3D Genome Construction from Hi-C Data

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Overview of Hi-C

- Hi-C is a method that uses high throughput DNA sequencing to determine genome-wide chromosomal interactions. It allows unbiased identification of chromatin interactions and a more random, automatic way of choosing target loci.

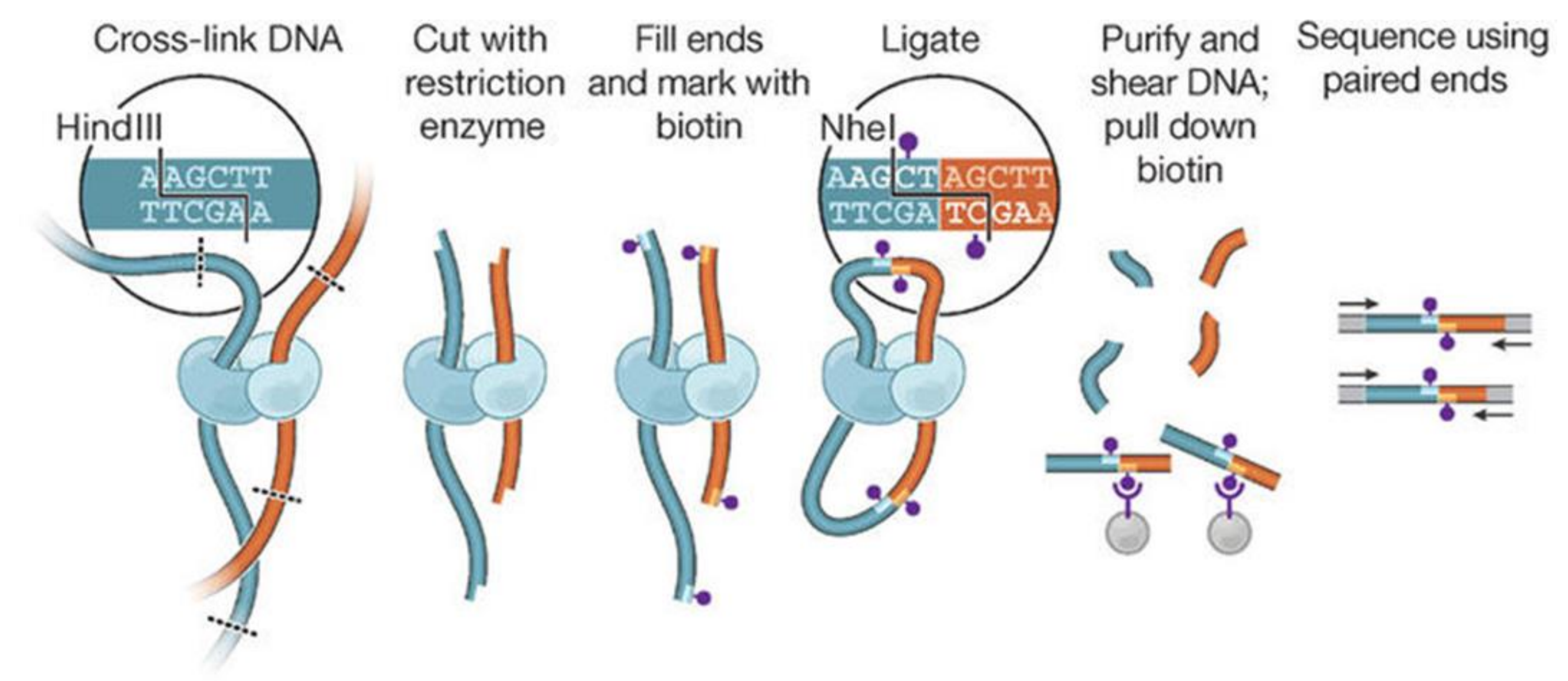


Figure 1: The Hi-C Technique

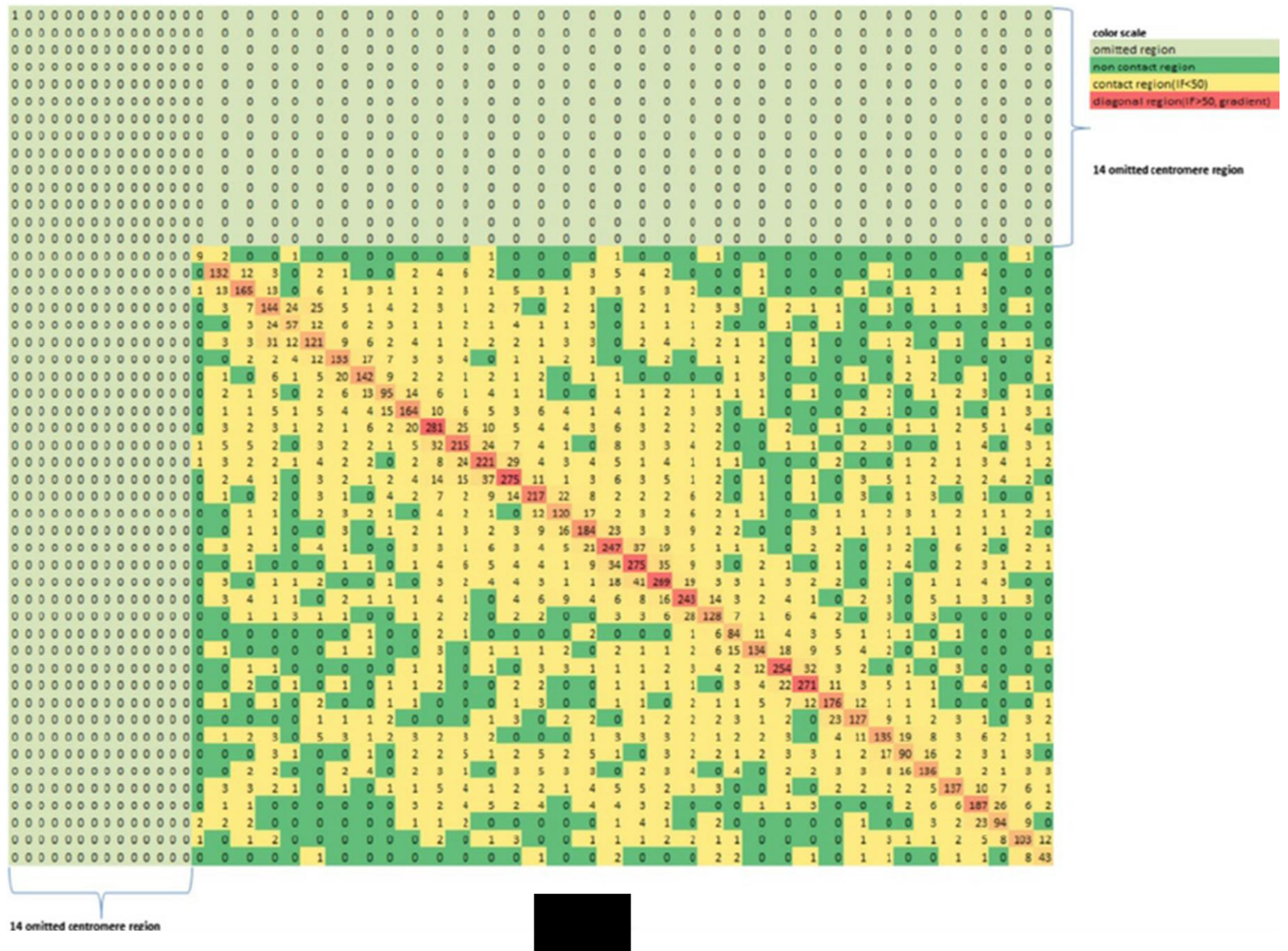
Figure 2: Paired-End Sequencing

