

## Stereo-Seq

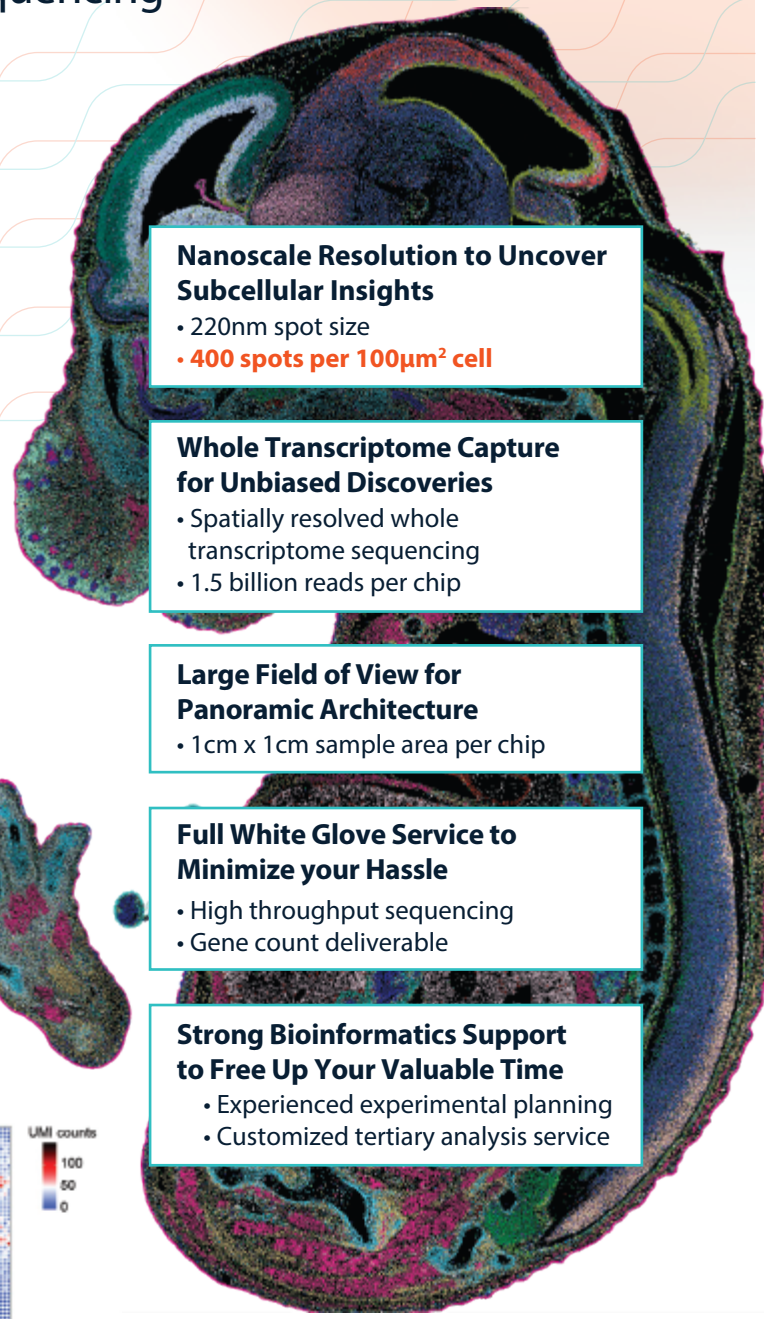
### Spatial Enhanced Resolution Omics-Sequencing

#### Unprecedented Nanoscale Subcellular Resolution with Large Field of View

Spatial transcriptomics sequencing fills up the knowledge gap in the understanding of cellular gene expression in relation to the morphological context, which is critical to decipher genetic functions.

Stereo-seq offers nanoscale subcellular resolution with a large field of view for spatial transcriptomics sequencing. It has demonstrated promising potential in spatial characterization of tumor microenvironment, construction of 3D transcriptomics model, spatiotemporal transcriptomics atlases in mammalian developmental biology and many more.

MiRXES Genomics provides an end-to-end service for Stereo-seq workflow, from tissue sectioning to bioinformatics tertiary analysis. Gene expression data is integrated with spatial information at nanoscale resolution to generate unprecedented details.



**Nanoscale Resolution to Uncover Subcellular Insights**

- 220nm spot size
- **400 spots per 100µm<sup>2</sup> cell**

**Whole Transcriptome Capture for Unbiased Discoveries**

- Spatially resolved whole transcriptome sequencing
- 1.5 billion reads per chip

**Large Field of View for Panoramic Architecture**

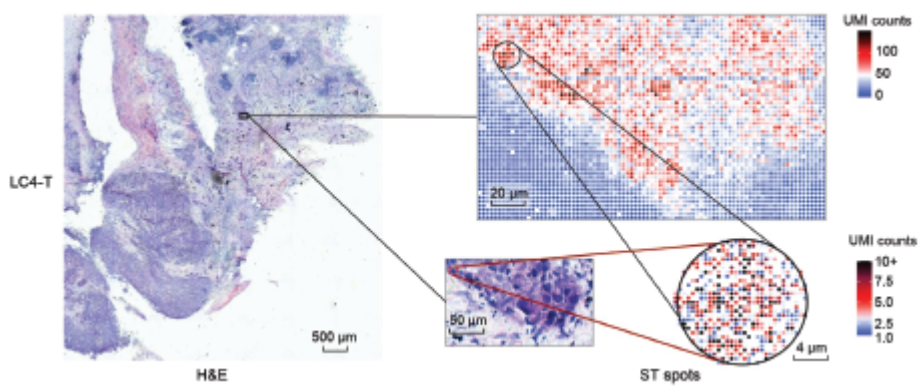
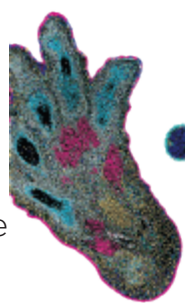
- 1cm x 1cm sample area per chip

