



**HAL**  
open science

## **metagWGS: a workflow to analyse short and long HiFi metagenomic reads Taxonomic profile HiFi vs Short reads assembly**

Joanna Fourquet, Jean Mainguy, Maïna Vienne, Céline Noirot, Pierre Martin, Vincent Darbot, Olivier Bouchez, Adrien Castinel, Sylvie Combes, Carole Iampietro, et al.

### ► **To cite this version:**

Joanna Fourquet, Jean Mainguy, Maïna Vienne, Céline Noirot, Pierre Martin, et al.. metagWGS: a workflow to analyse short and long HiFi metagenomic reads Taxonomic profile HiFi vs Short reads assembly. JOBIM 2022, Jul 2022, Rennes, France. Actes des exposés (keynotes, contributions orales, mini-symposia): JOBIM2022\_proceedings\_oral.pdf (23 Mo) et actes des posters et démos: JOBIM2022\_proceedings\_posters\_demos.pdf (19 Mo). 10.15454/1.5572369328961167E12 . hal-03771202

**HAL Id: hal-03771202**

**<https://hal.inrae.fr/hal-03771202>**

Submitted on 7 Sep 2022

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Joanna Fourquet<sup>1\*</sup>, Jean Mainguy<sup>1\*</sup>, Maina Vienne<sup>1</sup>, Céline Noiroi<sup>1</sup>, Pierre Martin<sup>1</sup>, Vincent Darbot<sup>3</sup>, Olivier Bouchez<sup>2</sup>, Adrien Castinel<sup>2</sup>, Sylvie Combes<sup>3</sup>, Carole Lampietro<sup>2</sup>, Christine Gaspin<sup>1</sup>, Denis Milan<sup>2</sup>, Cécile Donnadiou<sup>2</sup>, Geraldine Pascal<sup>3</sup> and Claire Hoede<sup>1</sup>

<sup>1</sup> INRAE, Université de Toulouse, UR875 MIAT, Bioinformatics, PF GenoToul Bioinfo, F-31326, Castanet-Tolosan, France (doi: 10.15454/1.5572369328961167E12)

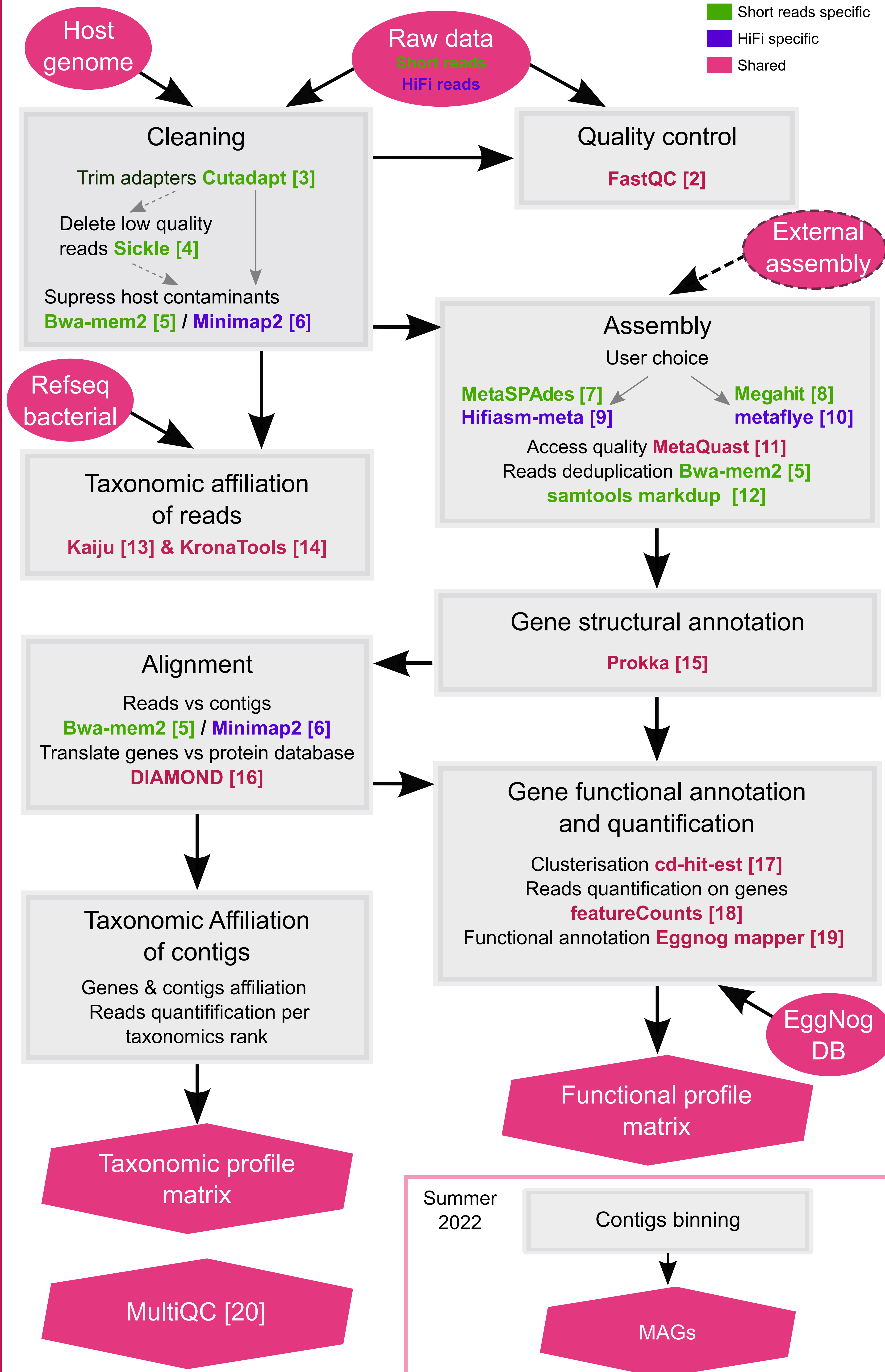
<sup>2</sup> INRAE, GeT-PlaGe, Genotoul – INRAE – 31326 Castanet-Tolosan, France (doi: 10.15454/1.5572370921303193E12)

