Now providing a more accurate tissue phenotyping and spatial heterogeneity characterization solution for pathological tissues with Stereo-seq
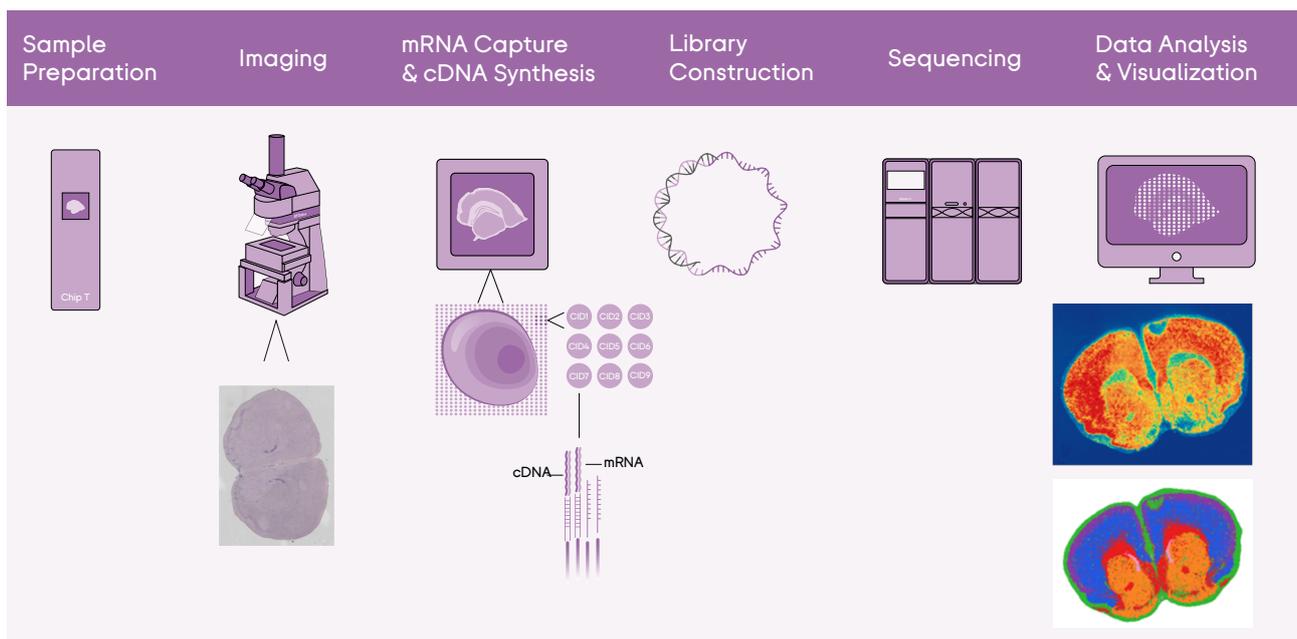
01 Stereo-seq Spatial Transcriptome Profiling on H&E Stained Tissue Section

STOmics Stereo-seq Transcriptomics Set for Chip-on-a-slide is intended for generating a spatially-resolved 3' mRNA library from biological tissue sections. Built upon DNA Nanoball (DNB) technology, STOmics Stereo-seq Transcriptomics Set for Chip-on-a-slide enables a "tissue-to-data" solution through *in situ* capture of the whole transcriptome, at nanoscale resolution and centimeter-sized field of view. This kit utilizes DNB patterned array chips loaded with spatially-barcoded probes that capture and prime poly-adenylated mRNA from tissue sections *in situ*. Each cDNA synthesized from mRNA captured on a particular spot is linked to its spatially-barcoded probe, allowing subsequent gene expression mapping of a tissue section following sequencing and visualization analysis using the StereoMap visualization platform.

Now compatible with tissue H&E staining, Stereo-seq workflow can obtain better tissue morphological information, to assist with tissue type identification, to obtain gene expression profile of specific tissue region, and to conduct downstream differential analysis between selected regions of interests.

