

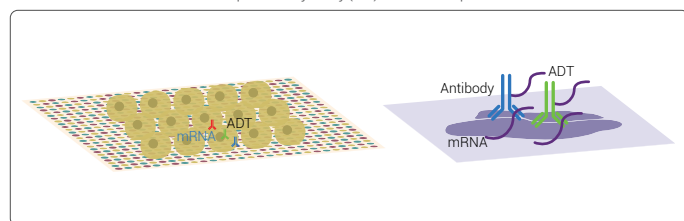
Stereo-CITE V1.1 Proteo-Transcriptomics Solution for Protein & RNA Co-Analysis

The Stereo-CITE Proteo-Transcriptomics Set enables simultaneous *in situ* detection of the whole transcriptome and 100+ proteins on the same tissue section – all with subcellular resolution. By integrating high-plex protein profiling with unbiased transcriptomics in a single experiment, Stereo-CITE empowers researchers to decode cellular phenotypes, interactions, and tissue architecture with unprecedented depth and clarity.

Technology Principle

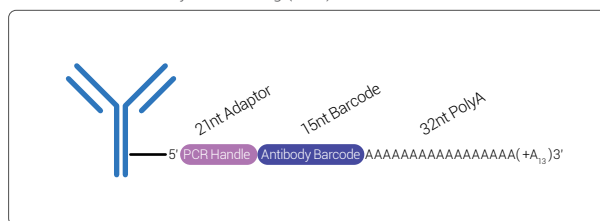
Utilizing the ultra-high resolution of Stereo-seq, Stereo-CITE combines Cellular Indexing of Transcriptomes and Epitopes by Sequencing (CITE-seq) with the Stereo-seq workflow. It captures mRNA and antibody-derived tags (ADTs) at nanoscale resolution across a centimeter-scale field of view. Through a streamlined “tissue-to-data” workflow, the system delivers spatial maps of transcriptome and protein expression via sequencing and visualization.

a. mRNA and ADT are both captured by Poly(dT) on the chip



More information: Liao S, Heng Y, Liu W, et al. Integrated Spatial Transcriptomic and Proteomic Analysis of Fresh Frozen Tissue Based on Stereo-seq [J].BioRxiv, 2023. doi: 10.1101/2023.04.28.538364.

b. Structure of antibody-derived tag (ADT)



Totalseq™A antibody-oligonucleotide conjugate.

Application Directions



Organ heterogeneity studies

01



Target discovery and drug development

02



Tumor microenvironment research

03



Immunotherapy

04

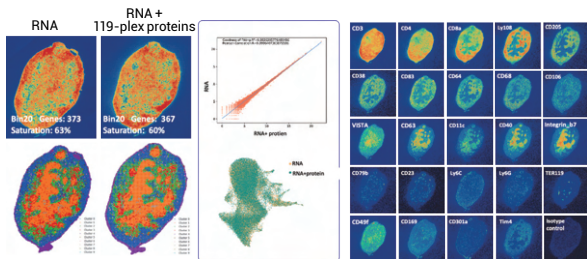
Product Highlights



Spatial *in situ* multi-omics

01

Unbiased spatial profiling of the whole transcriptome and hundreds of protein markers on the same tissue section.



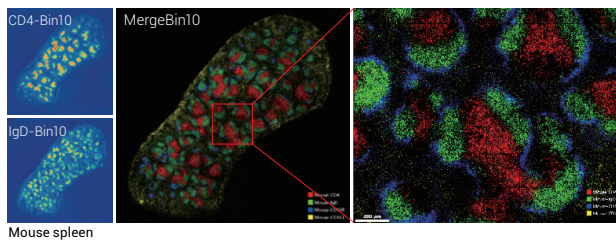
*Mouse thymus was used
*TotalSeq™-A Mouse Universal Cocktail V1.0 (Biolegen, Cat. No. 199901)



High Resolution

02

Subcellular resolution for both transcriptome and protein analysis.



