Metagenomic Sequencing

1. Sample Requirements

Sample Type	Amount(Qubit®)	Volume	Concentration	Purity(NanoDrop™)
Total DNA	≥ 200 ng	≥ 20 µL	≥ 10 ng/µL	OD 260/280=1.8~2.0, no degradation or RNA contamination

2. Sequencing Parameters

Platform	NovaSeq 6000
Read length	Paired-end 150 bp
Recommended sequencing depth	≥ 6G/12 G raw data
Data quality	Guaranteed ≥ 85% bases with Q30 or higher
*Turnaround time	Minimum 5 weeks from confirmation of library preparation to datareleasing without bioinformatic analysis

*Turnaround time varies depending on the project volume.

3. Data Analysis Contents

Shotgun Metagenomic Sequencing Standard Analysis
Data quality control: filtering reads containing adapter or with low quality, filtering host genome sequences
Assembly
Species annotation (microorganic sequences extracted from NCBI NR database, 2018-10)
Gene prediction
Gene annotation （KEGG, eggNOG, CAZy, ARDB databases)
Species/Gene/Function abundance statistics and cluster analysis
Comparative analysis (among samples)