

# Genomic & Transcriptomic applications for microorganisms studies

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GeT (Genome & Transcriptome) is a cutting-edge multi-site core facility in Toulouse (France), providing the academic and private scientific communities with technologies and expertise in the area of genomics and transcriptomics.

GeT-Biopuces is one of the four GeT sites. Located at INSA Toulouse, within the Toulouse Biotechnology Institute (TBI), the platform is ISO9001 & NFX50-900 certified and specialized in biotechnology and in the study of micro-organisms. Its missions are:

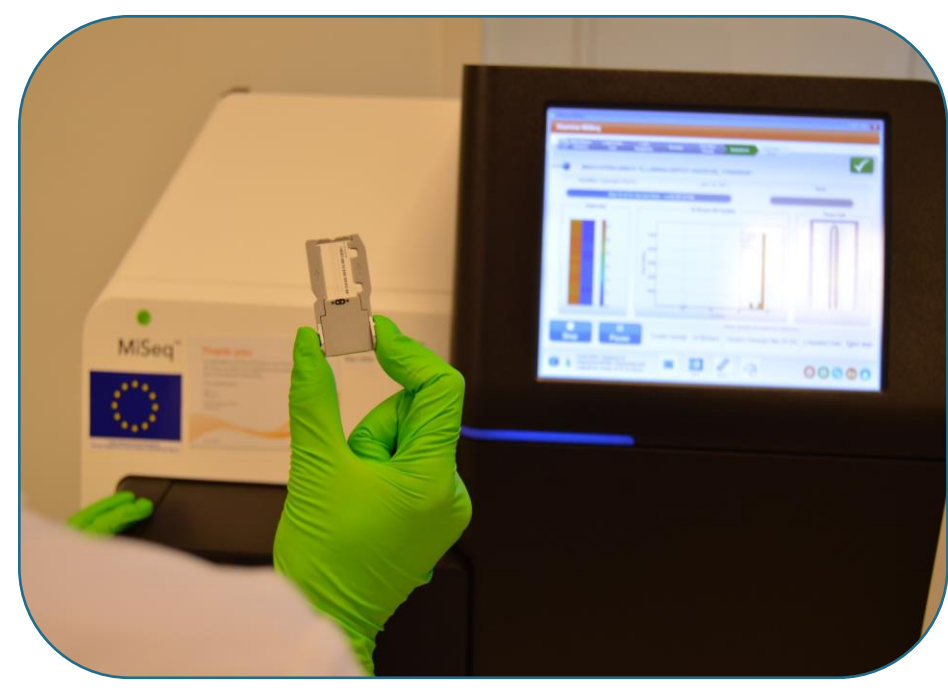
## SERVICES:

Sequencing, digital PCR, bioinformatic and statistic analysis

ADVICE AND SKILL TRANSFERT

DEVELOPMENT

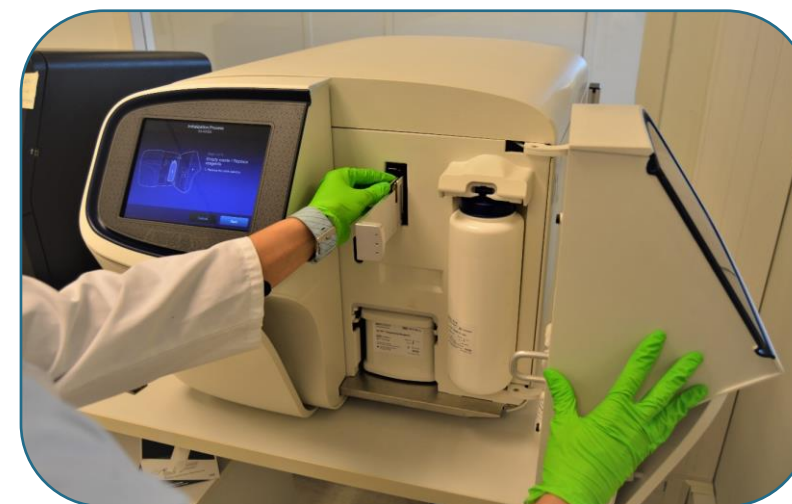
## EQUIPMENT:



MiSeq, Illumina



MinION, Oxford Nanopore



GeneStudio S5, ThermoFisher



QiaCuity One, Qiagen

SEQUENCING

SHORT  
READS

LONG  
READS

Digital PCR

Applications

Technologies

Input

Bioinfo  
Biostats  
analysis

Amplicons,  
16S, 18S, ITS

Illumina MiSeq

10 ng DNA

✓

Small genomes  
(bacteria and yeast)

