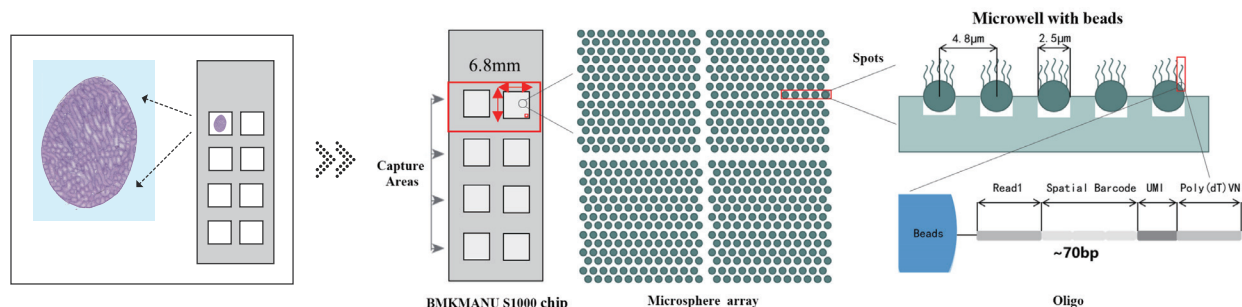
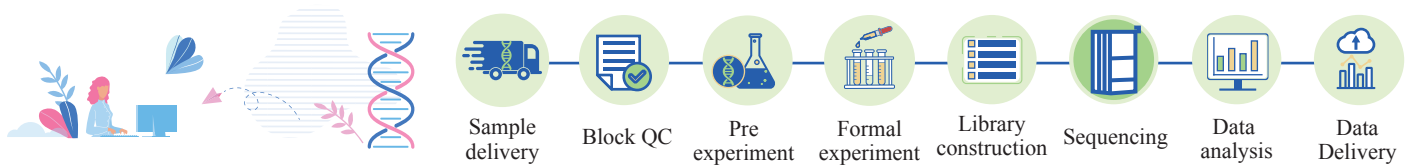


BMKMANU S1000 Spatial Transcriptome Sequencing

Spatial organization of cells is crucial in various biological processes, such as immune infiltration, embryo development, etc. Spatial transcriptome sequencing provides insights into gene expression and tissue architecture. BMKGene offers comprehensive spatial transcriptome sequencing services for higher resolution studies. Empowering diverse research with spatial gene expression profiles in heterogenous samples.



Service Workflow



Bioinformation

1. Raw Data Quality Control

2. Basic Analysis (BMKGene self-developed software BSTMatrix, compatible with downstream third-party software)

- Barcode splitting and data saturation assessment
- Reference genome alignment
- Image processing
- Gene expression quantification

4. Multi-samples analysis

- Data combination and re-clustering
- Marker gene identification of each cluster
- Spatial distribution of Top10 DEGs, Violin plot, t-SNE, UMAP scatter plot, Clustering heatmap
- Differential expression of a cluster between samples/groups (two or more samples/groups)
- Seurat data filtration and re-clustering
- GO/KEGG enrichment analysis of DEGs

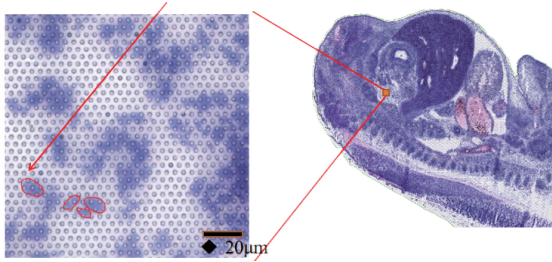
3. Inner-sample analysis

- Spot clustering according to expression matrix
- Gene expression: expression quantification and intensity distribution (two or more samples)
- Differential expression analysis; Marker gene identification of each cluster
- Spatial distribution of Top10 DEGs, Violin plot, t-SNE, UMAP scatter plot, Clustering heatmap
- Hierarchical clustering on DEGs
- Function annotation and enrichment on DEGs: GO and KEGG
- Data filtration and spot clustering (Seurat)
- Gene set enrichment of clusters

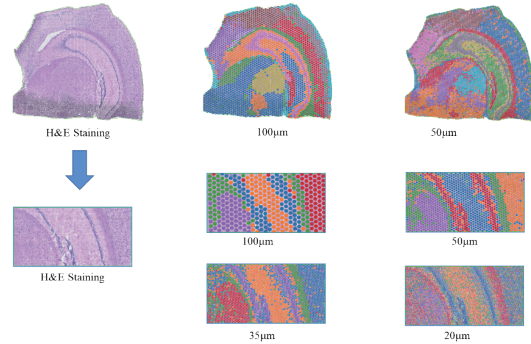
- Differential expression analysis between clusters
- Gene set enrichment of clusters

Service Advantages

① **Sub-cellular resolution:** Each capture area contained >2million spatial Bar-coded Spots with a diameter of 2.5 μm and a spacing of 5 μm between spot centers, enabling spatial transcriptome analysis with sub-cellular resolution(5 μm).



② **Multi-level resolution analysis:** Flexible multi-level analysis ranging from 100 μm to 5 μm to resolve diverse tissue features at optimal resolution.



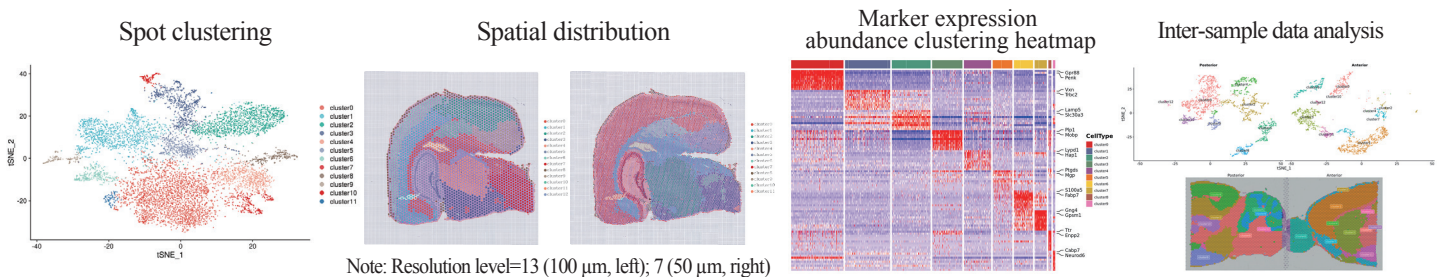
Service Specifications

Library	platform	Recommended Data Output
S1000 cDNA library	BMKMANU S1000-Illumina PE150	60 Gb/sample

Sample Requirements

Sample	Number	Size	RNA quality
OCT embedded tissue block	2-3 blocks/sample	Approx. 6.8x6.8x6.8 mm ³	RIN \geq 7

Demo Results



Featured Publications

Year	Journal	Title
2023	PNAS	Spatial transcriptomics reveals light-induced chlorenchyma cells involved in promoting shoot regeneration in tomato callus



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