<sup>3</sup> GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet Tolosan, France

\* These two authors contributed equally to this work

Corresponding author: [claire.hoede@inrae.fr](mailto:claire.hoede@inrae.fr)

## Production of whole metagenome assembly, functional and taxonomic profile

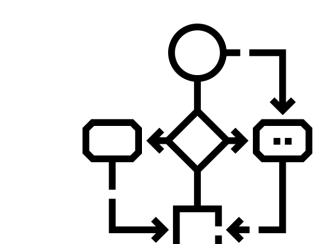


## Workflow features



### Type of NGS data:

whole genome shotgun sequencing (Illumina HiSeq3000 or NovaSeq, paired, 2\*150bp ; PacBio HiFi reads, single-end)



### Workflow:

a scalable and reproducible metagenomic analysis with a **nextflow** [1] pipeline using **Singularity** [21] container

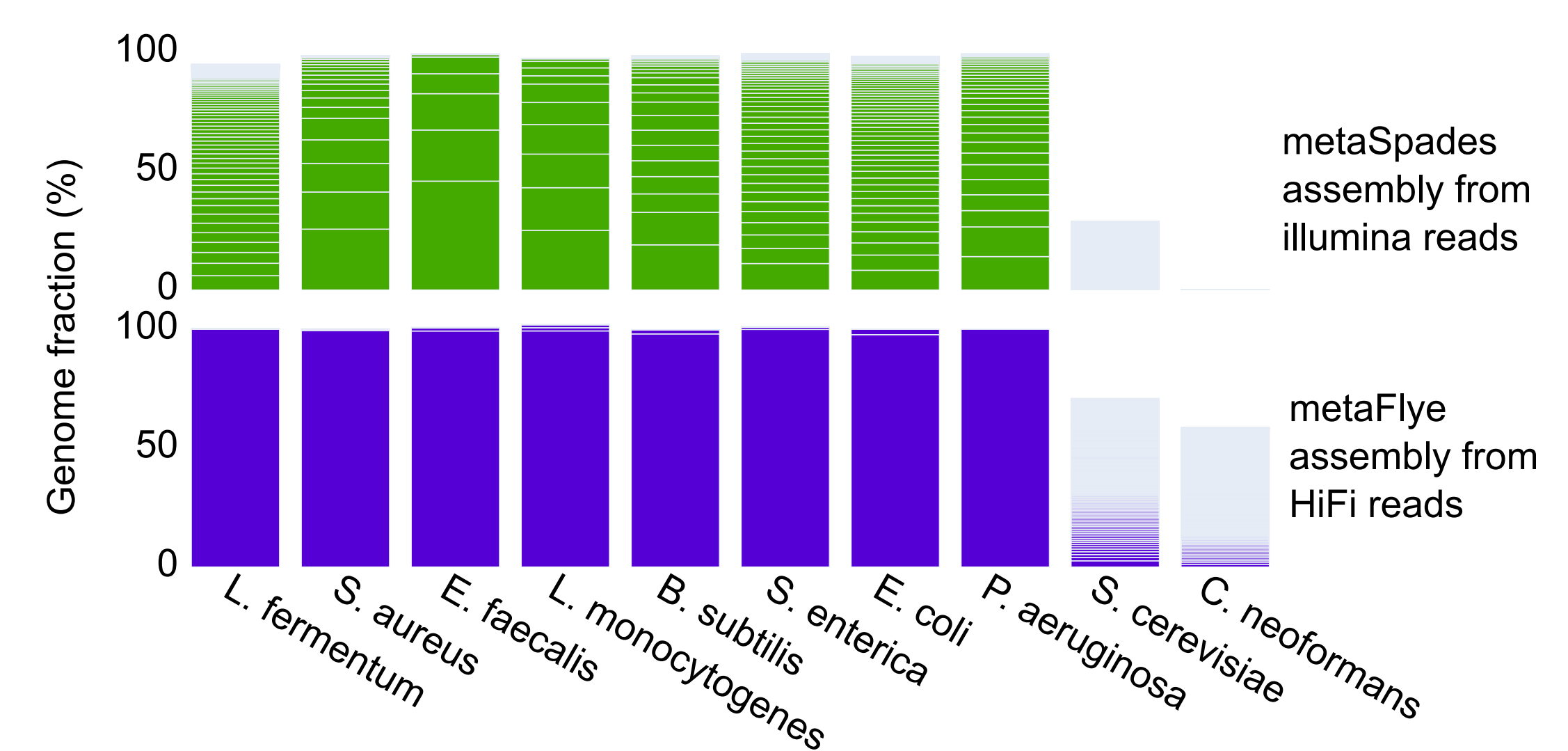


### Fully documented

<https://forgemia.inra.fr/genotoul-bioinfo/metagwgs>

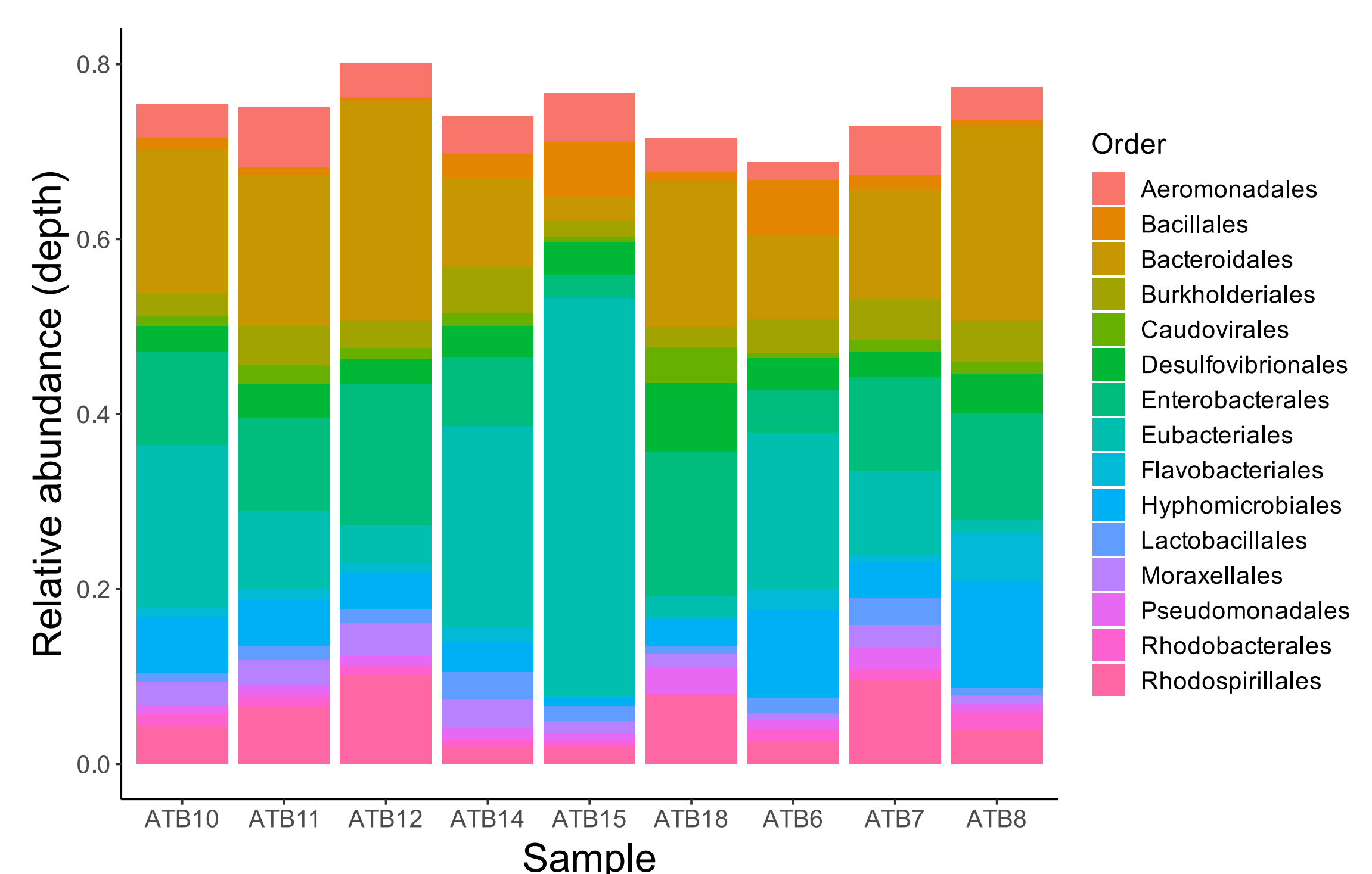
## Results examples

### HiFi vs Short reads assembly



**Bacterial genomes of mock Zymobionics are assembled in one contig by HiFi reads.** The genome fraction is the fraction of the reference genomes covers by the assembly. Each block in a bar represents a contig. Bacterial genomes are well covered by all assemblies but Illumina assembly is much more fragmented.

### Taxonomic profile



**Relative abundance of the 15 major orders of nine biofilms grown in bioreactors from sewage (example from ATB biofilm project).** Graph made from the taxonomic profile matrix generated by metagWGS. ATB15 is a sample that was exposed to ciprofloxacin (antibiotic) during the 14 days of culture.

## Perspectives

Annotation of Antibiotic Resistant Genes    Annotation of mobilome genes    Co-assembly