02 Application Highlights

- Combining tissue morphological information with spatial transcriptome profiling data for multi-modal analysis.
- Gain additional molecular insights from selected tissue region of interest (ROI).
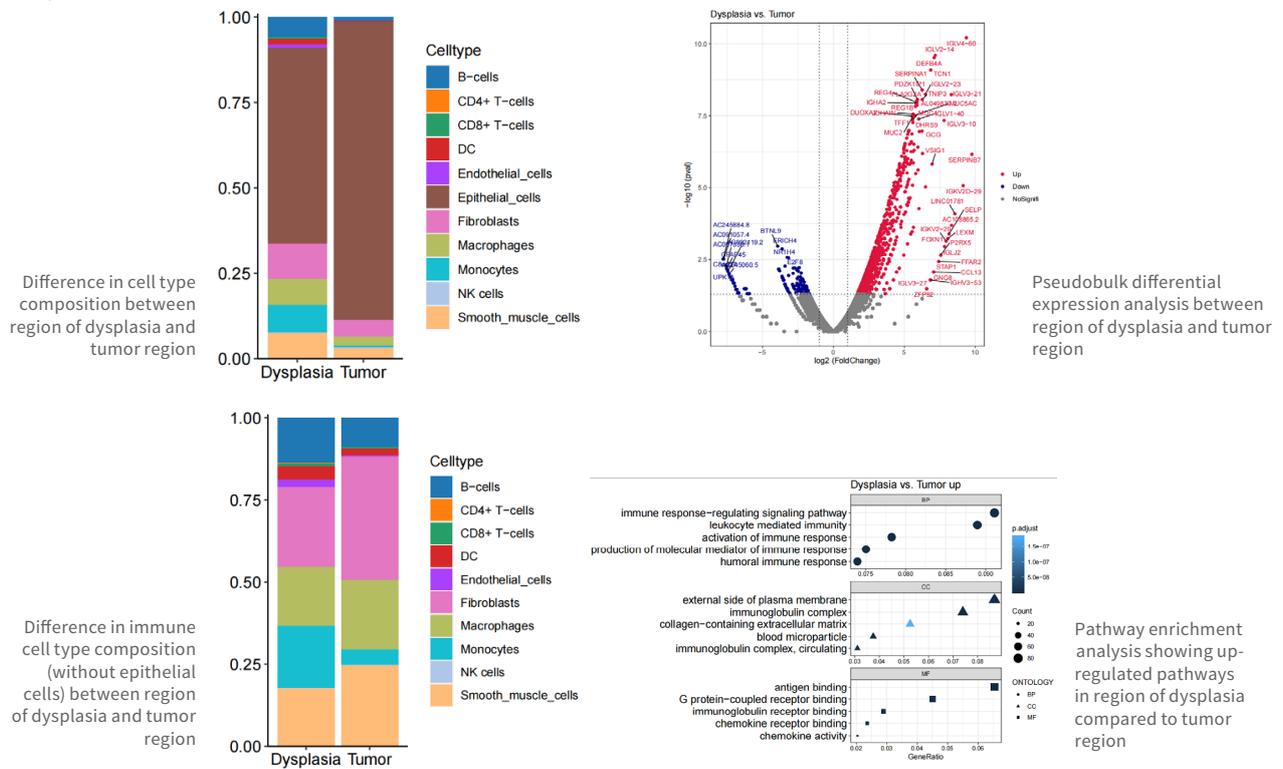- High resolution information obtained on pathological tissues.

