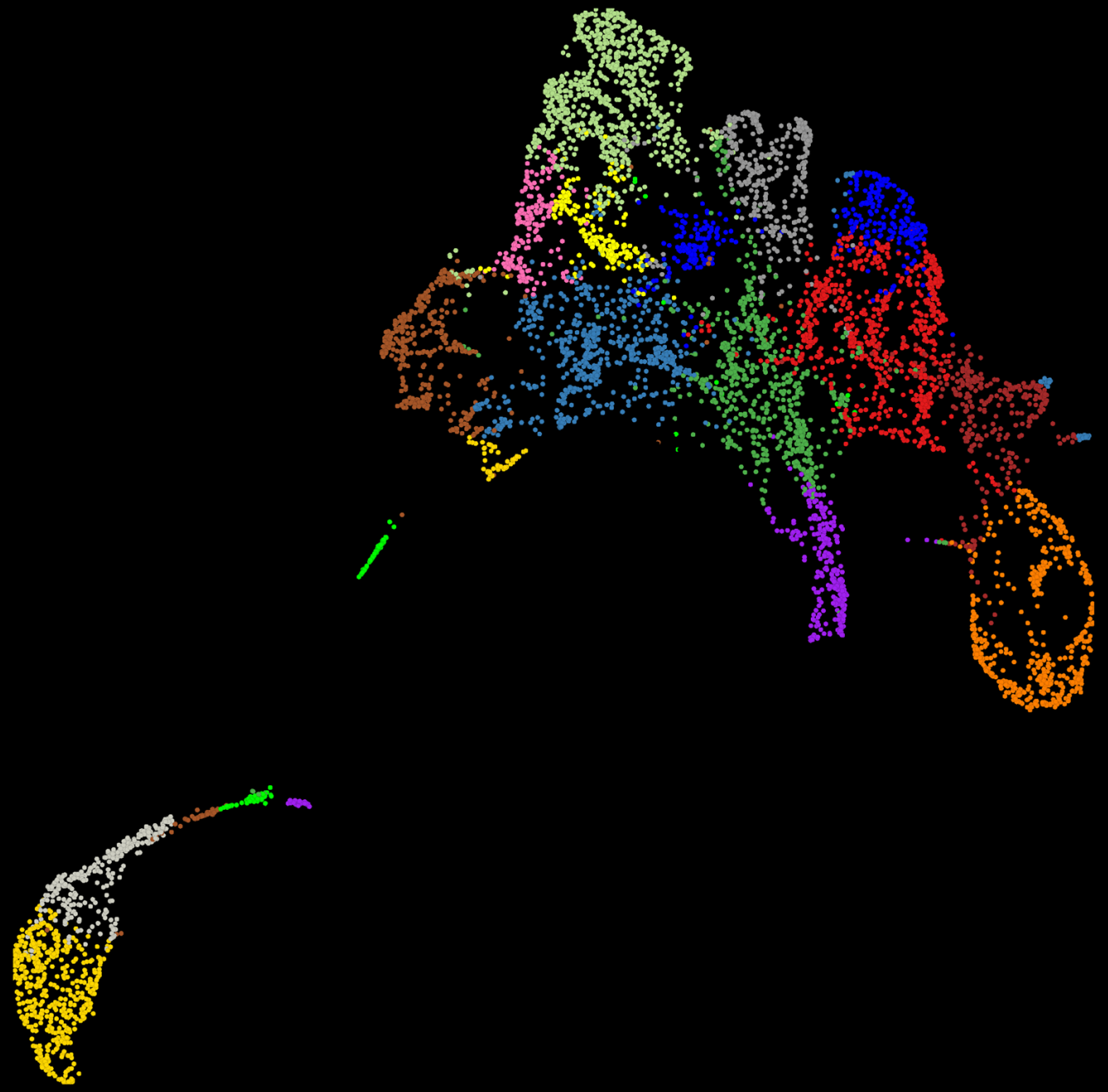
Visium Spatial



Your Local 10x Genomics Team

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10x GENOMICS

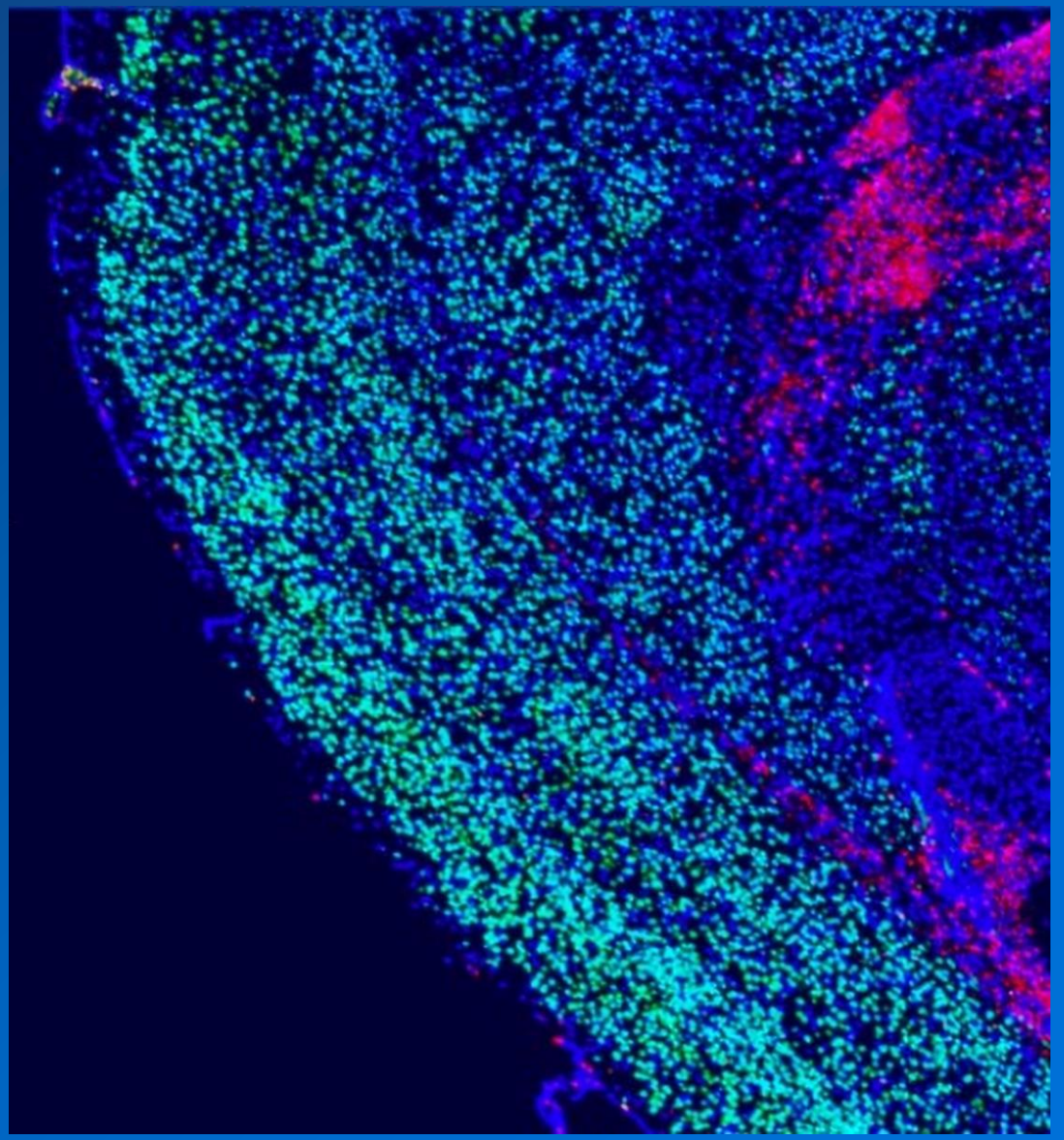
Master Biology with the 10x Toolkit

Visium Spatial

Josh Talboom, Ph.D.
Science & Technology Advisor (STA)
San Diego & OC, CA

GRT Hub Workshop - Spatial Transcriptomic Data Analysis
9/28/2023

The complexity of biology limits our understanding of disease and our abilities to improve human health.



Fundamental Challenges Remain in Treating Disease

Many diseases still pose major threats to public health

ALZHEIMER'S →

98%

failure in Alzheimer's drug development

Kim, C. Kwon et al. Alzheimer's Disease: Key Insights from Two Decades of Clinical Trial Failures. *Journal of Alzheimer's Disease* 1: 83–100 (2022).

CANCER →

20-30%

response rates for immune checkpoint blockade

Kumar, N, Papillon-Cavanagh, S, Tang, H, et al. A multi-omic single cell sequencing approach to develop a CD8 T cell specific gene signature for anti-PD1 response in solid tumors. *Int J Cancer*. Vol. 151 Issue 11. 2043–2054 (2022).

AUTOIMMUNE DISORDERS →

4+ yrs.

for diagnosis of autoimmune disorders

Diagnosing Autoimmune Diseases, *Benaroya Research Institute*, Oct. 2017, www.benaroyaresearch.org/blog/post/diagnosing-autoimmune-diseases.

10x Solutions Are Transforming the Understanding of Disease

10x provides the tools researchers use to solve the tough questions that remain in biology & disease

Cancer

Cell

Single-Cell Analyses Identify Brain Mural Cells Expressing CD19 as Potential Off-Tumor Targets for CAR-T Immunotherapies

nature medicine

A single-cell map of intratumoral changes during anti-PD1 treatment of patients with breast cancer

Autoimmune

Science

Single-cell eQTL mapping identifies cell type-specific genetic control of autoimmune disease

nature

Interpreting type 1 diabetes risk with genetics and single-cell epigenomics

Neuroscience

nature genetics

Single-nucleus chromatin accessibility and transcriptomic characterization of Alzheimer's disease

nature immunology

Microglia use TAM receptors to detect and engulf amyloid β plaques

Other fields

Science

Pathogenic variants damage cell composition and single cell transcription in cardiomyopathies

Cell Genomics

Retinal ganglion cell-specific regulation in primary open-angle glaucoma

10x GENOMICS

Getting the Best View of Biology and Disease

Overview of legacy and current “omic” methods

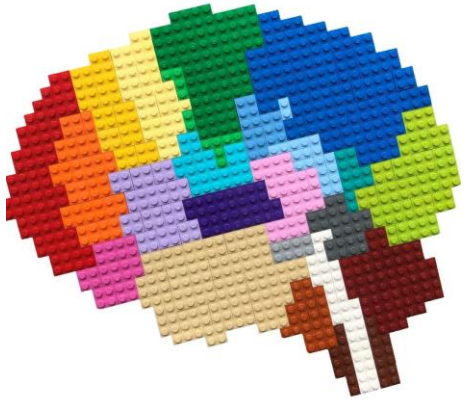
Bulk

- General snapshot of the whole target “ome”
- Lacks cellular or subcellular resolution and spatial context

Single Cell

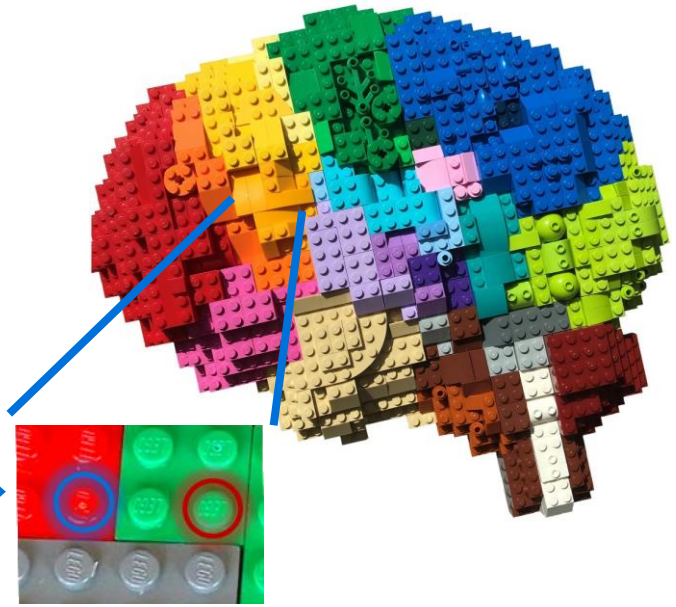
- Cell-by-cell view of the whole target “ome”
- Method unable to retain spatial context

Spatial



- 2D view of the whole target “ome” across several cells
- Valuable for initial discovery at the system, organ, or tissue level
- Current solutions do not offer single cell or subcellular resolution

In Situ



Images and concept courtesy of Bo Xia, NYU School of Medicine

- 3D view of 500-1000 “ome” targets in *situ* at subcellular resolution
- Suitable for focused deeper dives into cell-by-cell biological mechanisms
- Not practical for discovery at the system or organ level

Chromium

Visium

10x GENOMICS

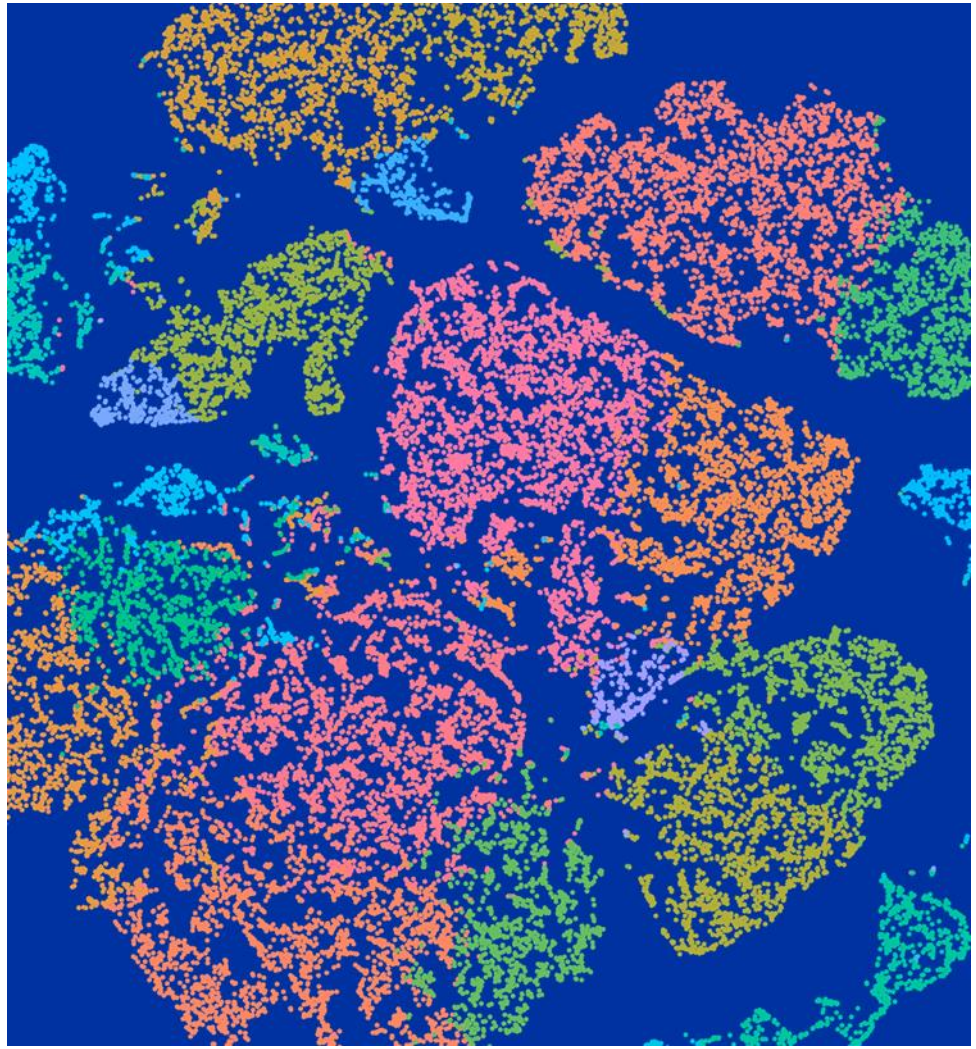
Toolkit

Xenium

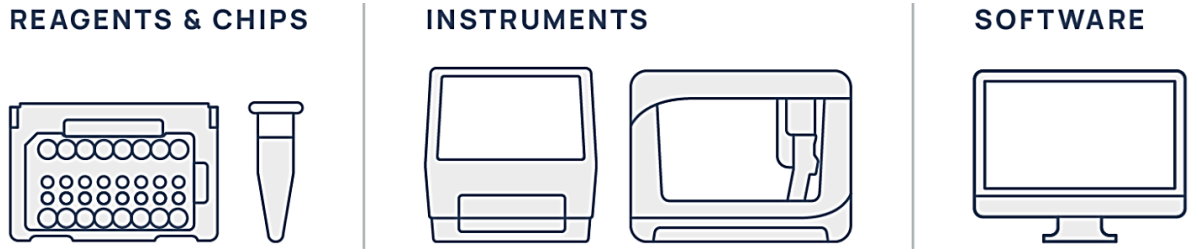

Chromium Single Cell

Chromium

RESOLVE TUMOR HETEROGENEITY, CELL BY CELL



- Partitions and barcodes cells in minutes
- Analyzes 100s to millions of cells
- Leverages scale of NGS while preserving cellular identity
- **FFPE compatible (*Gene Expression Flex*)**
- Perform Single Cell:
  - **Gene expression**
  - **Protein expression**
  - **Functional genomics by CRISPR**
  - **Immune repertoire and corresponding antigens**
  - **Epigenetics**
  - **Multiomic analyses**



Chromium – Replacing the Legacy Toolkit Across Biology

RNA

Gene expression

- Microarrays
- qPCR / PCR
- Bulk RNA-Seq
- ISH

CRISPR Screening

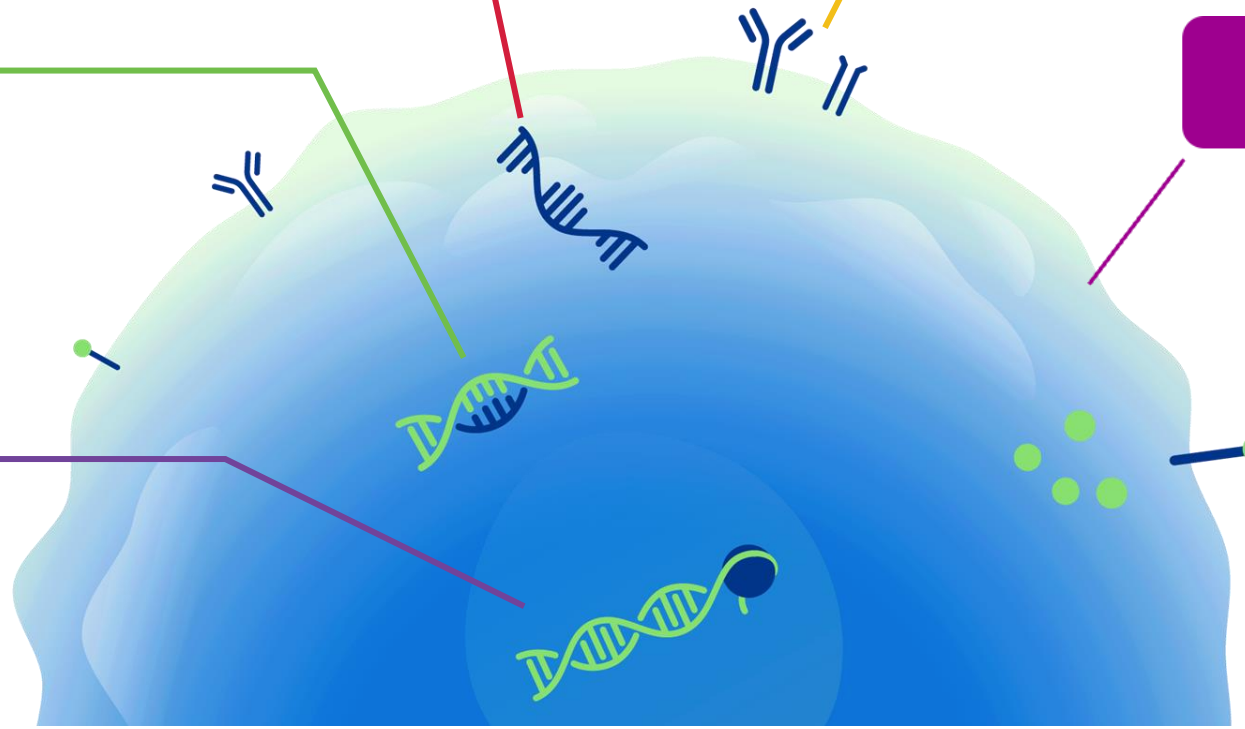
CRISPR functional genomics

- Liquid handlers
- High content imaging

Chromatin

Epigenomics

- ChIP and NGS-based methods



T- and B-Cell Receptors

Immune cell profiling

- Flow cytometry
- NGS methods

Fixed Samples

Gene Expression Flex
for fixed & FFPE

Proteins

Protein expression

- Western blots
- Affinity columns
- Protein microarrays
- Highly Multiplexed Imaging
- Microscopy
- FACS
- CyTOF
- IHC/IF

