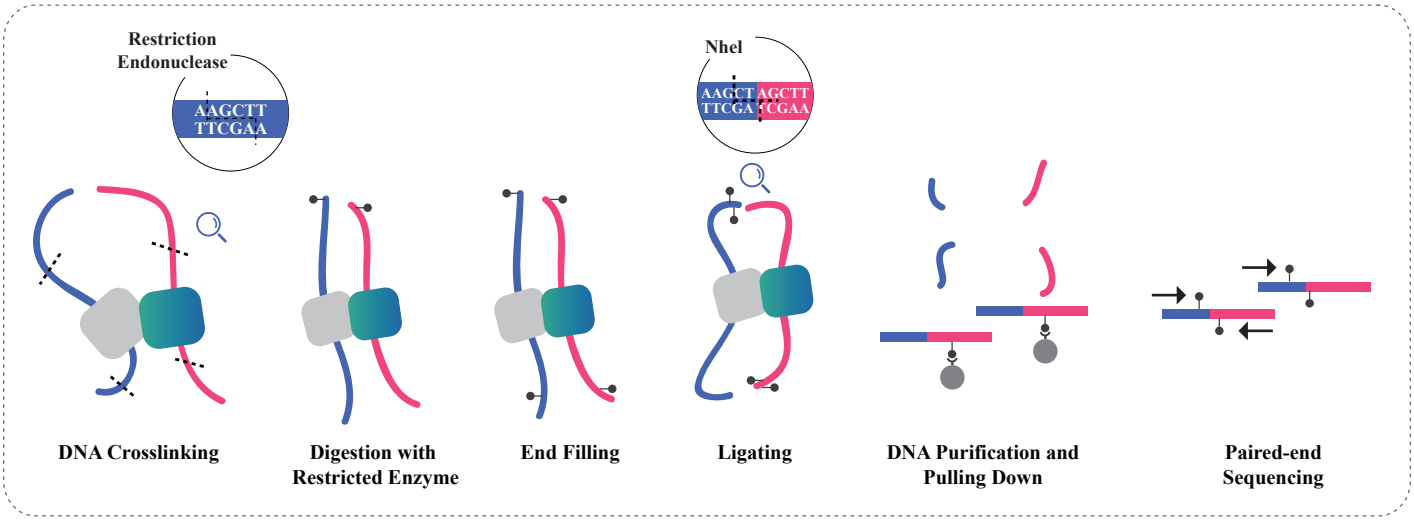
Hi-C based Chromatin Interaction

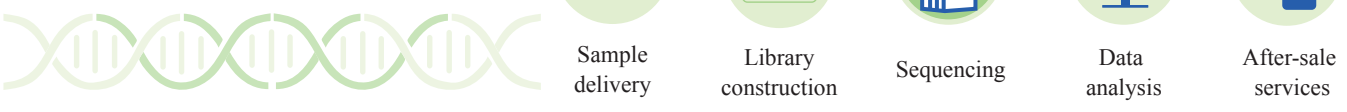
Hi-C technology is an advanced method used to study the three-dimensional structure of chromosomes and chromatin interactions. BMKGENE integrates chromosome conformation capture and high-throughput sequencing technologies to capture and analyze the physical interactions between different chromosomal regions in the genome. This provides valuable insights for researchers to understand the mechanisms of gene expression regulation, as well as to investigate gene regulation, chromatin remodeling, and genomic changes associated with diseases.

Technical Features



DNA fragments of long linear distance while close in spatial structures are fixed and enriched for Pair-end sequencing. This technology empowers us to reveal the interactions between chromosome compartments and 3D structure of genome, which provides vital clues for novel intergenetic regulatory mechanisms.

Service Workflow



Bioinformatics

1. Hi-C library QC

- Hi-C distribution assessment.
- Interaction decay exponents(IDEs).

2. Chromatin interaction

- Genome-wide Hi-C interaction profiling (cis/trans analysis);
- Genome-wide Hi-C interaction heatmap;
- Compartment A/B; • TAD; • Genome-wide Loop.

3. Differential analysis on 3D chromatin structure.

Service Advantages

- Extensive experience with over 1000 Hi-C libraries constructed for over 800 species.
- Over 100 published cases with an accumulative impact factor of over 900.
- Customized restrict enzyme design to ensure optimal Hi-C efficiency on different species. Up to 93% valid interaction pairs have been achieved.
- In-house patents and software copyrights for Hi-C experiments and data analysis.
- After-sale services: After-sale services are valid for 3 months upon project completion, including project follow-up, trouble-shooting, results Q&A, etc.

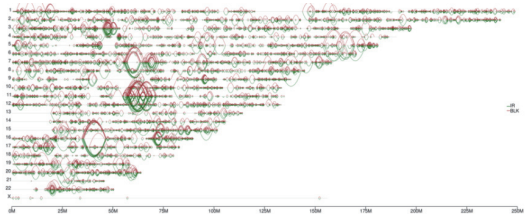
Service Specifications

Platform	Recommended Data	Resolution
Illumina PE150	Loop ≥ 150× TAD ≥ 50×	40 Kb; 10 Kb

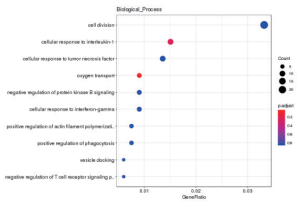
Sample Requirements

Frozen Tissue	Cells
1-2 g	10^7

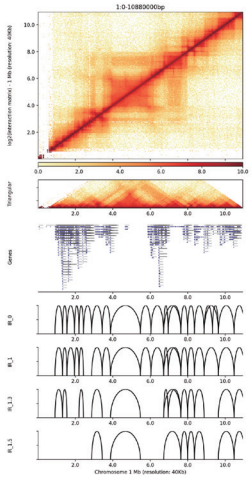
Demo Results



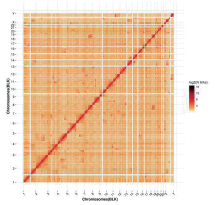
Genome-wide distribution of loops



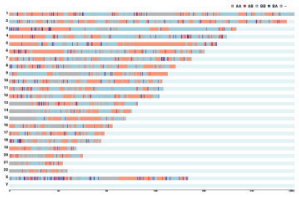
KEGG enrichment on differential TAD related genes



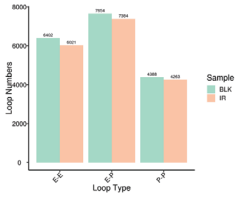
Visualization of TADs



Hi-C interaction heat map



Genome-wide distribution of A/B Compartment switching



Enhancer and promoter prediction on loop anchor sites analysis

Featured Publications

Year	Journal	Article	Applications	DOI
2021	Acta Pharmaceutica Sinica B	3D disorganization and rearrangement ofgenome provide insights into patho -genesis ofNAFLD by integrated Hi-C, Nanopore, andRNA sequencing	Disease treatment	10.1016/j.apsb.2021.03.022
2021	Neuro-Oncology	The comparative integrated multi-omics analysis identifies CA2 as a novel target for chordoma	Disease treatment	10.1093/neuonc/noab156

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