



THE 4<sup>th</sup> VIETNAM SCHOOL OF BIOLOGY (VSOB-4)

# Metagenome Analysis in One Health Practice – From 16S to Shotgun

*September 03<sup>rd</sup>-06<sup>th</sup>, 2025, ICISE, Quy Nhon, Vietnam*

# **Keynote 2**

# **Analysis of Gut Microbiome, Structure and Function in Vietnamese Adults**

*Presenter: Thuy Vy Nguyen, PhD*

# MICROBIOME – HOW TO STUDY IT ?



<https://scitechdaily.com/coral-microbiome-bacteria-fungi-and-viruses-is-key-to-surviving-climate-change/>



<https://biomemakers.com/blog/the-soil-microbiome-and-its-impact-on-plant-nutrition>



<https://ngheandost.gov.vn/hoat-dong-khcn/>

**WHO ARE THEY ? WHAT ARE THEY DOING ?**

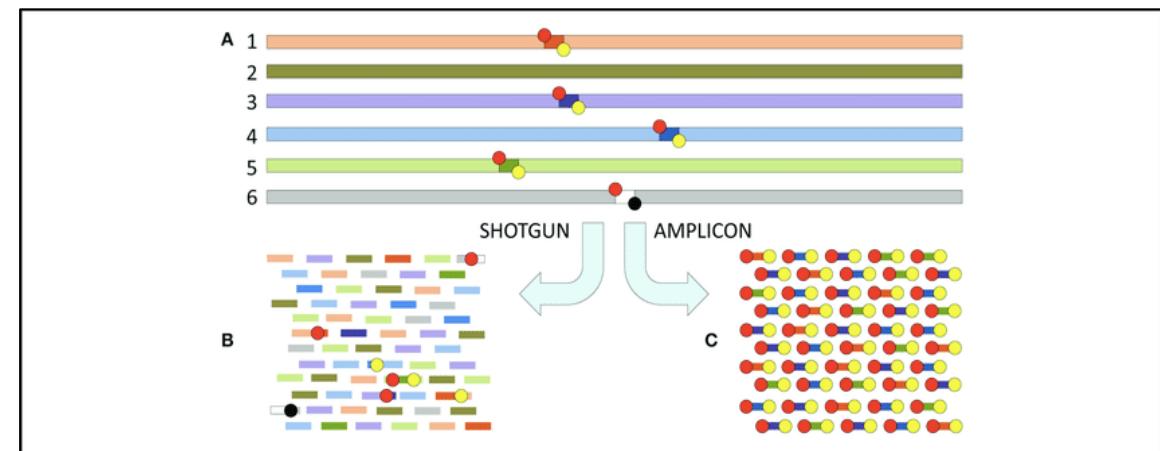
**Culture-based methods**



*Das and Singh, 2024*

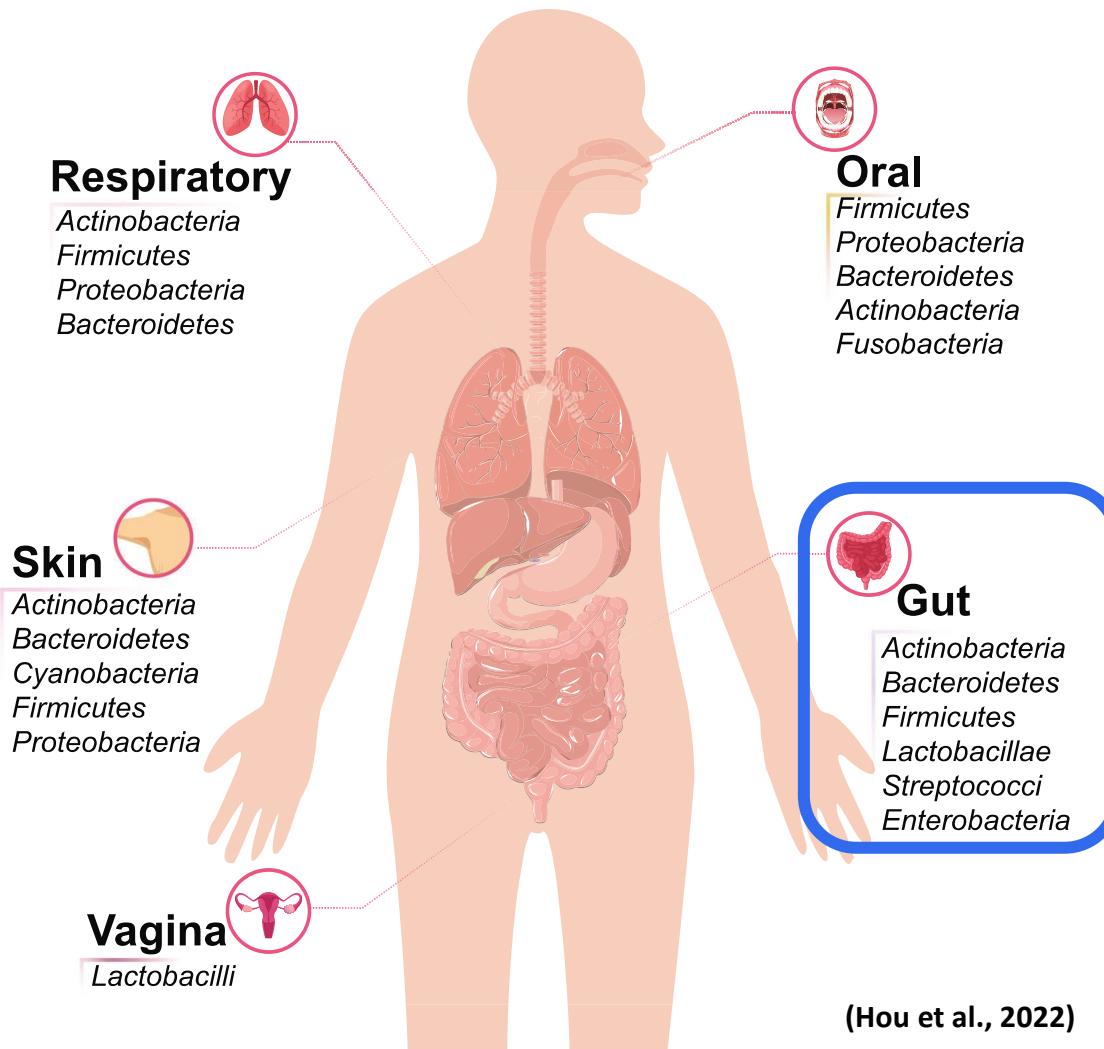
**Unculture-based methods**

**METAGENOMICS**



<https://sourdoughstartersfall20.wordpress.ncsu.edu/2020/10/09/so-lets-talk-about-sequencing-our-starters/>

