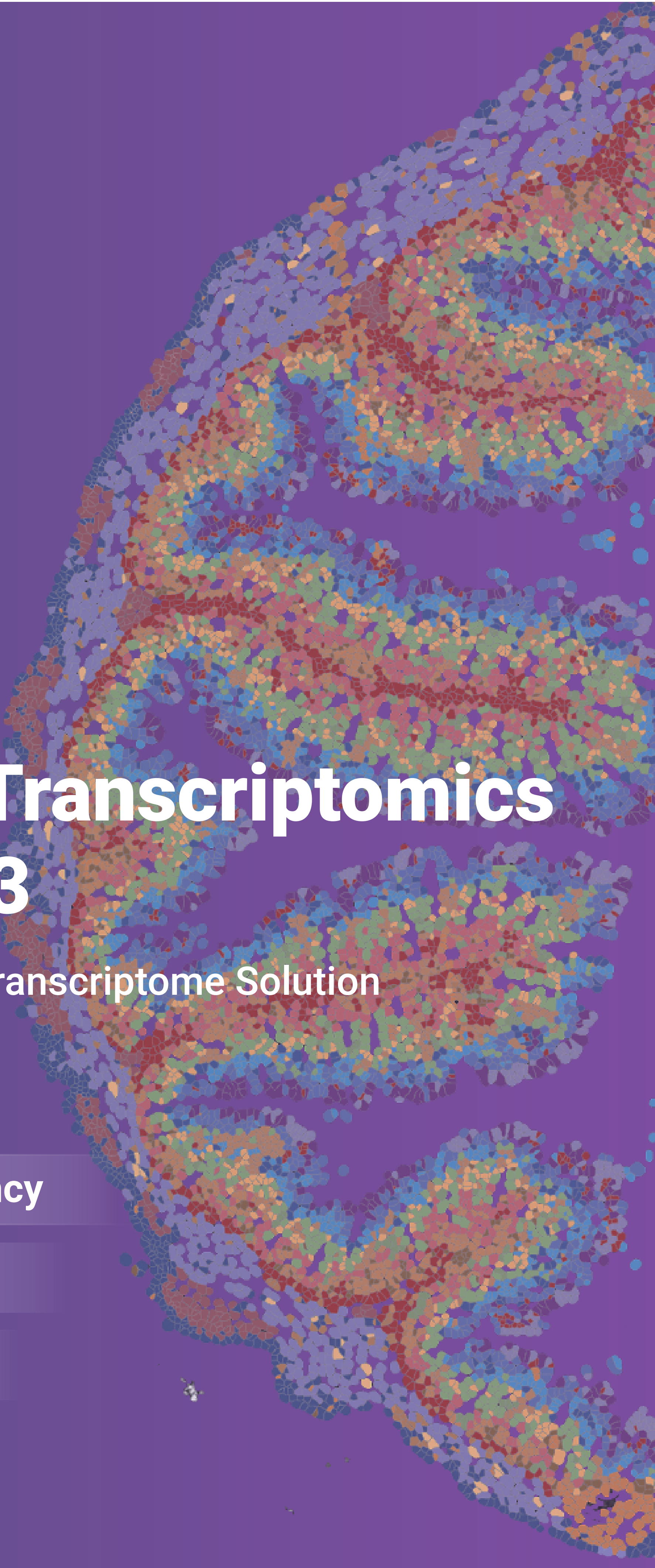
STOmics



# Stereo-seq Transcriptomics Solution v1.3

Level-up Spatial Whole Transcriptome Solution

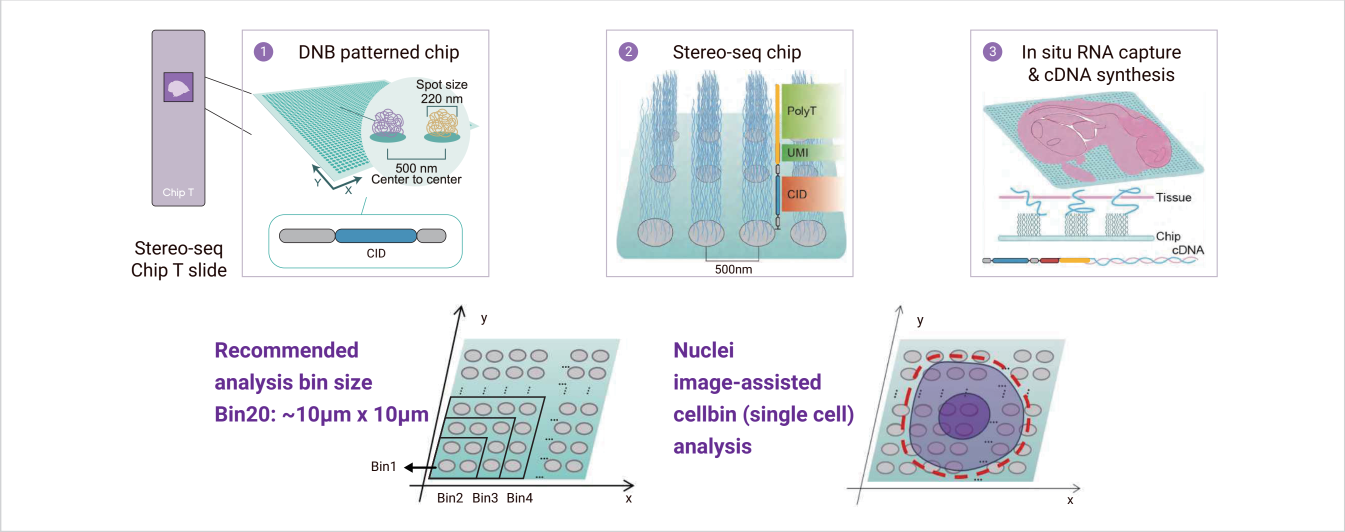
**Higher capture efficiency**

**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 