

# Microbiota Associated With Soils of Cacao and Coffee Farms with Potential Promoter Effect of Plant Growth in the Amazonas Region

Jois V. Carrion<sup>1</sup>, Maricela Chavez-Huigo<sup>1</sup>, Yadhira M. Olano<sup>1</sup>, Martha S. Calderon<sup>1,2</sup>, and Danilo E. Bustamante<sup>1,2</sup>

<sup>1</sup>Instituto de Investigación en Ingeniería Ambiental (INAM), Facultad de Ingeniería Civil y Ambiental (FICIAM), Universidad Nacional Toribio Rodríguez de Mendoza, Chachapoyas, Amazonas, Perú. <sup>2</sup>Instituto de Investigación para el Desarrollo Sustentable de Ceja de Selva (INDES-CES), Universidad Nacional Toribio Rodríguez de Mendoza, Chachapoyas, Amazonas, Perú.

## 1. Introduction

Soil health, with its resilience and biological diversity, is key to nutrient uptake and stress tolerance. However, the projected temperature increase by 2050 could reduce microbial diversity, increasing disease, and decreasing agricultural yields for cacao and cocoa farms. The use of molecular tools such as metabarcoding is key to identifying microbial species and their functions.

## 2. Objective

To decipher the biodiversity and functional profile of the microbiota in soils of cocoa and coffee crops in the Amazon region of Peru using the high-throughput sequencing method metabarcoding.

