

## Microbial Whole Genome Sequencing

### 1. Sample Requirements

Sample Type	Amount Qubit®	Volume	Concentration	Purity NanoDrop™
Genomic DNA	≥ 300 ng	≥ 20 µL	≥ 5 ng/µL	OD260/280=1.8~2.0, no degradation or contamination

### 2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 bp
Recommended sequencing depth	≥ 100x for bacterial genomes ≥ 50x for fungal genomes
Data quality	≥ 80% bases with Q30 or higher
*Turnaround time	Minimum 3 weeks from confirmation of library preparation to data releasing without bioinformatic analysis

\*Turnaround time varies depending on the project volume.

### 3. Data Analysis Contents

Bacterial and Fungal Re-sequencing Standard Analysis
Data quality control: filtering reads containing adapter or with low quality
Alignment with reference genome, statistics of sequencing depth and coverage
SNP/InDel calling, annotation and statistics
CNV calling, annotation and statistics
SV calling, annotation and statistics