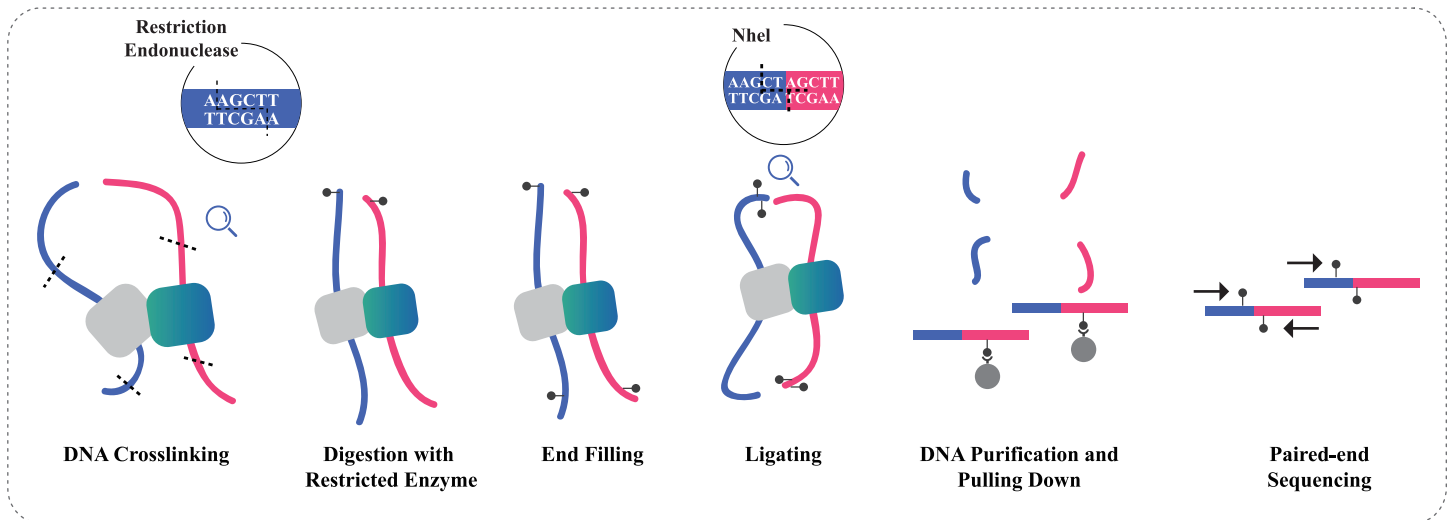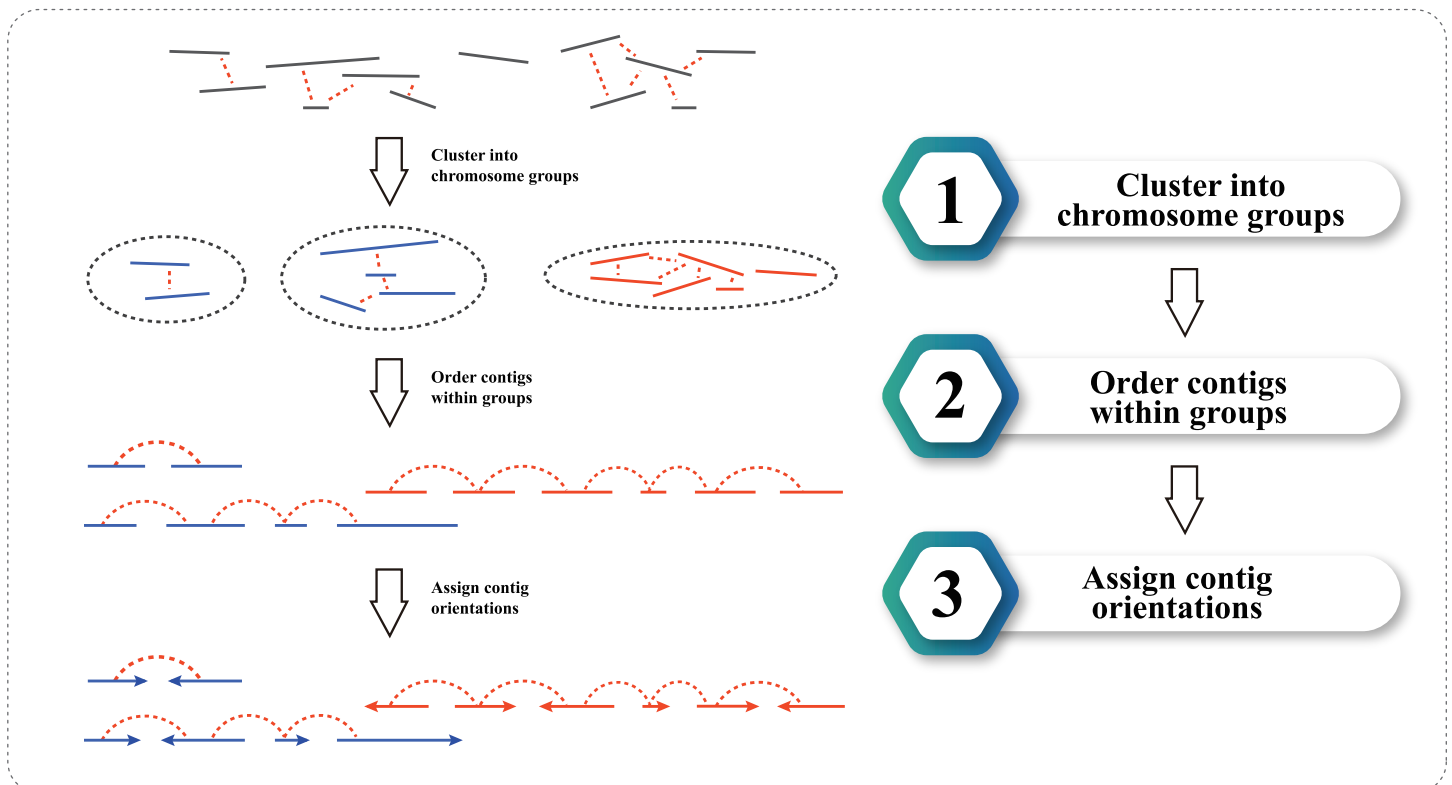# Hi-C based Genome Assembly

