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Within Reach

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Global Leaders in  
Single-Cell and Spatial

# Spatiotemporal Multi-Omics in Plant Research

To reveal the mysterious changes in  
plant growth and development





# About Omics Empower

Omics Empower (OE Biotech's subsidiary), a leader in single-cell transcriptomics research service provider since 2018, has revolutionized plant cell research with its cutting-edge spatiotemporal multi-omics technologies.

Our expertise in single-cell transcriptomics and spatial transcriptomics has been refined through the execution of over 17000 single-cell experiments spanning more than 2,000 tissue types, empowering over 340 scientific publications, including 33 on plant samples. Such extensive experience has enabled us to unravel the complex cellular heterogeneity that drives plant development, contributing significantly to the understanding of plant biology and driving advancements in the field.

Article Count

340+

Lab Exp

17,000+

Sample Type

2,000+

We partner with top-tier omics platforms to offer comprehensive services, from root to fruit, that reveal the intricate molecular mechanisms behind plant responses to environmental stimuli. Our efforts have been recognized with a high-impact publication in *Molecular Plant*, showcasing the global dynamic molecular profiles of stomatal lineage cell development.

Omics Empower remains committed to advancing plant science by delivering robust, reliable research services to the scientific community worldwide. Join us in exploring the dynamic world of plant cell function and development.



As the parent company of Omics Empower, Oebiotech has been a trailblazer in sequencing technology services in China since 2009. Now, we are poised to bring our expertise to the global stage. Over the past 15 years of dynamic growth, we have evolved into a biotechnology group enterprise with a team of over 600 dedicated professionals, ready to make a meaningful impact on the international arena.



## Empowering Research with Multi-Omics Innovations

We provide multi-omics technical services for life science research, including comprehensive products such as **single-cell sequencing**, **spatial omics**, **yeast libraries**, and **bioinformatics analysis**. We are committed to enhancing life through technology and benefiting humanity through scientific innovation.

# What Can We Do?

## Single-cell transcriptome sequencing

Unlocking the secrets of cellular diversity, our advanced single-cell transcriptomics platforms: “10x Genomics” and “MobiNova”, are revolutionizing the way we explore gene expression in plant cell development. These systems enable precise mRNA analysis from single cells, revealing the intricacies of cellular heterogeneity and uncovering new cell types under various conditions.

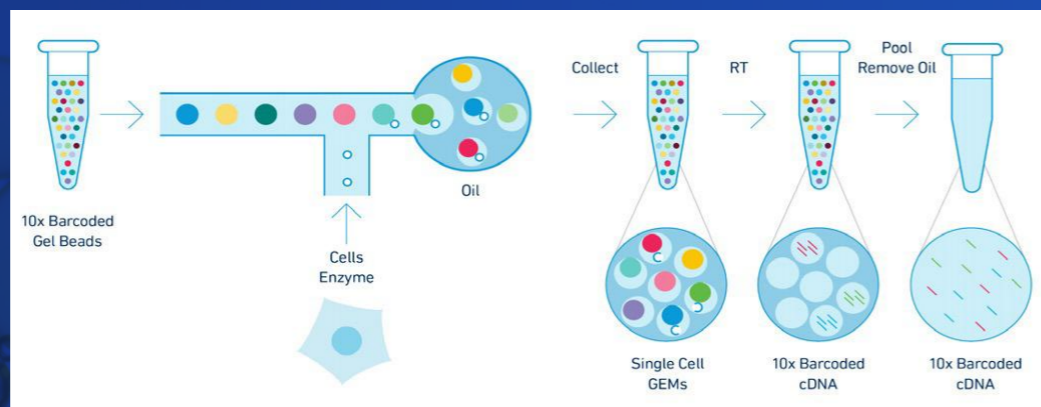
With our Omics Empower platform, we're not just sequencing cells, we're pioneering the future of cellular research, making groundbreaking discoveries accessible and intuitive for scientists spanning the globe.



# 10 x Chromium 3' single-cell transcriptome sequencing

The 10x Genomics Chromium system uses a microfluidic, GEMs microreaction system, employing sequence tags (cell barcodes and unique molecular identifiers/UMIs) to distinguish cell composition within a population and quantify transcripts within individual cells.

