18S rRNA Barcoding Metagenomics

microomics®
Small things that matter.

Service to analyse the taxonomic profile and diversity of **fungi and some unicellular organisms** present in all types of samples.
It also allows the identification of different genera of animals and plants.

18S rRNA is a unique gene of **eukaryotic organisms** with a highly conserved sequence, but with some hypervariable regions with sequences that are virtually **unique** for each **phylogenetic group**.
Selective sequencing of these hypervariable regions of DNA extracted from a sample allows analysis of the diversity and taxonomy present in the sample. The identification of eukaryotes is carried out by comparing the obtained sequences against a reference database.

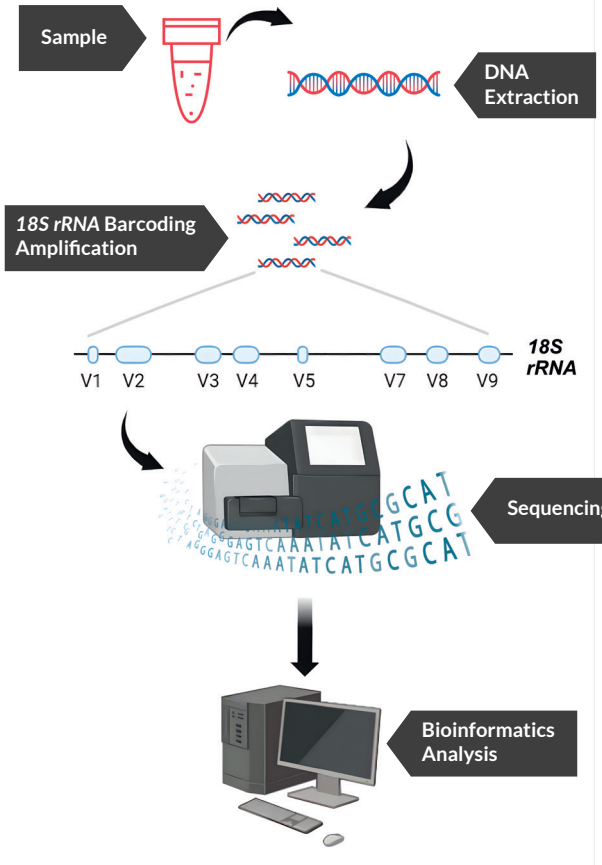
Consultancy and Study Design

Personalized scientific-technical consulting by our metagenomics experts for:

- Experimental Desing
- Sampling
- Project Tracking
- Results Delivery Meeting
- Drafting or Reviewing Publications

Molecular Biology Laboratory

A highly qualified team with extensive experience in metagenomics will carry out:



Sample quality control

Certified Cleanroom

Library Quality Control

Sample reception

- Biological sample reception 250 µl / 500 g*
  *According to the microbial load of the sample
- ADN up to 800 ng
  - Minimal volume = 40 µl
  - Minimal concentration = 20 ng/µl
  - Purity: OD260/280 = 1.8–2.0
    OD260/230 = 2.0

DNA extraction

- In anti-contamination **certified cleanroom**
- Experience with >50 different matrices
- Specific purification protocol

Amplification

- V4 and V8-V9 variable regions of the gene *18S rRNA*
- Possibility to customize the primers with other regions or with other more specific genes, such as *COI* or *LSU*, for example.
- **Use of positive and negative controls to monitor contamination**

