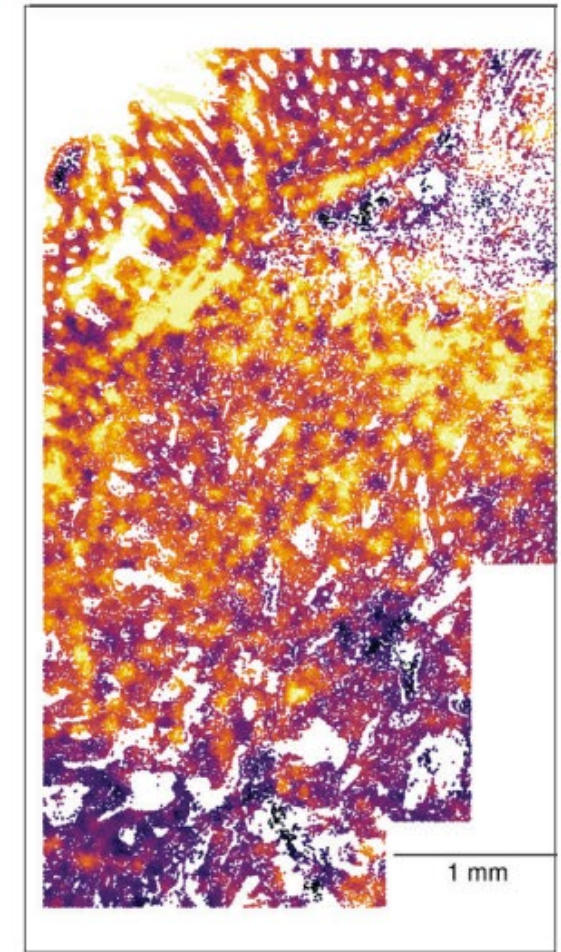
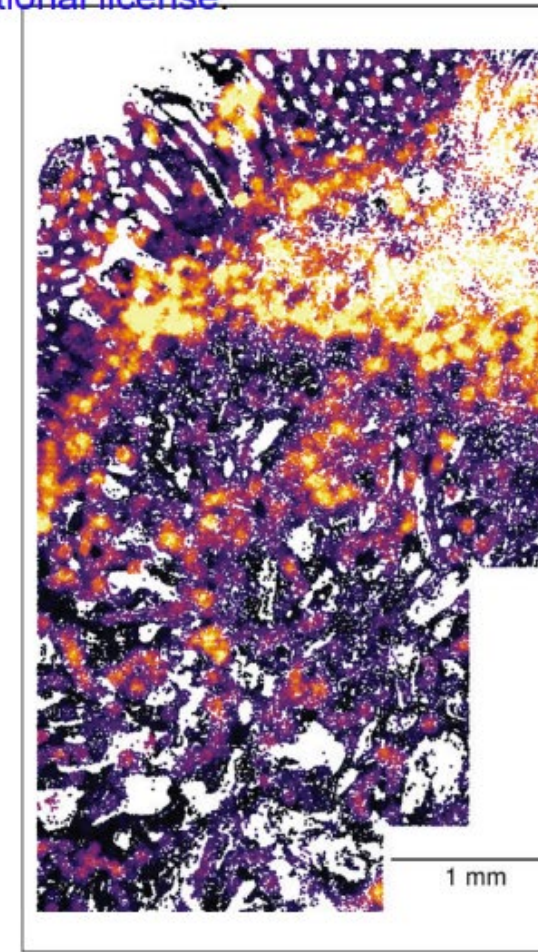
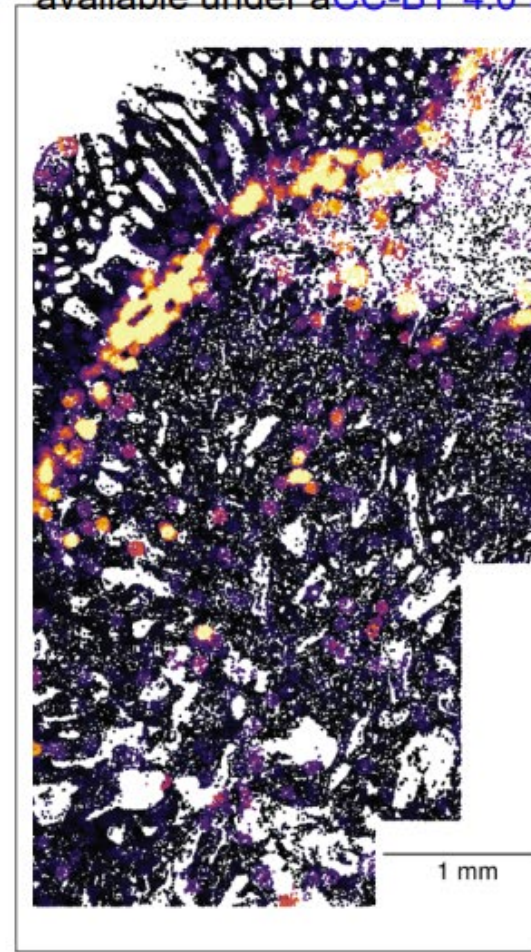
Patrick Danaher, Dan McGuire, Michael Patrick, David Kroeppler, Haiyan Zhai, Joachim Schmid, Joseph M. Beechem

doi: https://doi.org/10.1101/2023.09.19.558514

This article is a preprint and has not been certified by peer review [what does this mean?].



Abstract Full Text Info/History Metrics Preview PDF



No "human being" can examine 36 million spatial correlations, this method provides an automated, systematic method to focus on high-impact first-of-kind spatial discoveries

The “Holy-Grail” of Spatial Biology is Here

Explore Single-cell and Subcellular Imaging of the Whole Protein-coding Transcriptome (>18,000-plex)

nanoString

PRODUCTS

RESEARCH FOCUS

SUPPORT & RESOURCES

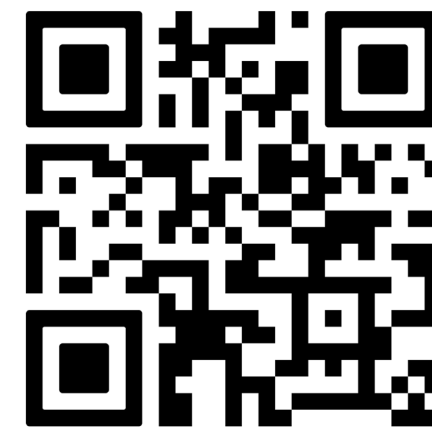
COMPANY



CosMx Human Pancreas FFPE Dataset

First Single-Cell Spatial Dataset with over 18,000 Genes

[REQUEST MORE INFORMATION](#)



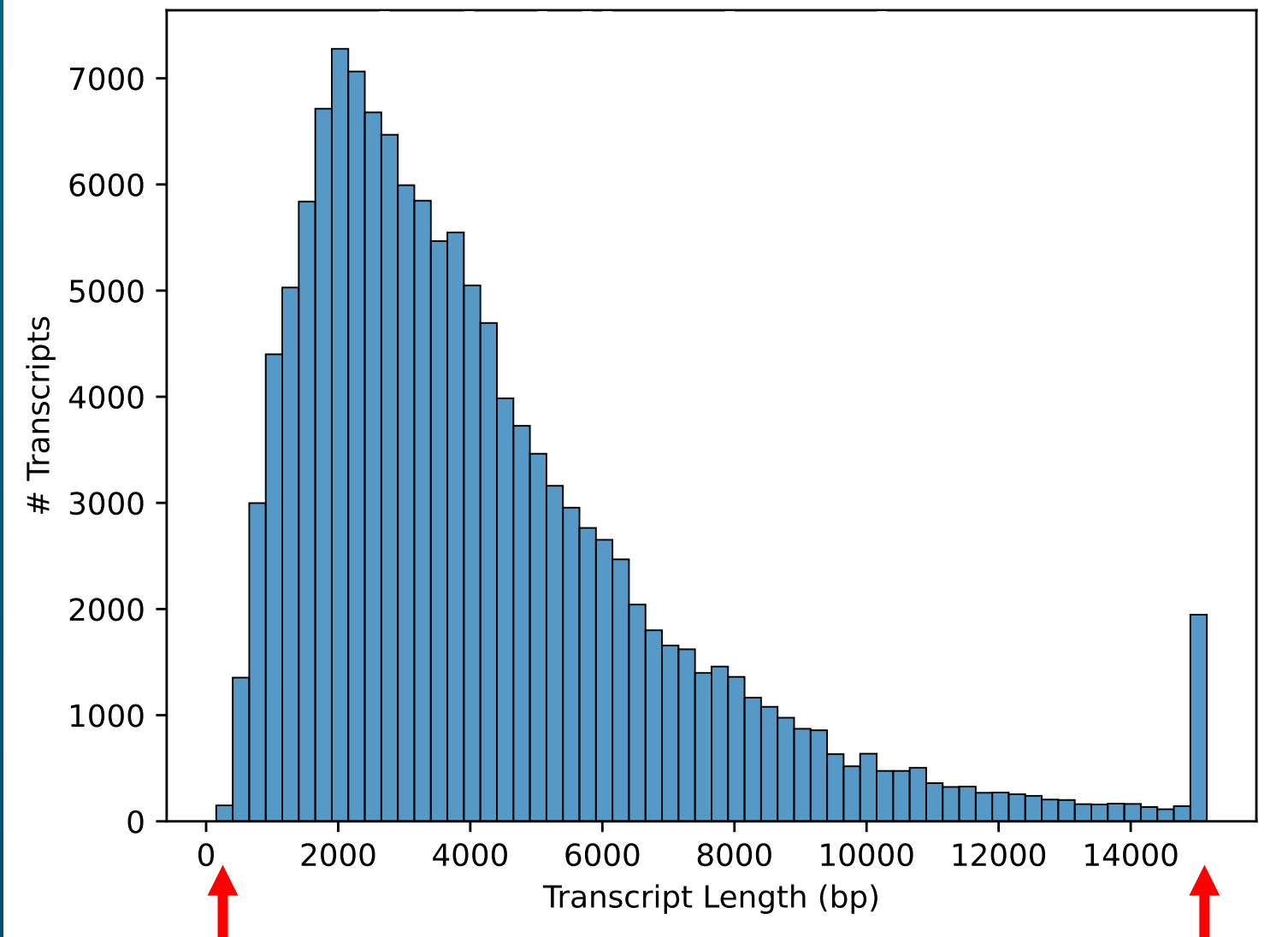
CosMx >18,000-plex dataset in public domain is here!