## 3. Material and methods

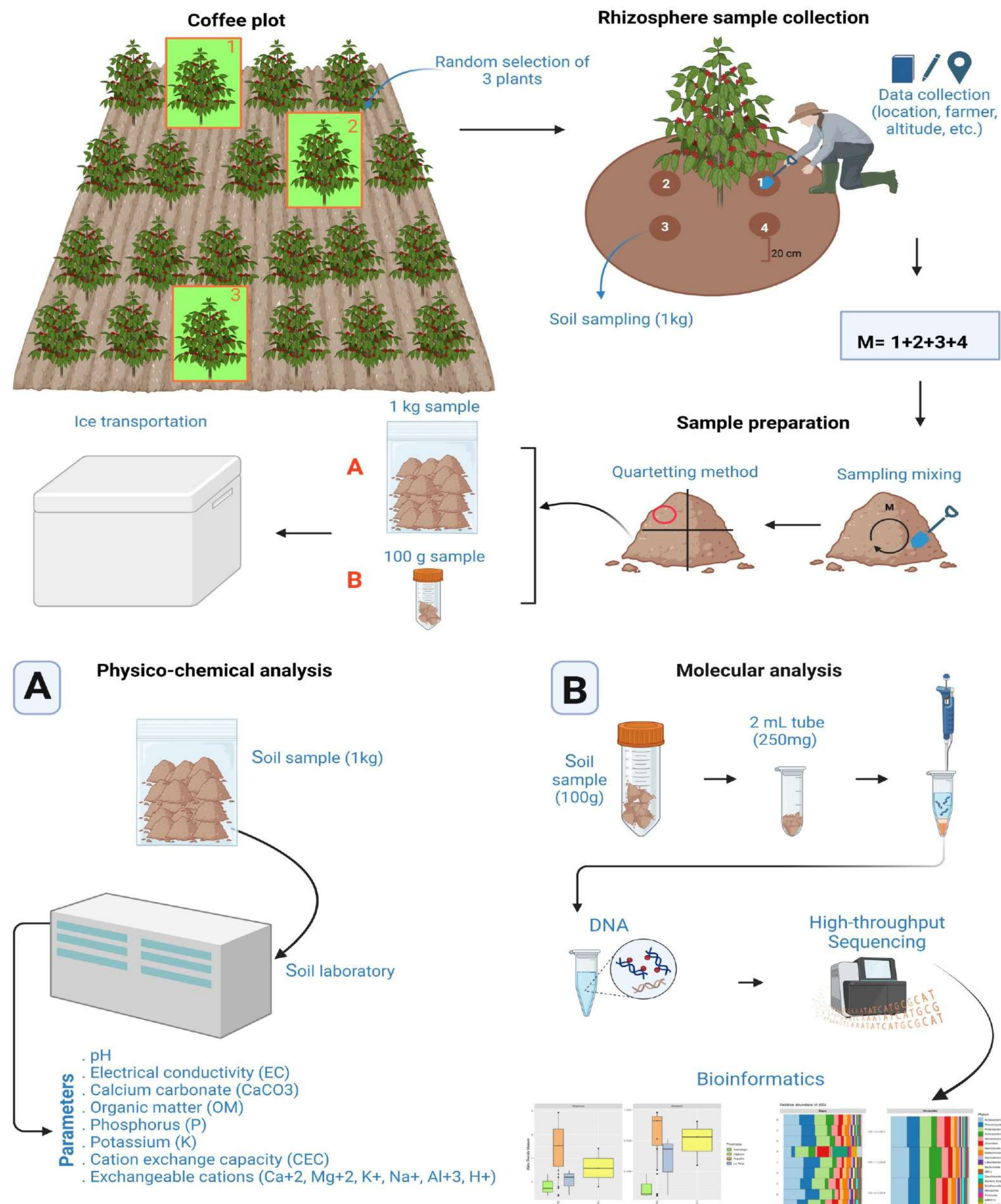


Figure 1. Sample collection process and laboratory work methodology

## 4. Results

- 32,988 in total ASVs. After normalization were found 19,874 in cocoa and 13,114 in coffee.
- Alpha cocoa diversity → Utcubamba is slightly more diverse than Bagua but not significantly.
- Coffee alpha diversity → Luya is slightly more diverse than Rodriguez but not significantly.
- Phylum Acidobacteriota, Planctomycetota, and Proteobacteria were the most predominant in cacao soils.
- Phylum Proteobacteria, Verrucomicrobiota, Acidobacteriota, and Actinobacteriota were the most predominant in coffee soils.
- Lipid and cofactor metabolic** pathways were predominant in cacao soils microbiota, while **amino acid and carbohydrate pathways** were in coffee soils microbiota.
- The categories of genetic information processing and cellular processes show higher activity in cocoa soils microbiota compared to coffee. This could reflect a higher metabolic complexity in the cocoa-associated microbiota.

## 5. Discussion

- This is the first study to describe the microbiota associated with cocoa and coffee soils in the Amazon region and Peru.
- Although the cocoa and coffee farming are very close to each other, their microbial composition is different.
- In our study, *Proteobacteria* was identified as the most abundant phylum, in contrast to the findings of Chica Cárdenas et al. (2024) in Colombia, where *Acidobacteriota* dominated the microbial community.
- The pathways most related to the growth-promoting effect in cocoa are “environmental information processing” and “metabolism” important for membrane transport and carbohydrate production. For coffee, the key pathways are “amino acid” and “carbohydrate metabolism” crucial for nutrition.

