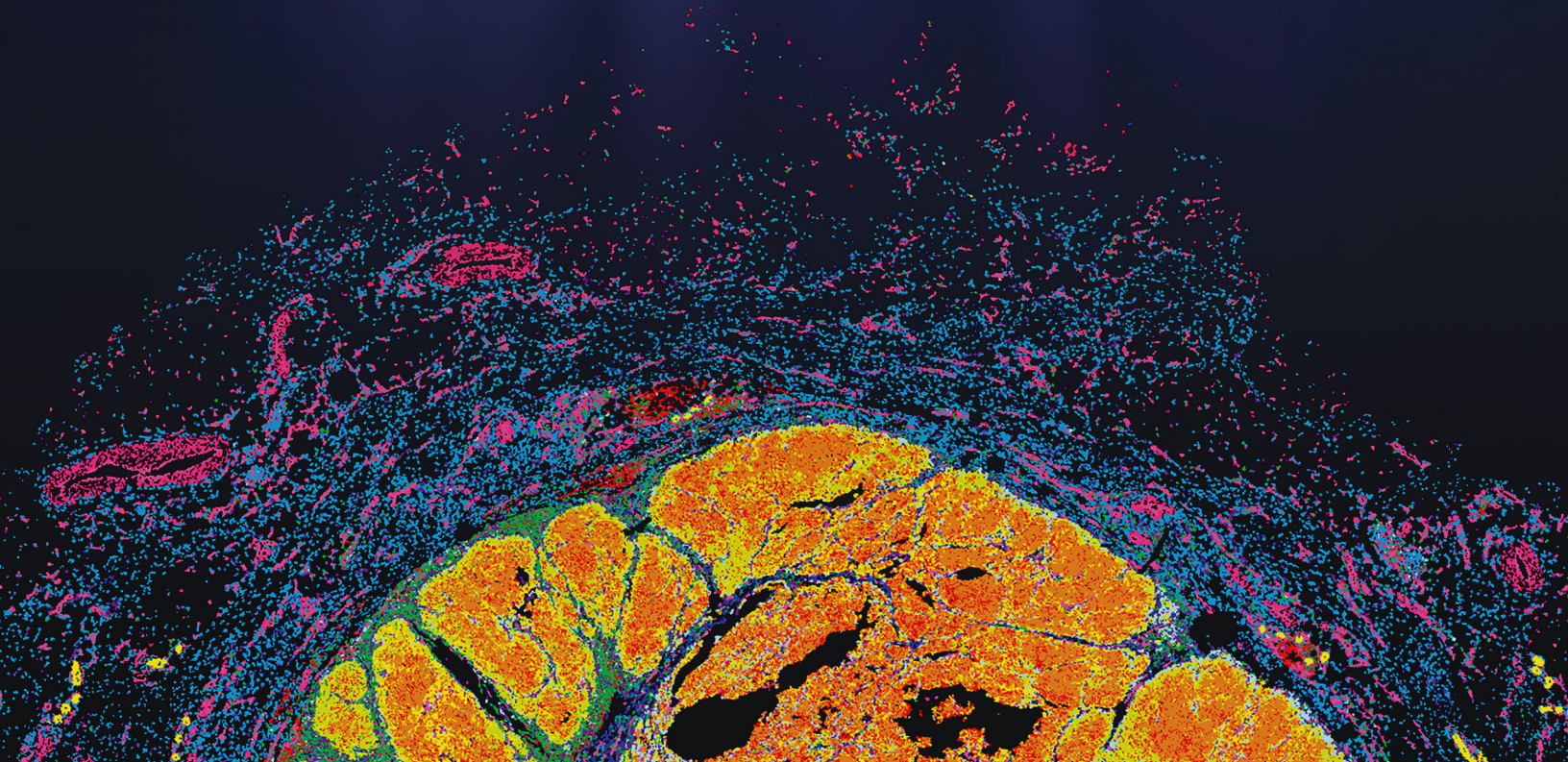


vizgen®

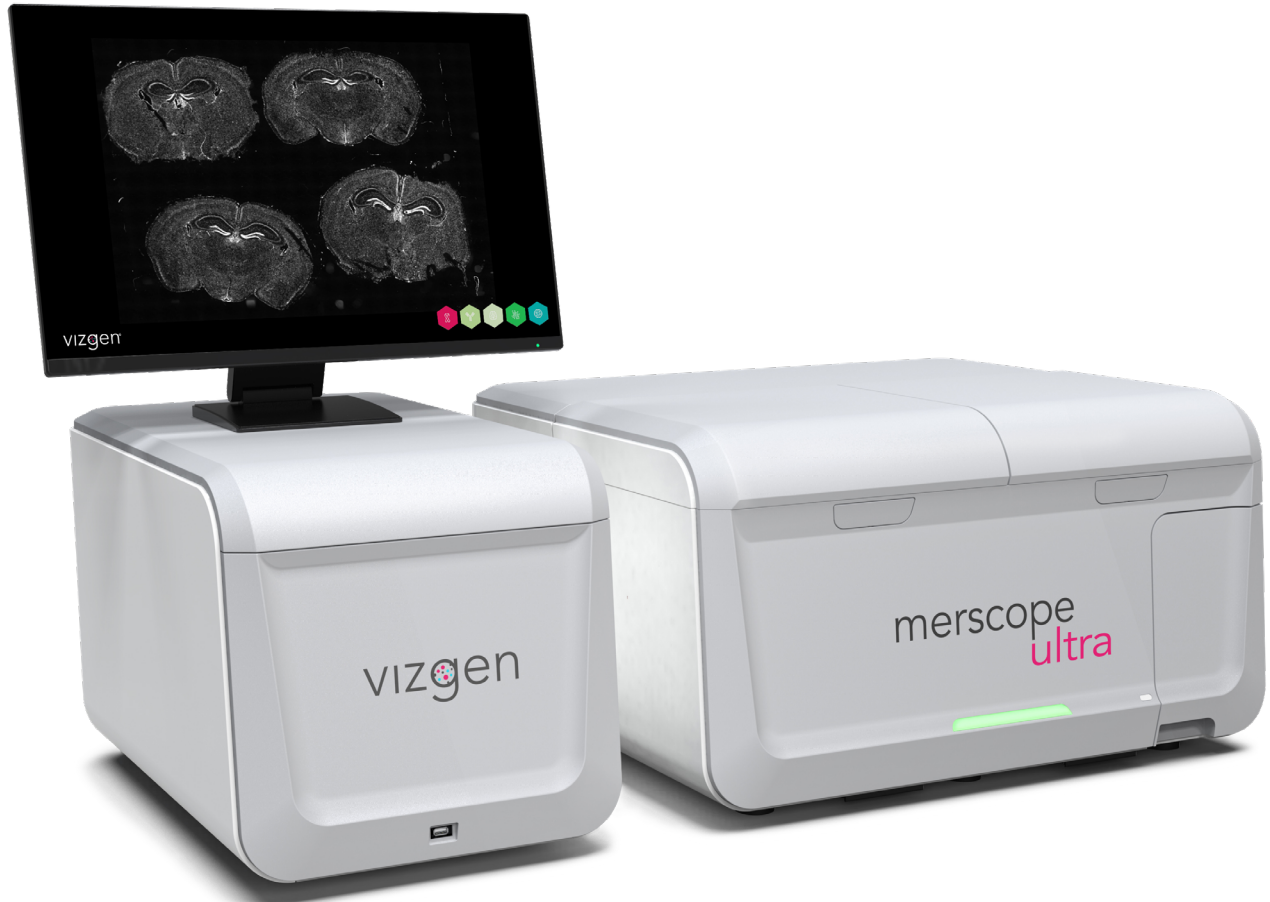
ultra

exploration

Explore the depths of spatial biology with MERSCOPE Ultra™.
Benefit from unmatched sensitivity, ultimate flexibility and an
expansive 3.0 cm² imaging area.

