

Dive deep into single-cell spatial genomics with the MERSCOPE™ Platform



Explore spatial genomics with data you can trust from the MERSCOPE™ Platform, the industry's first end-to-end solution for getting high-quality data from MERFISH experiments.

From instrument, reagents, and consumables to intuitive data visualization and analysis software, you'll have everything you need to unlock spatial discoveries today.



vizgen



What is spatial genomics?

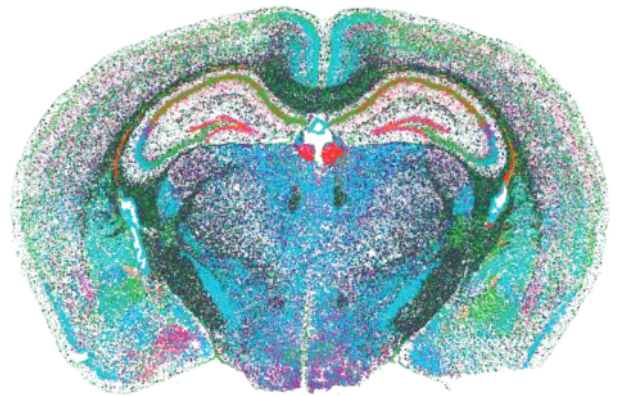
To truly understand cell biology and gene expression, researchers need tools that preserve the natural complexity of tissues. It is crucial to capture the heterogeneity of cells to know how tissues are organized and how individual cells interact. Spatial genomics—[Nature's Method of the Year 2020](#)—achieves all this and more.

With this technique, we can now generate complete biological maps of RNA expression, cell type, cell state, and the physical architecture of tissues. Spatial genomics provides an unprecedented depth of biological understanding, throwing open the doors to the next frontier of biotechnology.



Bulk and single-cell sequencing can yield genomic information that shows us part of the whole picture, but these techniques destroy native cellular structure.

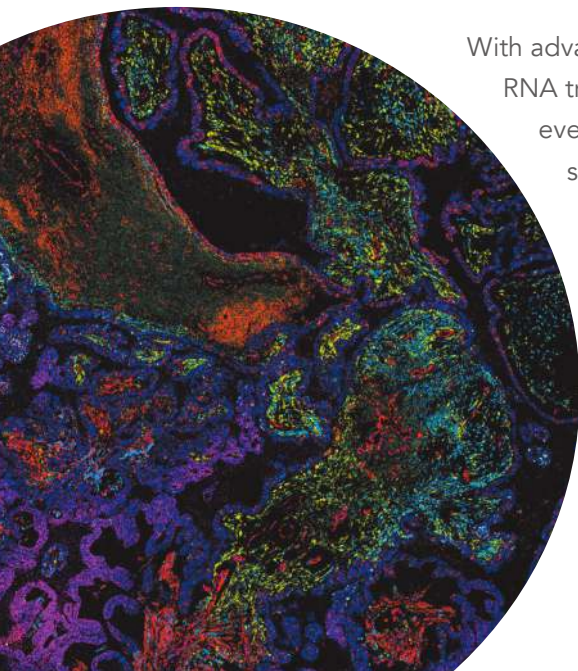
Spatial genomics with true single-cell resolution retains spatial context, detecting the localized expression of hundreds of genes to reveal the bigger picture.



Why pivot to spatial genomics?

With advanced spatial genomic techniques and technology, researchers can localize RNA transcripts with high specificity at a subcellular level with ≤ 100 nm resolution—even for the most lowly expressed genes. Other techniques such as single-cell sequencing require dissociation of the tissue, resulting in loss of tissue context. Spatial technologies maintain tissue structure while providing high effective multiplexing capacity, profiling hundreds or thousands of genes at once to enable exploration of individual cells, cell-cell interactions, or tissue level structures in a single sample.

By enabling in-depth analysis of key samples such as this FFPE human ovarian cancer tissue (left), spatial genomics has the potential to reveal information that can help elucidate the progress of disease development and inform eventual treatment.



Map the future of spatial genomics with Vizgen

Vizgen scientists are dedicated to pioneering the next generation of genomics, providing tools that demonstrate the possibilities of in situ single-cell spatial genomics, setting the standard for the field. Our end-to-end solutions are enabling researchers to gain new insight into the biological systems that govern human health and disease with spatial context.