# THE HUMAN GUT MICROBIOME

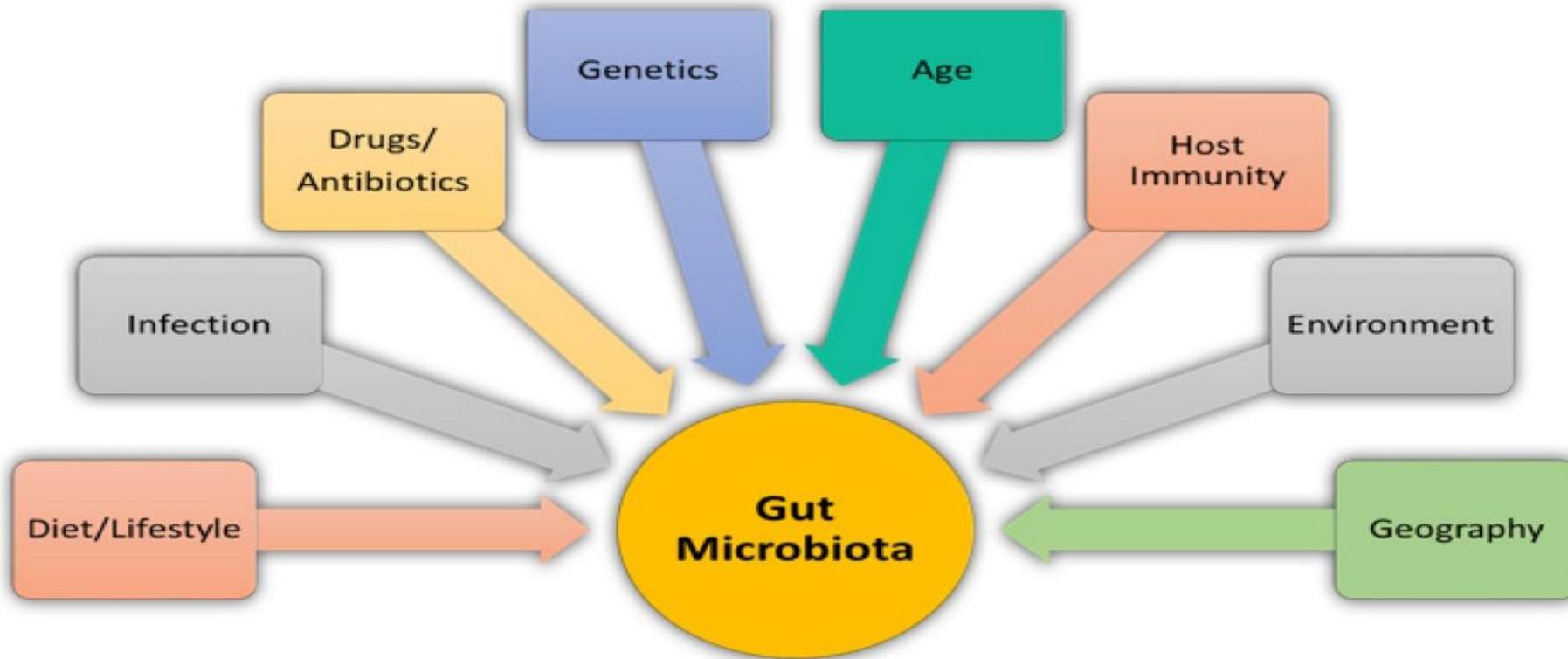


300-500 bacterial species/person

38 trillions of microbial cells

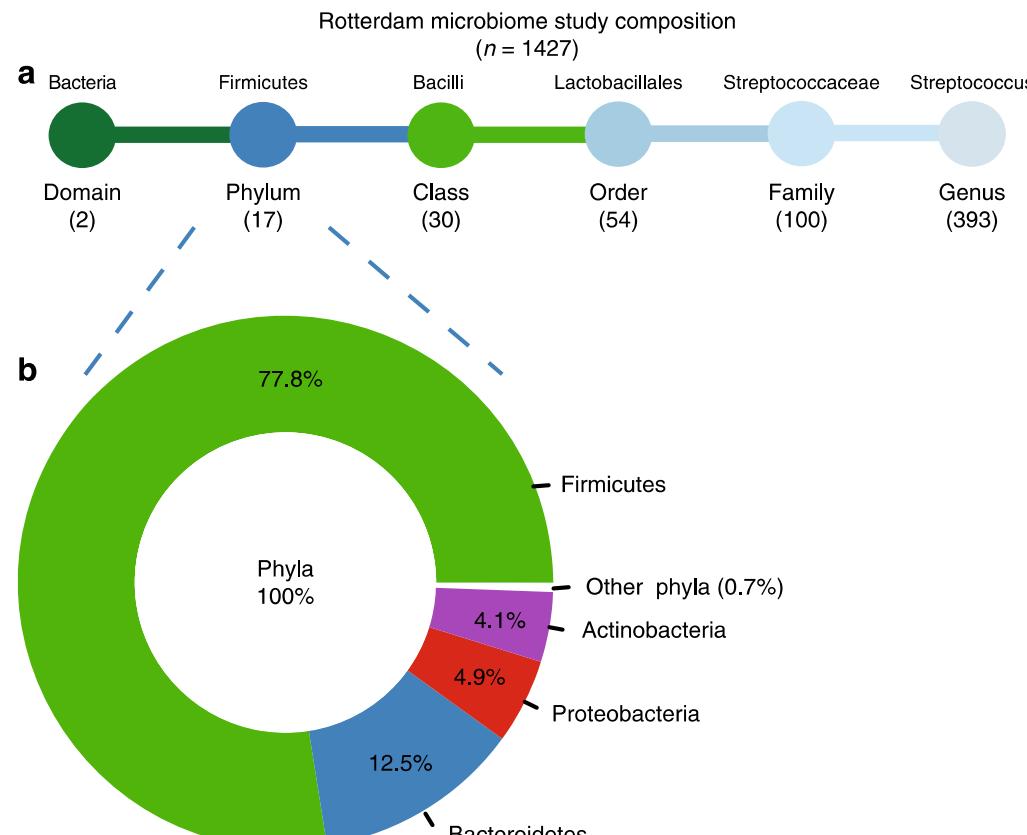
150 times more genetic informations than the host's

# FACTORS INFLUENCING THE GUT MICROBIOME

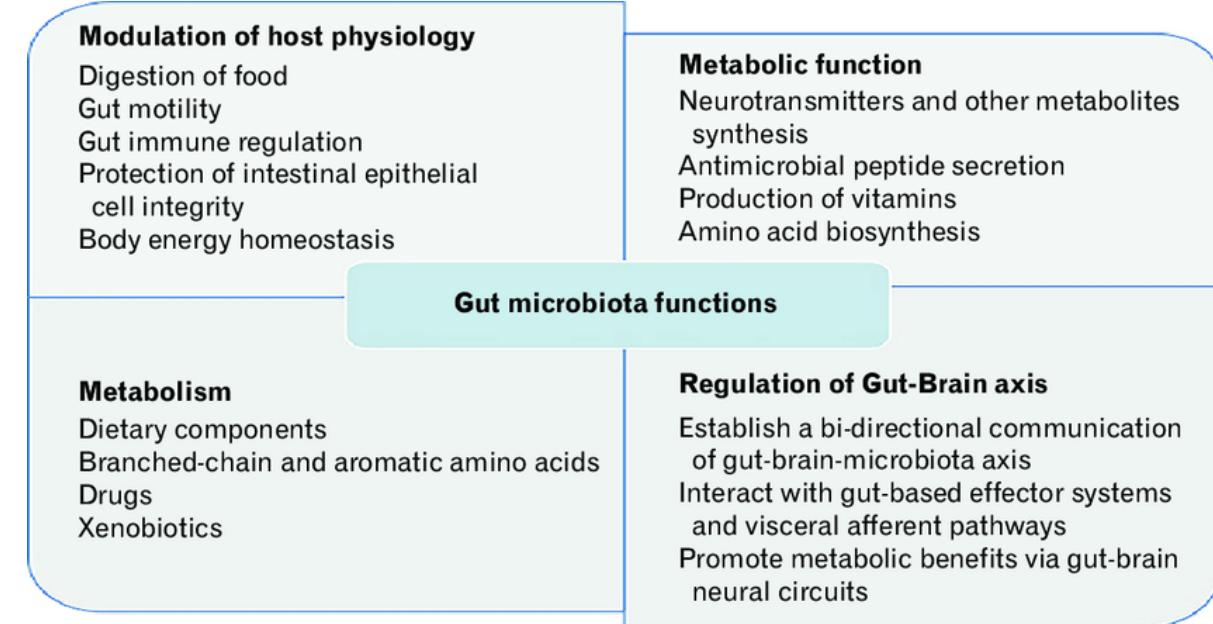


(Akbara et al., 2018)

