BGISEQ-500 Service Overview
BGI ChIP Sequencing

Service Description

ChIP Sequencing is widely used to analyze protein interactions with DNA. It combines chromatin immunoprecipitation (ChIP) with massively parallel DNA sequencing to identify binding sites of DNA-associated proteins, and can be used to precisely map global binding sites for any protein of interest. ChIP sequencing offers higher resolution and more precise and abundant information in comparison with array-based ChIP-chip.
Besides clean sequencing data output, BGI offers standard, advanced and customized bioinformatics services to suit your specific research needs.

Confidence:	Great correlation with HiSeq data.
Low input:	As low as 5ng ChIP-ed DNA/sample for human sample.
Comprehensive analysis:	Correlation analysis between ChIP-Seq and RNA-seq.

Sequencing Service Specification

The BGI ChIP-Seq Service will be performed with the BGISEQ-500 sequencing system, featuring combinatorial probe-anchor synthesis (cPAS) and DNA Nanoballs (DNB) technology[1] for superior data quality.

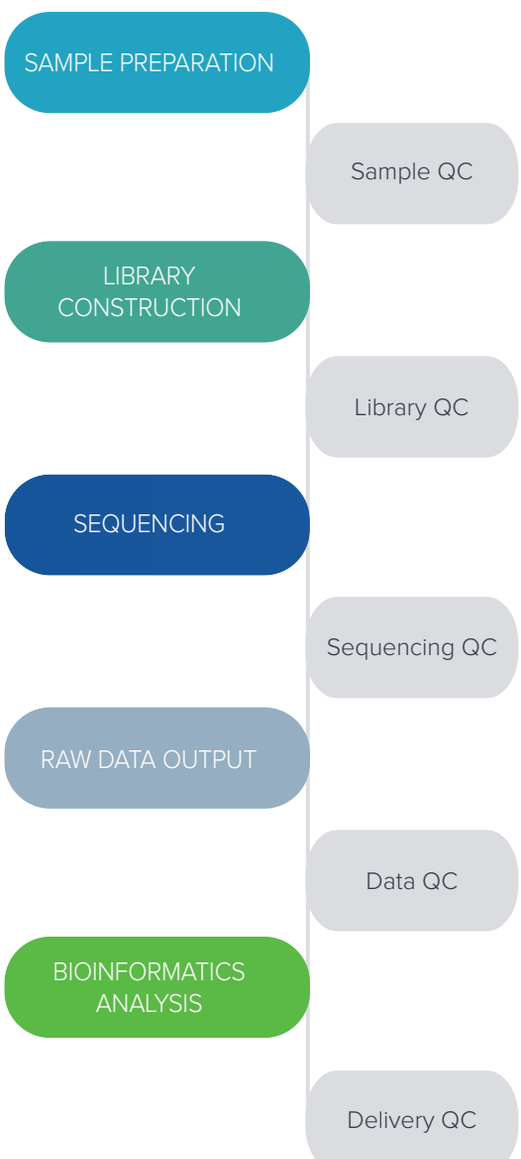
- 50bp Single-end sequencing reads
- Standard output 20 Million reads per sample
- Clean data and bioinformatics analysis are available in standard file formats
- Available data storage and bioinformatics applications
- Cloud-based data storage and delivery system

Turn Around Time

- Typical 25 working days from sample QC acceptance to final data delivery
- 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 high quality results.



Data Analysis

In addition to clean data output, BGI offers a range of standard, advanced and customized bioinformatics pipelines for your ChIP-Seq analysis project, including the correlation analysis of differential expression genes and peak-related genes.

Reports and output data files are delivered in industry standard FASTQ, and Excel file formats with publication-ready tables and figures.

