Novogene

Shallow Shotgun Metagenomic Sequencing

Shallow Shotgun Metagenomic Sequencing is a relatively recent application that bridges the gap between amplicon sequencing and deep shotgun metagenomic sequencing by offering a cost-friendly alternative to 16S rRNA amplicon sequencing. It offers species-level taxonomy with little to no PCR bias from amplification and offers taxonomy coverage across different taxa.

It addresses the challenges of amplification bias for today's microbiome studies and provides a less biased representation of microbial communities, similar to that of deep shotgun metagenomic sequencing. It is suitable for large-scale human microbiome studies.

Our Key Features & Advantages

Comprehensive Analysis
We provide expert bioinformatics analysis using the latest databases and software, generating high-quality and publication-ready data.

Effective Methodology
Our techniques enhance the generation of data from low-abundance species.
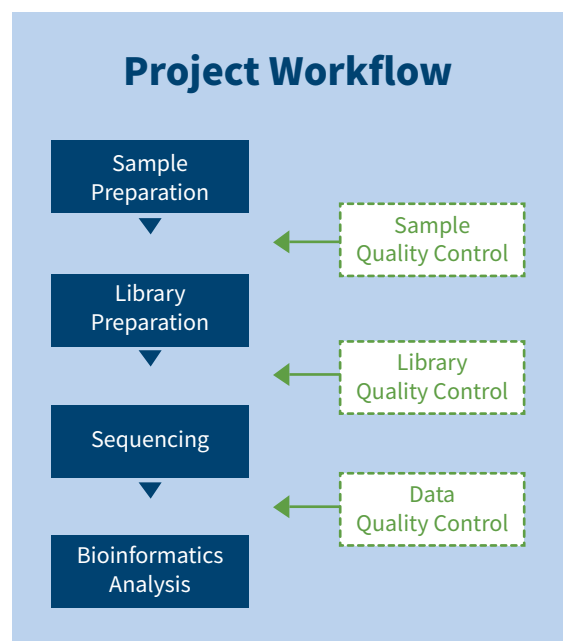
Outstanding Service
We provide high-quality sequencing (with a Q30 score ⩾ 85%), an efficient standard workflow, fast turnaround time, and cost-effective bioinformatics analysis.
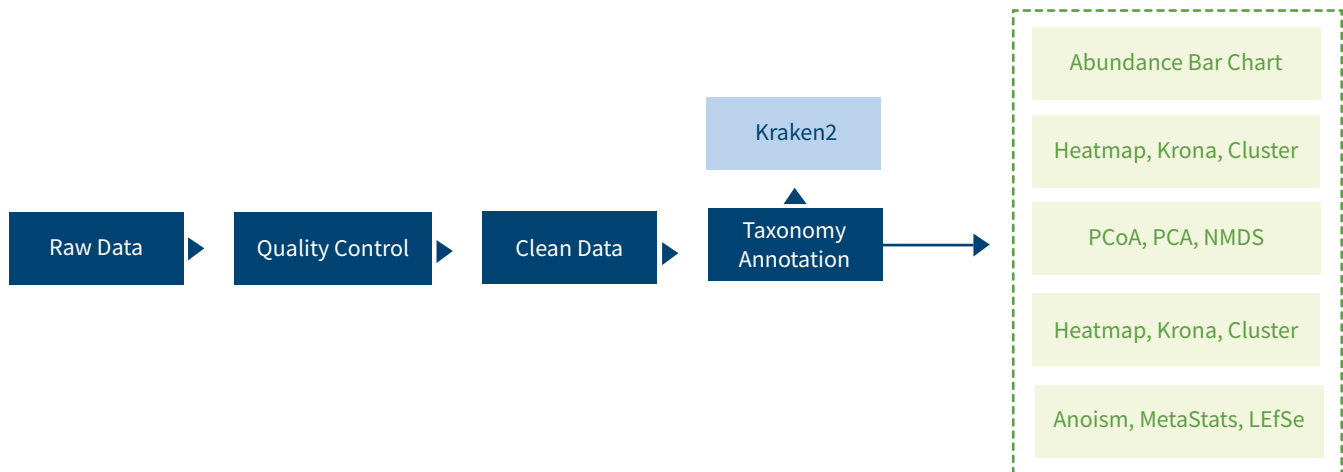
Real-time Project Management
Our Customer Service System (CSS) online platform allows for real-time project tracking 24/7, collaboration with your team and other helpful information.
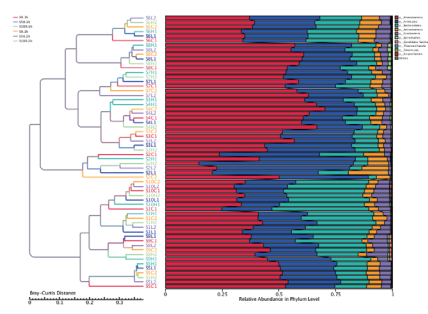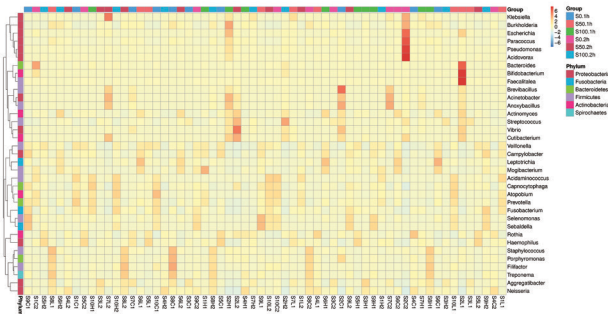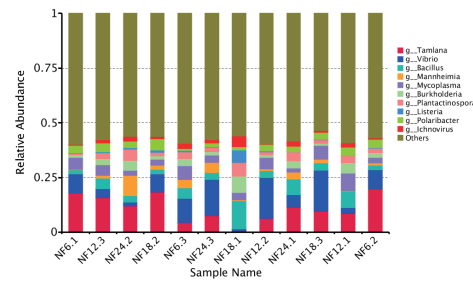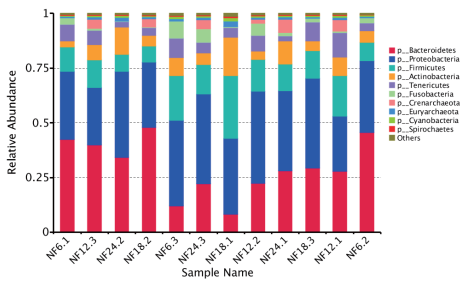
Project Workflow

Sample Preparation → Sample Quality Control

Library Preparation → Library Quality Control

Sequencing → Data Quality Control

Bioinformatics Analysis

Standard Analysis Pipeline

Raw Data → Quality Control → Clean Data → Taxonomy Annotation → Kraken2

- Abundance Bar Chart
- Heatmap, Krona, Cluster
- PCoA, PCA, NMDS
- Heatmap, Krona, Cluster
- Anoism, MetaStats, LEfSe

Examples of Analysis Content

Sample Requirements

Sample Type	Amount	Volume	Concentration	Purity
Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng / μL	OD260/280 = 1.8-2.0 No degradation, no contamination, no color