



STOmics

Stereo-seq Transcriptomics Solution V1.3

Level-up Spatial Whole Transcriptome Solution

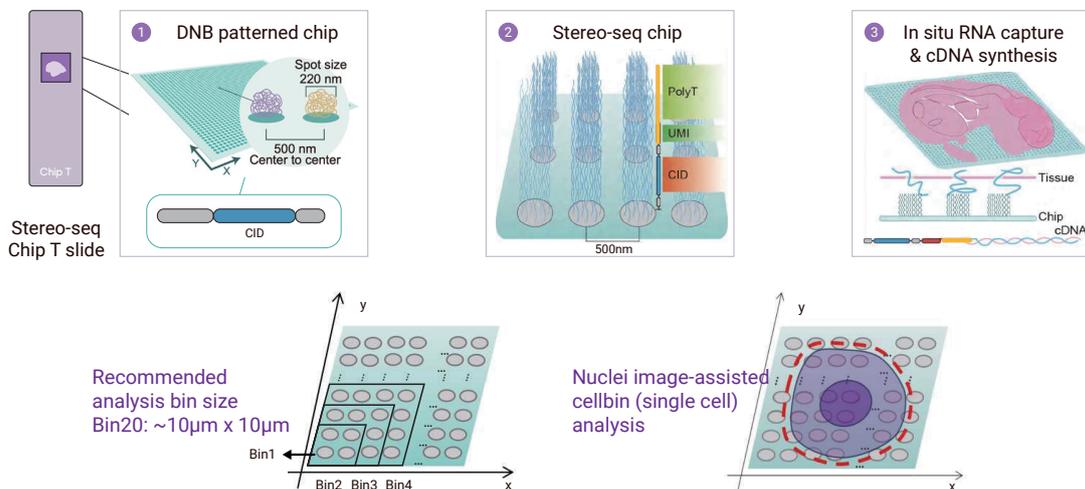
Higher capture efficiency

Broad compatibility

Faster workflow

Technology Introduction

STOmics' proprietary Stereo-seq (SpaTial Enhanced REsolution Omics-sequencing) technology provides researchers with a new tool to investigate spatial biology. We offer an unprecedented field-of-view and single-cell resolution, allowing for simultaneous study and analysis of the transcriptome at tissue, cellular, subcellular, and molecular levels using fresh frozen tissue.



Validated Tissue Types

Mouse			Human			Other
Whole brain	Ovary	Large intestine	Lung cancer	Thymus	Thyroid cancer	Monkey brain
Eye ball	Heart	Skin	Esophageal cancer	Pancreas	Kidney cancer	
Small intestine	Spleen	Lung	Colon cancer	Liver cancer	Ovarian cancer	
Kidney	Liver	Thymus	Skin hair follicler	Tonsil	Breast cancer	
Uterus	Tongue	Tumor-bearing	Endometrial carcinoma	lymph node metastasis		
And More...						

Product Features

• Single cell spatial discovery

Improved capture efficiency resulting in higher gene counts per cell, enabling precise spatial cellular phenotyping and exploration of cell-cell interaction within the tissue context.

• Broad compatibility

Compatible with a variety of tissue types and species as well as precious samples with low RIN values

