

Supplementary materials

Table S1. Identification of patients and patients' information's CDI, IBD and HCW

Identification	Age	Sex	T1	T2	T3	ATB Before	Treatment for CDI
CDI patients							
CDI 01	38 y	F	X	X	NR	No	Vancomycin 5d
CDI 02	66 y	F	X	X	X	No	Vancomycin 24h
CDI 03	94 y	M	X	D	D	NG	NG
CDI 04	54 y	M	X	X	X	No	Vancomycin 6d
CDI 05	60 y	F	X	X	X	Cefuroxim and Ceftriaxon	No
CDI 06	59 y	F	X	X	X	No	Piperacilline and Tazobactam 7d
CDI 07	56 y	F	X	X	X	Cefuroxim	Vancomycin 10d
CDI 08	72 y	F	X	X	X	Moxiflocin	Vancomycin 10d
CDI 09	59 y	M	X	X	X	No	Vancomycin 7d
CDI 10	58 y	M	X	X	X	Ceftriaxon and norfloxacin	No
CDI 11	66 y	F	X	X	NR	Metronidazole	Amoxicillin and clavulanic acid
CDI 12	66 y	M	X	X	X	Ceftriaxon and Metronidazole	No
CDI 13	71 y	F	X	X	X	Sulfamethozole trimethoprim	Probiotic
CDI 14	55 y	M	X	X	X	No	Vancomycin
CDI 15	71 y	M	X	NR	X	No	Vancomycin 14d
IBD patients							
IBD 01	57	F	X	X	X	No	/
IBD 02	81 y	M	X	X	NR	No	/
IBD 03	26 y	F	X	NR	X	No	/
IBD 04	57 y	F	X	NR	X	No	/
IBD 05	24 y	F	X	X	X	No	/
IBD 06	49 y	F	X	X	X	ATB 1 month before the donation	/
IBD 07	38 y	F	X	NR	X	No	/
IBD 08	42 y	F	X	X	X	No	/
IBD 09	52 y	M	X	X	NR	No	/
IBD 10	60 y	F	X	X	X	No	/
IBD 11	30 y	F	X	NR	NR	No	/

IBD 12	61 y	F	X	NR	X	No	/
IBD 13	60 y	F	X	X	X	No	/
IBD 14	56 y	M	X	NR	NR	No	/
IBD 15	58 y	F	X	X	X	No	/
HCW patients							
HCW 01	42 y	M	X	X	X	No	/
HCW 02	25 y	M	X	X	X	No	/
HCW 03	56 y	F	X	X	X	No	/

Legend:

D: deceased; d: days; h: hours; y: years old, F: female; M: male; NR: not realized; NG: not given; red colour: positive sample.

Table S2. Classification of faeces with Bristol scale stool and means of preserving the samples

Samples	T1		T2		T3	
	Freezing	Scale	Freezing	Scale	Freezing	Scale
IBD 01	No	5	No	5	No	5
IBD 02	No	5	No	5	NR	NR
IBD 03	No	5	NR	NR	No	4
IBD 04	No	3	NR	NR	No	4
IBD 05	No	4	No	4	No	4
IBD 06	No	6	No	5	X	6
IBD 07	No	5	NR	NR	No	4
IBD 08	No	4	No	4	No	3
IBD 09	No	4	X	4	NR	NR
IBD 10	No	4	No	4	No	5
IBD 11	No	4	NR	NR	NR	NR
IBD 12	No	4	NR	NR	X	4
IBD 13	No	3	X	4	X	4
IBD 14	No	5	NR	NR	NR	NR
IBD 15	No	4	No	4	X	4
PS 01	No	3	No	3	No	3
PS 06	No	4	No	4	X	4
PS 11	No	4	No	4	X	4
CDI 01	No	4	No	5	NR	NR
CDI 02	X	6	X	6	No	4
CDI 03	No	4	NR	NR	NR	NR
CDI 04	X	7	No	7	X	5
CDI 05	X	3	X	5	No	4
CDI 06	X	5	No	4	X	4
CDI 07	X	6	X	5	No	4
CDI 08	X	6	X	5	No	4
CDI 09	X	5	No	5	X	4
CDI 10	X	6	X	4	X	5
CDI 11	X	7	X	7	NR	NR
CDI 12	X	5	X	5	X	3
CDI 13	X	5	No	5	X	4
CDI 14	X	6	X	6	X	4

CDI 15	X	7	NR	NR	X	4
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Legend: X: Freezing; Score: 1 (constipation) to 7 (diarrhoea) (Bristol stool score) and 3 and 4 are normal faeces; NR: not realized; red colour: positive sample.

