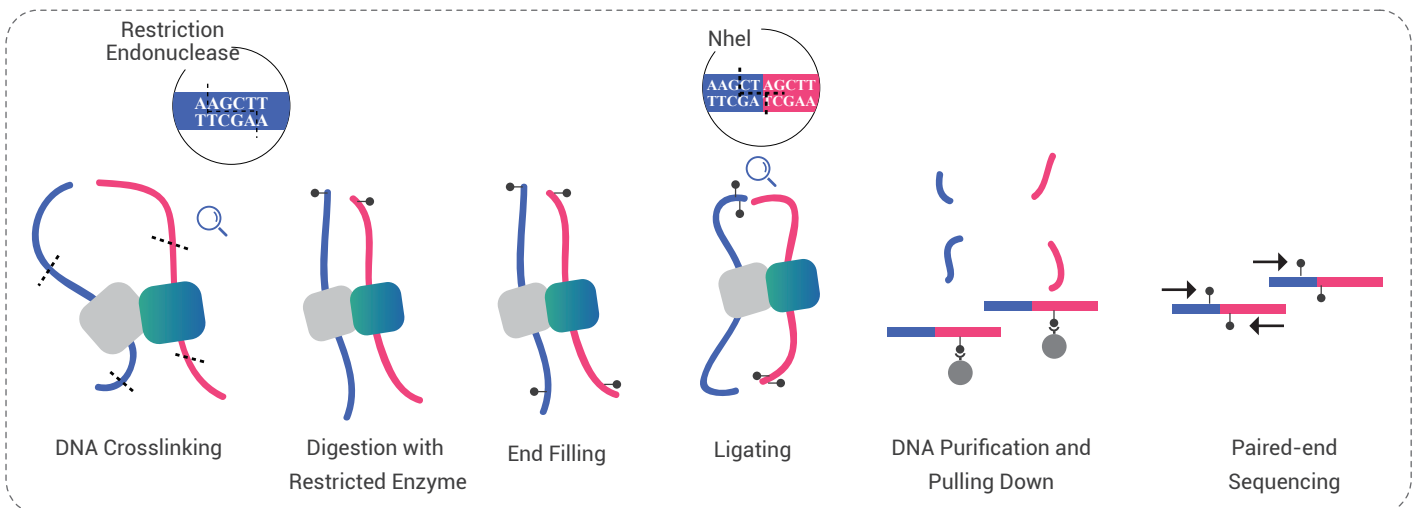


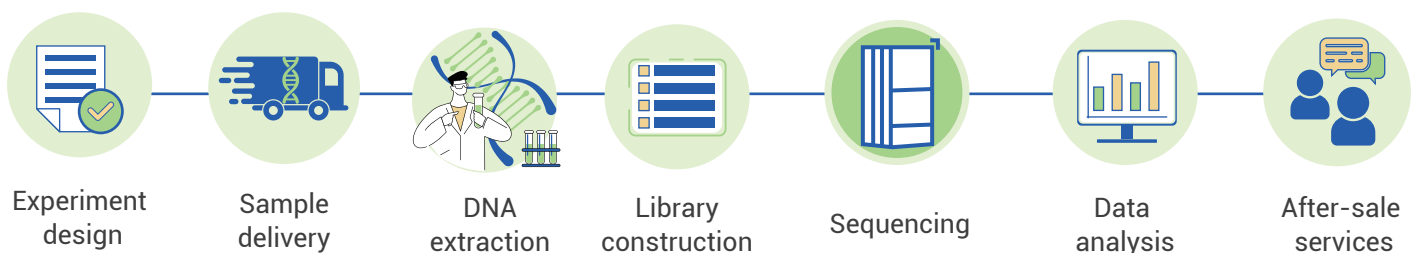
Hi-C based Genome Assembly

Hi-C is a technique that uses proximity-based interactions and high-throughput sequencing to capture chromosomal configurations. It is beneficial in enhancing genome assembly by identifying long-range and intricate interactions between genomic regions, which can aid in scaffolding and orienting contigs to construct chromosome-level genomes. BMKGENE has accomplished over 2000 successful cases and holds numerous patents in this area.

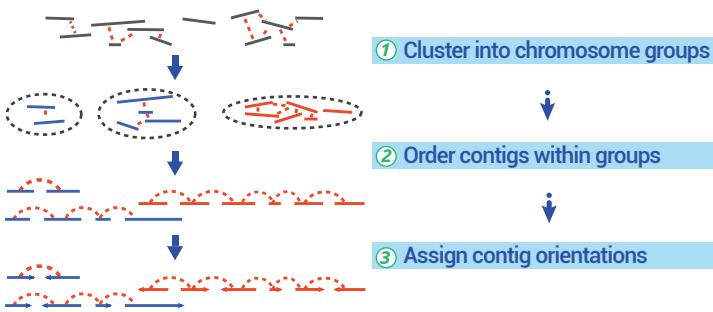
Technical Workflow



Service Workflow



Bioinformatics



Service Specifications

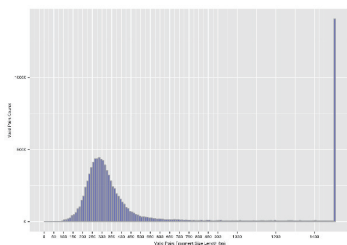
Library Type	Platform	Read Length	Recommended Strategy
Hi-C	Illumina/MGI	PE150	≥ 100X

Sample Requirements

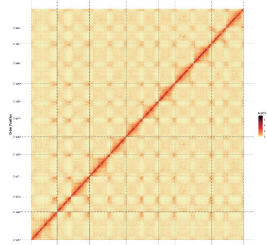
Animal	Fungus	Plants
Frozen tissue: 1-2 g per library Cells: 1×10^7 cells per library	Frozen tissue: 1 g per library	Frozen tissue: 1-2 g per library

*We strongly recommend sending at least 2 aliquots (1 g each) for the Hi-C experiment.

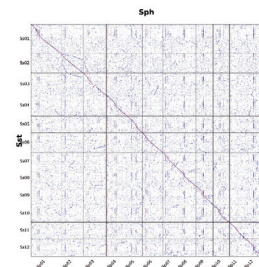
Demo Results



Hi-C library assessment



Hi-C heatmap



Collinearity analysis to evaluate assembly accuracy

Featured Publications



Biomarker Technologies (BMKGENE)

✉ info@bmkgene.com 🌐 www.bmkgene.com

Global Locations

Germany United Kingdom United States China

Service Advantages

- There is no need to construct a genetic population for contig anchoring;
- Higher marker density leads to higher contig anchoring ratio at above 90%;
- Extensive experience with over 2000 Hi-C libraries constructed for over 1000 species, including highly complex, polyploid and giant genomes;
- Over 200 published cases with an accumulative impact factor of over 2000;
- In-house patents and software copyrights for Hi-C experiments and data analysis;
- Proprietary visualization and tuning software enables manual block adjustments, including moving, reversing, undoing, and redoing.