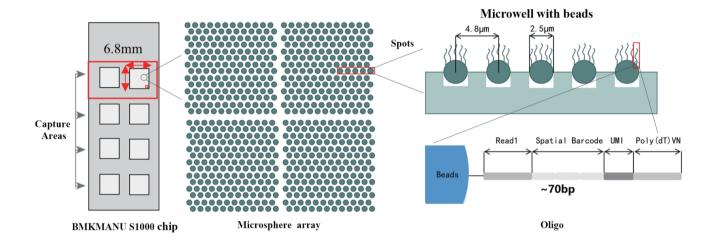
# BMKMANU S1000 Spatial Transcriptome Sequencing



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. With the development of technology, the ultra-clear tissue morphology and the real structural difference of spatial molecular expression need to be studied with higher resolution. 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.

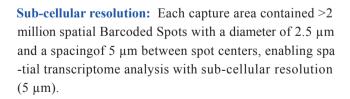
#### **Technical Scheme**

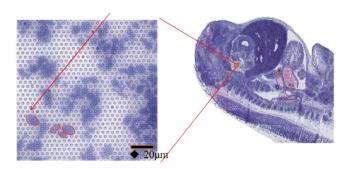


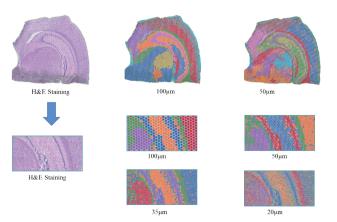
### **Advantages of BMKMANU S1000**



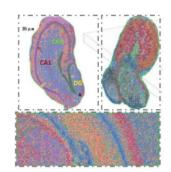
**Multi-level resolution analysis:** Flexible multi-level an -alysis ranging from 100 μm to 5 μm to resolve diverse tissue features at optimal resolution.

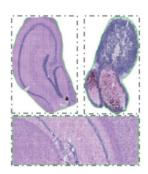






Comprehensive transcriptome profiling: Transcripts cap -tured from the entire tissue slide can be analyzed, wit -hout restriction on number of target genes and target area





## **Service Specifications**

Library	platform	Recommended Data Output	Sample Delivery
S1000 cDNA library	BMKMANU S1000- Illumina PE150	60 Gb/sample	OCT embedded cryo samples; FFPE samples (Optimal diameter: approx. 6x6x6 mm <sup>3</sup> )

## **Bioinformatics Analysis**

The data generated by BMKMANU S1000 is analyzed using the software "BSTMatrix", which is independently designed by BMKGENE, including:

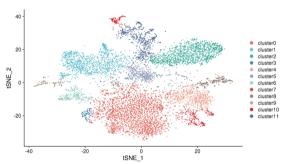
Gene expression matrix generation

HE image processing

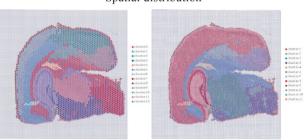
3 Compatible with downstream third-party software for analysis

4 Online "BSTViewer" helps to obtain visualization results at different resolutions.

Spot clustering

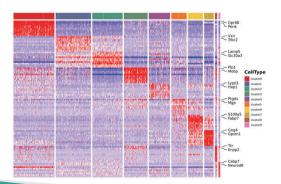


Spatial distribution



Note: Resolution level=13 (100 μm, left); 7 (50 μm, right)

Marker expression abundance clustering heatmap



Inter-sample data analysis

