

CRISPR Genome-Wide Off-Target Analysis Service Overview



Service Description

The emergence of the CRISPR-Cas9 system has triggered a technical revolution in mammalian genome editing. Compared to traditional gene-targeting strategies, CRISPR-Cas9 technology offers a more efficient and cost-effective approach for generating genetically modified animal models. However, off-target cleavage in CRISPR-mediated genome editing is a major concern in the analysis of phenotypes as well as the selection of therapeutic targets.^[1]

Whole genome sequencing (WGS) is a straightforward approach for an unbiased survey of the full genome, which can be used to identify off-target nuclease activity^[2].

Genome-wide Off-target Detection Advantages

- Unbiased, with the capability to screen out all potential off-target sites.^[3]
- The greatest sensitivity and precision for SNP/InDel detection.^[4]
- No cellular model restriction.^[1]
- Simple experimental designs.^[1]



Sequencing Service Specification

BGI Genome-wide Off-target Detection Services are performed with the DNBSEQ™ platform and standard bioinformatics pipeline for superior data quality and analysis results.



Sample Preparation and Services

- Library preparation (DNBSEQ™ platform).
- Human/Animal/Plant samples accepted.
- Appropriate sequencing strategies are recommended according to different data.

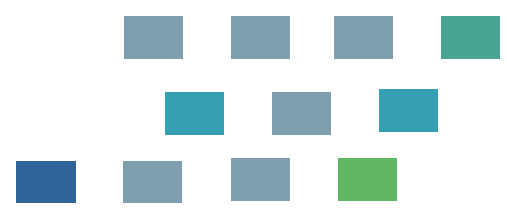
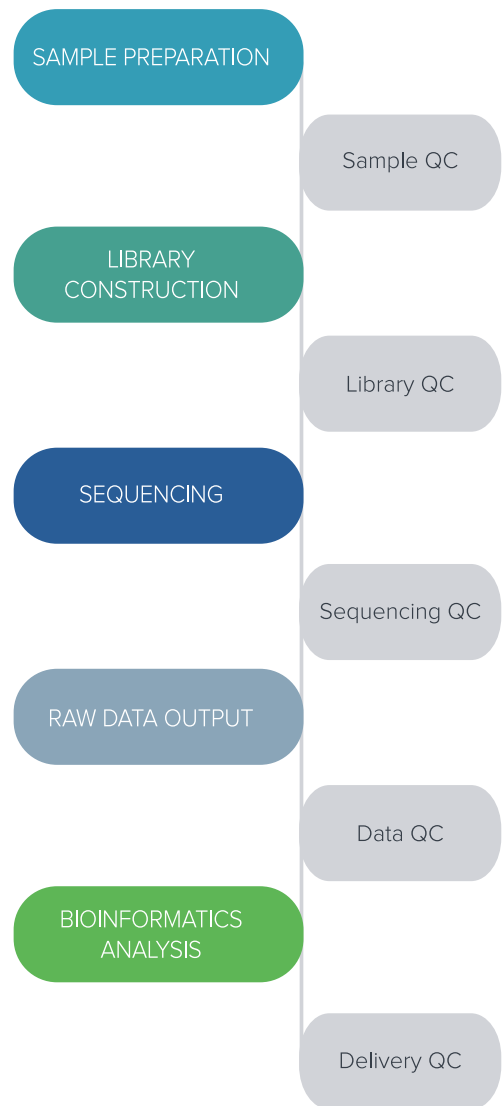


Turnaround Time

- Typical 31 working days from sample QC acceptance to data analysis report availability
- Expedited services are available; contact your local BGI specialist for details

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



Sequencing Technology

BGI Genome-wide Off-target Detection Services are performed on the DNBSEQ™ platform.

Data Analysis

Besides data output, BGI offers a range of standard and customized bioinformatics pipelines for your project. Reports and output data files are delivered in these file formats: FASTQ, BAM, VCF, JSON and TXT.

STANDARD BIOINFORMATICS ANALYSIS

- Assessment of sequencing reads
- Alignment of reads to reference genome, depth and coverage assessment
- SNP/InDel calling
- Specific variants detection (provide control sample)
- sgRNA homologous region analysis
- Editing efficiency analysis
- Off-target detection and statistics
- Off-target sites annotation
- Visualization of Analysis Results

CUSTOM ANALYSIS

Further customization of bioinformatics analysis to suit your unique project is available: Please contact your BGI technical representative.

Sample Requirements

DNA Sample	Library type	Mass	Concentration	Integrity (AGE)	Sample Purity
Regular Samples	PCR	≥200ng (Recommend ≥400ng)	≥8ng/μL	The band shown on gel electrophoresis has little degradation, or of fragment size greater than 20kb.	No contamination with RNA, protein or salt ions; colorless and transparent; non-sticky
	PCR-free	≥1μg (Recommend ≥2μg)	≥12.5ng/μL		

References

- [1] Dong Y, Li H, Zhao L. et al. Genome-Wide Off-Target Analysis in CRISPR-Cas9 Modified Mice and Their Offspring. G3 (Bethesda).;9(11):3645-3651(2019).
- [2] Atkins A, Chung CH, Allen AG, et al. Off-Target Analysis in Gene Editing and Applications for Clinical Translation of CRISPR/Cas9 in HIV-1 Therapy. Front Genome Ed.;3:673022(2021).
- [3] Chen S, Yao Y, Zhang Y, Fan G. CRISPR system: Discovery, development and off-target detection. Cell Signal. 70:109577(2020).
- [4] Foox, J., Tighe, S.W., Nicolet, C.M. et al. Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. Nat Biotechnol 39, 1129–1140 (2021).

BGI Offices

BGI Americas

One Broadway, 14th Floor
Cambridge, MA 02142,
USA

BGI Europe

Jutrzenki 12 A,
02-230 Warszawa,
Poland

BGI Asia

Building NO.7, BGI Park,
Yantian District Shenzhen,
Guangdong Province, China

BGI Australia

L6, CBCRC, 300 Herston
Road, Herston, Brisbane,
Queensland 4006, Australia

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We Sequence, You Discover