Microsynth

miCORE Resequencing

Attractive Prices Starting from One Sample

Comprehensive Service Package

From cell pellet or tissue sample to bioinformatic analysis, we have you covered. And not just that: We can ensure that the entire service package is completed in less than 5 weeks.

Cost-effective and Flexible Pricing

You are in control: You choose the start and end steps, while we offer highly competitive fixed rates tailored to your needs.

Experience Exceptional Customer Satisfaction

Our quality, speed, and outstanding customer service ensure exceptional levels of customer satisfaction.

Microsynth AG, Switzerland
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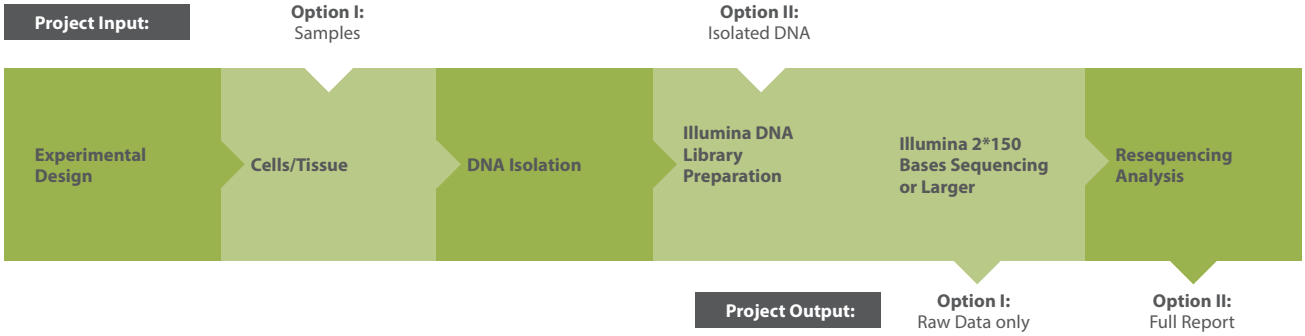
Overview miCORE Resequencing

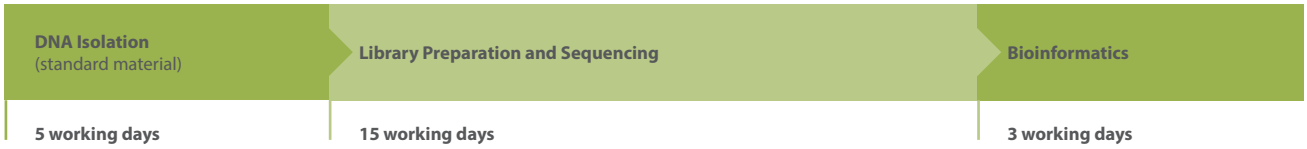
Bacterial or eukaryotic resequencing involves sequencing the entire genome and comparing the sequence to that of a known reference. The rapid generation of accurate genome sequence information is critical for detecting low-frequency mutations, finding important deletions and insertions, and discovering inherited or acquired genetic changes in individual genomes. From genome verification to the detection of virulence or suspected antibiotic resistance, or the localization of driver mutations, resequencing is used to answer a wide variety of questions. We are pleased to introduce our new one-stop service for resequencing. From low to high sample numbers, this service is available in two variants - with and without nucleic acid isolation.

Workflow and Service Description



DNA Isolation: Outsource DNA isolation to Microsynth. We have extensive experience with challenging samples and a standard pricing structure for many cell and tissue sample types.
Library Preparation: Library preparation includes QC of DNA samples and preparation of Illumina stranded libraries using indexes for multiplexing and equimolar pooling according to library quantification measurements.
Sequencing: Experience the ease of sequencing with our convenient per-sample data packages. From 1 Gb per bacterial sample to the desired coverage of the 148.8 Gb *Paris japonica* genome, you can easily adapt the sequencing throughput to your needs.
Bioinformatics: Sequenced reads are quality filtered and mapped to the reference genome (genbank format or equivalent), a prerequisite for this analysis. After best practice refinement, single nucleotide variations (SNVs) and small insertions and deletions (InDels) are detected and annotated. Multiple variant callers are used for sensitive and specific analysis. A user-friendly summary report is then provided to explain and structure the detailed output: raw data , mapping, variant calling, protein consequences of detected variations (Fastq, BAM/BAI, VCF, HTML and other standard formats). For bacteria, the basic service can be enhanced with the determination of resistance, virulence and mycotoxin genes and the detection of their genetic variations, if present.

Timeline



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

miCORE Resequencing Products

Laboratory:

20003 Resequencing - DNA Isolation
30000 Resequencing - Library Preparation
30750 Illumina Sequencing (1 Gb Reads Package, 2×150)

Bioinformatics Analysis:

30100 Resequencing - Bioinformatics (Bacteria)
30122 Resequencing - Bioinformatics (Eukaryotes)
30137 Add-on Bioinformatics - Toxicity, Virulence and Resistance Genes

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