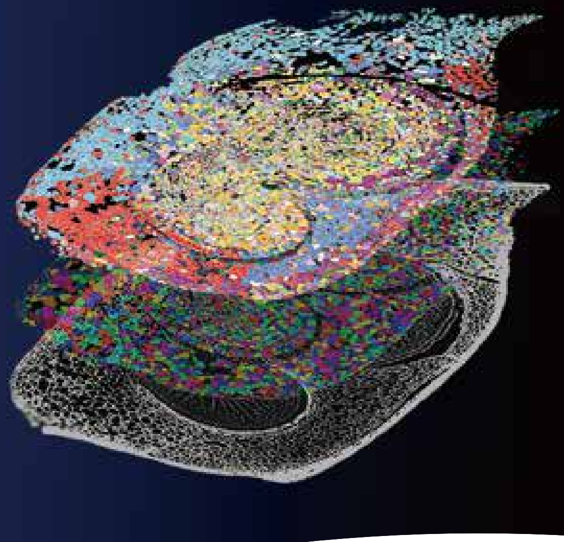
Plant Research

STOmics | MGI



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 type annotations

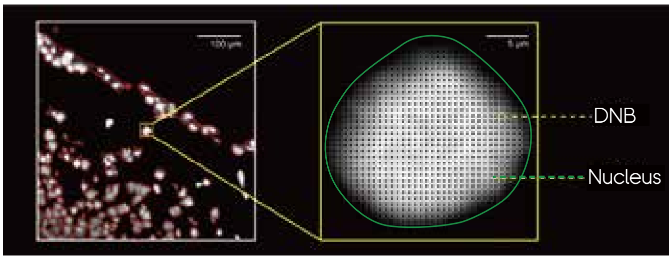


Figure 1. Stereo-seq capturing spots (DNBs) arranged down to single-cell resolution, allowing mRNA within one cell to be captured with hundreds of coordinate ID containing DNBs

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

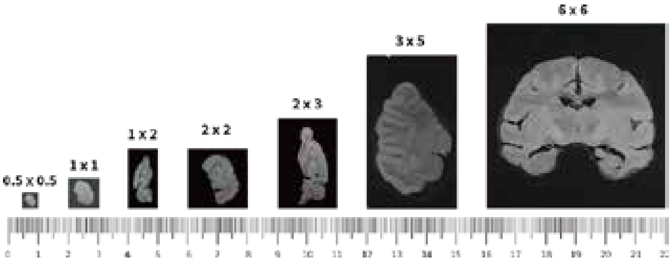
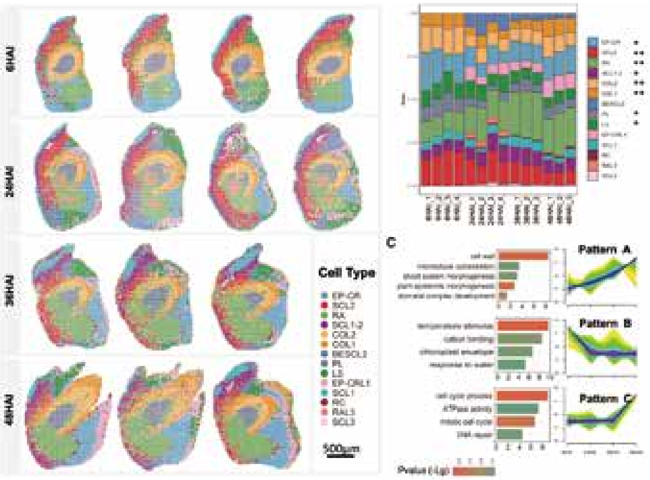


Figure 2. Demonstration of Stereo-seq chip at different sizes

Featured publication

Spatiotemporal transcriptomic landscape of rice embryonic cells during seed germination

Yao, Jie et al. Developmental Cell, 2024



Highlights

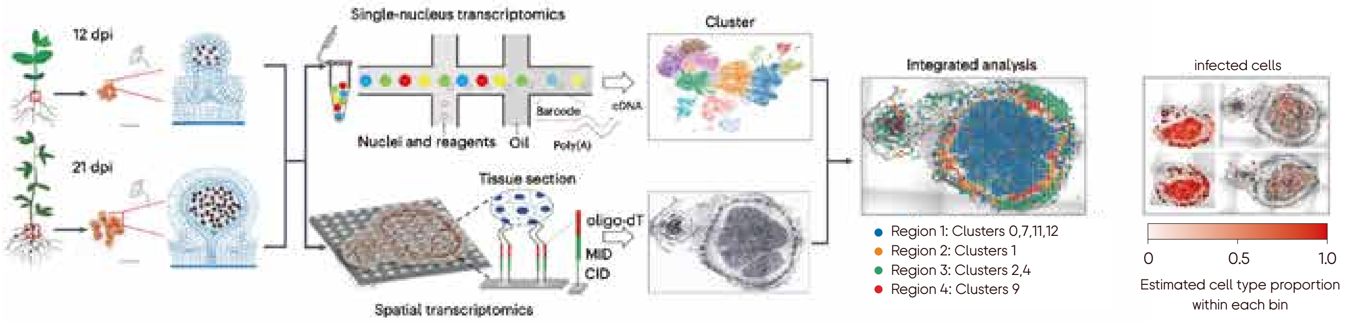
- Employed cutting-edge sequencing methods (Stereo-seq and scRNA-seq) to investigate rice seed germination
- Created an AI-driven cell segmentation model for analysis
- Uncovered novel embryo cell types and monitored gene expression at various stages
- Recognized essential gene - SCL2 - related to metabolism,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

Sample type: fresh frozen *Customer developed protocol.

Featured publication

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

Liu, Z., Kong, X., Long, Y. et al. Nat. Plants, 2023



Highlights

- 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
*Customer developed protocol.

Additional publications

Publication	Experiment snapshot	Link
Tracing the evolutionary and genetic footprints of atmospheric tillandsioids transition from land to air. *Nat Commun* 15, 9599 (2024)	Sample type: Fresh Frozen *Customer developed protocol.	
Mapping the molecular landscape of Lotus japonicus nodule organogenesis through spatiotemporal transcriptomics. *Nat Commun* 15, 6387 (2024)	Sample type: Fresh Frozen *Customer developed protocol.	
A spatial transcriptome map of the developing maize ear. *Nat. Plants* 10, 815–827 (2024)	Sample type: Fresh Frozen *Customer developed protocol.	
Chromosome-level genomes of three key Allium crops and their trait evolution. *Nat Genet* 55, 1976–1986 (2023)	Sample type: Fresh Frozen *Customer developed protocol.	
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)	Sample type: Fresh Frozen *Customer developed protocol.	

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