This enables single-cell gene expression profiling, allowing transcriptome analysis of thousands or even tens of thousands of cells.



- Technical Flow chart of 10xChromium single-cell transcriptome -  
(source 10xGenomics)

# MobiNova® 3' single-cell transcriptome sequencing

Empowering Life Sciences with Cost-Effective Innovations



## 1 Sample Preparation

Obtaining high-quality single-cell suspension from various sample types

## 2 Library Construction

Completing cell encapsulation, partitioning, and barcoding using patented MobiSeq technologies

## 3 Single-Cell Sequencing

Obtaining libraries compatible for various downstream NGS sequencing platforms such as Illumina sequencers

## 4 Data Analysis

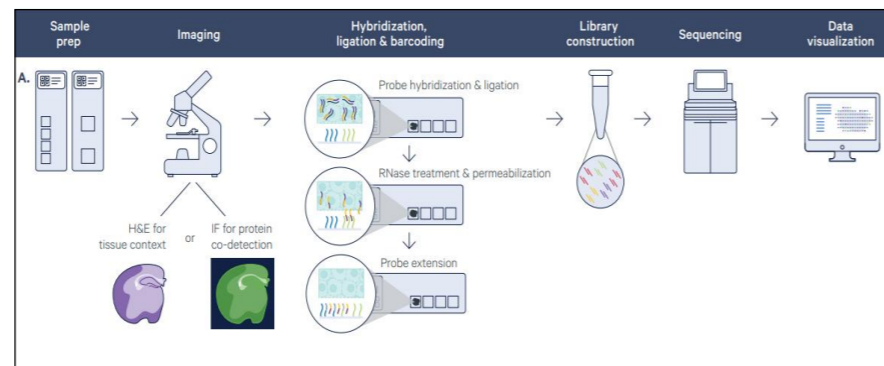
MobiVision software providing easy-to-use and informative data visualization and interpretation

- Technical flow chart of MobiNova single cell transcriptome (source MobiNova) -

# Single-cell Transcriptome Sequencing

Harnessing the power of single-cell transcriptome sequencing, we can comprehensively profile cellular composition and gene expression spanning tissues. However, this approach all short of capturing the spatial distribution of cells. To bridge this gap and unravel the intricate coordination among diverse plant cell types within tissues, we introduce high-throughput spatial transcriptome sequencing technology. This innovative method preserves the spatial integrity of plant tissues while enabling precise transcriptional profiling of cells at various locations, offering profound insights into the complexity of plant tissue architecture.

For plant sample analysis, Omics Empower recommends the cutting-edge 10x Genomics spatial transcriptomic solution, setting a new standard in spatial omics research.



- Technical flow chart of 10x Visium spatial transcriptome -  
(source 10xGenomics)

# How Should You Prepare Your Samples?

## Single-cell Transcriptome Plant Samples

### Fresh tissue samples-isolated protoplasts

- For whole plants planted in pots, the soil in the pots needs to be filled and compacted, and the soil needs to be kept moist; wrap and fix the soil in the pots with plastic wrap, put them into the sample bag and then pack them with a foam box. If necessary, fill or isolate the gaps with foam boards; pack the foam box into a box of appropriate size or a wooden frame and transport it at room temperature.
- For tissue culture seedlings in the vigorous growth period (each sample should have no less than 3 bottles, and the number can be increased or decreased as appropriate based on the amount of samples that can be collected); the tissue culture bottles should be placed in a foam box of appropriate size, and the gaps should be fixed and filled with foam boards and other materials to prevent the culture bottles from breaking during transportation. Transport at room temperature.

### Frozen tissue sample delivery-core extraction:

- Collect the required plant parts and quickly remove irrelevant tissues after sampling. If the root tissue is collected from the culture medium or soil, wash off the culture medium or soil with running water, absorb excess water with absorbent paper, and immediately freeze it with liquid nitrogen and transfer it to a -80°C refrigerator for storage, or transport it to the company with dry ice.



## Instructions for Delivery of Spatial Transcriptome Plant Samples

### Fresh tissue samples:

- The plant samples to be tested are cut and corrected to the appropriate embedded size according to the direction required for the research purpose, put the Leica embedded glue into the bottom of the embedded box, and put the trimmed plant samples into the embedded glue with tweezers, so that the samples are completely immersed in the embedded glue.
- Transfer the embedded box horizontally to dry ice for quick-freezing, then transfer to -80°C refrigerator, or transport the dry ice to the company.