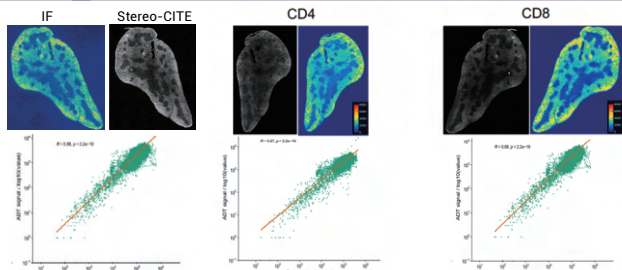
Mouse spleen



High Specificity

03

Same section correlation analysis showed a high correlation between spatial protein distribution and protein fluorescence signals from immunofluorescence staining.



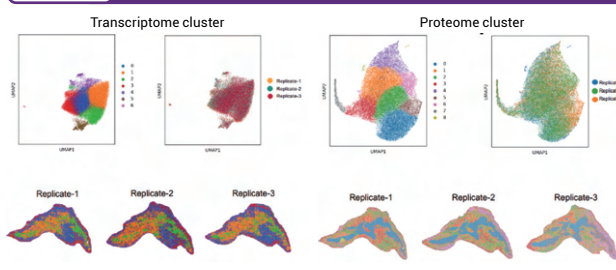
Mouse thymus



Reliable

04

Consistency analysis of three adjacent sections demonstrated good consistency between transcriptome and protein distributions.



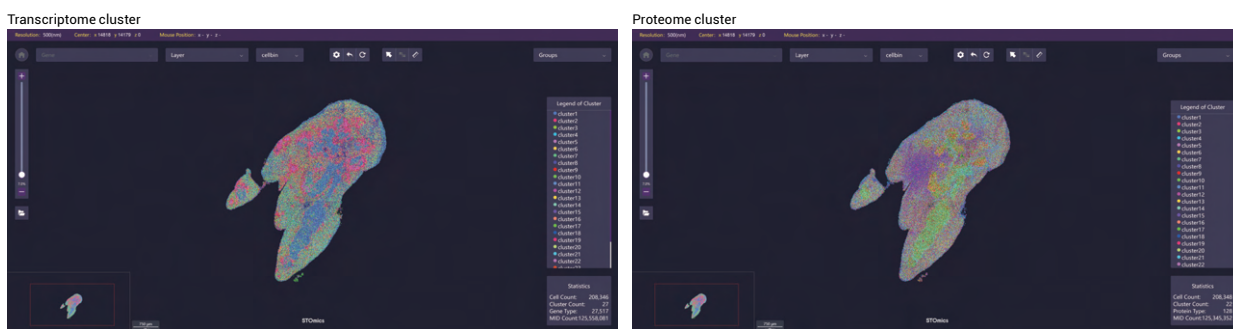
Mouse thymus



Robust bioinformatic analysis pipeline

05

Deliver spatial maps of transcriptome and protein expression via sequencing and visualization



Demo Data

Applications of Stereo-CITE in the multi-omics study of human paracancer lymph nodes

*Unpublished research data, not for citation

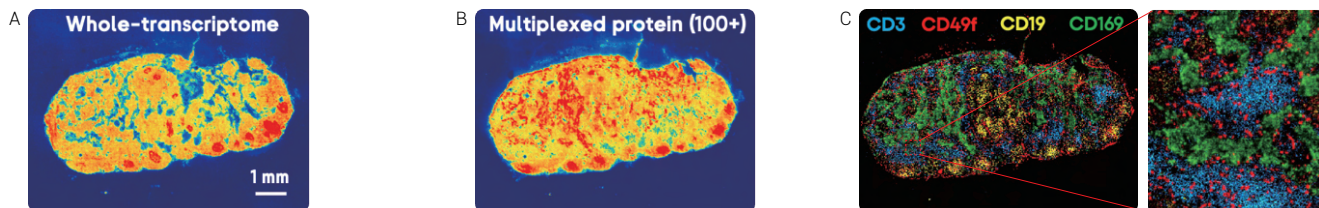
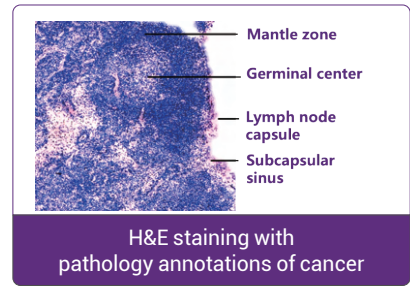
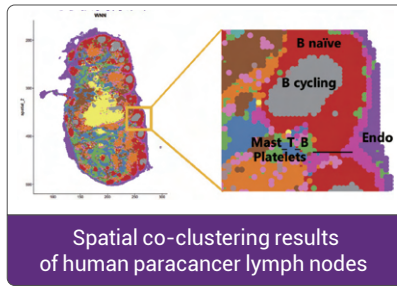
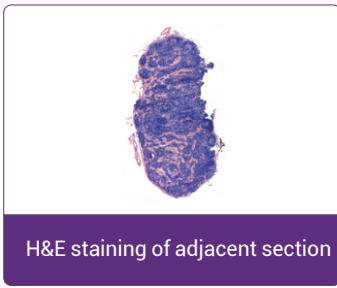