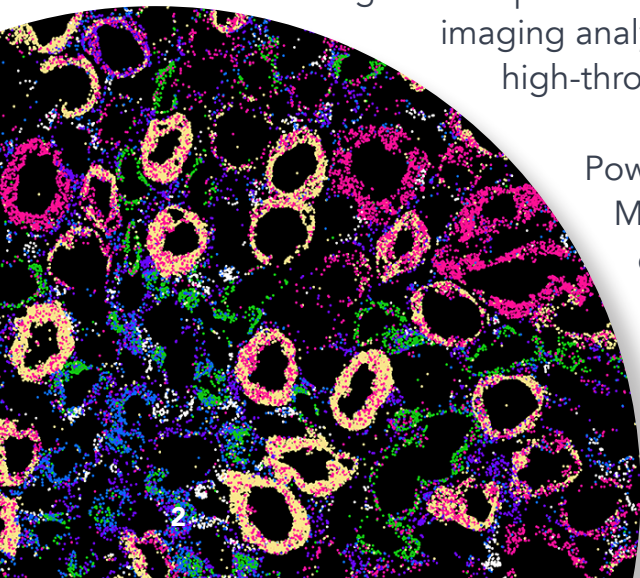


Introducing the MERSCOPE Ultra™: The Next Generation Spatial Genomics Platform



Position yourself at the forefront of scientific discovery with the Vizgen® MERSCOPE Ultra™, the next generation high plex, *in situ* single-cell spatial genomics platform. This end-to-end system automates sample imaging, imaging analysis, and cell segmentation, delivering high-resolution, high-throughput imaging without compromising sensitivity.

Powered by the trusted MERFISH technology, the MERSCOPE Ultra™ includes a high-performance analysis computer, along with the necessary reagents and software to accurately quantify and localize RNA and protein in tissue samples.



Largest Imaging Area

Explore spatial biology with an expansive 3.0 cm² imaging area, ideal for larger samples or multiple smaller samples.

Ultimate Flexibility & Customization

Tailor your research with fully customizable panels up to 1000 genes, species versatility and scalable imaging area.

High Spatial Resolution

Achieve detailed imaging from whole tissue sections to single-cell and sub-cellular levels.

Unparalleled Sensitivity

Experience the highest detection efficiency for capturing RNA transcripts, even those from lowly expressed genes.

Custom Panels & Features

Tailor your research with fully customizable panels, species versatility and scalable imaging area.

Uncompromised Quality

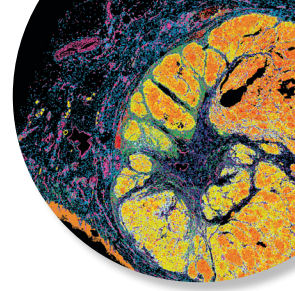
Benefit from exceptional, high-resolution optics combined with state-of-the-art processing power, delivering both speed and performance across a wide dynamic range. Transcripts appear as compact spots enabling better discrimination and more unique transcripts per cell.

Powered by MERFISH

Leverage proven MERFISH technology for unmatched sensitivity and resolution.

Supported by Experts

Access global technical support whenever you need it the most.

