Research

mirxes | genomics

Spatial Transcriptomics powered by

Stereo-seq™

SpaTial Enhanced REsolution Omics-sequencing

Unprecedented Nanoscale Subcellular Resolution with Large Field of View

Spatial transcriptomics sequencing bridges the knowledge gap between cellular gene expression and morphological context, which is critical to deciphering genetic functions.

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

Mirxes Genomics offers 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 a nanoscale resolution to reveal unprecedented details.

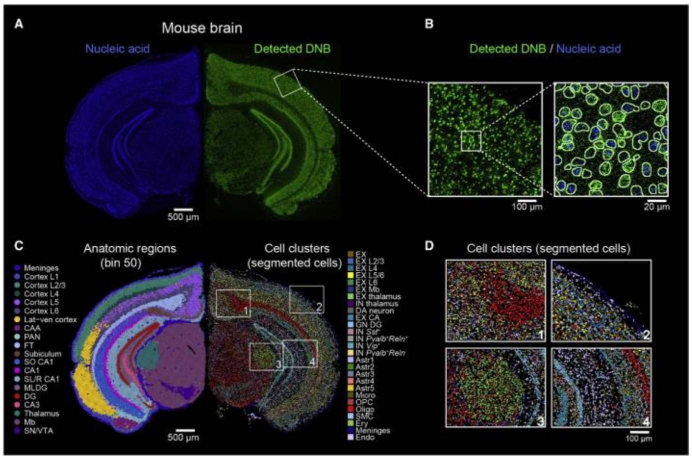


Figure: Stereo-seq dissects the adult mouse brain with cellular resolution
Chen et al., 2022, Cell 185, 1777–1792

Nanoscale Resolution to Uncover Subcellular Insights

- 220nm spot size
- 400 spots per 100µm^2 cell

Whole Transcriptome Capture for Unbiased Discoveries

- Spatially resolved whole transcriptome sequencing

Large Field of View for Panoramic Architecture

- Chip sizes from 1cm x 1cm up to 2cm x 3cm available

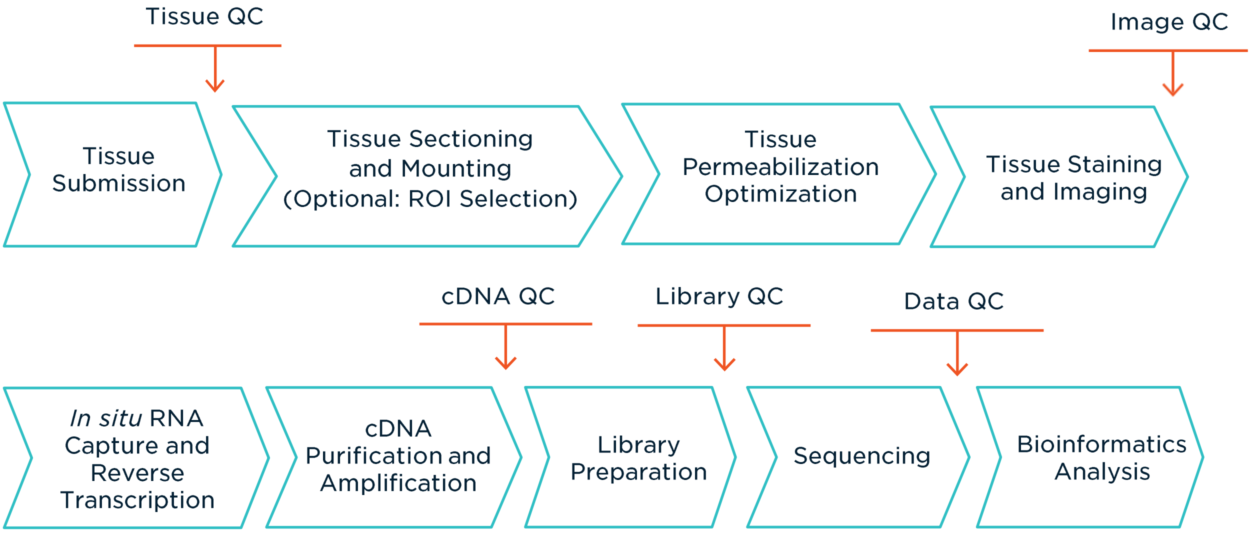
Full White Glove Service

- World's first Certified Service Provider
- Ultra-high throughput sequencing
- H&E staining on the same tissue section available

Expert Bioinformatics Support

- Pre-project planning
- Customizable tertiary analysis service

Spatial Transcriptomics Service Workflow



Sample Type	Available chip sizes and recommended data quantity[#] per chip	Sequencing Platform	Turnaround Time
Fresh Frozen Sample embedded in OCT	- 1 cm x 1 cm (1 billion raw reads) - 1 cm x 2 cm (2 billion raw reads) - 2 cm x 2 cm (4 billion raw reads) - 2 cm x 3 cm (6 billion raw reads)	DNBSEQ-T7	4-6 weeks from successful **determination of permeabilization time** to FASTQ data delivery

[#] The actual data output depends on sample quality

Bioinformatics Analysis and Support

Primary Analysis Package (Included)

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

Secondary Analysis Package (Add-on)

- QC statistics and Spatial Barcodes Maps
- Sequence Alignment Maps
- Gene Count Matrix

Additional Tertiary Analysis (Add-on)

- Spatial Gene Expression Cluster Analysis
- Spatial Copy Number Variation
- Cell Co-localization Analysis
- Trajectory Inference
- **Many other options upon request!**

Contact Us

Email: genomics@mirxes.com **Phone:** +65 6950 5864 **Website:** mirxes.com

Stereo-seq Brochure - MM-002-P_r00