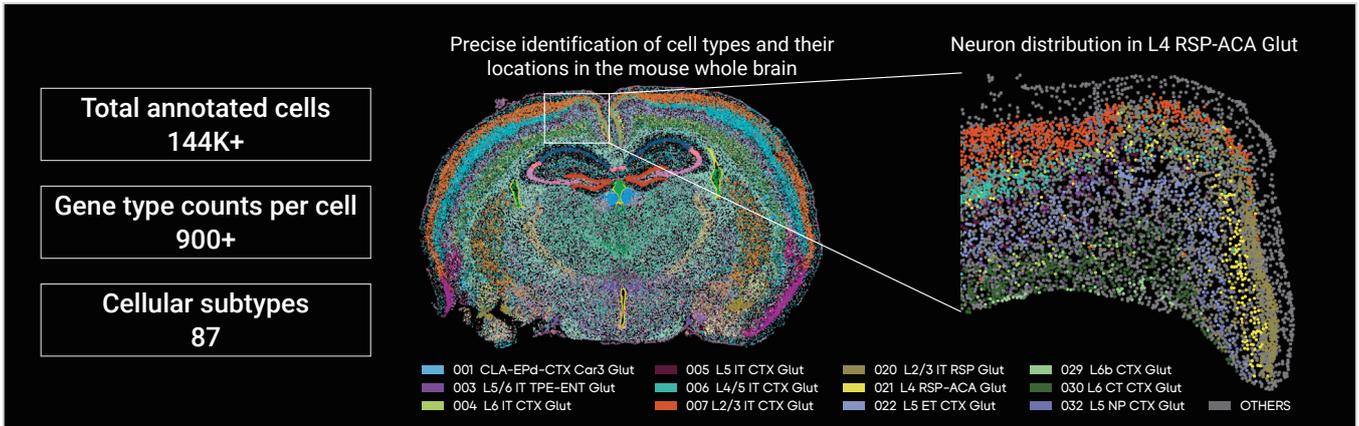
• Various sizes to meet your needs

Currently available in 0.5cm x 0.5cm or 1cm x 1cm chip sizes without compromising resolution.

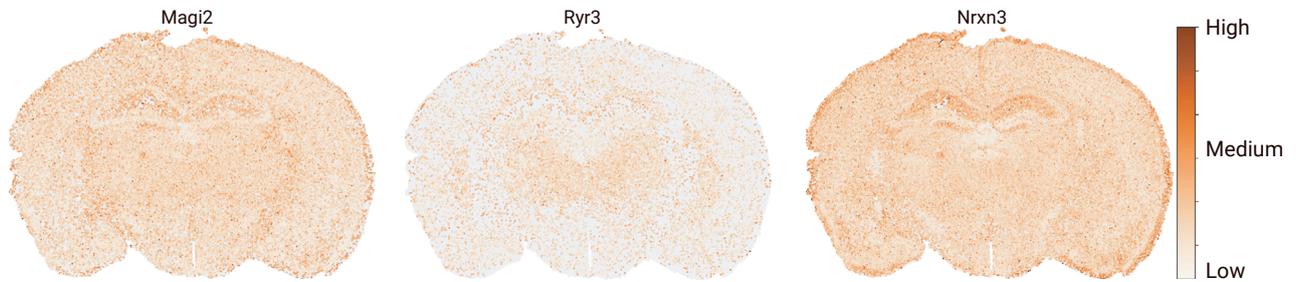
• Unbiased whole transcriptome profiling and more

Not limited by predetermined targets or throughput, enabling unbiased whole transcriptome discovery and the ability to combine multi-omics capabilities.

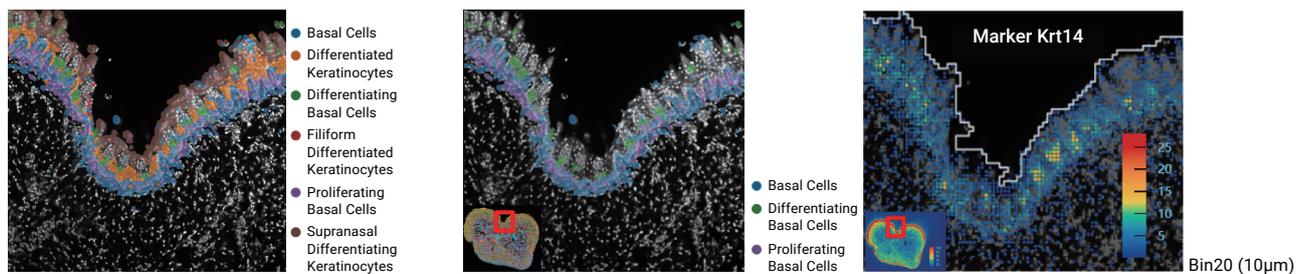
Demo Data



Uniquely expressed protein-coding genes demonstrated spatial distribution features in mouse brain