Chromium – Instrument

X

Chromium X

Next generation single cell system that runs all standard 80K cells/run assays and HT & Fixed assays with up to 1M cells/run

Chromium Single Cell

Gene Expression Flex

Remove the constraints of standard single cell workflows by profiling fixed RNA

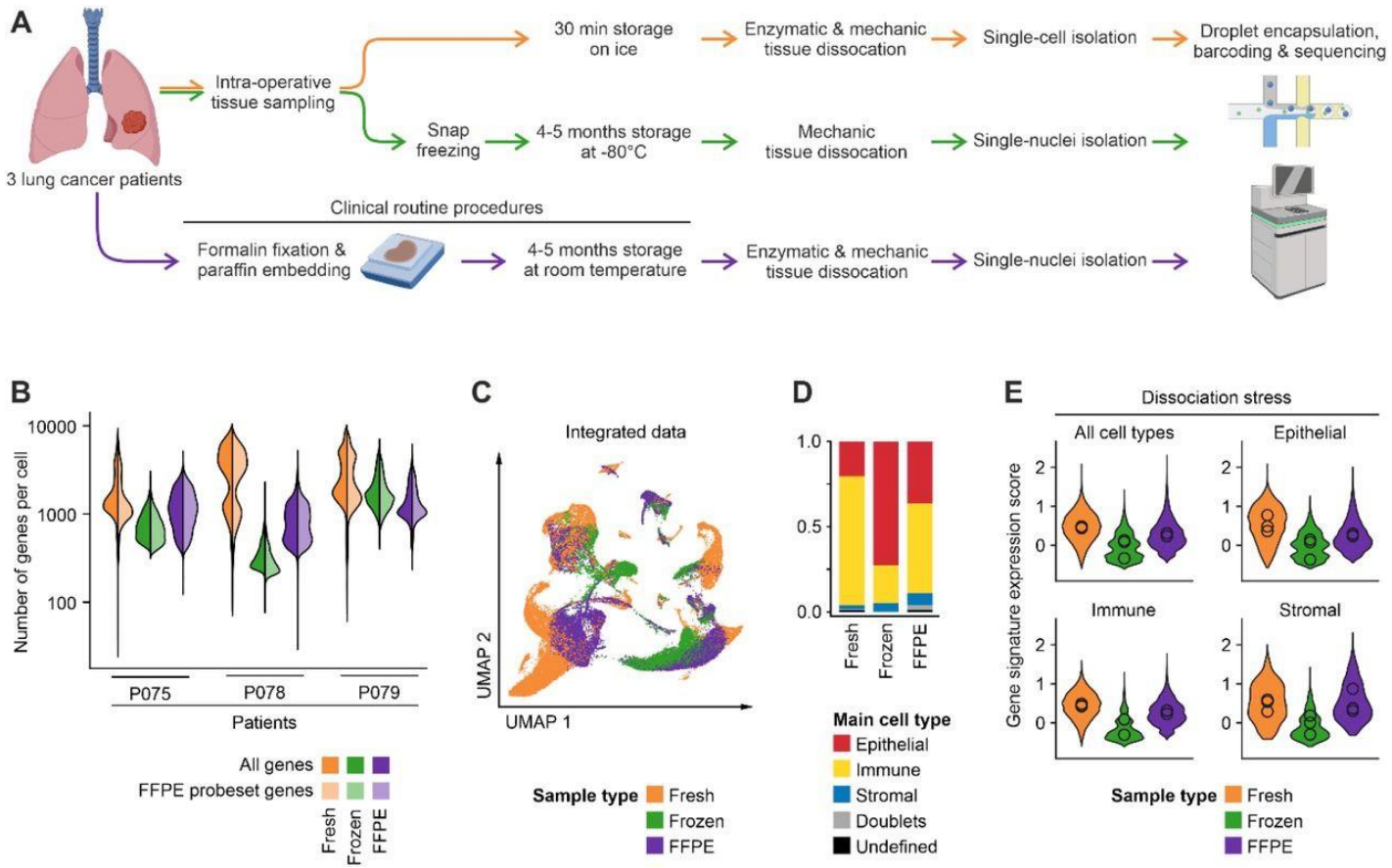
10x GENOMICS

Flex – Profiled Fresh & FFPE Lung Cancer Tissue

Trinks et al. bioRxiv, April 2023

Key Takeaways:

- Fresh and FFPE samples **generated high-quality single cell data**
- **Highly consistent behavior** between samples
- Flex made single-cell profiling of fresh tissue easier
- Flex enabled single-cell profiling of FFPE tissues & reduced cost:
  - Retrospective analysis annotated with **long-term clinical follow-up data**
  - Easy integration of **single cell and spatial data**
  - Facilitates routine insights utilizing **histological & molecular features**



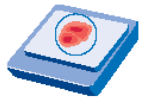
https://doi.org/10.1101/2023.04.25.538273

Flex – Flexibility

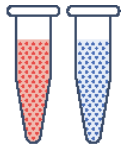
Multiple sample types, scale, & options

Broad sample compatibility

Fresh tissue
Frozen tissue



FFPE tissue



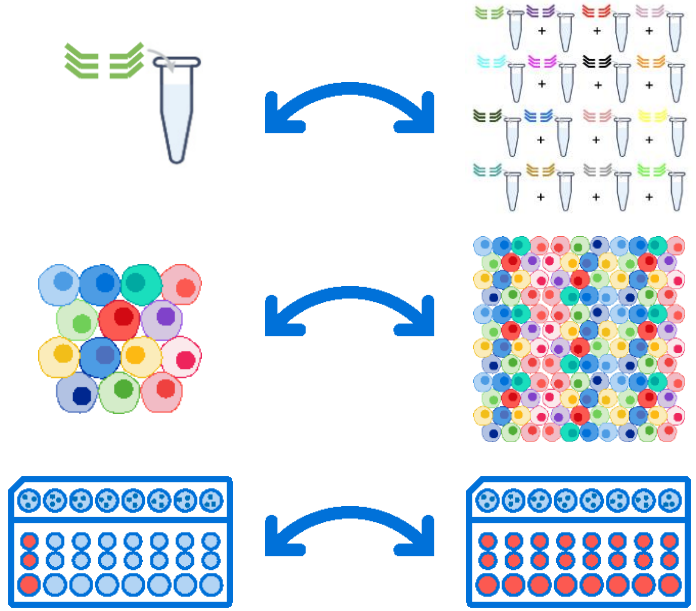
Cell suspensions
Nuclei suspensions

In-line multiplexing

Sample-specific barcode

5-fold increase in scale over other multiplexing techniques

Flexible sample and cell input number

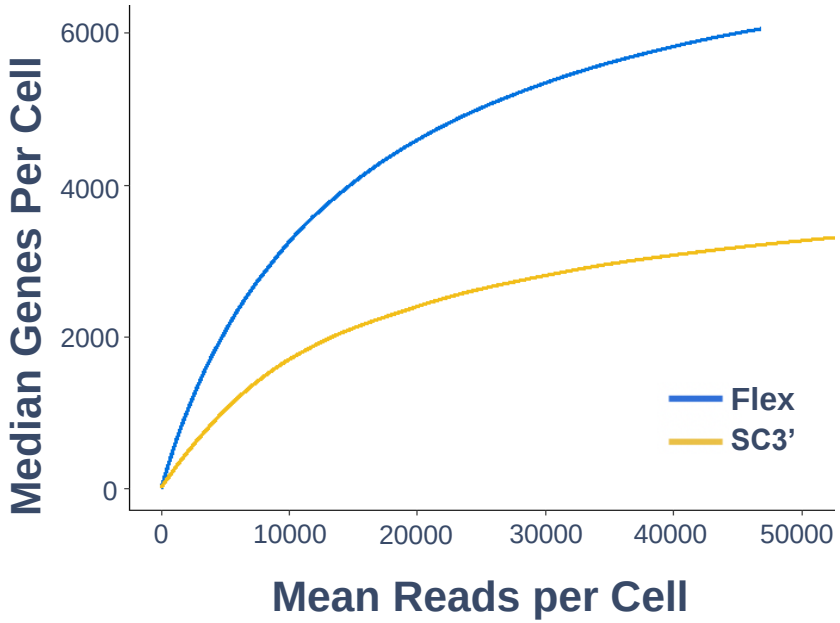


- Up to 128 samples per chip
  - *i.e.,16 samples per lane with the 4 x 16 Multiplex Kit*
- Up to 1M cells per chip
  - i.e., 128K cells per lane *with the 4 x 16 Multiplex Kit*

Flex - Industry Leading Single-Cell Sensitivity

High sensitivity at low read depth

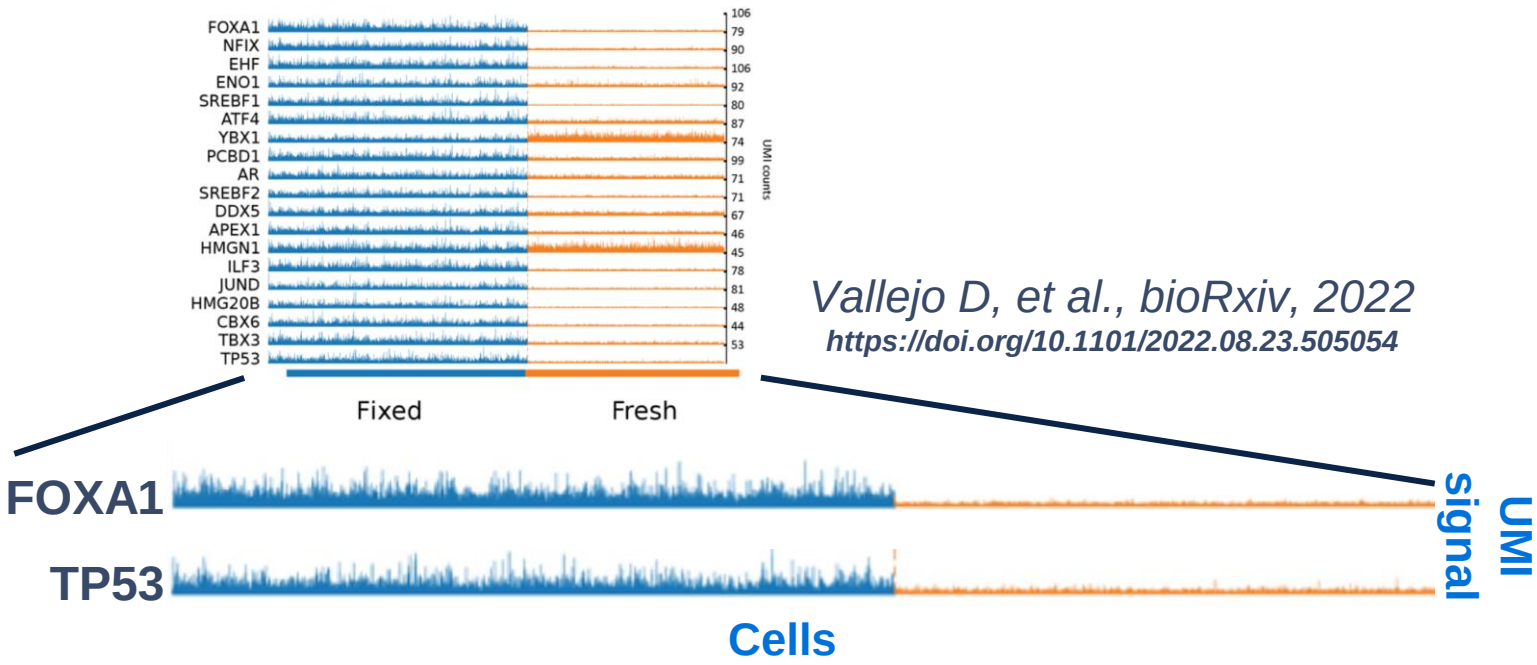
Ovarian cancer nuclei



Substantial reduction in sequencing cost

Transcription factor detection

Prostate cancer cell line (LNCaP)



Vallejo D, et al., bioRxiv, 2022
https://doi.org/10.1101/2022.08.23.505054

Chromium Single Cell Gene Expression Flex

Single Cell FFPE (scFFPE)

Utilizing the Flex assay to profile cells & nuclei from FFPE tissue

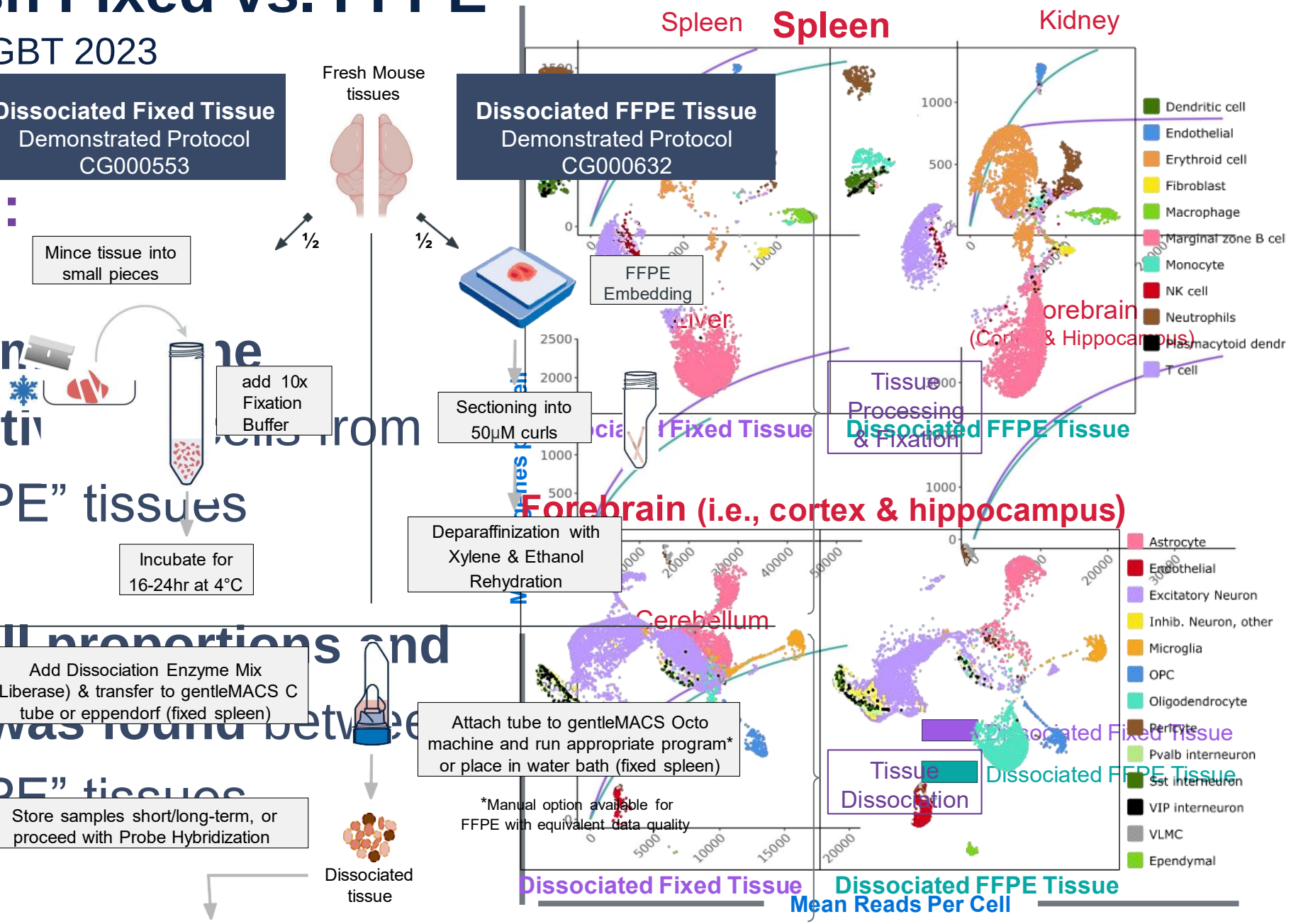
10x GENOMICS

scFFPE – Fresh Fixed vs. FFPE

10x data presented at AGBT 2023

Key Takeaways:

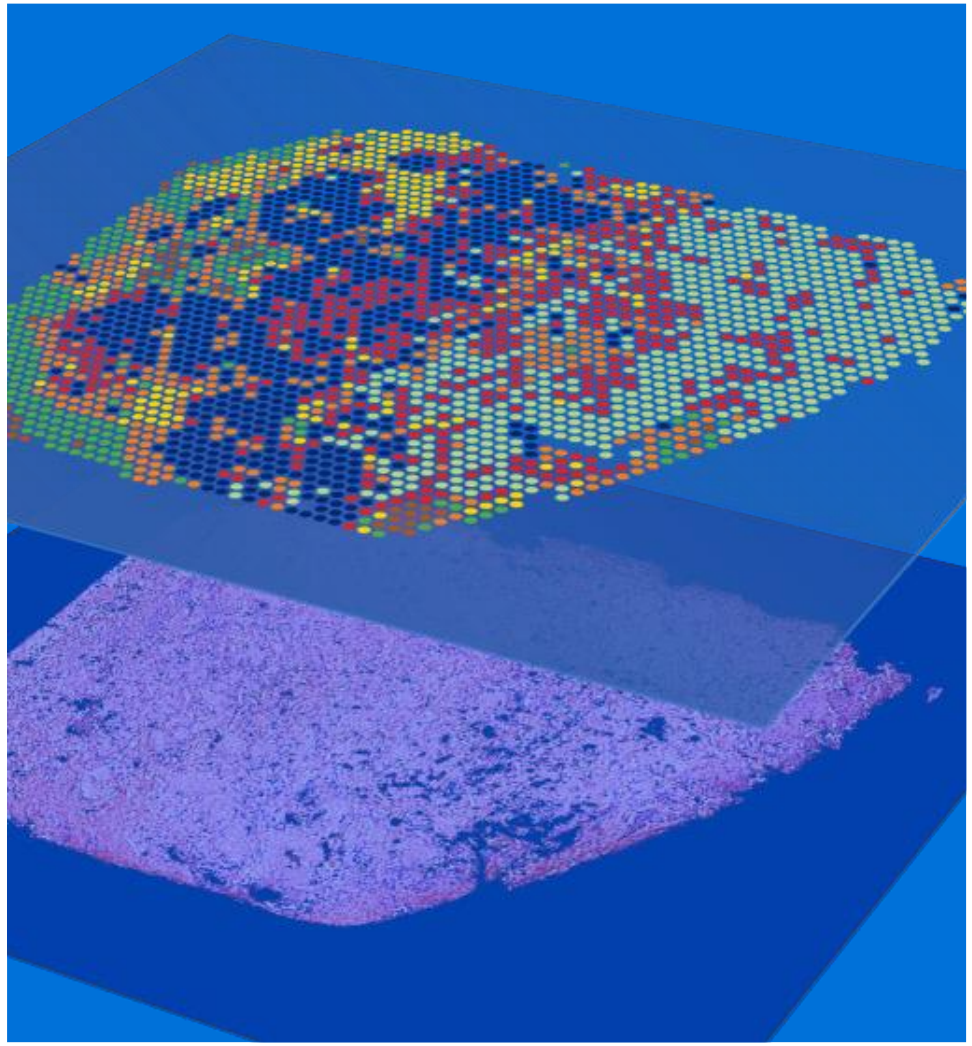
- **Flex showed similar gene detection sensitivities from cells from** “Fixed” and “FFPE” tissues
- **Comparable cell proportions and cell clustering was found between** “Fixed” and “FFPE” tissues



