

# Unlock Spatial Insights in Cardiac Tissue with Vizgen's Spatial Multi-omics Platform



The heart is structurally and molecularly complex; layered cardiomyocytes, fibroblasts, immune cells, vascular networks, and neural-crest-derived populations form intricate micro-neighborhoods. Understanding cardiac development and disease requires knowing what genes are expressed, and exactly where.

The Solution:

**vizgen**<sup>®</sup>

**MERSCOPE Ultra™ Platform and MERFISH 2.0™**

High-plex, single-cell spatial transcriptomics across large cardiac tissue areas for:

- Heart development
- Congenital defects
- Tissue remodelling
- Cardiomyocyte/fibroblast/vascular interplay



**vizgen**<sup>®</sup>

# The chromatin regulator *Ankrd11* controls cardiac neural crest cell-mediated outflow tract remodeling and heart function

Kibalnyk, Y., Afanasiev, E., Noble, R.M.N. et al. *Nat Commun* 15, 4632 (2024).  
<https://doi.org/10.1038/s41467-024-48955-1>

## Background

Cardiac neural crest cells (CNCCs) play a central role in heart development, particularly in remodeling the outflow tract (OFT).

Disruption of CNCC function can result in congenital heart defects, abnormal septation, and impaired ventricular performance.

Researchers used the MERSCOPE® Platform to perform spatial transcriptomics in embryonic heart tissue to examine how loss of the chromatin regulator *ANKRD11* affects OFT development.

## MERSCOPE platform enabled:

High-plex profiling of cncc-derived & neighboring cells

Spatially resolved altered states in oft

Mapping developmental signalling disruptions

Connecting gene regulation → cell misallocation → anatomical defects

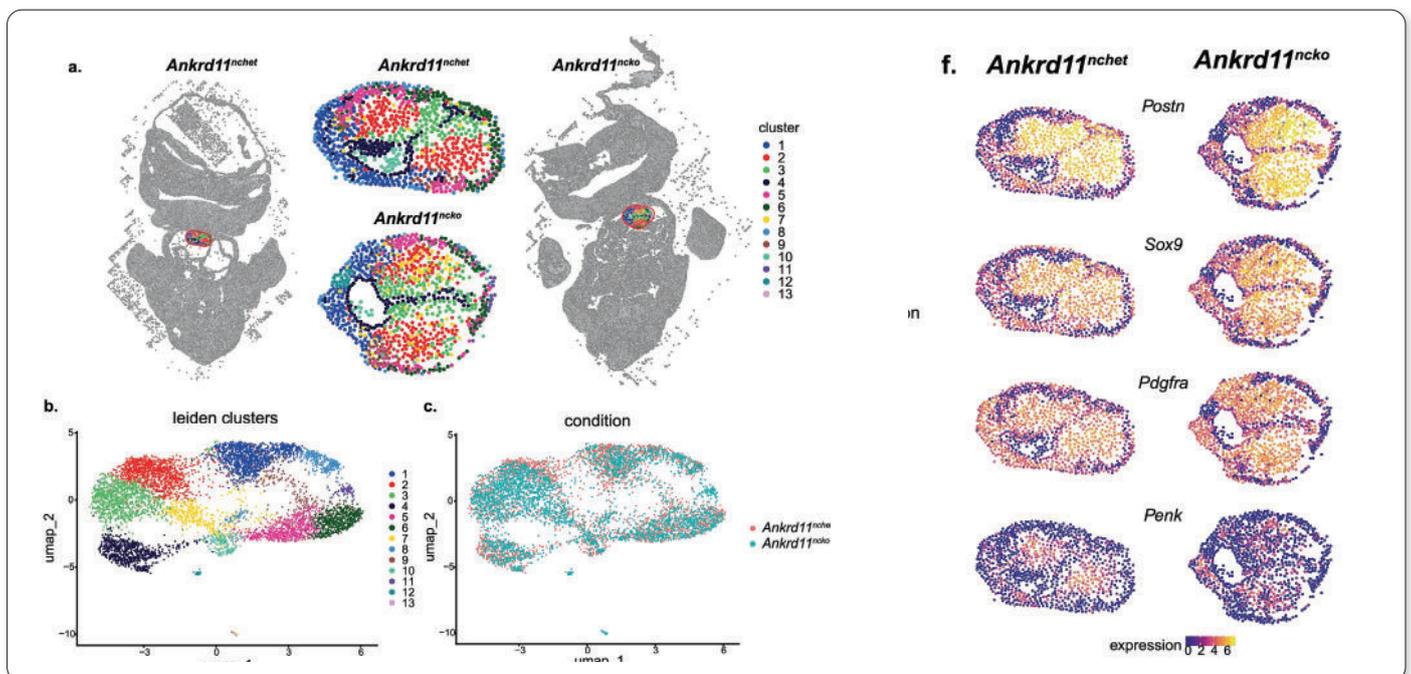
## Key findings:

