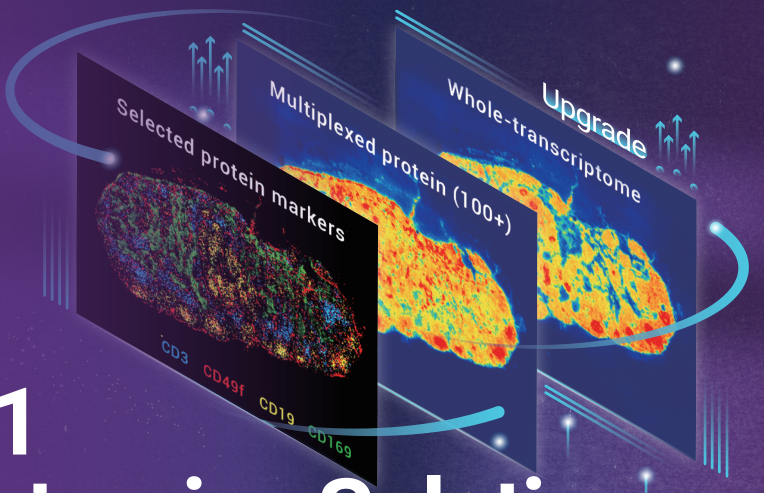
STOmics



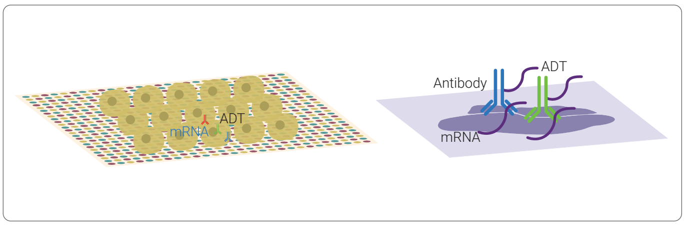
Stereo-CITE V1.1 Proteo-Transcriptomics Solution for Protein & RNA Co-Analysis

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 single-cell 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

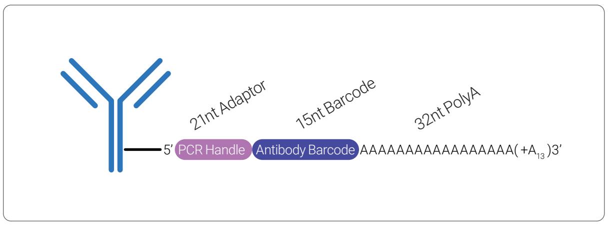
Utilizing the ultra-high resolution of Stereo-seq, Stereo-CITE combines Cellular Indexing of Transcriptomes and Epitopes by Sequencing (CITE-seq) with the Stereo-seq workflow. It captures mRNA and antibody-derived tags (ADTs) at nanoscale resolution across a centimeter-scale field of view. Through a 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

01 Organ heterogeneity studies

02 Target discovery and drug development

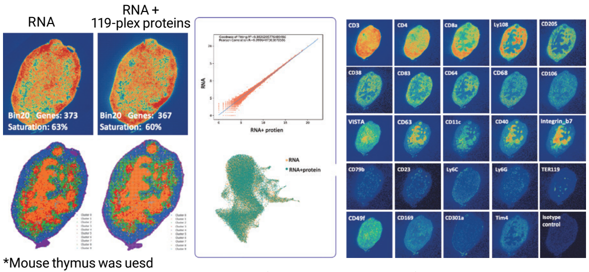
03 Tumor microenvironment research

04 Immunotherapy

Product Highlights

01 Spatial *in situ* multi-omics

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

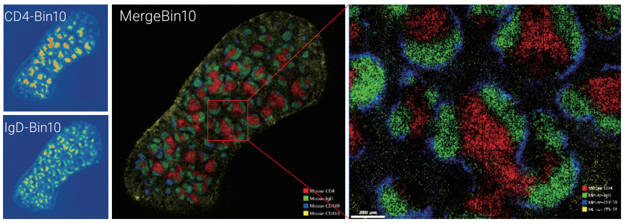


*Mouse thymus was uesd

*TotalSeq^{TM}-A Mouse Universal Cocktail,V1.0(Biolegen,Cat. No. 199901)

02 High Resolution

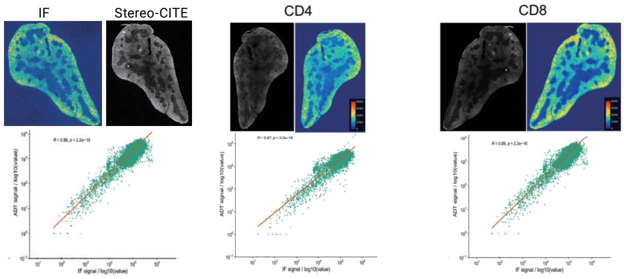
Subcellular resolution for both transcriptome and protein analysis.