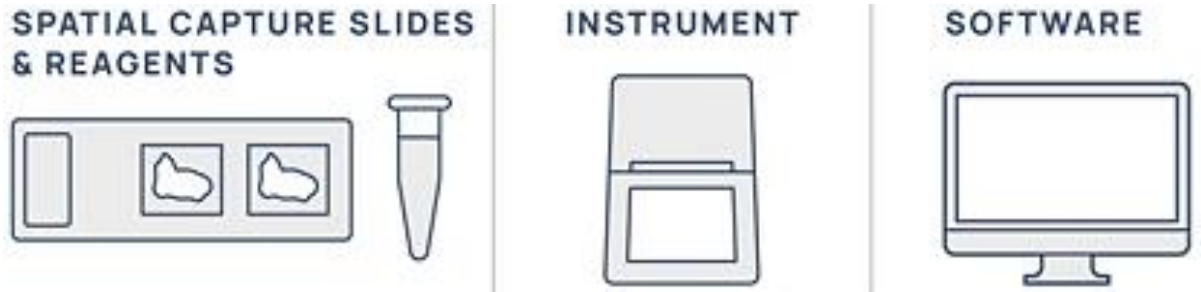
Visium Spatial

Visium

EXPLORE THE SPATIAL ARCHITECTURE OF GENE & PROTEIN EXPRESSION



- Histological & whole transcriptomic information from an entire tissue section
- Slide contains arrayed barcoded oligos representing spatial locations
- Leverages NGS while preserving spatial location
- Unbiased gene & protein expression in tissue context
- **Compatible with Fresh Frozen, Fixed Frozen, 4% PFA Fixed, & FFPE**



10X GENOMICS

Visium – How it Works

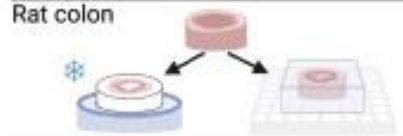
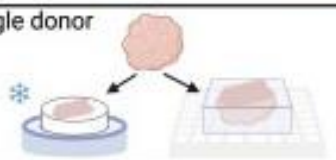
Visium – Use Case in Drug Discovery

Lyubetskaya et al., 2023, Cell Reports Methods

Key Takeaways:

- Over 80K Visium FF & FFPE spatial spots were profiled across several human & mouse tissues
- Transcriptional data with spatial context identified unique features across several tumors
- Cell-type & depth features are distinctly resolved across different tumors
- Tumor-specific biomarkers were identified in patient pancreatic cancer FFPE tissue samples

Experimental summary

	System and modality	Goal	Conclusion
Figure 2	Rat colon 	Determine resolution, fidelity, and reproducibility of ST using a normal, well structured tissue with our spatial validation framework	ST can reliably and with high resolution capture spatial information consistent with pathology annotation and known cell types
Figures 3-4	Syngeneic tumors 	Assess the ability of ST to capture tumor and microenvironment heterogeneity in a reductionist model	ST reflects inter and intra-tumoral heterogeneity, including immune infiltration and depth-specific biology, in two mouse syngeneic oncology models
Figure 5	Single donor 	Use a single donor to compare frozen and FFPE ST modalities to support viability of ST for FFPE clinical cohorts	The FFPE probes-based ST protocol was consistent with polyA-based frozen and FFPE protocols, with few notable exceptions due to non-specific probes
Figures 6-7	Clinical cohort 	Determine the utility of ST for putative target discovery in a clinical cohort	Analysis of a small clinical cohort with our spatial validation framework showed consistency between ST and digital pathology and allowed for the identification of putative tumor biomarkers

https://doi.org/10.1016/j.crmeth.2023.100340

Visium Spatial

Direct Placement Assays

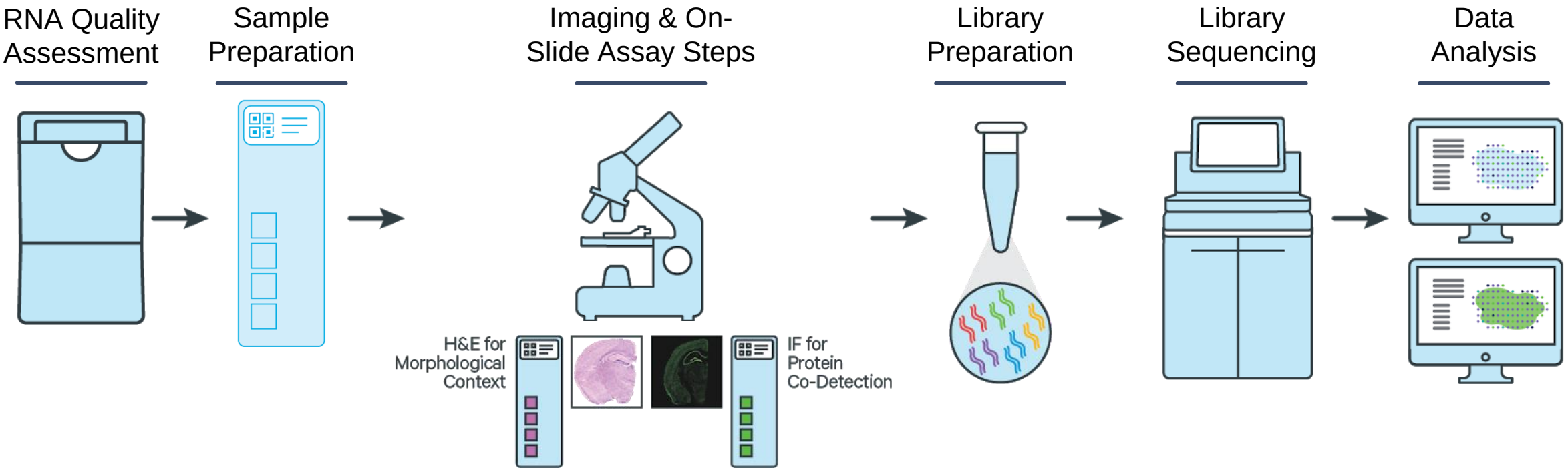
Keep the spatial context of gene expression without the need of an instrument

Fresh Frozen (RT-based) & FFPE (probe-based) v1

10x GENOMICS

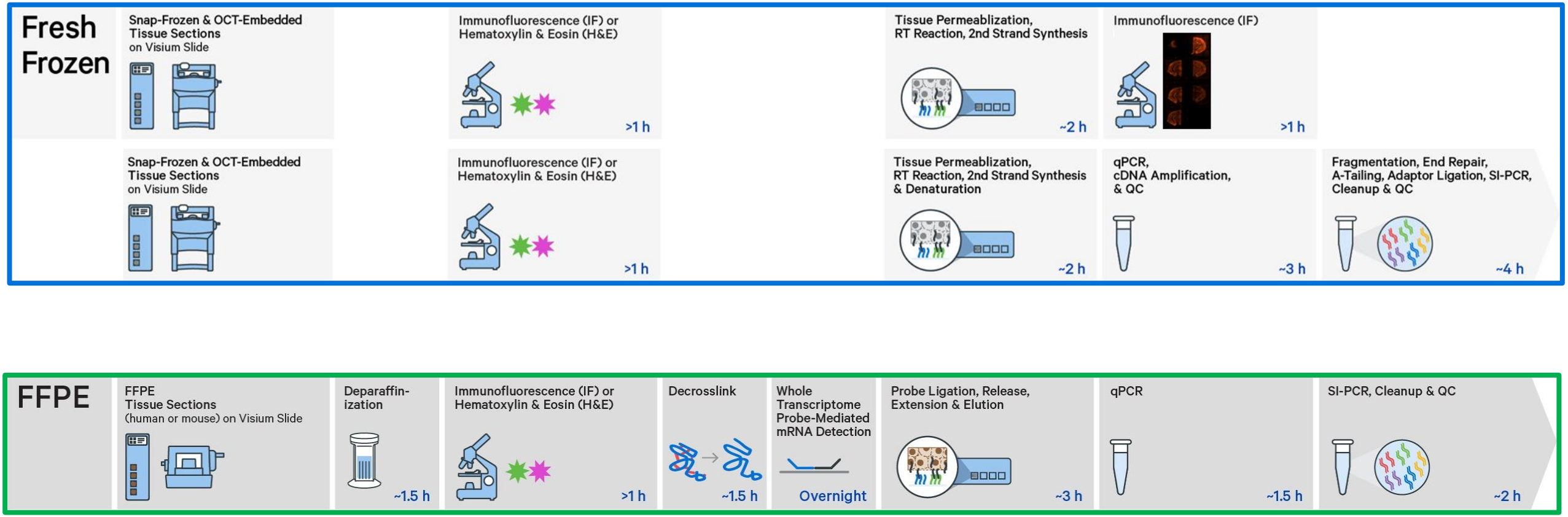
Visium – Direct Placement Workflow

No instrument required - Fresh Frozen & FFPE v1 assays



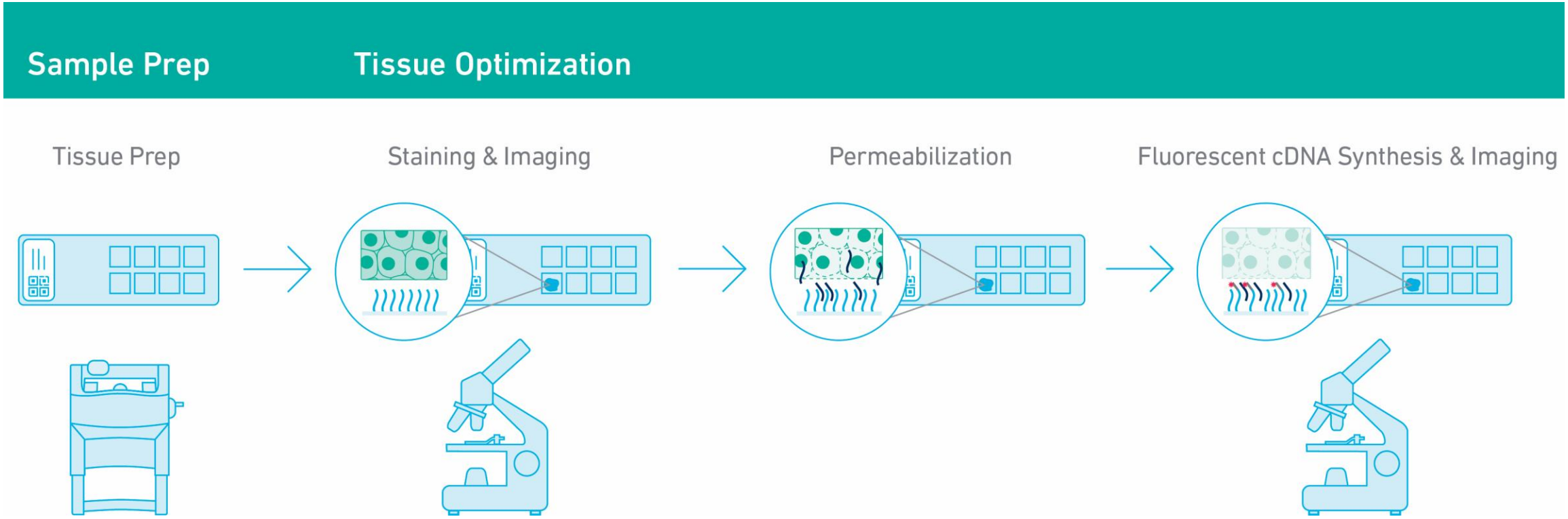
Visium – Direct Placement Workflows

No instrument required - Fresh Frozen & FFPE v1 assays



Visium – Fresh Frozen - Tissue Optimization Workflow

Direct placement v1 assay



1. Section Tissue on to Visium Slide

1. Fix Tissue
2. H&E Stain
3. BF Image

1. Non-Barcoded mRNA Capture

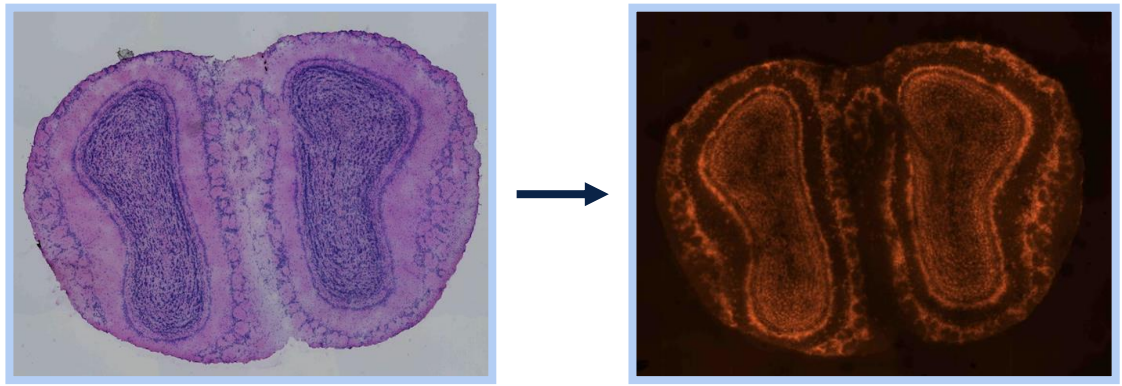
1. Remove Tissue
2. Fluorescent Image

Visium – Fresh Frozen - Tissue Optimization Workflow

Direct placement v1 assay

Purpose

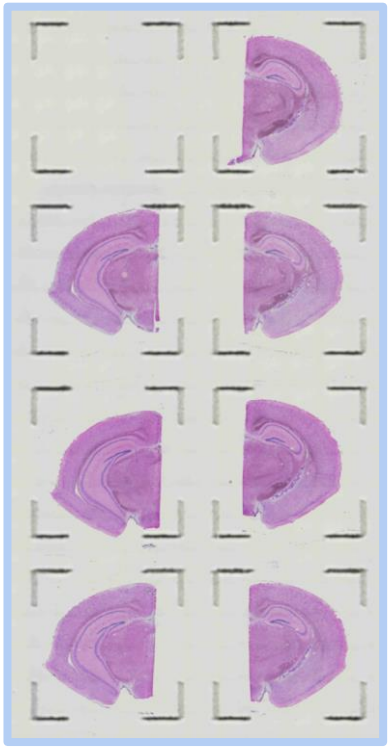
- To determine the optimal permeabilization time, ensure tissue compatibility, and become familiar with the workflow



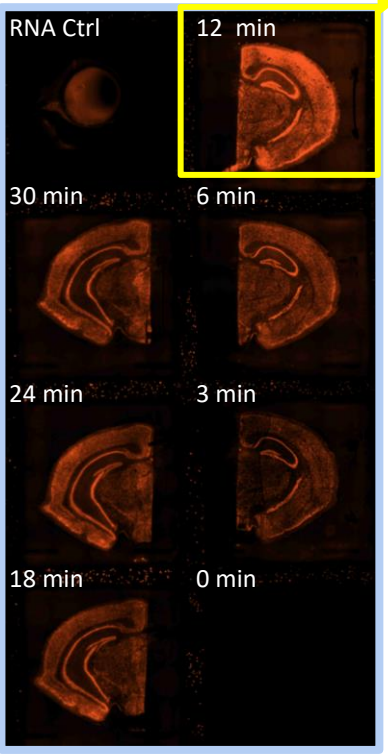
- Recommend testing serial sections of a single tissue type and section thickness per Tissue Optimization slide before proceeding to the Gene Expression experiment

Use optimal permeabilization time for Gene Expression Experiment

Brightfield image



Fluorescent image



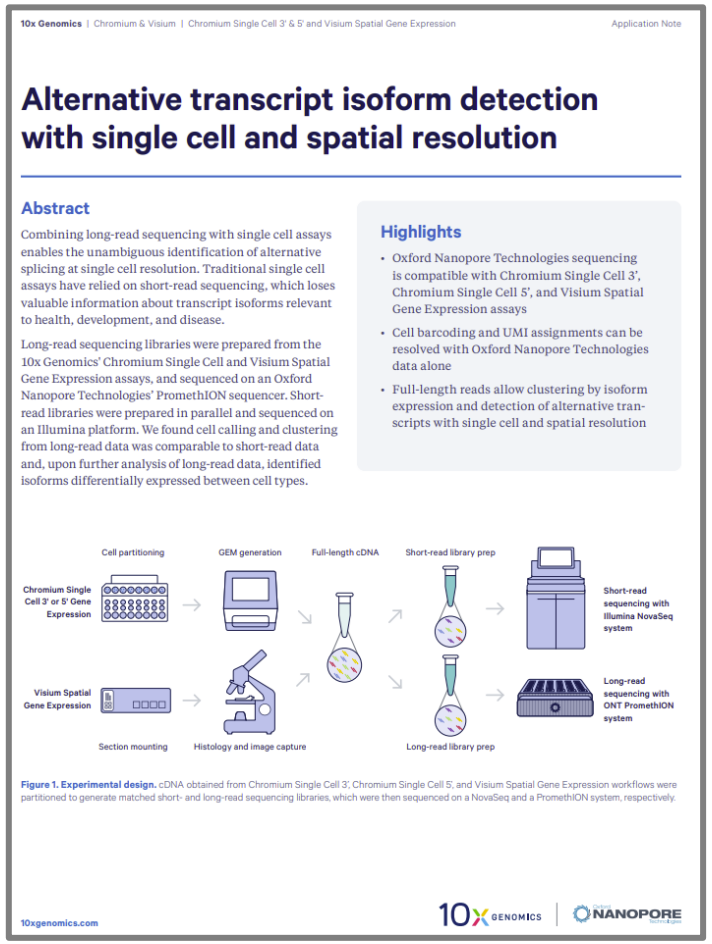
Mouse brain

Visium – Fresh Frozen - Isoform Detection

Enabling new insights via isoform-level alternative splicing for the 10x RT-based 3’, 5’, & Visium FF assays

PacBio Compatible

Oxford NANOPORE Technologies



10x Genomics | Chromium & Visium | Chromium Single Cell 3' & 5' and Visium Spatial Gene Expression — Application Note

Alternative transcript isoform detection with single cell and spatial resolution

Abstract

Combining long-read sequencing with single cell assays enables the unambiguous identification of alternative splicing at single cell resolution. Traditional single cell assays have relied on short-read sequencing, which loses valuable information about transcript isoforms relevant to health, development, and disease.

Long-read sequencing libraries were prepared from the 10x Genomics' Chromium Single Cell and Visium Spatial Gene Expression assays, and sequenced on an Oxford Nanopore Technologies' PromethION sequencer. Short-read libraries were prepared in parallel and sequenced on an Illumina platform. We found cell calling and clustering from long-read data was comparable to short-read data and, upon further analysis of long-read data, identified isoforms differentially expressed between cell types.