# COMPOSITION AND FUNCTIONS OF THE GUT MICROBIOME

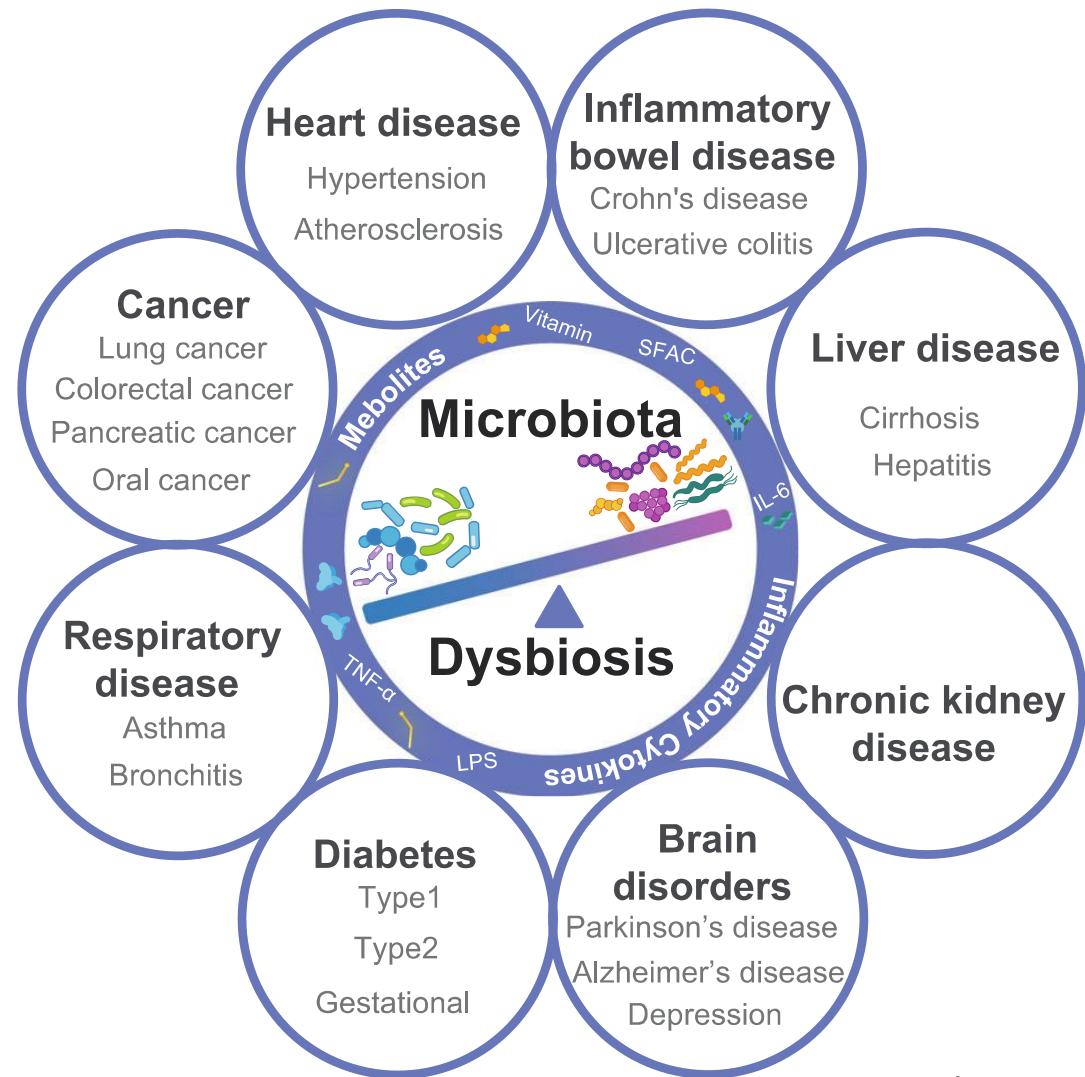


(Boer et al., 2019)



(Singh et al., 2020)

