Nøvogene

16S/18S/ITS 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 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 specialists can advise you on the appropriate analysis for your project.

Advantages & Highlights

Highly experienced

We have sequenced over 170,000 samples, resulting in nearly 30 published papers.

Effective methodology

- · 200-500bp insert DNA library,
- · Illumina NovaSeq PE250.
- 30K/50K/100K reads packages with bioinformatic analysis are available.
- Maximum TAT of 25 working days, starting from sample QC (Without analysis, ≤100 samples).
- · Additional 5 working days for data analysis.

Outstanding service

We provide high-quality sequencing, an efficient standardized workflow, fast turnaround times, and bioinformatic analysis at a cost-effective price.

Comprehensive analysis

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



Sample Requirements

SAMPLE TYPE	AMOUNT	CONCENTRATION	VOLUME	PURITY
Genomic DNA	≥ 200 ng	≥20 ng/μL	≥ 12 µl	OD260/280=1.8-2.0, no degradation or RNA contamination

Project Workflow

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Analysis Pipeline



Novogene Client Publication

The microbiota maintains homeostasis of liver-resident $\gamma\delta$ T-17 cells in a lipid antigen/CD1d-dependent manner (Li *et al*, 2017)





Reference

Li F, Chen Y, Bai L, *et al*. The microbiota maintains homeostasis of liver-resident γδT-17 cells in a lipid antigen/CD1d-dependent manner. *Nature Communication* (2017) 8: 13839

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