Mouse spleen

03 High Specificity

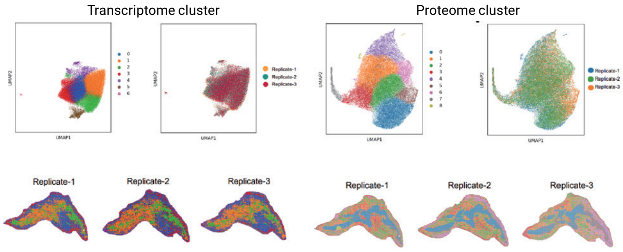
Same section correlation analysis showed a high correlation between spatial protein distribution and protein fluorescence signals from immunofluorescence staining.



Mouse thymus

04 Reliable

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

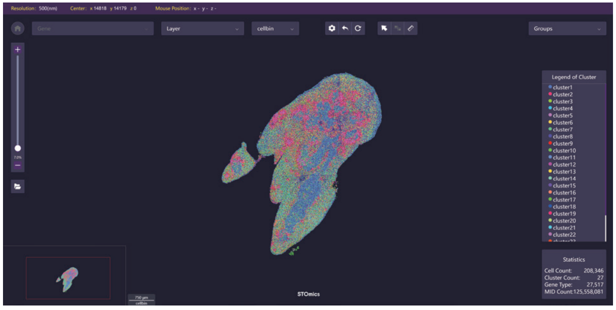


Mouse thymus

05 Robust bioinformatic analysis pipeline

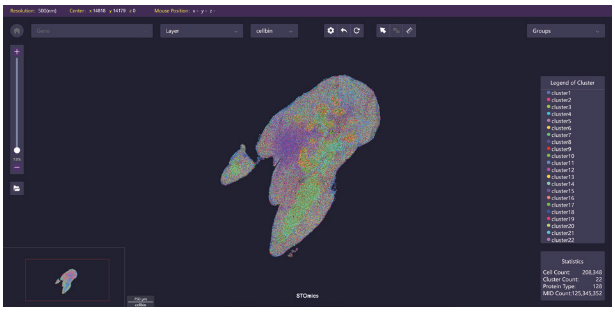
Deliver spatial maps of transcriptome and protein expression via sequencing and visualization

Transcriptome cluster



Statistics
Cell Count: 208,346
Cluster Count: 27
Gene Type: 27,517
MID Count:125,558,081

Proteome cluster



Statistics
Cell Count: 208,348
Cluster Count: 22
Protein Type: 128
MID Count:125,345,352

Demo Data

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

*Unpublished research data, not for citation

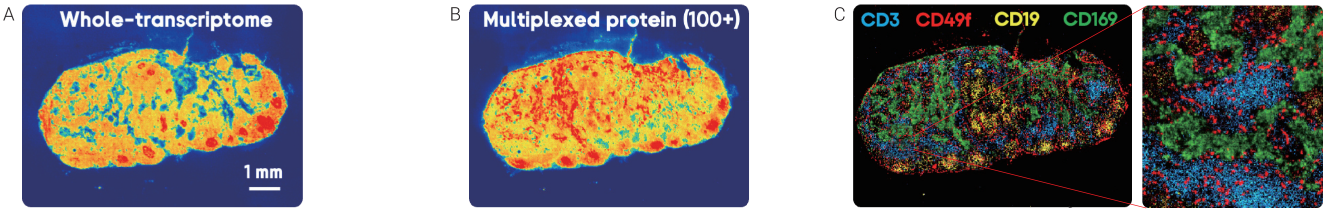
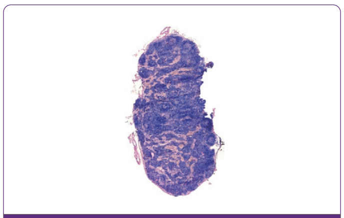