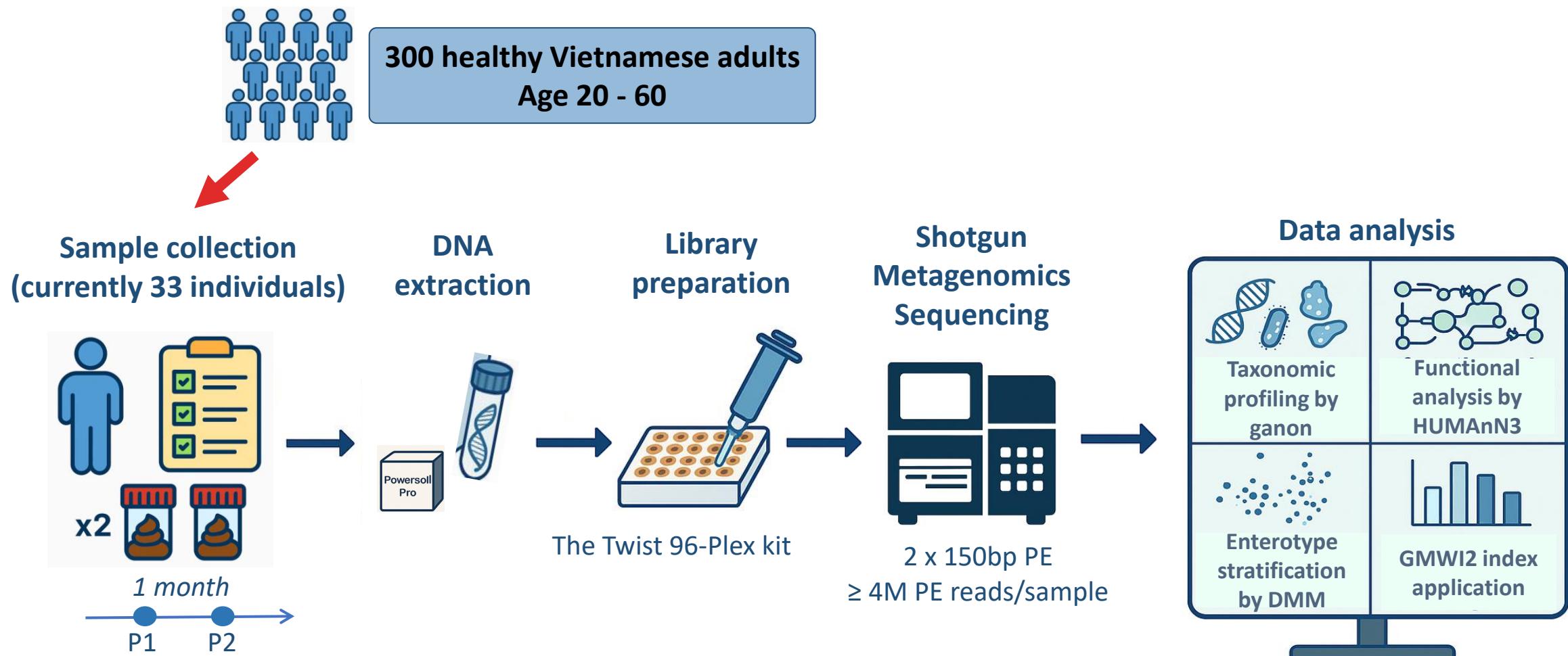
# GUT MICROBIOME AND HEALTH



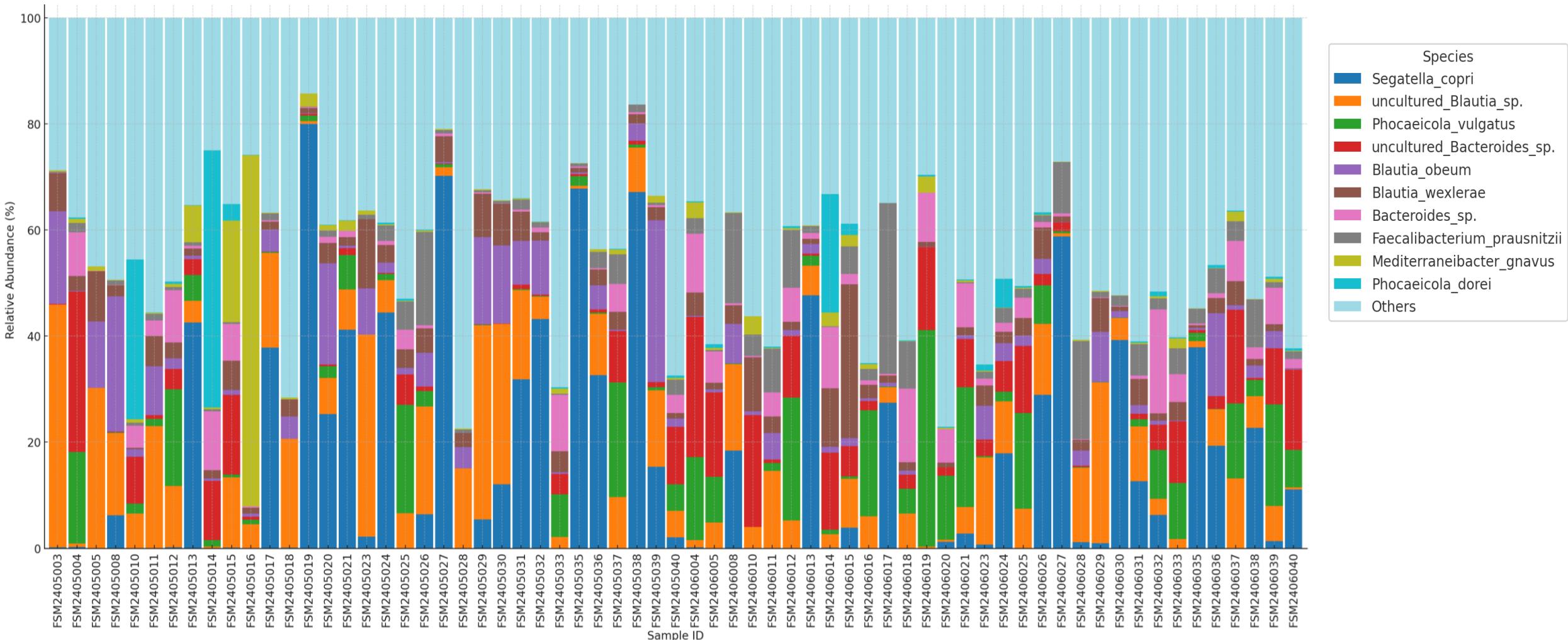
(Hou et al., 2022)

