

Incredible promotion for unbiased metagenome analysis by Next-Generation Sequencing technology – from 30 Euro per sample – Order online!

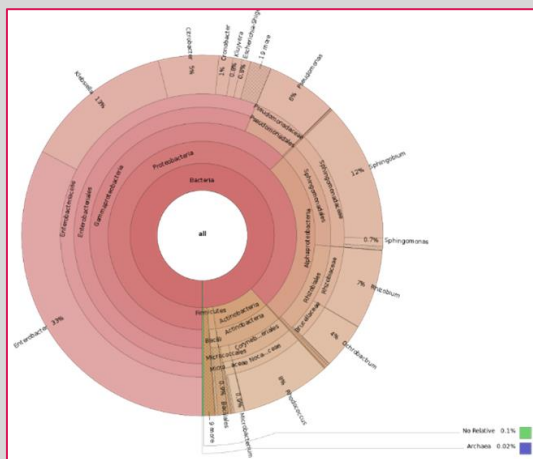
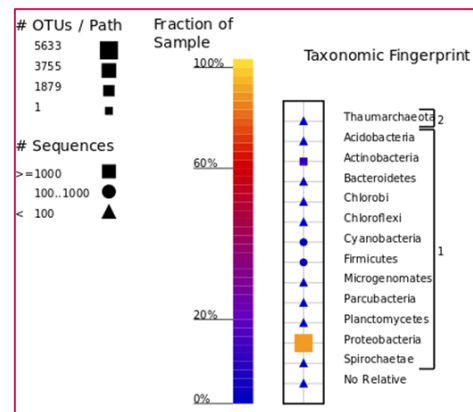
Metagenome genotyping

Next-Generation Sequencing is a very efficient tool when analyzing species in a given environment, commonly referred to as metagenome analysis. NGS has become the approach of choice due to its ability to identify all species in tested samples and is based on sequencing of pre-amplified hypervariable regions (such as 16S, 18S or ITS), traditionally used for species identification, and comparing thus obtained sequences with reference databases.

We apply a well-balanced sequencing strategy in order to achieve desired results.

We recommend and perform:

- Amplicon generation for 1-192 samples, pooling
- 250 b paired-end read sequencing with **output >20K reads/sample**, demultiplexing, analysis report. Optional advanced data analysis services available on request
- For selected primer sets this service is available starting from a single sample
- **Time to results:** less than 4 weeks



...and you can choose from:

SO-024 - Metagenome analysis, up to 24 samples

Includes Sample QC, Amplicon generation for up to **24 samples** using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-048 - Metagenome analysis, up to 48 samples

Includes Sample QC, Amplicon generation for up to **48 samples** using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-096 - Metagenome analysis, up to 96 samples

Includes Sample QC, Amplicon generation for up to **96 samples** using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing

SO-192 - Metagenome analysis, up to 192 samples

Includes Sample QC, Amplicon generation for up to **192 samples** using a single primer set, double indexing, library prep + QC, 1x 250 b paired-end sequencing, demultiplexing