[Home](#) » [Products](#) » [CosMx Spatial Molecular Imager](#) » [CosMx™ SMI Datasets](#) » [CosMx SMI Human Pancreas FFPE...](#)

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

CosMx Whole Transcriptome (>18,000-plex) Imaging Panel

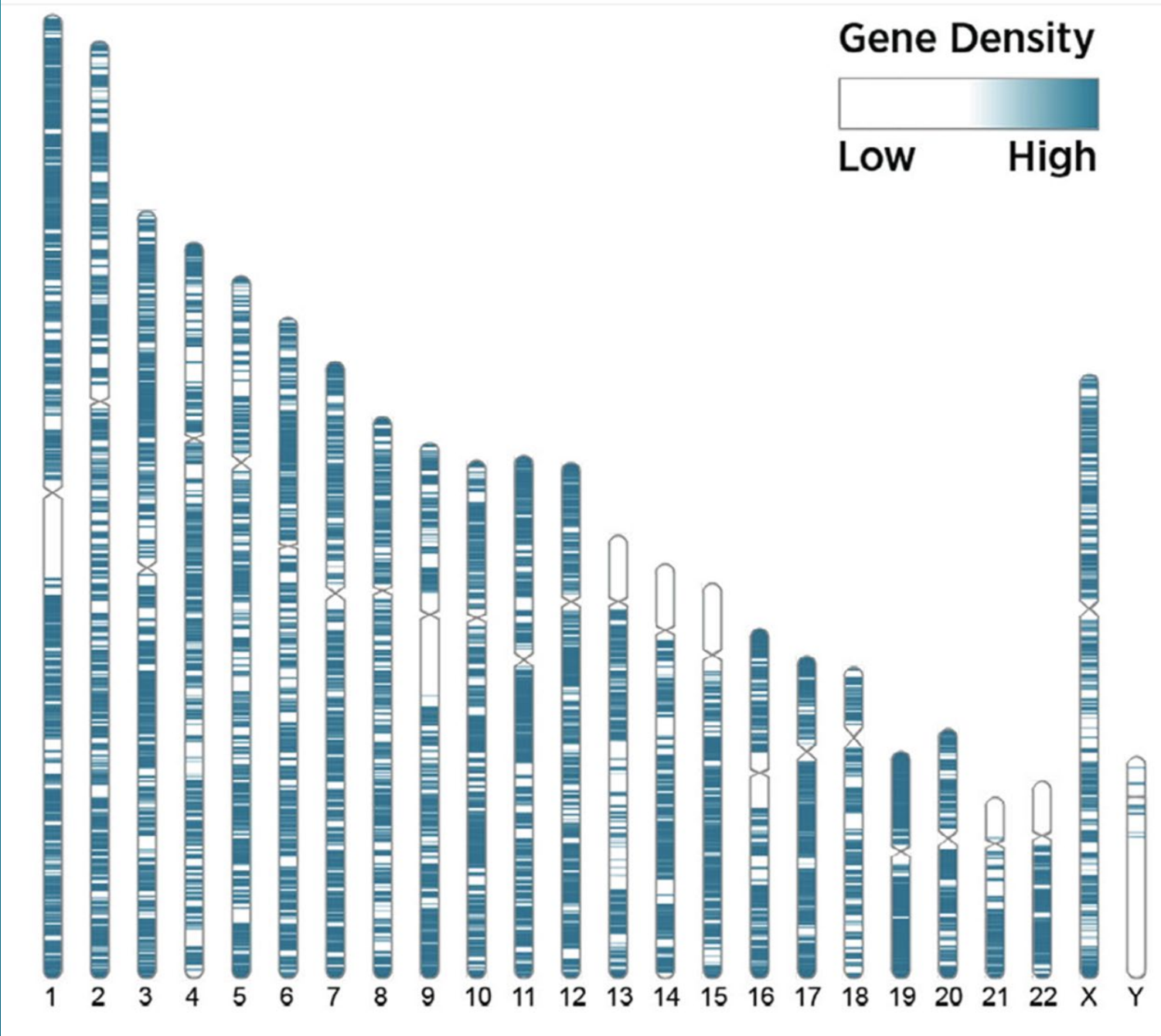
Distribution of Transcript Lengths that have CosMx imaging probes



Transcripts < 250 bp in length

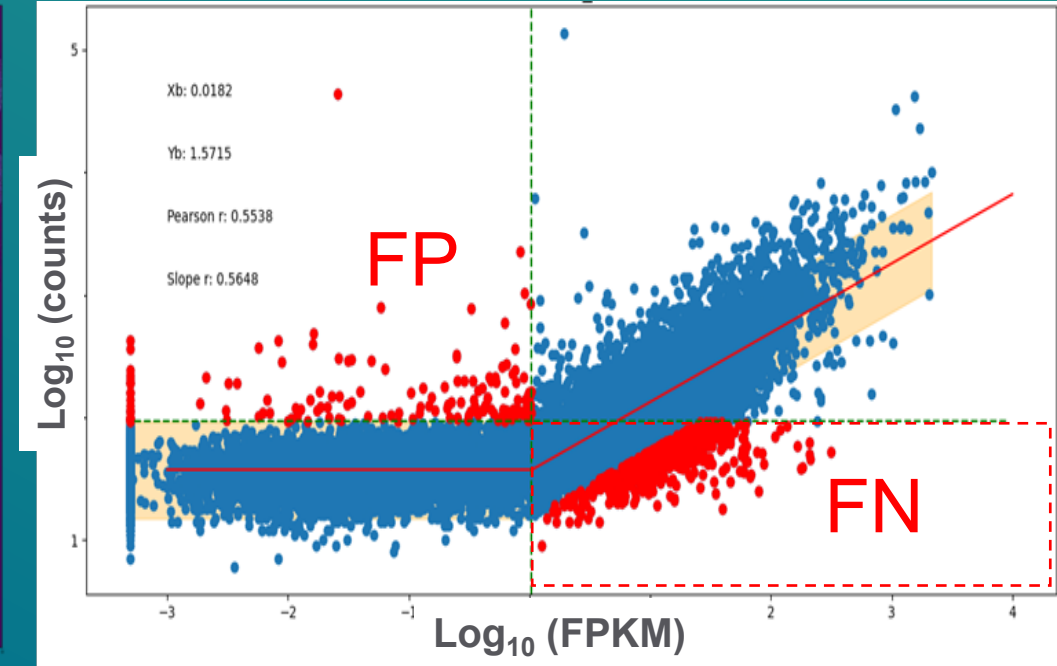
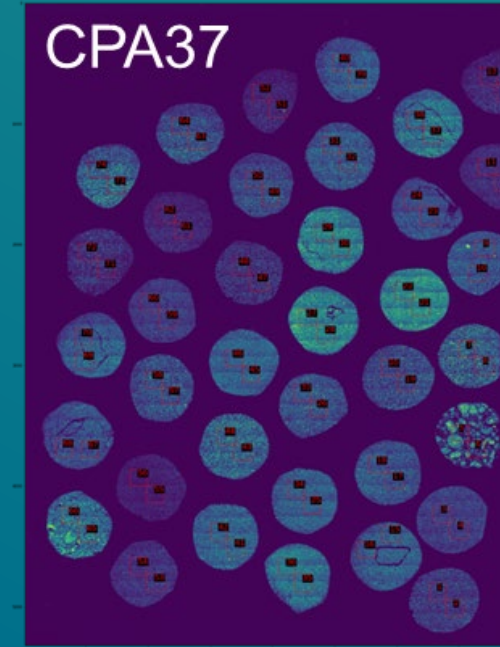
Transcripts ≥ 15 kB in length

Over 38,000 CosMx imaging probes distributed over 23 chromosomes

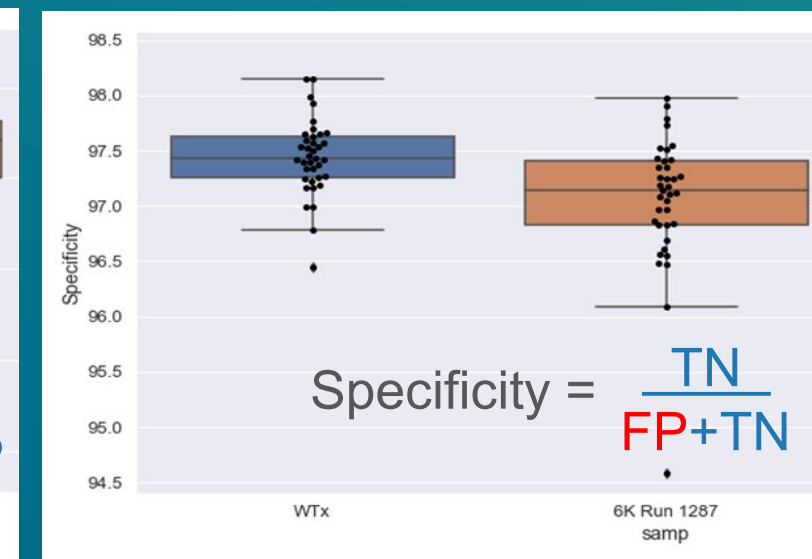
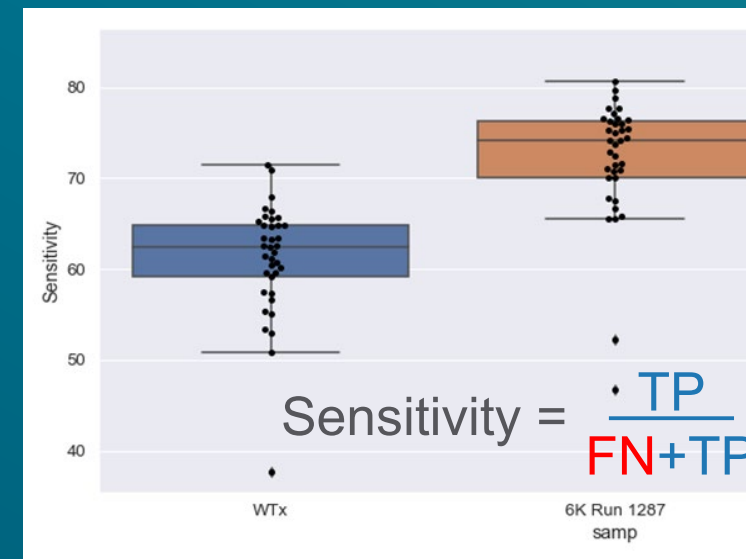


Establishing a Baseline Sensitivity and Specificity for CosMx pre-commercial WTx >18,000-plex Imaging Panel

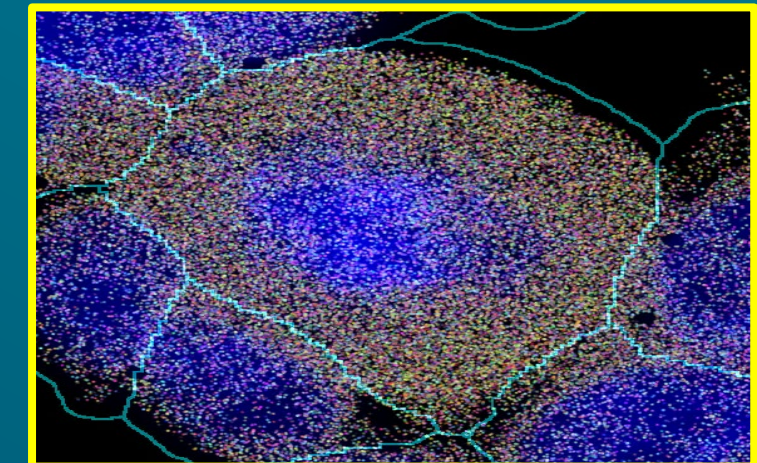
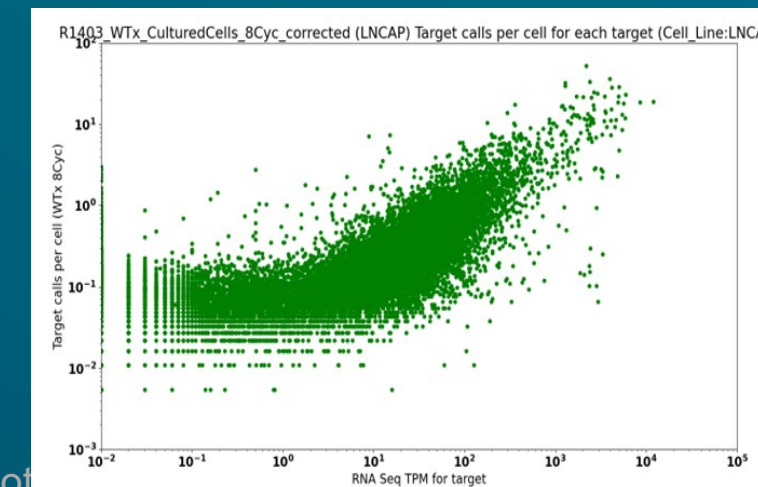
(1) Referenced against deep RNA-seq CCLE database (Broad)



(2) Pre-commercial Specs:
62.0% Sensitivity (1 FPKM break-point)
97.5% Specificity



