



Your Science, Within Reach

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*Global Leaders in
Single-Cell and Spatial*

Empowering Discovery with Single-Cell and Spatial Transcriptomic Technologies



How Our Solutions Can Benefit Your Research



About Omics Empower

Omics Empower, a trusted provider of single-cell and spatial transcriptomics services since 2018, is dedicated to advancing scientific discovery with cutting-edge multi-omics technologies. With years of expertise, we empower researchers with high-quality solutions to tackle complex scientific challenges and drive innovation in lifesciences.

Our expertise in single-cell and spatial transcriptomics has been refined through over 17,000 single-cell experiments across more than 2,000 tissue types, contributing to over 370 scientific publications. This extensive experience has enabled us to decode the intricate cellular heterogeneity underlying various biological processes, driving breakthroughs in biomedical research and advancing our understanding of health and disease.

Article Count	Lab Exp	Sample Type
370+	17,000+	2,000+

We've partnered with top-tier omics platforms to offer comprehensive services that reveal intricate molecular mechanisms underlying various biological processes, including disease progression and cellular development. Our work has been recognized with high-impact publications, demonstrating groundbreaking insights into the dynamic molecular profiles of health and disease.

Omics Empower remains committed to advancing biomedical research by delivering robust, reliable research services to the global scientific community. **Join us in exploring the complexities of cellular function and molecular dynamics.**

Global Leaders in Single-Cell and Spatial

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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 transcriptomics, 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 cell. These systems enable precise mRNA analysis from single cells, revealing the intricacies of cellular heterogeneity and uncovering new cell types under various conditions.

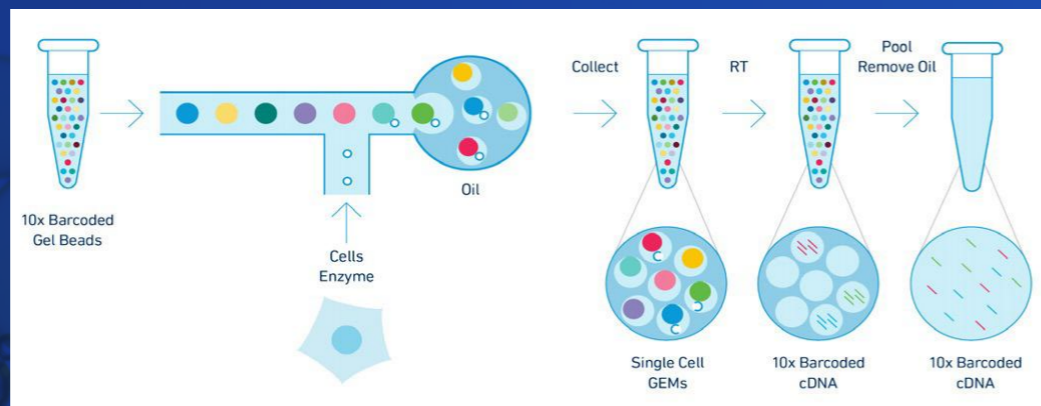
With our Omics Empower platform, we're not just sequencing cells, we're pioneering the future of cellular research, making groundbreaking discoveries accessible and intuitive for scientists spanning the globe.



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 10x Chromium 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

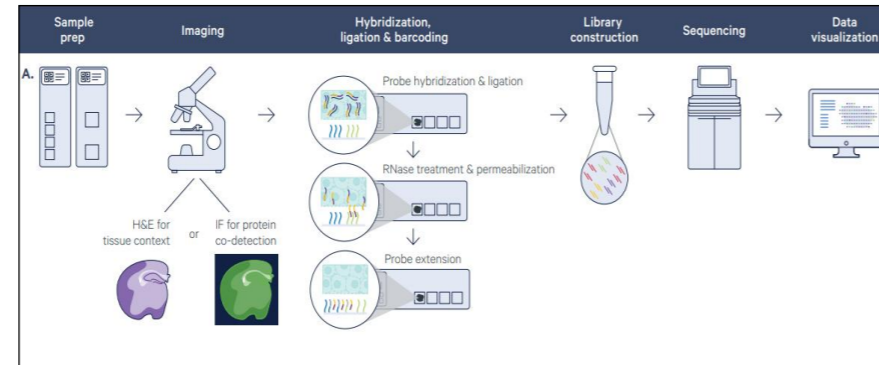
MobiVision software providing easy-to-use and informative data visualization and interpretation

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

Spatial 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 cell types within tissues, we introduce high-throughput spatial transcriptome sequencing technology. This innovative method preserves the spatial integrity of tissues while enabling precise transcriptional profiling of cells at various locations, offering profound insights into the complexity of tissue architecture.

