Microsynth

Bacterial Resequencing -

Attractive Prices Starting from One Sample

Cost-Effective and Fast

We offer cost-effective entry and fixed rates for small sample numbers. In other words, there's no need to think twice - simply outsource your entire bacterial resequencing project to Microsynth and you'll receive all the important information within ≤4 weeks.

High Quality

0.75 Gb sequence data generated by Illumina paired-end reads, 2*75 bp or longer. A comprehensive bioinformatics package is included.

Convenient and User-Friendly

All you need to do is provide us with the cell pellet or the isolated DNA and name the reference genome. Our webshop has been designed for user-friendly sample registration.

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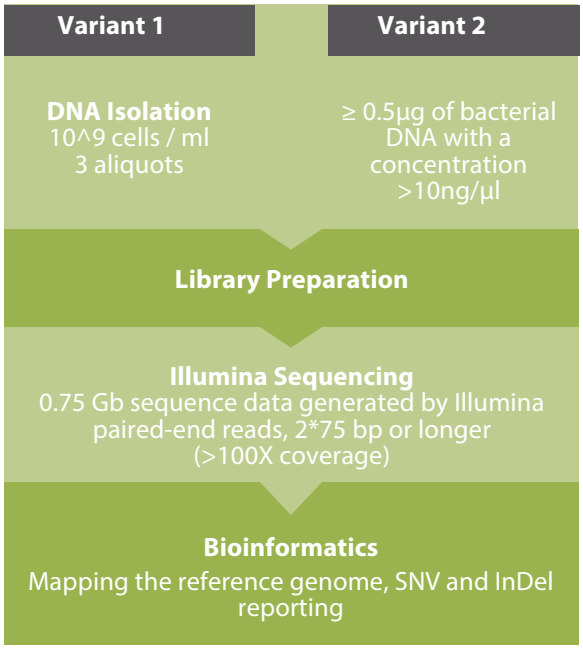
Introduction

Bacterial resequencing involves sequencing the entire genome and comparing the sequence to that of a known reference. The rapid generation of accurate microbial genome sequence information is critical for the detection of low frequency mutations, finding important deletions and insertions, and discovering other genetic changes between microbial strains. From genome verification to the detection of virulence or suspected antibiotic resistance, resequencing is used for a wide variety of topics.

We are pleased to introduce to you our new one-stop service for bacterial resequencing. Specifically tailored for low sample numbers, this new service is available in two variants - with and without nucleic acid isolation.

Workflow and Service Description



DNA Isolation: You may either perform the DNA isolation yourself or outsource this step to Microsynth. We have considerable experience in processing various sample matrices and DNA/RNA sources.

Library Preparation and Sequencing: After we have performed a quality check of your samples, Microsynth will construct Illumina libraries that will include specific adaptors with barcodes.

Bioinformatics: Sequencing reads are quality filtered and mapped against the reference genome that you provide. 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 that will explain and structure the in-depth output:
Raw data (Fastq-), Mapping (BAM/BAI-), Variant calling (VCF-), protein consequences of detected variations (HTML-files). The basic service can be enhanced with specific downstream analyses.

Products

- Bacterial Resequencing by NGS*
- Bacterial Resequencing by NGS including DNA Isolation*

**Fixed price per sample including bioinformatics. Delivery of data within ≤4 weeks for small sample amounts. Volume pricing is applied for quantities above 24 samples.*
Condition: genome size is ≤10 MB, reference genome available (genbank-format or comparable)

Related Services:

- Bacterial de novo sequencing
- MLST Analysis
- Genomic epidemiology
- Shotgun Metagenomics
- Amplicon Metagenomics

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