STOmics | MGI

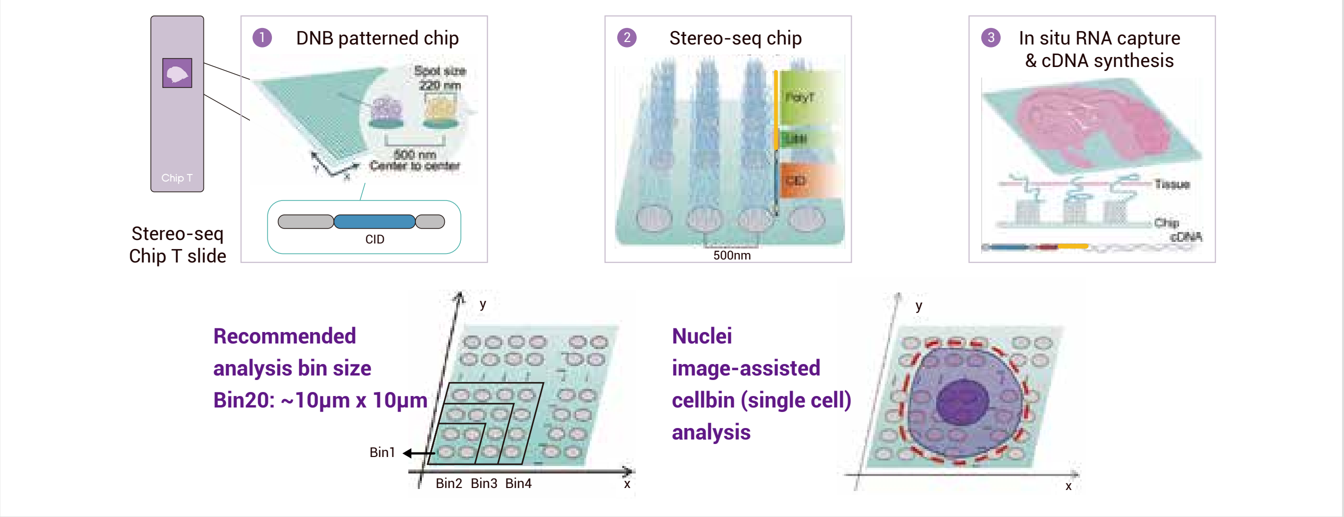
Stereo-seq Transcriptomics Solution v1.3

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 subcellular 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. The upgrade for the Large Chip Designs (LCD) will be available soon.

- **Unbiased whole transcriptome profiling and more**

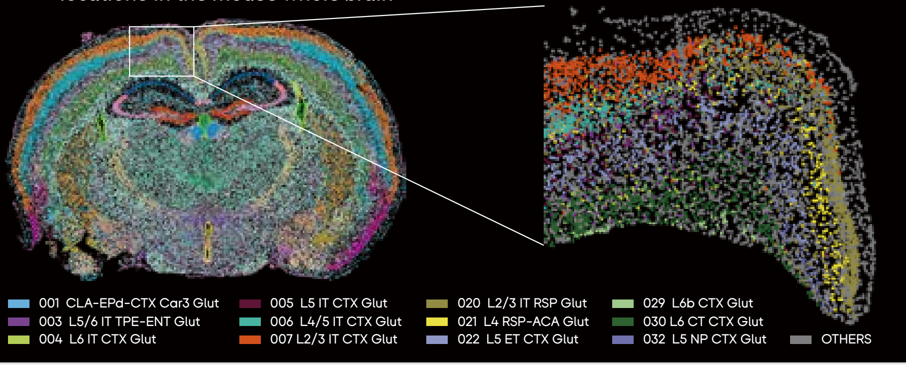
  Not limited by predetermined targets or throughput, enabling unbiased whole transcriptome discovery and the ability to combine multi-omics capabilities.

Demo Data

Total annotated cells
144K+

Gene type counts per cell
900+

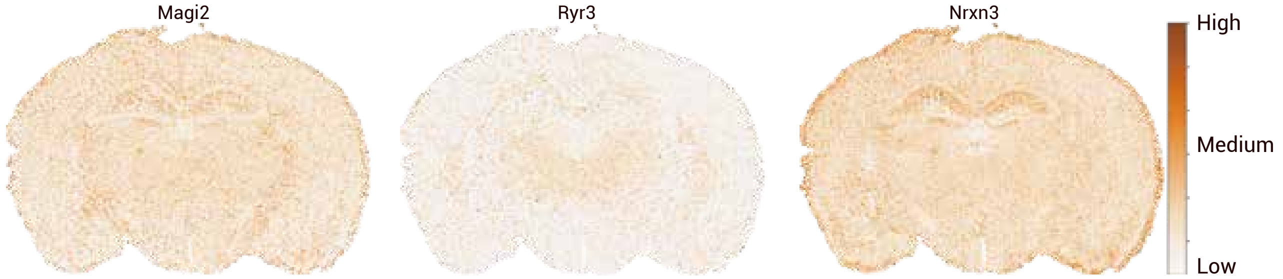
Cellular subtypes
87



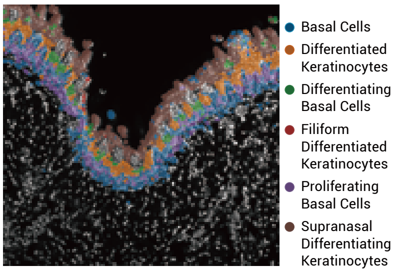
Precise identification of cell types and their locations in the mouse whole brain