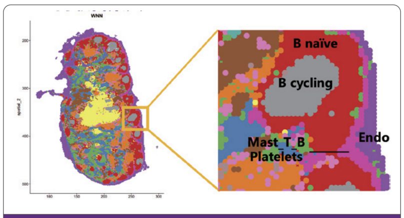
Fig 1 A. Human paracancer lymph nodes spatial gene expression profile at Bin20 (~10μm) B. Human paracancer lymph nodes spatial protein expression profile at Bin20 (~10μm). C. Pseudo-color image of 4 selected protein expressions.

Stereo-CITE recapitulated the organizational structure of human lymph nodes

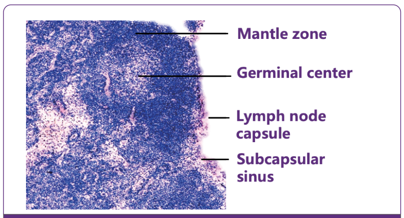
The figure below shows the comparison of the spatial co-clustering results with the H&E-stained image of adjacent sections. It was found that the multi-omics spatial co-clustering results perfectly recapitulated the tissue structure of the lymph nodes, which is highly consistent with prior biological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



H&E staining of adjacent section

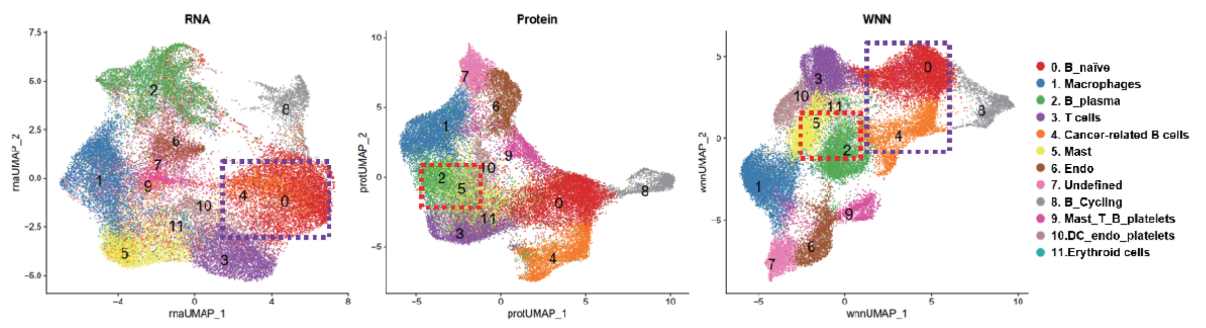


Spatial co-clustering results
of human paracancer lymph nodes



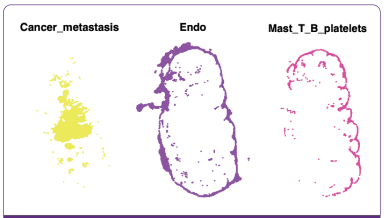
H&E staining with
pathology annotations of cancer

The joint analysis of RNA and protein information effectively distinguished Cluster 0 and 4, Cluster 2 and 5, which remain indistinguishable through RNA and protein-only clustering approaches. Stereo-CITE exemplifies the advantages of combining diverse omics data to achieve a more comprehensive understanding of biological systems.

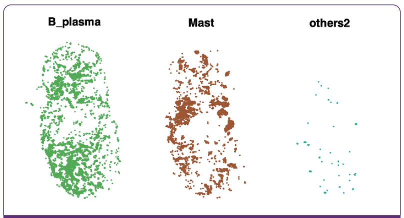


Joint analysis of RNA and protein information provides more accurate spatial clustering

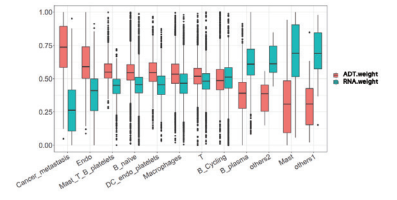
Protein and transcriptional information contribute to the clustering results differently. Statistical diagram demonstrated that proteomic information plays a key role in grouping cancer metastatic related cells, endothelial cells, mast cells and others, where transcriptome information is the main contribution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



