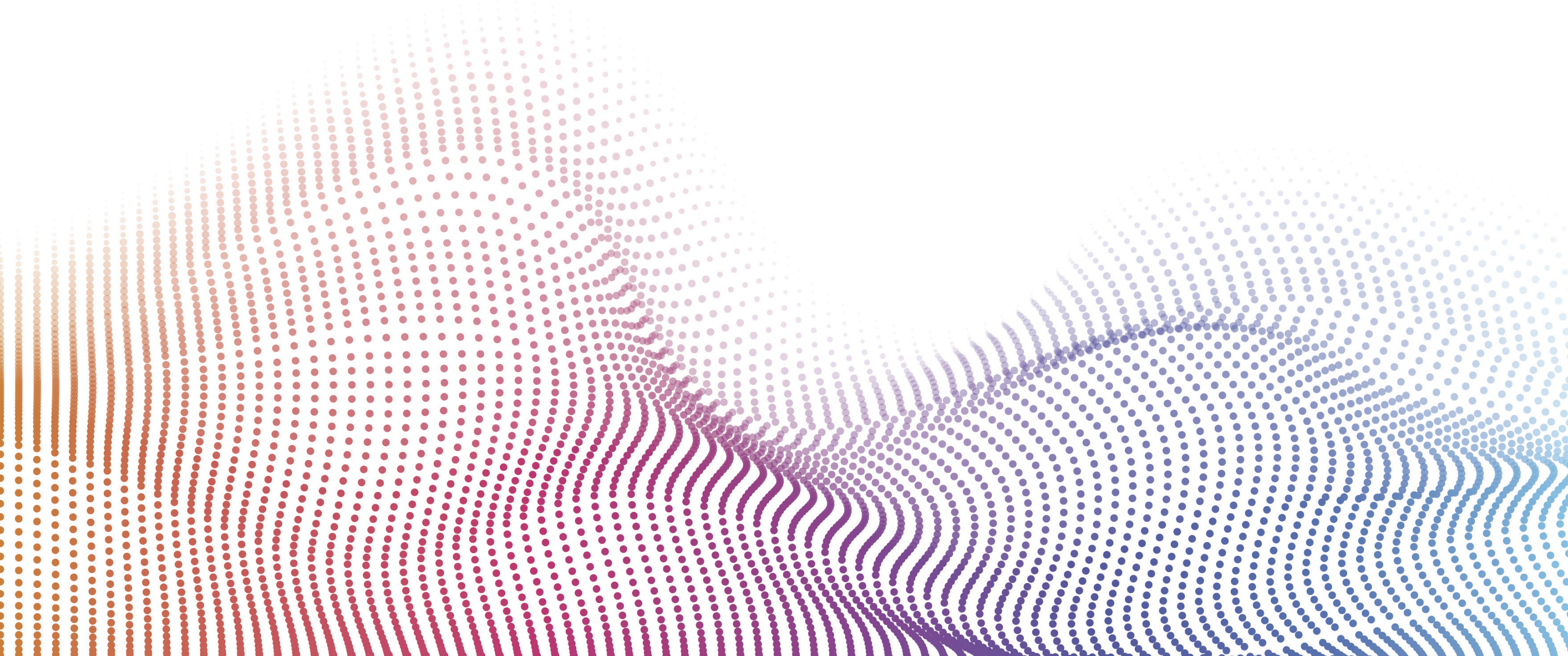
STOmics | MGI

STOmics

Stereo-CITE Product Note



Simultaneously characterizes hundreds of proteins along with expressed RNA to facilitate multi-omics study, cell phenotyping and biologically relevant mechanisms.

