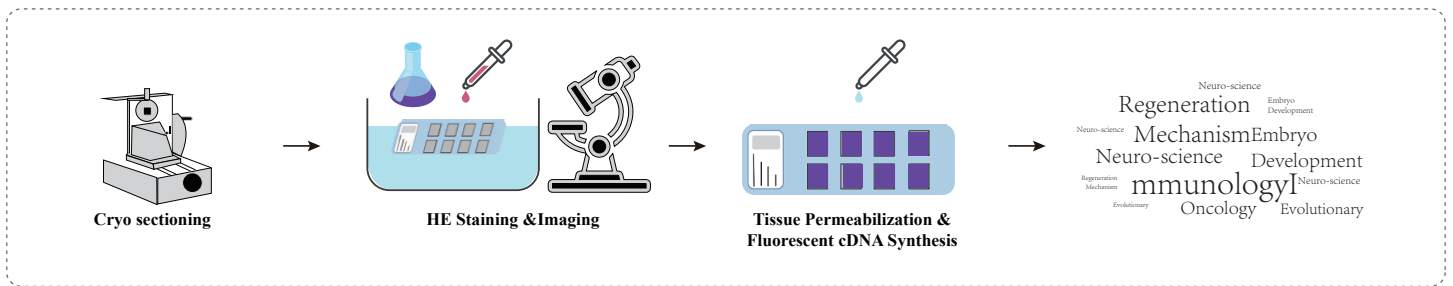


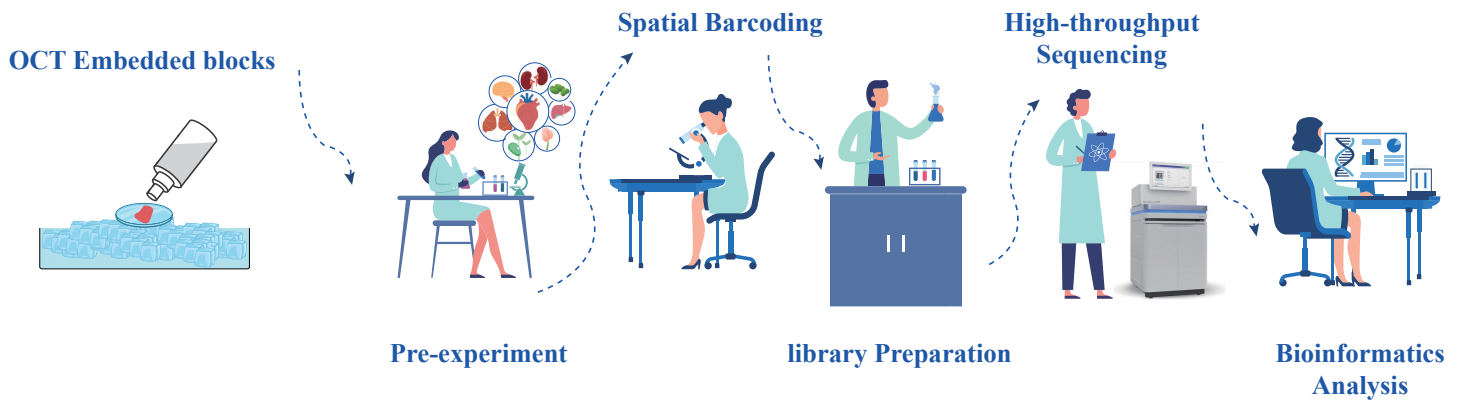
Spatial organization of cells plays vital role in various biological processes, such as immune infiltration, embryo development, etc. Spatial transcriptome sequencing, which indicates gene expression profiling while retaining information of spatial position, has provide great insights into transcriptome-level tissue architecture. BMKGENE provides comprehensive, one-stop spatial transcriptome sequencing service from samples to biological insights.

Spatial transcriptomics technologies empowered novel perspectives in diverse research arena by resolving gene expression profile with spatial content in heterogenous samples.

Technical Scheme



How to start your first Spatial Transcriptomics project with BMKGENE?



Service Specifications

Library	platform	Recommended Data Output	Sample Delivery
Spatial mRNA library	10X Visium Illumina PE150	60 Gb/sample	OCT embedded cryo samples; FFPE samples (Optimal diameter: approx. 6x6x6 mm ³)

Service advantages

- One-stop service integrates all experience and skill based steps, including cryo-sectioning, staining, tissue optimization, spatial barcoding, library preparation, sequencing and bioinformatics .
- Highly skilled technical group with experience in over 250 tissue types, 50+ species including human, mouse, mammal, fish and plants.
- Real-time update on entire project with full control of experimental progress.
- Comprehensive standard bioinformatics package with 29 analyses, 100+ high-quality figures.
- Customized data analysis and visualization available for different research requests.

Bioinformatics Analysis

Data Quality Control

Data output and quality score distribution
Gene detection per spot
Tissue coverage

Inner-sample Analysis

Gene detection
Spot clustering
Differential analysis among clusters

Inter-group Analysis

Data combination
Spot clustering of joint data
Differential analysis between groups