Neuron distribution in L4 RSP-ACA Glut

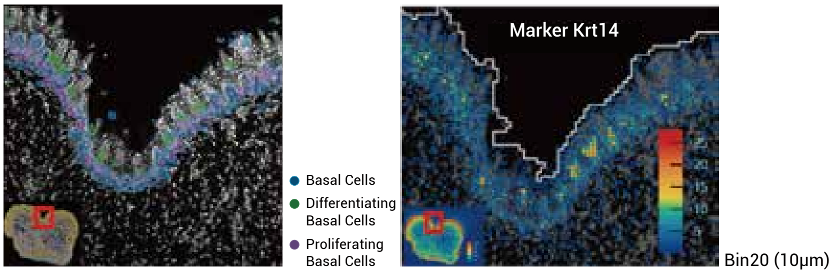
Uniquely expressed protein-coding genes demonstrated spatial distribution features in mouse brain



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

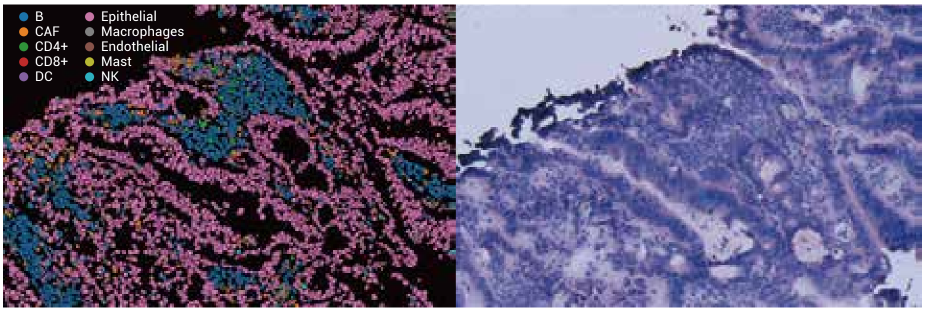


Epithelial cells exhibit a layer distribution from basal cells to keratinocytes.

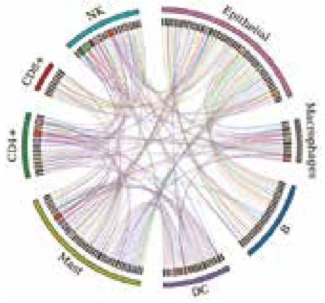


The pattern of marker gene expression is consistent with the distribution patterns of associated cells (basal cells).

Decode tumor microenvironment in CRC at single-cell resolution



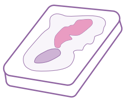
Stereo-seq reveals intricate anatomical structures and cellular



Intercellular communications of identified immune cell types in CRC samples

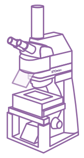
Stereo-seq Workflow

① Sample preparation



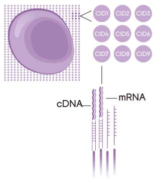
- Sectioning and mounting of fresh frozen (FF) samples（~10μm) on Stereo-seq Chip T Slide.

② Stain and image



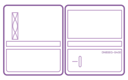
- Stain the tissue section with nuclei-stain (ssDNA) or hematoxylin and eosin (H&E) stain.
- Visualize it using an epi-fluorescence microscope or reflected brightfield microscope.

③ mRNA capture & cDNA synthesis

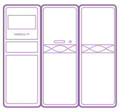


- Tissue permeabilization and mRNA release.
- Released mRNA is captured by spatially barcoded probes on Stereo-seq Chips.

④ Sequencing



DNBSEQ-G400



DNBSEQ-T7

- Sequence Stereo-seq Transcriptome FF library on DNBSEQ-G400 or DNBSEQ-T7.

⑤ Data analysis & visualization

Image processing — **StereoMap(Manual)** → **Reads processing & quantification** — **SAW** → **Visualization** — **StereoMap**

- Stereo-seq Analysis Workflow (SAW) to process your spatial gene expression data.
- Explore the results interactively with high-definition visualization software, StereoMap.

Product Specification

Product	0.5 cm x 0.5 cm chip	1 cm x 1 cm 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	0.5 cm x 0.5 cm	1 cm x 1 cm
Duration/hands-on operational time	1.5 day	1.5 day
Minimum Sequencing Depth	600M reads	2000M reads

Product name	Product code
Stereo-seq Permeabilization Set for Chip-on-a-slide V1.1	211SP11118
Stereo-seq Transcritpomics Set for Chip-on-a-slide V1.3	211ST13114
Stereo-seq Transcritpomics Set for Chip-on-a-slide (0.5cm * 0.5cm) V1.3	211ST13004
Stereo-seq 16 Barcode Library Preparation Kit V1.0	111KL160
Stereo-seq PCR Adaptor	301AUX001-02

Contact us

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