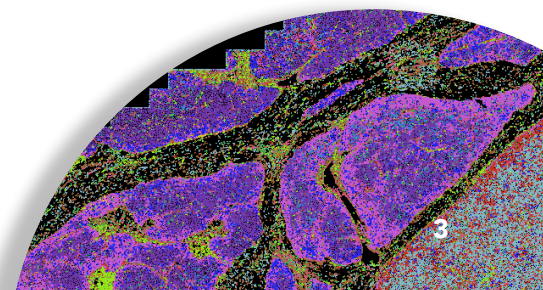


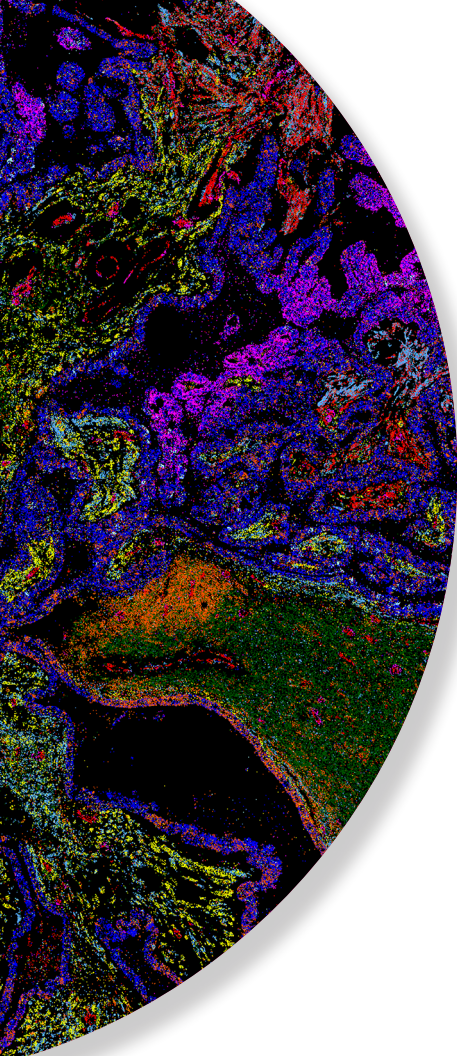
MERSCOPE vs MERSCOPE Ultra: Specifications Comparison

	MERSCOPE	MERSCOPE ULTRA
Vizgen Flow Chambers Supported	1) 1.0cm ² maximum imageable area	1) FCX-S (Standard): 1.25cm ² maximum imageable area 2) FCX-L (Large): 3cm ² maximum imageable area
Throughput	Up to 3.0cm ² per week	Up to 9.0cm ² per week
Multiplex Capacity	Up to 1000 genes	Up to 1000 genes
Optical Resolution	Oil immersion; High numerical aperture	Oil immersion; High numerical aperture objective
Transcript Localization Precision (X and Y)	≤ 20nm	≤ 20nm
Imaging Camera	Back-thinned cooled sCMOS camera	Back-thinned cooled sCMOS camera
On-Instrument Storage Capacity	15 TB	58 TB
Analysis PC Storage Capacity	15 TB	58 TB
Illumination Source	Multi-color laser	Multi-color laser
Automated Image Processing	Transcript decoding and cell segmentation	Transcript decoding and cell segmentation



Visit our website to explore the full output of a MERSCOPE® or MERSCOPE Ultra™ experiment.





Why pivot to spatial genomics?

Spatial genomics with true single-cell resolution preserves spatial context, detecting the localized expression of hundreds of genes and revealing broader biological insights.

- Localize RNA transcripts with high specificity at a subcellular level with ≤ 20 nm resolution—even for the most lowly expressed genes.
- Maintain tissue structure while providing highly effective multiplexing capacity, making it ideal for exploring individual cells, cell interactions, and tissue structures in a single sample.
- Spatial transcriptomics has the potential to reveal information that can help elucidate the progress of disease development and inform eventual treatment.

Maximizing spatial data quality

To make the most of spatial genomics, reliable and high-quality data is essential. Vizgen scientists focus on key metrics that define superior spatial data, drawing from extensive experience in multiplexed spatial transcriptomics.