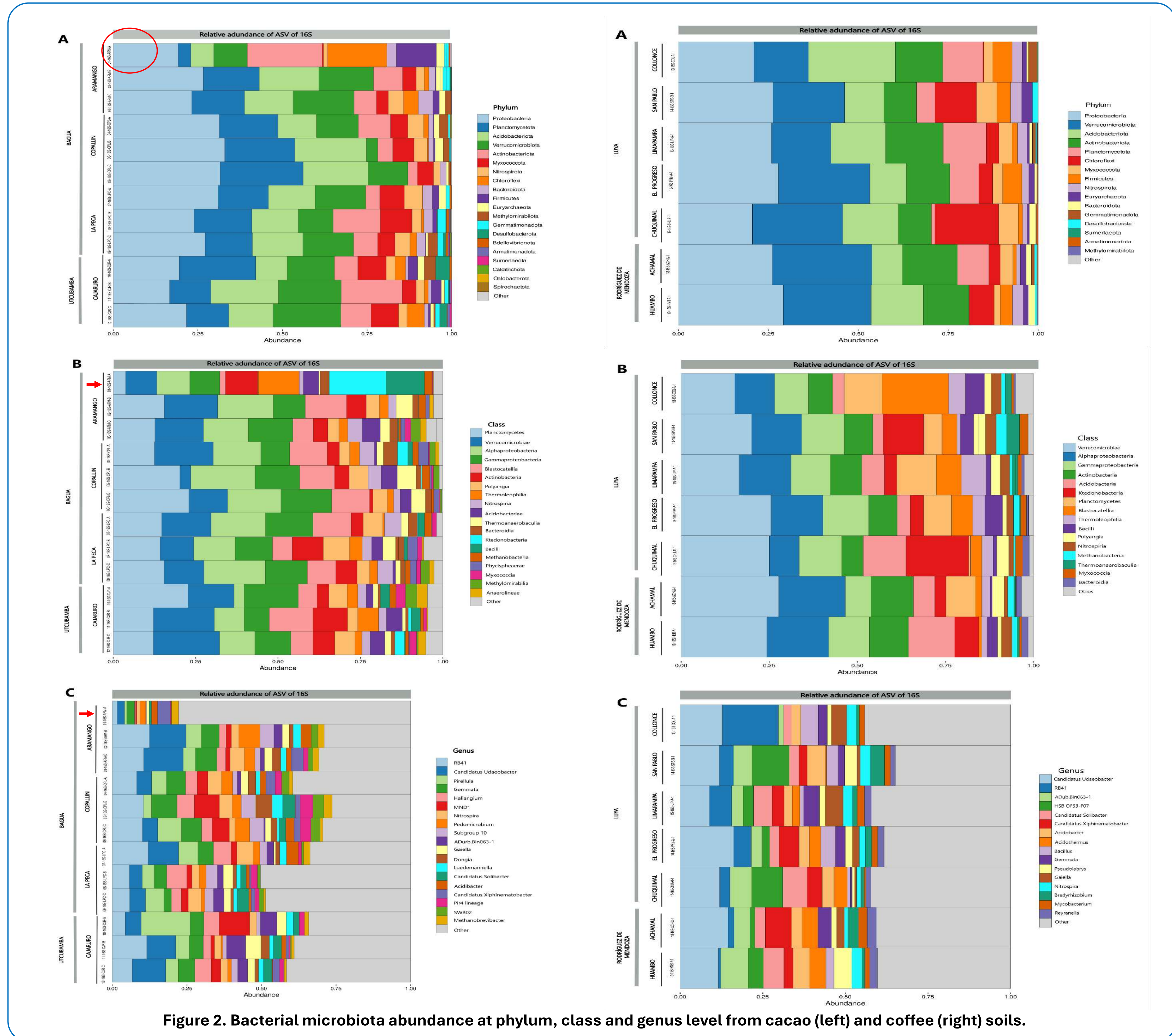


Figure 2. Bacterial microbiota abundance at phylum, class and genus level from cacao (left) and coffee (right) soils.