### Frozen tissue samples:

- Store at -80°C and ship to the company on dry ice.



# Omicsempower's Core Competencies!

We have integrated globally recognized cutting-edge analytical platforms.

Our drive for innovation has resulted in a state-of-the-art, 1000 square meter spatial multi-omics platform that fuses cutting-edge tech with research prowess.

Our dedication to superior spatial multi-omics services is evident in our advanced infrastructure and partnerships with top research institutions. We're set to fuel scientific breakthroughs worldwide with our progressive tech solutions.

## Our offerings include



### Single-cell RNA Sequencing

Utilizing 10x Chromium, BD Rhapsody, and MobiNova systems, we provide deep insights into cellular heterogeneity and gene expression dynamics.



### High-Throughput Sequencing

Equipped with Illumina X Plus and MGI DNBSEQ-T7 sequencers, we deliver large-scale, accurate sequencing services to support comprehensive genomic research.



### Spatial Transcriptomics

With 10x Visium FF, 10x Visium CytAssist, 10x Xenium *in Situ*, and Stereo-seq technologies, we offer detailed understanding of the spatial organization of gene expression within tissues.



### Bioinformatics Analysis

Focus on providing in-depth bioinformatics analysis to help you extract valuable biological insights from complex data.

# Accelerate Your Research!

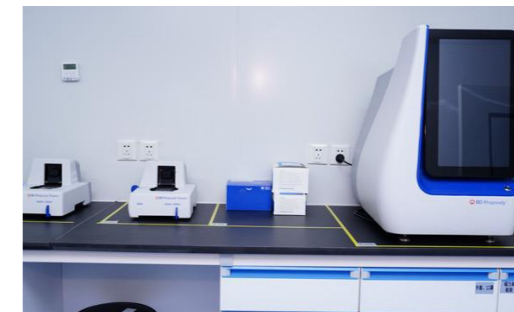
## Single-cell transcriptome experimental



10x Chromium Controller



10x Chromium X



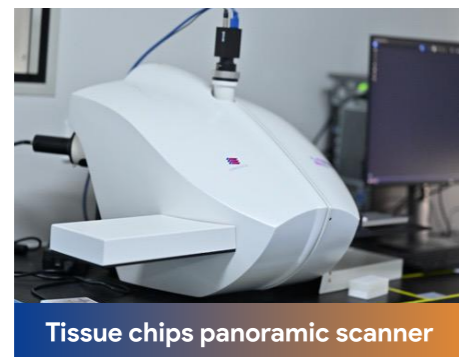
BD Rhapsody™Scanner



MobiNova®-100



# Spatial transcriptome experimental



Tissue chips panoramic scanner



10x Genomics Visium CytAssist



10x Genomics Xenium



Stereo-seq microscope

# High-throughput sequencing



MGI DNBSEQ-T7



Illumina X plus

# What Our Clients Have Published?

## Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in *Gossypium bickii*

IF: 17.1

Published in: February 2023

Technical services provided:  
**10x Genomics single-cell transcriptome sequencing**

Material:  
**Bechners cotton (*Gossypium bickii*) cotyledons**

### Research background

Cotton (*Gossypium* spp.) is a vital economic crop, with cottonseeds rich in oil and protein. Pigment glands, unique defensive structures within the genus *Gossypium*, contain gossypol as a primary compound, which plays a significant role in resistance of cotton to pests and diseases. However, the toxicity of gossypol to humans and ruminant animals limits the utilization of cottonseed resources. Australian wild cotton species, such as *Gossypium bickii*, exhibit a desirable trait known as “delayed formation of pigment glands in cotyledons,” characterized by low gossypol and gland-free seeds, allowing for enhanced use of cottonseed resources. The presence of gossypol-containing pigment glands in the plant aids in maintaining resistance to pests and diseases, underscoring the breeding value of these species. Understanding the biological processes and potential molecular mechanisms underlying pigment gland morphogenesis is essential for developing new low-gossypol cotton cultivars with gland-free seeds and gland-containing plants.

