

Microbial *De novo* Sequencing

1. Sample Requirements

1.1 Illumina platform (350 bp insert DNA Library)

Sample Type	Amount(Qubit®)	Volume	Concentration	Purity “(NanoDrop™)”
Genomic DNA	≥ 1 µg	≥ 20 µL	≥ 20 ng/µL	OD260/280=1.8-2.0; no degradation or contamination

1.2 PacBio platform (SMRTbell® DNA Library)

Sample Type	Amount(Qubit®)	Volume	Concentration	Purity “(NanoDrop™)”
HMW Genomic DNA	≥ 10 µg	≥ 50 µL	≥ 100 ng/µL	OD260/280=1.8-2.0; no degradation or contamination

2. Sequencing Parameters

Platform	Illumina HiSeq X
Read length	Paired-end 150 bp
Recommended sequencing depth	≥ 50x for bacterial and fungal genome
Data quality	Guaranteed ≥ 80% bases with Q30 or higher
*Turnaround time	Minimum 6 weeks from confirmation of library preparation to data releasing without bioinformatic analysis;

Platform	PacBio Sequel
Read length	≥ 10 kb or 20 kb
Recommended sequencing depth	≥ 100× for bacterial genomes ≥ 50× for fungal genomes
Data quality	Contig N50 ≥ 20 kb, Scaffold N50 ≥ 1 Mb
*Turnaround time	Minimum 6 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 Draft Map Standard Analysis
Data quality control: filtering reads containing adapter or with low quality
Genome preliminarily assembles
Genome survey: genome size, GC distribution, repeat rate
Genome component analysis: gene structure prediction, repetitive sequences, non-coding RNAs
Gene function annotation: NR, GO, COG, KEGG, and Pfam

Bacteria Complete Map Standard Analysis
Data quality control: filtering reads containing adapter or with low quality
Genome advanced assemble
Genome survey: genome size, GC distribution, repeat rate
Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs, CRISPR, prophage analysis, gene island analysis
Gene function annotation: KEGG, SwissPort, NR, GO, COG
Genome cycle graph

Fungus Fine Map Standard Analysis
Data quality control: filtering reads containing adapter or with low quality
Genome advanced assemble
Genome survey: genome size, GC distribution, repeat rate
Genome component analysis: gene structure prediction, repeat sequences, non-coding RNAs
Gene function annotation: NR, GO, KOG, and KEGG