Hi-C is a method designed to capture chromosome configuration by combining probing proximity-based interactions and high-throughput sequencing. The intensity of these interactions is believed to be negatively correlated with physical distance on chromosomes.

Technical Work Flow

| DNA Crosslinking | Digestion with Restricted Enzyme | End Filling | Ligating | DNA Purification and Pulling Down | Paired-end Sequencing |

The interaction intensity captured by Hi-C sequencing provides vital guidance in clustering, ordering , and orienting of assembled sequences in a draft genome and anchoring those onto a certain number of chromosomes. This technology empowers a chromosome-level genome assembly in absence of a population-based genetic map.
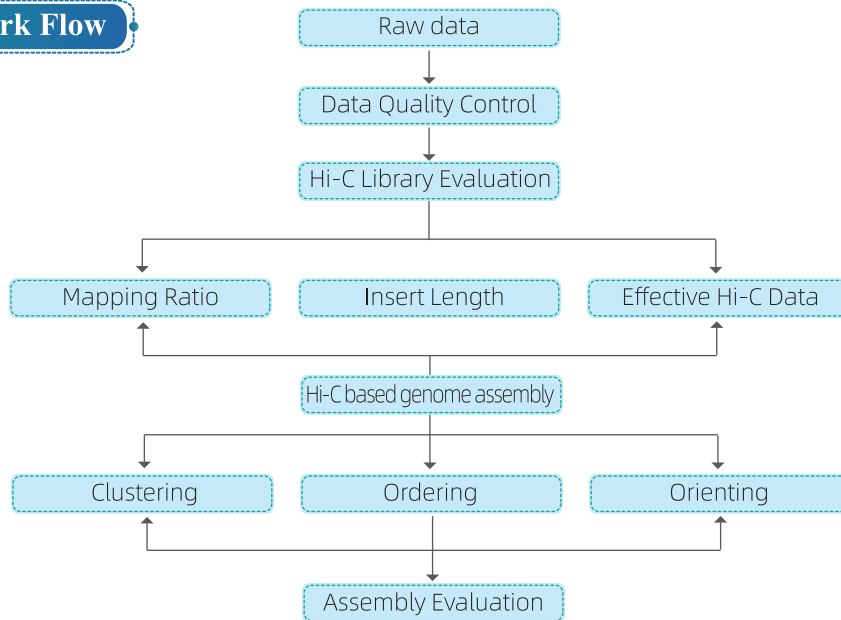

1. Cluster into chromosome groups
2. Order contigs within groups
3. Assign contig orientations

Service Work flow

Sample Delivery → Hi-C library preparation experiment → Hi-C library QC → Sequencing → Hi-C data QC → Bioinformatics analysis

Service Specifications

Sequencing Platform	Library size	Recommended depth	Estimated turn-around time	Assembly
Illumina NovaSeq 6000	300-350 bp	Simple genome ≥ 100 × Complex genome ≥ 150 ×	3 months (Depending on species)	Anchoring ratio ≥ 90% (Depending on species)

Service Advantages

- No need in constructing genetic population for contig anchoring;
- Higher marker density leading 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 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 redo;

Bioinformatics Work Flow

Raw data → Data Quality Control → Hi-C Library Evaluation → (Mapping Ratio, Insert Length, Effective Hi-C Data) → Hi-C based genome assembly → (Clustering, Ordering, Orienting) → Assembly Evaluation