MICROBIOMA ITALIANO: preliminary analysis of the Italian gut microbiome composition

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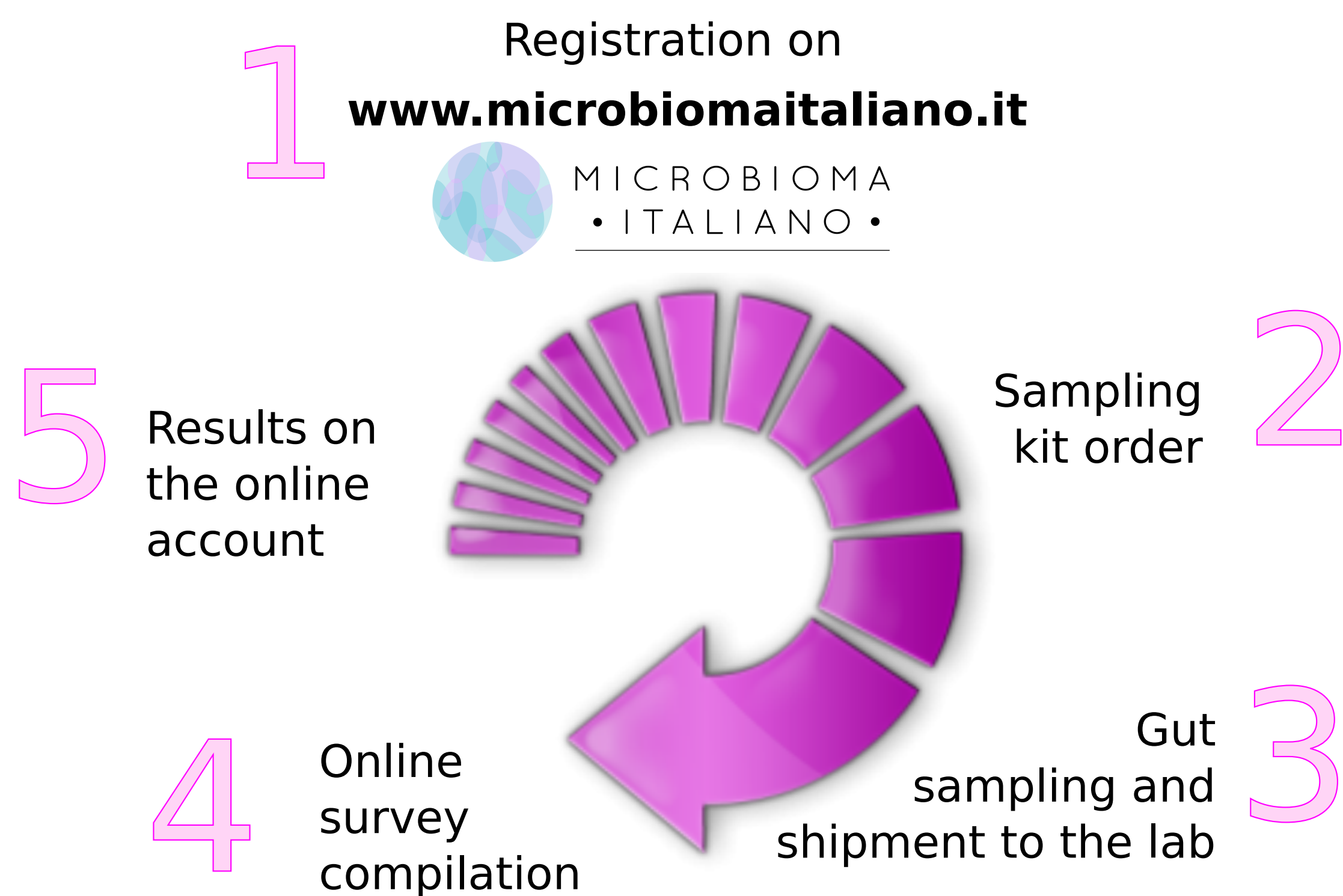[3]Faculty of Medicine, Polytechnic University of Marche, Roma square 22, 60121 Ancona, Italy

INTRODUCTION

Human microbiome is a complex field, in which the sample size strongly affects the reliability of the results [Qin et al. (2010)]. Many studies showed that gut microbiome is very different across populations and countries [Yatsunenko T. et al. (2012)], thus some large studies have focused on the microbiome of specific countries (i.e. American Gut or British Gut projects).

