

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%).



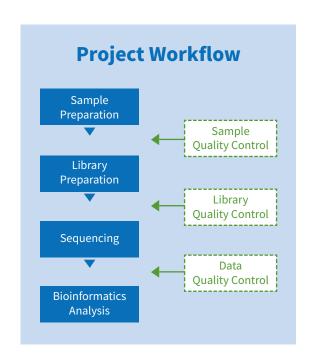
Extensive Experience

We have sequenced hundreds of thousands of samples, resulting in nearly 30 published articles.



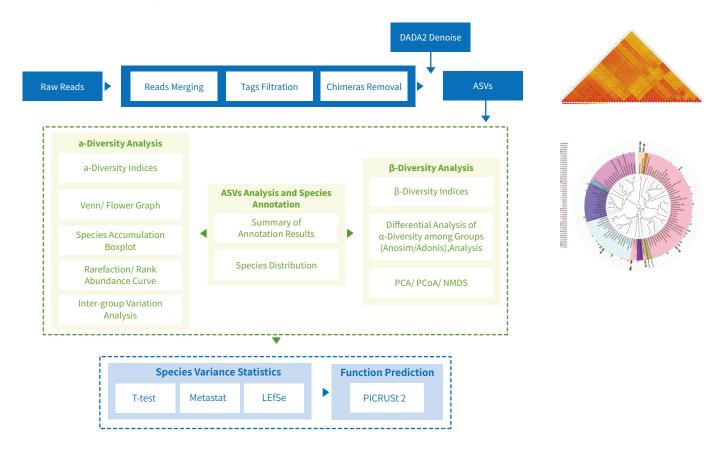
Outstanding Service

We provide high-quality sequencing (with Q30 score \geq 75%), an efficient standard workflow, fast turnaround time, and cost-effective bioinformatics analysis.





Standard Analysis Pipeline



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
Genome Biology	14.028	Influenza infection elicits an expansion of gut population of endogenous Bifidobacterium animalis which protects mice against infection (2020)
Nature Communications	11.878	Soil fungal networks maintain local dominance of ectomycorrhizal trees (2020)
Advanced Science	15.804	Sexual Dimorphism of Gut Microbiota Dictates Therapeutics Efficacy of Radiation Injuries (2019)

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