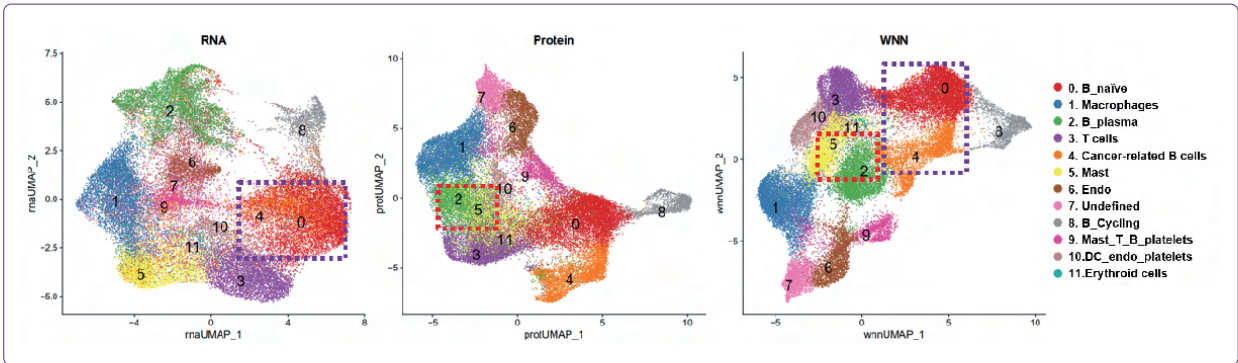
Fig 1 A. Human paracancer lymph nodes spatial gene expression profile at Bin20 (~10µm) B. Human paracancer lymph nodes spatial protein expression profile at Bin20 (~10µm). C. Pseudo-color image of 4 selected protein expressions.

Stereo-CITE recapitulated the organizational structure of human lymph nodes

The figure below shows the comparison of the spatial co-clustering results with the H&E-stained image of adjacent sections. It was found that the multi-omics spatial co-clustering results perfectly recapitulated the tissue structure of the lymph nodes, which is highly consistent with prior biological and histological knowledge.

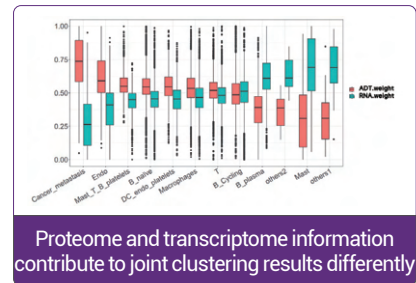
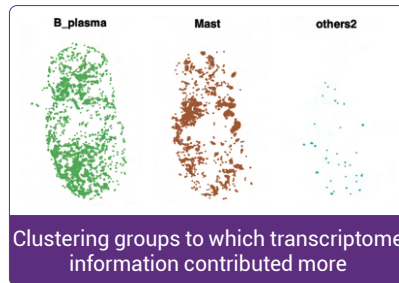
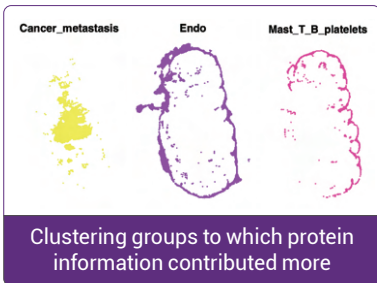


The figure below shows the comparison of the spatial co-clustering results with the H&E-stained image of adjacent sections. It was found that the multi-omics spatial co-clustering results perfectly recapitulated the tissue structure of the lymph nodes, which is highly consistent with prior biological and histological knowledge.