STANDARD BIOINFORMATICS ANALYSIS

- Data filtering
- Alignment to the reference genome
- Peak scanning and annotation
- Identification of differential peaks between samples
- Identification of differential peaks between groups
- Differential peaks annotation

ADVANCED BIOINFORMATICS ANALYSIS

- Motif Analysis

CUSTOMIZED BIOINFORMATICS ANALYSIS

- Statistics of the epigenetic modification level and mRNA expression level of related genes
- The distribution of epigenetic modification level in different gene categories
- Overall connection of epigenetic modification level and the mRNA expression level in different gene categories
- The relationship of the ratio of epigenetic modification and the ratio of mRNA expression in a pair of samples
- Clustering analysis based on epigenetic modification level and mRNA expression level
- Calculate different level of epigenetic modification when mRNA expression level is different
- GO, Pathway analysis, related functional excavation and verification of the genes that differences exist in both epigenetic modification and mRNA expression
- Further customization of Bioinformatics analysis to suit your unique project is available: Please contact your BGI technical representative.

BGISEQ-500 Sequencing Technology

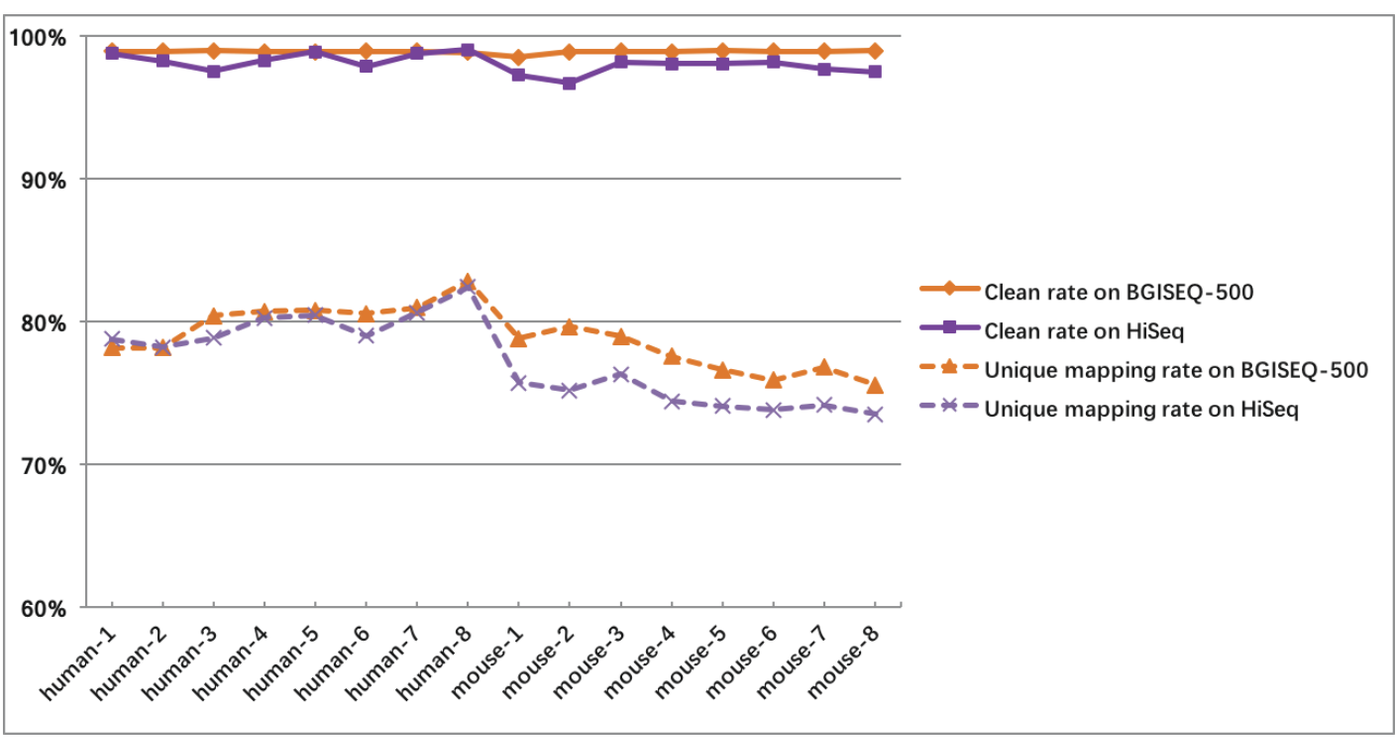
BGISEQ-500 is an industry leading high-throughput sequencing system, powered by combinatorial Probe-Anchor Synthesis (cPAS) and improved DNA Nanoballs (DNB) technology [1].

