

BGI Empowers its Multi-Omics Solutions by Utilizing PacBio Revio Long-Read Sequencing Platform

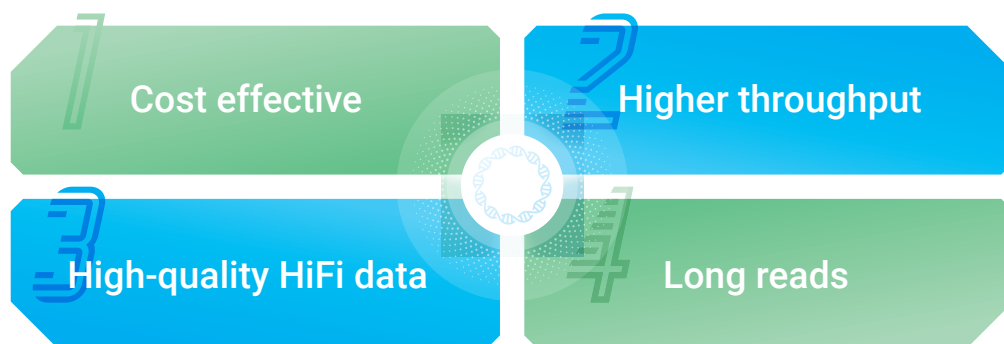


Service Description

Long-read sequencing can effectively solve some of the insurmountable problems in short-read sequencing and significantly improve the detection rate of large structural variation sites by constructing long fragment libraries.

Service Specification

BGI Long-read Sequencing Services are performed with the PacBio Revio long-read sequencing platform, and standard bioinformatics pipeline, which enables superior data quality , analysis results, higher throughput, and lower sequencing costs.



Multiple Types of Long-read Sequencing Services

BGI offers multiple services based on PacBio long-read sequencing, as well as supporting low-input library construction.

All projects are supported by the professional laboratory and bioinformatics infrastructure.

Plant & Animal Genome Sequencing

- Plant & Animal *de novo* sequencing
- T2T genome & pan-genome research
- Haplotype-resolved *de novo* assembly
- Plant & Genome whole genome resequencing: SV calling

Human Whole Genome Sequencing

- SV calling
- Total variation detection
- Population cohort study
- T2T genome and phasing

Long-read Transcriptome

- Full-length isoform RNA sequencing
- Profile expression at isoform resolution
- Reveal transcript structure information without assembly
- Single-cell Isoform sequencing

Epigenome Sequencing

- Methylation detection

Pre-made library sequencing

- Sequencing only for PacBio Revio system

Microbial Genome Sequencing

- Bacterial/Fungal *de novo* sequencing
- 16S Full-length sequencing

Request for Information or Quotation

Contact a BGI representative to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics.

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BGI Genomics



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We Sequence, You Discover