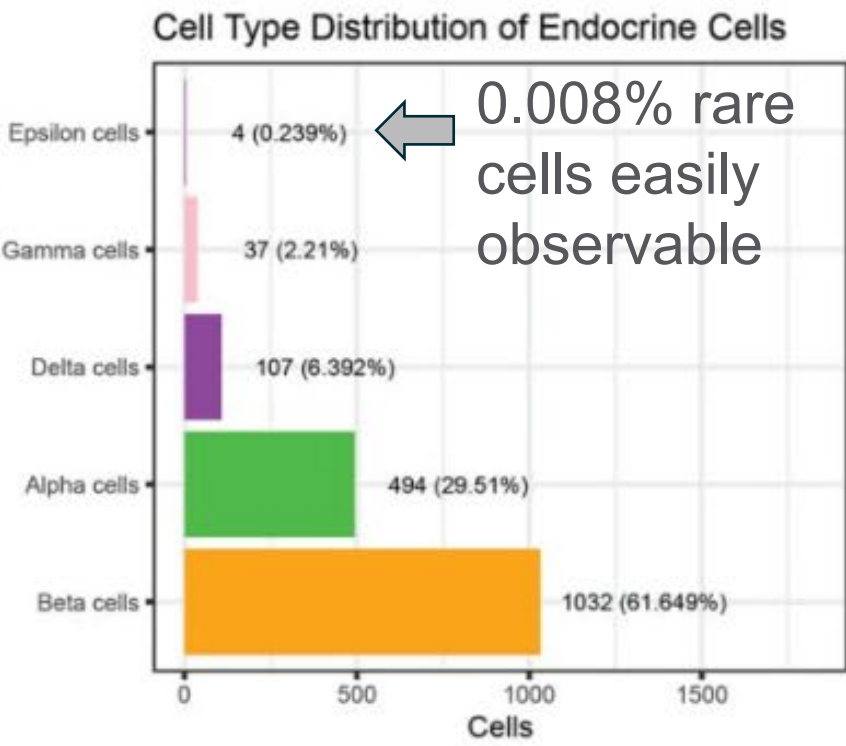
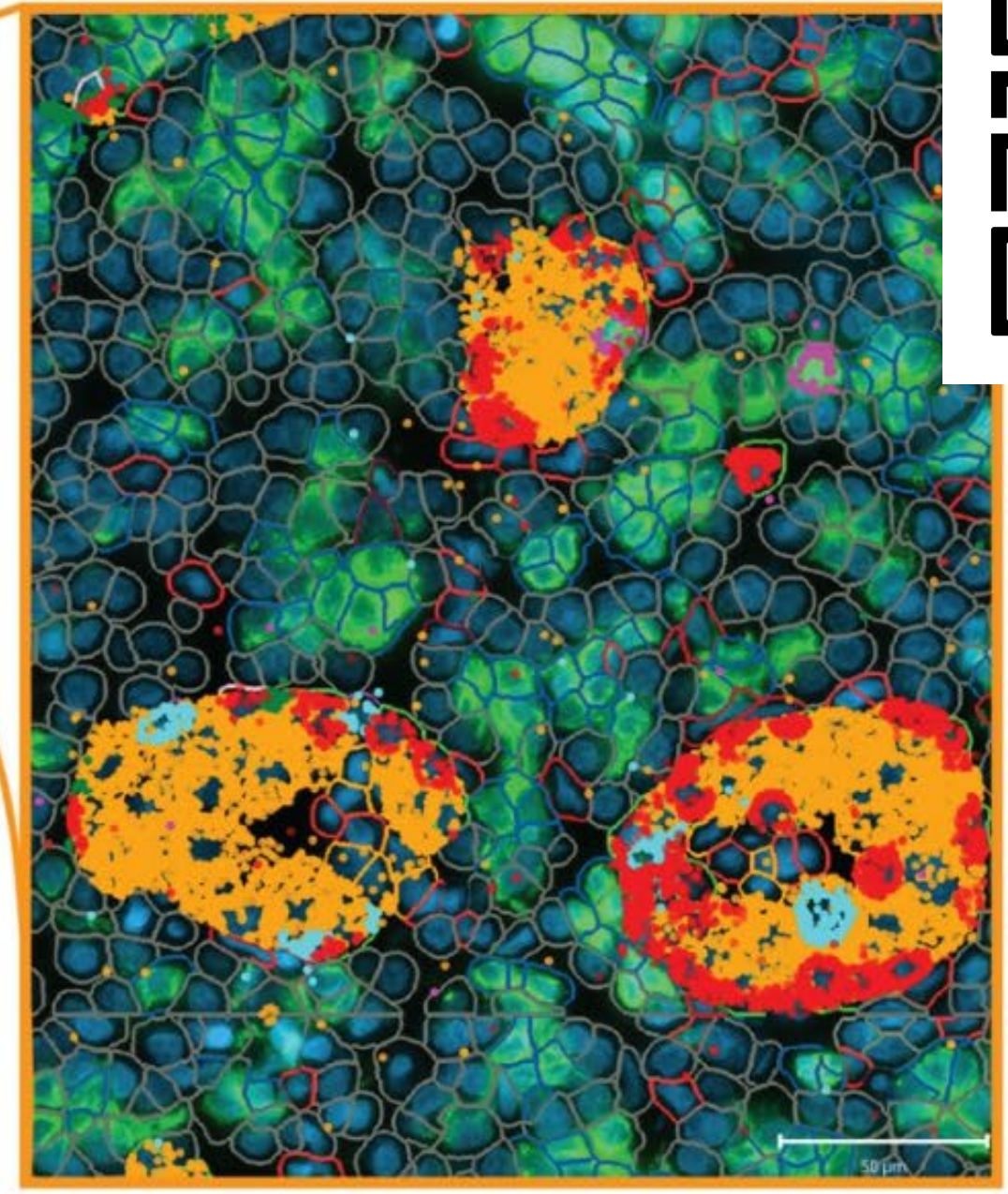
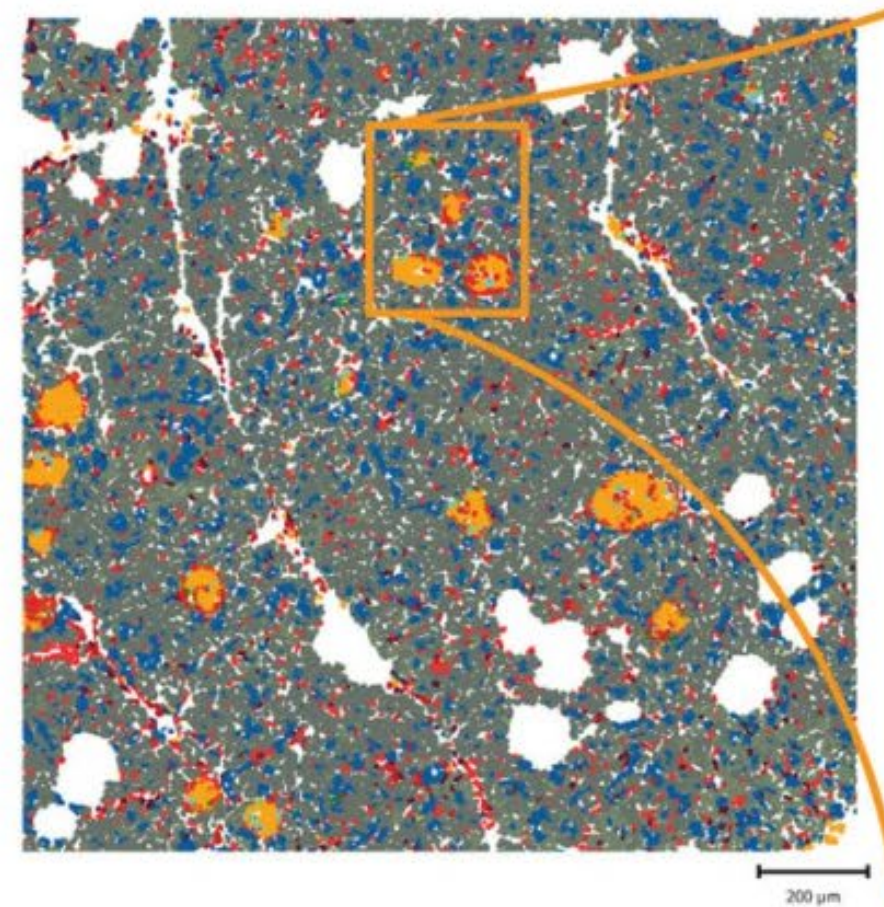
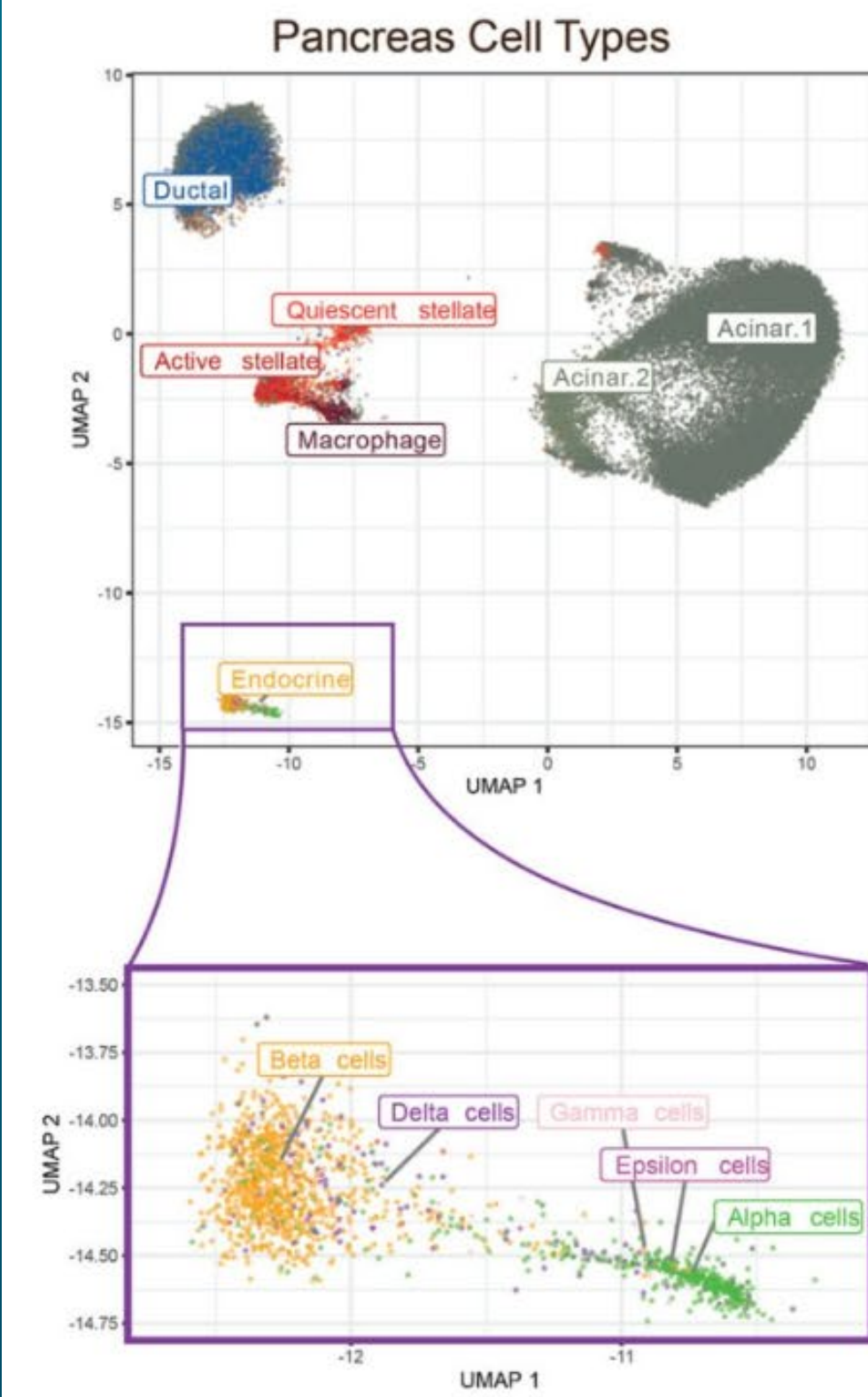
(3) “Bonus”: Typical Fixed-cells yield up to 10,000 transcripts per cell at less than 1-cent per cell!