Processing of Hi-C Data

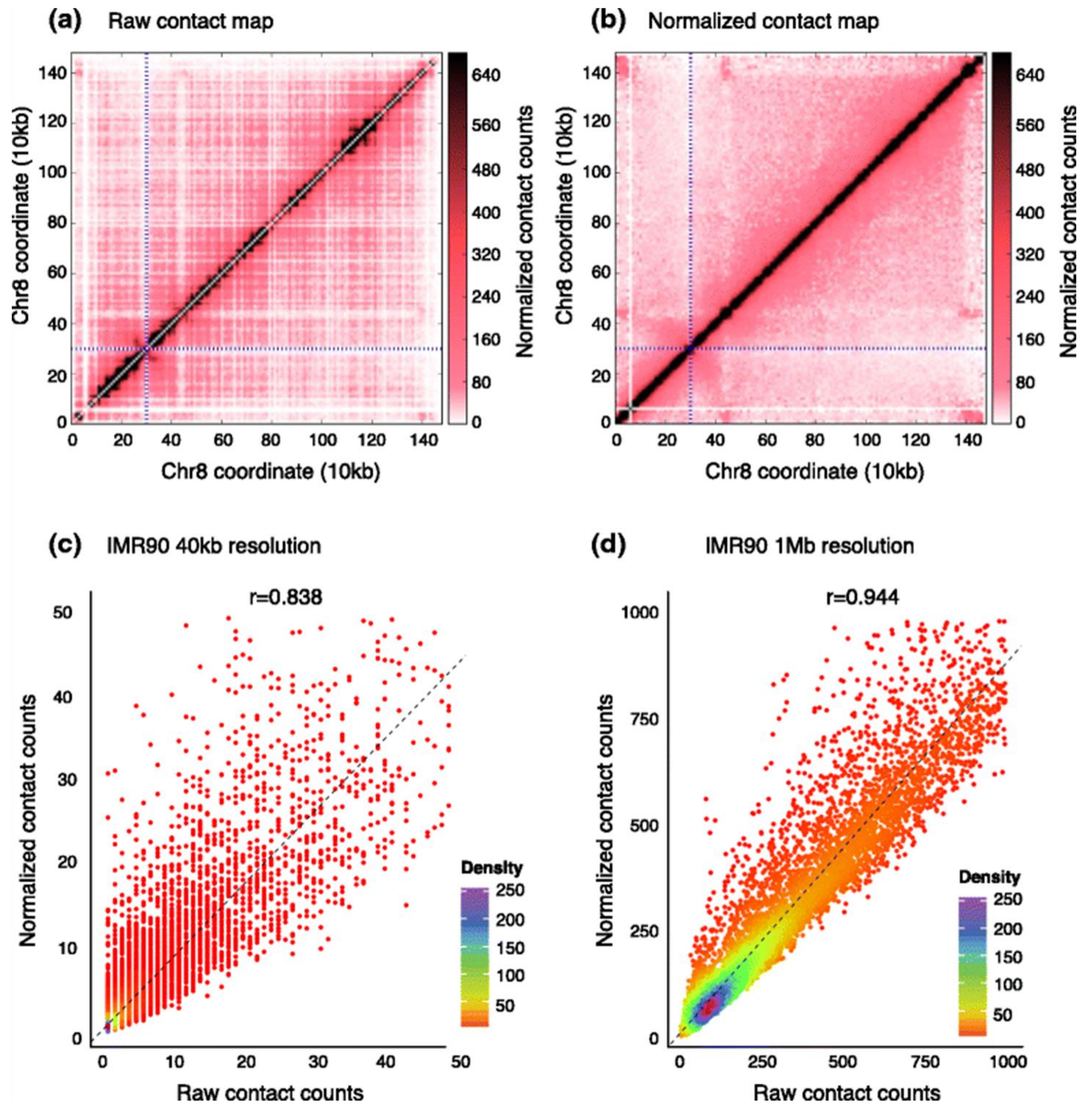
Get FASTQ read files

Convert mapped Hi-C reads to readable format

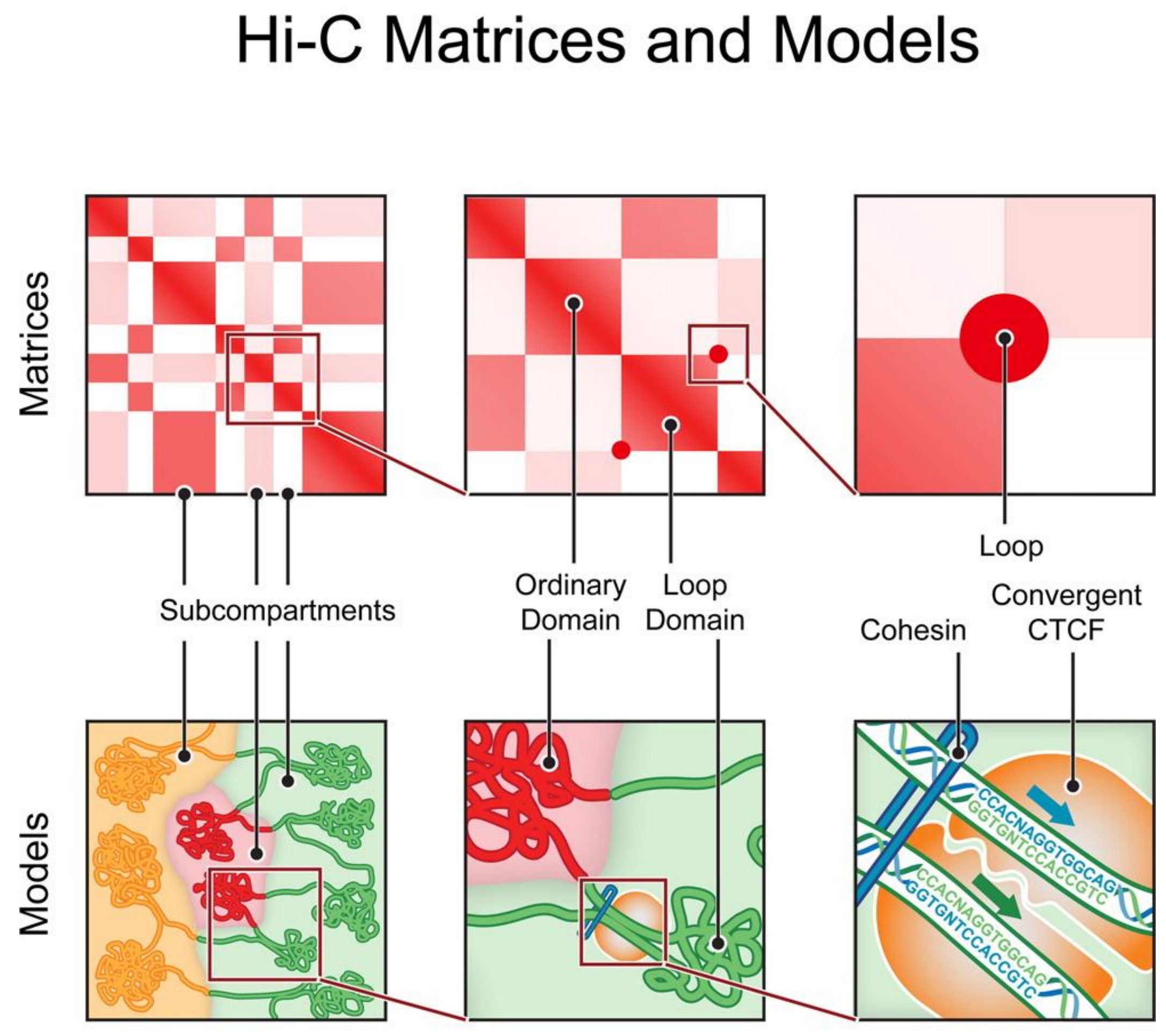
Extract contact matrices from readable format



Normalize Hi-C contact matrices



Genome Construction



- Using algorithms that transform Hi-C contact data of a chromosome or genome into an ensemble of probable 3D conformations for the dataset
- Two examples are LorDG and 3DMax

