

The Vizgen logo features the word "vizgen" in a white, lowercase, sans-serif font. The letter "o" is replaced by a circular icon containing several small, colored dots in red, green, and blue. The background of the entire image is a dark, swirling pattern of purple and blue dots, creating a tunnel-like effect that draws the eye towards the center.

vizgen®

Spatial biology's next era is here with MERFISH 2.0

# From Surface Structures to Subcellular Depths

More transcripts, more cells, more insights



# Explore more of biology— with data you can trust



## Detect more cell types

Identify rare and abundant cells with enhanced sensitivity and specificity



## Resolve subcellular detail

Preserve transcript localization for precise phenotyping and segmentation



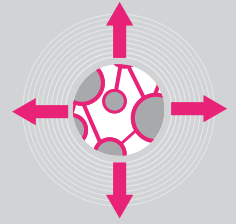
## Map tissue architecture

Explore spatial organization and microenvironments with reproducible results



## Reveal molecular crosstalk

Investigate pathways, rare cells, and interactions that drive disease and therapy

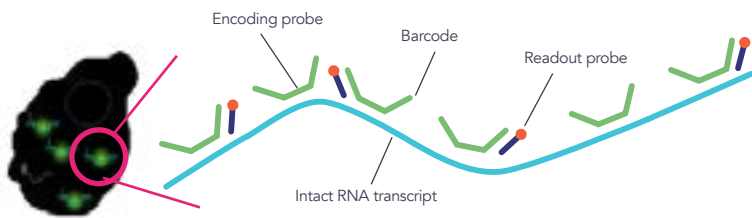


## Go further with low-quality samples

Confidently work with FFPE and other degraded tissues using MERFISH 2.0's optimized chemistry

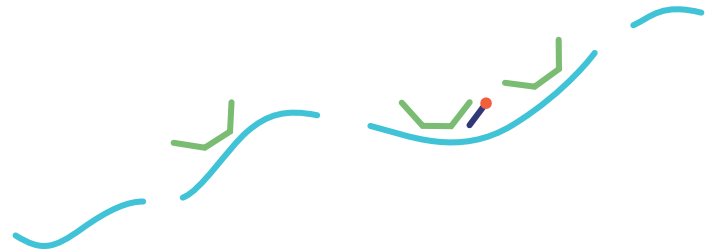
## How MERFISH 2.0 handles challenging samples

### High quality RNA samples and traditional MERFISH



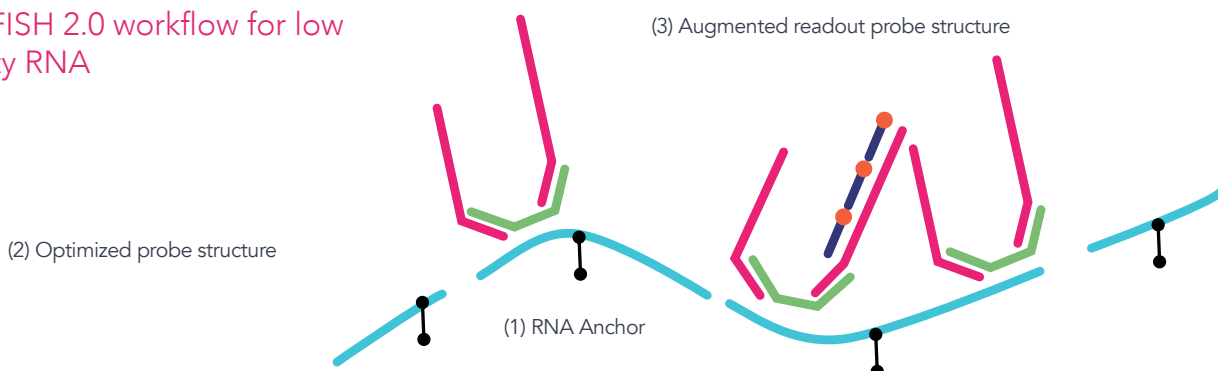
In intact RNA samples, multiple encoding probes bind along the transcript, generating strong fluorescent signals at the '1' barcode positions

### Low quality RNA samples and traditional MERFISH



In degraded samples, such as archival FFPE tissues, RNA fragmentation leads to fewer probe binding sites, reducing signal intensity. At lower RNA quality, background noise can obscure signals, making transcript quantification more challenging

### MERFISH 2.0 workflow for low quality RNA



# MERFISH: A proven platform, now more powerful

Multiplexed Error-Robust Fluorescence In Situ Hybridization (MERFISH) combines combinatorial labeling, sequential imaging, and error-robust barcoding to deliver single-cell spatial transcriptomics at scale. MERFISH 2.0 builds on this foundation with enhanced chemistry for greater sensitivity, expanded sample compatibility, and even clearer insights.