Table S3 – Significant taxa using linDA models in R studio v4.2.2 between *C. difficile* positive and *C. difficile* negative group.

	$\log_2\text{FoldChange}$	<i>p</i> _{adj}
<i>Clostridioides</i>	3.03878103	1.38E-05
<i>Colidextribacter</i>	-1.8746591	0.0016972
<i>Monoglobus</i>	-1.9788814	0.0016972
UCG.003	-1.543897	0.00288813
<i>Anaerostipes</i>	-2.3853769	0.0032462
<i>Enterococcus</i>	3.2322434	0.00376198
<i>Oscilibacter</i>	-1.5685798	0.00376198
<i>Clostridiales</i> <i>ge</i>	-1.6838486	0.00376198
<i>Lachnospira</i>	-2.3245454	0.00376198
<i>Oscillospira</i>	-1.1121663	0.00517723
<i>Butyricicoccus</i>	-1.7785305	0.00762989
<i>Lachnospiraceae</i> NK4A136 group	-2.4230547	0.0085659
<i>Clostridia</i> <i>ge</i>	-1.9161461	0.01312289
<i>Enterobacteriales</i> <i>ge</i>	1.77432568	0.01489544
<i>Sutterella</i>	-1.927567	0.01489544
<i>Lachnospiraceae</i> UCG.004	-1.9382879	0.01489544
<i>Romboutsia</i>	-2.4449953	0.01489544
<i>Oscillospiraceae</i> <i>ge</i>	-1.5896989	0.01716848
<i>Fusicatenibacter</i>	-2.6163993	0.01716848
<i>Enterobacteriaceae</i> <i>ge</i>	2.18702628	0.02230039
<i>Haemophilus</i>	0.75252042	0.03028035
<i>Coriobacteriales</i> <i>ge</i>	-1.3208606	0.03028035
<i>Lachnospiraceae</i> ND3007 group	-2.0977945	0.03028035
<i>Agathobacter</i>	-2.2609146	0.03028035
<i>Marvinbryantia</i>	-1.1760316	0.03480656
<i>Ruminococcaceae</i> <i>ge</i>	-1.7545244	0.03480656
<i>Butyricicoccaceae</i> <i>ge</i>	-0.7260133	0.03513151
<i>Rhodospirillales</i> <i>fa</i> <i>ge</i>	-1.3629844	0.04454008
<i>Bilophila</i>	0.84579423	0.04778817

