









FREE NGS Grade **DNA Extraction Service** 

# 16s/ITS Amplicon Metagenomic Sequencing Services

**Amplicon Sequencing In-House Service Provider** 



## Limited Time Offer from February to June 2024

25% Off 16s/ITS Amplicon Metagenomic Sequencing Services, inclusive of complimentary NGS Grade DNA extraction for selected sample types (Water filtered paper or material, Gut content, Soil, Sludge and Stool).



### Conducted with **ISO Certified Protocols**

Standard protocol recommended by Illumina, verified, and validated by ISO Accreditation body (ISO 17025), maintaining the consistency and accuracy of the results.



### 200k Raw Reads for **Each Sample**

Ensures more accurate results, reduce biasness, and maximise discovery of ASV available in the samples.



### **Fast Turnaround Time**

As fast as 6 weeks after QC has been passed.



## **Prompt Technical Support**

Post-sequencing technical support from our Bioinformatics team.

# **Applications** offered by 1st BASE



#### 16s rDNA Amplicon Metagenomic Sequencing

The 16S rRNA amplicon metagenomic sequencing technique is a microbiome analysis to uncover and study the diversity of Bacteria within a given sample. Choose between the 16s region of V1 – V9 for better resolution in your data, or simply choose region V3-V4 for uncovering general diversity in your samples.



#### **ITS Amplicon** Metagenomic Sequencing

The ITS amplicon metagenomic sequencing is a sensitive method for Fungal diversity analysis in your environmental samples. Choose between region ITS 1 or ITS 2 depending on the nature of Fungi within your environmental samples.



#### Custom Metagenomics Sequencing

Custom Metagenomic amplicon libraries are targeting population of organisms (Such as aquatic animal, plant or many more) using targeted specific genes. Just provide us your primer sequence of interest to get started.



<sup>\*</sup> Terms and conditions apply, scan QR code for details.

# Bioinformatics Deliverables



- Data QC and trimming
- ASV table generation and Taxonomic characterization
- ASV Analysis and Species Annotation, including KRONA results, Heatmap, Taxonomic Abundance and up to 5 Venn diagrams\*
- Alpha-diversity Analysis, including Alpha Indices table with ANOVA, Rarefaction curve, Rank abundance curve

- Beta-diversity Analysis, including Ordination (CCA, RDA, DPCoA, NMDS, MDS, PCoA), Unifrac distance analysis, UPGMA (Unweighted Pair-group Method with Arithmetic Means)
- 6 Phylogenetic Trees, including ASV co-occurrence networks & Metacoder
- 7 Statistics Between Groups: DESeq2, ANOSIM, LEFSE
- Metagenome Functional Prediction using Picrust2 (only applicable for 16s)

# **Key Diagrams**



**Taxa Barplot** 



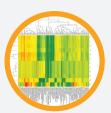
Heatmap



**Distant Matrix** 



**Alpha Diversity** 



**Picrust** 



Top 10 Taxa (Boxplot) Krona Chart



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UPGMA



Venn Diagram

# **What Our Customer Are Saying**

#### 66 Bioinformatic support has been very helpful! 77

Apical Scientific has provided excellent support from sample preparation to amplicon data analysis. The analysis report was comprehensive and the figures provided were attractive and neatly organised. More importantly, the local bioinformatic support has been very helpful where we have had interactive discussion and received professional advice to ensure our research is properly designed and correctly analysed. Thank you Apical Scientific for such a great assistance and help throughout our research journey at UPM!

Dr. Amalia Mohd. Hashim

Biotech Faculty, UPM (September 2022)