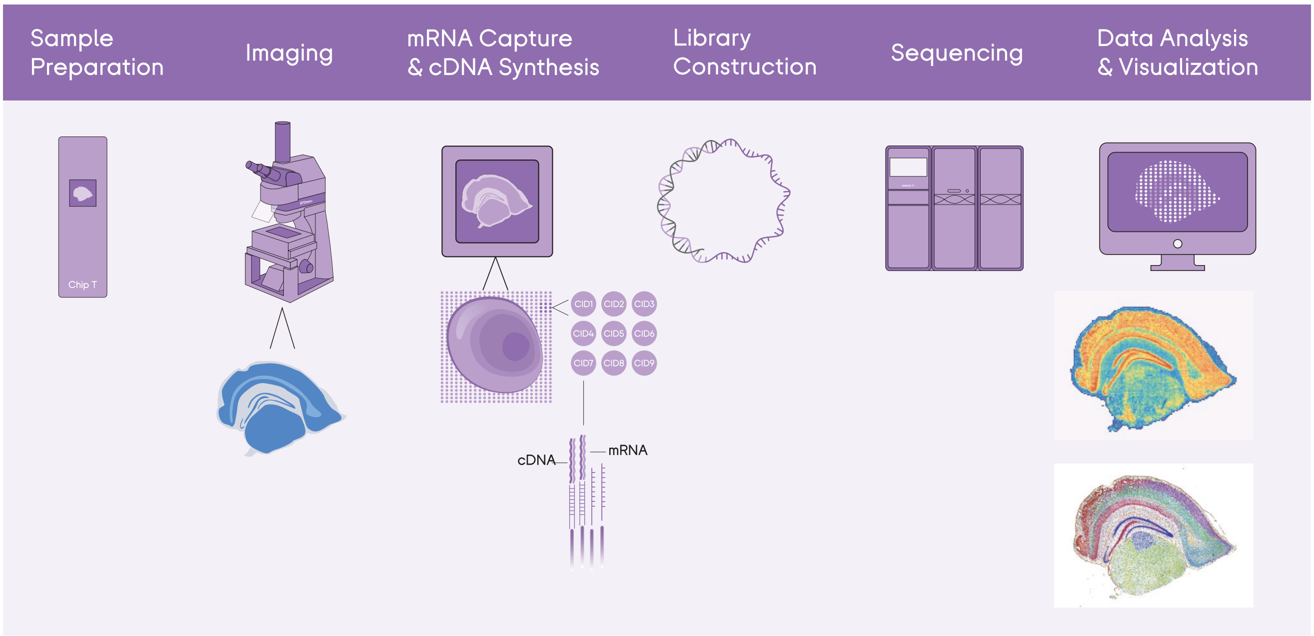
01 Stereo-CITE Proteo-Transcriptomics solution for Protein & RNA co-analysis

Combined with Cellular Indexing of Transcriptomes and Epitopes by Sequencing (CITE-seq), STOmics Stereo-CITE Proteo-Transcriptomics Set is intended for simultaneous detection of the whole transcriptome and high-plex protein on the same tissue section. Built upon DNA Nanoball (DNB) technology, STOmics Stereo-CITE Proteo-Transcriptomics Set enables a "tissue-to-data" solution through *in situ* capture of the whole transcriptome, at nanoscale resolution and centimeter-sized Field of View (FOV). The Stereo-seq Chip T (poly-T-based chip) is loaded with capture probes containing spatial coordinate information. Through a series of biochemical processes, the probes can capture mRNA molecules and antibody-derived tags (ADTs) *in situ* within the tissue, perform cDNA synthesis, and obtain transcriptome plus multi-protein spatial distribution information of the entire tissue through sequencing and a complementary visualization platform.

The advanced bioinformatics analysis tools now perform a comprehensive analysis of proteome and transcriptome. This feature enables researchers to profile spatial expression maps of both the whole transcriptome and multi-plex proteins on the same section at a large field-of-view. Stereo-CITE facilitates the study of tissue heterogeneity and associated biological significance in complex (disease) tissues, leading to a broader understanding of spatial omics studies.

02 Application highlights

- **Spatial in situ multi-omics**
  Unbiased spatial profiling of whole transcriptome and hundreds of protein markers on the same tissue section.
- **High Resolution**
  Subcellular resolution for both transcriptome and protein analysis.
- **High-plex protein detection**
  High detection efficiency of 100+ plex proteins with antibody combinations of your choice from in-house validated vendor.
- **Spatial protein profiling via high-throughput sequencing**
  No auto-fluorescence interference or antigen instability caused by multiple rounds of detection.