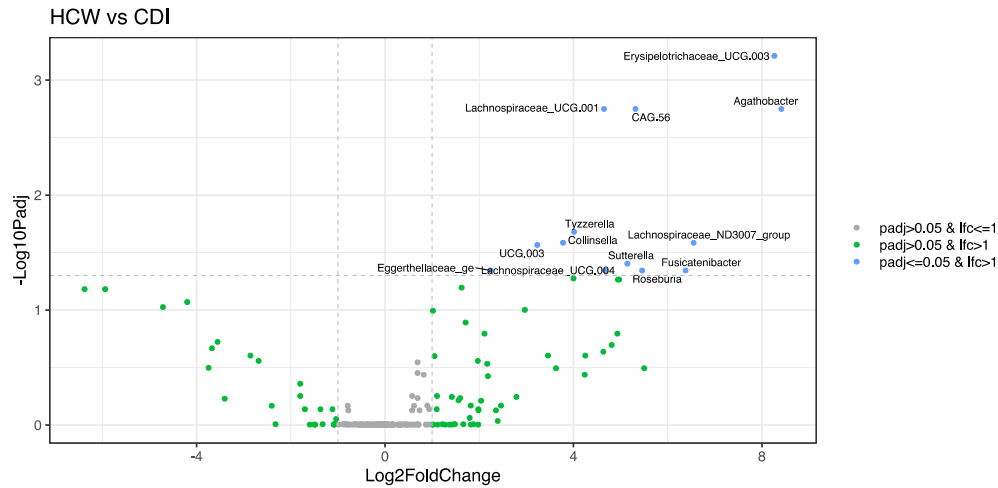


Figure S1. Group effect of bacterial microbiota. Linear model for differential abundance in Rstudio v4.2.2 (linDA) using groups and patients as variable. Here a representation of \log_2 fold change of the HCW group between CDI group. Two thresholds are present: The first one is fixed at $-\log_{10}(\text{padj}) > 0.05$ and the seconde is fixed at -1 and +1 \log_2 fold change. The grey dots are the genera with $\text{padj} > 0.05$ and with an effect size ≤ 1 ; the green dots are the genera with $\text{padj} > 0.05$ and with an effect size > 1 ; the blue dots are the genera with $\text{padj} \leq 0.05$ and with an effect size > 1 .