Highlights

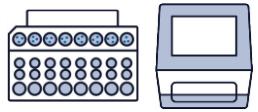
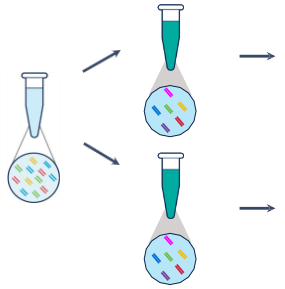
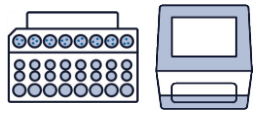
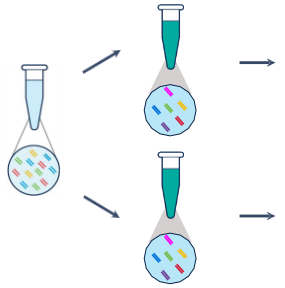
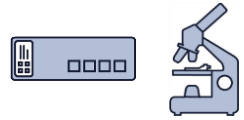
- Oxford Nanopore Technologies sequencing is compatible with Chromium Single Cell 3', Chromium Single Cell 5', and Visium Spatial Gene Expression assays
- Cell barcoding and UMI assignments can be resolved with Oxford Nanopore Technologies data alone
- Full-length reads allow clustering by isoform expression and detection of alternative transcripts with single cell and spatial resolution

Figure 1. Experimental design. cDNA obtained from Chromium Single Cell 3', Chromium Single Cell 5', and Visium Spatial Gene Expression workflows were partitioned to generate matched short- and long-read sequencing libraries, which were then sequenced on a NovaSeq and a PromethION system, respectively.

10xgenomics.com

10x GENOMICS | NANOPORE

10x Technical Note

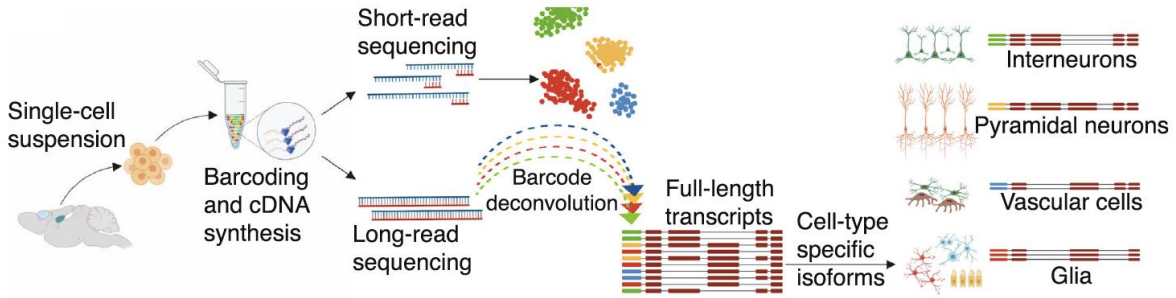
Tissue type	Assay	Sample barcoding	Library Preparation	Sequencing
	3’ GEX			Illumina PacBio
	5’ GEX & V(D)J			Illumina
	Spatial GEX			ONT

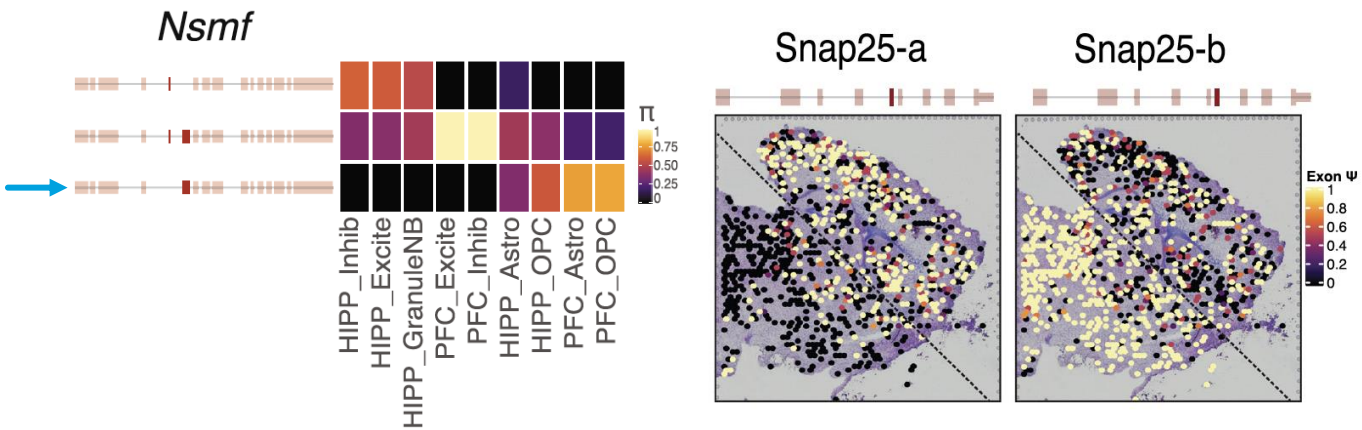
Visium – Fresh Frozen - Isoform Detection

Joglekar et al., Nat Comm, 2021

Key Takeaways:

- 10x Genomics Single Cell and **Visium Spatial Gene Expression** solutions were combined with **long-read sequencing** to investigate the **differential isoform expression (DIE)** between brain regions
- Adding **spatial analysis anchored single-cell DIE observations and localized mRNA splicing**
- Spatial transcriptomics combined with long-read sequencing yields a spatially resolved splicing map, **bringing closer a full isoform map of the brain**





doi.org/10.1038/s41467-020-20343-5

Visium Spatial

CytAssist Enabled Assays

Simplifies Visium prep/workflow & broadens sample access

FFPE/probe-based v2

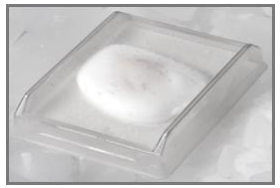
10x GENOMICS

Visium – CytAssist Simplifies Prep & Broadens Access

Precision analyte capture and spatial barcoding

FFPE samples

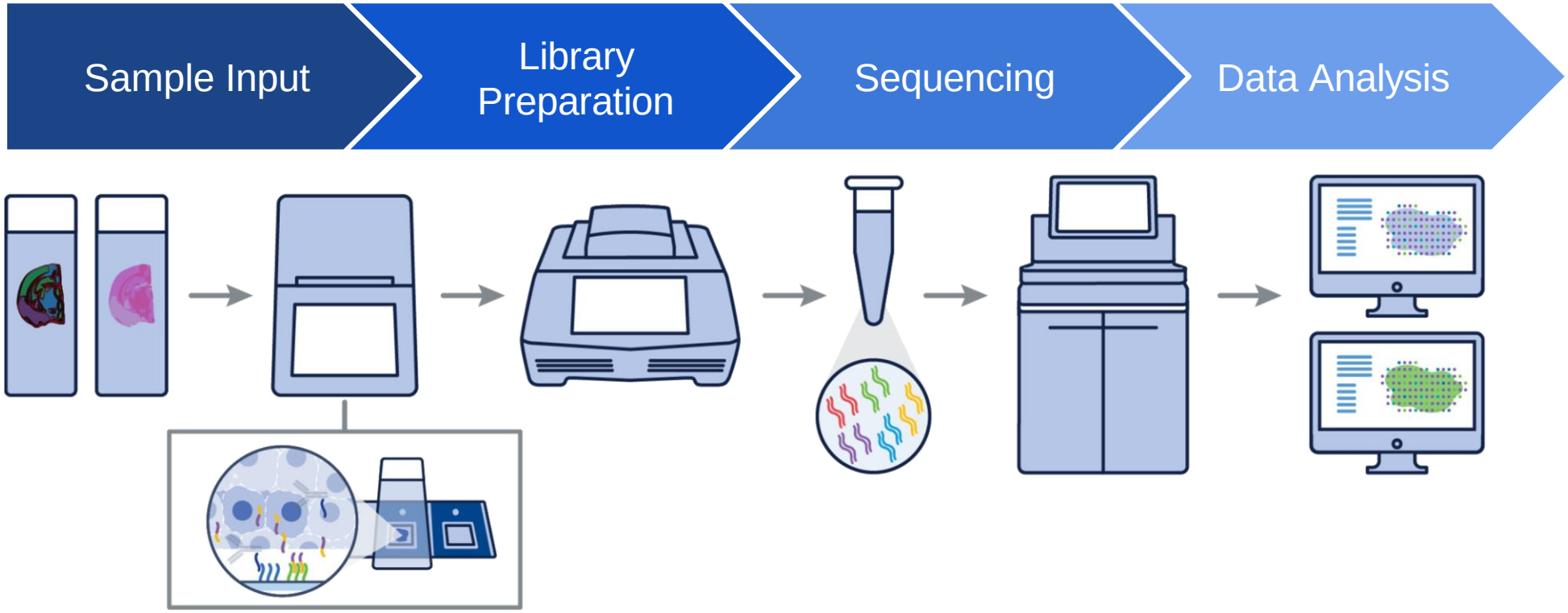
Archived FFPE samples



Fresh Frozen AND
Fixed Frozen samples

- Improved gene sensitivity and specificity
- Broader tissue type compatibility
- Access to archival samples
- Improved spatiality
- Streamlined workflow
- Enables protein + gene expression

Visium CytAssist – Workflow



Sample Preparation
User-supplied human samples
Freshly Placed FFPE Sections
Archived H&E Slides

Library Preparation
Visium CytAssist
10x Genomics Kits
User-supplied third-party reagents

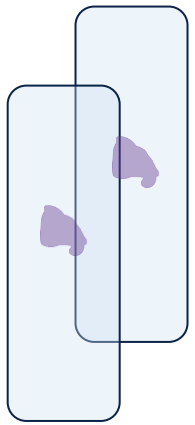
Sequencing
10x Genomics library-compatible sequencer (e.g., Illumina sequencer)

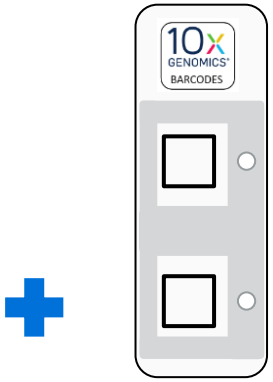
Analysis
Space Ranger analysis pipeline
Loupe Browser visualization tool

Visium CytAssist – Workflow

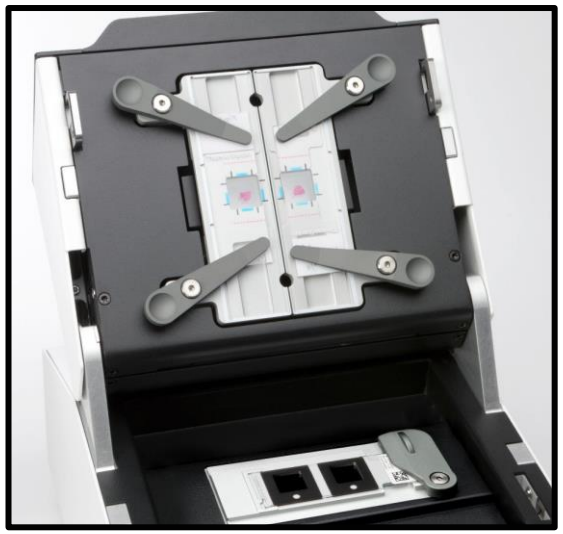
Seamlessly integrate with standard histology FFPE & FF sample preparation

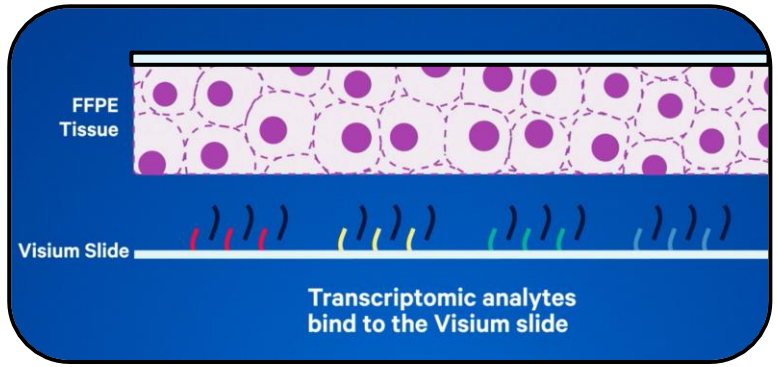
Two tissue slides
Stained sections on standard glass slides

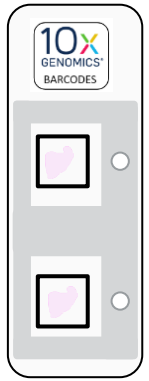




Visium Slide
Two capture areas

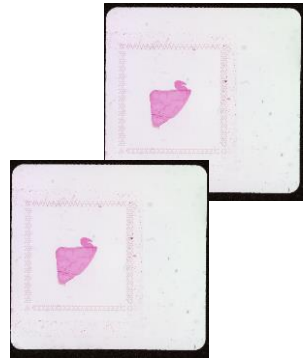






Visium Slide
Target probes now captured on slide

Two tissue images
Spatial orientation for sequencing data



Visium CytAssist – Rescues Challenging Sample Type

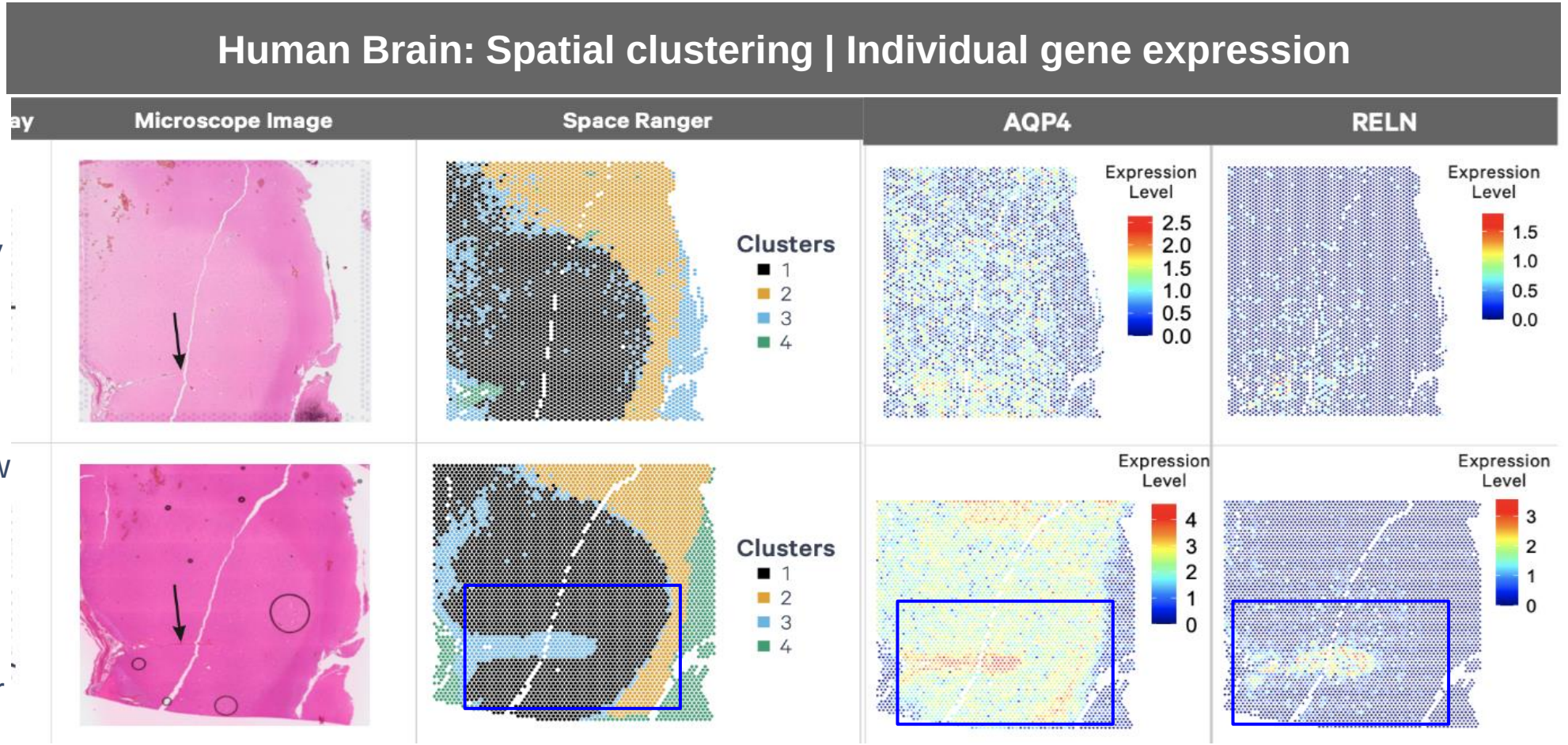
Human Brain | Spatial Clustering | Individual Gene Expression

Spatial Clustering

- Boxed region highlights layers of gene clusters forming around a capillary

Individual Gene Expression

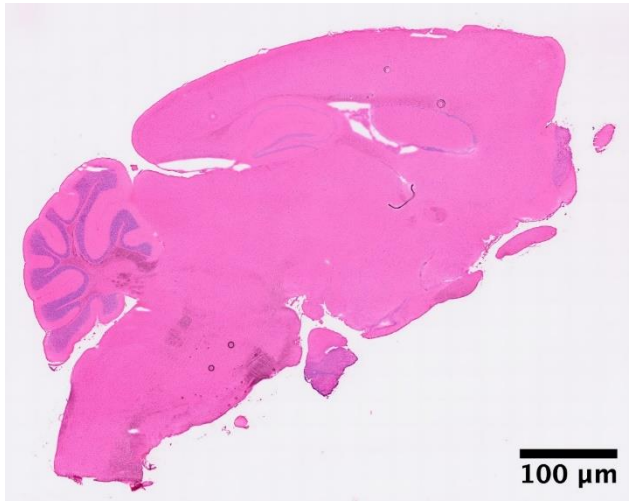
- Gene maps from DP show less distinction between signal and background
- AQP4 and RELN regulates the blood- brain barrier, seen in the cluster near the capillary



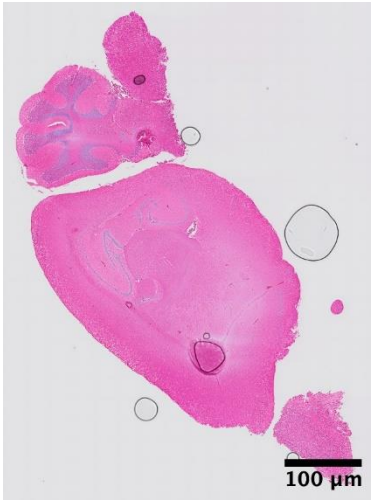
Visium CytAssist – Robust Performance Across Samples