The cPAS chemistry works by linking a fluorescent probe to a DNA anchor on the DNB, followed by high-resolution digital imaging. This combination of linear amplification and DNB technology reduces the error rate while enhancing the signal. In addition, the size of the DNB is controlled in such a way that only one DNB is bound per active site in the flow cell. This patterned array technology not only provides sequencing accuracy, but it also increases the chip utilization and sample density.

Sequencing data performance

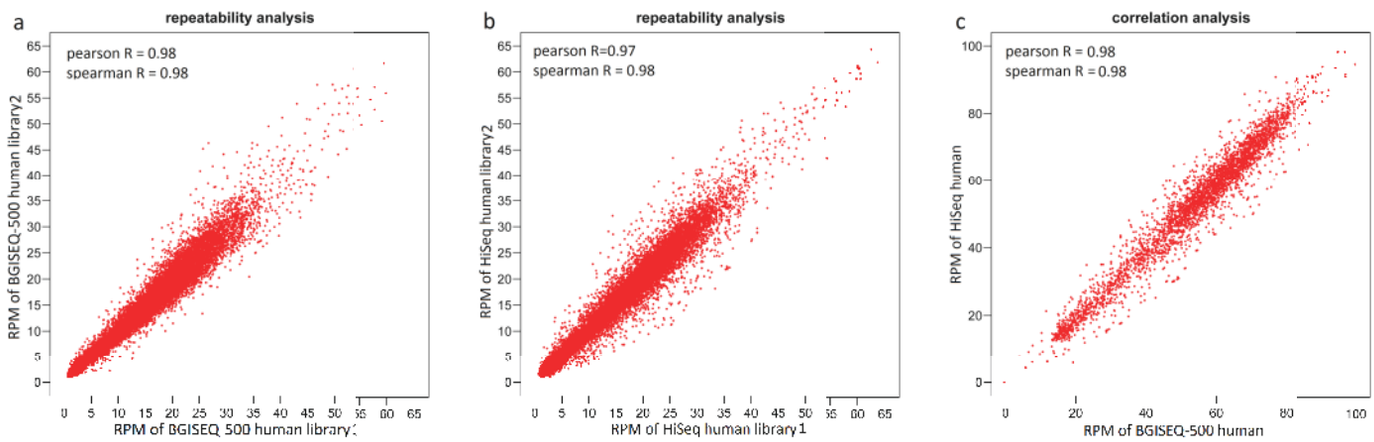
Excellent agreement of data quality between HiSeq and BGISEQ-500

The plot below shows the high sequencing data quality of human HeLa cell libraries and mouse libraries on BGISEQ-500 as compared to the HiSeq platform. By applying the same filtering criteria, the clean rate and unique mapping rate from the same samples are consistent on both platforms.



