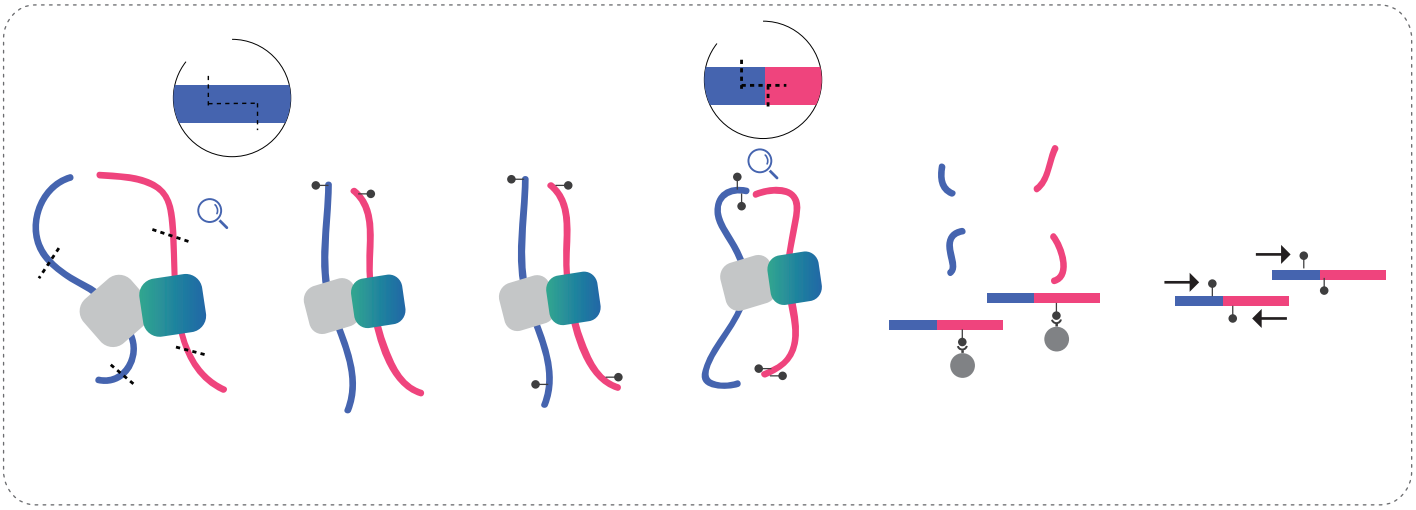
BMKGENE

# Hi-C based Chromatin Interaction

## Product Introduction

Accumulative evidence has shown that spatially arranged chromatin interactions play a vital role in gene expression regul-ation. The 3D folding of chromosomes brings distant regulatory elements into close spatial proximity, by which regulation of genes can be achieved. Hi-C is a method designed to capture chromosome configuration by combining probing proximity-based interactions and high-throughput sequencing.

## 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 re-gulatory mechanisms.

## Service Workflow

Sample delivery → Library construction → Sequencing → Data analysis → After-sale services

## Bioinformation List

**1. Hi-C library preparation and sequencing**

- Correlation between Hi-C libraries;
- Interaction decay exponents(IDEs).

**2. Chromosome 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.

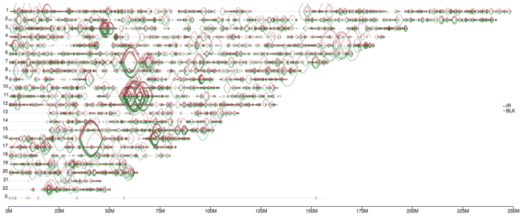
## Service Specifications

| Platform | Recommended data | Resolution | Turnaround Time |
|---|---|---|---|
| Illumina PE150 | Loop ≥ 150×<br>TAD ≥ 50 × | 10 Kb<br>40 Kb | 50-80 days<br>(Depending on species) |

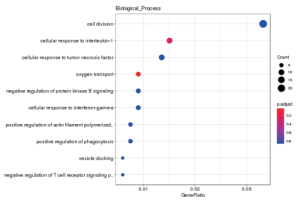
## Sample Requirements

| Frozen tissue | Cells |
|---|---|
| 1-2 g | 10^7 |

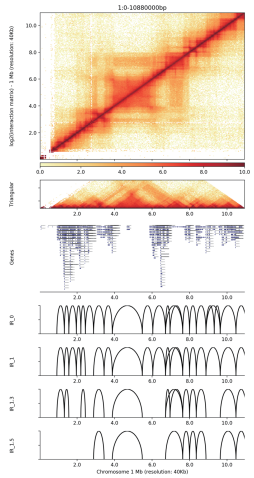
## Demo Results



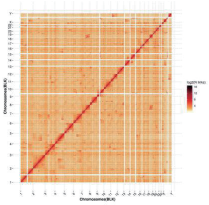
Genome-wide distribution of loops



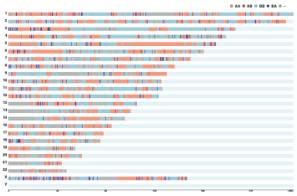
KEGG enrichment on differential TAD related genes



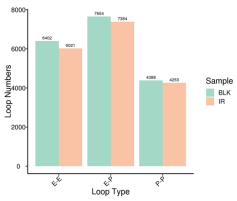
Visualization of TADs



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 | Paper | 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 | doi.org/10.1093/neuonc/noab156 |

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