The MERSCOPE Platform

MERFISH

- High sensitivity
- Scalable multiplexing
- Uncompromised accuracy
- Error robust barcoding



MERSCOPE

- Automated in situ imaging
- Sample and species flexibility
- Exceptional resolution minimizes optical crowding
- Comprehensive reagent and kit offerings for specialized applications



SOFTWARE

- Customizable gene panel design
- Interactive visualization
- Seamless data analysis
- Class-leading cell segmentation



SUPPORT

- Focus on customer success
- Field Service Engineers (FSEs)
- Field Applications Specialists (FASs)
- Lab services

INNOVATION

- Continuous expansion of offerings
- Leadership and passion for scientific breakthroughs



MERFISH: The leading spatial genomics technology

[MERFISH \(multiplexed error-robust fluorescence *in situ* hybridization\)](#) technology expands on the capabilities of single molecule FISH (smFISH) by using combinatorial labeling, sequential imaging, and error-robust barcoding to detect RNA with sub-micron accuracy. This gives researchers a window into the intracellular organization of the transcriptome within every cell.

First published in 2015, MERFISH has since amassed over 60 peer-reviewed publications, with more exciting discoveries every year. With robust, valuable datasets and trustworthy data quality, this technology is supercharging biological research by giving scientists confidence in their spatial genomics analysis.

MERFISH workflows involve four major steps:

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

Preparation

Tissue samples are mounted on slides and permeabilized.

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

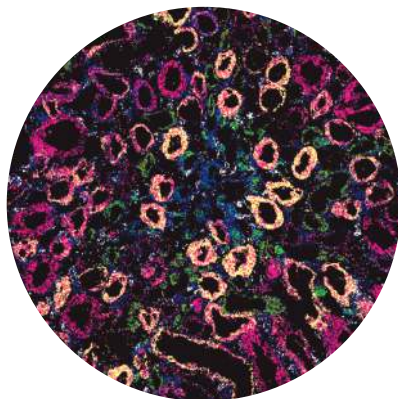
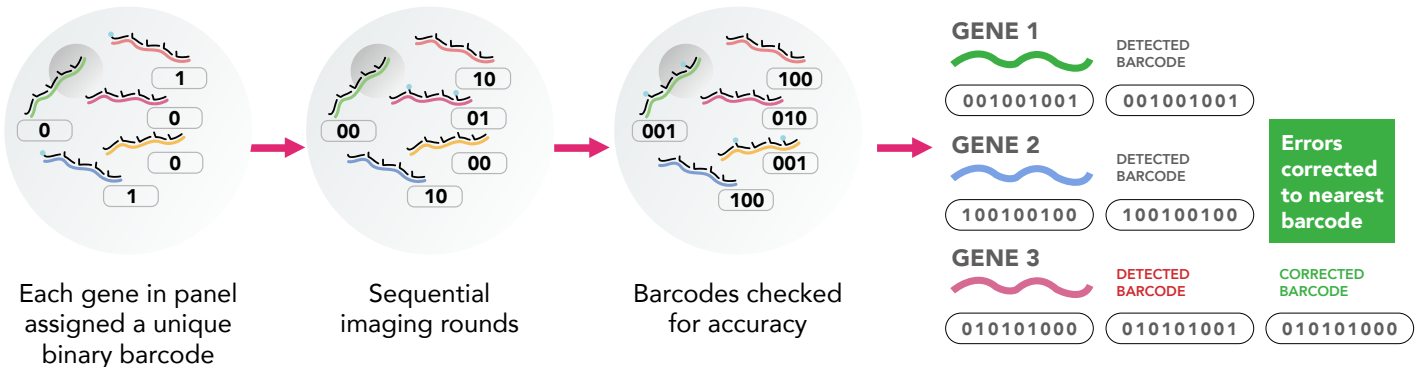
Hybridization

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

Clearing

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

Imaging



The system's error-correcting barcoding scheme and combinatorial labeling ensure the highest detection accuracy of transcripts while offering dramatically increased multiplexing capacity. 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 correlate with bulk RNA-seq data and are highly reproducible. MERFISH technology is extremely flexible, allowing for custom probe design and offering compatibility with a wide range of tissue types.