Loss of *Ankrd11* disrupts cncc differentiation & positioning

Mis-organized oft layers & reduced structural integrity

Vpt + cellpose2 distinguished cnccs from cardiomyocytes, fibroblasts, vascular cells

Integrated molecular → cellular → structural insights



## MERFISH identified CNCC clusters in the OFT at E11.5

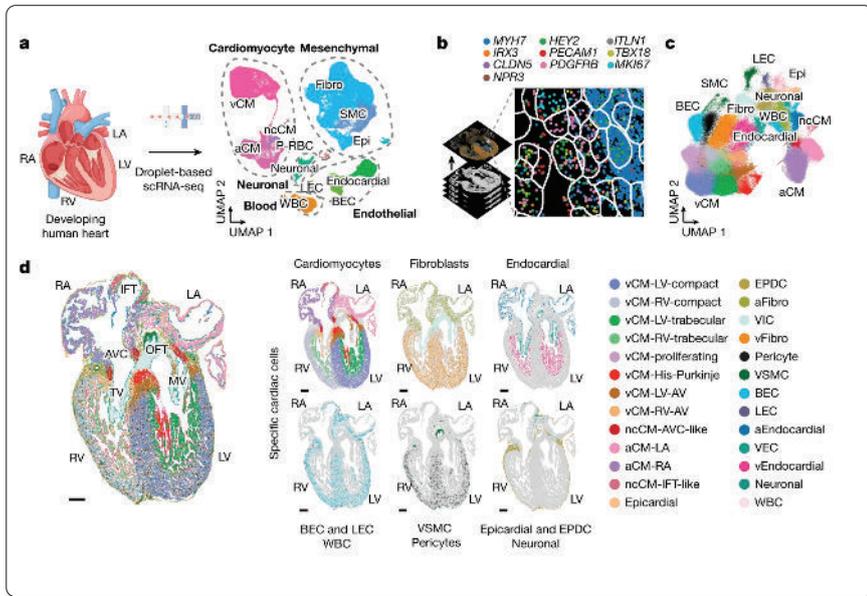
a, Plot showing the spatial position of cells from representative transverse sections of E11.5 *Ankrd11<sup>ncheta</sup>* (left) and *Ankrd11<sup>ncko</sup>* (right) embryos subjected to MERFISH with a custom 140 gene panel. b, c Plots showing the position of OFT cells from all samples in UMAP-space. f Plots showing spatial positions of OFT cells colored according to normalized gene expression.

# Spatially organized cellular communities form the developing human heart

Farah, E.N., Hu, R.K., Kern, C. et al.

*Nature* 627, 854-864 (2024).

<https://doi.org/10.1038/s41586-024-07171-z>



**Molecular and spatial human heart cell atlases reveal a diverse range of cell populations during heart development.**

a, Left, schematic of experiment. Right, scRNA-seq identifies a diverse range of distinct cardiac cells that create the developing human heart (UMAP) of ~143,000 cells. b, Schematic shows how 238 cardiac-cell-specific genes were spatially identified using MERFISH. c, Approximately 250,000 MERFISH-identified cardiac cells were clustered into specific cell populations as shown by UMAP and coloured accordingly in d. d, Identified MERFISH cells were spatially mapped across a frontal section of a 13 p.c.w. heart (left) and shown according to major cell classes (right).

**MERFISH was used to build the first large-scale human heart spatial atlas.**

## Key findings include:

12 major cell classes, 39 cell populations, 75 sub-types

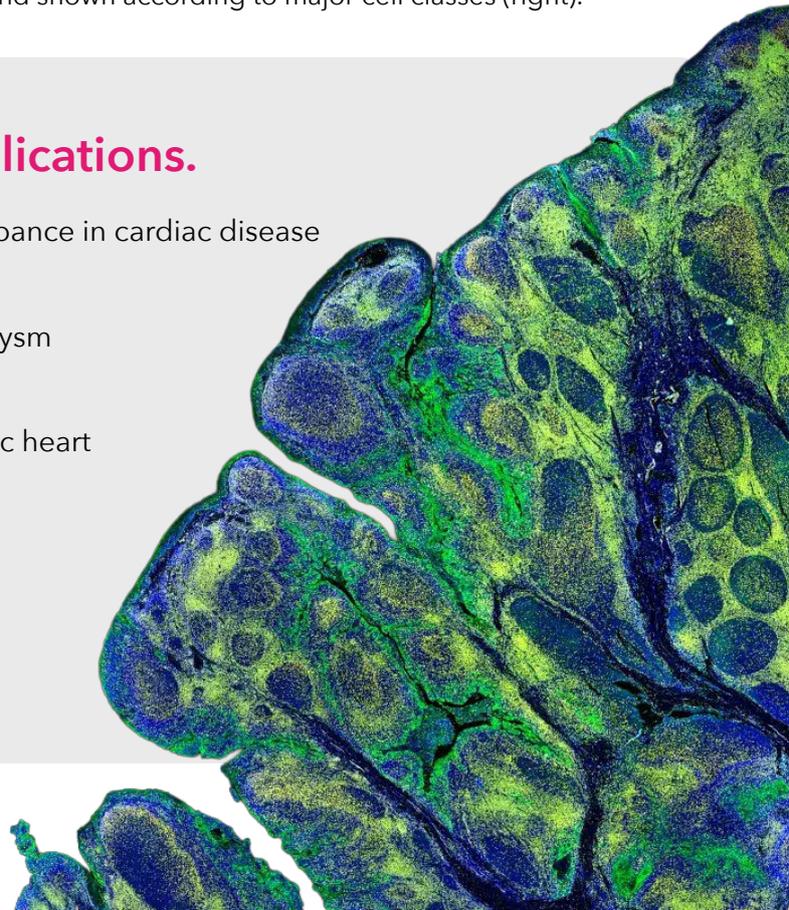
Discovery of laminar cardiomyocyte layers across the ventricular wall

