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Exploring the Common Human Gut Eukaryotic Microbiota around the World

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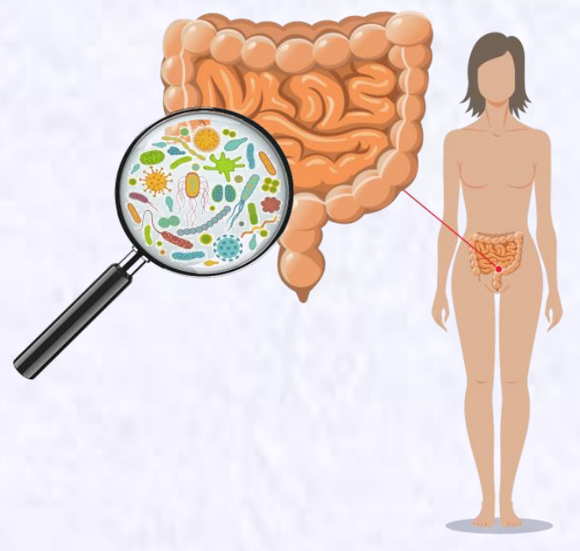
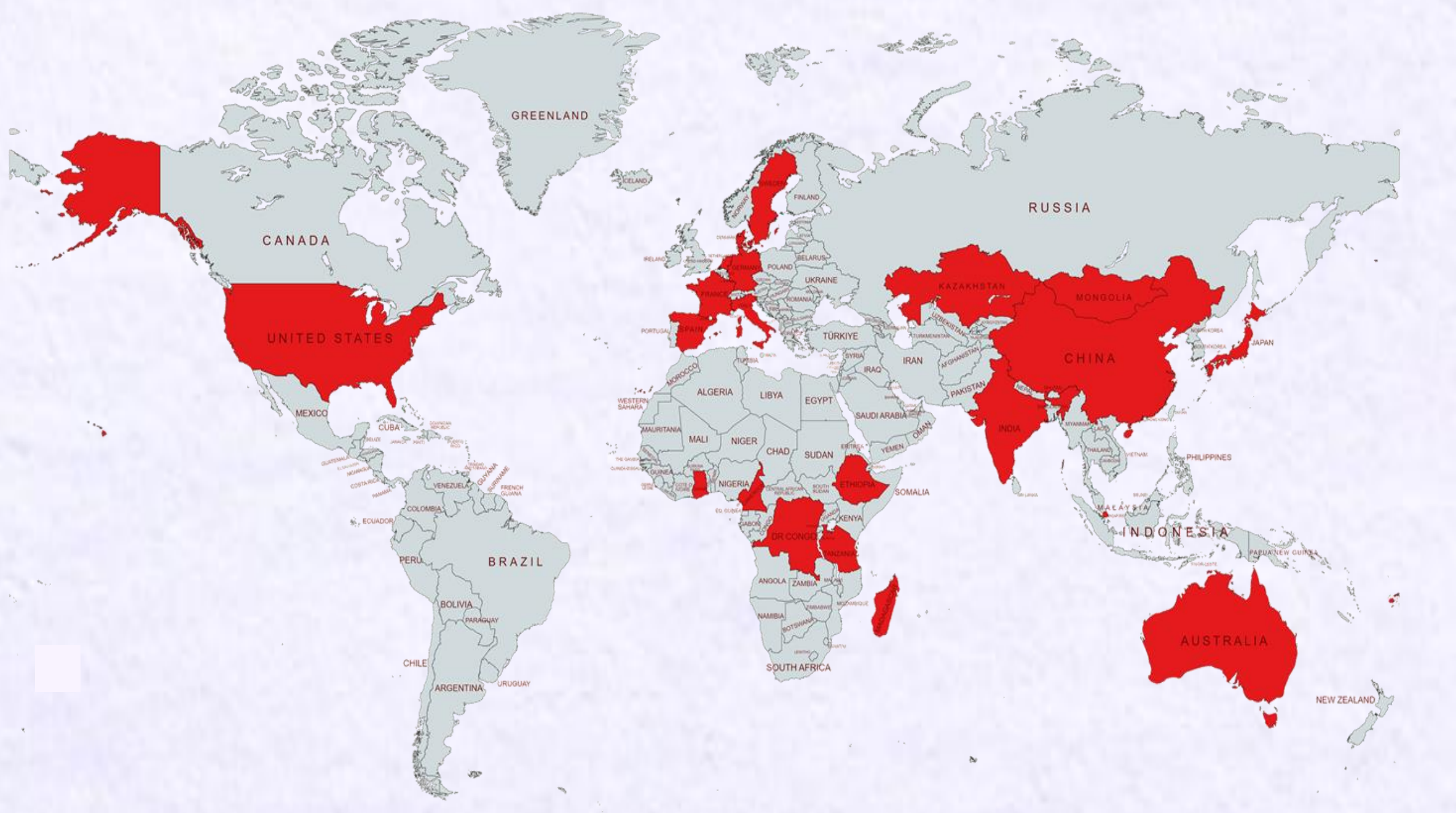
INTRODUCTION