Bring spatial genomics into your lab with MERSCOPE

Position yourself at the forefront of scientific discovery with the [MERSCOPE™ Platform](#), the industry's first high plex, *in situ* single-cell spatial genomics platform. We integrated the power and potential of MERFISH technology with high-resolution imaging, fluidics, image processing, and automation to deliver an end-to-end solution that helps scientists explore spatial context with minimal challenges. This easy-to-use system includes the instrument, reagents, and software needed to accurately quantify and localize RNA in tissue samples.

HIGH CELL THROUGHPUT

Profile up to several hundred thousand cells in a single sample at low cost per cell

FLEXIBILITY

Ability to run on many sample or tissue types, including fresh, fixed frozen, or FFPE human and mouse tissue

EFFECTIVE MULTIPLEXING

Cover 1000 genes in a single sample with custom gene panel design, imaging 1 cm² area in ~1 day

HIGH SPATIAL RESOLUTION

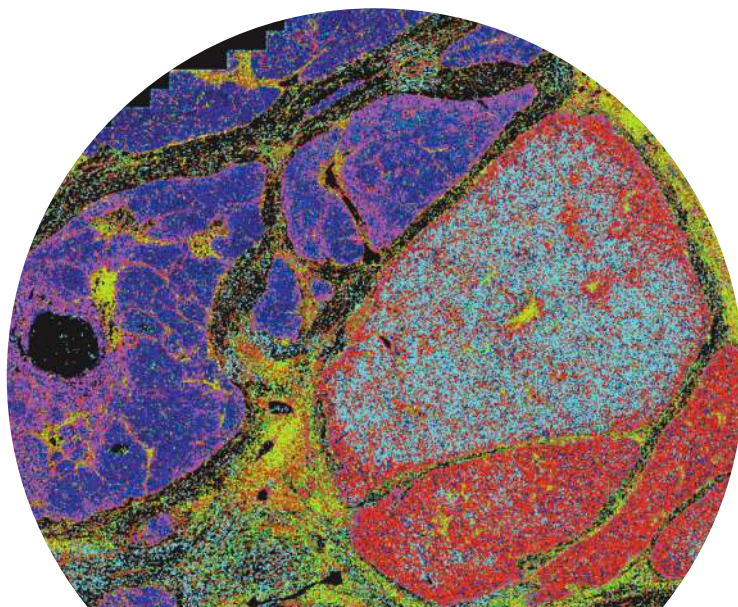
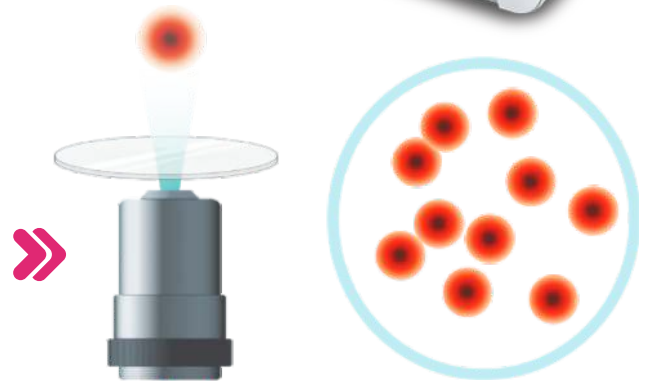
From whole tissue section to single-cell and sub-cellular imaging

UNPARALLELED SENSITIVITY

Highest detection efficiency for capturing RNA transcripts, even for lowly expressed genes

EXCEPTIONAL OPTICS

High-resolution optics result in single transcript spots appearing compact, enabling better discrimination between spots and more unique transcripts detected per cell



Visit our website to explore the full output of a MERSCOPE experiment and access FFPE human immune-oncology, mouse liver, and mouse brain receptor data releases.



Analyzing spatial data

Spatial genomics information is only useful if you also have the tools to make sense of it. The [MERSCOPE™ Vizualizer](#) software makes the most of spatial genomics data, enabling users to interact, analyze, and interpret even the most complex spatial transcriptomics datasets generated by a MERFISH experiment.

