

MetaTranscriptomics

18S

Shotgun Metagenomics

16S

ITS



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Microbiome
THE GENOMICS OF THE MANY



We provide full support on study design to ensure correct sequencing and bioinformatics strategies are used to meet your project goals. Our experts will consult with you about your specific requirements. Any metadata attached to samples will be used to perform statistical analysis in our default analysis pipelines.

Discover new organisms and explore the dynamic nature of microbial populations.

SERVICES LIST

16S-18S-ITS-based metagenomics / metabarcoding



Combine many samples in a single test for cost-effective qualitative and quantitative analysis.

- Mitochondrial / plastid 16S depletion
- OTU clustering, taxonomy, assignment, alpha/beta diversity, PCoA and taxonomic enrichment testing (on request).
- Sample stratification on metadata factors

Shotgun Metagenomic Sequencing



Taxonomic analyses and functional characterization: get insight on microbial composition and possible metabolic processes in the community.

- Comprehensively sample all genes in all organisms present in a sample
- Characterize the biological functions associated with the community and identify novel genes
- Identify biomarkers, i.e. taxa and functions that stratify communities of various types

MetaTranscriptomics



Disclosing activity by identifying genes that are expressed in a particular microbial environment throughout an unbiased RNA-seq.

- Insights in the gene activity and functional/pathway diversity by detecting how many genes are expressed in a community across all species
- Identifying the most important functionality/pathway required for the survival
- Assembly of novel transcripts
- Biomarker discovery by assessing changes in expression levels between different conditions/communities
- rRNA and host mRNA depletion

Virus detection and identification



Multiplex-Amplicon-Seq and Ultra-low RNA-Seq for the analysis of emerging infectious diseases in human and plants.

- Direct assessment of clinical samples with low virus abundance
- Understand the epidemiology and evolution of the virus in large cohorts

Purification of gDNA/RNA from various starting materials/matrixes