FFPE

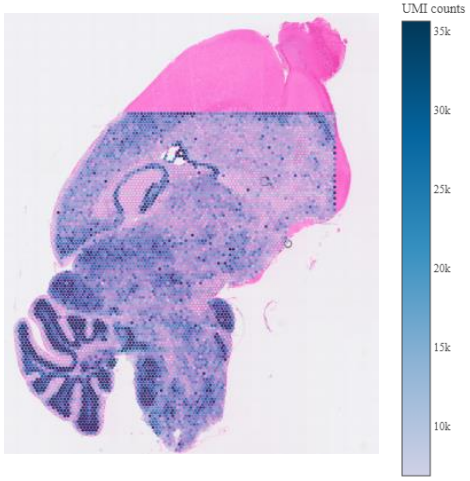
Fresh Frozen

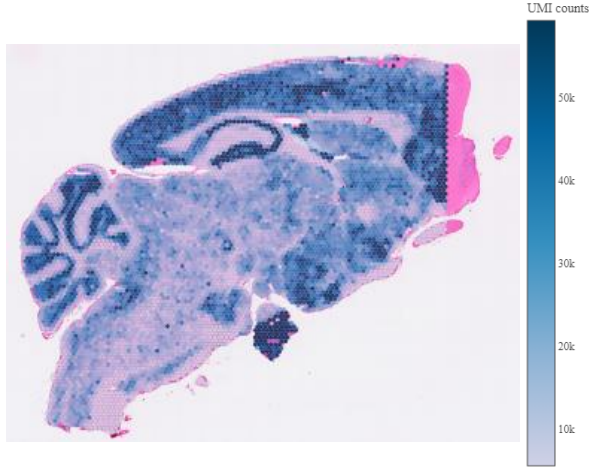


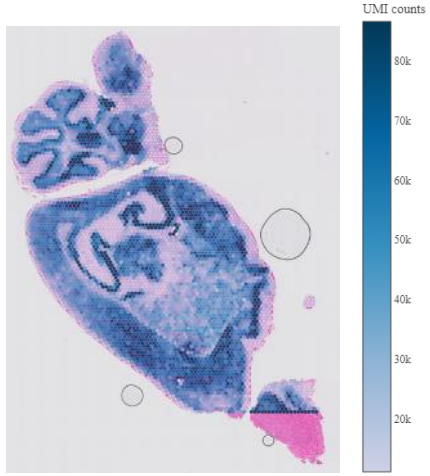
Fixed Frozen



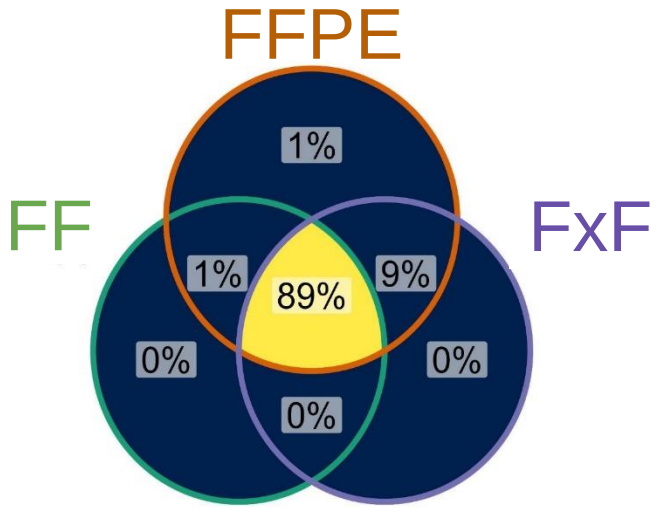
UMIs detected per spot



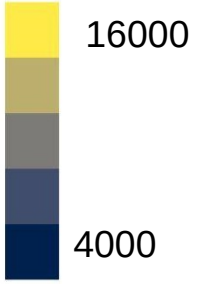




Total Genes Detected per Sample Prep Method



# of genes detected



Visium Spatial – CytAssist Enabled

Gene and Protein Expression

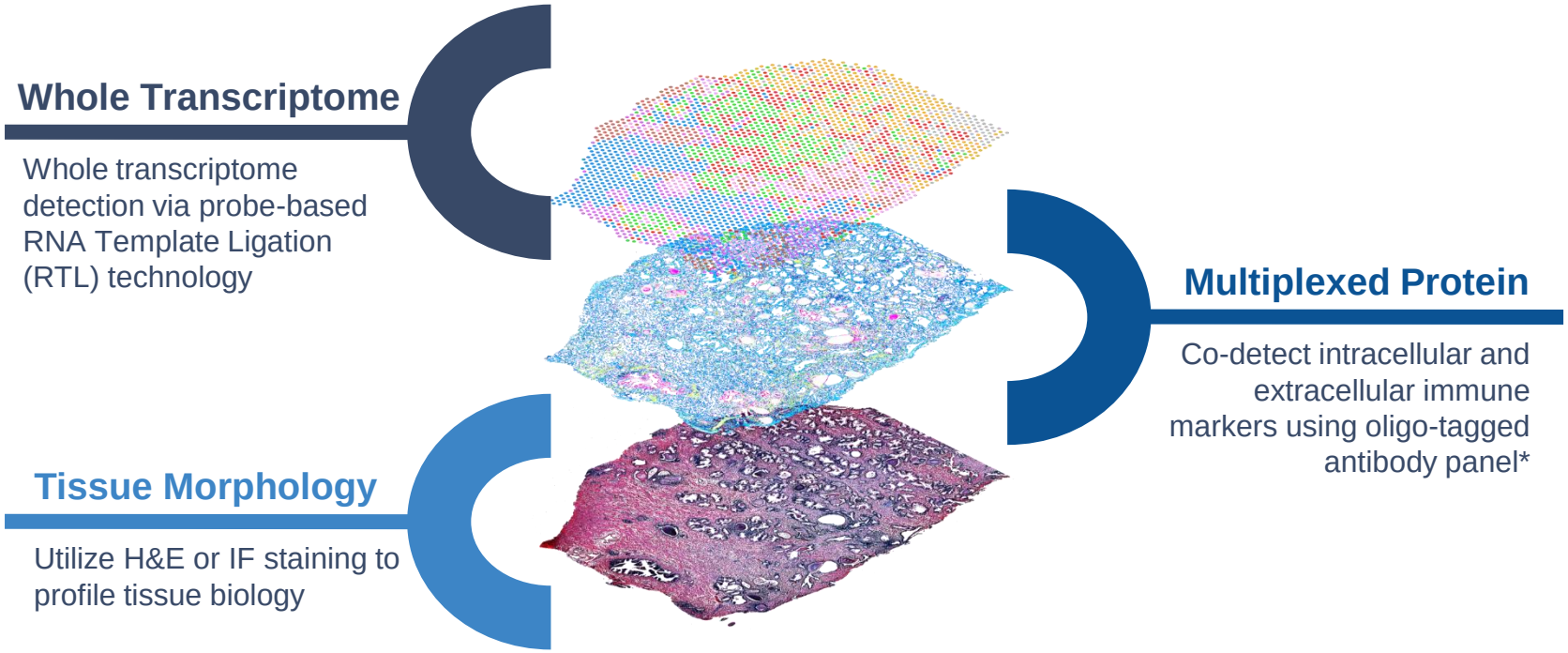
Broaden data collection from the same tissue section

FFPE/probe-based v2

10x GENOMICS

Visium CytAssist – Spatial Gene and Protein Overview

Probes and oligo-tagged antibodies enable RNA and protein co-detection

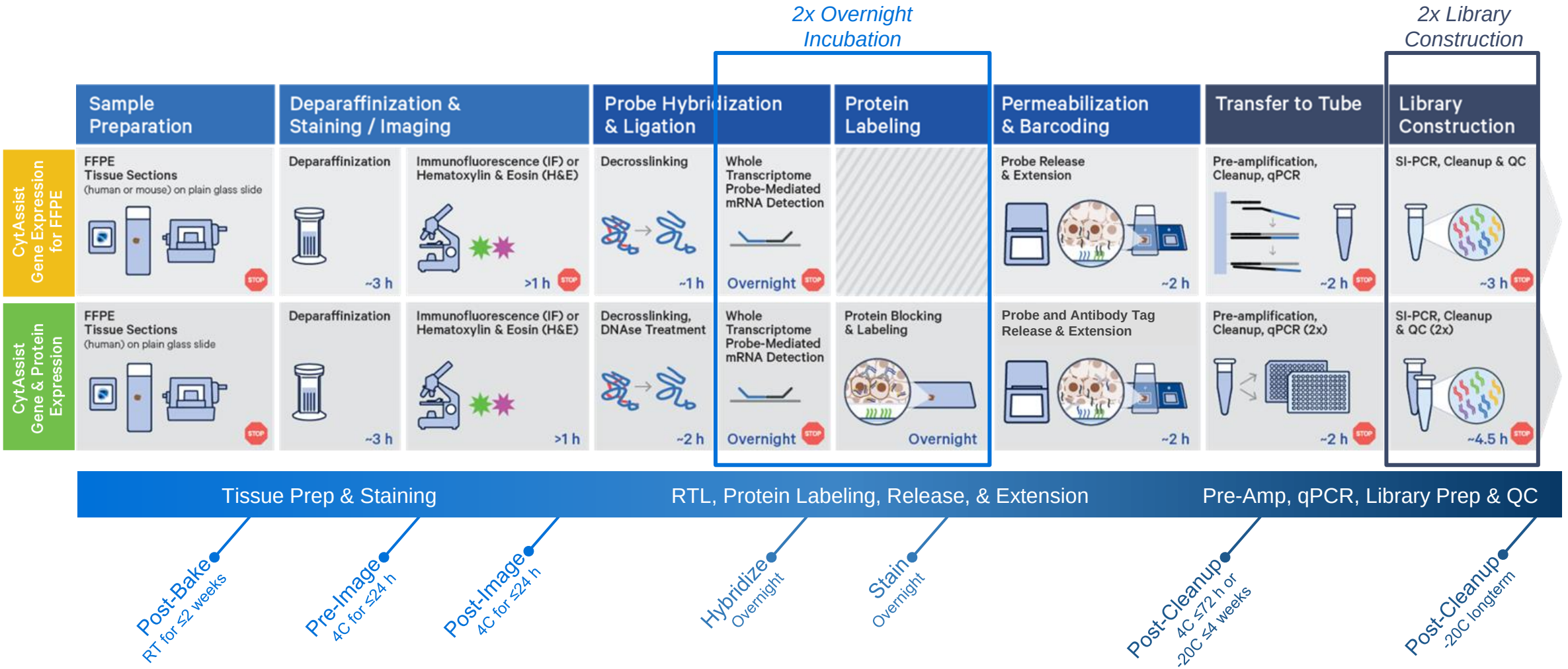


**Additional targets may be detected by spiking in oligo-tagged antibodies*

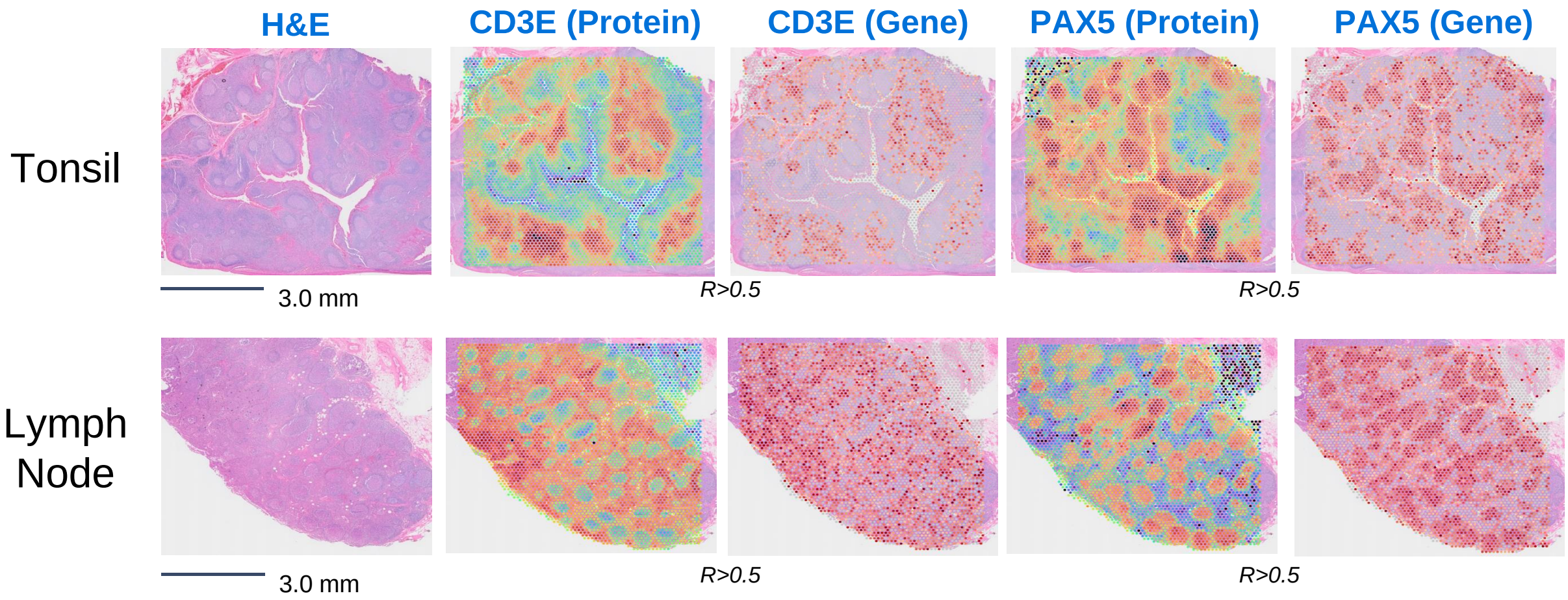
Visium CytAssist – Workflow

Spatial Gene and Protein Expression

Addition of an overnight step and ~3 hours of workflow

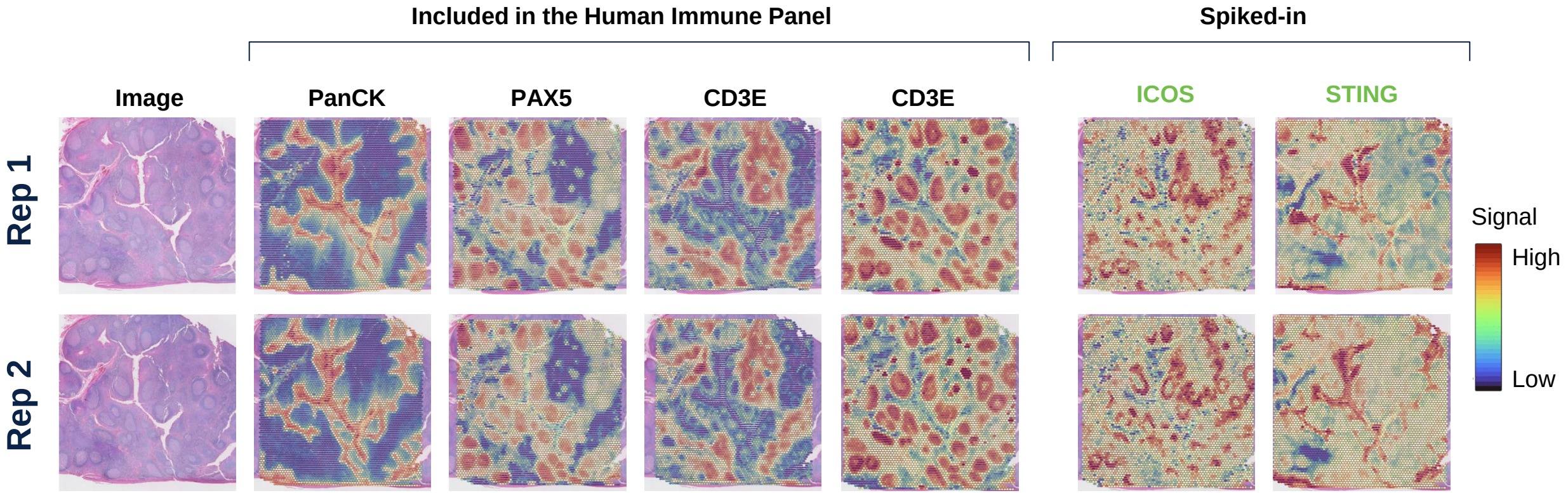


Visium CytAssist – Gene & Protein on a Single Tissue Section



Visium CytAssist – Antibody Spike-In Data

Human Tonsil



Visium Spatial – CytAssist Enabled

Roadmap: Visium HD

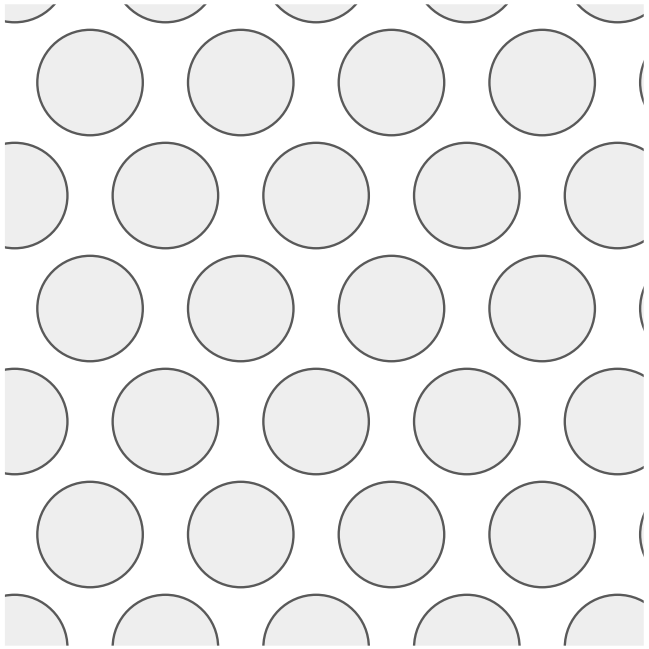
Enabling NGS-based whole-transcriptome at 2 µm resolution

