Plant and Animal Low Pass Whole Genome Sequencing

Leverage the speed and accuracy of complete genomic information for your breeding programs

Service Description

Plant and animal research, including phylodiversity investigation, agricultural trait discovery, genomic selection, GWAS, and molecular breeding, need more information in a shorter time and at a lower cost point, than legacy technology such as genotyping arrays can provide.

Low-pass whole genome sequencing (LP-WGS) outperforms arrays by delivering an order of magnitude more data, greater statistical power, and enhanced variant discovery capabilities at >99% accuracy, at pricing that enables much more affordable large scale research.

With the combination of revolutionary, high-capacity DNBSEQ™ sequencing technology and Gencove's analysis platform, BGI's low pass whole genome sequencing service enables researchers to stretch their research budgets further and commercial breeders to confidently make optimal genomic selection decisions to get to market faster with their best-in-breed.

Service Highlights

- Low DNA input amounts
- Even coverage of reads
- Much less duplication
- True PCR-Free
- Index hopping free

Sequencing Service Specification

BGI Plant and Animal low pass whole genome sequencing services are executed with the DNBSEQ™ sequencing system.

Sample preparation and services

- PCR and PCR-Free library methods are available
- 100bp and 150bp paired-end sequencing available
- Raw data, standard and customized data analysis
- Available data storage and bioinformatics applications

Sequencing Quality Standard

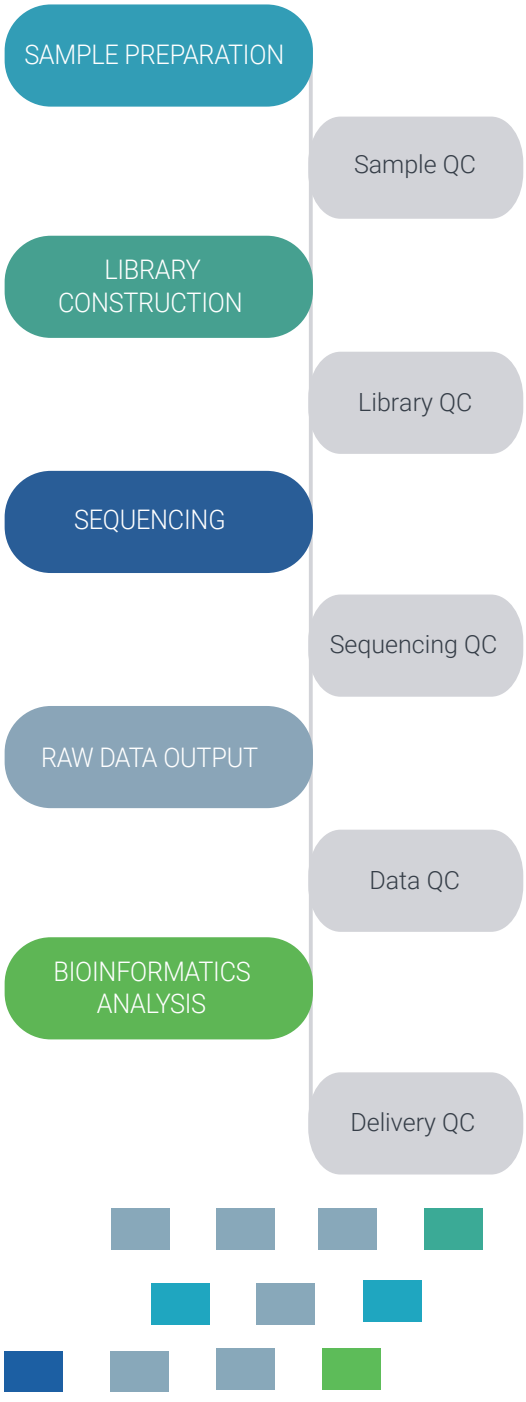
- Guaranteed ≥80% of clean bases with quality score of ≥Q30

Turnaround Time

- Typical 25 working days from sample QC acceptance to filtered raw data availability
- Expedited services are available; Contact your local BGI specialist for details