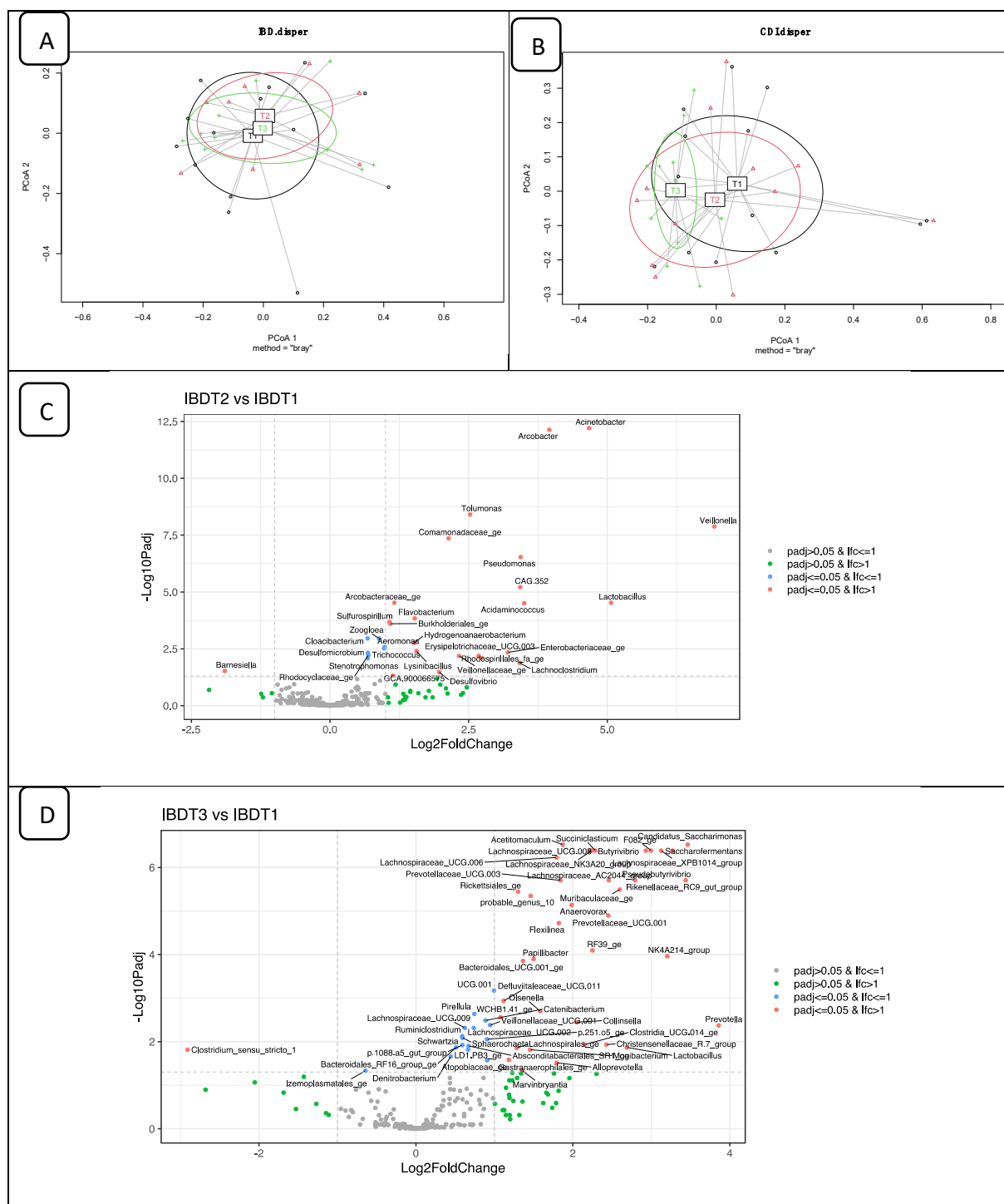


Figure S2 – Time effect on bacterial microbiota

Analysis of β -diversity using betadisper with vegan package in Rstudio v4.2.2. Betadisper analyzed beta-dispersion on the basis of Bray-Curtis dissimilarity matrix. Dissimilarity (beta dispersion) between groups was assessed using the Adonis₂ test. IBD time 1 group is represented in black, in IBD time 2 group is represented in red; in IBD time 3 group is represented in green;

Analysis of β -diversity using β -disper in Rstudio v4.2.2. CDI time 1 group is represented in black, in CDI time 2 group is represented in red; in CDI time 3 group is represented in green;

(C) Linear model for differential abundance in Rstudio v4.2. (linDA) using times and patients as variable for T2 vs T1 in IBD group. Here a representation of \log_2 fold change of the *C. difficile* positive group between *C. difficile* negative group. Two thresholds are present: the first one is fixed at $-\log_{10}(p_{adj} > 0.05)$ and the second one is fixed at -1 and +1 \log_2 fold change. The grey dots are the genera with $p_{adj} > 0.05$ and with an effect size ≤ 1 ; the green dots are the genera with $p_{adj} > 0.05$ and with an effect size > 1 ; the blue dots are the genera with $p_{adj} \leq 0.05$ and with an effect size ≤ 1 and the red dots are the genera with $p_{adj} \leq 0.05$ and with an effect size > 1 .

(D) Linear model for differential abundance in Rstudio v4.2. (linDA) using times and patients as variable for T3 vs T1 in IBD group. Here a representation of \log_2 fold change of the *C. difficile* positive group between *C. difficile* negative group. Two thresholds are present: the first one is fixed at $-\log_{10}(p_{adj} > 0.05)$ and the second one is fixed at -1 and +1 \log_2 fold change. The grey dots are the genera with $p_{adj} > 0.05$ and with an effect size ≤ 1 ; the green dots are the genera with $p_{adj} > 0.05$ and with an effect size > 1 ; the blue dots are the genera with $p_{adj} \leq 0.05$ and with an effect size ≤ 1 and the red dots are the genera with $p_{adj} \leq 0.05$ and with an effect size > 1 .