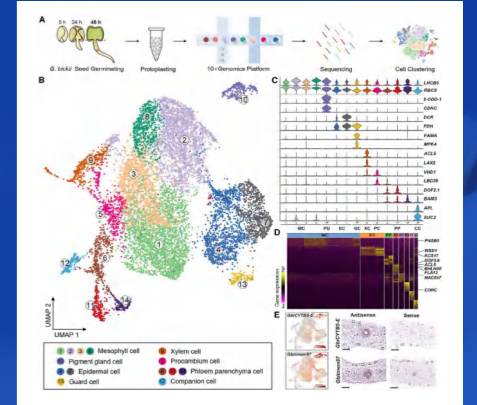


Fig 1. Construction of the single-cell transcriptome map of cotton cotyledon

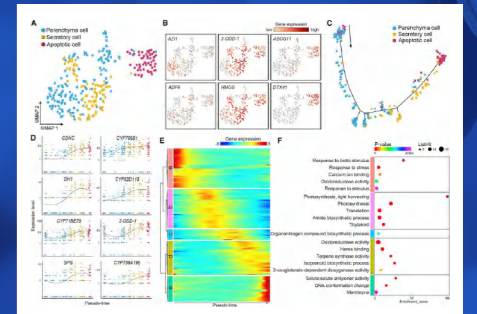


Fig 2. Developmental trajectory of pigment gland cells

# Spatial transcriptomics uncovers sucrose post-phloem transport during maize kernel development

Published in the journal: *Nature Communications*

IF: 14.7

Technical services provided:  
10 x Visium spatial transcriptome sequencing

Published in: November 2023

Material:  
Corn grain during the grain filling period

## Research background

Maize is one of the most widely cultivated and highest-yielding crops globally, with an average annual production reaching 1 billion tons. The maize kernel is a highly complex system, comprising millions of cells, including the diploid maternal seed coat, the triploid endosperm of the progeny genotype, and the diploid embryo. Studying cell types and functional regions in kernel development is crucial for understanding the molecular mechanisms of spatially and temporally specific gene expression in maize kernels, enabling the optimal use of genetic resources, including elite genes from various inbred lines and wild maize. However, traditional approaches based on visible tissue morphology or microscopy fail to distinguish morphologically similar but functionally distinct cell subpopulations. In particular, the endosperm adjacent to the scutellum (EAS), a critical interface for embryo and endosperm interactions, closely resembles surrounding cells, making these essential subpopulations difficult to differentiate. These cells mediate embryo-endosperm signaling, nutrient transport, and other biological functions, yet direct evidence of their roles has been lacking. Consequently, new technologies are urgently needed to differentiate the heterogeneous tissue cells within maize kernels and to accurately identify functionally significant cell subpopulations that are challenging to classify. Constructing in situ hybridization maps and analyzing gene functions during the grain-filling stage holds significant potential for advancing maize kernel improvement.

