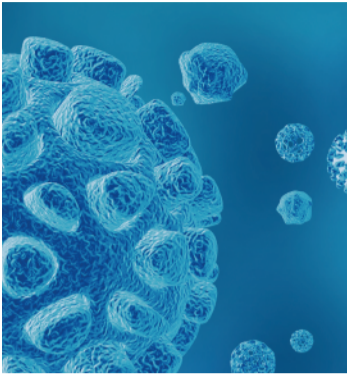


# 16S/18S/ITS Amplicon Metagenomic Sequencing



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.

### Outstanding service

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

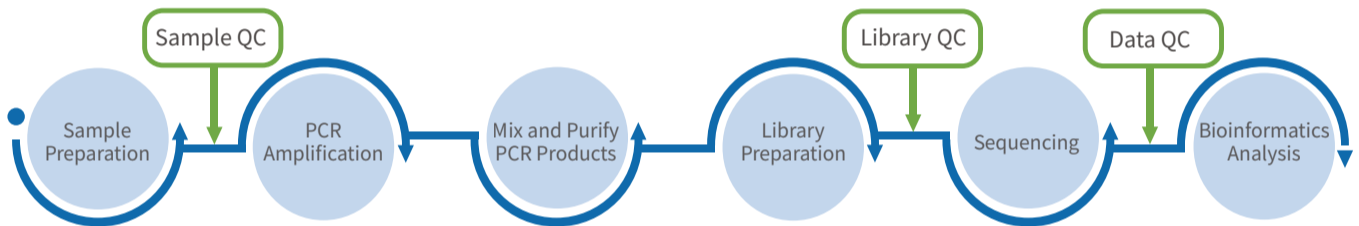
### Effective methodology

- 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.

### Comprehensive analysis

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

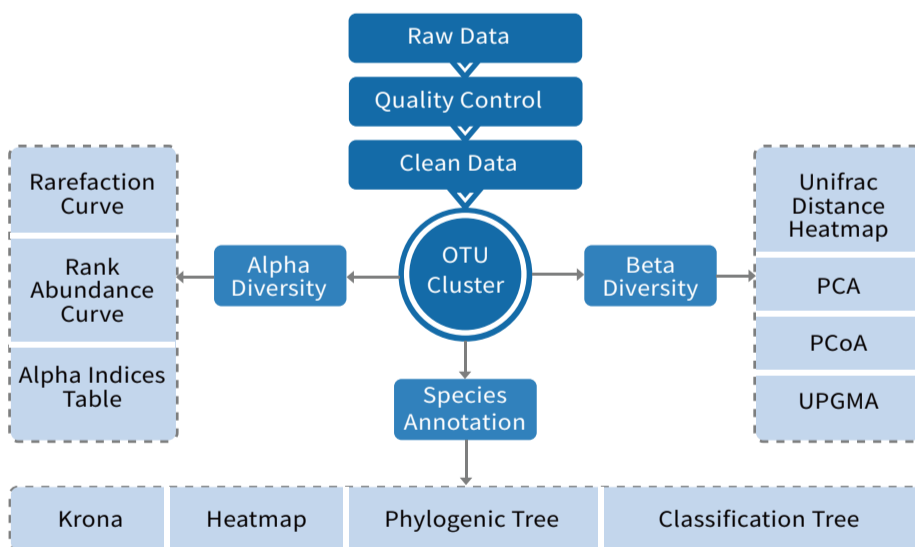
## Project Workflow



## 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

## Analysis Pipeline



## Novogene Powered Publications

Year	Journal	Title
2019	<i>Cell Host &amp; Microbiome</i>	Drosophila Histone Demethylase KDM5 Regulates Social Behavior through Immune Control and Gut Microbiota Maintenance
2018	<i>Microbiome</i>	Gut-dependent microbial translocation induces inflammation and cardiovascular events after ST-elevation myocardial infarction
2018	<i>Bioresource Technology</i>	Evaluating the impact of bamboo biochar on the fungal community succession during chicken manure composting
2017	<i>Nature Communications</i>	The microbiota maintains homeostasis of liver-resident γδT-17 cells in a lipid antigen/CD1d-dependent manner
2017	<i>Microbiome</i>	Gut microbiota dysbiosis contributes to the development of hypertension

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