ThermoFisher  
GeneStudio S5

10 ng DNA

✓

RNAseq with  
ribodepletion

ThermoFisher  
GeneStudio S5

500 ng total  
RNA

✓

DNAseq

Oxford Nanopore  
MinION

1 µg DNA

✓

Plasmids/Fosmids

Oxford Nanopore  
MinION

100 ng DNA

✓

Copy Number  
Variation

QiaCuity One

1 ng DNA

✓

Microbe detection

QiaCuity One

< 1 ng DNA

✓

Gene expression

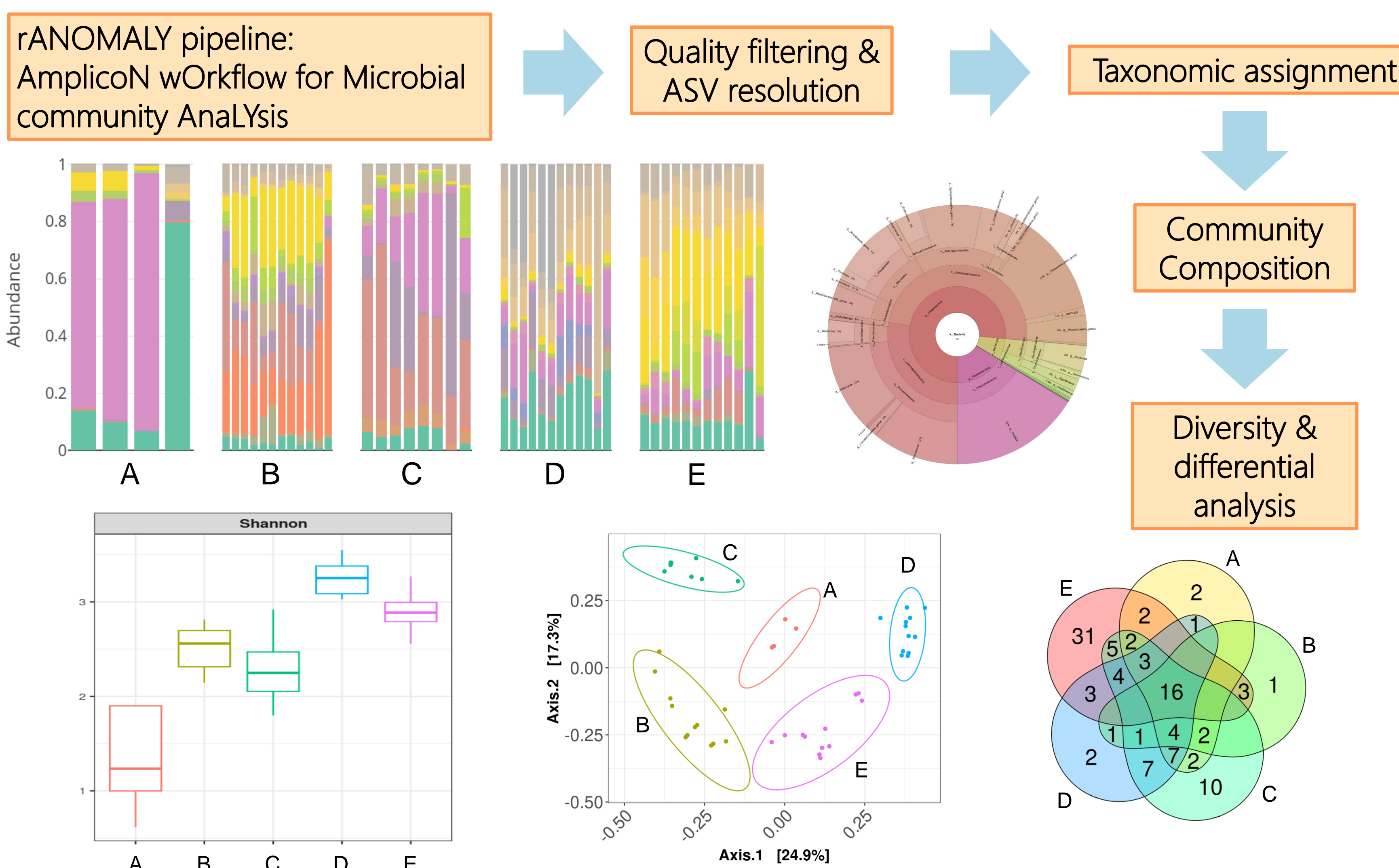
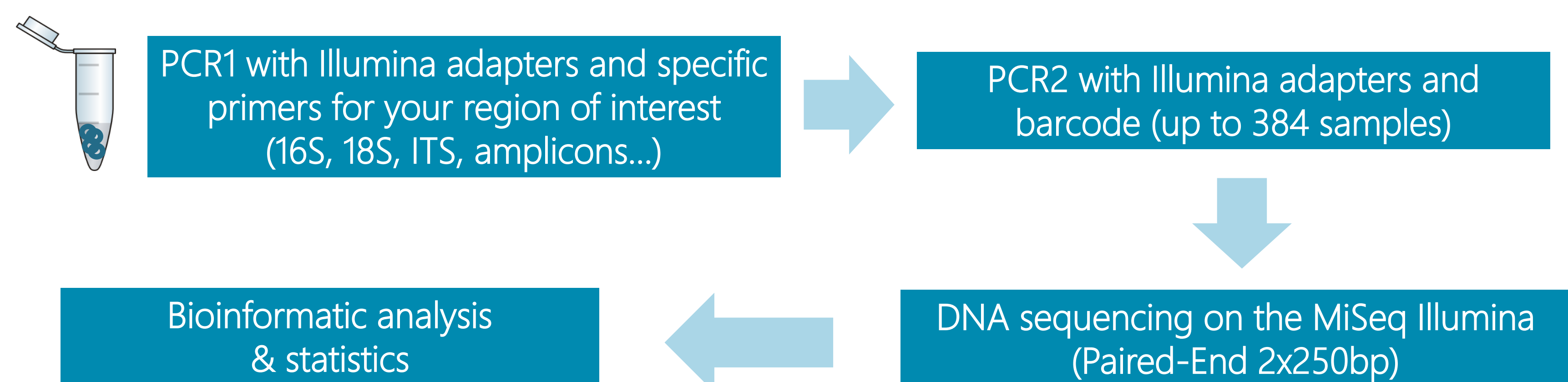
QiaCuity One