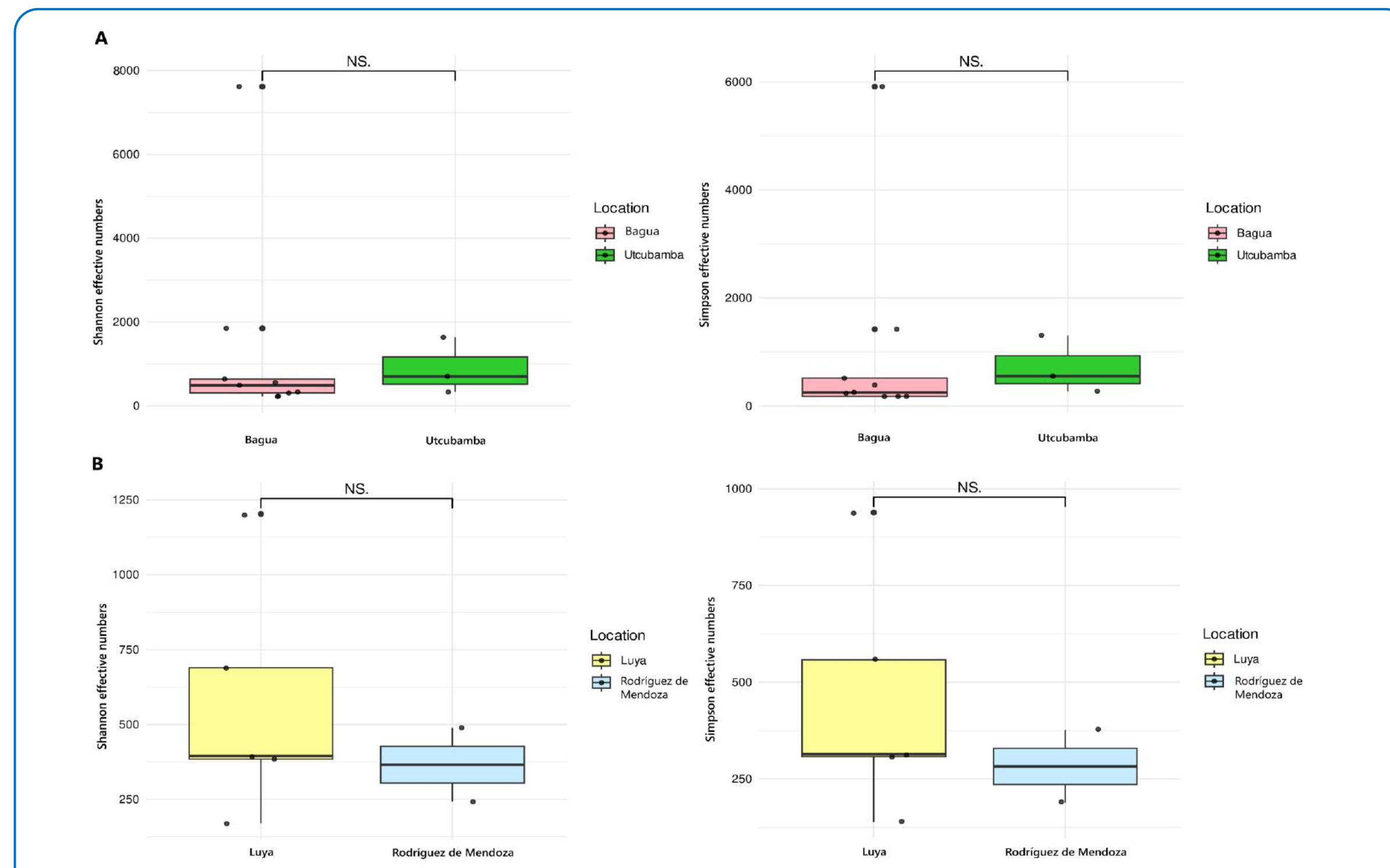


Figure 3. Shannon and Simpson's effective diversity for cocoa (A) and coffee (B) soils microbiota.