100s of peer-reviewed publications referencing MERFISH

“Method of the Year 2020: spatially resolved transcriptomics”

nature methods

## MERFISH 2.0 further optimizes the four major steps:

### 1 - Preparation

Tissue is mounted and permeabilized; protein co-detection is optional. MERFISH 2.0 improves RNA anchoring for better integrity and access.

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

### 2 - Clearing

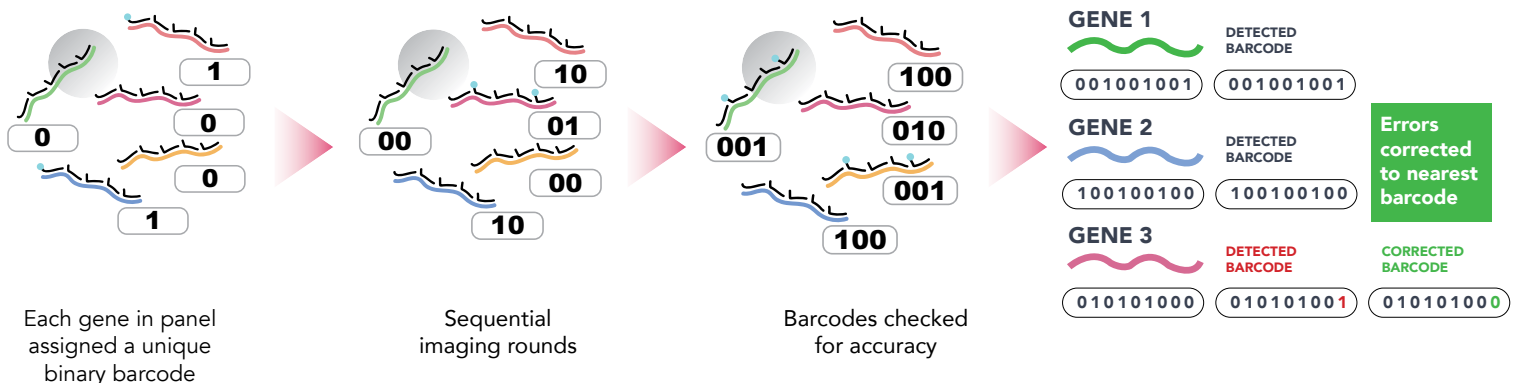
Gel embedding clears background while preserving probes. Ensures clean imaging with minimal signal interference.

### 3 - Hybridization

Thousands of encoding probes bind RNA targets. Optimized binding increases occupancy and readout success.

### 4 - Imaging

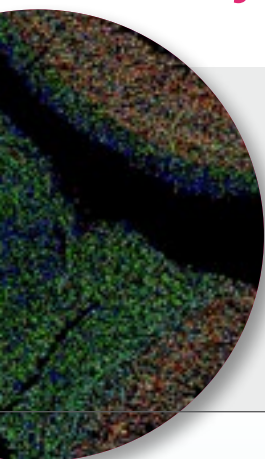
Barcoded genes are decoded via sequential imaging rounds. More readout probes amplify signal and boost accuracy.



“ We decided on MERFISH due to the high sensitivity and the relatively low requirements for tissue samples. Our expectations were greatly surpassed by the astonishing (subcellular) resolution of MERFISH 2.0, especially when compared to MERFISH 1.0. This will allow us to mechanistically test the main hypothesis of the project using this data alone, Thank you very much!

University Hospital Tübingen, Germany

# Sample compatibility: ready-to-run or ready-to-explore



Sample category

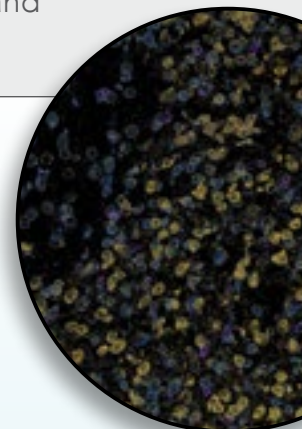
Vizgen support provided

Vizgen lab-validated

Ready-to-run protocols, QC metrics, in-house data

Customer-optimized

General guidance, tissue-specific support, and best practices



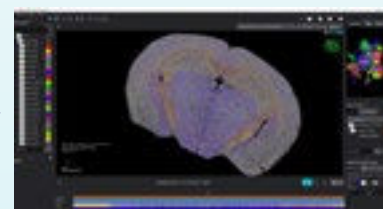
## A complete ecosystem for deeper discovery

A complete end-to-end solution with the MERSCOPE Ultra powered by MERFISH 2.0

Sample preparation

Data acquisition

Data analysis & visualization



High resolution | High sensitivity | Scalable | Flexible | High fidelity data

// MERFISH and MERSCOPE are the perfect companion to achieve high quality spatial transcriptomic data which are extremely important to dissect the complexity of the tumor microenvironment. Thanks to MERFISH 2.0 we obtained incredible data also with pancreatic ductal adenocarcinoma (PDAC) tissue for which suboptimal RNA quality - given by the high RNase tissue content - will not be a technical constraint anymore. //

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