# RESEARCH PROJECT

## ANALYSIS OF THE GUT MICROBIOME OF HEALTHY VIETNAMESE PEOPLE BY SHOTGUN METAGENOMIC SEQUENCING

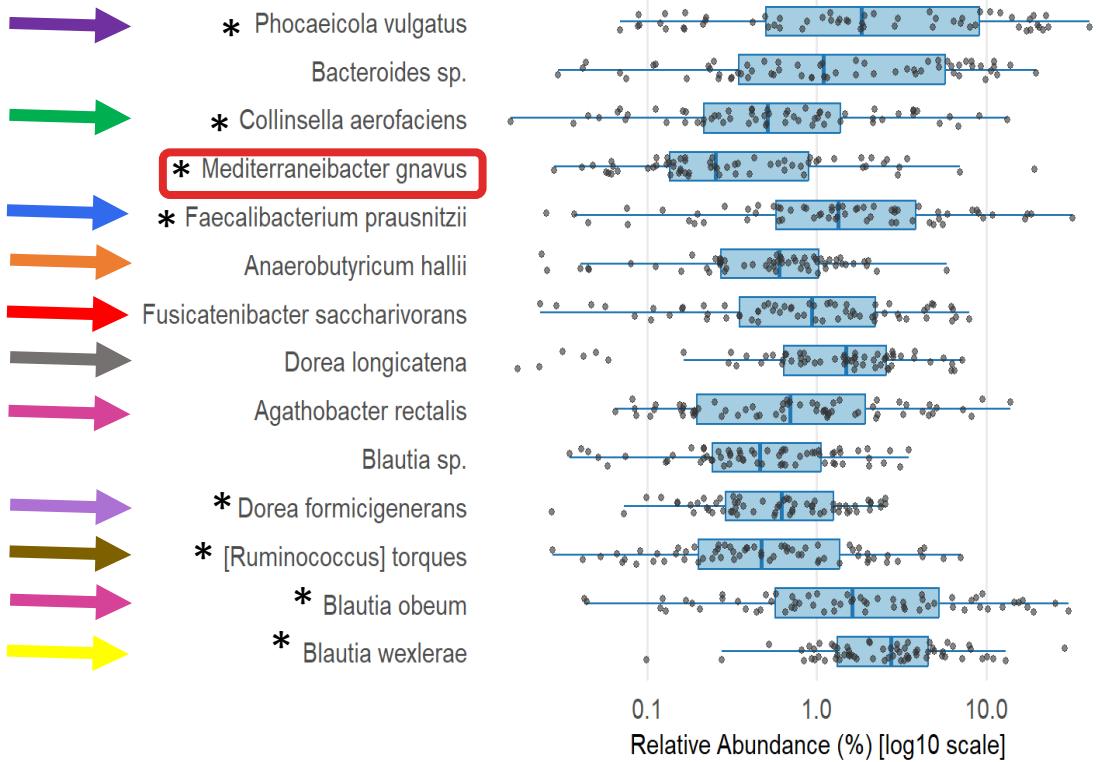


# TAXONOMIC PROFILING OF GUT MICROBIOME SAMPLES

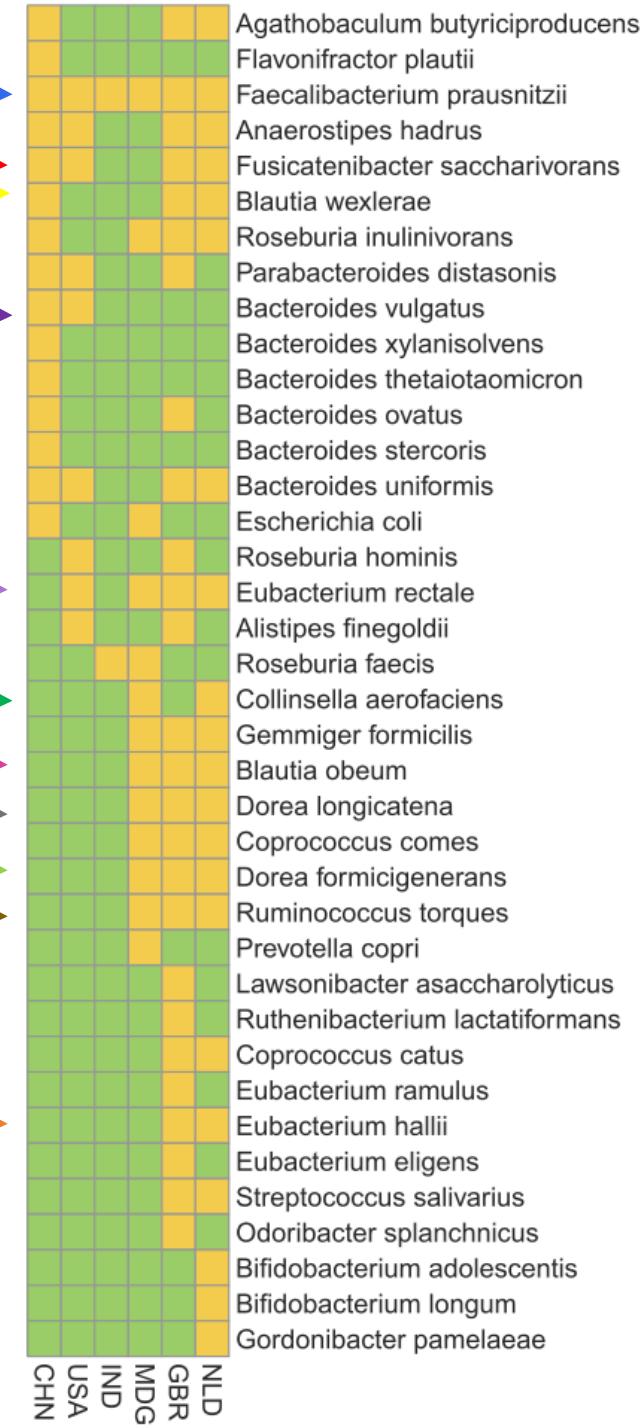


# CORE MICROBIOME FOUND IN VIETNAMESE METAGENOMES

Prevalence > 80%, Abundance > 0.01%

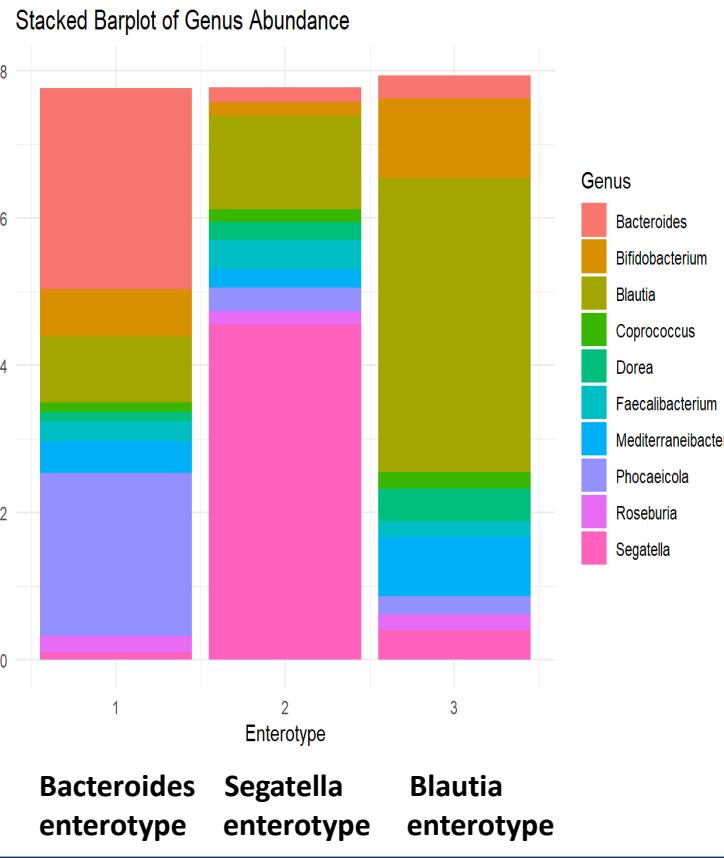


(Sheng et al., 2024)

