Advancing Your Research with Spatial Genomics

In the past half-century, multiomic analysis—genomics, proteomics, transcriptomics, and beyond—has revolutionized our understanding of biology. However, there is still a vast wealth of information left to uncover through the integration of spatial context and transcriptomic data to understand how cells function in their native environment.

vizgen

WHAT IS SPATIAL GENOMICS?

You may have heard multiple terms floating around in your field—3D biology, spatial genomics, spatial transcriptomics, or spatial biology. These all refer to the same discipline: spatially resolved transcriptomics, which was declared _Nature's Method of the Year 2020_ for its ability to "elucidate single-cell heterogeneity and define cell types while also retaining spatial information."

Bulk and single-cell sequencing have taken us this far. However, now we can generate complete biological maps of RNA expression, cell type, cell state, and the physical architecture of tissues. Spatial genomics provides a deeper biological understanding and is thus an obvious next step in biotechnology.

Bulk and single-cell sequencing can show us parts of the whole picture
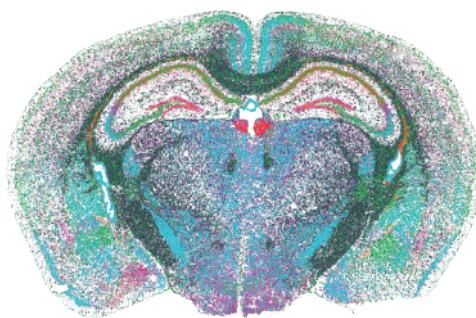

Spatial genomics with true single-cell resolution offers highly multiplexed direct _in situ_ detection and valuable insight into the bigger picture

Bulk and single-cell sequencing (represented on the left) can simultaneously profile a multitude of cells on a genomics level, but these methods require the destruction of the native cellular structure. In contrast, in situ spatial genomics approaches (represented on the right) can quantify hundreds of genes at single-cell resolution while retaining spatial context.

WHY PIVOT TO SPATIAL GENOMICS?

Spatial genomics is the next frontier of life science research. This approach accomplishes the same goals achieved by other techniques, such as distinguishing cell types and obtaining single-cell RNA sequencing data. But spatial genomics goes one step further, retaining spatial information and allowing scientists to characterize cell state, cell-cell interactions, and surrounding context. As a result, these methods offer unprecedented insight into the cellular heterogeneity of tissues. Knowing the precise locations of specific cells, such as T cells or GABA-receptive microglia, can help inform the progress of disease development and eventual treatment.
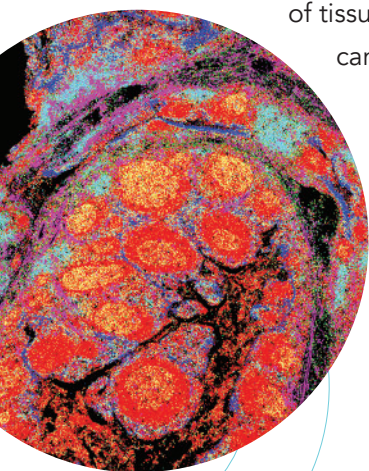

With advanced spatial genomic techniques and technology, researchers can achieve superior resolution and sensitivity. Advanced methods like MERFISH can localize RNA transcripts at a subcellular level with ≤100 nm resolution. These capabilities make it possible to detect and locate even the rarest of RNA species. Other techniques miss these lowly expressed genes, some which may significantly influence cells' functionality, like **nonsensory G-Protein coupled receptors (GPCRs) in brain tissue**. Spatial technologies can deliver these quality data metrics with high multiplexing throughput, profiling hundreds or thousands of genes at once.

Discovery and translational researchers alike are leveraging spatial genomic technologies to advance fundamental biological understanding and human health. From mouse brains to human cancer tumors, researchers can examine cellular and sub-cellular data within a wide range of tissues. This capability will help us understand neural connectivity in the brain, gene-dependent responses to cancer treatment, and more.