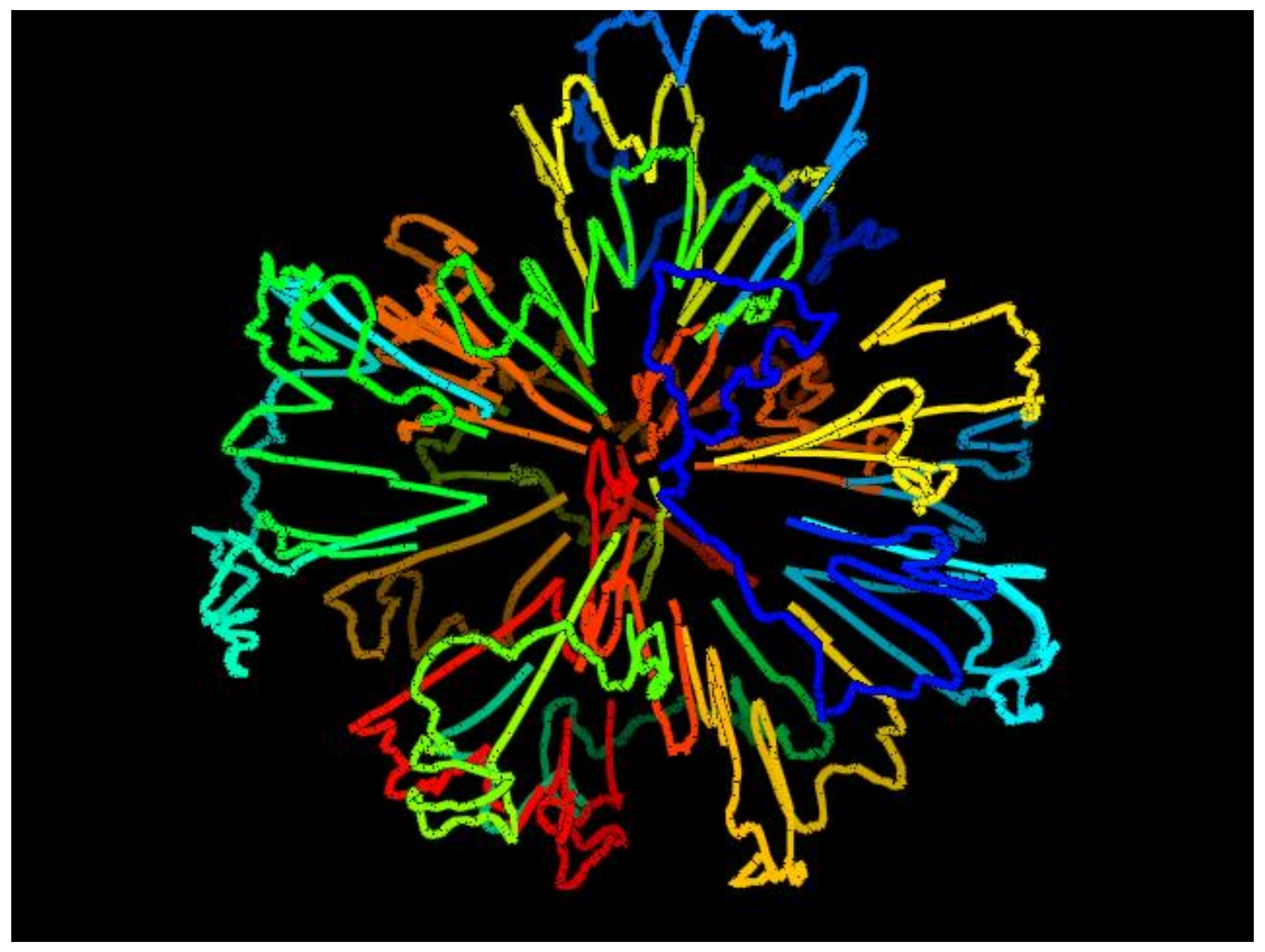


Figure 3: Genome Structure

References/Acknowledgments

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