OBJECTIVES

Microbioma Italiano (Italian Microbiome Project) is a citizen science project that aims to map the Italian lifestyle with its microbiome, defining the typical gut composition for this Country.

1 Registration on **www.microbiomaitaliano.it**

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2 Sampling kit order

3 Gut sampling and shipment to the lab

4 Online survey compilation

5 Results on the online account

Microbioma Italiano is building an open source database, a tool for doctors and health-professionals to monitor and study their patiens.

METHODS

Since September 2015 we have sequenced 98 samples with the connected survey. We extracted DNA using Mobio powerfecal kit and sequenced V3-V4 16S hypervariable regions with Illumina Miseq platform, 300PE approach. Bioinformatic analysis were performed by means QIIME 1.9.1 with closed-reference approach for OTU clustering and identification against Greengenes 13-8 ver.

RESULTS

We obtained an average of 281141 reads (minimum 52467; maximum 584004) that showed an average of 448 OTUs (minimum 146; maximum 1142).
Archaea were found in 36% of the samples.
The most abundant bacterial *Phyla* were: *Bacteroidetes, Firmicutes, Verrucomicrobia* and *Proteobacteria.*

Bar plot showing class level composition of the 98 samples.
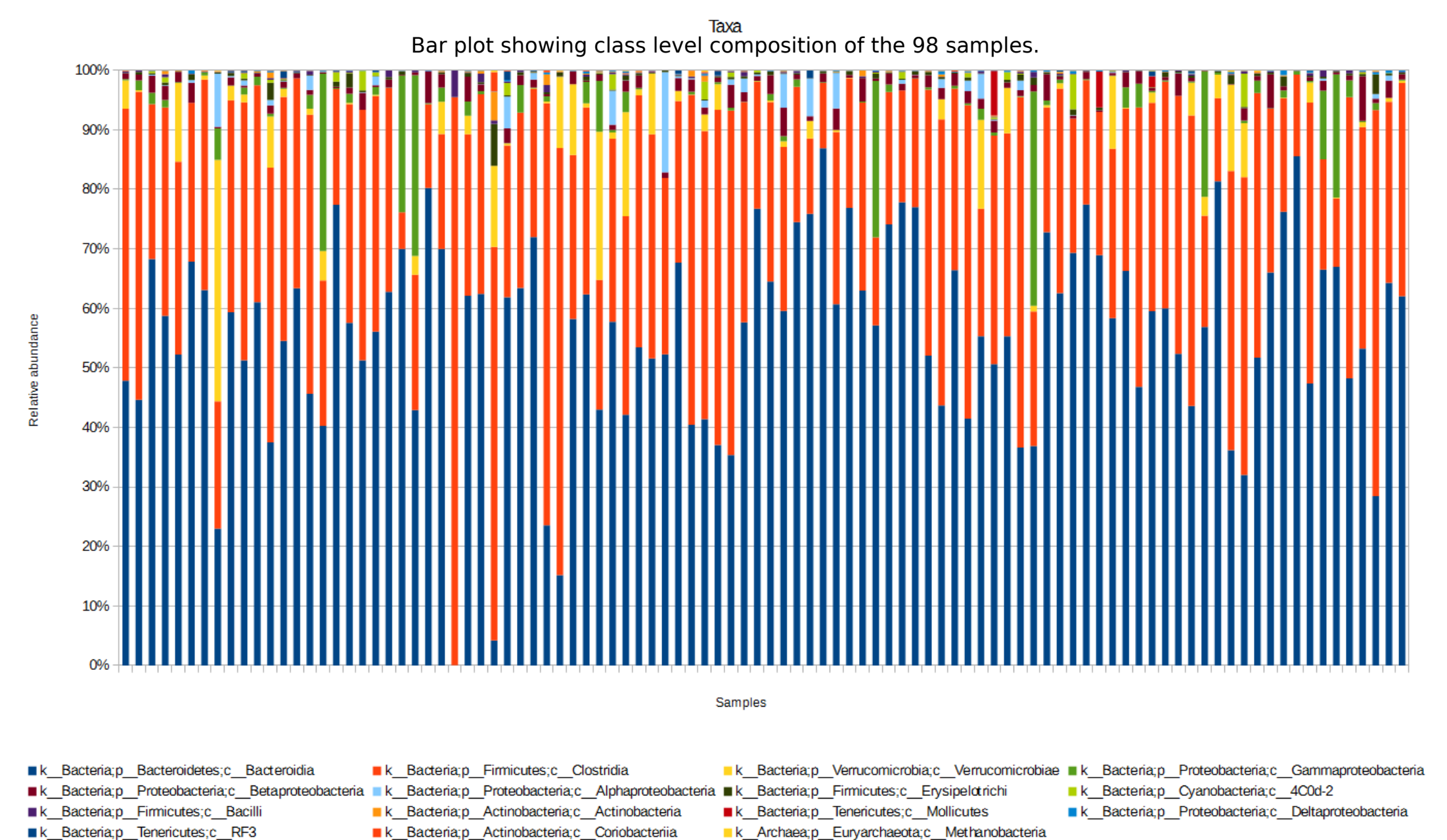
Among the others, we analyzed the effect of diet, daily water, antibiotics (within 3 months) and probiotics intake on the number of total