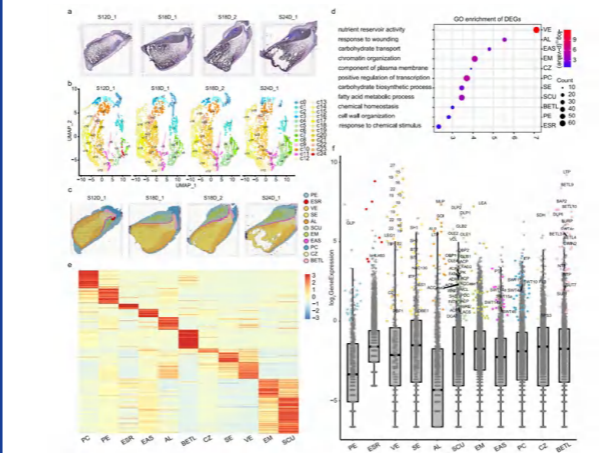


Fig. 1. Spatial analysis of the three grouting stages

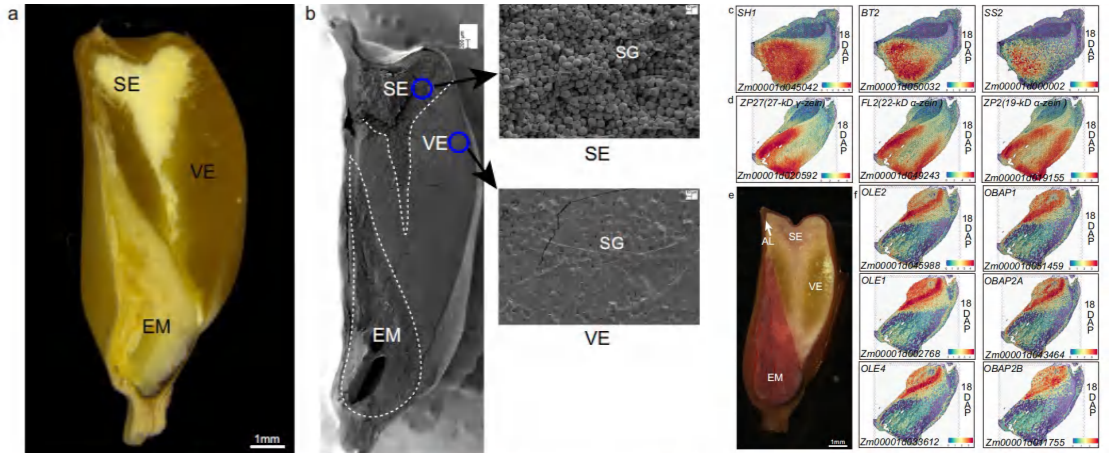


Fig. 2. Spatial specific accumulation of starch, protein and oil in corn seeds

# Partial List of Articles

No.	Year of Publication	Journal	2023 Impact Factor	Article Title	Sample Type	Applied Technology
1	2020	<i>Molecular Plant</i>	17.1	Global Dynamic Molecular Profiling of Stomatal Lineage Cell Development by Single-Cell RNA Sequencing	Arabidopsis	10x Genomics single-cell transcriptomics
2	2020	<i>Frontiers in Plant Science</i>	4.1	Single-Cell RNA Sequencing Efficiently Predicts Transcription Factor Targets in Plants	Rice leaves	10x Genomics single-cell transcriptomics
3	2022	<i>Plant Journal</i>	6.2	Identification of Novel Regulators Required for Early Development of Vein Pattern in the Cotyledons by Single-Cell RNA-Seq	Arabidopsis	10x Genomics single-cell transcriptomics
4	2022	<i>Crop Journal</i>	6.0	Single-cell RNA sequencing reveals the landscape of maize root tips and assists in identification of cell-type-specific nitrate-response genes	Maize root tips	10x Genomics single-cell transcriptomics
5	2022	<i>International Journal of Molecular Sciences</i>	4.9	Identification of the Regulators of Epidermis Development under Drought- and Salt-Stressed Conditions by Single-Cell RNA-Seq	Arabidopsis	10x Genomics single-cell transcriptomics

No.	Year of Publication	Journal	2023 Impact Factor	Article Title	Sample Type	Applied Technology
6	2023	<i>Molecular Plant</i>	17.1	Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in <i>Gossypium bickii</i>	<i>Gossypium bickii</i>	10x Genomics single-cell transcriptomics
7	2023	<i>Plant Communications</i>	9.4	Combining single-cell RNA sequencing with spatial transcriptome analysis reveals dynamic molecular maps of cambium differentiation in the primary and secondary growth of trees	<i>Populus</i>	10x Genomics single-cell transcriptomics
8	2023	<i>Plant Communications</i>	9.4	Transcriptional Landscape of Cotton Roots in Response to Salt Stress at Single-cell Resolution	Cotton roots	10x Genomics single-cell transcriptomics
9	2023	<i>Nature Communications</i>	14.7	Spatial transcriptomics uncover sucrose post-phloem transport during maize kernel development	<i>Maize kernel</i>	10x Genomics single-cell transcriptomics
10	2024	<i>Developmental Cell</i>	10.7	The soil emergence-related transcription factor PIF3 regulates root penetration by interacting with the receptor kinase FER	Arabidopsis	10x Genomics single-cell transcriptomics
11	2024	<i>eLife</i>	6.4	Root-specific secondary metabolism at the single-cell level: A case study of the metabolism and regulation in the roots of tea plants ( <i>Camellia sinensis</i> )	Tea roots	10x Genomics single-cell transcriptomics