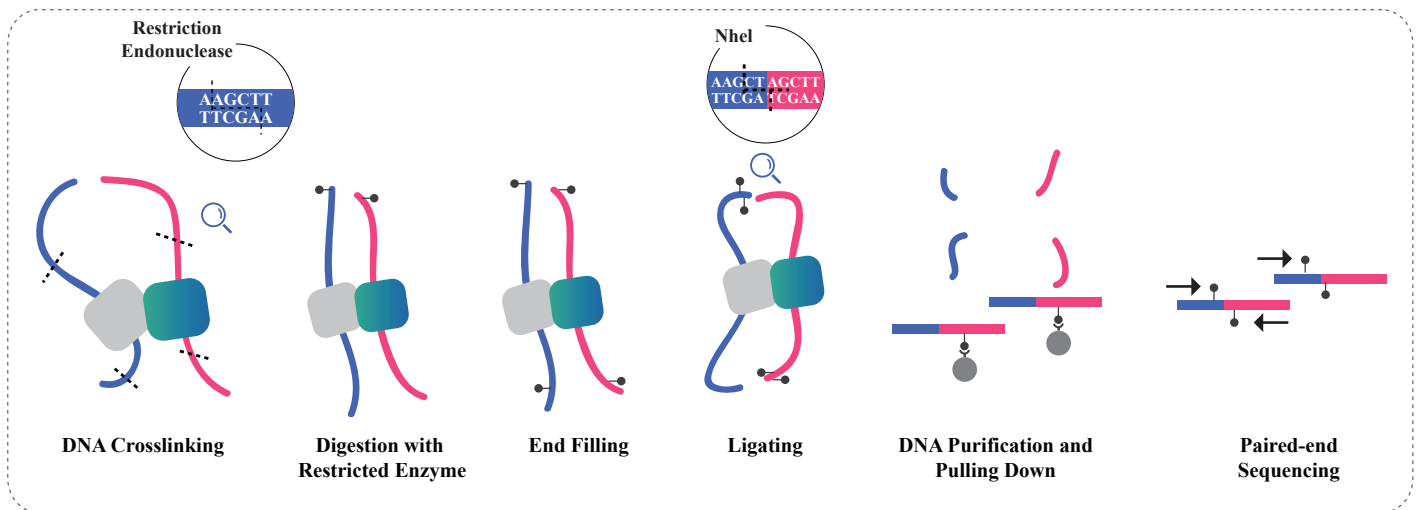


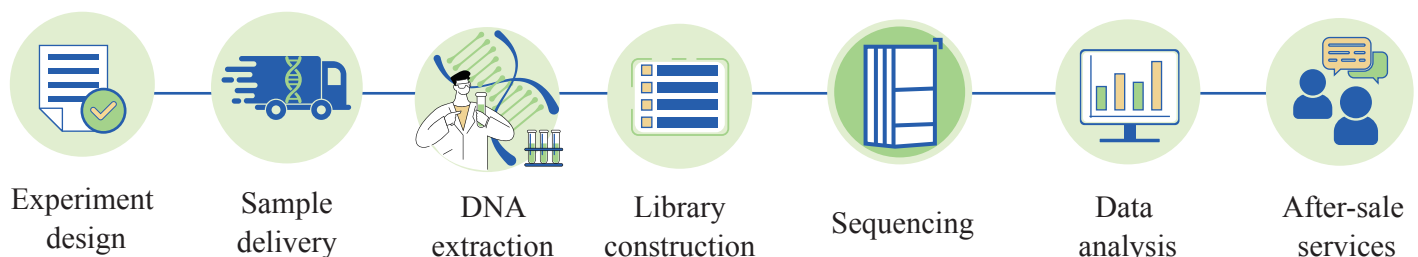
# Hi-C based Genome Assembly

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 1000 successful cases and holds numerous patents in this area.

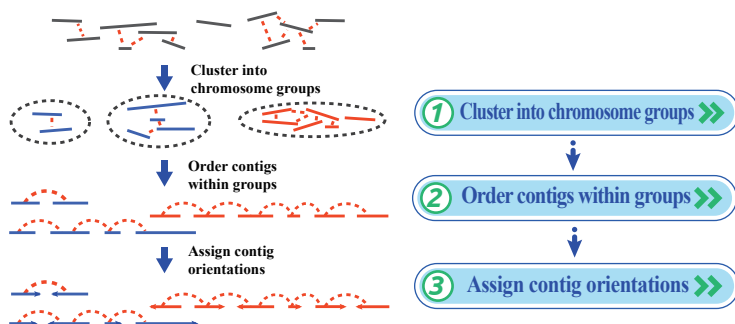
## Technical Work Flow



## Service Workflow



## Bioinformatics



## Service Advantages

- No need in constructing genetic population for contig anchoring;
- Higher marker density leads to higher contigs anchoring ratio at above 90%;
- Extensive experience with over 1000 Hi-C libraries constructed for over 800 species, including highly complex, polyploid or giant genomes;
- Over 100 published cases with an accumulative impact factor of over 900;
- In-house patents and software copyrights for Hi-C experiments and data analysis;
- Self-developed visualized data tuning software, enables manual block moving, reversing, revoking and redoing.

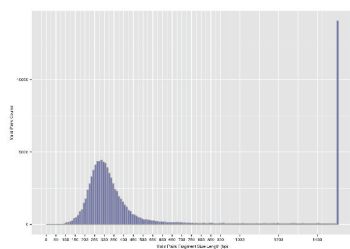
## Service Specifications

Library Type	Platform	Read Length	Recommend Strategy
Hi-C	Illumina	PE150	≥ 100X

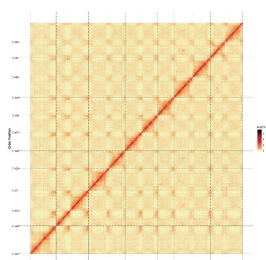
## Sample Requirements

Animal	Fungus	Plants
Frozen tissue: 1-2g per library Cells: 1e7 cells per library	Frozen tissue: 1g per library	Frozen tissue: 1-2g per library
*We strongly recommend sending at least 2 to 4 aliquots (1 g each) for the Hi-C experiment.		

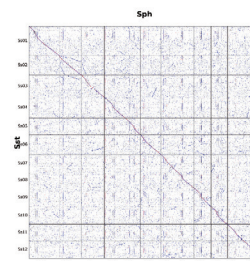
## Demo Results



Hi-C library assessment



Hi-C interaction heatmap



Genome assembly accuracy verification using collinearity analysis

## Featured Publications



## Biomarker Technologies (BMKGENE) GmbH

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