



**miCORE Amplicon Metagenomics**  
Full-Service Accomplished Within 5 Weeks

### **Complete Service Bundle**

From high-quality sample isolation to library preparation, sequencing and in-depth bioinformatic analysis, we've got every step of the process covered. And we guarantee that the full service package will be completed in less than 5 weeks.

### **Cost-effective and Modular Pricing Structure**

Choose the initiation and completion stages according to your preferences, and we will present you with exceptionally competitive fixed rates tailored to your needs.

### **Enjoy Unparalleled Customer Satisfaction**

Our commitment to quality, rapid delivery, and exceptional customer service ensures an unparalleled level of satisfaction for our valued customers.

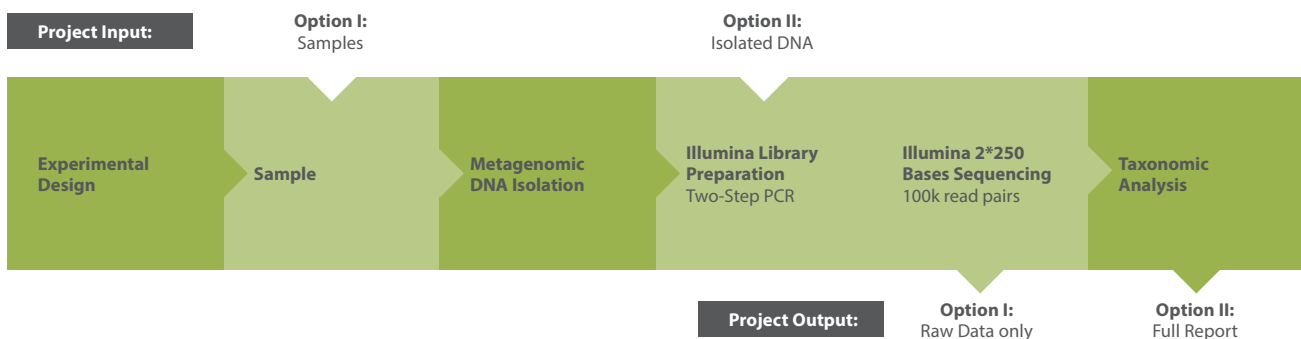
## Overview miCORE Amplicon Metagenomics

Explore the bacterial potential with Microsynth's miCORE Amplicon Metagenomics service. This marker-based technique leverages the power and sensitivity of next-generation sequencing (NGS) to gain in-depth knowledge of the taxonomic composition of your samples.

Discover microbial communities in environmental samples, taxonomic shifts and effects under experimental conditions, microbial diversity for well being, or pathogenic potential in a medical setting. Choose from our state-of-the-art bioinformatic analysis modules

to reveal taxonomic composition, effects of treatment or environmental factors, and functional potential of your samples at a glance. Microsynth's miCORE Amplicon Metagenomics service is designed to support your research with precision and efficiency.

## Workflow and Service Description



**DNA Isolation:** Outsource your DNA isolation to Microsynth. We have extensive experience with challenging samples and a standard pricing structure for many sample types, from forest soil to feces.

**Library preparation:** Library preparation includes DNA sample QC, two-step PCR Illumina library preparation using standard primer sets, indexes for multiplexing and equimolar pooling according to library quantification measurements.

**Sequencing:** Experience the ease of sequencing with our convenient fixed 100k read pairs per sample data package: Sequencing delivers 100,000 read pairs (100,000 forward reads + 100,000 reverse reads) per sample. More than enough to uncover even the rarest species within very complex communities.

**Bioinformatics:** Bioinformatics for 16S/ITS sequencing includes full service from quality control, clustering of reads into OTUs (zOTUs/amplicon sequence

variants), assignment of taxonomic profiles, calculation of  $\alpha$ -diversity and rarefaction curves to publication-ready plots and interactive krona charts. Taxonomic assignment is provided at any level down to genus level (and species level where possible). Additional modules can be booked at additional cost, if technically feasible, to shed light on the functional potential of the detected communities or to analyze statistical confidence in a comparative setting.

## Timeline



We also offer an express service option for an additional fee to expedite the sequencing of your samples.

## miCORE Amplicon Metagenomics Products

Laboratory:

**20005** DNA Isolation for Amplicon Metagenomics

**30088** Amplicon Metagenomics Sequencing

Bioinformatics Analysis:

**30102** Amplicon Metagenomics Analysis

**30202** Amplicon Comparative Statistics

**30207** Amplicon Functional Profiling (16S)