1 pg total  
RNA

✓

## Metagenomic Sequencing

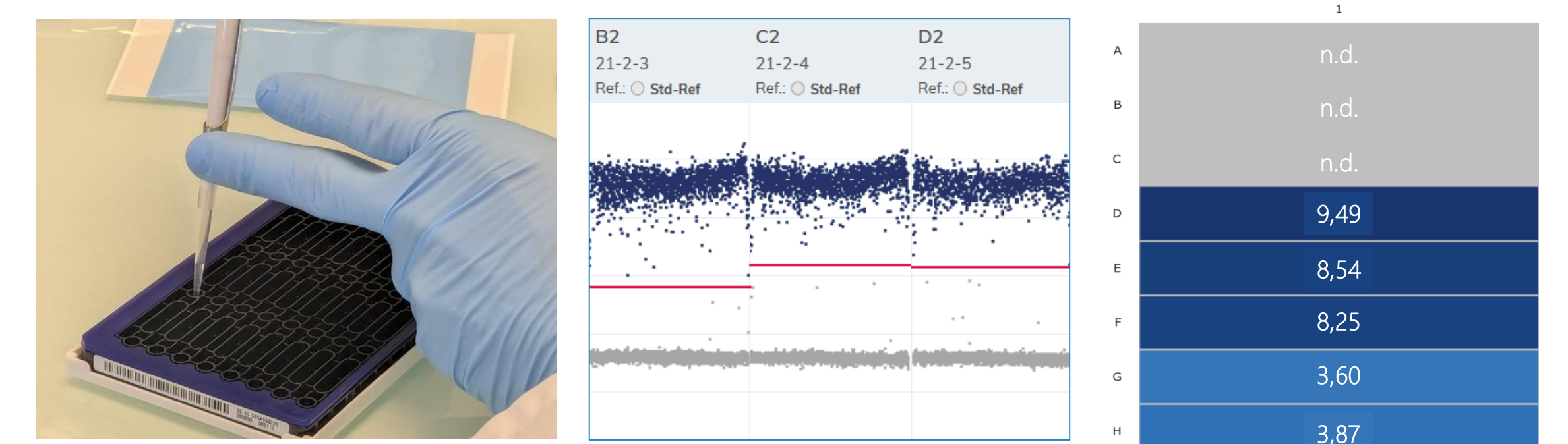
By using our comprehensive metagenomic sequencing and analysis pipeline, start analyzing DNA extracted from complex samples of interest without the need to cultivate micro-organisms. This approach provides you with a global view of the diversity and functions of microbial communities present in a given environment. Explore the composition, abundance and interactions in a microbiota, whatever its origin (human, animal, environment, etc.).