In recent years, thanks to advances in massive sequencing technologies, many large-scale metagenomic studies have been carried out to characterise the complex consortium of microorganisms that constitute the human gut microbiome. However, the vast majority of these are mainly focused on bacteria, leaving aside the role of eukaryotes (1).



Moreover, the few existing studies that have focused on microbial eukaryotes use the 18S ribosomal gene sequence, while whole genome sequencing (WGS) studies are scarcer (2).

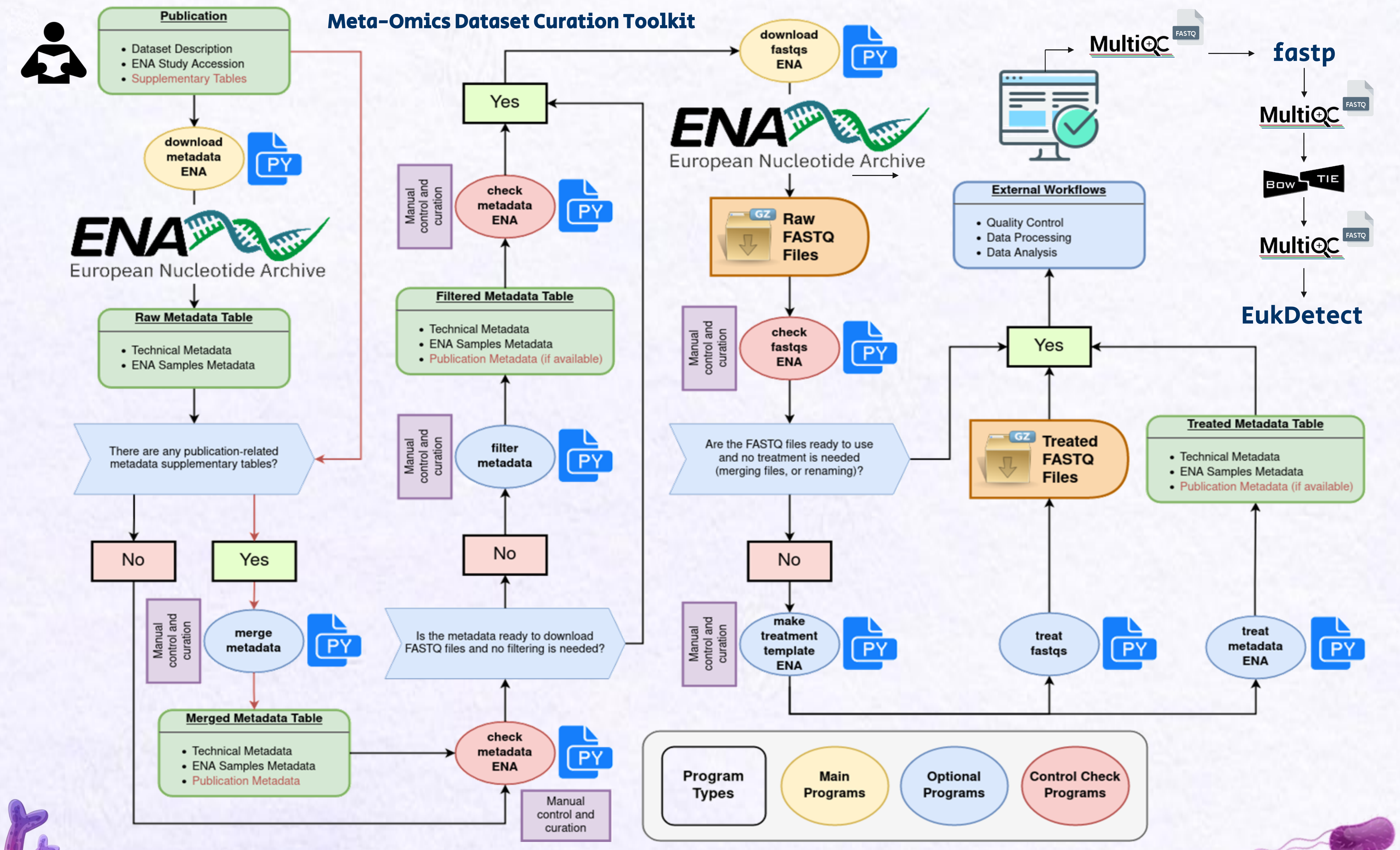
Therefore, this study aims to explore the common eukaryotic members in the microbiota of healthy individuals across different human populations worldwide.



