SERVICE OVERVIEW

16S/18S/ITS Amplicon Sequencing

Service Description

Over 99% of natural microorganisms can not be isolated and cultured clonally, while traditional isolation and culture-dependent methods challenge the study of microorganisms in their natural environment.

Metagenomic studies of genetic material that is directly recovered from environmental samples, have benefitted greatly from advanced NGS technology as a method for the exploration of microbial biodiversity.

16S and 18S rDNA are hypervariable regions in the 16S or 18S rRNA genes in bacteria and fungi, while ITS (Internal Transcribed Spacer) is the spacer DNA between the small-subunit and large-subunit rRNA genes in bacteria, fungi and archaea.

Sequence comparison of 16S/18S/ITS regions is widely used in taxonomy and molecular phylogeny because of the easy amplification by PCR, even from low quantities of DNA, while they have a high degree of variation even between closely related species.

Sequencing Service Specification

Our 16S/18S/ITS Amplicon Sequencing services are executed with DNBSEQ sequencing system.

Sample Preparation and Services

- PCR will be used to isolate different 16S/18S/ITS regions
- PE300 sequencing by DNBSEQ
- Sequencing data are available in standard file formats
- Custom bioinformatic data analysis is available
- Data storage services are available

Sequencing Quality Standard

- Up to ≥ 80% of bases with a ≥Q30 quality score, depending on the chosen sequencing strategy
- Recommended sequencing coverage is dependent on the complexity of the sample

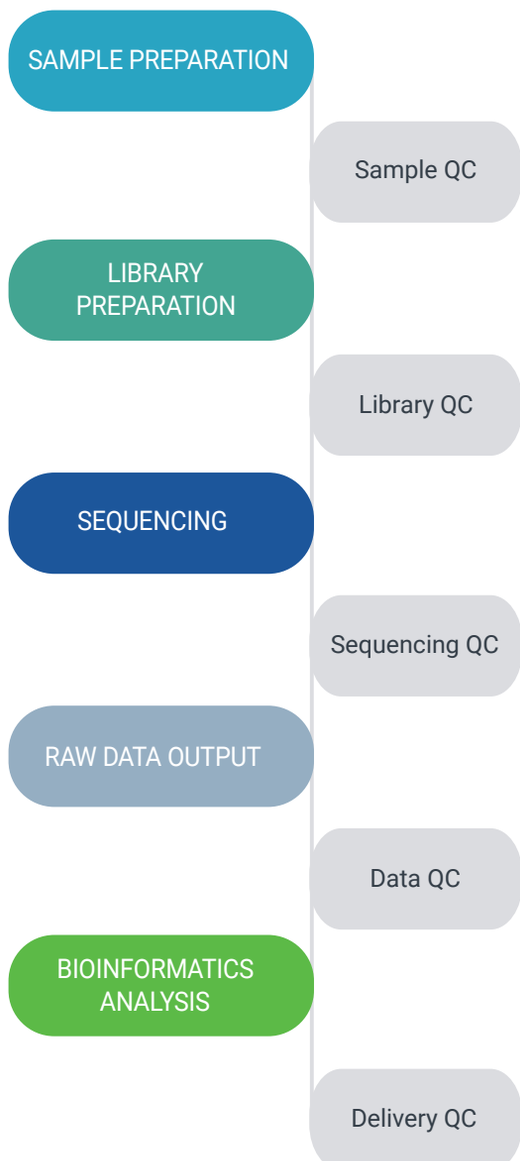
Turn Around Time

- Typical 35 working days from sample QC acceptance to data availability
- Expedited services are available, contact our specialist for details

Quality Data | Fast TAT | Cost Effective

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



Data Analysis

Besides clean data output, we offer a range of standard and customized bioinformatics pipelines for your sequencing project. Reports and output data files are delivered in industry standard file formats:FASTQ, .xls and .png.

STANDARD ANALYSIS

- Data filtration
- Overlap paired-end reads to form tags
- Tags are clustered into OTU. PCA, Venn diagram. A rank curve will be generated based on OTU abundance
- Species are classified by OTU annotation, based on which a species profiling histogram, heat map and a phylogeny tree will be provided
- Alpha diversity indexes are generated for in single sample
- Beta diversity and clustering analysis are performed for multiple samples
- Comparative analysis is used to screen significant differences in multiple samples

CUSTOMIZED ANALYSIS

Further customization of Bioinformatics analysis to suit your unique project is available:
Please contact our technical representative.

Sample Requirements

We can process intact genomic DNA:

	SAMPLE REQUIREMENT	CONCENTRATION
Genomic DNA	> 0ng(recommend≥50ng)	> 0ng/μL

Request for Information or Quotation

If you have any questions or would like to discuss how we can meet your specific needs or for expert advice on experiment design, from sample to bioinformatics, please don't hesitate to contact us at:

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