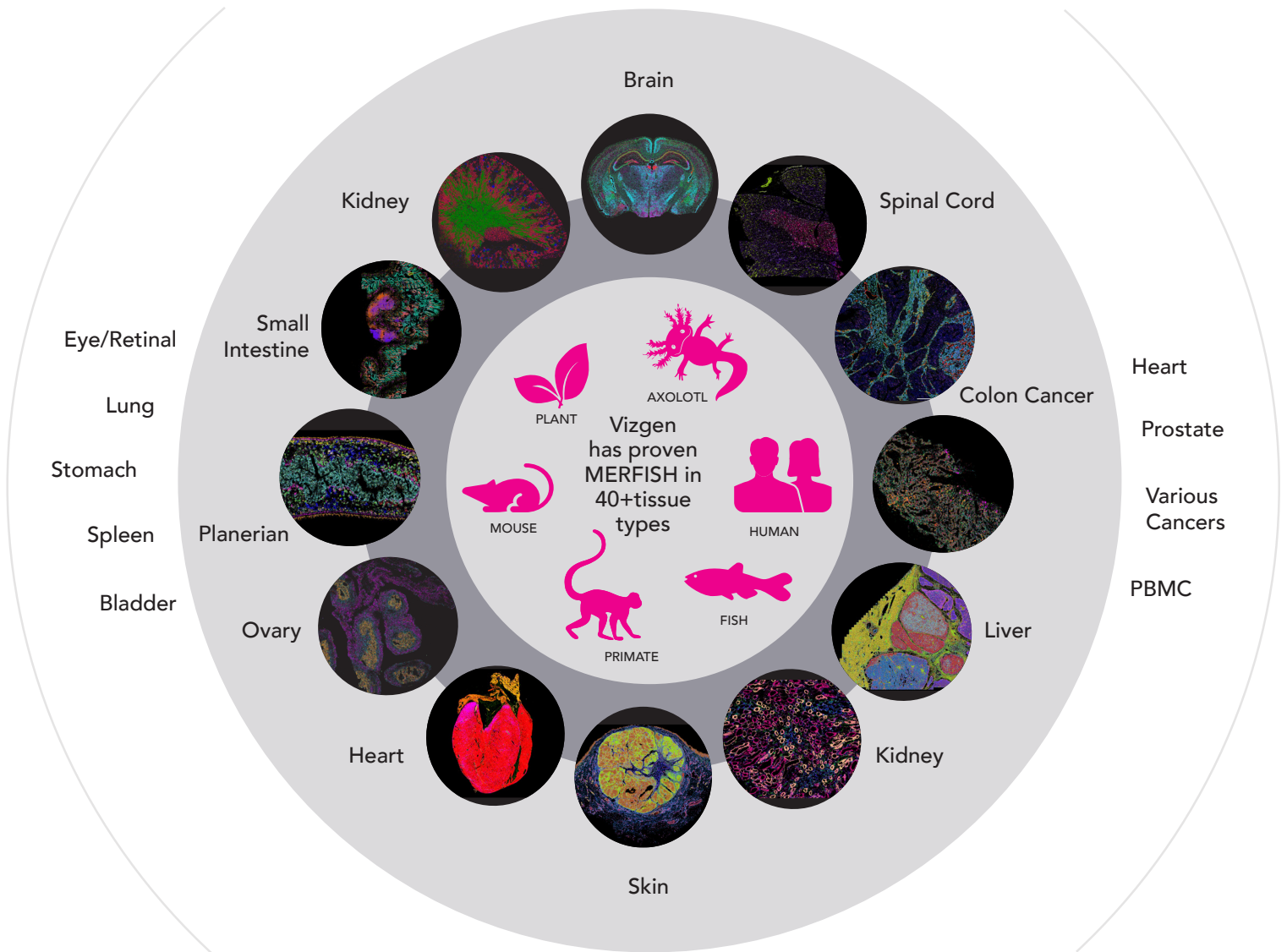
Key Quality Metric	Sensitivity	Specificity	Information Density	Effective Multiplexing Capacity
Central Question	How many transcripts of each targeted RNA species are detected?	How many transcripts are identified correctly?	How many transcripts can the technology identify in a cellular volume?	How many different genes can the technology accurately profile at once?
Biological Significance	Many biologically relevant transcripts are expressed at low copy numbers.	Lower noise allows more transcriptomic variations to be discovered and stand out above the noise.	Characterizing subtle variations between individual cells requires sufficient information about each cell.	Measuring more biomarkers better characterizes the complexity inherent to a biological system.

Choosing the right technology for spatial genomics

Choosing the right technology for spatial experiments is critical for ensuring that you don't need to sacrifice data quality in one area for another or limit your experimental options. MERSCOPE Ultra™ provides the highest quality data by integrating cutting-edge optical technology,

fluidics, automation, and data processing to produce spatial genomics data answers in one shot. With the platform's sample input flexibility, you'll be able to obtain reliable data from the tissue samples that interest you most.