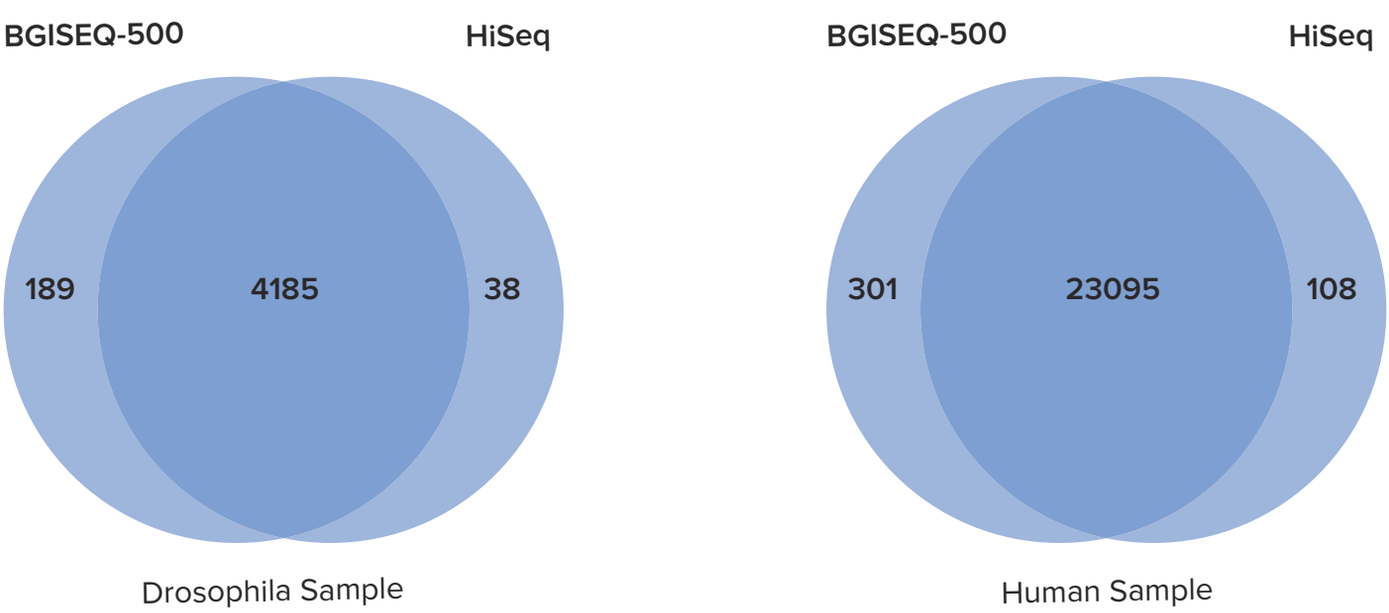
Excellent agreement of reads per million (RPM) between HiSeq and BGISEQ-500

The scatter plots below compare the reads per million (RPM) values of human HeLa cell sample sequenced on the BGISEQ-500 and HiSeq platforms. The coefficients of sequencing repeatability on both platforms are high (Figures a, b). There is a high correlation between BGISEQ-500 and HiSeq platforms as well (Figure c).



Excellent agreement of peak number detection between HiSeq and BGISEQ-500

The figures below show the comparison of detected peak numbers on both HiSeq and BGISEQ-500 platforms from the same samples[2]. The common peak detection rate of both drosophila and human HeLa cell sample are higher than 99%, while both platforms have a small amount of their own uniquely detected peaks.



Sample Requirements

We can process DNA samples of human, plant, animal and microbial samples, with the following general requirements:

	DNA Amount and Concentration	Minimum Volume
ChIP-ed DNA	Amount ≥ 10ng, Concentration ≥ 1 ng/μl	15 μl
ChIP-ed DNA (human sample only)	Amount ≥ 5ng, Concentration ≥ 1 ng/μl	15 μl

References

[1] Human genome sequencing using unchained base reads on self-assembling DNA nanoarrays

Drmanac R, Sparks AB, Callow MJ, Halpern AL, Burns NL, Kermani BG, Carnevali P, Nazarenko I, Nilsen GB, Yeung G, *et al*.

Science (2010) 327(5961):78–81 doi:10.1126/science.1181498

http://science.sciencemag.org/content/327/5961/78.full

[2] ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia

Stephen G. Landt,Georgi K. Marinov,Anshul Kundaje, *et al*.

Genome Res. 2012 Sep;22(9):1813-31. doi: 10.1101/gr.136184.111

https://www.ncbi.nlm.nih.gov/pubmed/22955991

Want to learn more?

Contact your local BGI account representative for the most affordable ChIP-sequencing rates in the industry, to discuss how we can meet your specific project requirements or for expert advice on experiment design, from sample to bioinformatics.

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