**Full White Glove Service to Minimize your Hassle**

- High throughput sequencing
- Gene count deliverable

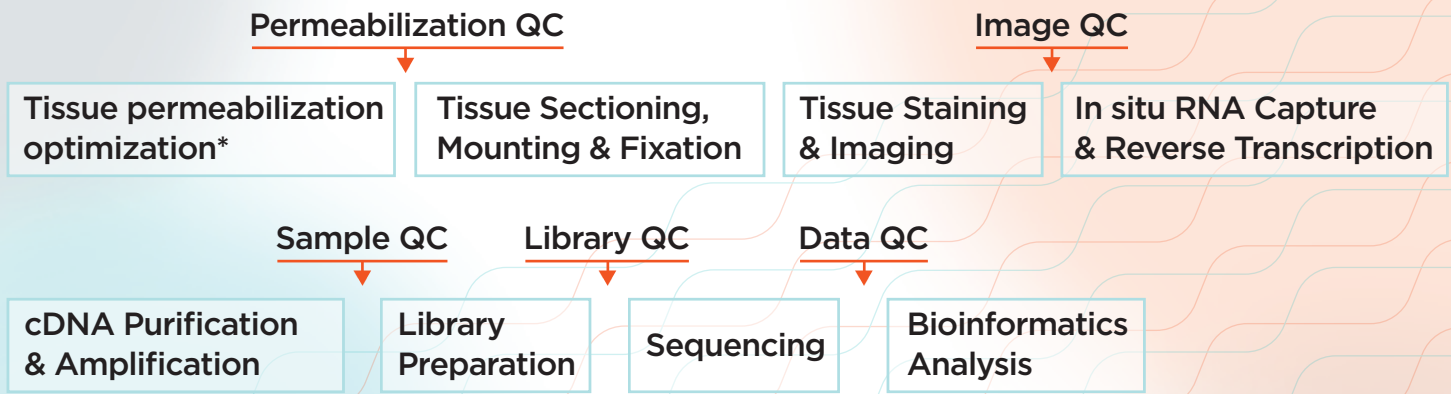
**Strong Bioinformatics Support to Free Up Your Valuable Time**

- Experienced experimental planning
- Customized tertiary analysis service



Wu et al., 2021, <https://doi.org/10.1101/2021.10.21.465135>

## Stereo-Seq Service Workflow



Sample Type	Chip Size	Expected Data Quantity	Sequencing Platforms	Turnaround Times
Fresh Frozen Sample (> 10µM) embedded in OCT (Extra sections required for tissue permeabilization optimization*)	1 cm x 1 cm	1.5G reads per chip	DNBSEQ-G400 or DNBSEQ-T7	4 Weeks from successful sample QC to data delivery

\* Repeated optimization is NOT needed for the same tissue type

## Bioinformatics Analysis

### Primary Analysis Package (FOC)

- Fastq Files
- Stained Tissue Image(s)
- Barcode to Position Mapping File
- QC Statistics

### Secondary Analysis Package

- Primary Analysis
- Sequence Alignment Map File
- Gene Count Matrix
- Barcode Mapping Information
- QC Statistics

### Additional Tertiary Analysis

- Spatial Gene Expression Pattern Analysis
- Spatial Copy Number Variation
- Trajectory Inference
- Velocity
- Ligand-receptor Analysis
- Many other options

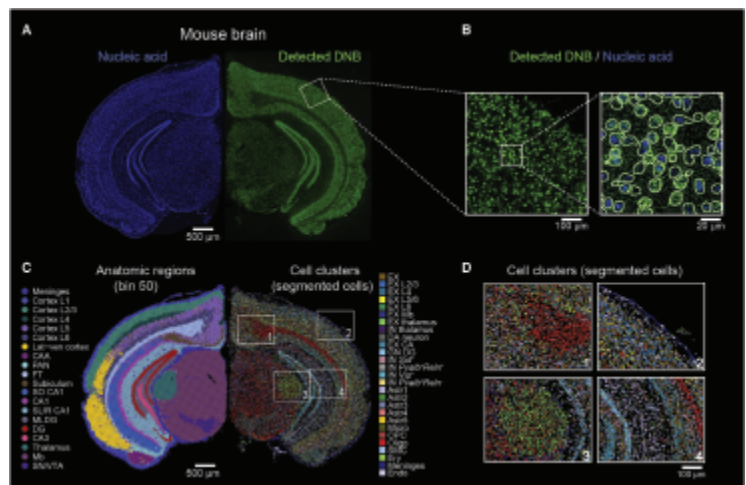


Figure: Stereo-seq dissects the adult mouse brain with cellular resolution  
Chen et al., 2022, Cell 185, 1777–1792