16S/18S/ITS Amplicon Metagenomic Sequencing

1. Sample Requirements

Sample Type	Amount(Qubit®)	Concentration	Volume	Purity(NanoDrop™)
Genomic DNA	⩾ 200ng	⩾ 20 ng/μL	⩾ 12 μL	OD260/280=1.8~2.0 no degradation or contamination

2. Sequencing Parameters

Platform	**Illumina NovaSeq 6000**
Read length	Paired-end 250 bp
Recommended sequencing depth	30 kb/50 kb/100 kb raw reads
Data quality	Guaranteed ⩾ 75% bases with Q30 or higher
***Turnaround time**	Within 4 weeks from project verification to data releasing without bioinformatic analysis

*Turnaround time varies depending on the project volume.

3. Data Analysis Contents

16S/18S/ITS Amplicon Metagenomic Sequencing Standard Analysis
Data quality control
OTUs cluster and phylogenetic relationship construction
Species annotation
Alpha diversity analysis (Observed species, Goods coverage, Chao1, ACE, Shannon, Simpson Index)
Beta diversity analysis (Unifrac distance heatmap, PCA, PCoA, UPGMA)
Ternaryplot
NMDS analysis
LefSE analysis
Metastats analysis
Species T-test analysis
MRPP, Anosim, Adonis, Amova analysis
Comparative analysis of alpha diversity indices
Comparative analysis of beta diversity indices
naryplot

16S/18S/ITS Amplicon Metagenomic Sequencing Advanced Analysis
Spearman, CCA/RDA, VPA analysis
Network analysis
PICRUSt analysis