Sample Preparation | Imaging | mRNA Capture & cDNA Synthesis | Library Construction | Sequencing | Data Analysis & Visualization

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

03 Characterizing spatial gene expression profile on histology images

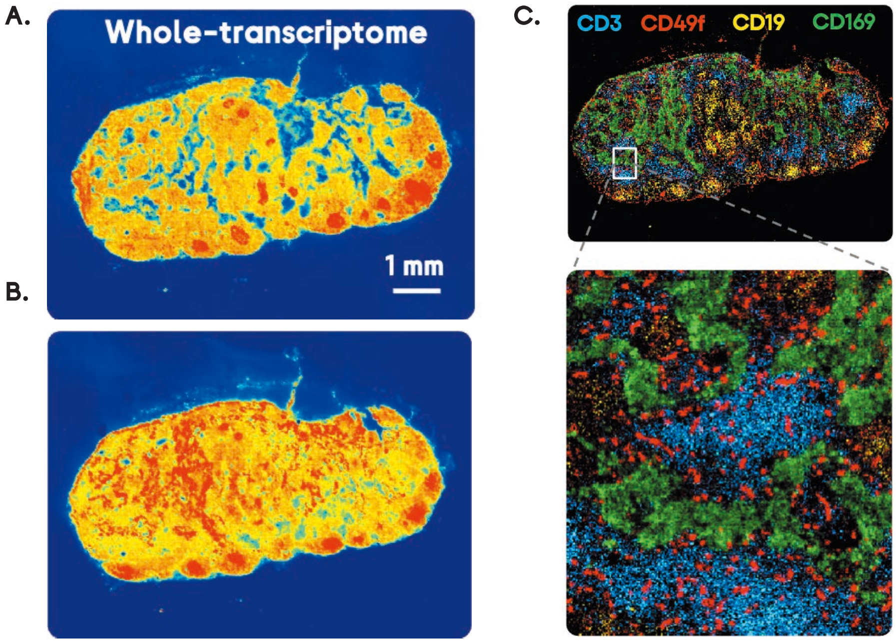
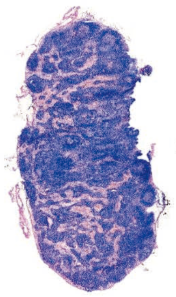


Figure 1.
A. Human paracancer lymph nodes spatial gene expression profile at Bin20 (~10μm)
B. Human paracancer lymph nodes spatial protein expression profile at Bin20 (~10μm).
C. Pseudo-color image of 4 selected protein expressions.

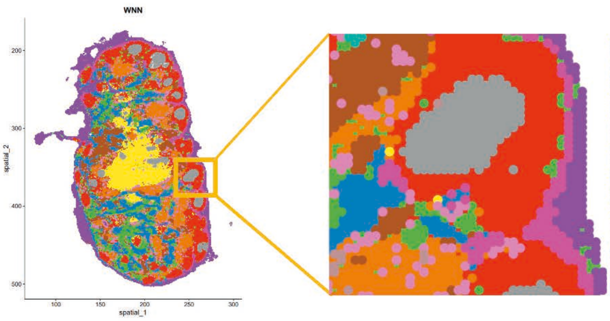
04 Stereo-CITE recapitulated the organizational structure of human lymph nodes

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. It was observed that the mantle area was composed of mainly naive B cells, the germinal center was composed of mainly cycling B cells, the capsule was composed of mainly endothelial cells, and the subcapsular sinus was composed of mainly mast cells, T cells, B cells, and platelets, which is highly consistent with prior biological and histological knowledge.

