Novogene

Amplicon Metagenomic Sequencing

16S/18S/ITS Amplicon Metagenomic Sequencing is frequently used to identify and differentiate microbial species.

Short (<500 bp) hypervariable regions of conserved genes or intergenic regions, such as 16S of bacteria and archaea or 18S/ITS of fungi, are amplified by PCR and analyzed using next-generation sequencing (NGS) technology. The resulting sequences are compared against microbial databases.

Applications range from identifying a single species in pure culture and characterizing the microbiota of animals or plants to comparing species diversity and population structure from various environmental sources or geographic regions.

Our Key Features & Advantages

Comprehensive Analysis

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

Effective Methodology

Our method features high amplification efficiency of sample DNA (> 95%).

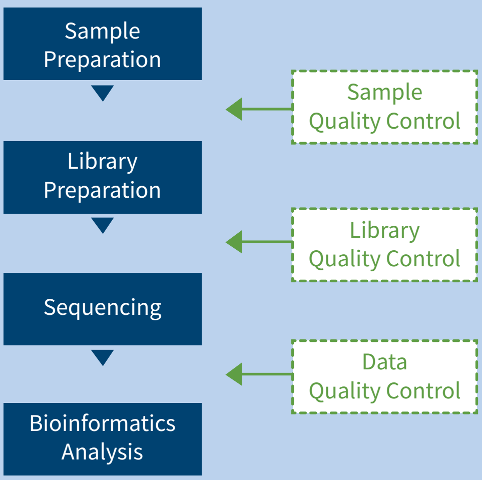
Outstanding Service

We provide high-quality sequencing (with Q30 score ⩾ 75%), 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

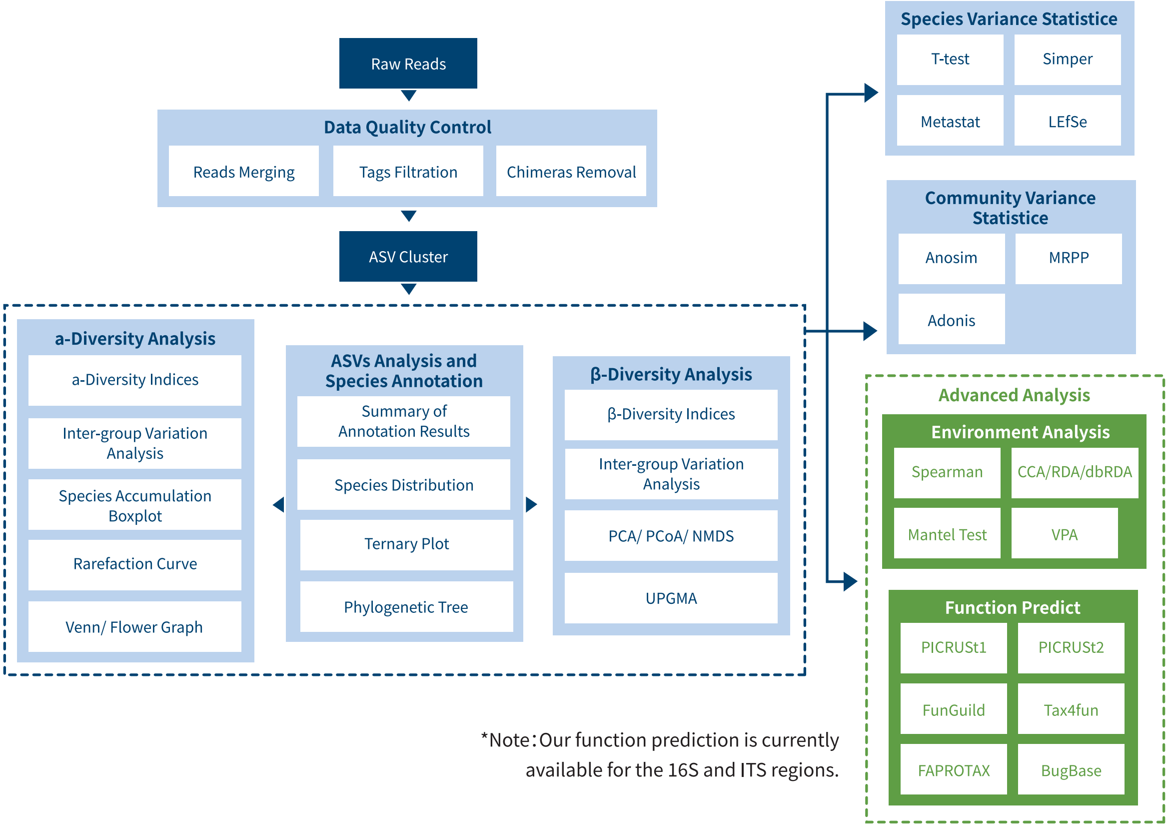
Library Quality Control

Sequencing

Data Quality Control

Bioinformatics Analysis

Standard Analysis Pipeline



Raw Reads

Data Quality Control
- Reads Merging
- Tags Filtration
- Chimeras Removal

ASV Cluster

a-Diversity Analysis
- a-Diversity Indices
- Inter-group Variation Analysis
- Species Accumulation Boxplot
- Rarefaction Curve
- Venn/ Flower Graph

ASVs Analysis and Species Annotation
- Summary of Annotation Results
- Species Distribution
- Ternary Plot
- Phylogenetic Tree

β-Diversity Analysis
- β-Diversity Indices
- Inter-group Variation Analysis
- PCA/ PCoA/ NMDS
- UPGMA

Species Variance Statistice
- T-test
- Simper
- Metastat
- LEfSe

Community Variance Statistice
- Anosim
- MRPP
- Adonis

Advanced Analysis

Environment Analysis
- Spearman
- CCA/RDA/dbRDA
- Mantel Test
- VPA

Function Predict
- PICRUSt1
- PICRUSt2
- FunGuild
- Tax4fun
- FAPROTAX
- BugBase

*Note：Our function prediction is currently available for the 16S and ITS regions.

Sample Requirements

Library Type	Sample Type	Amount	Volume	Concentration	Purity NanoDrop
PCR Free Library (Amplicon)	Genomic DNA	⩾ 200 ng	⩾ 20 μL	⩾ 10 ng/μL	OD260/280=1.8~2.0 No degradation, no contamination

Publications

Listed below are some publications that were supported by Novogene solutions. We have successfully sequenced more than 250,000 samples, including soil, water, feces, sludge, and other samples.

Journal	IF	Title
Resources, Conservation, and Recycling	13.716	Biosynthesis and recycling of magnetite nanocatalysts from Fe-rich sludge (2022) Synergetic effects of microbial-phytoremediation reshape microbial
Journal of Hazardous Materials	10.58	Synergetic effects of microbial-phytoremediation reshape microbial communities and improve degradation of petroleum contaminants (2022)

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