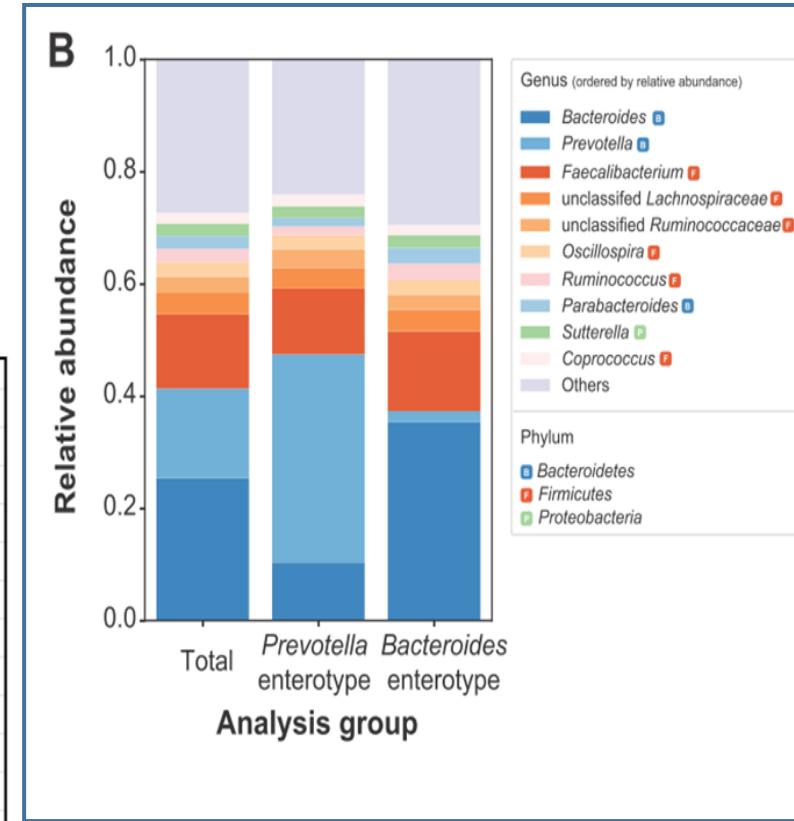


# ENTEROTYPE STRATIFICATION IN DIFFERENT COHORTS

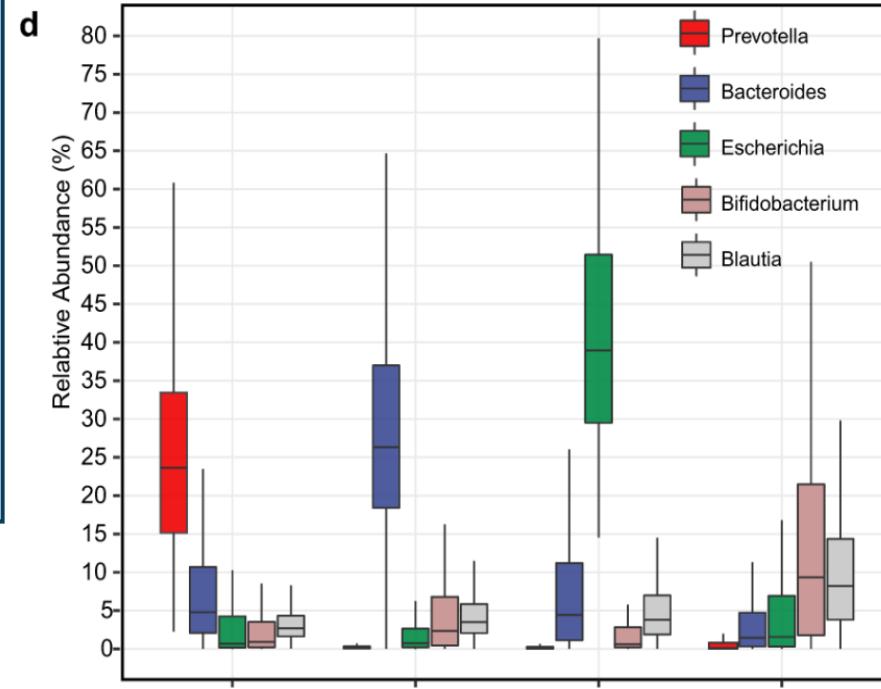
## Vietnamese cohort



## Korean cohort



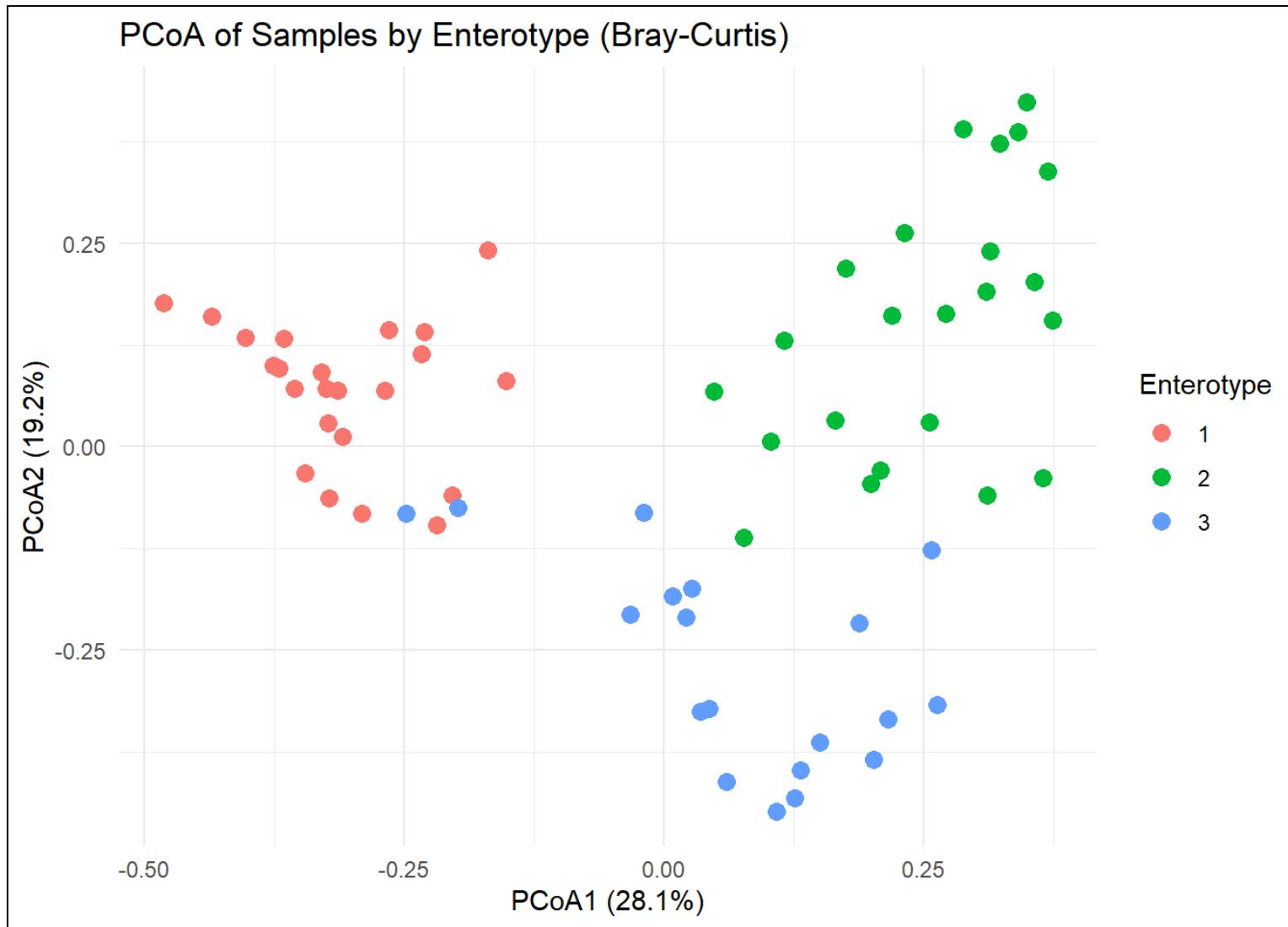
## Chinese cohort



(Lu et al., 2021)

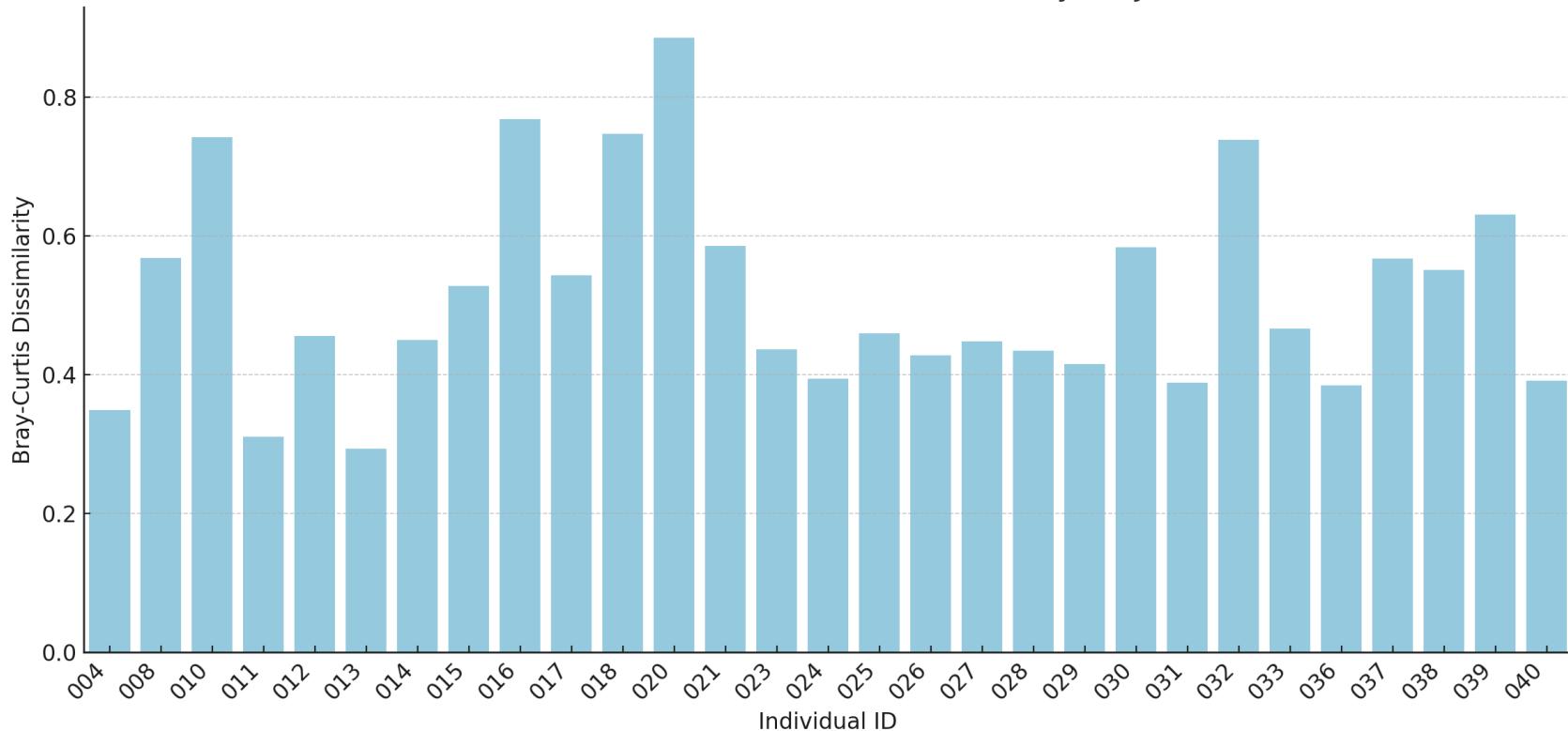
(Lim et al., 2021)