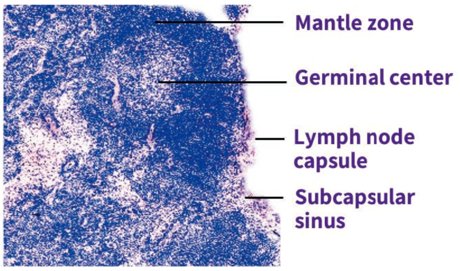
H&E staining of adjacent section



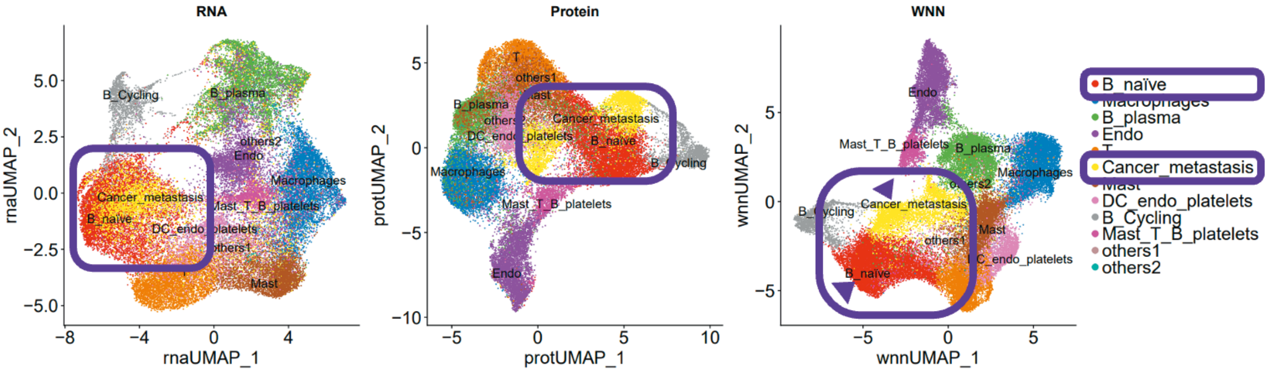
Spatial co-clustering results of human paracancer lymph nodes



H&E staining with pathology annotations of cancer

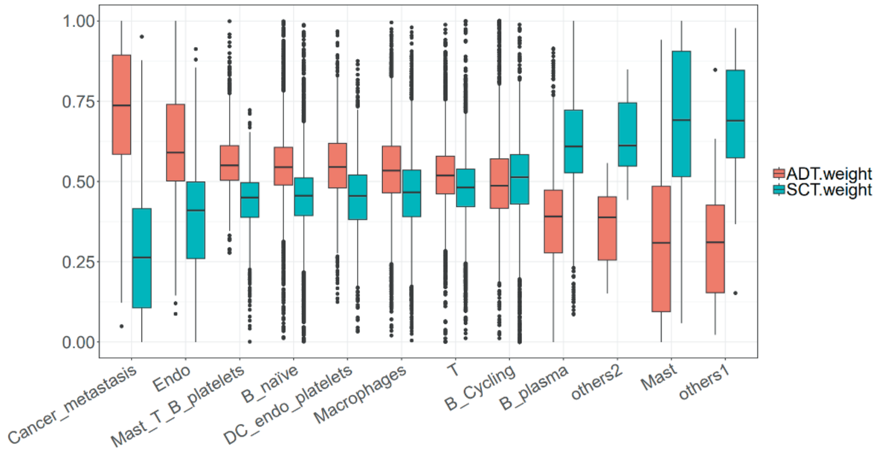


Co-clustering proves to be an effective approach for the integration of multiple omics analyses. Specifically, the method enables a clear separation of the red and yellow clusters, which remain indistinguishable through RNA and protein-only clustering approaches. Stereo-CITE exemplifies the advantages of combining diverse omics data to achieve a more comprehensive understanding of biological systems.

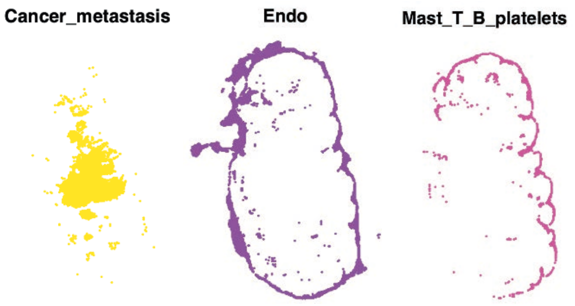


05 Joint analysis of RNA and protein information provides more accurate spatial clustering

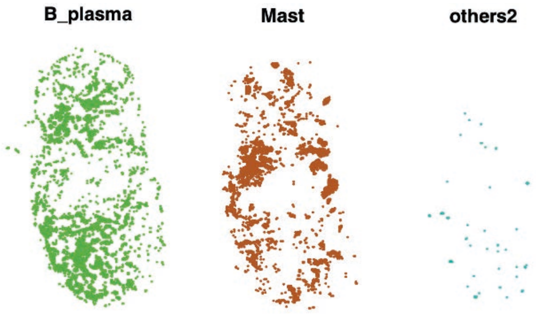
Protein and transcriptional information contribute to the clustering results differently. Statistical diagram demonstrated that proteomic information plays a key role in grouping cancer metastatic related cells, endothelial cells, mast cells and others, where transcriptome information is the main contribution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