- 22RV1
- 769P
- A172
- CCRF-CEM
- COLO201
- DAUDI
- DU4475
- H1648
- H596
- HCC1806
- HDLM2
- HEL
- HEPG2
- HL60
- HS578T
- HUH7
- HUT78
- IGROV1
- KG1
- MALME3M
- MEC1
- MV411
- OPM2
- SKLMS1
- SKMEL2
- SKODW
- SNU16
- SNU475
- SR
- SUDHL1
- SUDHL6
- SW948
- T47D
- THP1
- TT
- U118MG
- U87MG



First (in the world) FFPE Spatial Single-cell Whole Transcriptome Public Data Release: healthy human pancreas



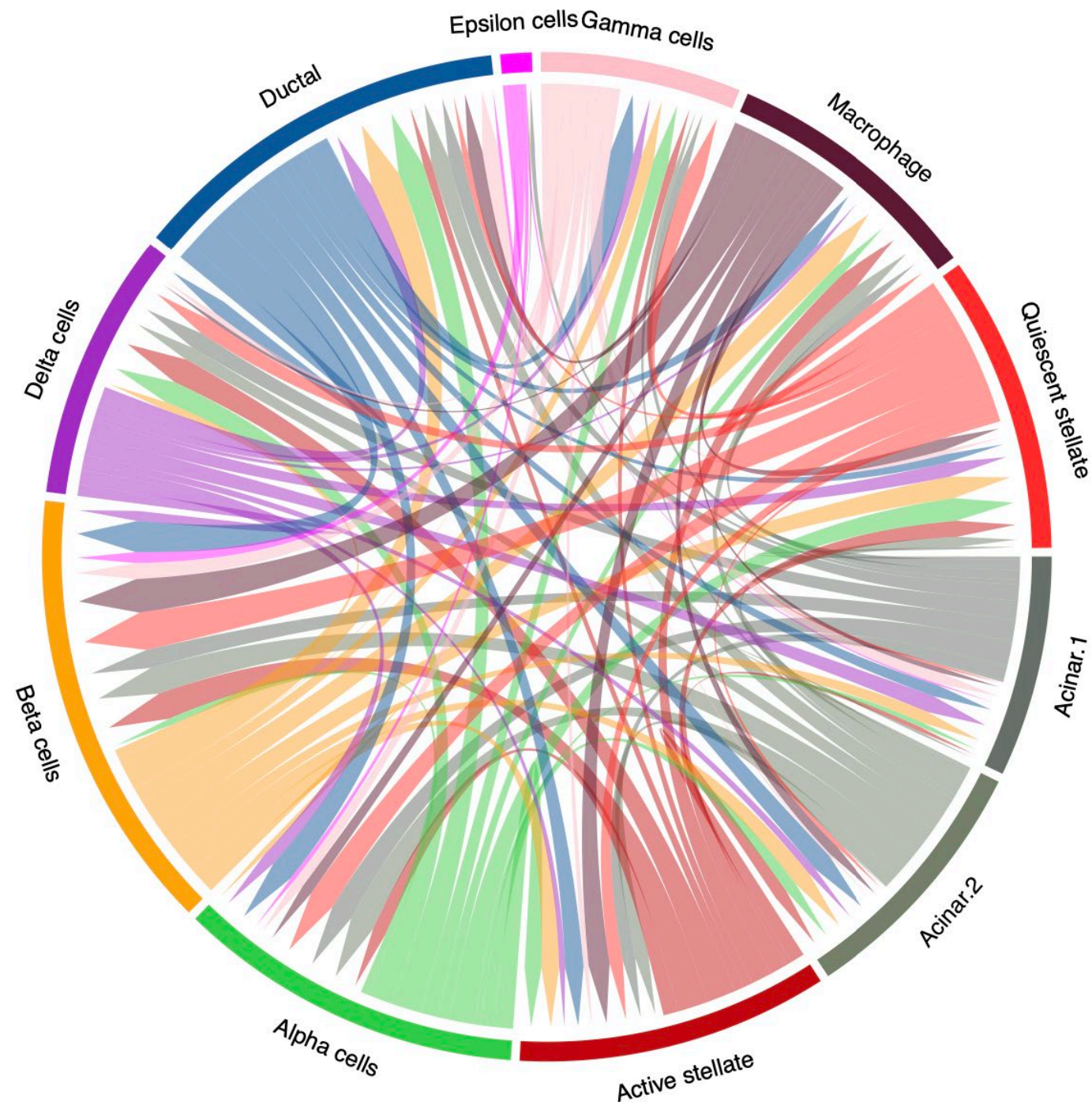
0.008% rare cells easily observable

GCG (Alpha cells)
 INS (Beta cells)
 PPY (Gamma cells)
 SST (Delta cells)
 GHRL (Epsilon cells)

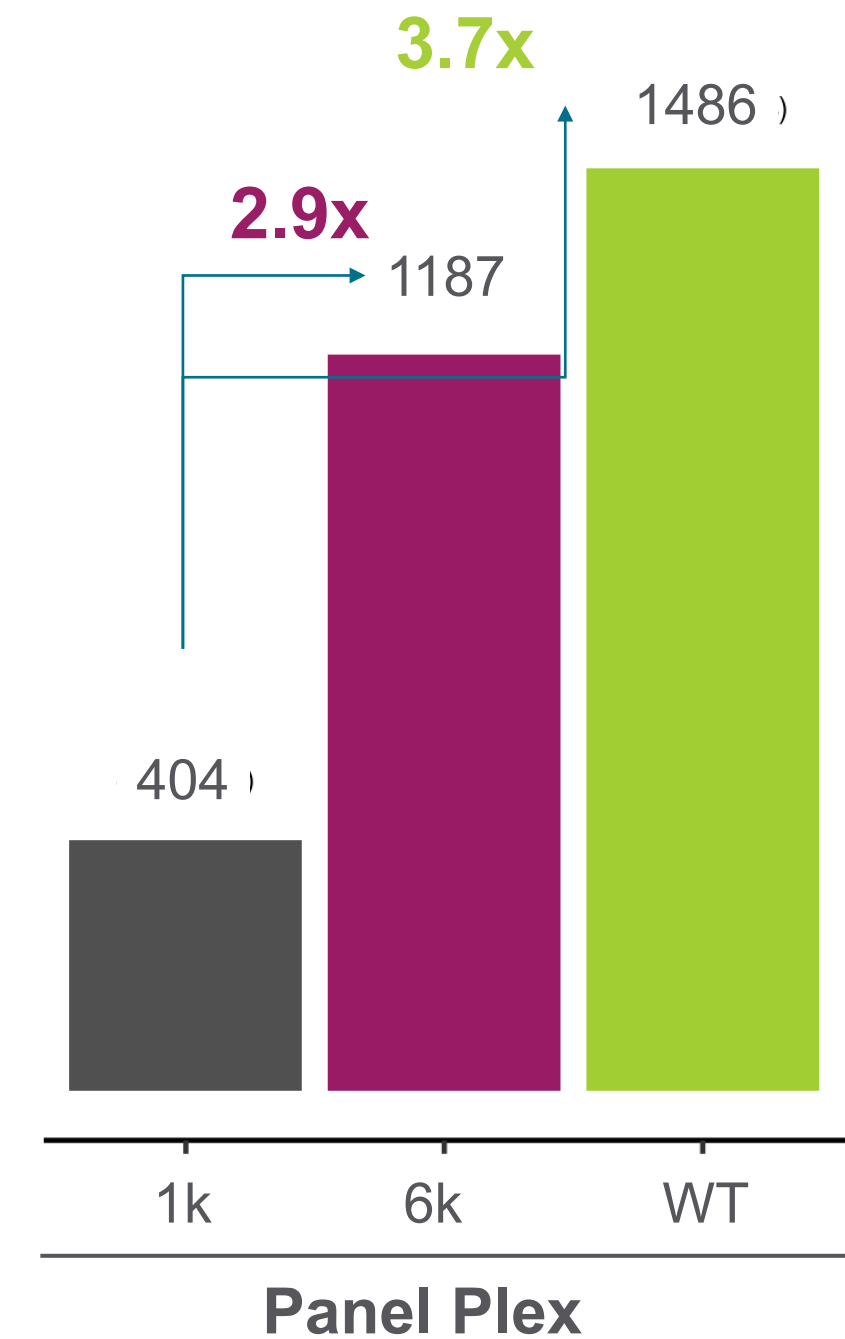
DAPI
 PanCK

CosMx WTx Panel: “Listens In” on “Conversations” Between Cells

Pancreas Cell-to-Cell “Conversations”
Arrows Represent Receptor-Ligand Interactions