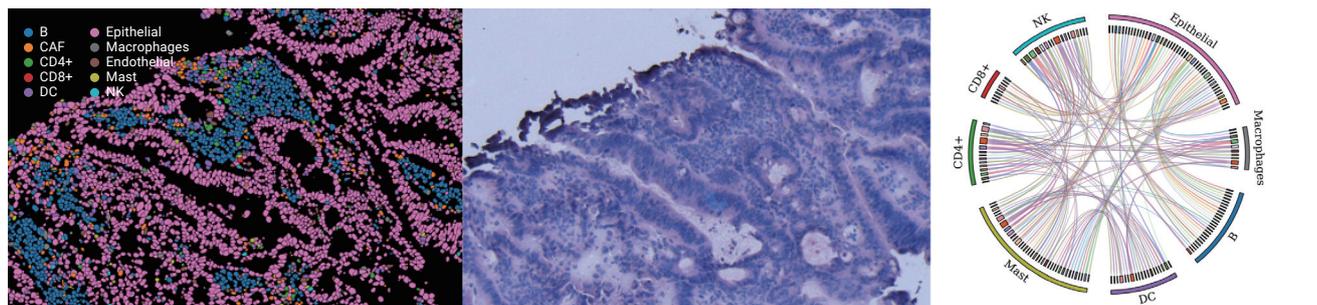
Precise spatial single-cell analysis enables well-defined tissue stratification



Epithelial cells exhibit a layer distribution from basal cells to keratinocytes.

The pattern of marker gene expression is consistent with the distribution patterns of associated cells (basal cells).

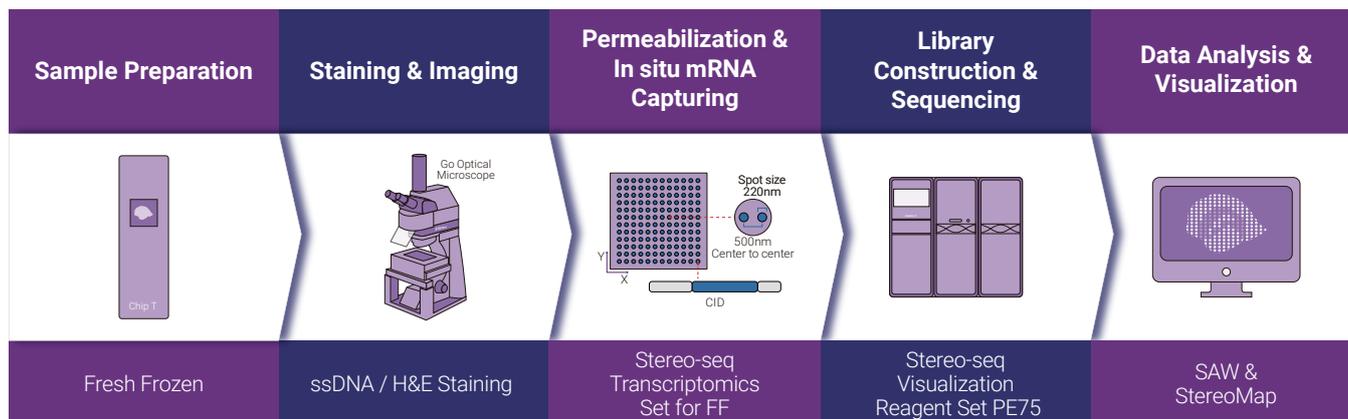
Decode tumor microenvironment in CRC at single-cell resolution



Stereo-seq reveals intricate anatomical structures and cellular composition

Intercellular communications of identified immune cell types in CRC samples

Stereo-seq Workflow



Product Specification

Product	0.5cm x 0.5cm chip	1cm x 1cm chip
Detection scope	Unbiased whole transcriptome	
Data output bin size (minimum)	Bin 1 (500nm)	
Data visualization and analysis bin size (recommended)	Single-cell segmentation (Cellbin) or Bin 20 (10 μm)	
Additional instrumentation	Not required	
Sample type	Fresh frozen	
Analysis software included (free)	StereoMap & SAW	
Capture area size	0.5cm x 0.5cm	1cm x 1cm
Duration/hands-on operational time	1.5 day	1.5 day
Minimum Sequencing Depth	600M reads	2000M reads

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.
211ST13114	211ST13114-CG	Stereo-seq Transcriptomics Set for Chip-on-a-slide V1.3	4 RXN	V1.3	For generating a spatially-resolved 3' mRNA library from biological tissue sections.
211ST13004	211ST13004-CG	Stereo-seq Transcriptomics Set for Chip-on-a-slide (0.5cm x 0.5cm) V1.3	4 RXN	V1.3	
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.

Manufactured by
STOmics

Reach out to us to learn more:

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