**Bibliography:**  
Theil S, Rifa E. rANOMALY: Amplicon workflow for Microbial community Analysis. F1000Res. 2021 Jan 7;10:7. doi: 10.12688/f1000research.27268.1. PMID: 33537122; PMCID: PMC7836088.

## Digital PCR

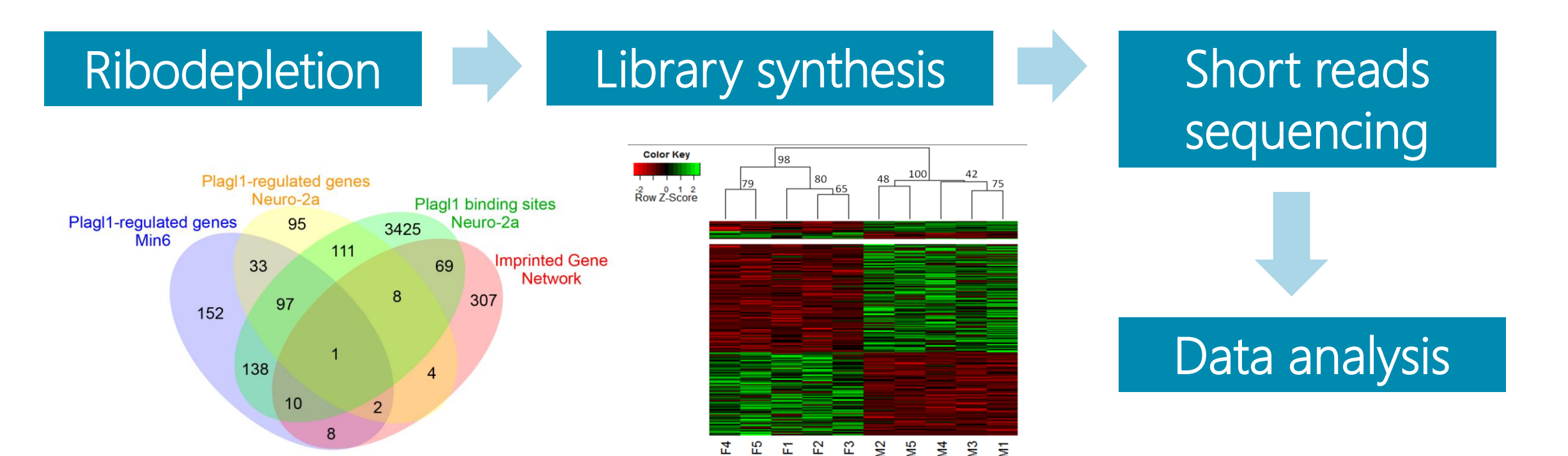
This flexible, solid partitioning-based new technology allows you to split your sample into several thousands elementary PCR reactions (8,500 or 26,000 partitions), to search for rare events, work on difficult samples rich in inhibitors, or precisely determine differences as low as 10% between samples. No need for standards, quantification is absolute and up to five different targets can be multiplexed.



- COPY NUMBER VARIATION : Determine the copy number of your genes of interest with unprecedented precision
- MICROBE DETECTION : Absolute quantification of bacteria, fungi and viruses, even in trace amounts
- GENE EXPRESSION : Measure very low expression levels, catch tiny changes very precisely, and easily multiplex up to 5 targets

## Transcriptomic Sequencing

Get an exhaustive view of the differential expression between conditions in order to identify mechanisms of antimicrobial resistance, impact of stress, ...



**Bibliography:**  
Séguela A., Della-Negra O., Gautier R., Hamelin J., Milferstedt K., Servin R., Teste M. and Canlet C. (2025). Integrated Co-extraction Protocol for Transcriptomic and 1H NMR Metabolomic Analysis of Multi-species Biofilms. Bio-protocol 15(5): e5237. DOI: 10.21769/BioProtoc.5237.  
V. Cuffe-Gauchard, J. Aube, J.-R. Lagade, L. Bignon, J.-P. Lafontaine, I. Hernandez-Avila, N. Marsaud, B. Shillito, L. Amand, E. G. Roussel, M.-A. Cambon. bioRxiv 2024.07.23.604794; FISH, a new tool for in situ preservation of RNA in tissues of deep-sea mobile fauna. doi: https://doi.org/10.1101/2024.07.23.604794