Our intuitive software seamlessly combines spatial context at the single-cell level to assist researchers with gaining valuable biological insights. With the tool, you can easily generate high-resolution images and visualize MERFISH data.

Data output from a MERSCOPE measurement

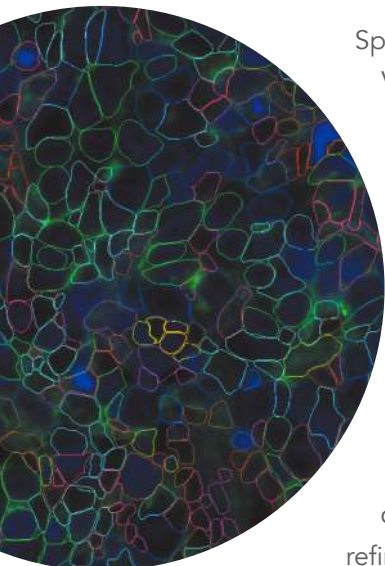


Vizgen Data Output



Visualization and Analysis

- List of all detected transcripts and their spatial locations in three dimensions (.CSV)
- Mosaic images (.TIFF)
- Output from cell segmentation analysis
 - Transcripts per cell matrix (.CSV)
 - Cell metadata (.CSV)
 - Cell boundaries (.Parquet)



Spatial analysis of cells and detected transcripts is dependent on accurate detection of cells. Vizgen has integrated and developed multiple segmentation methods and tools that can parse individual cells even within highly dense tissue sections. These intuitive tools provide researchers with the means to correctly assign transcripts to cells and enable downstream cell annotation.

MERSCOPE 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 combining these resources to create spatially-resolved transcriptional atlases and more.

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.

Innovation is at the core of who we are, so stay on the lookout for expanded data analysis offerings from Vizgen scientists and data experts in the future.

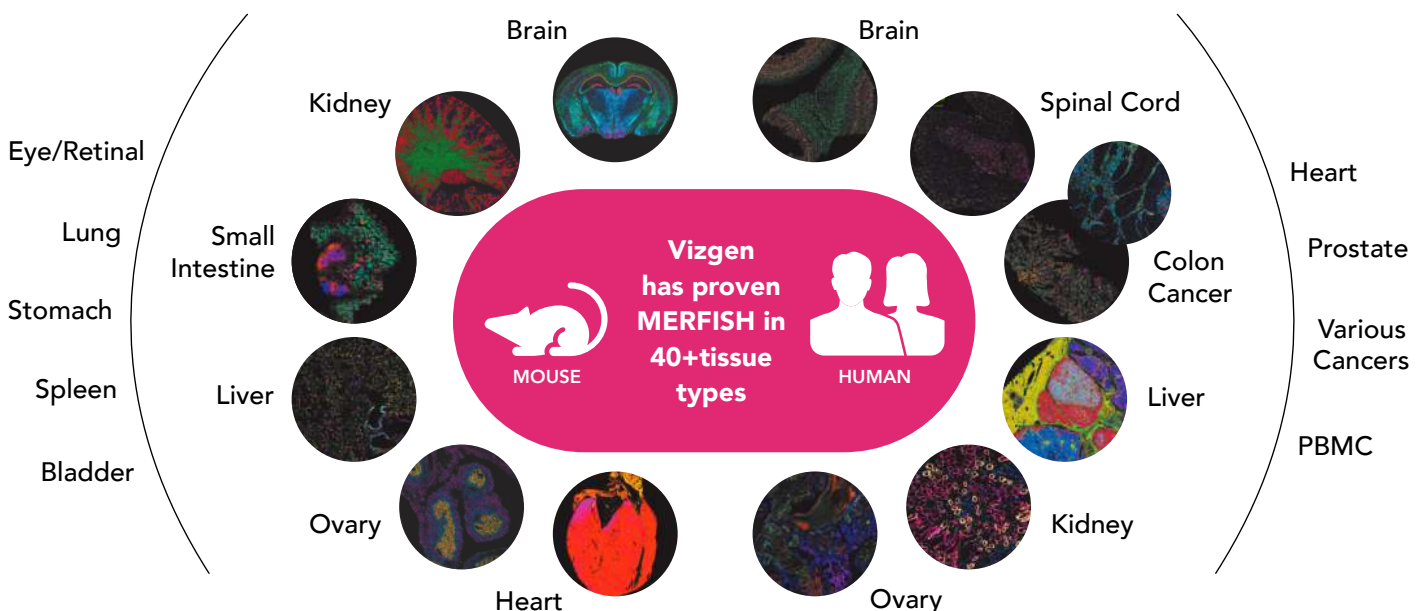
Getting the best spatial data from every experiment