For 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 10x Genomics)

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

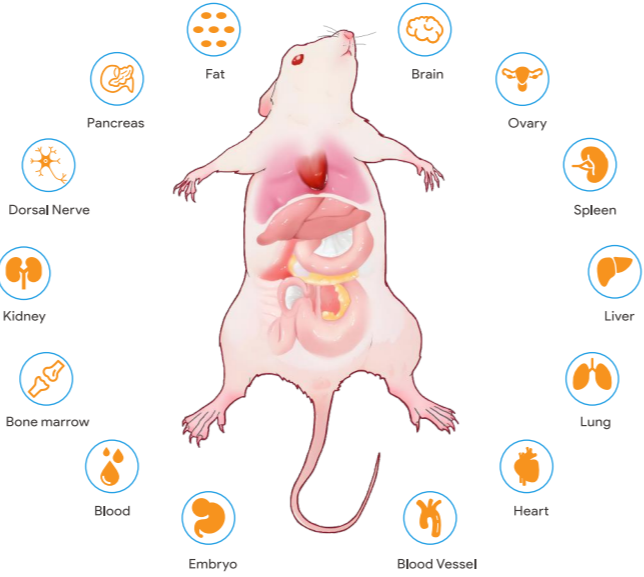
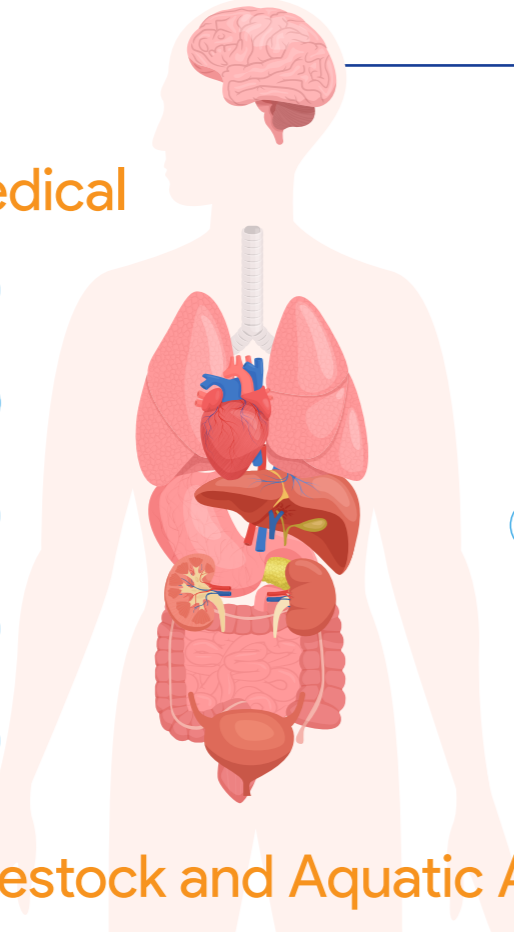
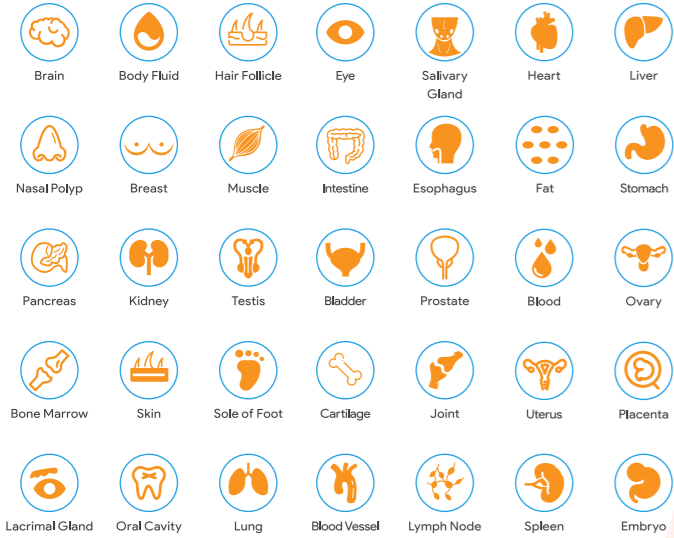