## Acknowledgements

**SeqOcln** financed by FEDER funds (Programme Opérationnel FEDER-FSE\_Midi-Pyrénées et Garonne 2014-2020)

ATB\_Biofilm funded by PNREST Anses, 2020/01/142



Projet cofinancé par le Fonds Européen de Développement Régional

[1] P. Di Tommaso et al. Nextflow enables reproducible computational workflows. *Nat Biotechnol.*, 35(4):316-319, 2017.  
 [2] S. Andrews. FastQC: A Quality Control Tool for High Throughput Sequence Data [Online]. Available at <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>, 2010.  
 [3] M. Martin. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet journal*, 17(1):10-12, 2011.  
 [4] NA Joshi, JN Fass. Sickle: A sliding-window, adaptive, quality-based trimming tool for FastQ files [Software]. Available at <https://github.com/najoshi/sickle>, 2011.  
 [5] H. Li et al. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics*, 25(14):1754-60, 2009.  
 [6] H. Li, Minimap2: pairwise alignment for nucleotide sequences. *Bioinformatics*, 34:3094-3100, 2018.  
 [7] S. Nurk et al. MetaSPAdes: a new versatile metagenomic assembler. *Genome Res.*, 27(5):824-834, 2017.  
 [8] D. Li et al. MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics*, 31(10):1674-6, 2015.  