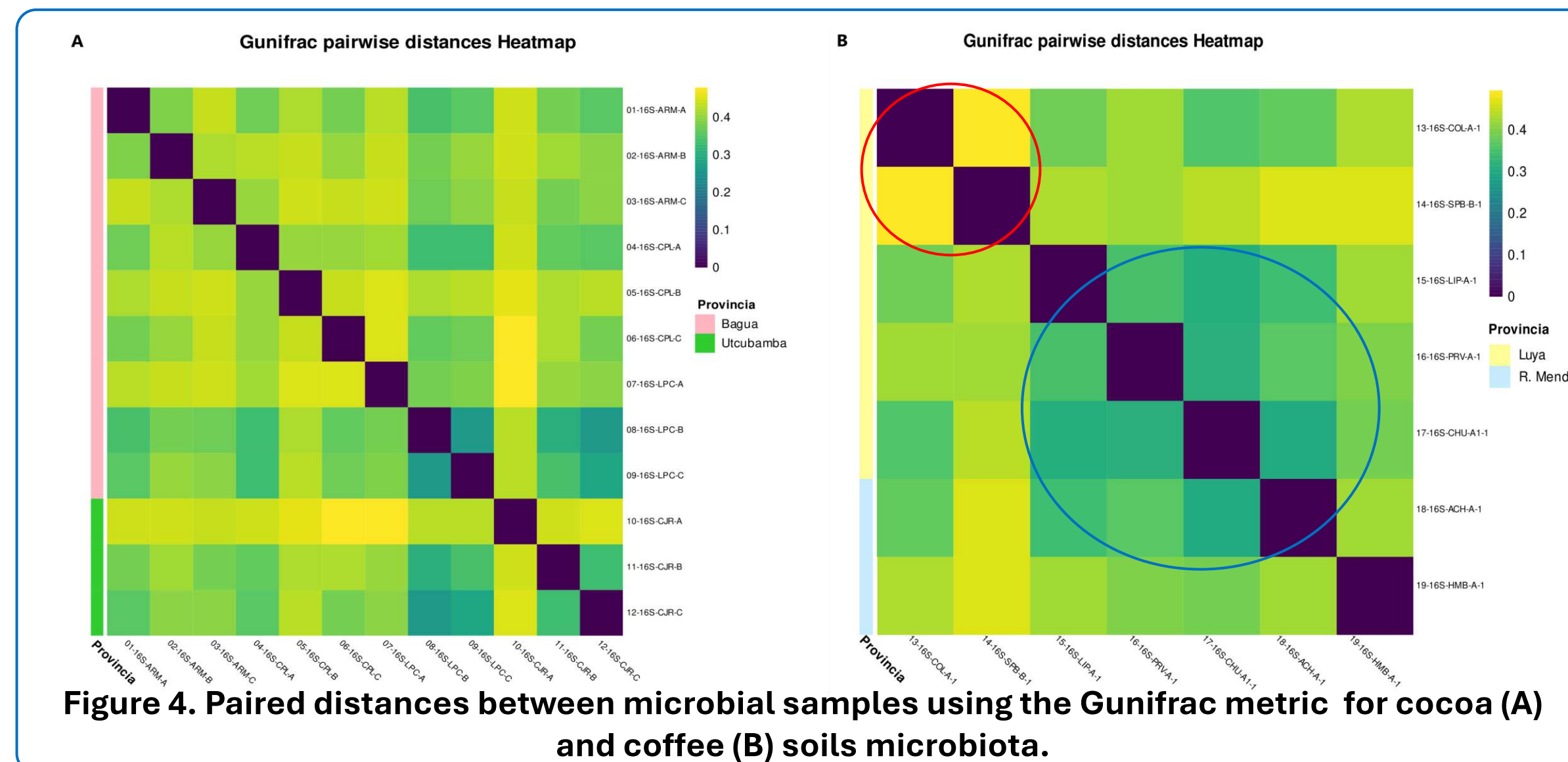


Figure 4. Paired distances between microbial samples using the Gunifrac metric for cocoa (A) and coffee (B) soils microbiota.