Proteome and transcriptome information contribute to joint clustering results differently



Clustering groups to which protein information contributed more



Clustering groups to which transcriptome information contributed more

Stereo-seq's multi-omics solutions bring greater possibilities and less effort to gaining research insights

06 Product Reagents

Stereo-seq Permeabilization Set for Chip-on-a-slide

Part Number	Product		Specification	Description
211SP118	Stereo-seq Permeabilization Kit	111KP118	8 RXN	For determining permeabilization parameters to optimize mRNA capture
	Stereo-seq Chip P Slide (1cm*1cm)	210CP118	8 EA	
	STOmics Accessory Kit	1000033700	5 PCS	

Stereo-CITE Proteo-Transcriptomics Set

Part Number	Product		Specification	Description
211PT114	Stereo-seq Transcriptomics T Kit	111KT114	4 RXN	For generating a spatially-resolved 3' mRNA library and ADT (protein) library from the same biological tissue sections
	Stereo-seq Chip T Slide (1cm*1cm)	210CT114	4 EA	
	STOmics Accessory Kit	1000033700	5 PCS	
	Stereo-seq Protein Assisted Kit	212KA114	4 RXN	

Stereo-seq Library Preparation Kit

Part Number	Product	Specification	Description
111KL114	Stereo-seq Library Preparation Kit	4 RXN	For constructing STOmics Library

Stereo-seq 16 Barcode Amplification Kit, 16 RXN

Part Number	Product	Specification	Description
111KB016	Stereo-seq 16 Barcode Amplification Kit, 16 RXN	16 RXN	16 barcode kit for preparing for and constructing of Stereo-CITE libraries.

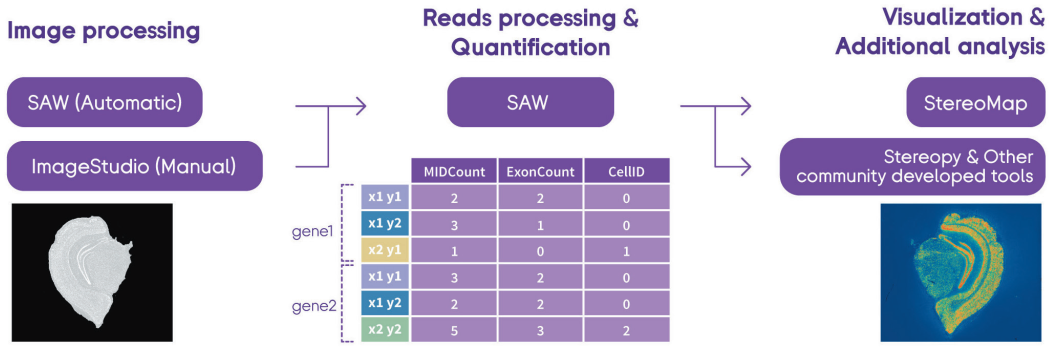
Stereo-seq PCR Adaptor

Part Number	Product	Specification	Description
301AUX001	Stereo-seq PCR Adaptor	2 EA	Compatible with PCR thermal cycler as a heating unit

User manuals and documentations: **https://en.stomics.tech/resources/sop**

07 Intuitive Software Pipelines and Suits

ImageStudio image processing software, **SAW** (Stereo-seq Analysis Workflow) and **StereoMap** visualizaiton platform are offered free of charge to users and enables them to discover spatial biology knowledge with multiplexed tissue images.



		MIDCount	ExonCount	CellID
gene1	x1 y1	2	2	0
	x1 y2	3	1	0
	x2 y1	1	0	1
gene2	x1 y1	3	2	0
	x1 y2	2	2	0
	x2 y2	5	3	2

Learn more:
https://en.stomics.tech/BioinfoTools

Version : June 2024

Reach out to us to learn more:

Web: en.mgi-tech.com

Email: MGI-service@mgi-tech.com