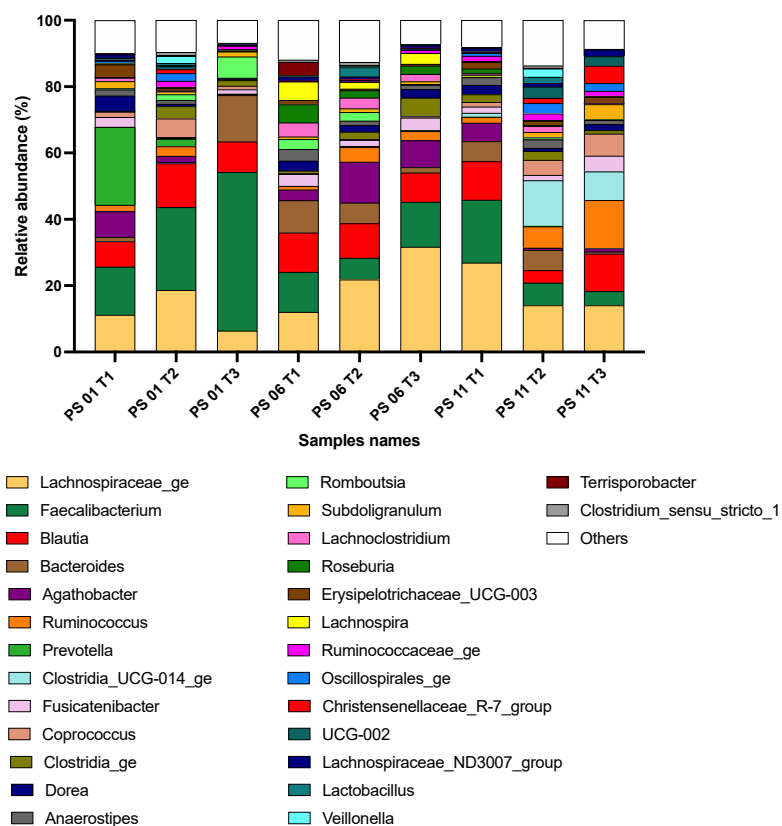


Figure S3 – Evolution of gut microbiota (mean cumulative relative abundance) of bacterial genera for clinical group through time in HCW groups

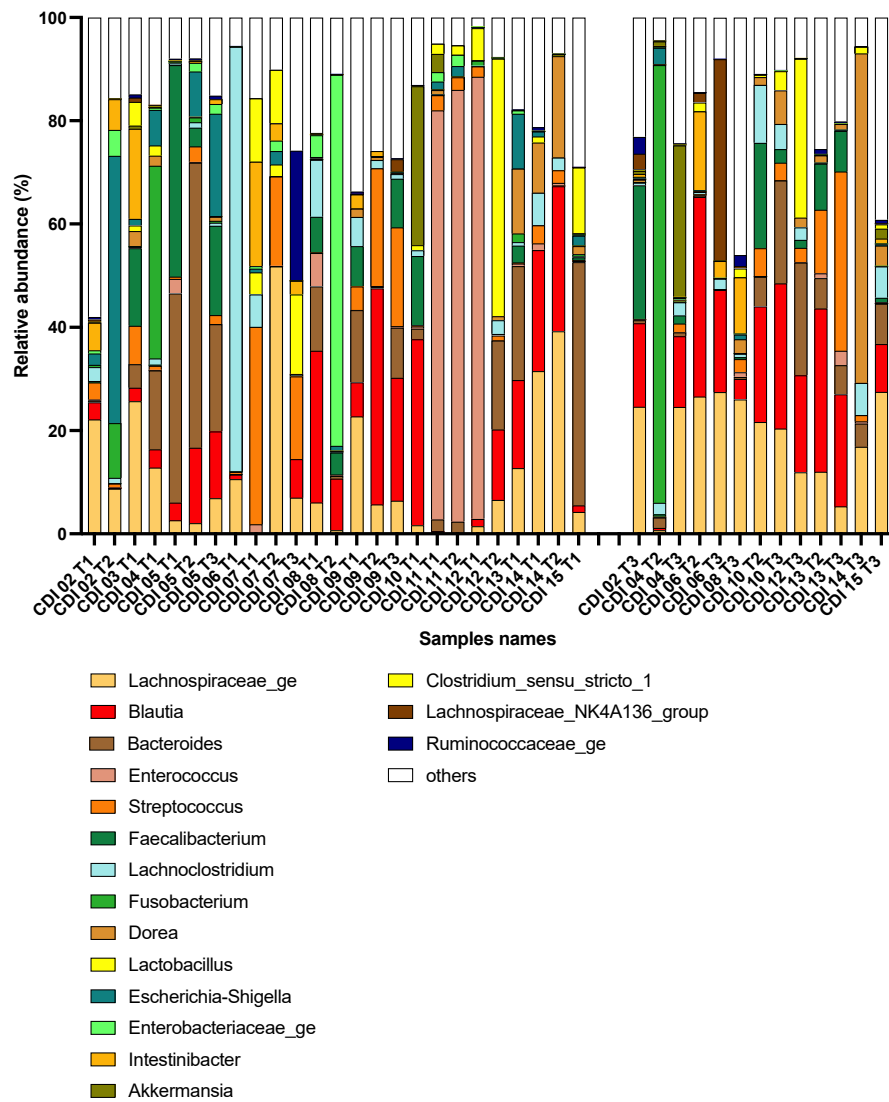


Figure S4 – Evolution of gut microbiota (mean cumulative relative abundance) of bacterial genera for clinical group through time in CDI groups