FFPE/probe-based v2

Visium CytAssist – Roadmap

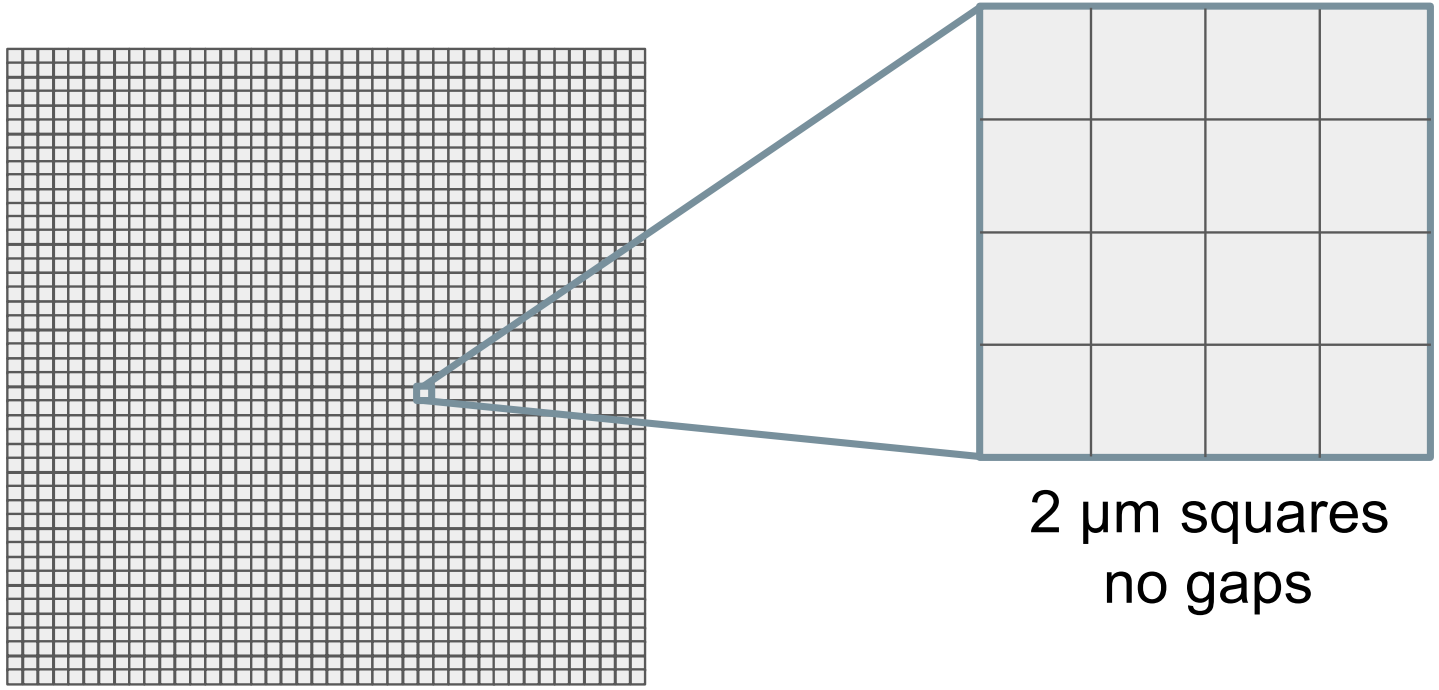
Visium HD

Visium



55 µm spots, hexagonally arranged

Visium HD



8 µm squares, no gaps

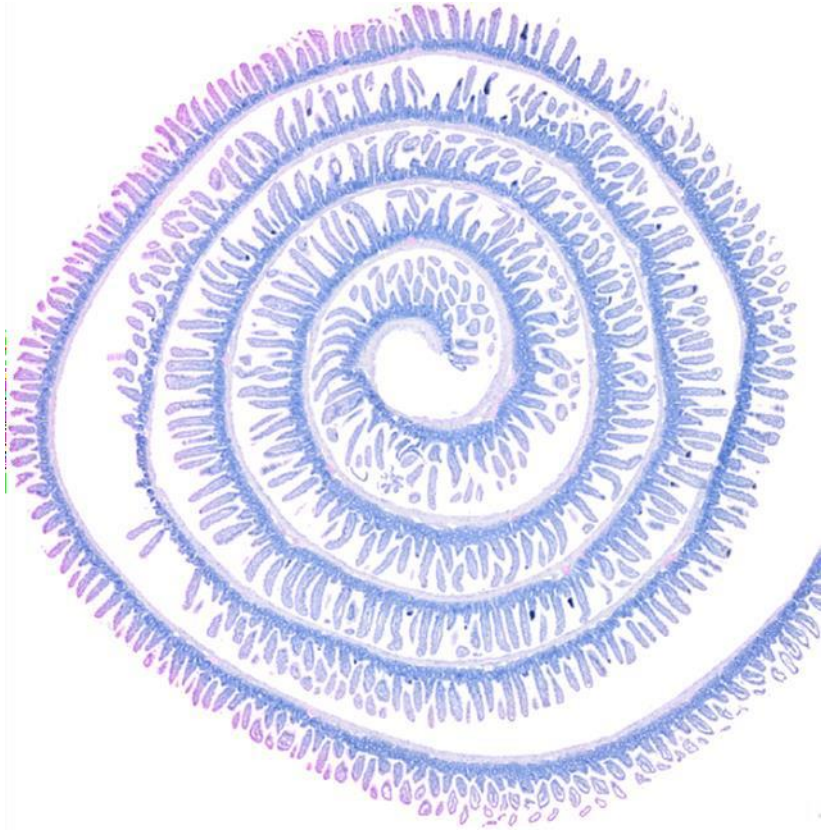
2 µm squares no gaps

Actual feature size

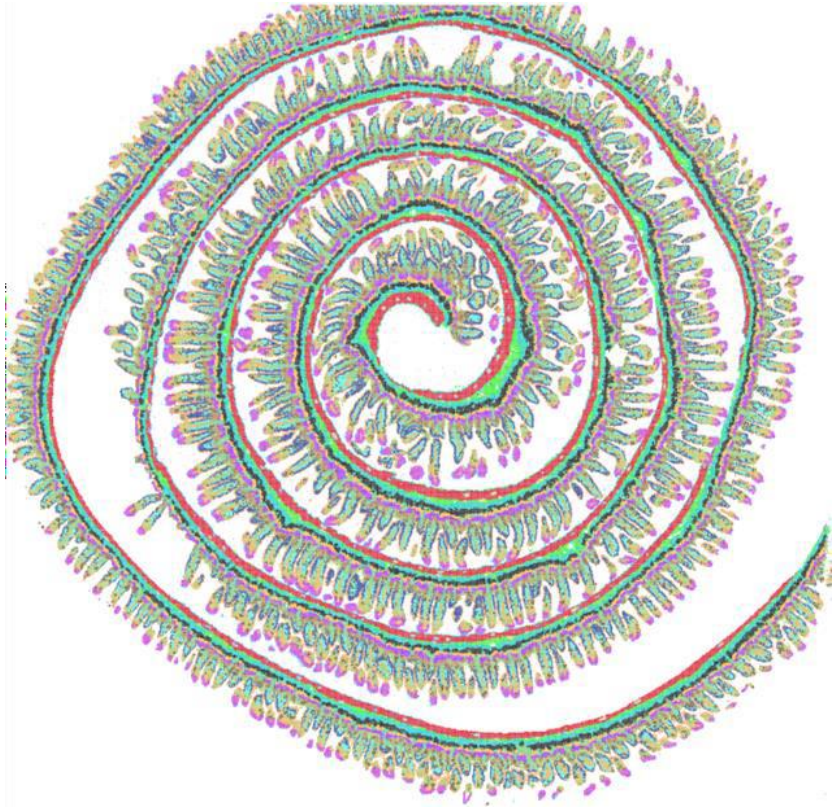
CytAssist – Higher Resolution: Visium HD

FFPE mouse intestine

H&E staining

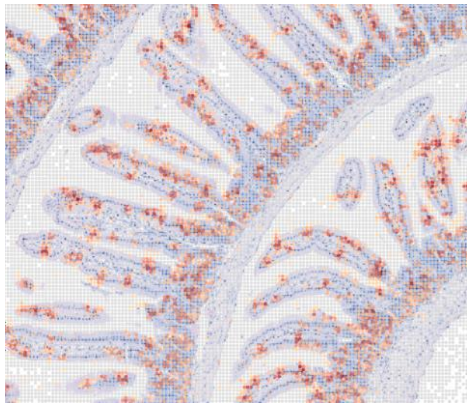


Unbiased clustering data

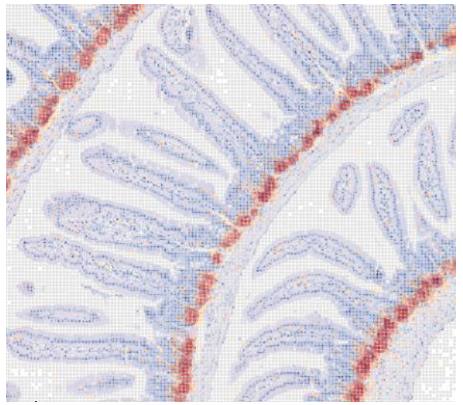


Marker gene expression

Muc2 (goblet cell marker)



Lyz1 (paneth cell marker)

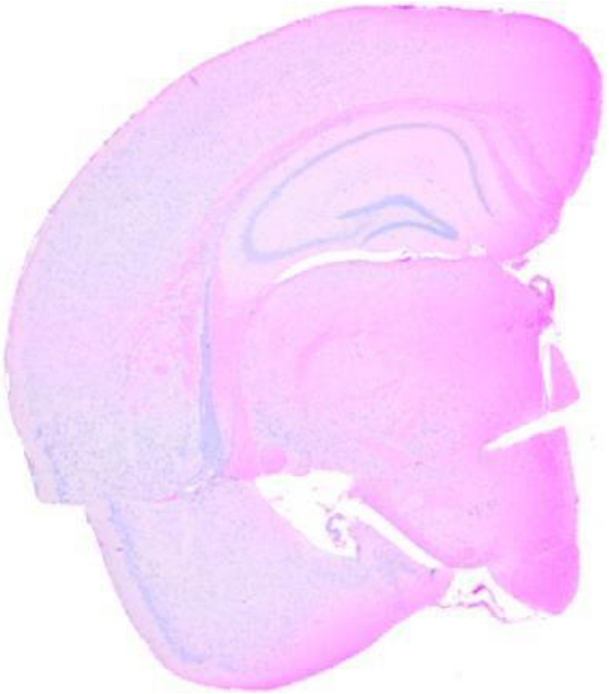


R&D consumables, reagents, workflows, software being used to generate and process the data

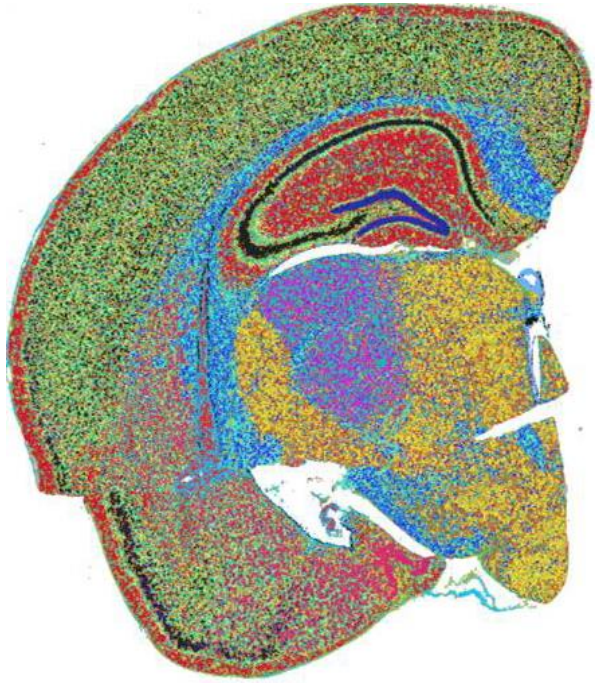
CytAssist – Higher Resolution: Visium HD

FFPE mouse brain

H&E staining

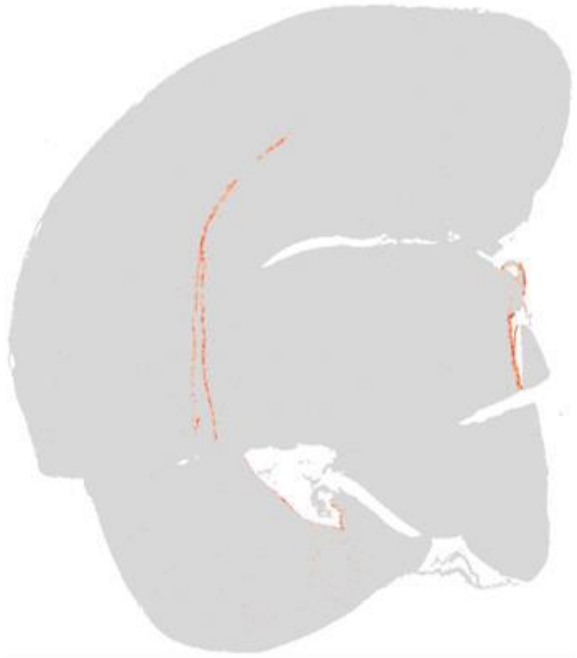


Unbiased clustering data



Marker gene expression

Ccdc153
(ependymal cell marker)



Clic6
(choroid plexus marker)

R&D consumables, reagents, workflows, software being used to generate and process the data

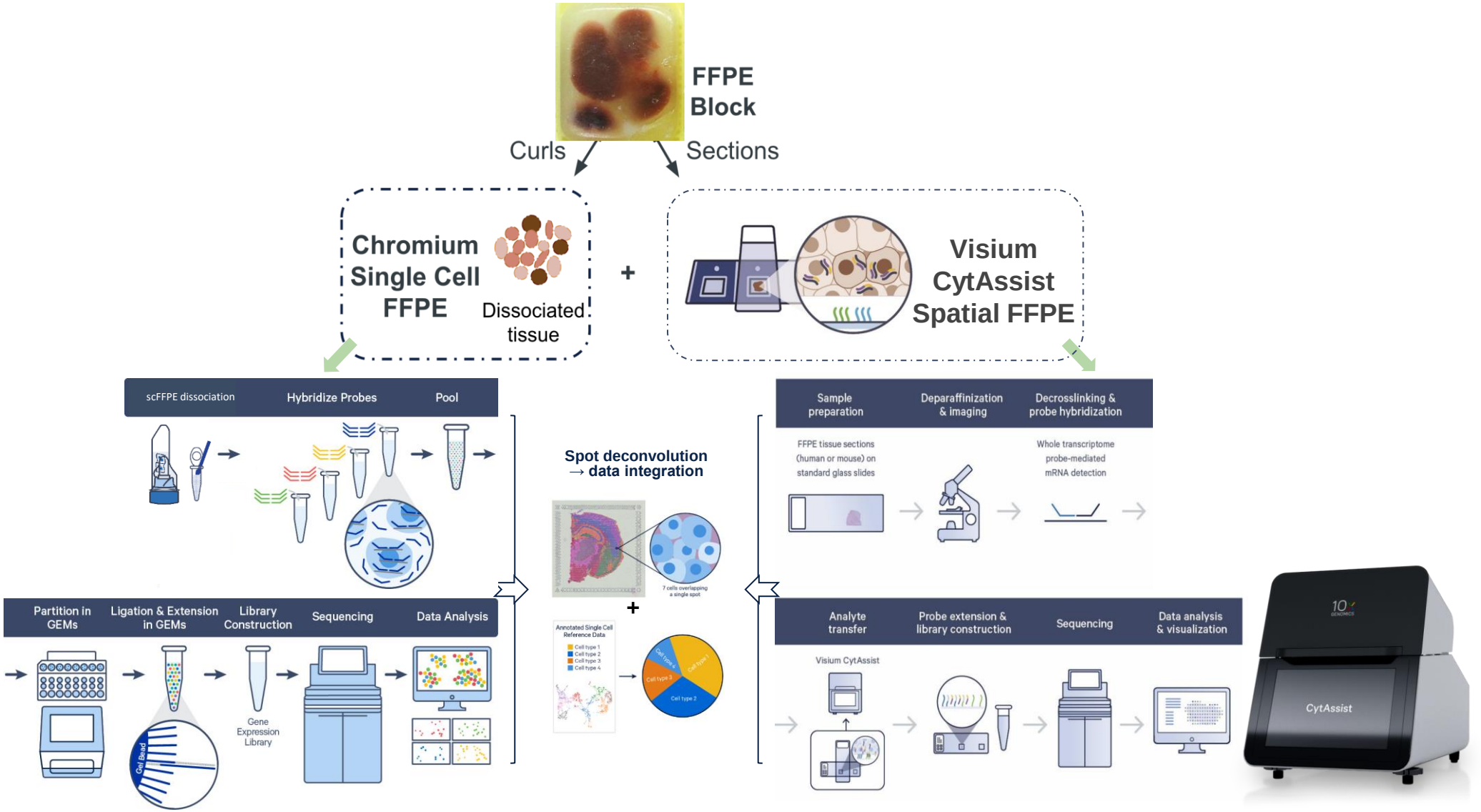
Chromium Single Cell & Visium Spatial

Data Integration

Uniting data from Chromium Flex’s scFFPE with Visium’s FFPE on CytAssist

Data Integration – Flex and CytAssist from same FFPE Tissue

Example using FFPE human prostate cancer tissue



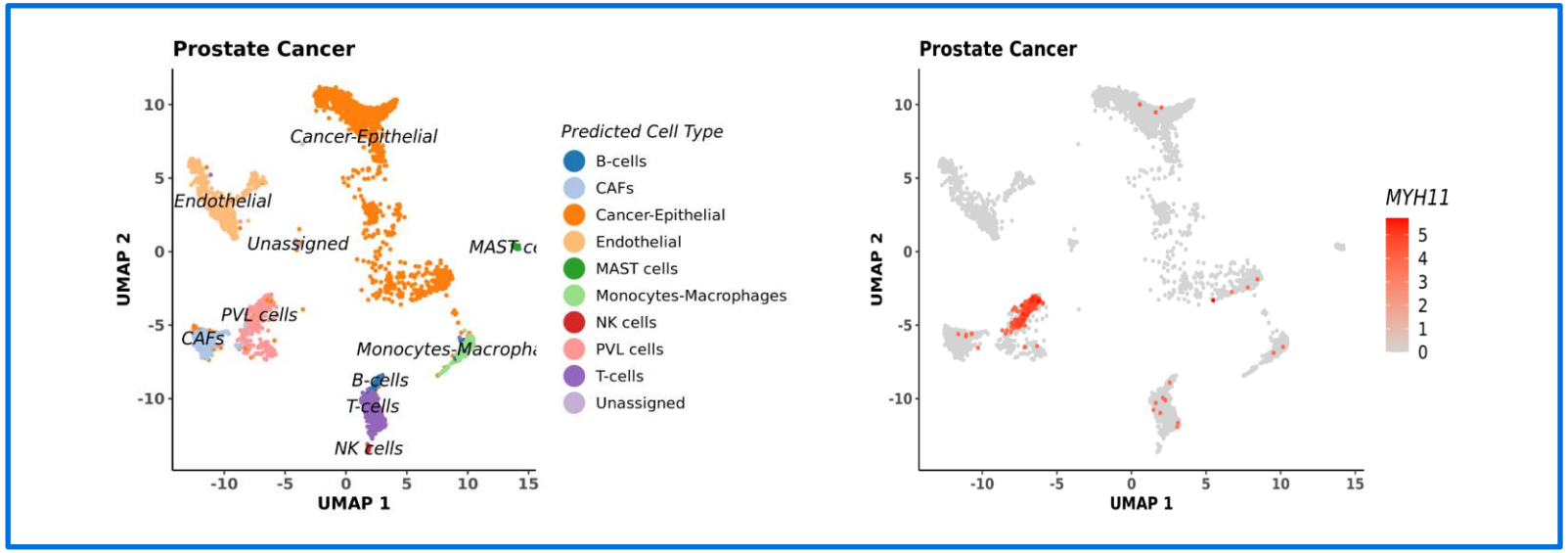
Data Integration – Flex and CytAssist from same FFPE Tissue

Example using FFPE human prostate cancer tissue

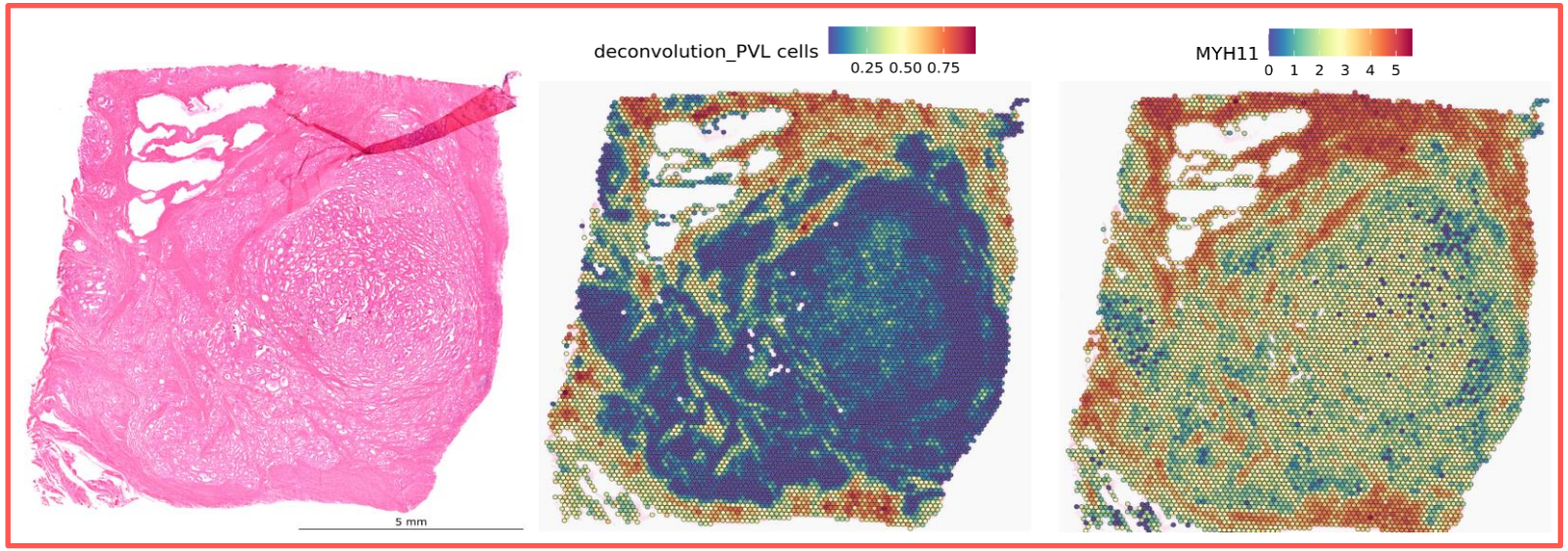
Key Takeaways:

- Combine single-cell resolution with spatial context
- Uncover new biological insights
- Enabled by shared probe architecture

scFFPE



CytAssist



Chromium Flex & Visium CytAssist

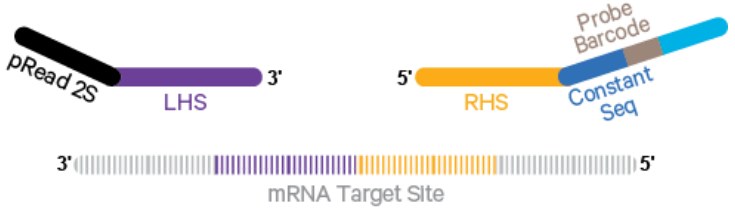
Probe Customization

Unlock limitless possibilities via cross-platform shared chemistry

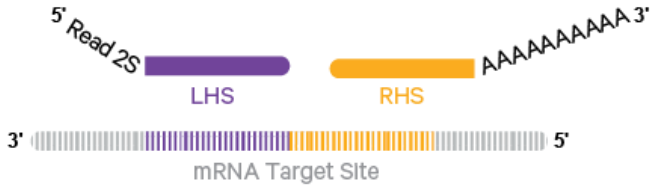
10x Probe-Based Chemistries

Provide highly specific & customizable workflows

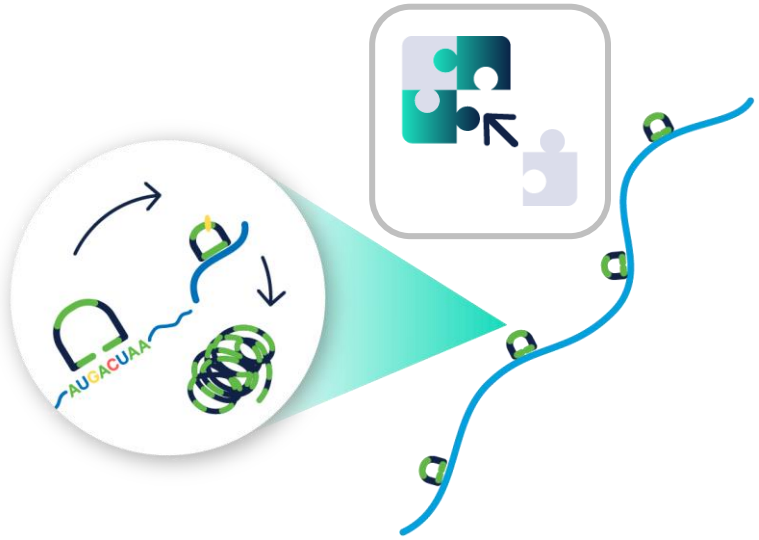
Chromium Gene Expression Flex



Visium for FFPE



Xenium



Technical Note

CG000621 | Rev B

Custom Probe Design for Visium Spatial Gene Expression and Chromium Single Cell Gene Expression Flex

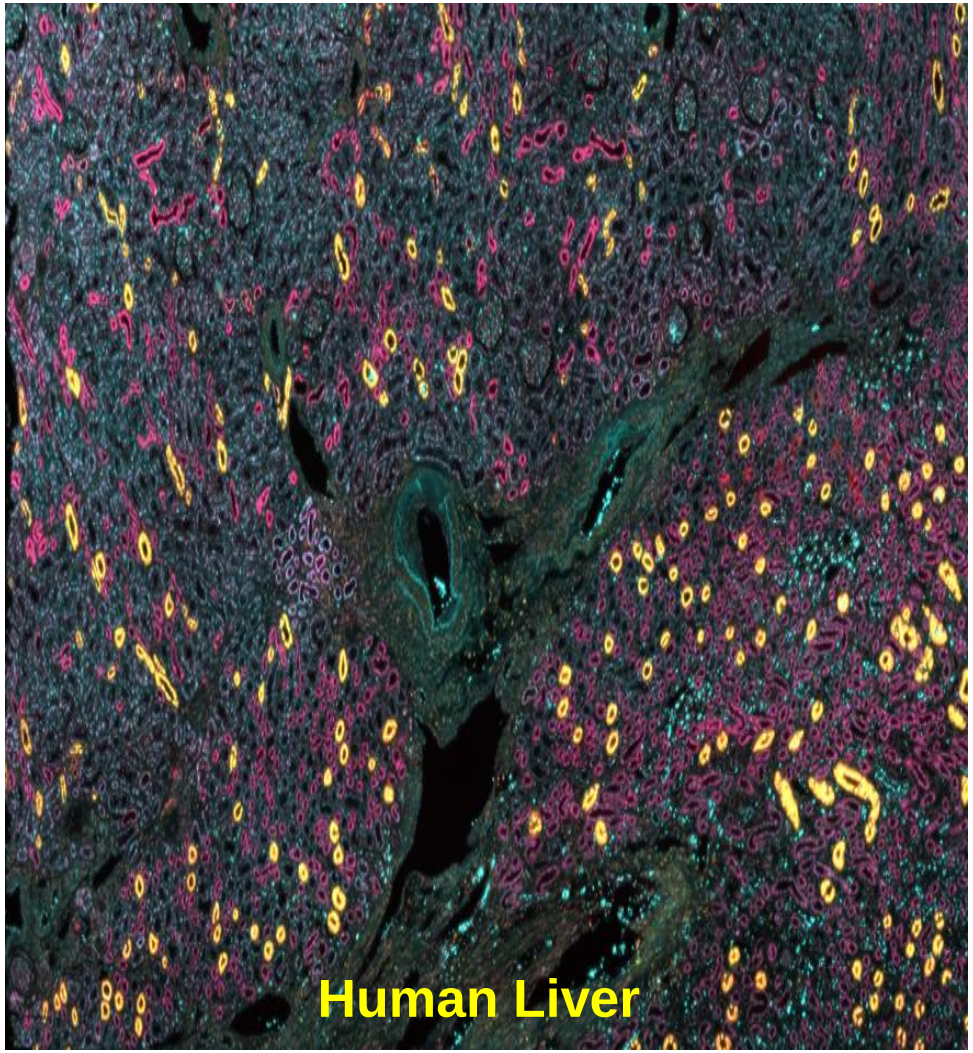
Introduction

10x Genomics Visium Spatial Gene Expression technology for FFPE enables spatial transcriptomic insights by analyzing mRNA in tissue sections derived from fixed tissue samples. Chromium Single

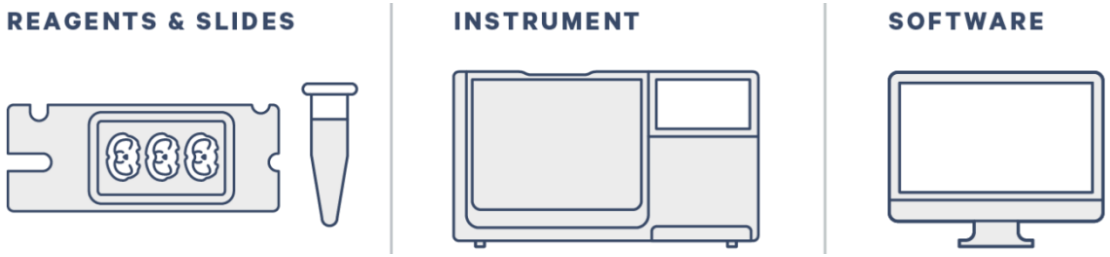

Xenium In Situ

Xenium

UNCOVER CELL-CELL INTERACTIONS DRIVING FUNCTION



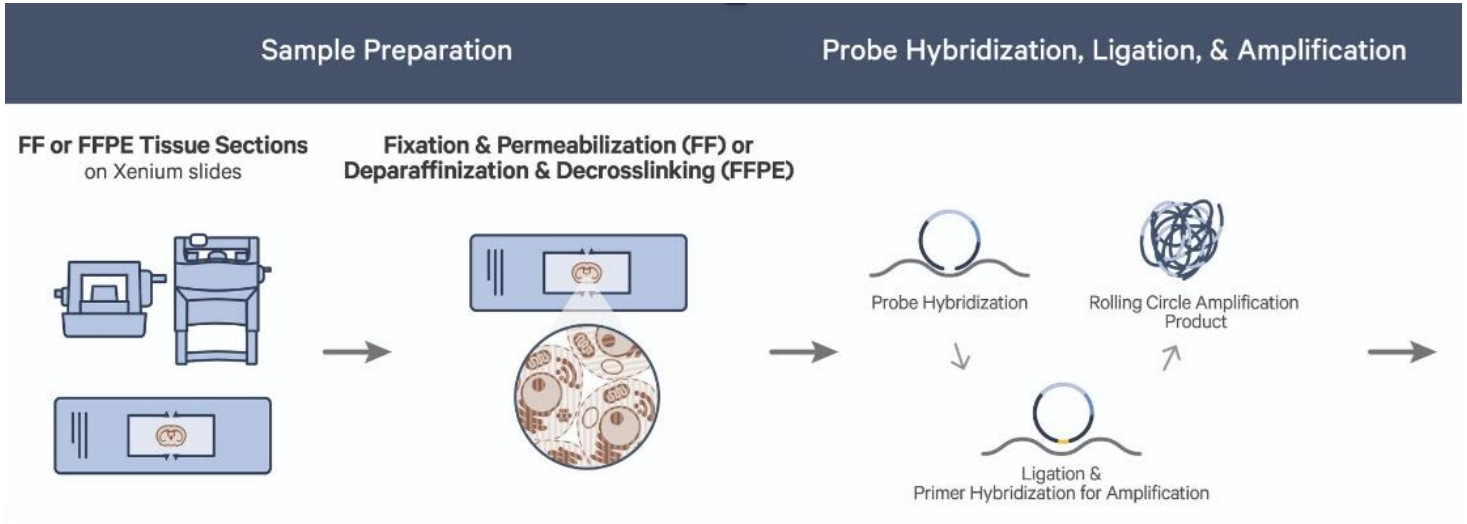
- Reveal the relationship between cellular structure and function with single base-pair resolution
- End-to-end in situ platform with imaging readout (no NGS required)
- Hundreds of RNA targets with subcellular resolution
- Highly specific and sensitive
- High throughput, fast time to results
- **Compatible with Fresh Frozen and FFPE**



10X GENOMICS

Xenium – A Simple Workflow with 3-4hrs of Hands-On Time

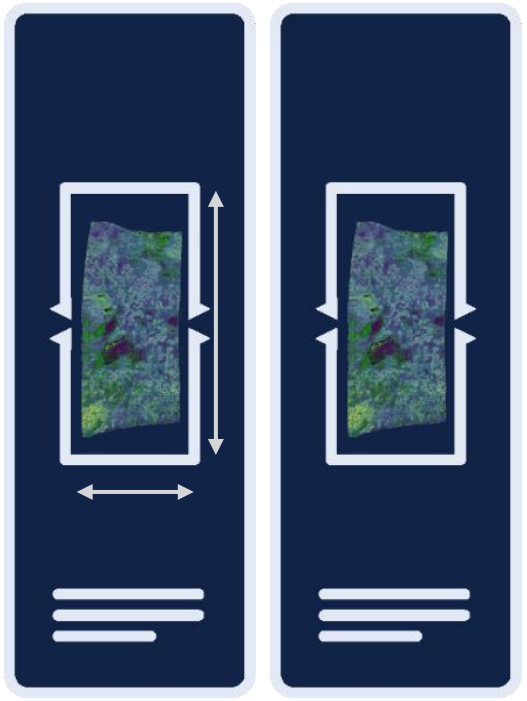
From sections to instrument start in 2-3 days



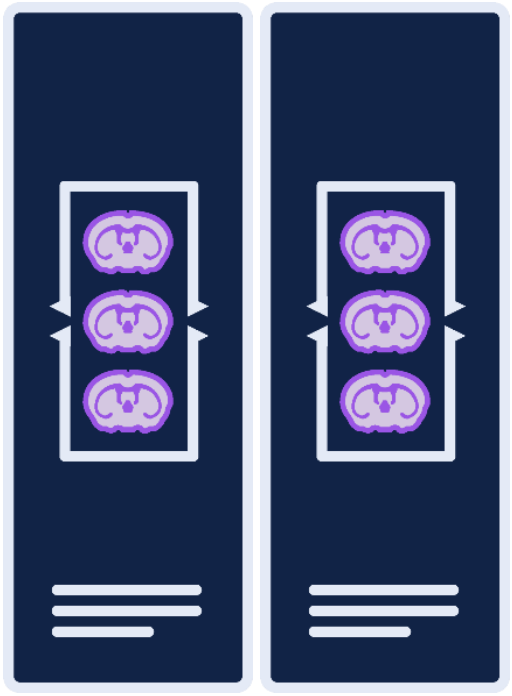
Simple and robust benchtop workflow with only ~4 hours hands on time

Fully automated decoding and end-to-end analysis

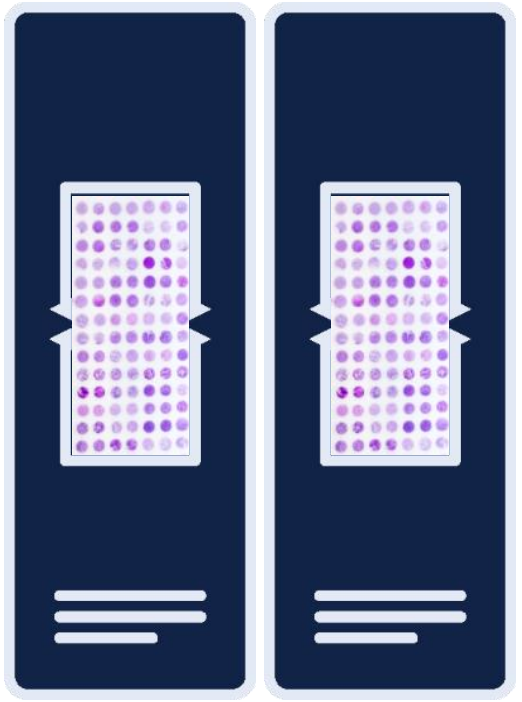
Xenium – Leading Analyzable Area for Maximum Flexibility