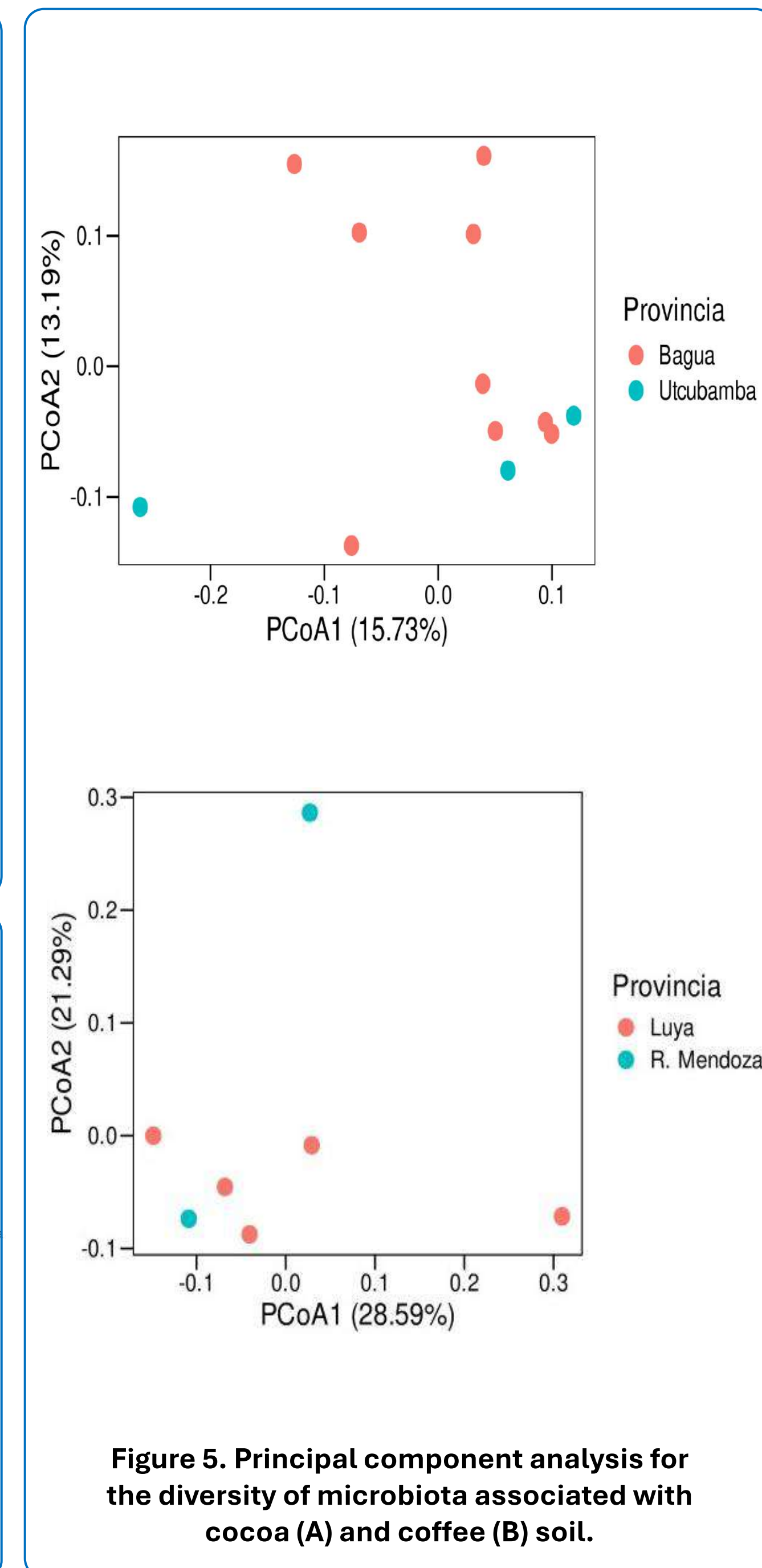


Figure 5. Principal component analysis for the diversity of microbiota associated with cocoa (A) and coffee (B) soil.

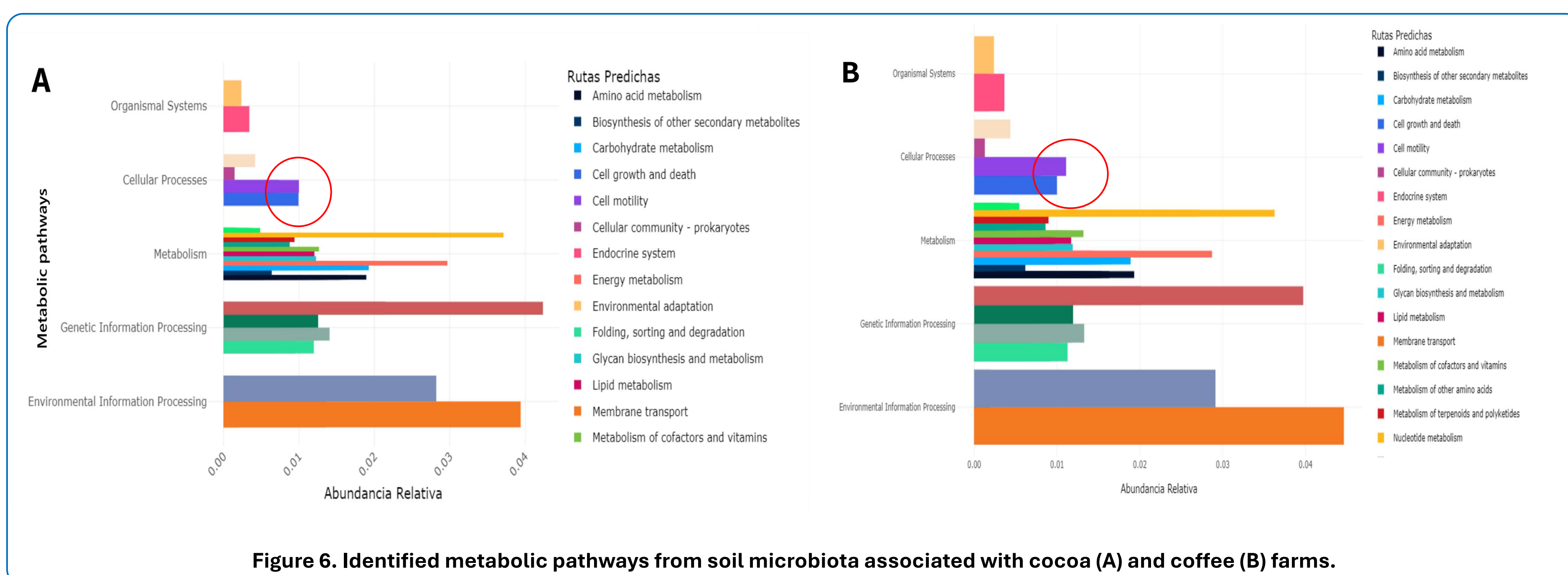


Figure 6. Identified metabolic pathways from soil microbiota associated with cocoa (A) and coffee (B) farms.