Joint analysis of RNA and protein information provides more accurate spatial clustering

Protein and transcriptional information contribute to the clustering results differently. Statistical diagram demonstrated that proteomic information plays a key role in grouping cancer metastatic related cells, endothelial cells, mast cells and others, where transcriptome information is the main contribution in the cell type identification of B_plasma and Mast groups.

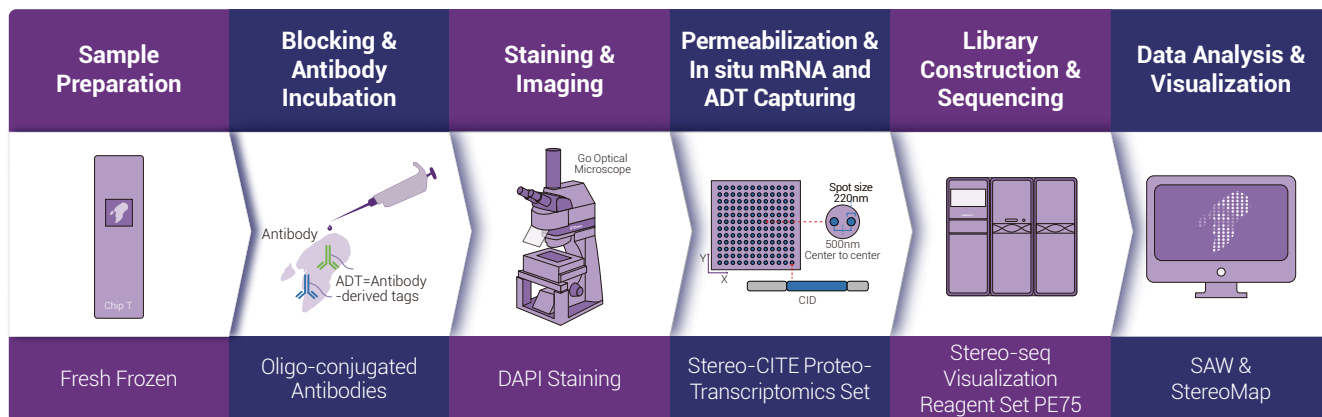


Validated Tissue Types

| Human | | | Mouse |
|-------------|-----------------|-------------------|-------------------|
| Tissue type | | | Tissue type |
| Lung cancer | Lymph node | Esophageal cancer | Esophageal cancer |
| Tonsil | Cervical cancer | Colon cancer | Spleen |
| Thymus | Lymphoma | Renal cancer | Liver |
| Esophagus | Gastric cancer | | |

*More sample types are being adapted and will be added to the list.

Stereo-CITE Workflow



Ordering Information

| Catalog Number | Set Name | Specifications | Version | Description |
|----------------|--|----------------|---------|--|
| 211SP11118 | Stereo-seq Permeabilization Set for Chip-on-a-slide V1.1 | 8 RXN | V1.1 | For determining permeabilization parameters to optimize mRNA capture. |
| 211PT11114 | Stereo-CITE Proteo-Transcriptomics Set V1.1 | 4 RXN | V1.1 | For generating a spatially-resolved 3' mRNA library and ADT (protein) library from the same biological tissue sections. |
| 212KA11114 | Stereo-seq Protein Assisted Kit | 4 RXN | V1.1 | This accessory kit provides additional reagents required for proteo- transcriptomic workflows and is included in the Stereo-CITE Proteo-Transcriptomics Set V1.1. Can be ordered separately. |
| 111KL160 | Stereo-seq 16 Barcode Library Preparation Kit | 16 RXN | V1.0 | Designed for library preparation of samples using Stereo-seq technology, enables the addition of sample barcodes and library construction. |
| 301AUX001 | Stereo-seq PCR Adaptor | 2 EA | / | Compatible with PCR thermal cycler as a heating unit. |

Resources

User manuals and documentations:

<https://en.stomics.tech/resources/documents/list.html?types=Stereo-CITE%20Solution%20V1.1>

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Website: <https://en.stomics.tech/>



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