# DISTRIBUTION OF SAMPLES INTO 3 ENTEROTYPES

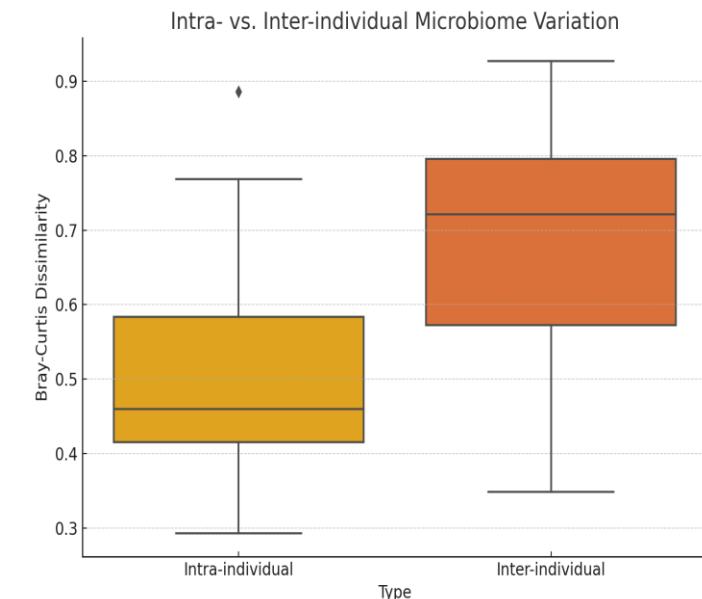


# COMPOSITIONAL VARIABILITY OF THE GUT MICROBIOTA

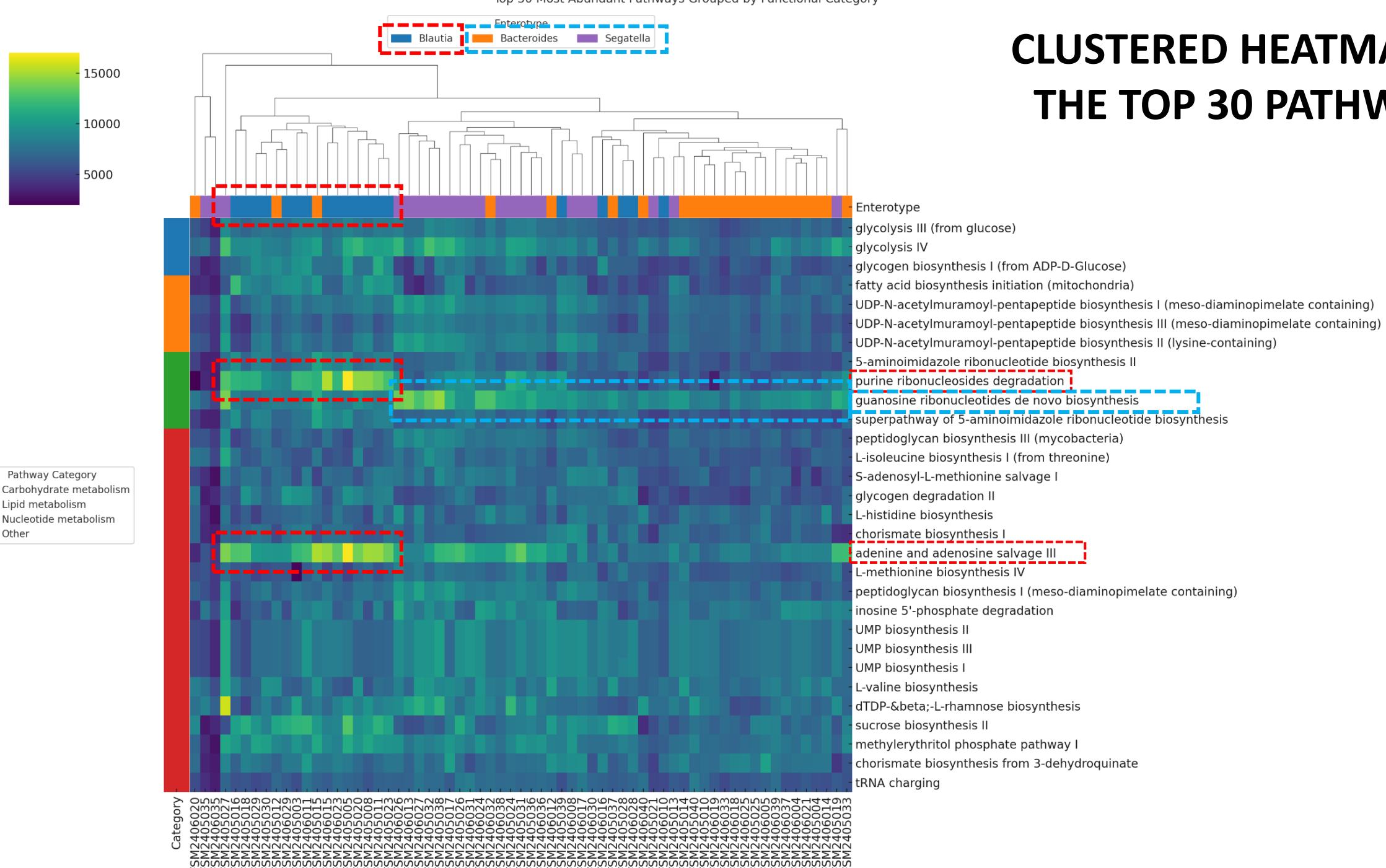
Compositional variability of the gut microbiota for the 29 individuals estimated by the Bray-Curtis dissimilarity



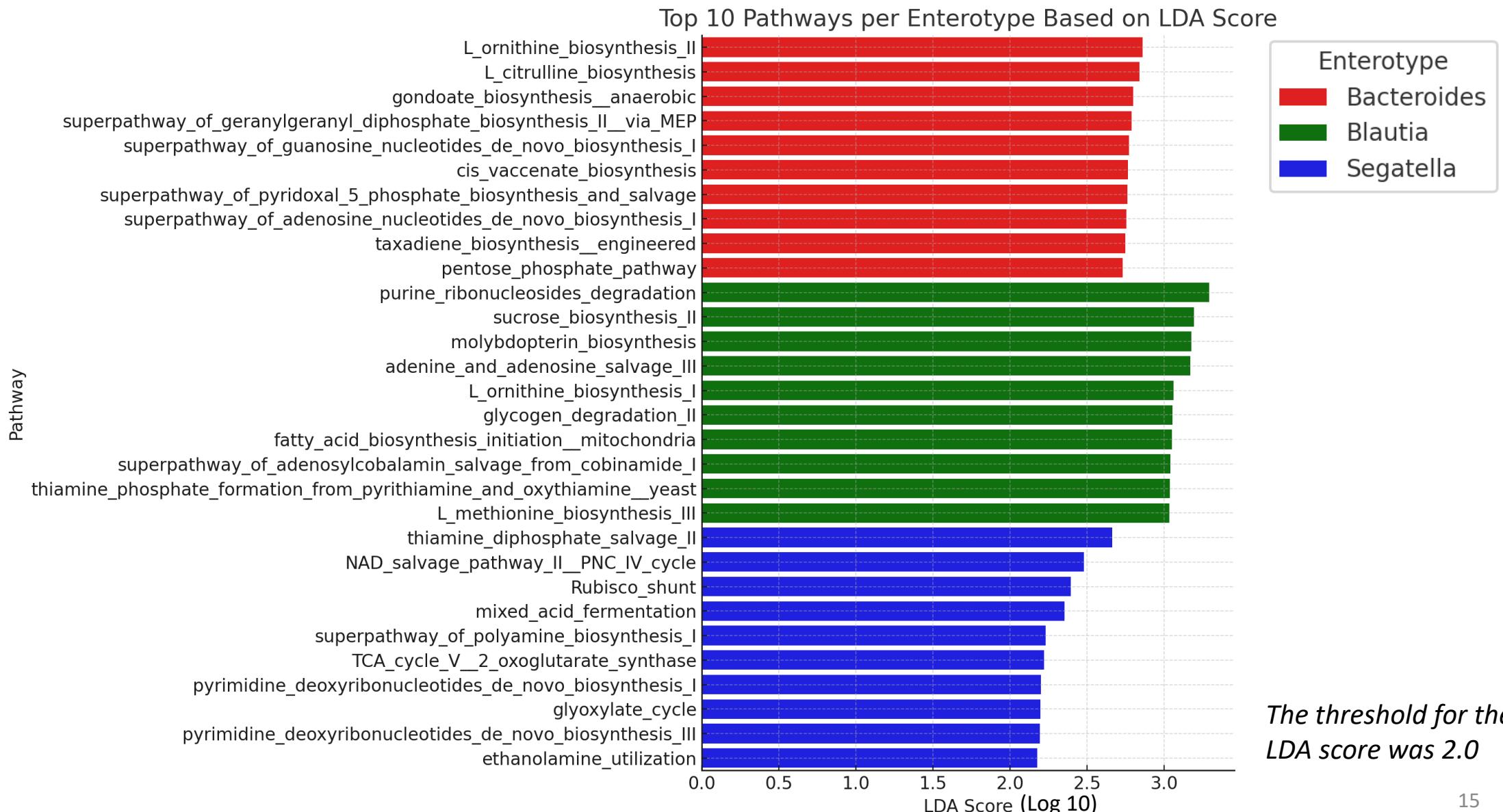
Boxplots of intra- and inter-individual Bray-Curtis dissimilarity