Clustering groups to which protein
information contributed more



Clustering groups to which transcriptome
information contributed more



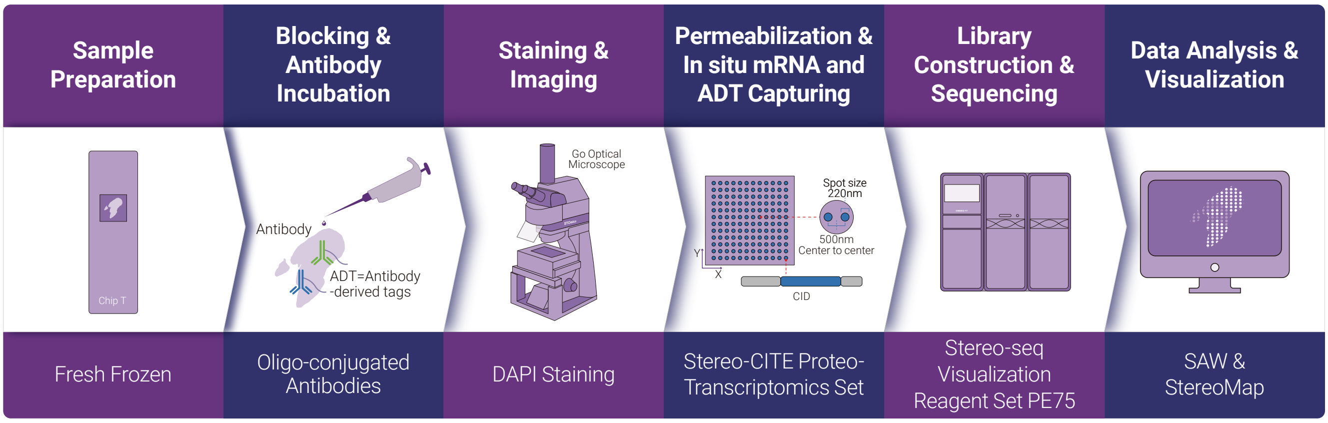
Proteome and transcriptome information
contribute to joint clustering results differently

Validated Tissue Types

<table>
<tr><th colspan="6">Human</th><th>Mouse</th></tr>
<tr><th colspan="6">Tissue type</th><th>Tissue type</th></tr>
<tr><td colspan="2">Lung cancer</td><td colspan="2">Lymph node</td><td colspan="2">Esophageal cancer</td><td>Esophageal cancer</td></tr>
<tr><td colspan="2">Tonsil</td><td colspan="2">Cervical cancer</td><td colspan="2">Colon cancer</td><td>Spleen</td></tr>
<tr><td colspan="2">Thymus</td><td colspan="2">Lymphoma</td><td colspan="2">Renal cancer</td><td>Liver</td></tr>
<tr><td colspan="3">Esophagus</td><td colspan="3">Gastric cancer</td><td></td></tr>
</table>

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

Stereo-CITE Workflow



Sample Preparation	Blocking & Antibody Incubation	Staining & Imaging	Permeabilization & In situ mRNA and ADT Capturing	Library Construction & Sequencing	Data Analysis & Visualization
Fresh Frozen	Oligo-conjugated Antibodies	DAPI Staining	Stereo-CITE Proteo-Transcriptomics Set	Stereo-seq Visualization Reagent Set PE75	SAW & StereoMap

Ordering Information

Catalog Number	Catalog Number (US use only)	Set Name	Specifications	Version	Description
211SP11118	211SP11118-CG	Stereo-seq Permeabilization Set for Chip-on-a-slide V1.1	8 RXN	V1.1	For determining permeabilization parameters to optimize mRNA capture.
211PT11114	211PT11114-CG	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	212KA11114-CG	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.
111KL11160	111KL11160-CG	Stereo-seq 16 Barcode Library Preparation Kit	16 RXN	V1.1	Designed for library preparation of samples using Stereo-seq technology, enables the addition of sample barcodes and library construction.
301AUX001	301AUX001-CG	Stereo-seq PCR Adaptor	2 EA	/	Compatible with PCR thermal cycler as a heating unit.

Resources

Visit https://en.stomics.tech/ to start your spatial journey.

Manufactured by

STOmics

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

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