Bioinformatics Analysis

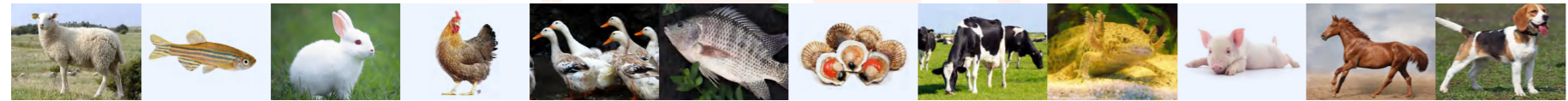
Focus on providing in-depth bioinformatics analysis to help you extract valuable biological insights from complex data.

Where Can It Be Used?

Applicable Fields - Medical



Applicable Fields - Livestock and Aquatic Animal



Accelerate Your Research!

Single-cell transcriptome platform



10x Chromium Controller



10x Chromium X



BD Rhapsody™Scanner



MobiNova®-100

Spatial transcriptome platform



10x Genomics Visium CytAssist



Tissue chips panoramic scanner



10x Genomics Xenium



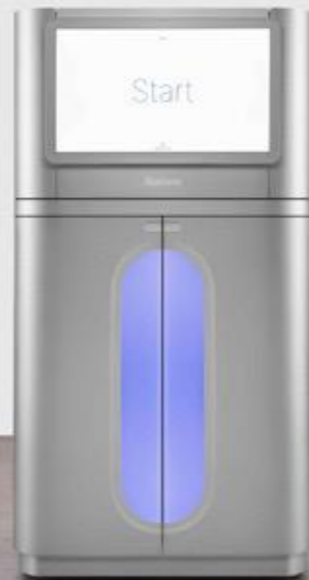
Stereo-seq microscope



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MGI DNBSEQ-T7

Illumina X plus



What Our Clients Have Published?

Global Leaders in
Single-Cell and Spatial

Progenitor-like exhausted SPRY1+ CD8+ T cell spotentiate responsiveness to neoadjuvant PD-1 blockade in esophageal squamous cell carcinoma

IF: 50.3

Published in: October 2023

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

Material:
Tumor samples from 14 ESCC patients before and after treatment.

Research background

Esophageal cancer is the seventh most common malignant tumor globally. In China, both the number of new cases and deaths each year account for more than half of the global total, imposing a significant disease burden. More than 90% of cases in China are esophageal squamous cell carcinoma (ESCC). Clinically, nearly 70% of ESCC patients are diagnosed at a locally advanced stage, where direct surgery alone yields poor outcomes. Therefore, the current standard treatment strategy for locally advanced esophageal cancer is a neoadjuvant approach, which involves administering chemoradiotherapy before planned surgery. However, the overall efficacy remains suboptimal, with 40% to 60% of patients experiencing recurrence after surgery, most commonly in the form of distant metastasis. Thus, there is a clinical need for more effective systemic neoadjuvant strategies to improve the survival prognosis of esophageal cancer patients.

In recent years, based on the results of several Phase III clinical trials, PD-1 inhibitors combined with chemotherapy have become the standard first-line treatment for advanced esophageal cancer. The application of immunotherapy has also gradually expanded to resectable esophageal cancer patients. There have been several domestic and international studies reporting the efficacy and safety of neoadjuvant immunotherapy in resectable locally advanced esophageal cancer. Among them, the pathological complete response rate (pCR) of neoadjuvant immunotherapy combined with chemotherapy in locally advanced ESCC patients ranges from 25% to 39.2%. However, this neoadjuvant immunotherapy strategy still faces challenges such as inconsistent patient response and unclear targets for improving benefits. Although PD-L1 expression is considered a theoretical biomarker for benefiting from immunotherapy (PD-1/PD-L1 inhibitors), there remains controversy in the international academic community regarding whether PD-L1 can effectively predict whether esophageal cancer patients will benefit from immunotherapy. Therefore, there is a need to seek more reliable biomarkers for immunotherapy efficacy.

