

## Plant and Animal Whole Genome Re-Sequencing

### Service Description

Plant and animal whole genome re-sequencing (WGRS) involves sequencing the entire genome of a plant or animal and comparing the sequence to that of a known reference genome. Re-sequencing of the plant and animal genome will identify genetic variations such as SNPs and Indels and discover other genetic changes of the sequenced species. It has been used for the identification of functional genes and markers of important traits to facilitate molecular breeding and to improve agricultural production and conservation.

### Highlights of DNBSEQ™ Technology

- Even coverage of reads
- Much less duplication
- True PCR-Free
- Index hopping free

### Sequencing Service Specification

BGI Plant and Animal Whole Genome Re-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  $\geq 90\%$  of clean bases with quality score of Q20
- Standard sequencing coverage of 10-30X is recommended for the study of individuals and 5-10X for population studies



#### Turnaround Time

- Typical 30-40 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.



## Data Analysis

Besides clean data output, BGI offers a range of standard and customized bioinformatics pipelines for your whole genome re-sequencing project.

Reports and output data files are delivered in industry standard file formats: FASTQ, BAM, VCF, .xls, .png

### STANDARD ANALYSIS

- Data Filtering
- Alignment
- SNP/InDel/SV/CNV calling, annotation and statistics

### 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 $\geq 1 \mu\text{g}$ , Concentration $\geq 12.5 \text{ ng}/\mu\text{l}$	15 $\mu\text{l}$
Low Input Samples	Intact genomic DNA $\geq 200 \text{ ng}$ , Concentration $\geq 2.5 \text{ ng}/\mu\text{l}$	15 $\mu\text{l}$
True PCR-Free	Intact genomic DNA $\geq 1.5 \mu\text{g}$ , Concentration $\geq 12.5 \text{ ng}/\mu\text{l}$	15 $\mu\text{l}$

## Request 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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