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

Explore histology with spatial molecular knowledge

03 **Characterizing Spatial Gene Expression Profile on Histology Images**

Histological information provided by H&E-stained tissue section is useful for selecting tissue region of interest related to specific scientific questions for exploring potential molecular mechanisms. Here, we demonstrated the difference in spatial molecular characteristics between precancerous (dysplasia) region and cancerous (tumor) region from tissue-level to cell-level in colorectal cancer tissues.
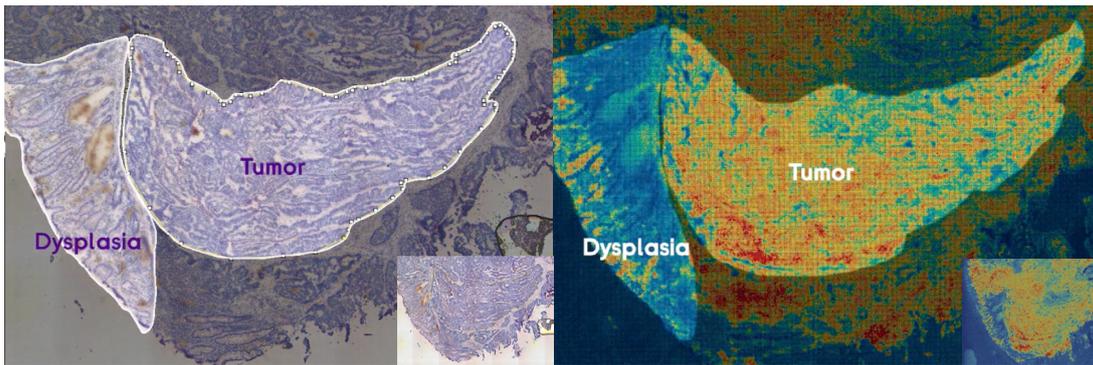
Significant differences in cell composition between region of dysplasia and the tumor region were discovered through annotation of the Stereo-seq transcriptome data corresponding to these two regions. Compared with the tumor region, the region of dysplasia had higher immune cell infiltration. Further analysis at the molecular level revealed that region of dysplasia was enriched with significant immune responses, suggesting specific immune microenvironment characteristics within the region of dysplasia.

Difference in cell type composition between region of dysplasia and tumor region

Pseudobulk differential expression analysis between region of dysplasia and tumor region

Difference in immune cell type composition (without epithelial cells) between region of dysplasia and tumor region

Pathway enrichment analysis showing up-regulated pathways in region of dysplasia compared to tumor region

With Stereo-seq's high resolution feature, we were able to explore and reveal the different characteristics of dysplasia and tumor region at the tissue, cell and molecular levels respectively, and the corresponding analytical results also provided insights and breakthrough points for related research in dysplasia.

04 **Stereo-seq Gene Expression & H&E Demo Display**
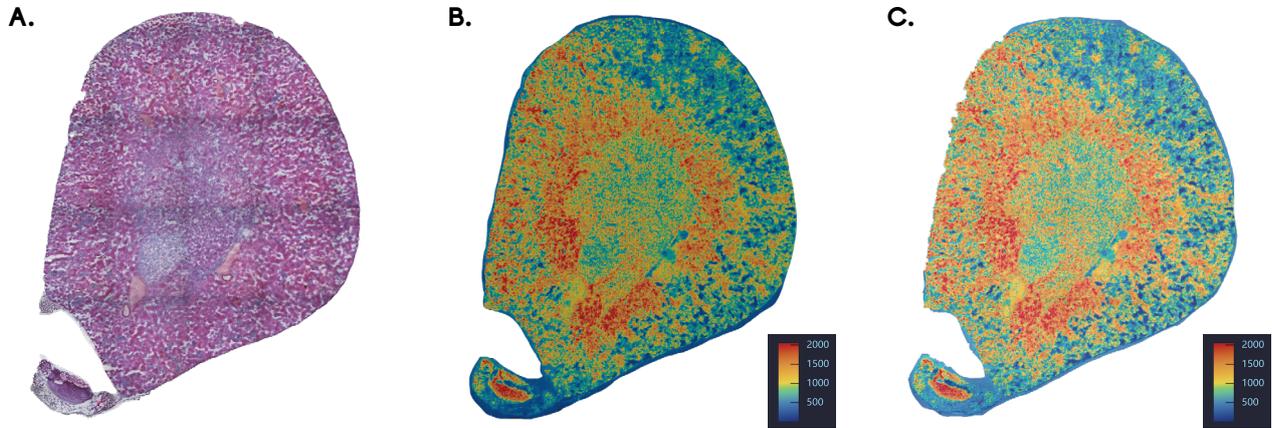
Mouse Kidney

A.