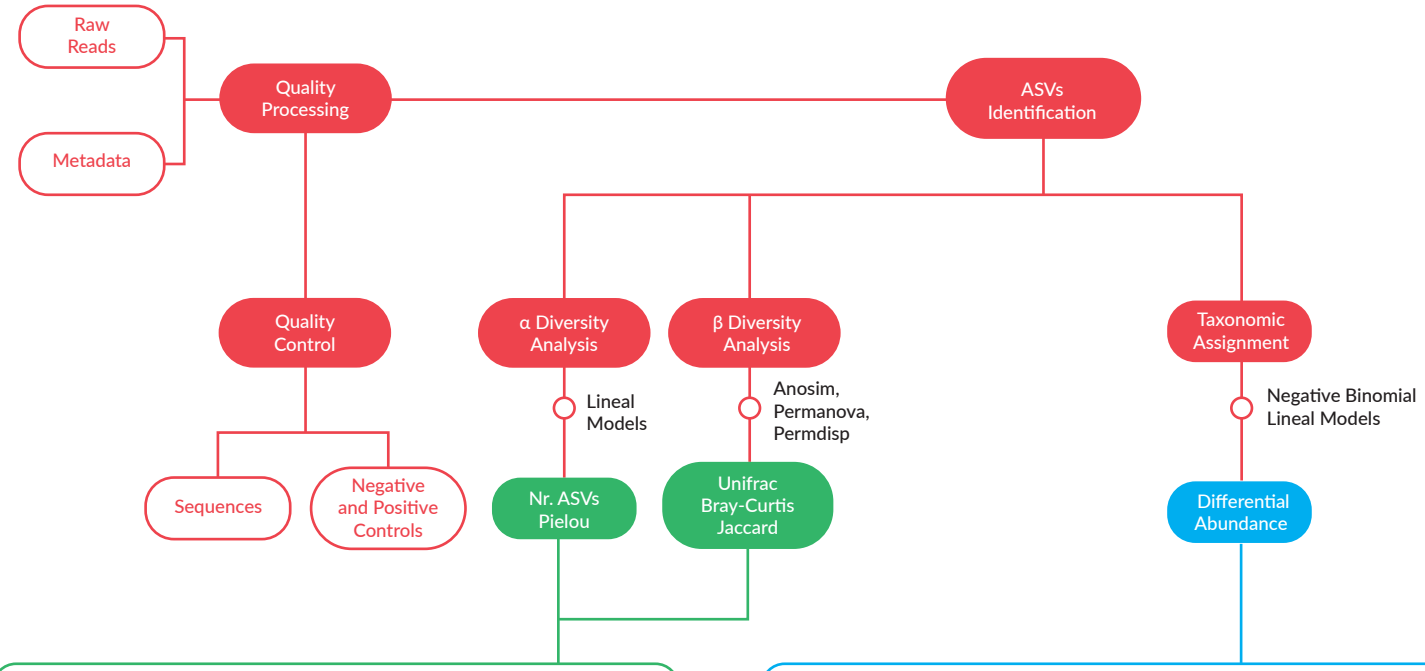
Sequencing

- Illumina MiSeq 2x300 pb
- 60.000 guaranteed reads per analysis

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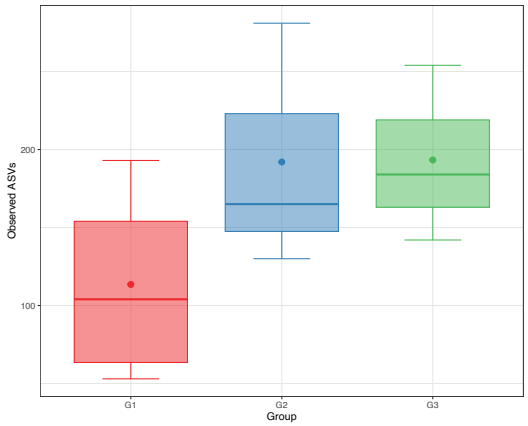
Bioinformatic and Statistical Analysis

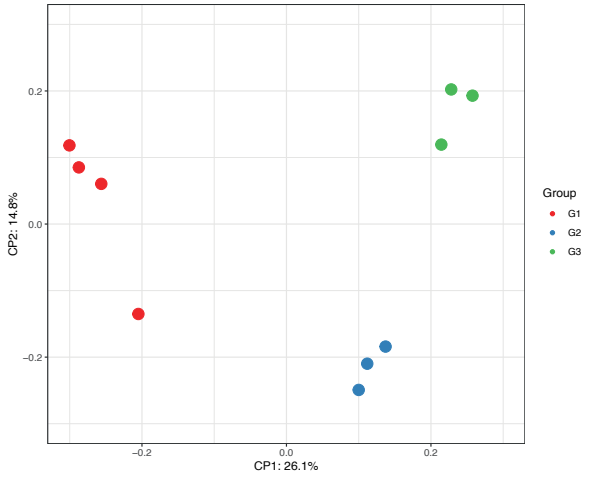
Our Bioinformatics Department has **pipelines designed to customize each analysis** according to the study's needs, addressing:



Diversity Analysis

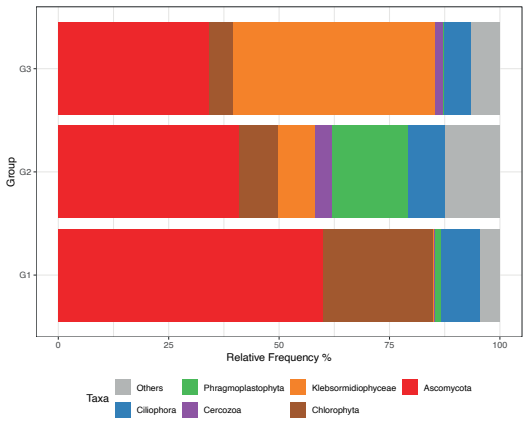
Study of the eukaryotic diversity present in each sample (α) and among samples (β).





Taxonomic Assignment

Identification of eukaryotic organisms present in the sample with **high taxonomic resolution** down to the **genus level**. Adapted approach for some species.



Association or correlation studies with qualitative or quantitative variables.

Complementary services

Customized bioinformatics analysis: bioinformatics analysis consulting service, **which includes 2 hours of post-delivery analysis in any complete study.**

Express service: possibility of reducing the turnaround time for the complete analysis.

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