SGI – BACTERIAL WGS SERVICE

Bacterial Whole Genome Sequencing

Platform :

Next Generation Sequencing

Whole Genome Sequencing (WGS) of bacterial genomes is becoming more and more relevant for the medical sector and research as general. It enables high resolution characterization of bacteria in terms of properties that include antibiotic resistance, molecular epidemiology, and virulence. As for research as general, studying the novel bacterial genomes can open the opportunity for discovering new biotechnologies that useful for the humankind.

With our advanced Next Generation Sequencing platform and in-house bioinformatician, SGI offers Bacterial WGS Service for both de-novo or by reference sequencing depend on the customer research's needs.
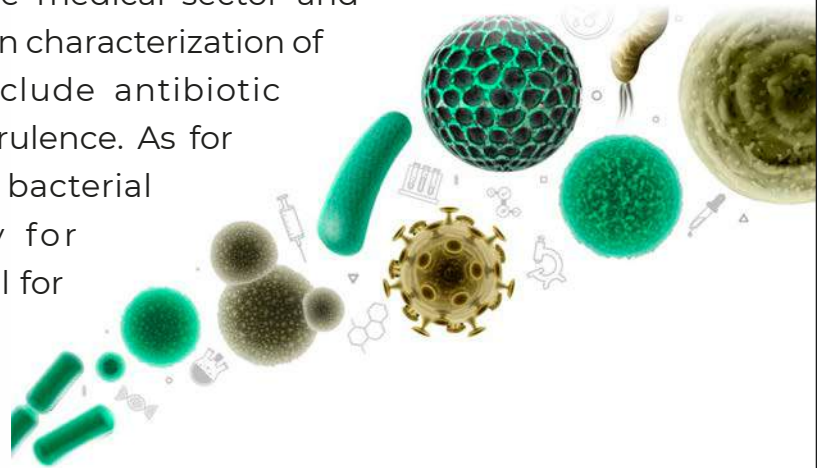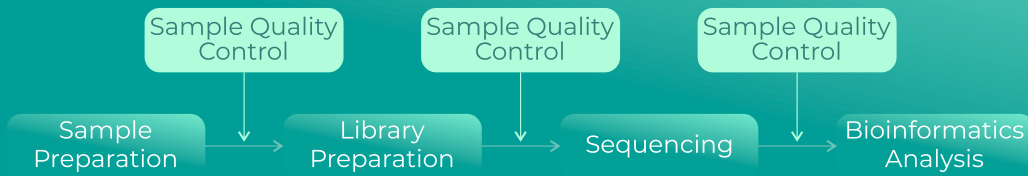
KEY Technology :

High accuracy, low Adapter Rate, low Duplication Rate, and low Index Hopping.

Our end-to-end workflow can support you with a broad range of species.

Project Workflow

Sample Quality Control	Sample Quality Control	Sample Quality Control

Sample Preparation → Library Preparation → Sequencing → Bioinformatics Analysis

Sample Requirements

▶ Raw materials

Sample Type	Minimum Requirement
Fresh Cell Culture from Single Colony	$\geq 1 \times 10^7$ cells

Wrap the samples with parafilm thoroughly and please ensure there is sufficient amount of ice gel in the package.

▶ gDNA

Mass	Concentration	Integrity	Minimum Requirement
> 1 µg	$\geq 12{,}5$ ng / µl	The band shown on gelelectrophoresis has little degradation, or of fragment size greater than 20kb	No contamination with RNA, protein or salt ions; colorless and transparent; non-sticky. *) Ensure purify of the sample

- Customers need to provide sample analysis in one of the following methods: Qubit, AGE, Agilent 2100, or other equivalent insruments.

- **The solvent composition of the sample must be indicated**. SGI will perform the gDNA quality test before entering the NGS protocol.

▶ *What will you get :*

-Without Data Analysis
   Raw data sequencing (fastq files)

-With Data Analysis
   Raw data sequencing (fastq files)

   Standard analysis :
   - Project Summary
   - Data Summary
   - Assembly Summary
   - Comparative Genomics

TAT: approx. 2 months