ADVANCING BIOLOGICAL UNDERSTANDING
Spatial genomics is revolutionizing how researchers collect and analyze data in various fields
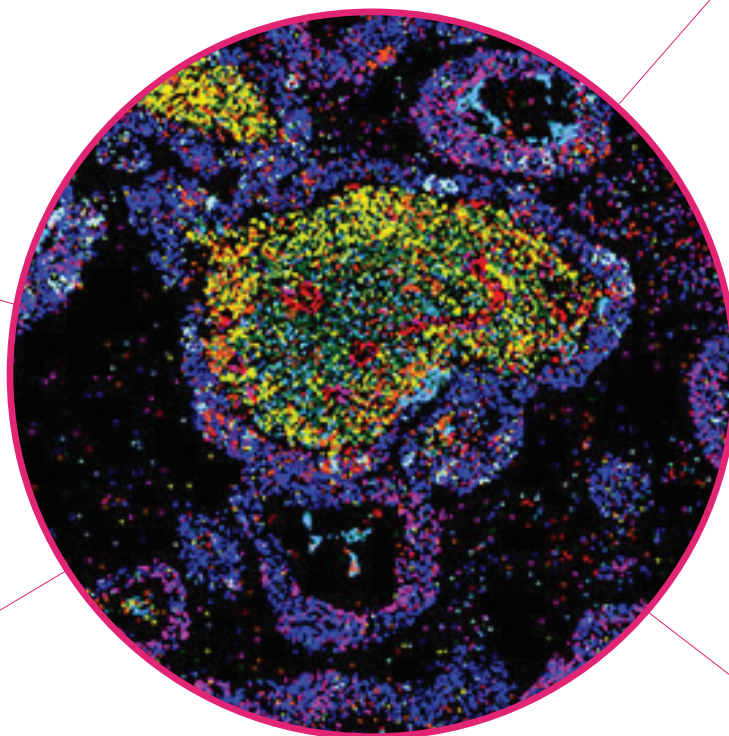
Neuroscience

Oncology

Infectious Disease

Immunology

Development Biology & Regenerative Medicine

Fluorescence *in situ* hybridization (FISH) technology has been a fixture of spatial biology for decades. This method involves fluorescent probes that bind specific RNA transcripts; the probes hybridize to fixed tissues allowing scientists to image RNA expression patterns with a fluorescence microscope.

After the widespread adoption of FISH, researchers subsequently developed single molecule FISH (smFISH), which uses multiple probes for individual RNA targets to achieve much higher resolution and yield more quantitative data. This technology evolution culminated in the development of **multiplexed error-robust FISH (MERFISH)**, which retains the *in situ* sensitivity of FISH, but uses a massively multiplexed barcoding scheme to dramatically increase gene throughput and reduce errors. Compared to other options such as slide-seq or array-based sequence methods, MERFISH offers the highest detection efficiency and resolution for spatially profiling the transcriptome. With **over 20 peer-reviewed studies** published since 2015, MERFISH has already made its mark on the scientific community—but this is just the beginning.

EXCEPTIONAL DETECTION EFFICIENCY
Characterize the gene expression profile of entire tissues, even lowly expressed genes, with the highest sensitivity and accuracy
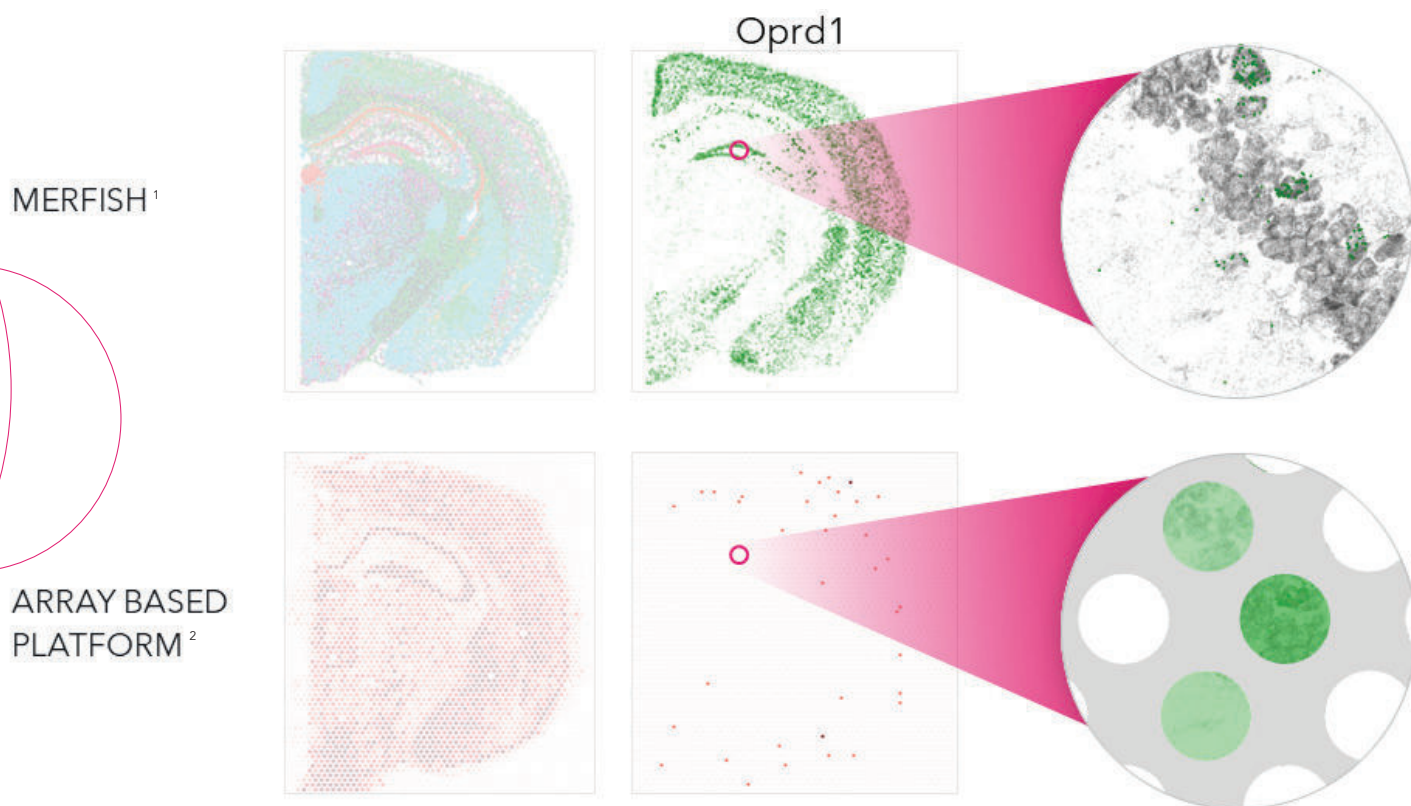