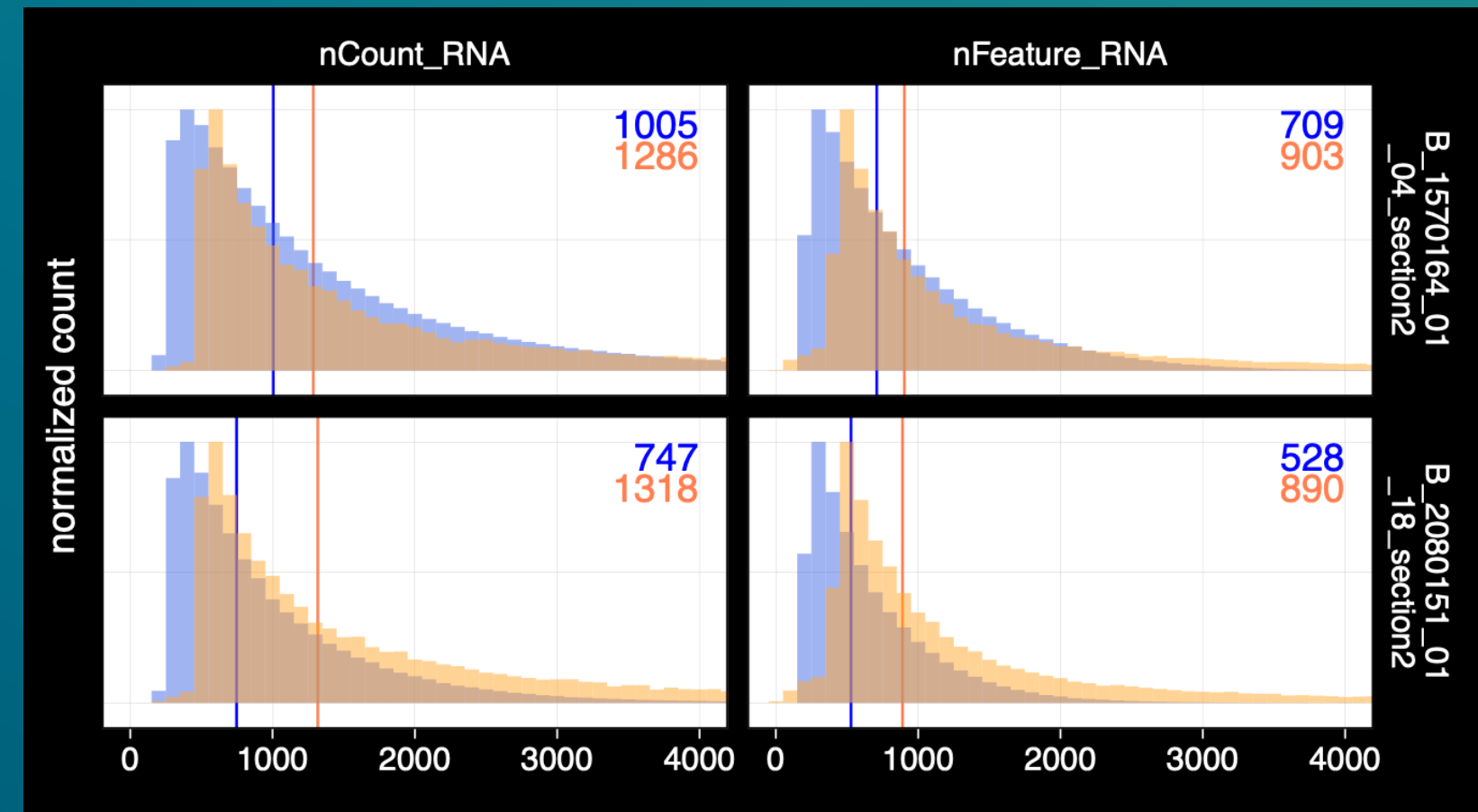
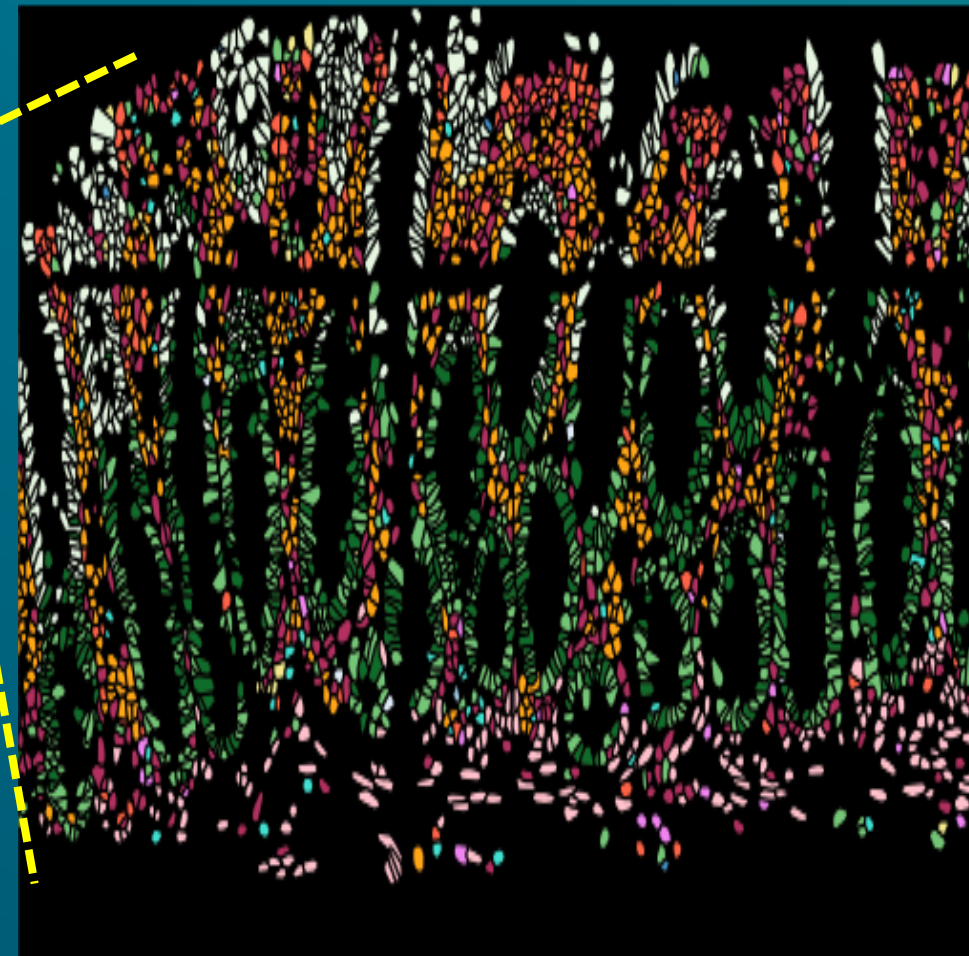
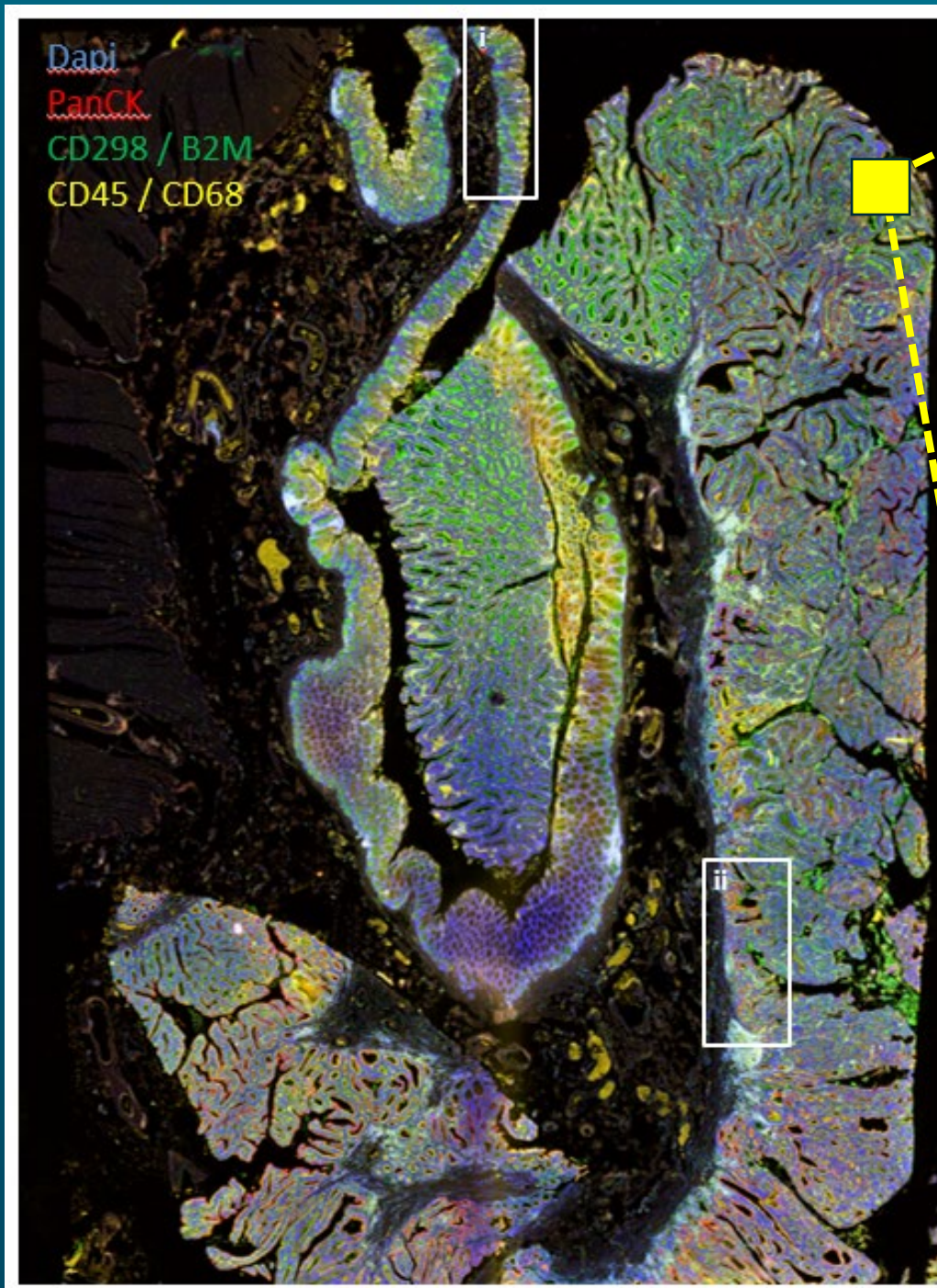


Interactions Detected by CosMx Panel Plex
Number of Receptor-Ligand Interactions

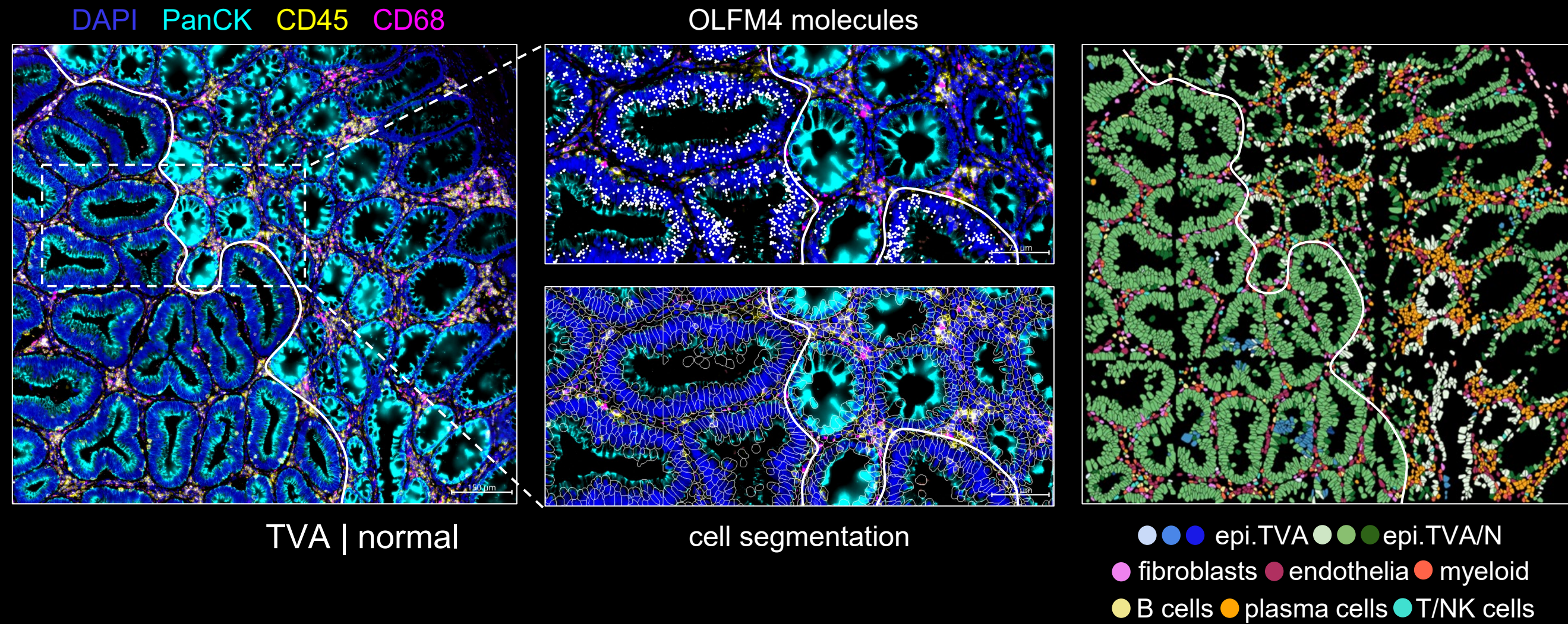


CosMx WTx Panel: True single-cell Spatially-resolved Whole Transcriptome with Dr. Holger Heyn (CNAG, Barcelona)