Flexibility in species and gene samples is critical



Compatible sample types include fresh or fixed frozen, adherent or suspended cells and FFPE

MERFISH: Ultra high-sensitivity spatial genomics technology with sub-micron accuracy

MERFISH (multiplexed error-robust fluorescence in situ Hybridization) enhances single-molecule FISH by using combinatorial labeling, sequential imaging, and error-robust barcoding to detect RNA with sub-micron accuracy, revealing the intracellular organization of the transcriptome within cells. Since its introduction in 2015, MERFISH has been featured in over 200 publications, driving advancements in spatial genomics. Its robust, high-quality datasets give researchers confidence in their analyses.

The system's error-correcting barcoding and combinatorial labeling ensure precise transcript detection and increased multiplexing. If background fluorescence does cause a readout error, the system can easily assign the readout to the nearest correct barcode. While MERFISH does not require sequencing, the measurements taken with MERSCOPE or MERSCOPE Ultra correlate with bulk RNA-seq data and are highly reproducible. Additionally, MERFISH is flexible, supporting custom probe designs and compatibility with various tissue types.

MERFISH workflows involve four major steps:

1 - Preparation

Tissue samples are mounted on slides and permeabilized.

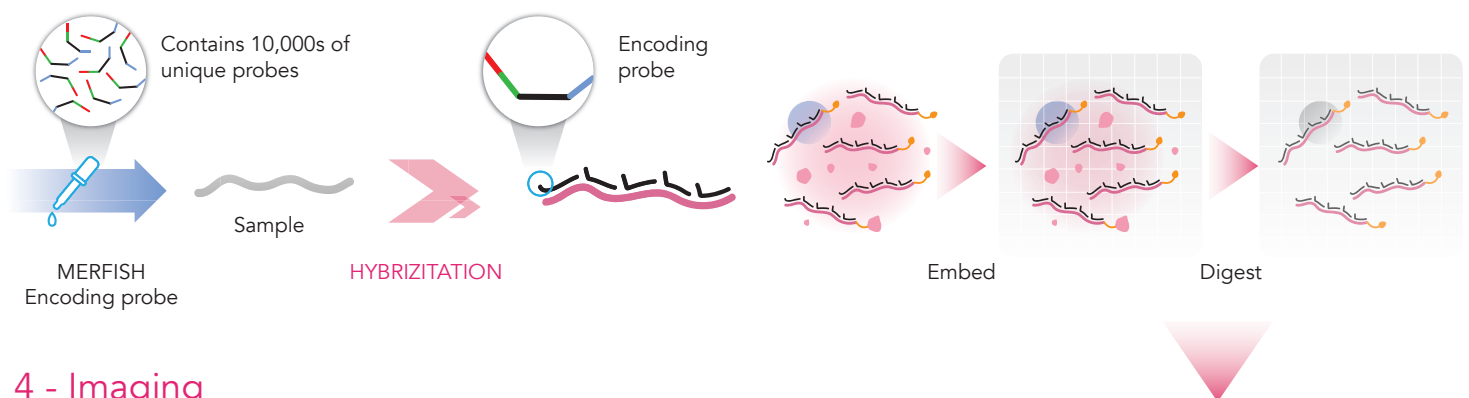
Staining for protein co-detection can be added at this stage