 [9] H. Cheng. Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. *Nat Methods*, 18:170-175, 2021.  
 [10] M. Kolmogorov. metaFlye: scalable long-read metagenome assembly using repeat graphs. *Nature Methods*, 17,1103-1110, 2020.  
 [11] A. Mikheenko. MetaQUAST: evaluation of metagenome assemblies. *Bioinformatics*, 32: 1088-1090, 2016  
 [12] P. Danecek. Twelve years of SAMtools and BCFtools. *GigaScience* 10: giab008, 2021.  
 [13] P. Menzel et al. Fast and sensitive taxonomic classification for metagenomics with Kaiju. *Nat Commun.*, 7:11257, 2016.  
 [14] BD Ondov et al. Interactive metagenomic visualization in a Web browser. *BMC Bioinformatics*, 12(1):385, 2011.  
 [15] T. Seemann. Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, 30(14):2068-9, 2014.  
 [16] B. Buchfink. Sensitive protein alignments at tree-of-life scale using DIAMOND. *Nat Methods*, 18: 366-368, 2021.  
 [17] L. Fu et al. CD-HIT: accelerated for clustering the next-generation sequencing data. *Bioinformatics*, 28(23):3150-2, 2012.  
 [18] Y. Liao et al. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. *Bioinformatics*, 30(7):923-30, 2014.  
 [19] C. Cantalapiedra. eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. *Mol Biol Evol* 38: 5825-5829, 2021  
 [20] P. Ewels et al. MultiQC: Summarize analysis results for multiple tools and samples in a single report. *Bioinformatics*, 32(19):3047-8, 2016.