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**

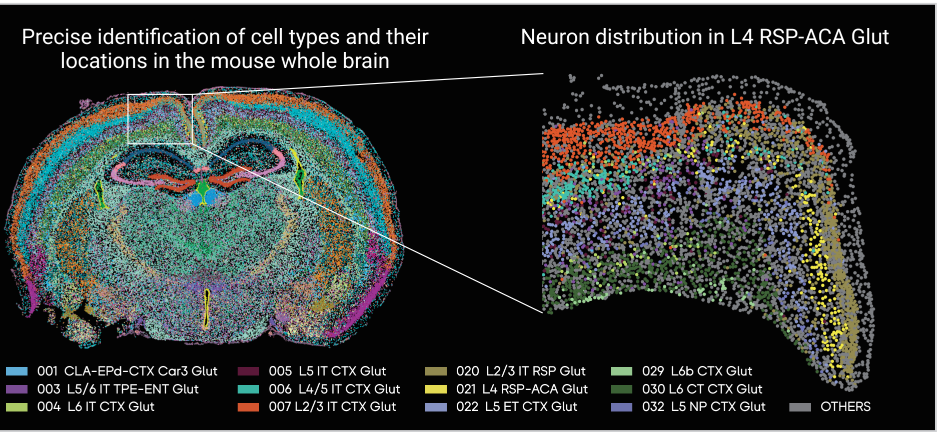
  Not limited by predetermined targets or throughput, enabling unbiased whole transcriptome discovery and the ability to combine multi-omics capabilities.