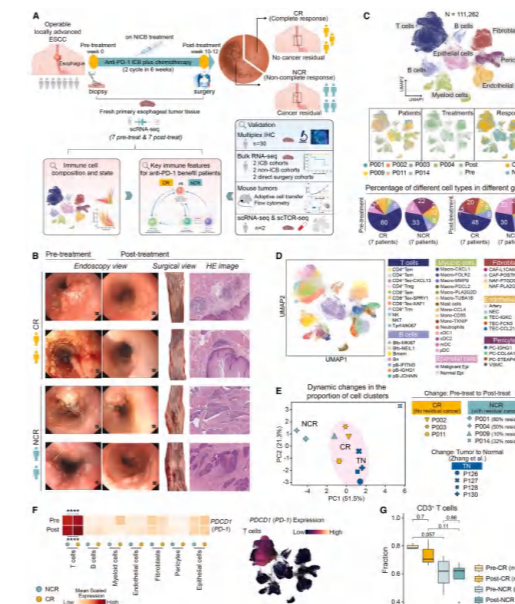


Fig 1. Cytological overview of esophageal squamous cell carcinoma before and after immunotherapy.

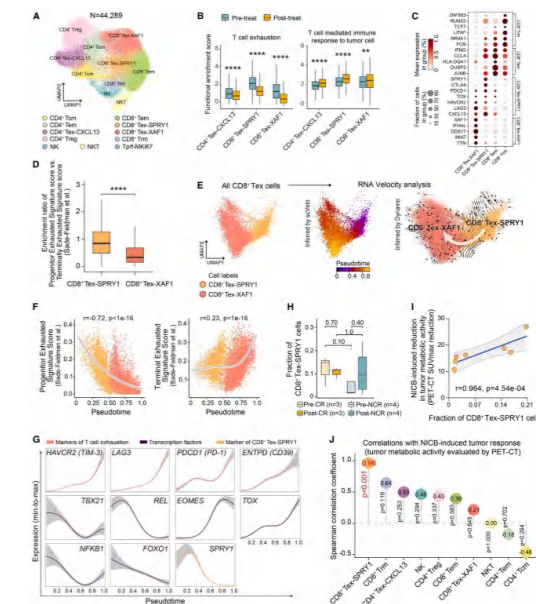


Fig 2. Identification of precursor exhausted cell-like CD8+ Tex

Eosinophils promote pulmonary matrix destruction and emphysema via Cathepsin L

IF: 40.8

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

Published in: October 2023

Material:
Mouse emphysema tissue model

Research background

Chronic obstructive pulmonary disease (COPD) is a widely prevalent disease globally, with emphysema and small airway disease being the main characteristics of COPD. Studies using various elastase perfusion models have shown that repeated exposure to elastase significantly induces eosinophilia and subsequent emphysematous changes in the lungs. Moreover, many studies using smoking-induced murine COPD models have also found that the increased expression of matrix metalloproteinases (MMPs) in macrophages and the role of cathepsin S (CTSS) in neutrophil-related COPD are crucial for the development of emphysema. In addition, therapies targeting Th2 or eosinophilic inflammation, such as interleukin (IL)-5 and IL-33/ST2, have been beneficial for COPD patients. However, monoclonal antibodies targeting the IL-5 receptor do not alleviate disease exacerbations. Compared to other eosinophil-related diseases such as asthma, the exact role of eosinophils in the pathophysiology of COPD has not been fully understood, while the exact role of eosinophils in asthma is still under investigation.

