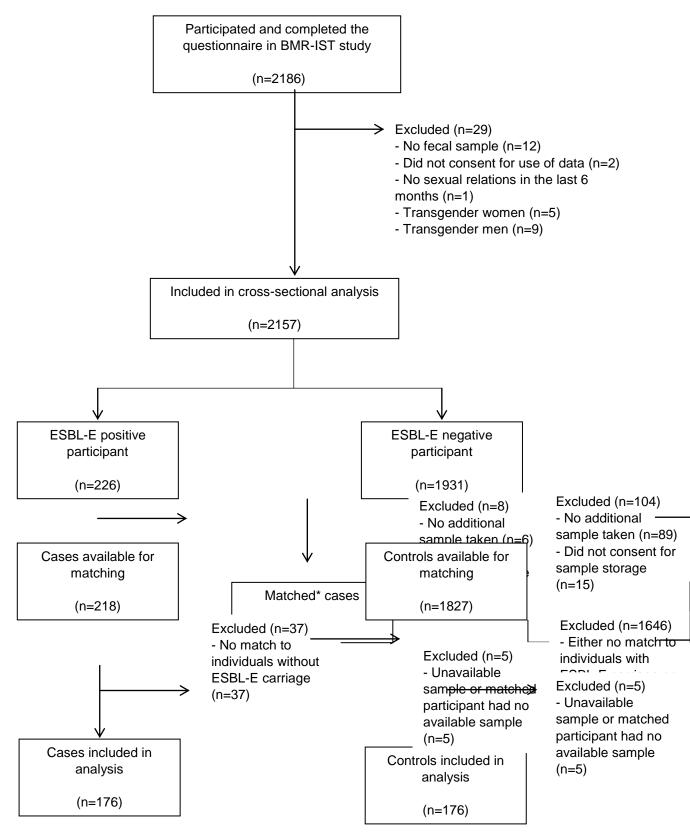
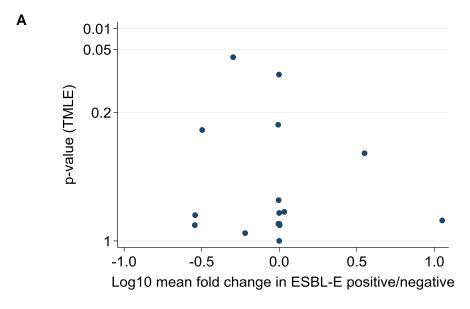
Figure 1. Participant flow chart

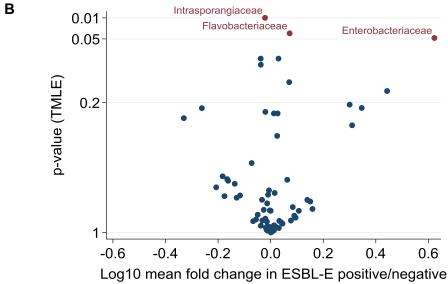


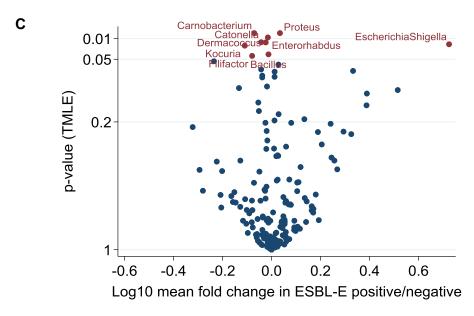
*Individuals were matched on the following characteristics: sexual group, ESBL-E prevalence of countries traveled in the previous 12 months, number of sexual partners in the previous 6 months [log(n+1)-transformed], geographic origin, and any antibiotic use in the previous 6 months.

Abbreviations: BMR-IST study, Bactériers MultiRésistantes-Infectious sexuellement transmissibles study; ESBL-E, extended spectrum β-lactamase-producing Enterobacterales.

Figure 2. Differences in relative abundances of gut microbiome between individuals with and without ESBL-E carriage



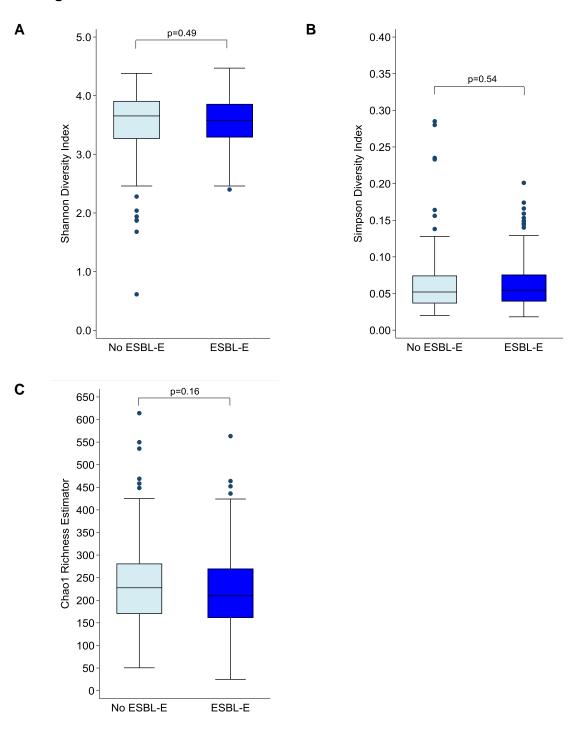




The mean \log_{10} difference in relative abundances at the phylum (**A**), family (**B**), and genus (**C**) level between cases and controls are plotted in function of their p-value. These values were obtained using targeted maximum likelihood estimation. Variance was estimated using an ensemble of machine learning techniques.

Abbreviations: ESBL-E, extended spectrum β-lactamase-producing *Enterobacterales*.

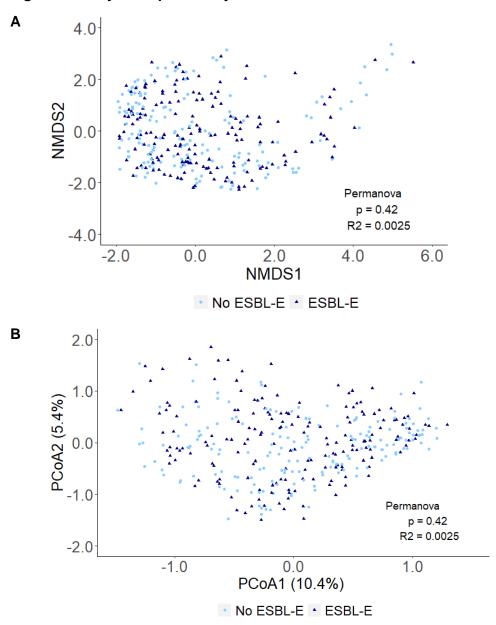
Figure 3. Analysis of α -diversity between those with and without ESBL-E carriage



Box-plots representing the distributions of the Shannon Diversity Index (**A**), Simpson Diversity Index (**B**) and Chao1 Richness Estimator (**C**), according to ESBL-E carriage status. Distributions were compared between participants with and without ESBL-E carriage using the Kruskal-Wallis rank test. Two participants with a Simpson Diversity Index above 0.40 were excluded from the graph in panel **B**.

Abbreviations: ESBL-E= Extended-Spectrum β-Lactamase-Producing *Enterobacteales*.

Figure 4. Analysis of β-diversity between those with and without ESBL-E carriage



Non-metric multidimensional scaling ordination (A) and Principal Coordinates Analysis (B) plot of dissimilarities for microbial communities between individuals with and without ESBL-E carriage. Dissimilarities were calculated using the Bray-Curtis method. Analyses were based on relative abundances.