To take full advantage of expanded possibilities for spatial genomics experiments, scientists need their tools and techniques to produce maximally reliable, usable data. But in a cutting-edge field, what metrics set high-quality spatial data apart from the rest? Based on years of experience in highly multiplexed spatial transcriptomics, Vizgen scientists prioritize these four key questions:

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 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 provides the highest quality data by integrating cutting-edge optical technology, fluidics, automation, and data processing to produce spatial genomics data at the unparalleled level of quality scientists have come to expect from MERFISH. With the platform's sample input flexibility, you'll be able to obtain reliable data from the tissue samples that interest you most.

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



Everything you need to dive into spatial biology

Vizgen's MERSCOPE Platform includes everything you need to bring spatial genomics into your own lab. You can also access our lab services to leverage our in-house sample processing and data analysis expertise to accelerate your scientific research and yield fundamental insights faster.

MERSCOPE™ Platform Reagents and Consumables List

PRODUCT	DESCRIPTION
MERSCOPE Slide Box (20 SLIDES & 10 SLIDES)	Sample slides for MERSCOPE instrument that are functionalized for tissue samples to enable Vizgen sample preparation protocols.
MERSCOPE Non-Beaded Slide Box (20 SLIDES)	Sample slides for MERSCOPE instrument that do not have fiducial beads to enable adherent cells to adhere to slide.
MERSCOPE FFPE Slide Box (10 SLIDES)	Sample slides for MERSCOPE instrument functionalized for FFPE tissues to enable Vizgen FFPE sample preparation protocols.
MERSCOPE Gene Panels (20 SAMPLES)	Custom gene panels comprised of encoding probes. Currently available in three sizes: up to 140 genes, up to 300 genes, and up to 500 genes.
MERSCOPE Gene Imaging Kit	Imaging reagent kits containing the reagents and cartridge for running a measurement on the MERSCOPE platform. Currently available in three sizes: up to 140 genes, up to 300 genes, and up to 500 genes.
MERSCOPE Cell Boundary Stain Kit (20 SAMPLES)	Kit containing a 3-protein staining reagent for cell segmentation in dense tissues. Compatible with human and mouse samples.
MERSCOPE Sample Prep Kit (20 SAMPLES)	Kit containing sample preparation reagents for 20 samples. Compatible with fixed, fresh frozen tissue, and cultured cells.
MERSCOPE FFPE Sample Prep Kit (10 SAMPLES)	Kit containing sample preparation reagents for 10 FFPE samples. Compatible with FFPE tissues only.
MERSCOPE Protein Stain Kit (20 SAMPLES)	Kits containing oligo-conjugated secondary antibodies and reagents for co-detecting proteins during a MERFISH experiment.
MERSCOPE Protein Verification Kit (5 SAMPLES)	Kit containing reagents to verify protein co-detection using MERSCOPE Protein Stain Kits.
MERSCOPE Sample Verification Kit (5 SAMPLES)	Kit containing smFISH probes and imaging reagents to do a single imaging run. Currently available for human and mouse.
MERSCOPE PanCancer Pathways Panel 500 Gene (HUMAN)	MERSCOPE 500 gene predesigned panel targeting canonical signaling pathways in human cancer tissue samples.
MERSCOPE PanNeuro Cell Type Panel 500 Gene (MOUSE)	MERSCOPE 500 gene predesigned panel providing ability to cell type major cells in mouse brain tissue samples.
MERSCOPE Immuno-Oncology Panel 500 Gene (HUMAN)	MERSCOPE 500 gene predesigned panel allows characterization of tumor and immune behavior at cellular and subcellular levels across multiple different types of cancers.

Research Use Only. Not for diagnostic procedures.



Visit [Vizgen.com](https://vizgen.com) to jump-start your spatial journey.

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?**

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