B.

C.

Figure 1.   **A.** H&E-stained image of mouse kidney section mounted on Stereo-seq Chip **B.** Mouse kidney spatial gene expression profile at bin20 (~10μm). **C.** Mouse kidney spatial gene expression profile at bin20 (~10μm) overlaying with H&E-stained image of the same section.
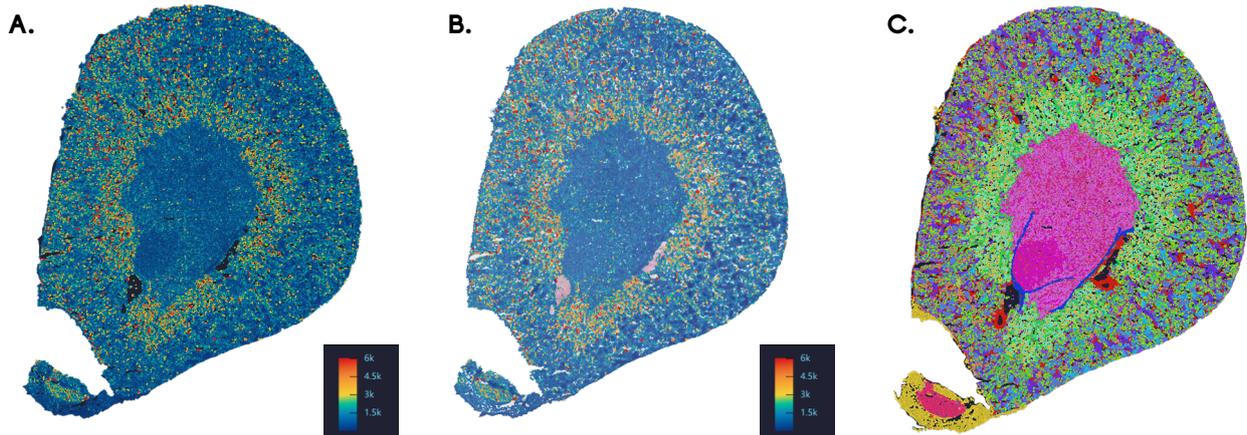
A.

B.

C.

Figure 2.   **A.** Spatial single-cell gene expression heatmap of mouse kidney (Cellbin*). **B.** Mouse kidney spatial single-cell gene expression heatmap overlaying with H&E-stained image of the same section (Cellbin*). **C.** Mouse kidney single-cell clustering results (Cellbin)

*The upper limit of the heatmap bar has been customized to 6K (MID count)

05 **Key Features**

❶ Enabling precise mapping of gene expression patterns within tissue sections, providing detailed spatial information.

❷ Providing intuitive and user-friendly interface for multi-model data visualization, exploration, and analysis, making it accessible to researchers with varying levels of computational expertise.

❸ Combining spatial transcriptomics with H&E-stained images allows for correlation of gene expression patterns with tissue morphology and pathology, enhancing the understanding of complex biological processes.

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

06 Product Reagents

Perform Stereo-seq in your own laboratory with Stereo-seq Kits.

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-seq Transcriptomics Set for Chip-on-a-slide				
Part Number	Product		Specification	Description
211ST114	Stereo-seq Transcriptomics T Kit	111KT114	4 RXN	For generating a spatially-resolved 3' mRNA library from biological tissue sections
	Stereo-seq Chip T Slide (1cm*1cm)	210CT114	4 EA	
	STOmics Accessory Kit	1000033700	5 PCS	

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

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

Stereo-seq H&E Mounting Medium			
Part Number	Product	Specification	Description
1000041969	H&E Mounting Medium	50 µL	Mounting medium used for adhering the coverslip to H&E-stained tissue section

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.

Image processing

SAW (Automatic)

ImageStudio (Manual)
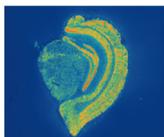
Reads processing & Quantification

SAW

		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

Visualization & Additional analysis

StereoMap

Stereopy & Other community developed tools

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