2 - Hybridization

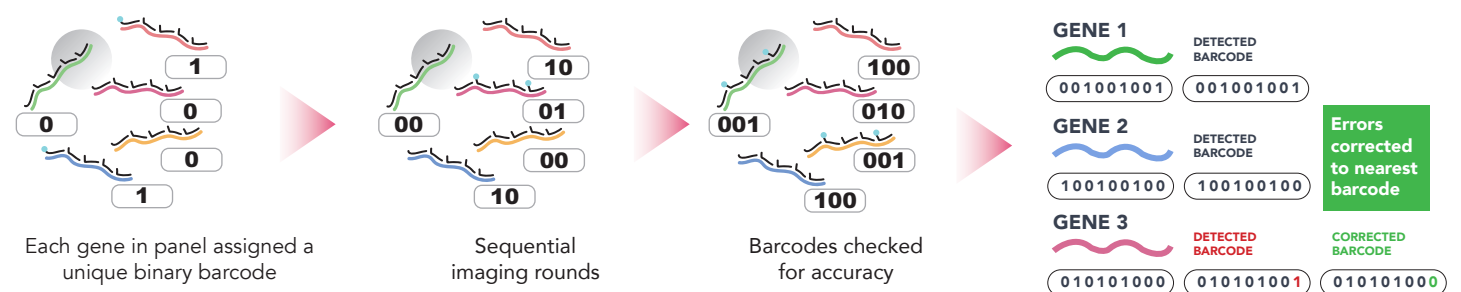
Embedding tens of thousands of unique encoding probes onto the sample.

3 - Clearing

Using a gel embedding and clearing process to remove unnecessary components while preserving transcripts and bound probes.



4 - Imaging



Order will vary based on tissue preservation type (FFPE or FF)

Data output from a MERSCOPE measurement

List of all detected transcripts

.csv
.parquet

Mosaic images

.tiff

Transcripts per cell matrix

.csv

Cellmeta data

.csv

Cell boundaries

.parquet

Cell clustering annotations

.csv
.h5ad

Vizgen Data Output



Visualization and Analysis

Visualizer: Analyze and interpret complex datasets



Spatial genomics data is only as valuable as the tools used to analyze it. The MERSCOPE® Visualizer software enhances the utility of spatial genomics data, empowering users to interact with, analyze, and interpret even the most complex spatial transcriptomics datasets generated by a MERFISH experiment.

Democratizing Data Output

Segmentation:

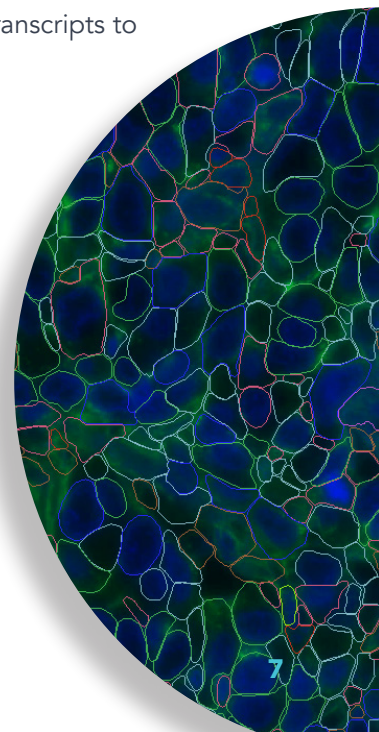
The MERSCOPE Ultra platform integrates multiple segmentation methods and tools, allowing for the precise parsing of individual cells, even within highly dense tissue sections. This ensures accurate assignment of transcripts to cells, facilitating downstream cell annotation.

Integration with 3rd party tools:

Data outputs are compatible with multiple third-party single-cell gene expression analysis software platforms, including Seurat, Scanpy, BioTuring, and Heavy-AI. Researchers are already leveraging these resources to create spatially resolved transcriptional atlases and more.

Open-source VPT tool:

The Vizgen Post Processing Tool (VPT) helps you divide a billion transcripts into a million cells. VPT is a free, open-source command line tool that enables users to reprocess and refine the single-cell results of MERSCOPE experiments. The tool's flexible nature allows integration with other segmentation methods. With an emphasis on scalable, reproducible analysis, VPT can be run on a workstation, cluster, or be deployed in a cloud computing environment.



vizgen®



Our complete spatial genomics solution offers an unprecedented view of the spatial organization of biological systems and will enable researchers to gain deeper insights in a wide range of biological domains, from fundamental biology, to medicine, to clinical diagnosis.

What will you discover? Visit [Vizgen.com](https://vizgen.com) to jump-start your spatial journey.

