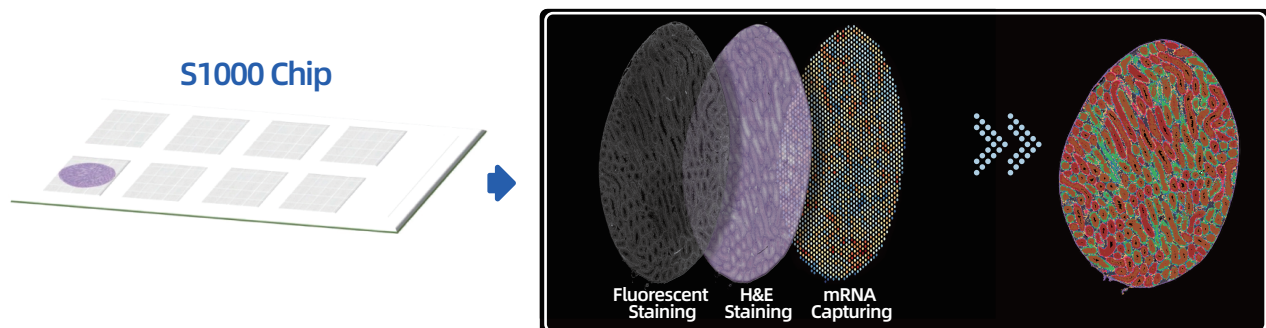
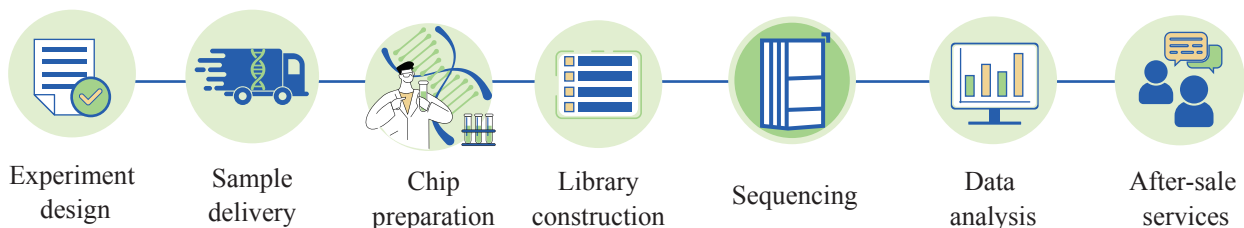


BMKMANU S1000 Spatial Transcriptome Sequencing with Cell Segmentation

BMKGENE's cell segmentation technology, developed for subcellular-level, high-resolution spatial transcriptomics using the BMKMANU S1000 chip, enables transcriptomic analysis at the cellular level in spatial dimensions. Combining fluorescence staining, HE staining, and RNA sequencing on a single chip, our "three-in-one" analysis algorithm accurately identifies cell structures for subsequent cell-based transcriptomic research.



Service Workflow



Bioinformatics

Raw Data Quality Control

- 1 Q-score distribution
- 2 Nucleotide distribution
- 3 Raw data assessment
- 4 Image processing

BSTMatrix Analysis

- 5 Statistics on data yield
- 6 Reference genome alignment
- 7 Gene expression quantification

- 8 Multi-resolution statistics and clustering analysis
- 9 Cell split statistics and clustering analysis

Spots-Based Clustering Analysis

- 10 Data quality control
- 11 Dimensionality reduction clustering analysis for spots
- 12 Differential expression analysis of cluster
- 13 Function annotation and enrichment on DEGs

Service Advantages

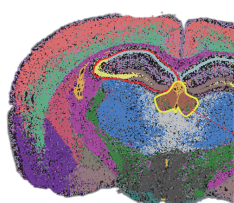
- Spatial transcriptomics allows for the study of gene expression in the context of tissue architecture and cellular organization, providing a more comprehensive understanding of biological processes.
- Spatial transcriptomics enables the identification of cell types and their spatial distribution within tissues, as well as the visualization of gene expression patterns in relation to specific structure features.
- BMKMANU S1000 chip has sub-cellular resolution up to 5 mm.
- Accompanied by user-friendly Windows software can be personalized analysis.
- Experience with hundreds of cases.

Service Specifications

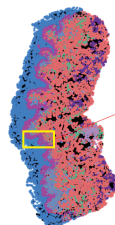
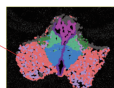
Library	Sequencing strategy	Data recommended	Quality Control
S1000 cDNA library	Illumina PE150	150 Gb/sample	OCT embedded cryo samples; Optimal diameter: approx. 6.8x6.8x6.8 mm ³

Sample Requirements

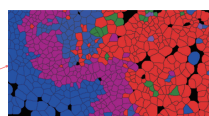
Blocks Number	RNA Quality
Three blocks per sample: Block 1: Experiment Block 2,3: Back-up	RIN ≥ 7



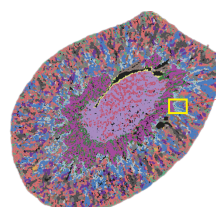
Mouse brain



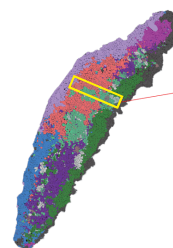
Oral skin



Demo Results



Mouse kidney



Plant callus



Featured Publications

Year	Journal	Article	Application
2023	PNAS	Spatial transcriptomics reveals light-induced chlorenchyma cells involved in promoting shoot regeneration in tomato callus	Plant Spatial Transcriptomics



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