2 sections
10.5 x 22.5mm

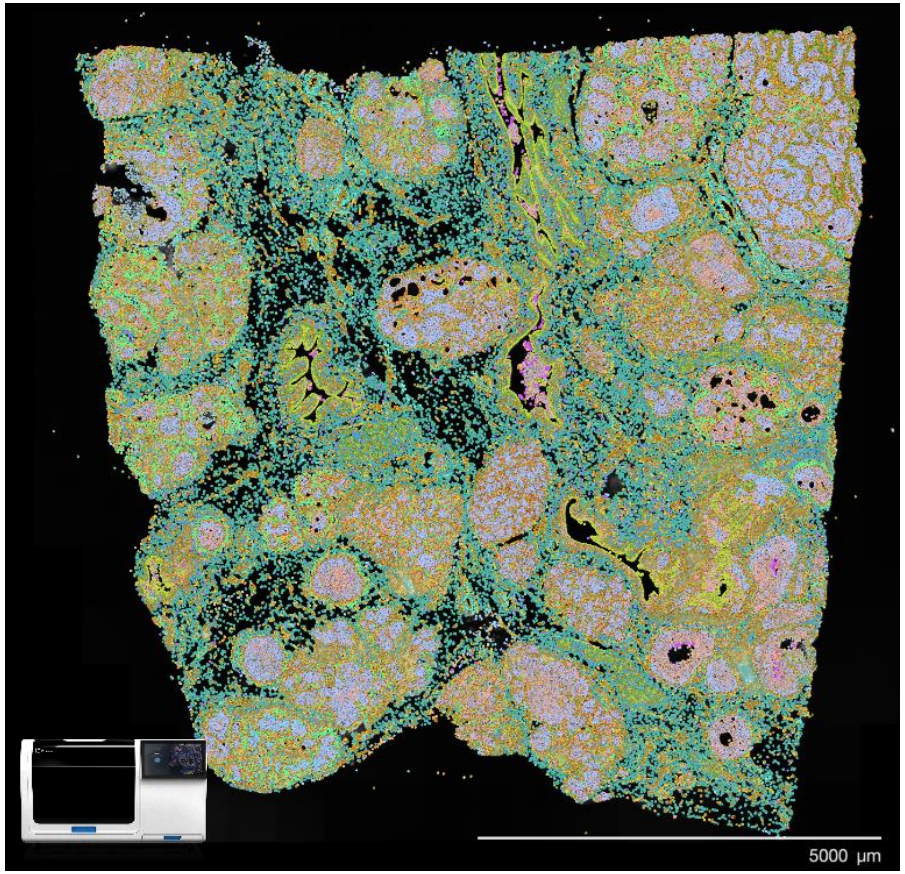


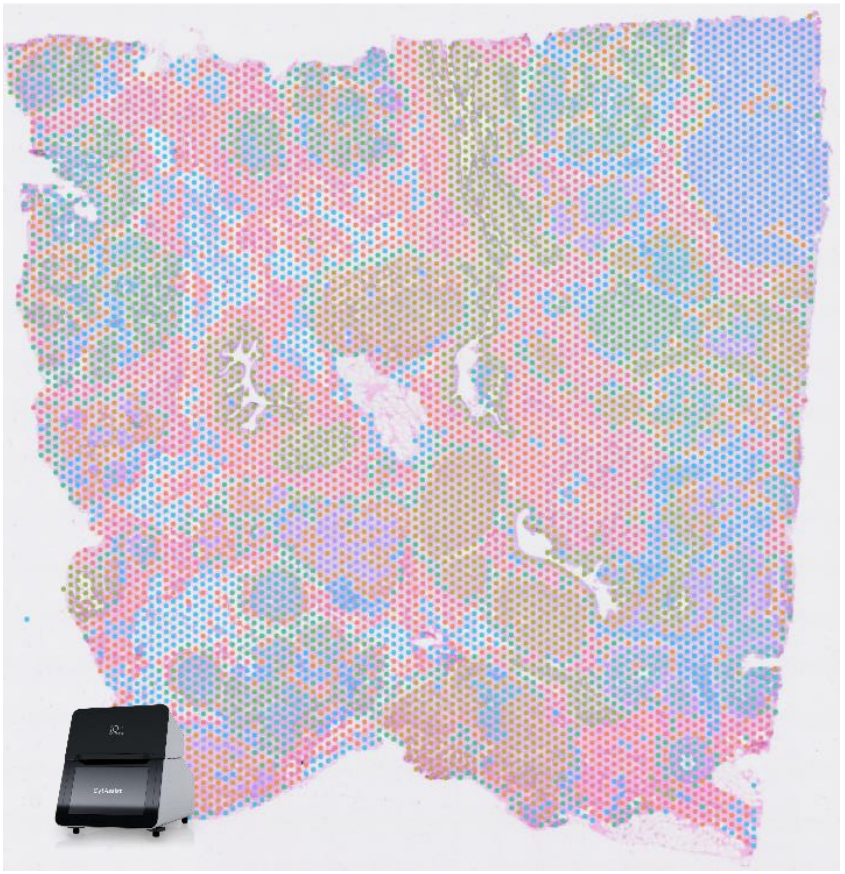
6 mouse brains
6 x 10mm



196 biopsies
1mm TMA

Xenium – Post Run: Whole-Transcriptome - Visium Cytassist



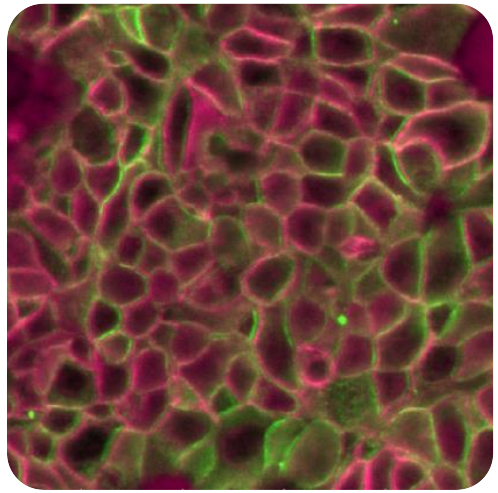


Human FFPE breast infiltrative ductal carcinoma

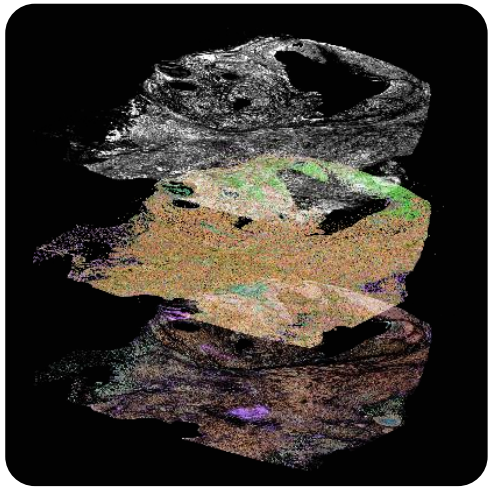
Xenium – Roadmap

Broader cell segmentation, protein multiomics, and increased RNA plex

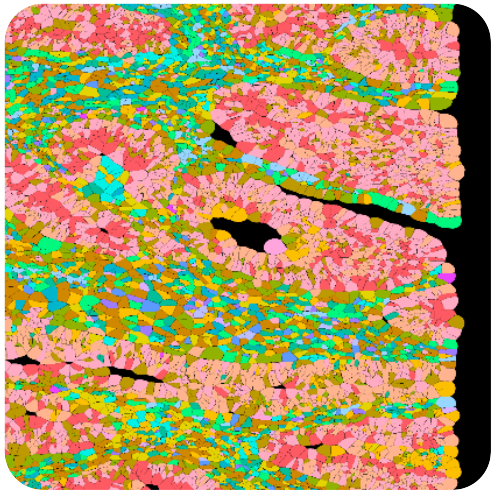
Expected in 2024



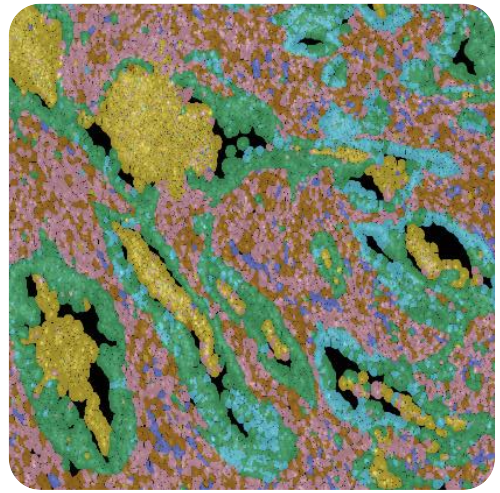
Multimodal cell segmentation



Fully integrated Protein & RNA



~2000 plex panel + custom



~5000 plex panel + custom

*Final product release timelines and configurations subject to change

Xenium – Rapid Adoption in the World's Leading Labs

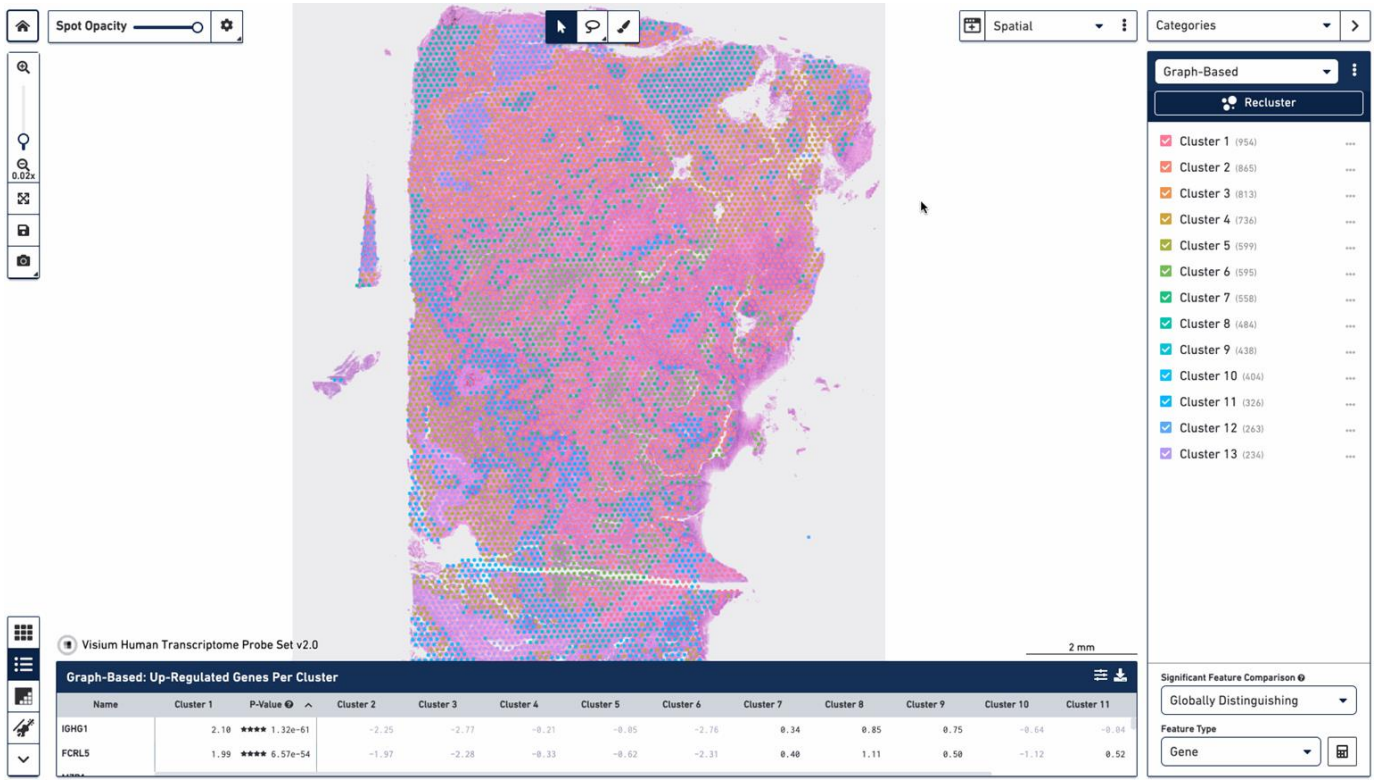
10x Genomics Surpasses 100 Xenium Analyzer Shipments

PR Newswire - Tue Aug 29, 3:30PM CDT Partnership Content

Rapid growth and adoption of Xenium Analyzer demonstrates strength of company's innovation engine, broad commercial reach and operational scale

Conclusion

Explore Visium datasets with Loupe Browser 7.0 Today



- Explore clustering, visualize genes of interest, annotate tissue regions, and calculate differential expression without any coding!
- **Download Loupe Browser free** and explore public datasets, including TMAs and variety of mouse and human tissues
- Redesigned Version 7.0 now available!

Visium CytAssist: Ready to Explore More

Simplifying spatial sample preparation and broadening sample access

Your Sample, Your Spatial Story

- ✓ Spatial Gene Expression for FFPE
- ✓ Spatial Gene & Protein Expression for FFPE
- ✓ Spatial Gene Expression for Fresh Frozen
- ✓ Spatial Gene Expression for Fixed Frozen
- ✓ Spatial Gene Expression for Tissue Microarrays
- ✓ Spot Deconvolution
- ✓ Validation of Xylene Alternatives

Coming Soon

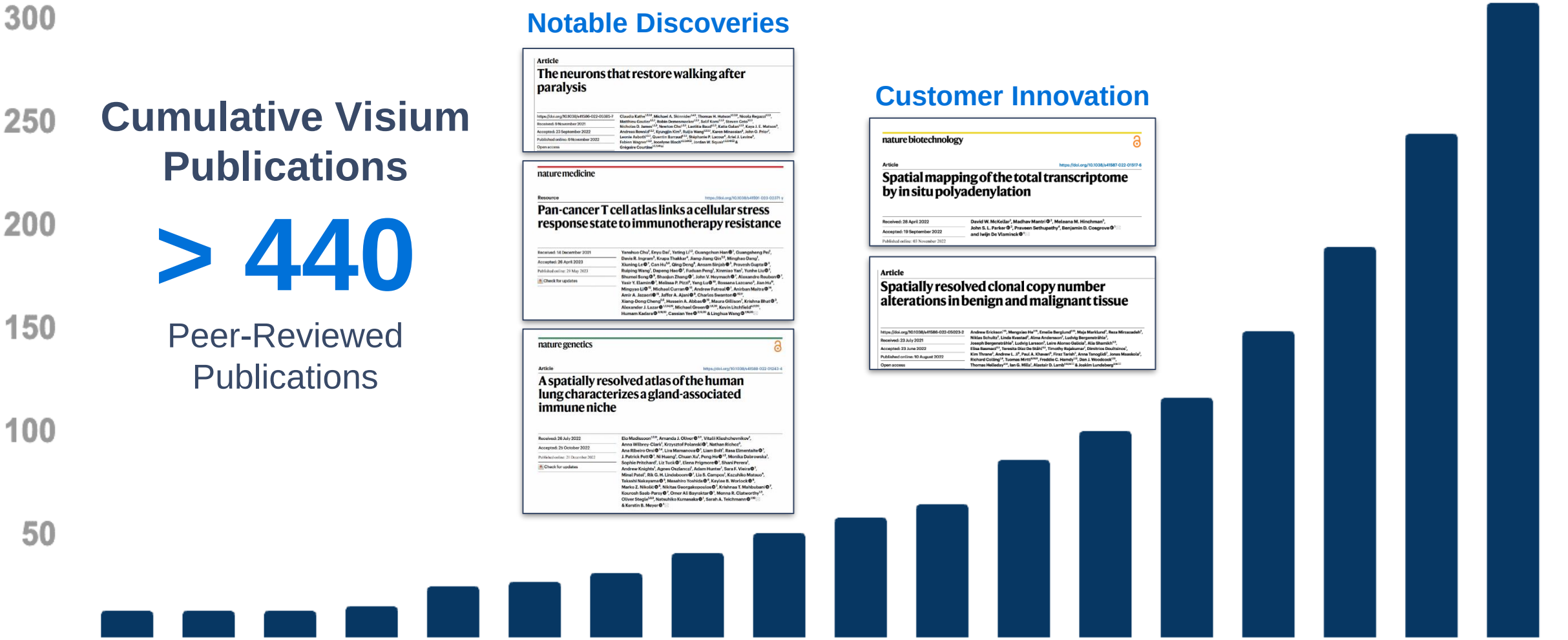
- Sample Prep Recommendation for Skin & Bone
- Visium HD Spatial Gene Expression

Visium Is Powering Impactful Research

Cumulative Visium Publications

> 440

Peer-Reviewed Publications



Notable Discoveries

Article

The neurons that restore walking after paralysis

nature medicine

Resource

Pan-cancer T cell atlas links a cellular stress response state to immunotherapy resistance

nature genetics

Article

A spatially resolved atlas of the human lung characterizes a gland-associated immune niche

Customer Innovation

nature biotechnology

Article

Spatial mapping of the total transcriptome by in situ polyadenylation

Article

Spatially resolved clonal copy number alterations in benign and malignant tissue

Biology’s Most Comprehensive Toolkit

Thank you
Want More Information?
Please Request a Follow-Up Meeting!

Chromium
Gene Expression Flex

Visium
CytAssist

Xenium
In Situ

Christine Kao
Sales Executive
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Tu Luu
Sales Associate
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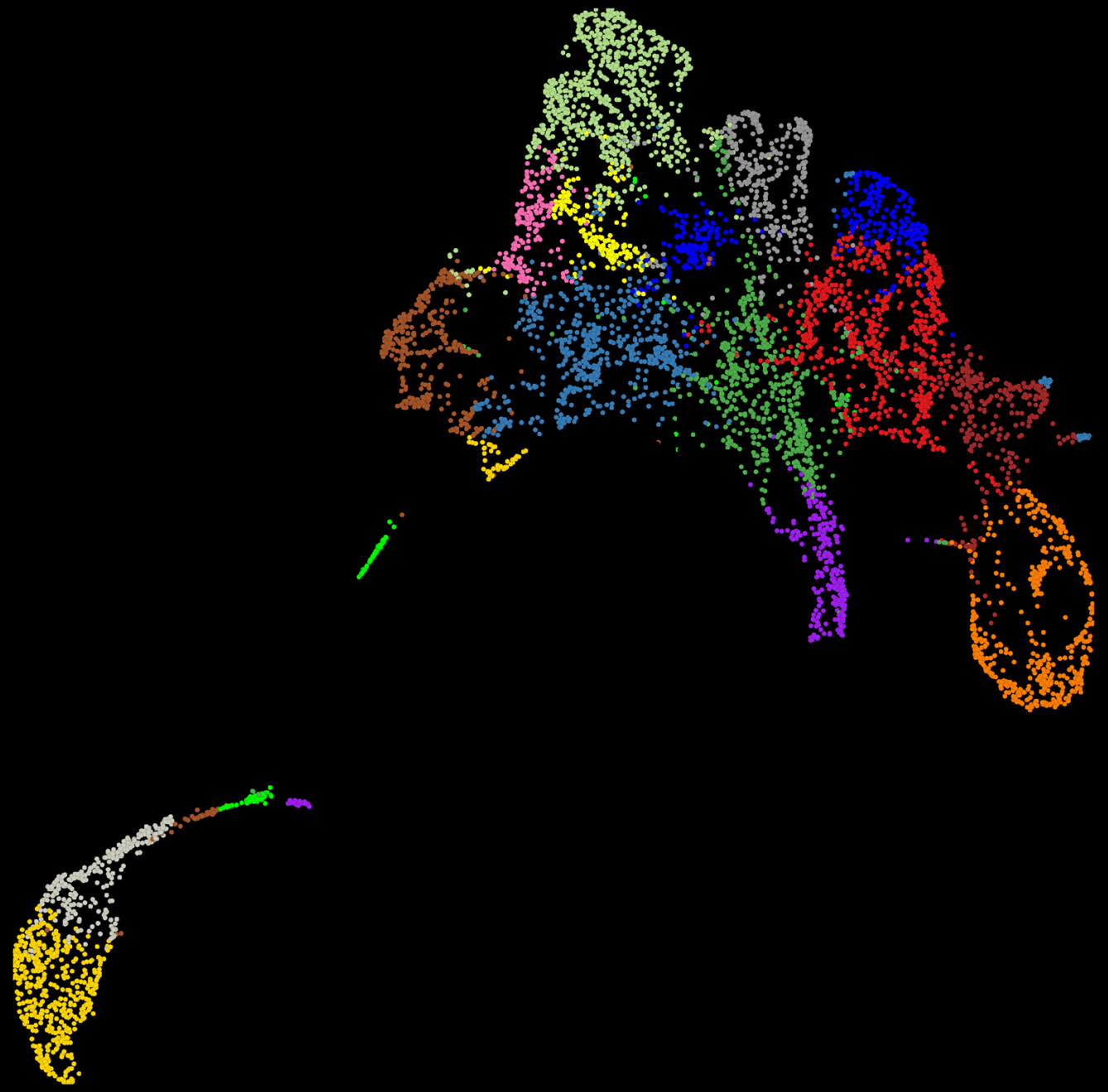
Visium Spatial



Appendix

scFFPE – Tested Tissues

Manual protocol - liberase + pestle dissociation

Tested Tissue	Age of Block	Amount of Tissue	Cells After Dissociation	Median UMIs per Cell (10k rps)	Median Genes per Cell (10k rps)
Human Healthy Lung	0 yo	50 um	~500k	~1500	~1000
Human Lung Cancer	0 yo	50 um	~1m	~1700	~1100
Human Breast Cancer	2 yo | 10 yo	50 um	~2.3m | ~1.7m	~1000 | ~1200	~700 | ~1000
Human Alzheimer's Brain	3 yo	50 um	~350k	~1500	~1100
Human Glioblastoma	1 yo	50 um	~750k	~2000	~1400
Human Reactive Lymph Node	6 yo	50 um	~6.5m	~1100	~700
Human Healthy Lymph Node	4 yo	50 um	~2.3m	~1200 (5k rps)	~700 (5k rps)
Human Pancreas	3 yo	50um	~500k	~1500	~900
Human Healthy Liver	5 yo	50um	~350k	~1200 (5k rps)	~700 (5k rps)
Human Liver Cancer	4 yo	50um	~550k	~1500	~600
Human Ovarian Cancer	2 yo	50um	~1.5m	~1700	~1200
Human Skin Melanoma	5 yo	50um	~200k	~2500 (5k rps)	~1700 (5k rps)
Human Prostate Cancer	3 yo	50um	~700k	~1100	~750
Human Colorectal Cancer	2 yo	50um	~550k	~1500	~1000
Human Healthy Kidney	3 yo	50 um	~500k	~2000	~1300
Human Endocervical Cancer	3 yo	50 um	~1.1m	~1000	~700

Visium CytAssist – Human Immune Cell Profiling Panel

Composition – 35 antibodies sourced from Abcam and BioLegend

Target	Cell Type or Marker	Clone ID	Vendor
alphaSMA	Structural marker	EPR5368	Abcam
CD3E	T cells	SP162	
CD4	T cells	EPR6855	
CD11b	Myeloid cells	EP1345Y	
CD11c	Dendritic cells	EP1347Y	
CD14	Myeloid cells	EPR3652	
CD16	Granulocytes/NK cells	EPR16784	
CD20	B cells	EP459Y	
CD27	Functional B cells	EPR8569	
CD31	Endothelial cells	EPR3094	
CD40	T and B lymphocytes	EPR20735	
CCR7/CD197	Functional B cells	EPR23192-57	
CXCR5	T cells	EPR23463-30	
EPCAM	Epithelial cells	EPR20532-222	
PDL1	Checkpoint marker	73-10	

Target	Cell Type or Marker	Clone ID	Vendor
BCL2	Apoptotic marker	100	BioLegend
CD8A	T cells	C8/144B	
CD19	B cells	R109	
CD21	Dendritic and B cells	Bu32	
CD45RA	Functional T cells	HI100	
CD45RO	Functional T cells	UCHL1	
CD66b	Neutrophils	6/40c	
CD68	Macrophages	BL13756	
CD163	Macrophage marker	QA19A16	
CD138	Plasma cells	DL-101	
HLA-DR	Myeloid cells	LN3	
PanCK	Structural marker	AE-1/AE-3	
PAX5	B cells	1H9	
PCNA	Cell proliferation marker	PC10	
PD1	Checkpoint marker	NAT105	
Vimentin	Mesenchymal cells	O91D3	
IgG2a	Isotype controls	MG2a-53	BioLegend
IgG1 k		MOPC-21	
IgG2b k		MPC-11	
IgG2a		RTK2758	

View Abcam or BioLegend website for IHC images and other details about antibody clones in Human Immune Cell Profiling Panel

10x products are empowering impactful science

Cumulative count as of the 3rd quarter of 2023

5,500+