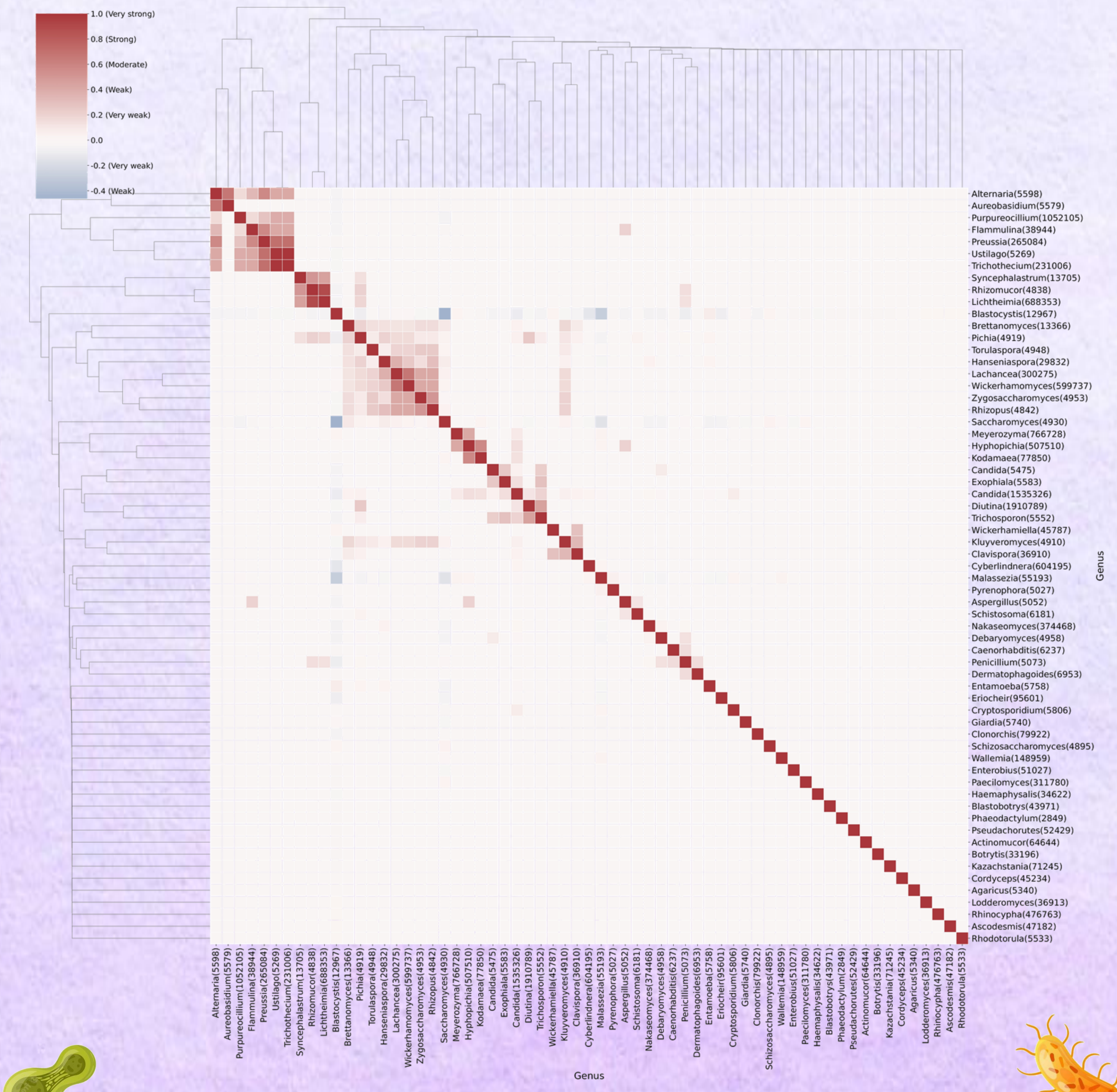
33 DATASETS 6021 SAMPLES 4353 INDIVIDUALS 22 COUNTRIES

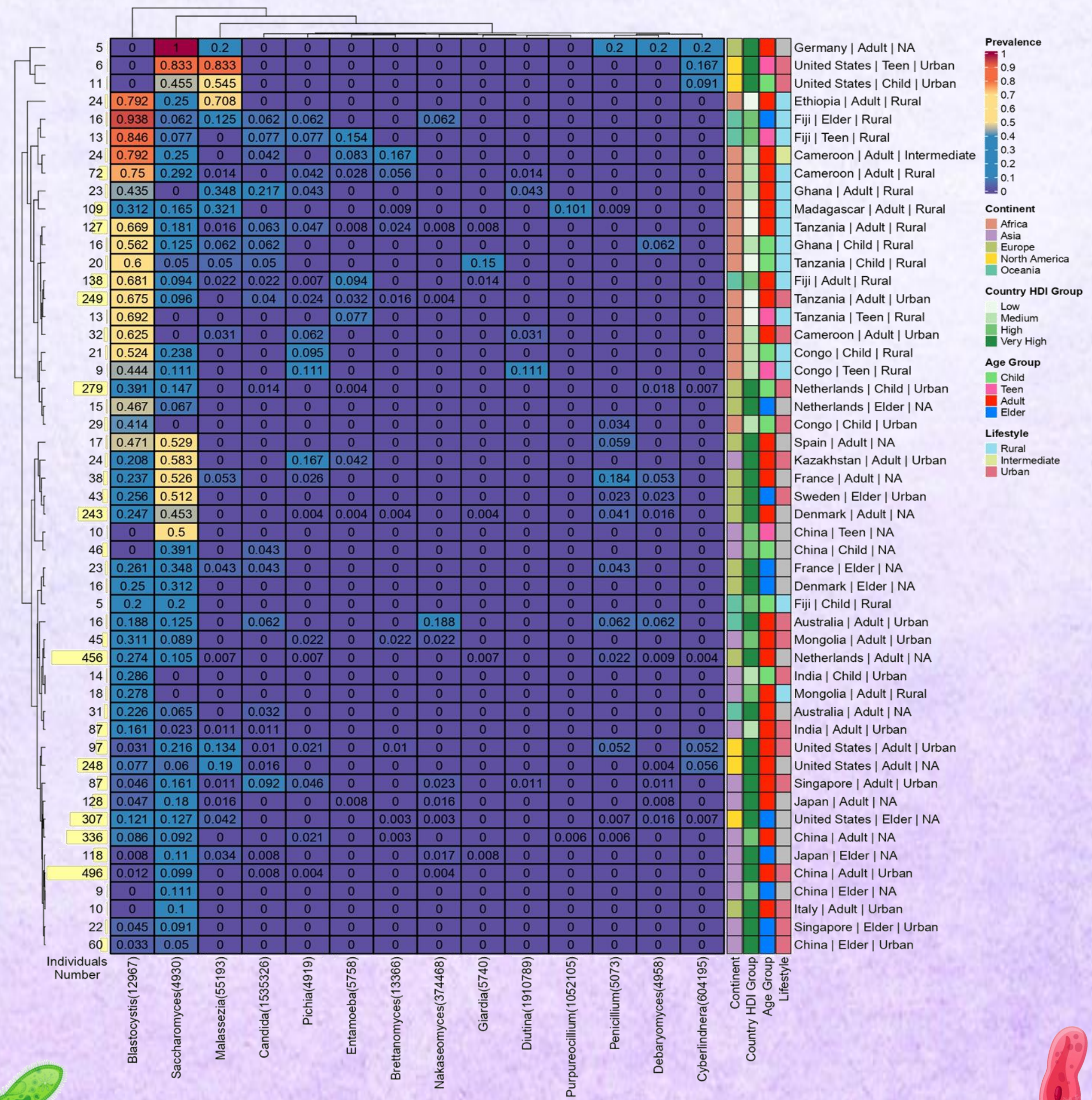
METHODS

1) **Meta-Omics Dataset Curation Toolkit:** a workflow that provides a standardised methodology for curating and processing raw metadata of public projects hosted in the European Nucleotide Archive (ENA) repository.
2) **Quality Control:** fastp (3), MultiQC (4) and Bowtie2 (5) have been used to process the raw data.
3) **EukDetect:** an eukaryotic taxonomic profiler engineered to work with WGS metagenomic data (6).



RESULTS





CONCLUSIONS & NEAR FUTURE

In conclusion, it is neither possible to confirm nor refute the presence or absence of a global eukaryotic core. Nevertheless, due to the heterogeneity in the number of individuals, the existence of some specific regional cores has been cautiously demonstrated. This evidences the future need to continue exploring the eukaryotic fraction of the human microbiome.

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