OTU using non parametric two-sample t-test. Only antibiotics use showed a significative decrease of the OTU number (p<0.01).
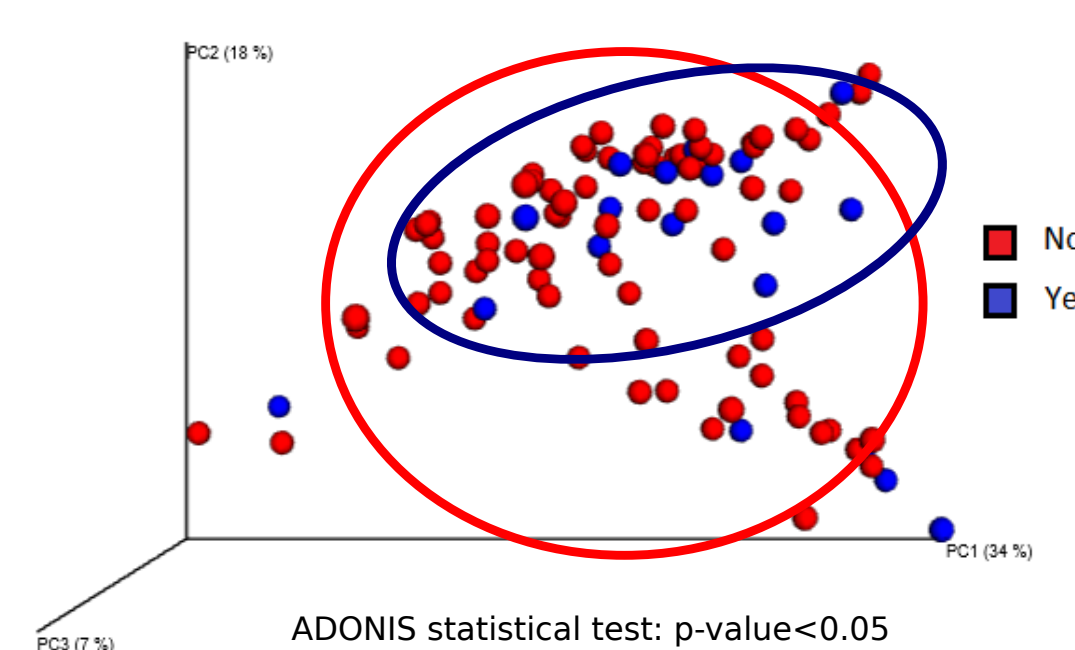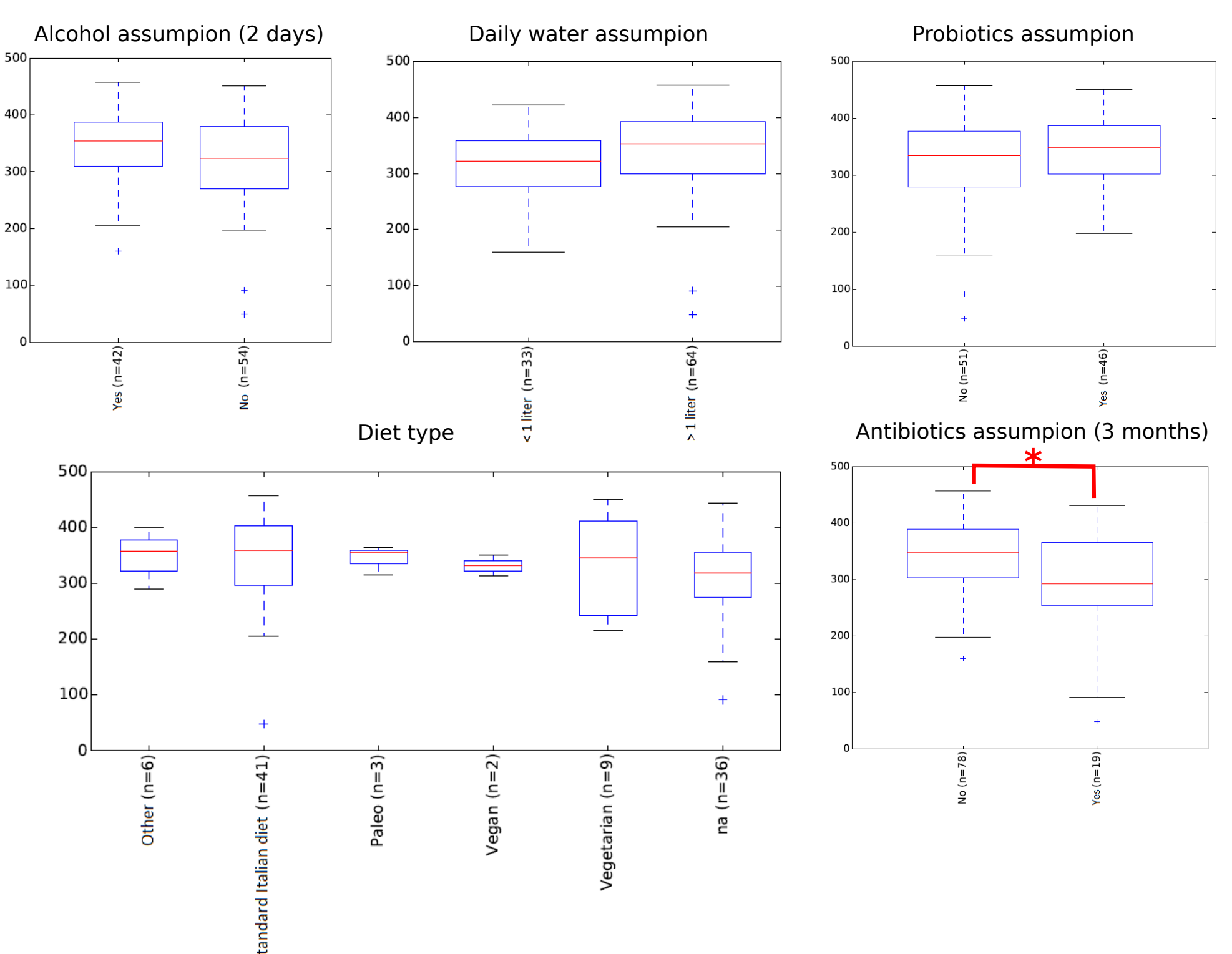
The weighted PCoA showed a higher community structure variability in control samples (No) than in antibiotics - treated samples (Yes).

ADONIS statistical test: p-value<0.05

CONCLUSIONS

- Microbioma Italiano is mapping the gut microbiome composition of the Italians in order to build an open source database;
- out of 98 complete samples, the most influencing factor in the composition of the gut seems to be the antibiotics intake;
- we need more samples to accurately analyze the different variables influencing the gut microbiome.