70X MORE TRANSCRIPTS PER GENE DETECTED WITH MERFISH

[1] Vizgen Data Release V1.0. May 2021
[2] 10x Genomics Data Release V1 December 2019

# BRINGING SPATIAL GENOMICS INTO YOUR LAB WITH MERSCOPE™

Getting started with spatial genomics can feel daunting, but researchers now have access to an all-in-one platform solution that provides everything a lab needs to begin running spatial experiments. The **MERSCOPE Platform** is Vizgen's complete technology solution that integrates the power of MERFISH technology with high-resolution imaging, fluidics, image processing, and automation to help scientists explore spatial context with minimal challenges. Because scientists can design custom gene panels for MERSCOPE experiments, this platform is incredibly versatile across applications and fields of study. In addition to the instrument, reagents, and consumables you need to run advanced spatial genomics experiments, the MERSCOPE Platform includes intuitive software that provides support for spatial data visualization and analysis.
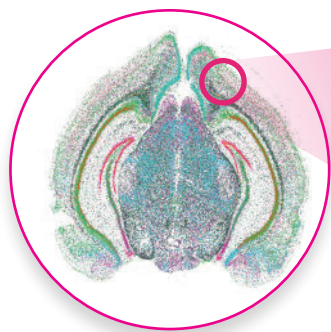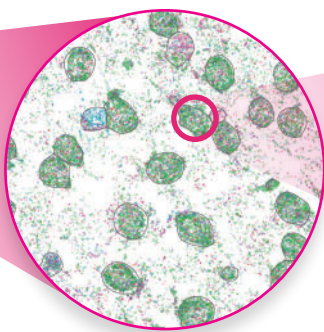
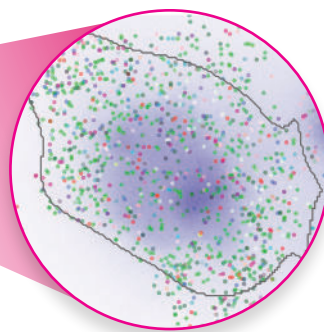| WHOLE SECTION	WIDE FIELD OF VIEW	SUB-CELLULAR
9 x 7 mm	200 x 200 micron	12 x 12 micron
Organization of tissue	**Cell interaction/function**	**L2/3 IT Glutamatergic neuron**

The MERSCOPE Platform brings your spatial genomics workflow from tissue sample to sub-cellular levels, allowing you to uncover tissue organization, cell function and interactions, and gene expression within individual cells.

ENTER THE SPATIAL DIMENSION

Scientists like you are only beginning to tap into the potential unlocked by spatial genomics. With MERFISH technology measurements generated by the MERSCOPE platform, researchers can conduct spatial genomic experiments with unparalleled sensitivity and throughput. *"In the hands of the research community, I believe that MERSCOPE will be a powerful tool for standardizing the way we characterize different cell types, not just in the brain, but also in the rest of the body, ultimately bringing a deeper level of understanding to all life science research,"* says Hongkui Zeng, Ph.D., Executive Vice President and Director of the Allen Institute for Brain Science.
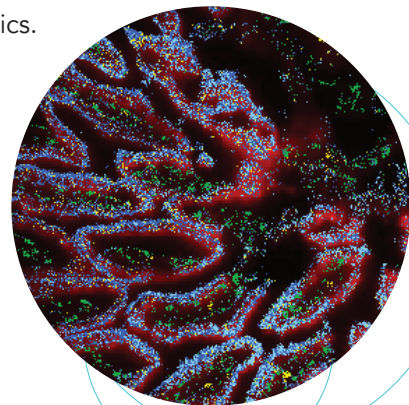
What will you discover? Learn more about spatial genomics and Vizgen today.

CLICK HERE

vizgen