BMKGENE

De Novo Genome Assembly

De Novo Genome Assembly constructs genomes from raw sequencing data without a reference genome. It's crucial for understanding biology and has diverse downstream research applications. Long read sequencing improves the assembly accuracy and quality. BMKGENE offers tailored solutions from sequencing to chro -mosome-level assemblies and annotation.

One-stop Genome Assembly Solution

Genome survey | Long-read sequencing | Genome assembly | Hi-C based chromosome-level genome assembly | Genome annotation

Service Workflow

Experiment design → Sample delivery → DNA/RNA extraction → Library construction → Sequencing → Data analysis → After-sale services

Bioinformatics

Genome Survey:

- Evaluation of genome size.
- Assessment of genome heterozygos -ity, repeat sequence proportion and genome GC content.

Long Read Sequencing:

- Data Quality Control

Hi-C based assembly:

- Data process and assessment & HiC library assessment.
- Hi-C based contigs anchoring.
- Assessment on Hi-C based contigs anchoring.

De Novo Genome Assembly:

- Raw data process and assessment.
- Genome assembly.

Genome Annotation:

- Whole-genome annotation: coding gene, repetitive sequence, transposon element, non-coding RNA, pseudogene.
- Function annotation: NR, eggNOG, GO, KEGG, TrEMBL, Swiss-prot, Pfam, InterPro.

Service Advantages

- Equipped with full spectrum of sequencing platforms: one-stop genome assembly solution.
- Flexible sequencing and assembling strategies fulfilling diverse genomes with different features.
- Highly skilled bioinformatician team with great experience in complex genome assemblies, including polyploids, giant genomes, etc.
- Over 160 successful cases with an accumulative published impact factor of over 1600.
- Turn-around-time as fast as 3 months for chromosome-level genome assembly.
- Solid technical support with a series of patents and software copyrights in both experimental side and bioinformatics.

Service Specifications

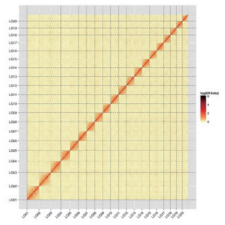
Content	Platform	Read Length	Coverage
Genome Survey	Illumina NovaSeq	PE150	≥ 50X
Genome Sequencing	PacBio Revio	15 kb HiFi Reads	≥ 30X
Hi-C	Illumina NovaSeq	PE150	≥ 100X

Note: Adequate sequencing depth is necessary for complex genomes.

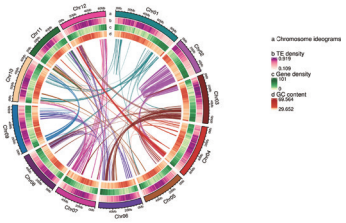
Sample Requirements

- It is recommended that all samples used for sequencing assembly come from the same individual.
- Transcriptome sequencing is suggested to assist genome annotation. It is recommended to collect mixed samples from different tissues and time periods for sequencing.

Demo Results



Hi-C Interaction Heatmap



Genome Circos Map
(TE density, gene density, GC content)

Featured Publications

Year	Journal	Title
2023	Nature Genetics	Super-pangenome analyses highlight genomic diversity and structural var -iation across wild and cultivated tomato species
2023	Nature Genetics	Genome assembly and genetic dissection of a prominent droughtresistant maize germplasm
2023	Nature Genetics	De novo genome assembly and analyses of 12 founder inbred lines provide insights into maize heterosis
2023	Nature Communications	Revealing evolution of tropane alkaloid biosynthesis by analyzing two gen -omes in the Solanaceae family
2023	Nature Communications	Common evolutionary trajectory of short life-cycle in Brassicaceae ruderal weeds

BMKGENE

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