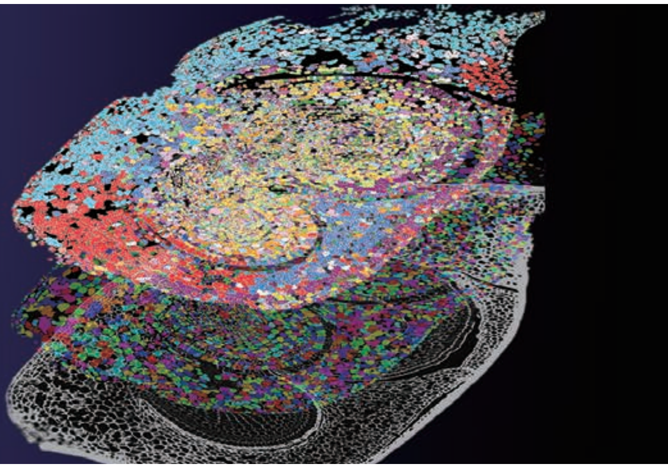
# Unveiling Plant Biology with Stereo-seq

## True single-cell spatial transcriptomics



Understanding spatial gene expression in plants is vital for advancing research on development, evolution, and environmental interactions. While RNA's role in cellular function is well-characterized in animals, it remains underexplored in plants. Stereo-seq, a single-cell resolution spatial transcriptomics technology with whole transcriptome capturing, enables detailed analysis and scientific discovery of plant tissue structures, cellular interactions, and receptor-ligand networks.

## Technology Highlights

- Subcellular resolution allowing visualization on cellular heterogeneities and efficient cell types annotations

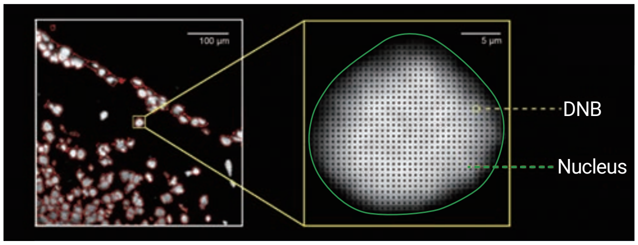


Figure 1. Stereo-seq capturing spots (DNBs) arranged down to single cell resolution, allowing mRNA within one cell to be captured with hundreds of coordinate ID containing DNBs

- Multiple chip sizes allowing various tissue types and scalable capture areas

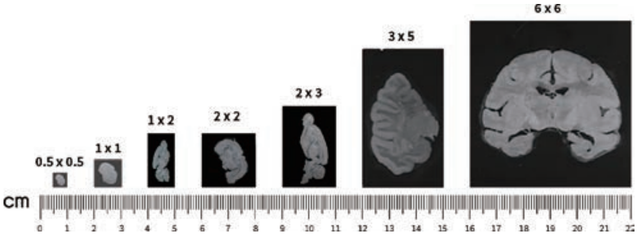
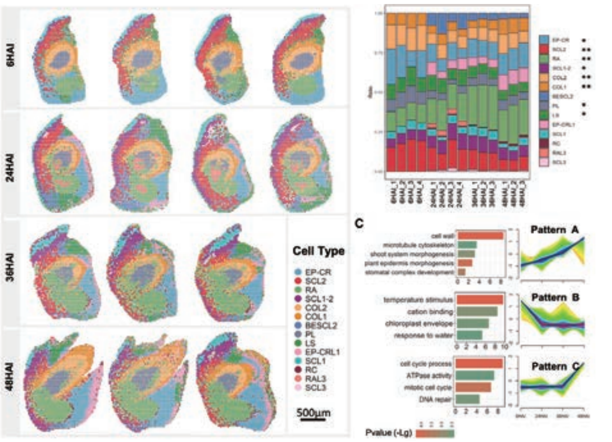


Figure 2. Demonstration of Stereo-seq chip at different sizes

## Featured Publication

### Spatiotemporal transcriptomic landscape of rice embryonic cells during seed germination

*Yao, Jie et al. Developmental Cell, 2024*

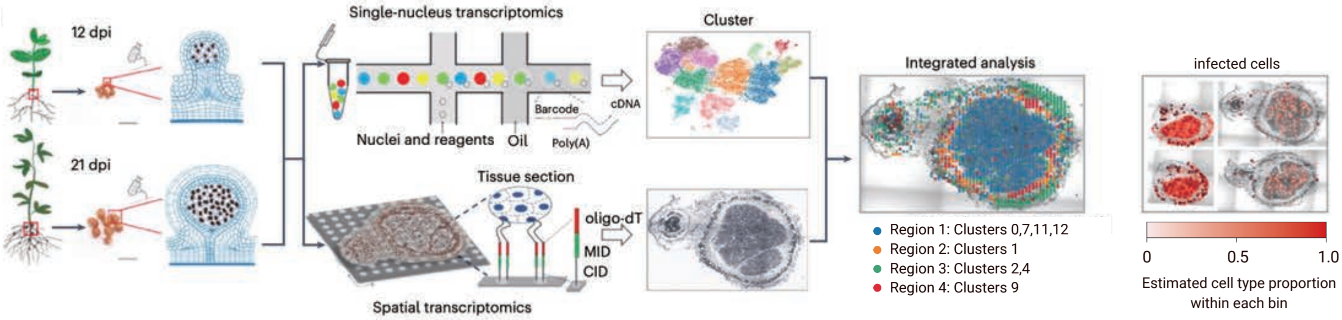


- Employed cutting-edge sequencing methods (Stereo-seq and scRNA-seq) to investigate rice seed germination
- Created an AI-driven cell segmentation model for analysis
- Uncovered novel embryo cell types and monitored gene expression at various stages
- Recognized essential gene - SCL2 - related to metabolism, biosynthesis, and hormone regulation signaling
- Sample type: fresh frozen

## Featured Publication

### Integrated single-nucleus and spatial transcriptomics captures transitional states in soybean nodule maturation

*Yao, Jie et al. Developmental Cell, 2024*



- Developed a high-resolution spatial transcriptomics gene expression profile for soybean nodules across various developmental stages
- Identified specialized uninfected cells as well as transitional infected cells
- Provided new insights into the rhizobium-legume interaction symbiosis
- Sample type: fresh frozen

## Addtional Publications

| Publication | Link |
|---|---|
| Tracing the evolutionary and genetic footprints of atmospheric tillandsioids transition from land to air. *Nat Commun* 15, 9599 (2024) | |
| Mapping the molecular landscape of Lotus japonicus nodule organogenesis through spatiotemporal transcriptomics. *Nat Commun* 15, 6387 (2024) | |
| A spatial transcriptome map of the developing maize ear. *Nat Plants* 10, 815–827 (2024) | |
| Chromosome-level genomes of three key Allium crops and their trait evolution. *Nat Genet* 55, 1976–1986 (2023) | |
| Spatial transcriptomics reveals light-induced chlorenchyma cells involved in promoting shoot regeneration in tomato callus. *Proc. Natl. Acad. Sci. U.S.A.* 120 (38) e2310163120 (2023) | |

Please note: All the publications referenced above utilized fresh frozen samples and implemented customized protocols specific to their studies.

**To learn more, visit completegenomics.com/spatial-transcriptomics**

General Inquiry: info@completegenomics.com