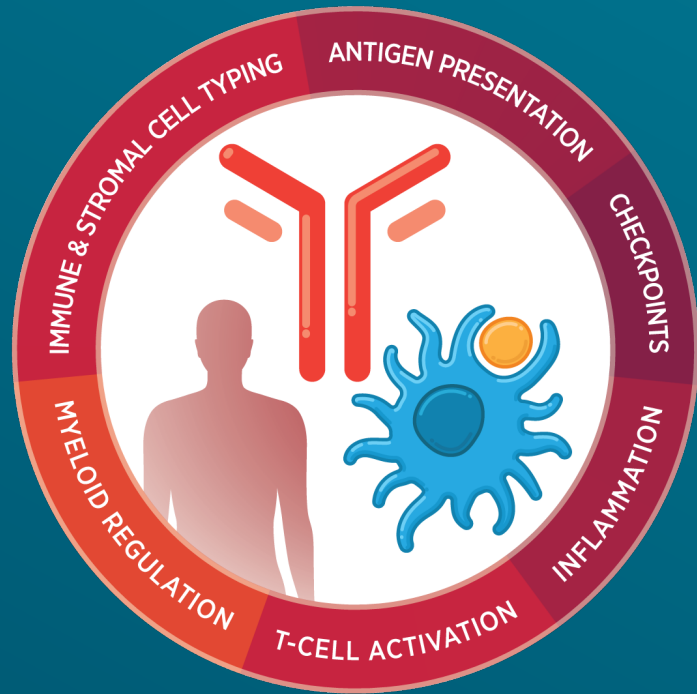
- Total single cells = 1.4 Million cells
- Transcripts = over 1.4 Billion
- Transcripts per cell > 1,000
- Neg-Probes per cell < 1.0
- Close to snRNA-seq on all key metrics
- Less than 1-cent per transcriptome



CosMx WTx – Spatially-Aware Cell State Profiling



Spatial Proteomics with CosMx SMI



CosMx™ Human IO Protein Panel

Protein Spatial Biology at subcellular resolution

HIGH PLEX

Visualize 64 protein targets plus 4 segmentation markers

HIGH THROUGHPUT

1 slide/day with 1.0 cm² tissue area

CUSTOMIZABLE

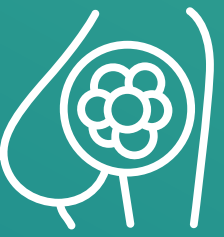
Add up to 8 additional custom protein targets (3Q 2023)

EXPANDING MENU

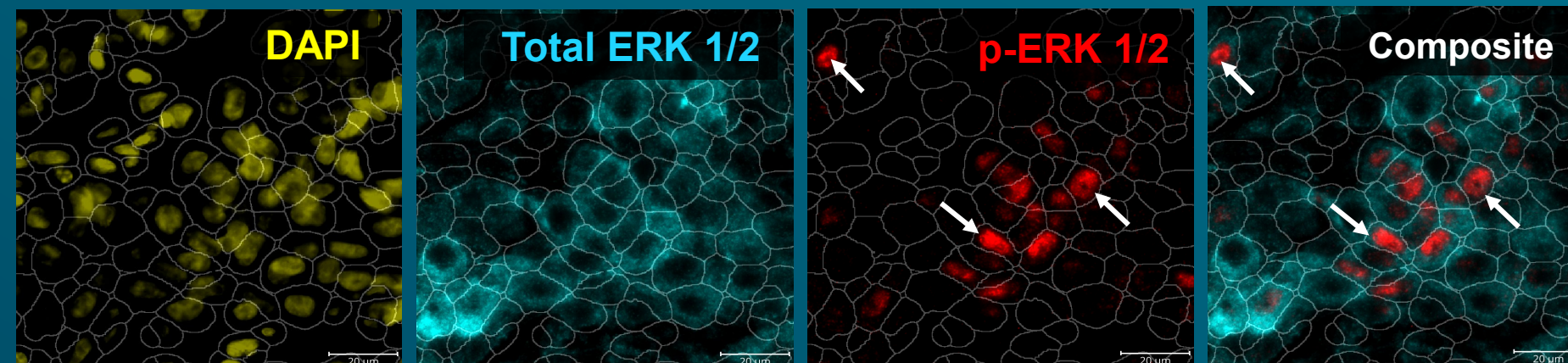
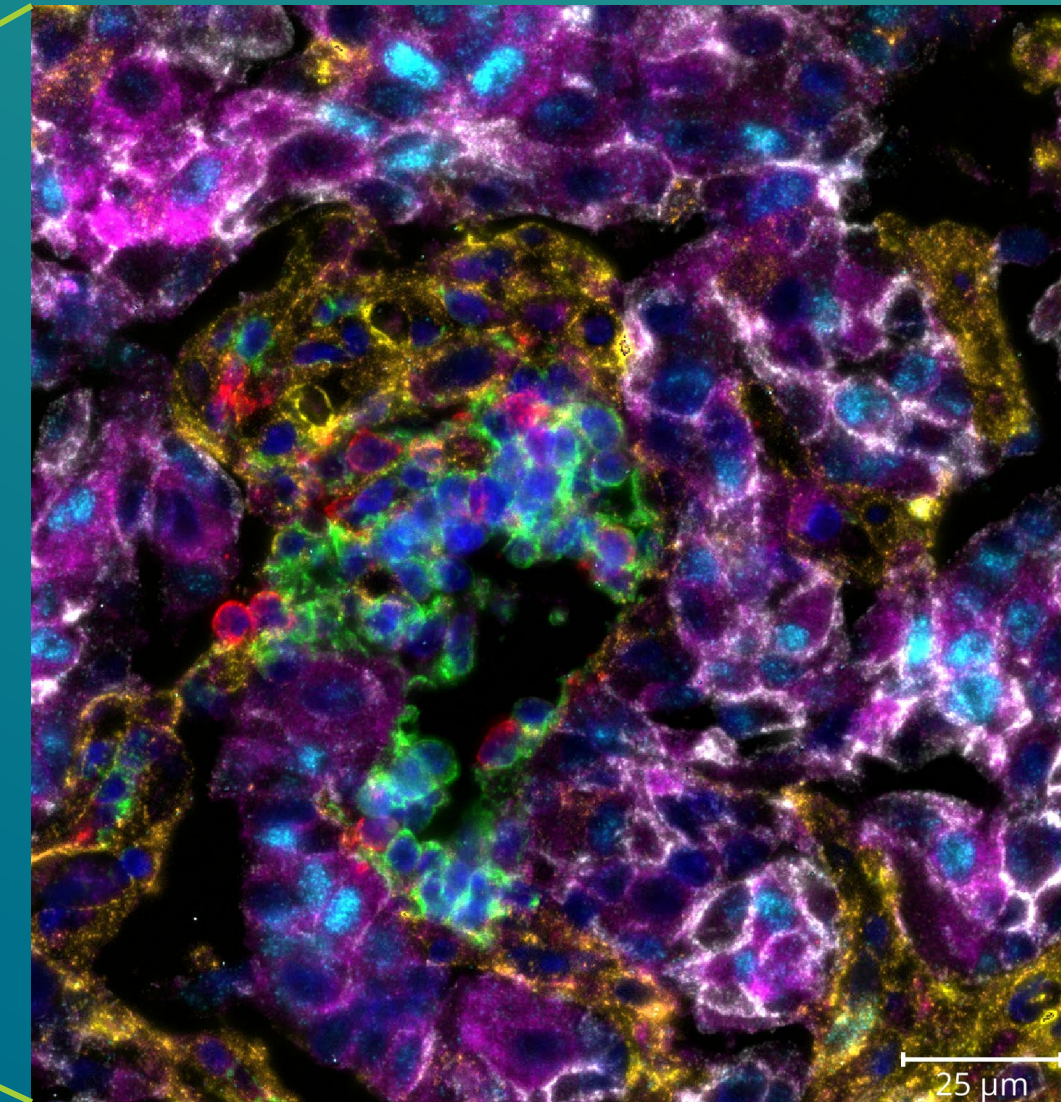
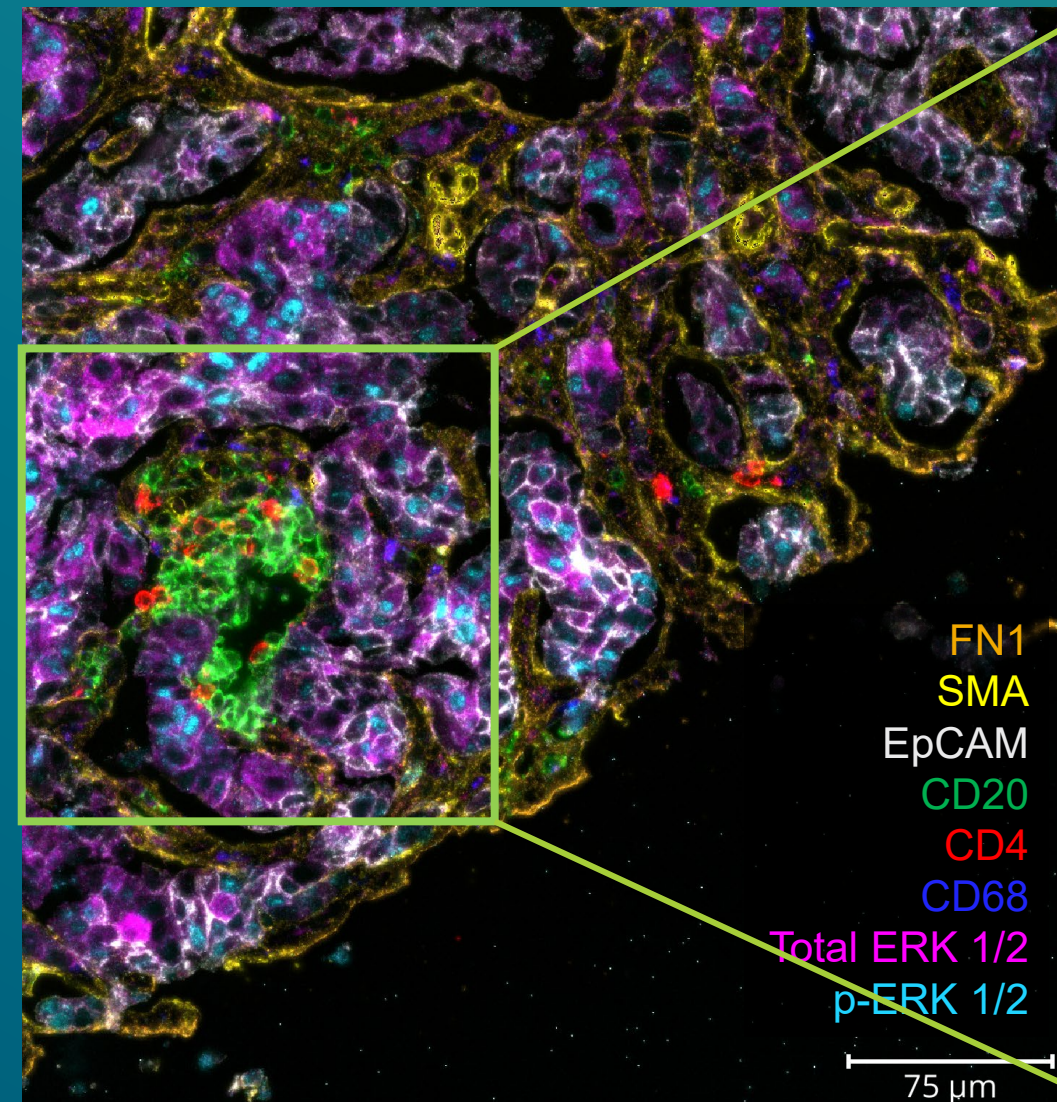
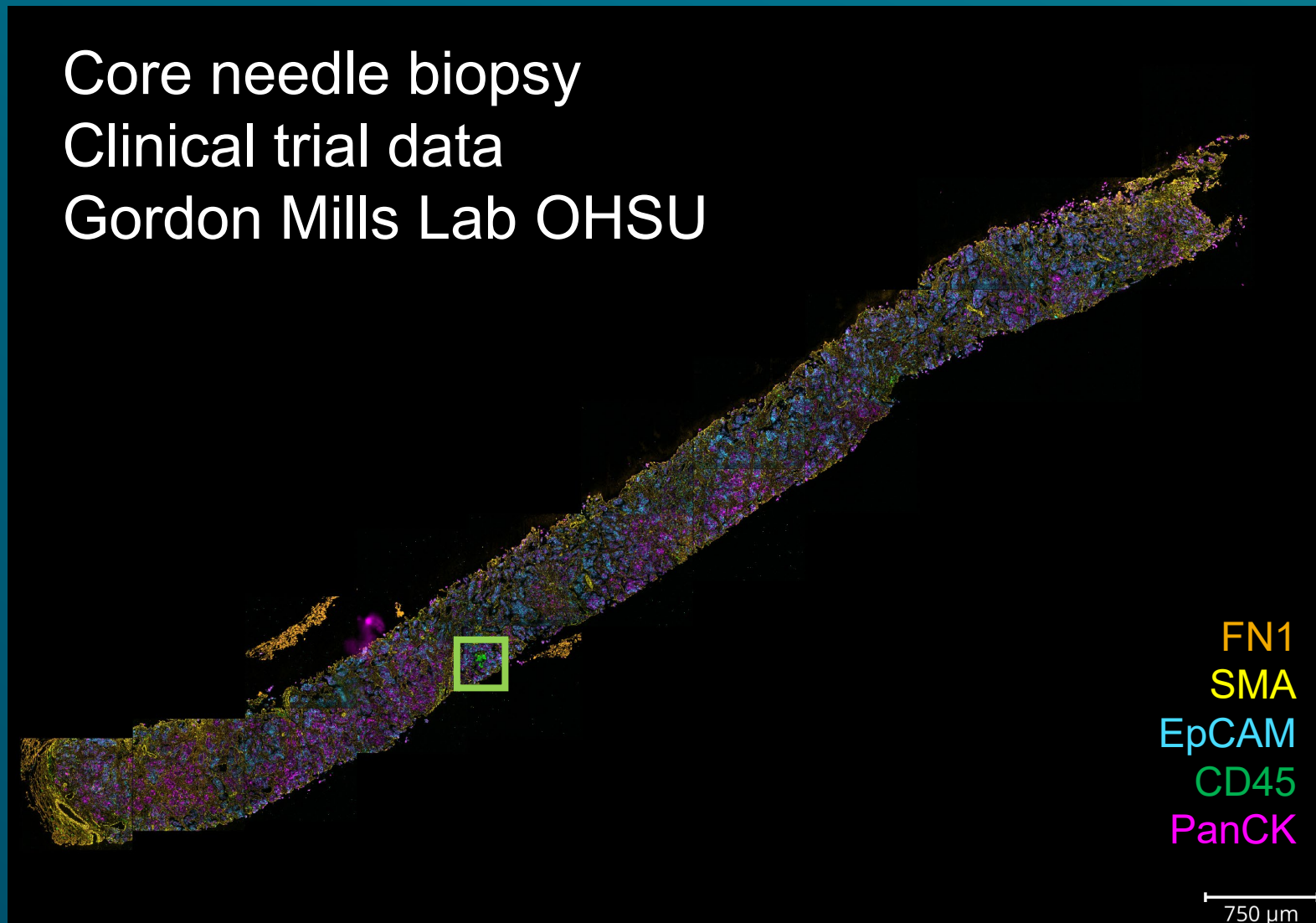
Mouse Neuroscience Panel (3Q 2023)