# CLUSTERED HEATMAP OF THE TOP 30 PATHWAYS



# LEFSE ANALYSIS OF FUNCTIONAL BIOMARKERS OF 3 ENTEROTYPES



# GUT MICROBIOME WELLNESS INDEX (GMWI)

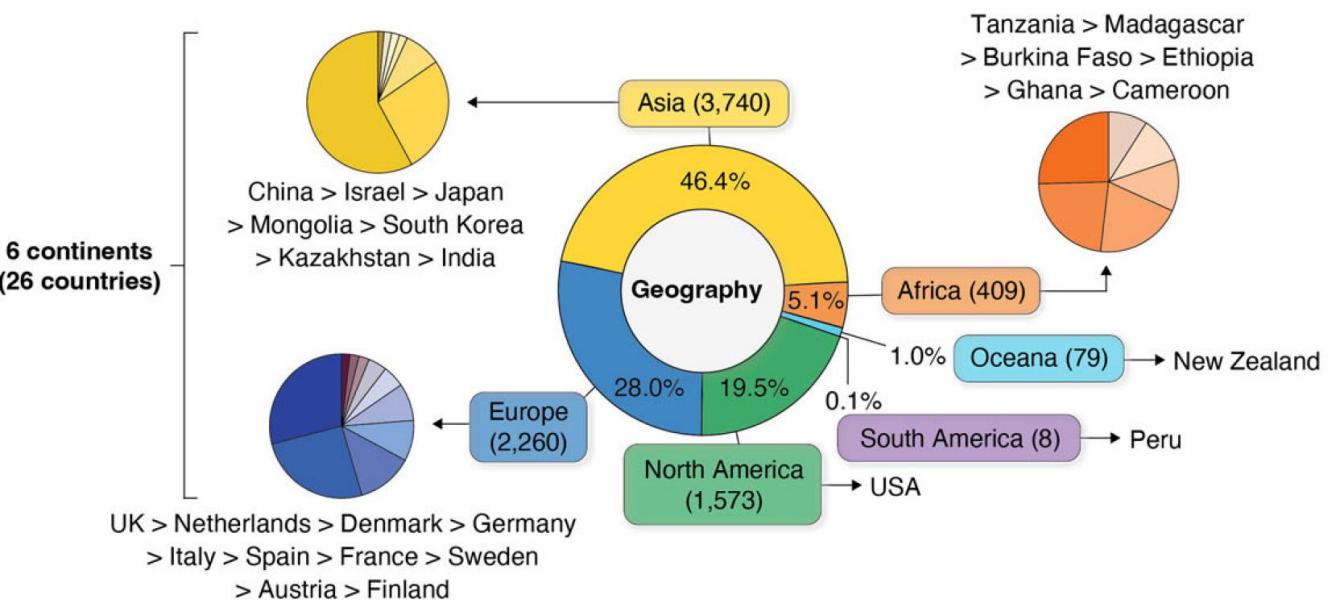
Standardized health status indicator based on gut microbiome taxonomic profiles

8069 stool shotgun metagenomes (26 countries & 6 continents):

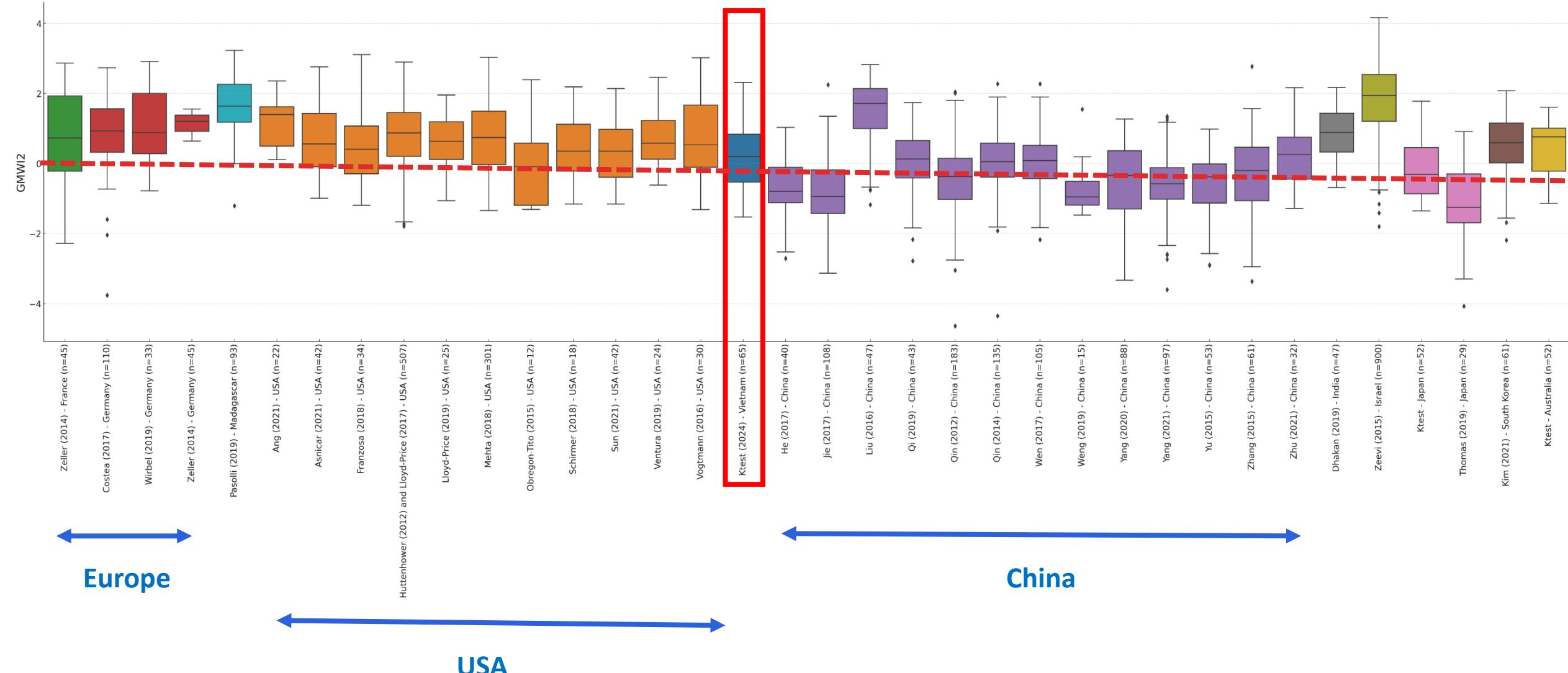
- 5557 healthy
- 2522 diseased (11 diseases including multiple sclerosis, ankylosing spondylitis, rheumatoid arthritis, ulcerative colitis, nonalcoholic fatty liver disease, T2D, Crohn's disease, Graves' disease, colorectal cancer, liver cirrhosis, atherosclerotic cardiovascular disease)

Accuracy of 79.9% in distinguishing healthy from non-healthy individuals

GMWI2 (+): Healthy; GMWI2 (-): Non-healthy; GMWI2 = 0: neither healthy nor non-healthy



# GMWI2 BY COHORTS



## IN SUMMARY

The core microbiome in our cohort includes 14 species, with a prevalence of 80% and a abundance of 0.01%. Bacterial species such as *Segatella copri*, *Mediterraneibacter gnavus* are characteristics in prevalence and abundance to Vietnamese cohort.

Our cohort can be classified into three enterotypes - Prevotella, Bacteroidetes and Ruminococcus, dominated by *Segatella copri*, Bacteroides sp. and Blautia sp.

Application of GMWI2 as an indicator to assess health status of Vietnamese people based on taxonomic profile showed comparable values to those of different countries in Europe, the USA, Asia.

Functional analysis of the GM in Vietnamese cohort showed 30 pathways, with dominant functional categories specific to each enterotype

# ACKNOWLEDGEMENTS

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