Spatial “cellular communities” involving cardiomyocytes, fibroblasts, and endothelial cells

Identification of PLXN-SEMA signaling networks driving ventricular wall morphogenesis

## Other selected cardiology publications.

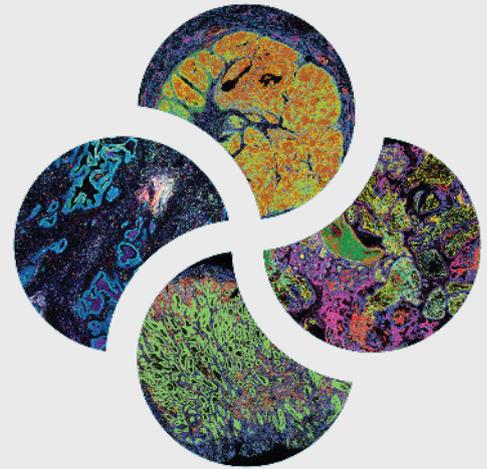
- Immune-mediated denervation & sleep disturbance in cardiac disease  
Ziegler et al., *Science* 2023
- Spatial transcriptomics in thoracic aortic aneurysm  
Mizrak et al., *ATVB* 2023
- Endothelial cell signatures in mouse embryonic heart  
Chen et al., *Circ Res* 2024
- Dystrophic trajectory in muscle development  
Chen et al., *Genome Research* 2024
- GATA4-linked aortic root dilation  
Bramel et al., *Nat Cardiovasc Res* 2024



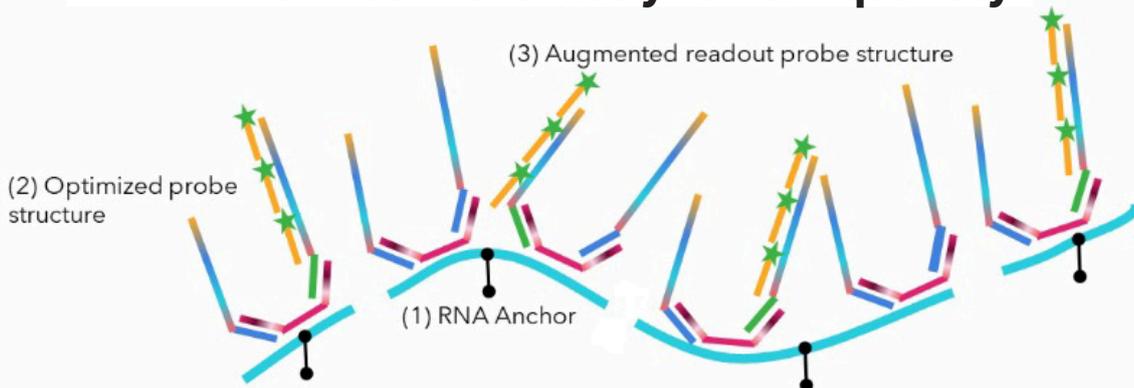
# Explore more of spatial biology,



## MERSCOPE Ultra™ Platform and MERFISH 2.0™



### MERFISH 2.0™ chemistry for low-quantity RNA



## Platform Benefits

### High-plex MERFISH 2.0™ chemistry

- Improved sensitivity & robustness
- Hundreds → ~1,000 genes
- FFPE & fresh frozen cardiac compatibility

### Large-area imaging with MERSCOPE Ultra™

- Up to 3 cm<sup>2</sup> tissue per run
- Whole-section imaging: ventricles, atria, septum, OFT, large vessels

### Accurate segmentation with VPT

- Handles dense cardiomyocytes and connective tissue
- Refined single-cell boundaries with dystrophin protein
- Reliable transcript assignment
- Strong spatial neighbourhood analysis