Inflammation	M2 Macrophage	CD8 T Cells	Immune Cell Migration	NK Cells	Tregs	Background		
	Dendric Cells	CD4 T Cells	Hematopoietic	Monocyte	Total Immune	Adipose	Endothelia	Fibroblasts
Checkpoint	Cytotoxicity	Antigen Presentation	Exhausted T Cells	Interferon	MHC2	Stroma		
	Myeloid Suppression	Memory T Cells	Neutrophils	Plasma Cells		Proliferation	Wnt Signaling	Tumor Suppressor
T Cell Activation	B Cells	Naive T Cells	Th Cells			Epithelia	Receptor Tyrosine Kinase	
	Macrophage	Myeloid Activation				Apoptosis	DNA Damage	
T Cells	Myeloid					Tumor	Antigen	
						Growth Factor Signaling	MAPK	
						Oncogene		

Explore Subcellular Localization and Post Translational Modifications

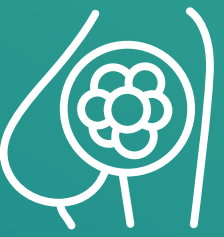


Core needle biopsy
Clinical trial data
Gordon Mills Lab OHSU

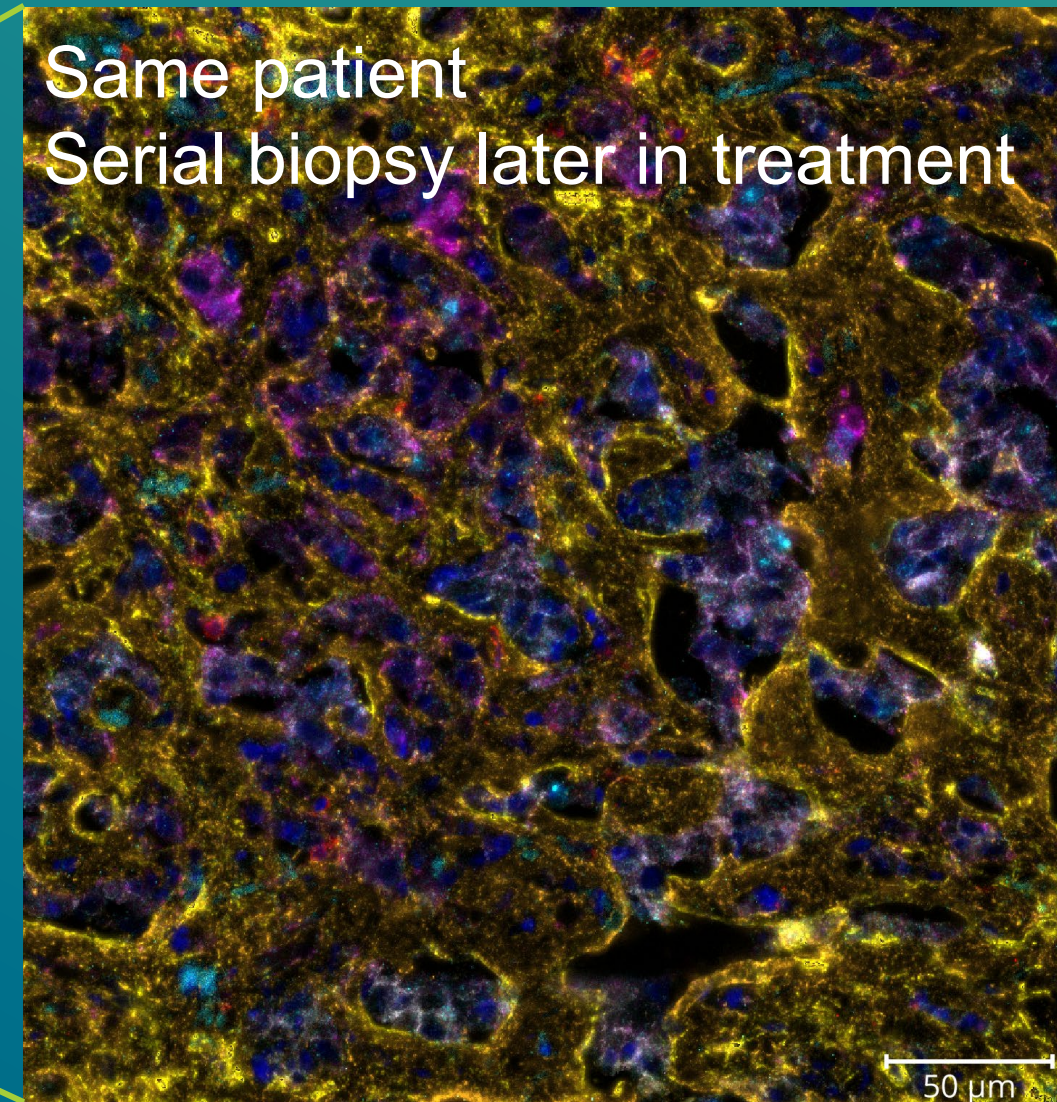
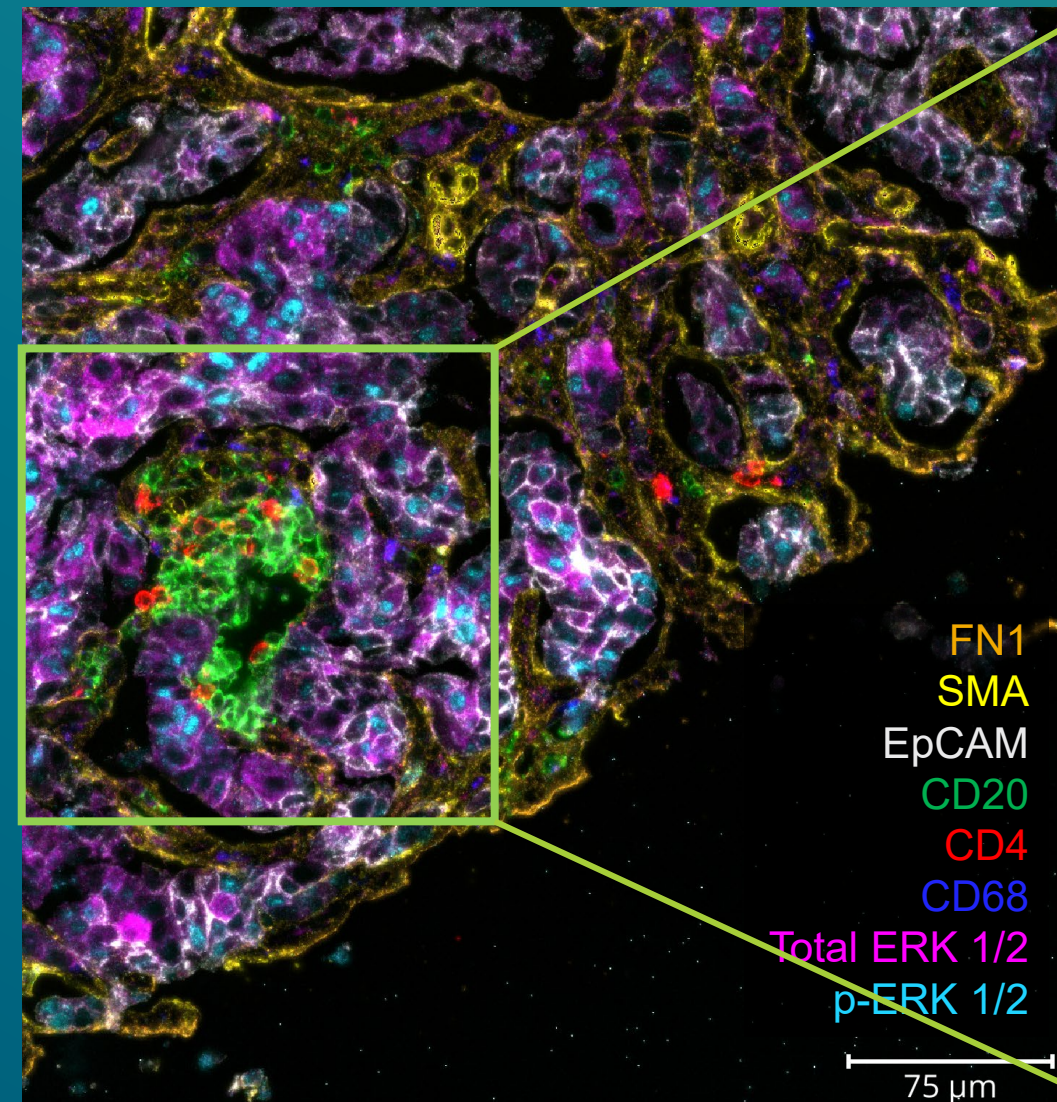
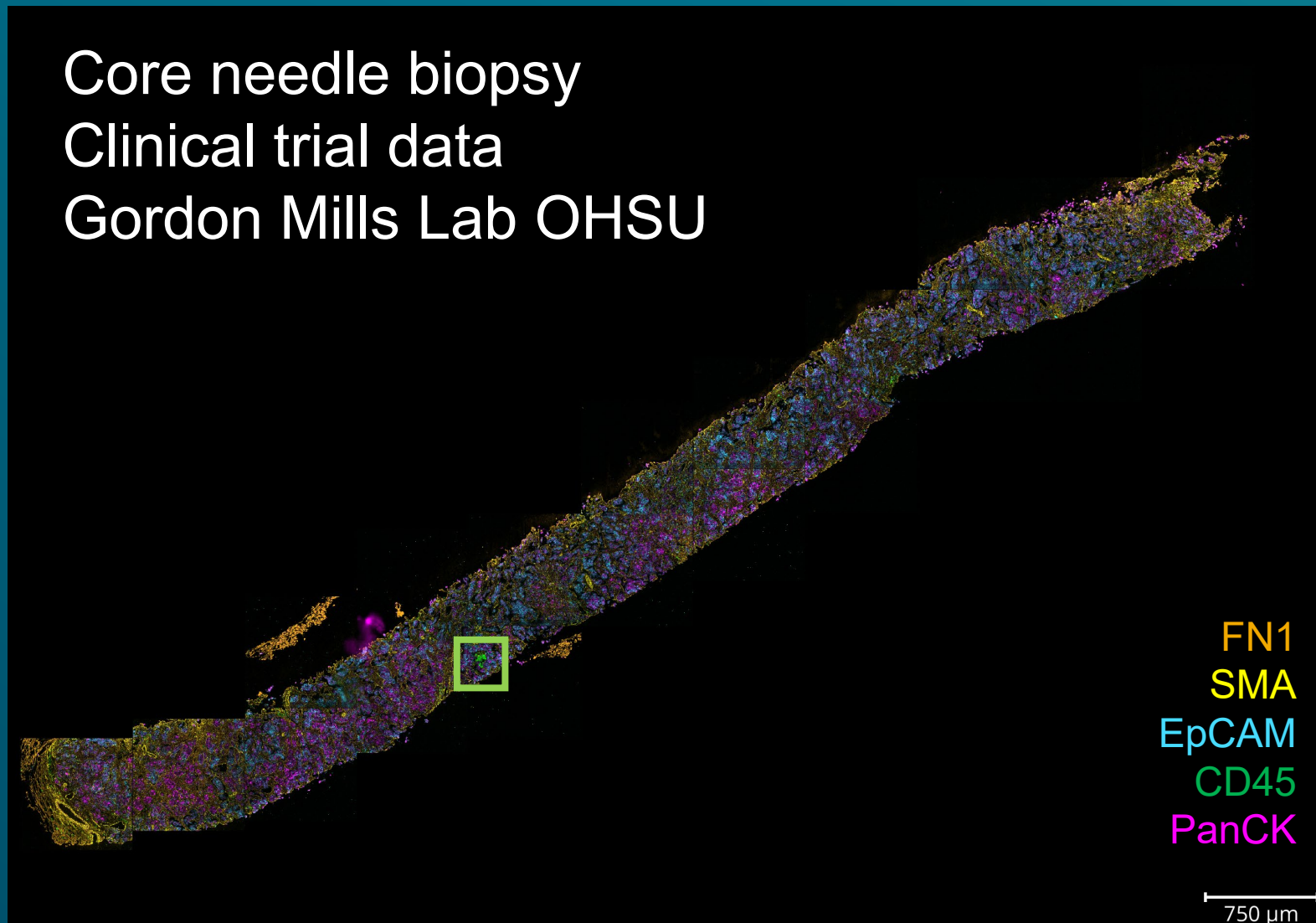