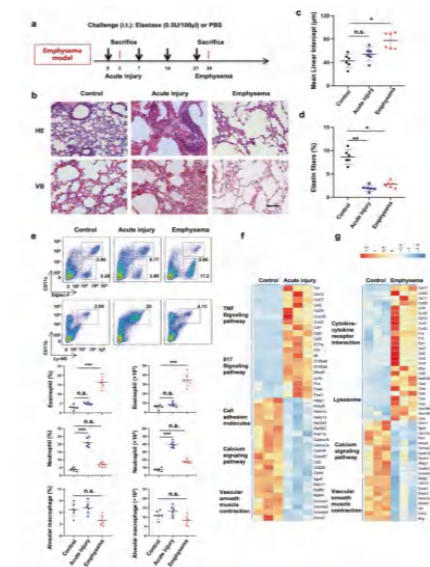


Fig. 1. Eosinophil aggregation in chronic elastase-induced emphysema

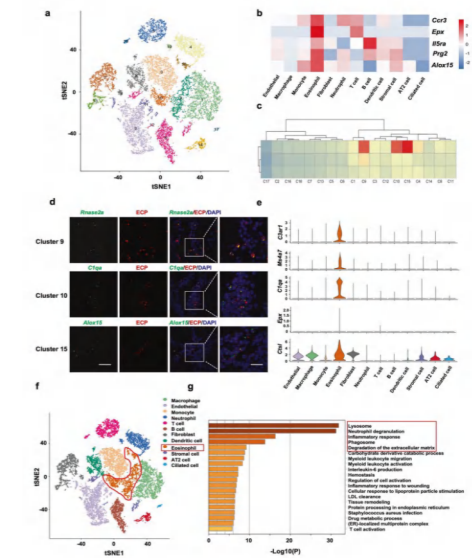


Fig 2. Characteristics of lung cell subpopulations

Partial List of Articles

No.	Year of Publication	Journal	Impact Factor	Article Title	Sample Type	Applied Technology
1	2024	<i>Advanced Materials</i>	29.4	Neutrophil Membrane-Camouflaged Polyprodrug Nanomedicine for Inflammation Suppression in Ischemic Stroke Therapy	Brain tissue	Single-cell RNA sequencing
2	2023	<i>Cancer Cell</i>	50.3	Progenitor-like exhausted SPY1+ CD8+ T cells potentiate responsiveness to neoadjuvant PD-1 blockade in esophageal squamous cell carcinoma	Esophageal cancer	Single-cell RNA sequencing immune repertoire
3	2023	<i>Signal Transduction and Targeted Therapy</i>	39.3	Eosinophils promote pulmonary matrix destruction and emphysema via Cathepsin L	Lung tissue	Single-cell RNA sequencing
4	2023	<i>Cancer Discovery</i>	38.3	Targeting Microglial Metabolic Rewiring Synergizes with Immune Checkpoint Blockade Therapy for Glioblastoma	Brain-sorted CD45+ cells	Single-cell RNA sequencing
5	2023	<i>Cell Host & Microbe</i>	30.3	Bacteroides methylmalonyl-CoA mutase produces propionate that promotes intestinal goblet cell differentiation and homeostasis	Colon tissue	Single-cell RNA sequencing

No.	Year of Publication	Journal	Impact Factor	Article Title	Sample Type	Applied Technology
6	2023	<i>Cell Metabolism</i>	29.0	Bone marrow immune cells respond to fluctuating nutritional stress to constrain weight regain	<i>Bone marrow</i>	Single-cell RNA sequencing
7	2023	<i>Molecular Plant</i>	27.5	Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in <i>Gossypium bickii</i>	<i>Lobe</i>	Single-cell RNA sequencing
8	2023	<i>Nature Communications</i>	16.6	Spatial transcriptomics uncover sucrose post-phloem transport during maize kernel development	<i>Corn kernel</i>	Spatial transcriptome sequencing
9	2024	<i>Nature Biotechnology</i>	46.9	Decoder-seq enhances mRNA capture efficiency in spatial RNA sequencing	<i>Olfactory bulb</i>	Spatial transcriptome sequencing
10	2024	<i>Nature Genetics</i>	30.8	Multi-omic profiling of clear cell renal cell carcinoma identifies metabolic reprogramming associated with disease progression	<i>Clear cell renal cell carcinoma</i>	Spatial transcriptome sequencing
11	2024	<i>International Journal of Surgery</i>	15.3	In situ tissue profile of rat trigeminal nerve in trigeminal neuralgia using spatial transcriptome sequencing	<i>Trigeminal nerve tissue</i>	Spatial transcriptome sequencing