# Demo Data

Total annotated cells
144K+

Gene type counts per cell
900+

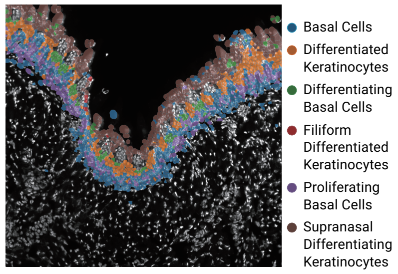
Cellular subtypes
87


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

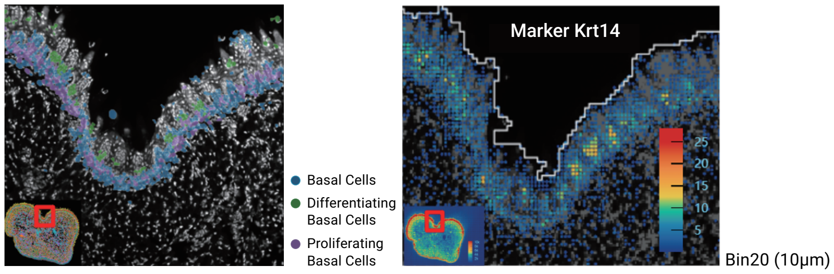
Neuron distribution in L4 RSP-ACA Glut

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

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

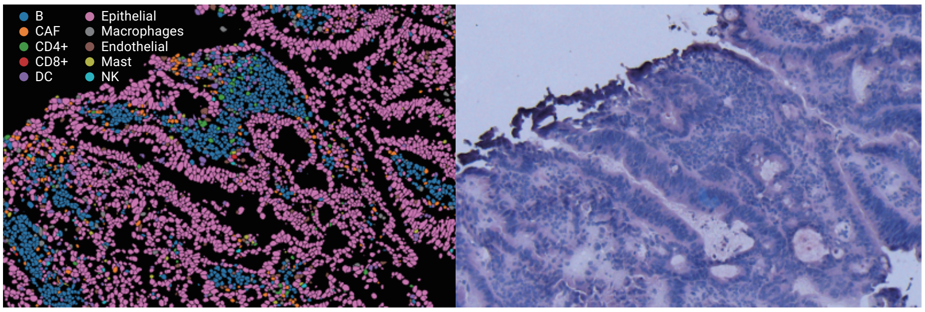


Epithelial cells exhibit a layer distribution from basal cells to keratinocytes.

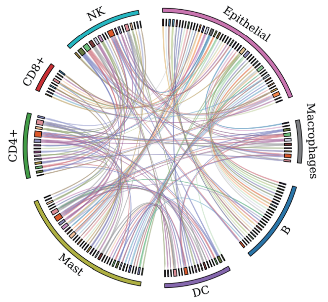


The pattern of marker gene expression is consistent with the distribution patterns of associated cells (basal cells).

## Decode tumor microenvironment in CRC at single-cell resolution



Stereo-seq reveals intricate anatomical structures and cellular composition



Intercellular communications of identified immune cell types in CRC samples

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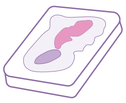
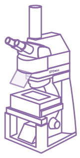
# Stereo-seq Workflow

### ① Sample preparation



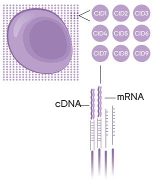
- Sectioning and mounting of fresh frozen (FF) samples （~10μm) on Stereo-seq Chip T Slide.

### ② Stain and image



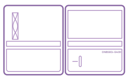
- Stain the tissue section with nuclei-stain (ssDNA) or hematoxylin and eosin (H&E) stain.
- Visualize it using an epi-fluorescence microscope or reflected brightfield microscope.

### ③ mRNA capture & cDNA synthesis

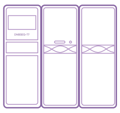


- Tissue permeabilization and mRNA release.
- Released mRNA is captured by spatially barcoded probes on Stereo-seq Chips.

### ④ Sequencing



DNBSEQ-G400



DNBSEQ-T7

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

### ⑤ Data analysis & visualization

**Image processing** — **Reads processing & quantification** — **Visualization**

StereoMap(Manual) → SAW → 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 | No 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 |

Reach out to us to learn more:

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