Translocation of phosphorylated ERK1/2 to nucleus

Explore Subcellular Localization and Post Translational Modifications



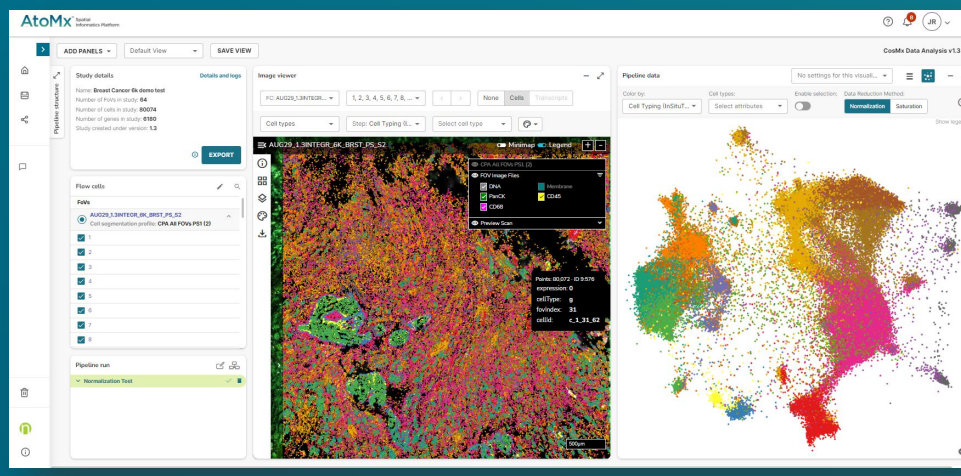
Core needle biopsy
Clinical trial data
Gordon Mills Lab OHSU



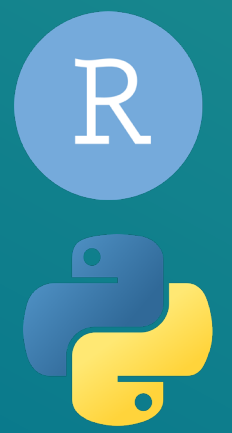
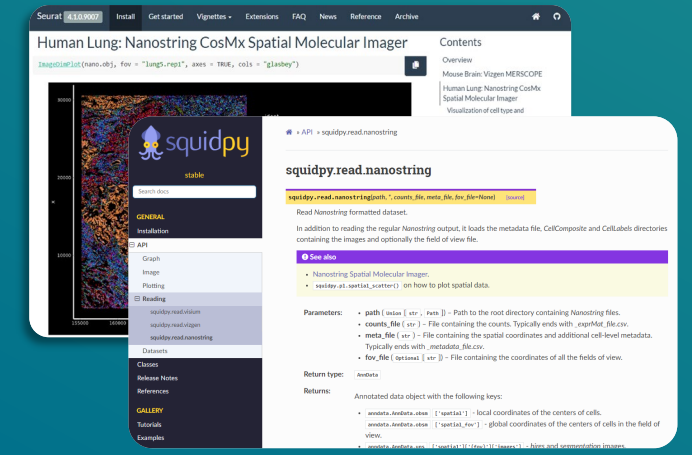
Decreased MAPK/ERK
signaling following therapy

First of its Kind Informatics Continuum for Spatial that Scales to any Plex or Sample Number

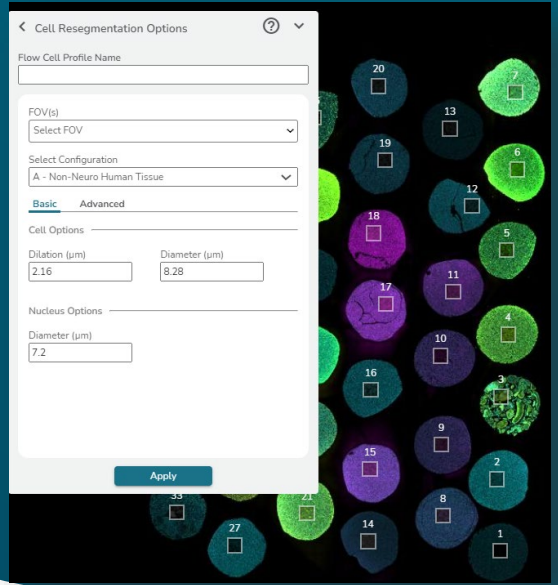
Iterative, Multi-sample, Custom Analytics suite



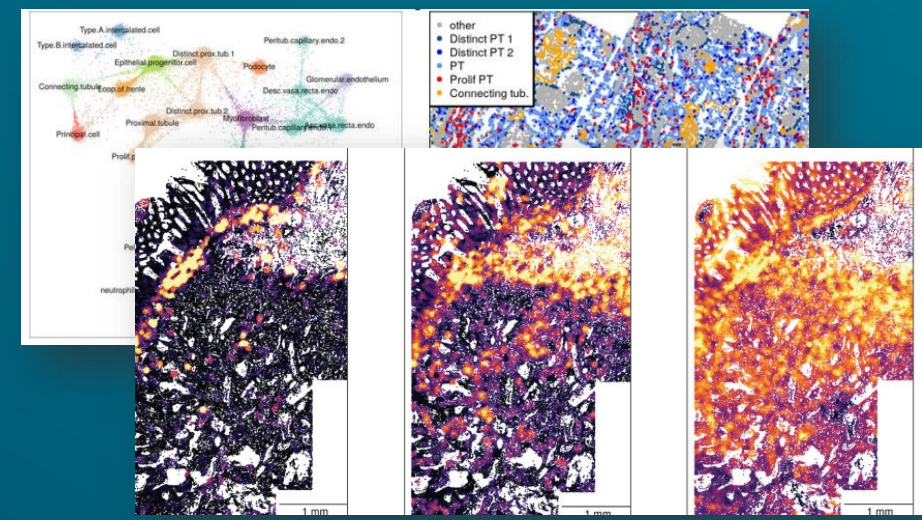
Opensource Portable



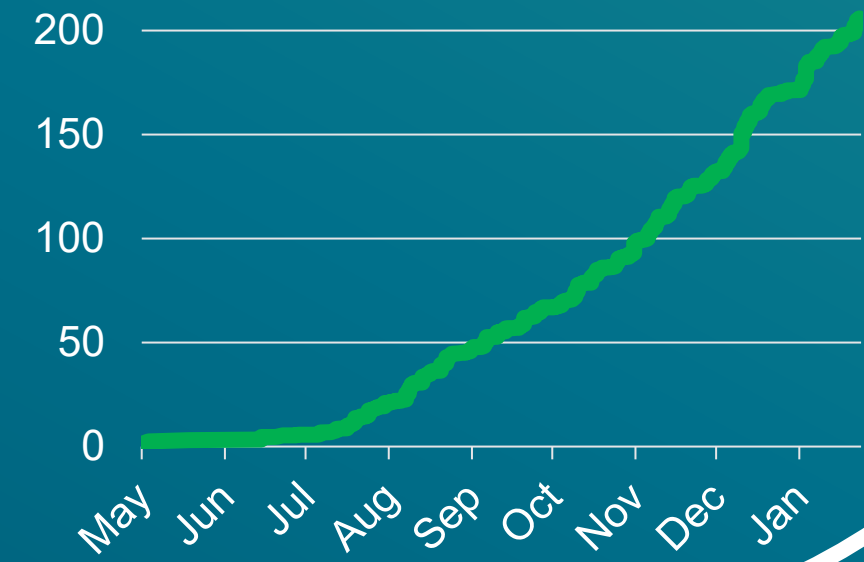
Machine-learning Cell Segmentation Toolkit



NSTG-open-source Algorithms



>200M Cells analyzed



AtoMx™

Spatial Informatics Platform

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

nanoString®

Spatial-Multi-Omics for Systems-Biology

GeoMx for in-situ **FUNCTION** at sample high-throughput
CosMx for in-situ subcellular resolution at tremendous
single-cell number and low single cell cost (< 1cent/cell)

GeoMx[®]
Digital Spatial Profiler

AtoMx[™]
Spatial Informatics Platform

CosMx[®]
Spatial Molecular Imager

- Whole Transcriptome
- High Throughput
- Data matches tissue architecture
- Highest-protein plex
- Highest multi-omic plex

- Single-Cell Resolution
- Entire Tissue Section
- Highest Multiplex & Sensitivity
- Best Cell-Segmentation
- Transformatively less expensive than sc-RNAseq

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