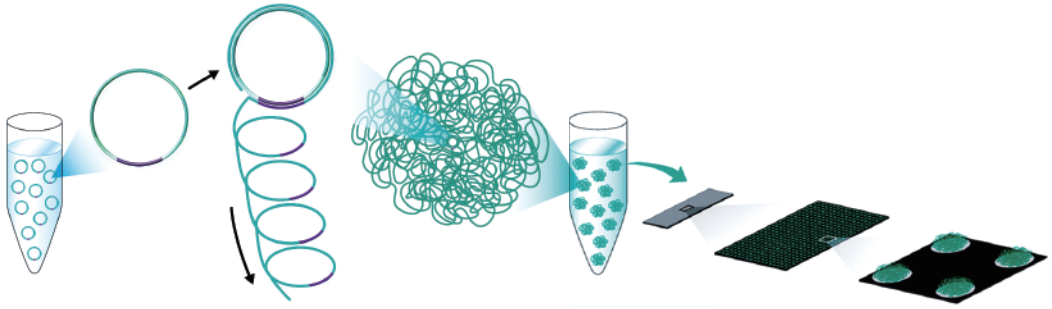
Project Workflow

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.



DNBSEQ™ Sequencing Technology

DNBSEQ™ is an innovative high-throughput sequencing technology, first developed by BGI's Complete Genomics subsidiary in Silicon Valley. The system is powered by combinatorial Probe-Anchor Synthesis (cPAS), linear isothermal Rolling-Circle Replication and DNA Nanoballs (DNB™) technology, followed by high-resolution digital imaging.
The combination of linear amplification and DNB technology reduces the error rate while enhancing the signal. The size of the DNB is controlled in such a way that only one DNB is bound per active site on the flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.The result is ultra-high output of up to 1400 Gb/run.



Gencove's Imputation and Analysis Platform

Gencove's platform enables highly accurate variant calling from low-pass sequencing data. Imputation accuracy outperforms that of the common genotyping arrays providing more statistical power for discovery. In addition, Gencove's platform returns ancestry, CNV and microbiome analysis for every sample.
Once sequenced, the data is uploaded to the Gencove platform, where they are compared to a fully sequenced and assembled standard haplotype genome. This step, called imputation, results in millions of over 99% accurate variant calls for every sample. We set up and validated LP-WGS for a variety of plant, agricultural animal, companion animal, and model organisms including cattle, pig, chicken, dog, cat, rat, mice, corn, soybean, peas, and rice. Sample data are shown below.
Output data files are delivered in industry standard BAM and VCF files.

Samples results of concordance studies in different species performed with different industry partners

SPECIES	SEQUENCING COVERAGE	SITES CALLED AFTER IMPUTATION	CONCORDANCE WITH WGS	REFFERENCE PANEL SIZE(INDIVIDUALS)
Cattle	0.4×	70 million	99.30%	946
Chicken	0.5×	26 million	99.00%	124
Dogs	1×	46 million	99.20%	435
Cats	0.4×	56 million	98.40%	78
Corn	1×	81 million	99.30%	277

Data Analysis

Besides clean data output, BGI offers a range of standard and customized bioinformatics pipelines for your low pass whole genome sequencing project. Reports and output data are delivered in industry-standard file formats: FASTQ, BAM, VCF, .xls, .png
Our standard analysis includes data filtering, alignment SNP/InDel/SV/CNV calling, annotation and statistics. The following additional analysis along with custom requests are also available.

ADVANCED ANALYSIS

- Population evolution analysis
- Point mutation detection (wild vs. mutant)
- Linkage map construction and QTL mapping
- GWAS analysis
- BSA analysis

CUSTOMIZED ANALYSIS

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

Sample Requirements

We can process your gDNA, whole blood, cell line, fresh frozen tissue and FFPE samples from a variety of species, with the following general requirements:

	DNA AMOUNT AND CONCENTRATION	MINIMUM SAMPLE VOLUME
Regular Samples	Intact genomic DNA ≥ 1 μg, Concentration ≥ 12.5 ng/μl	15 μl
Low Input Samples	Intact genomic DNA ≥ 200 ng, Concentration ≥ 2.5 ng/μl	15 μl
True PCR-Free	Intact genomic DNA ≥ 1.5 μg, Concentration ≥ 12.5 ng/μl	15 μl

Request for Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry and 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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We Sequence, You Discover