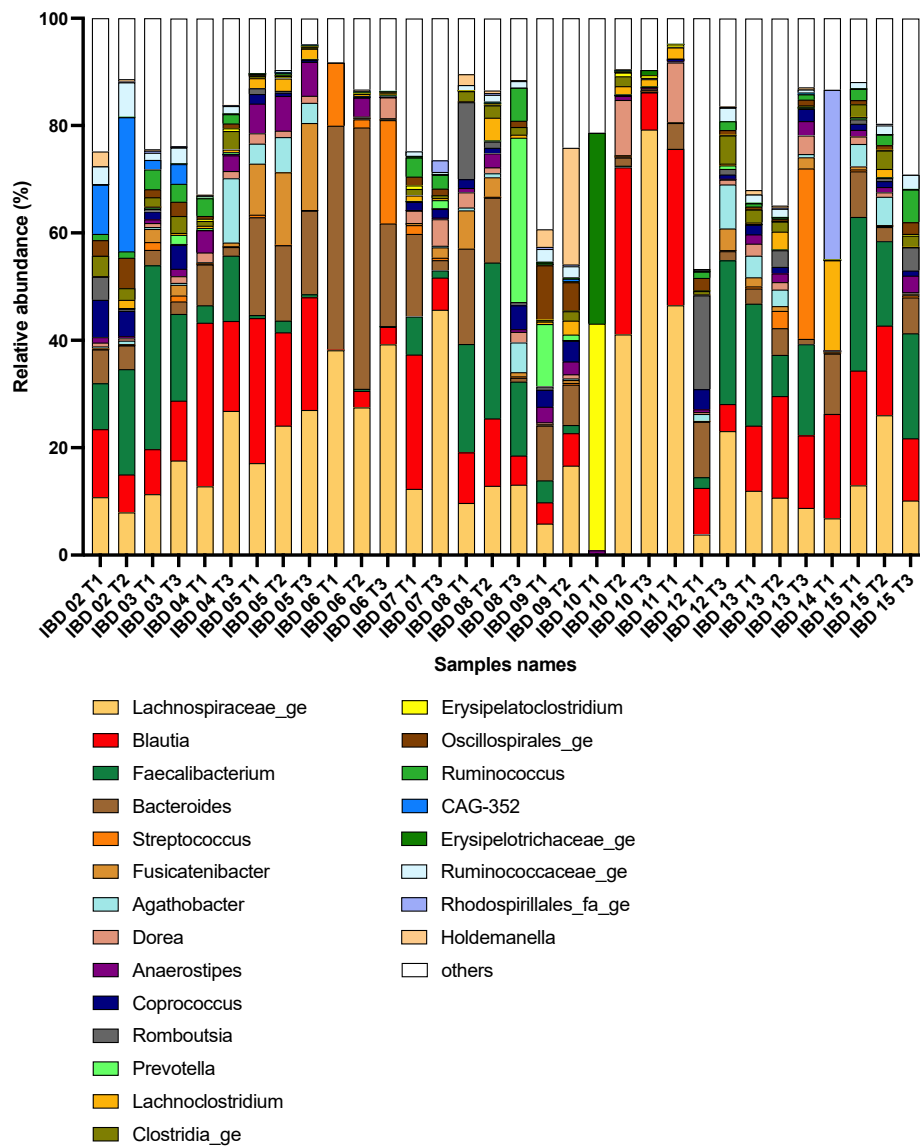


Figure S5 – Evolution of gut microbiota (mean cumulative relative abundance) of bacterial genera for clinical group through time in IBD groups

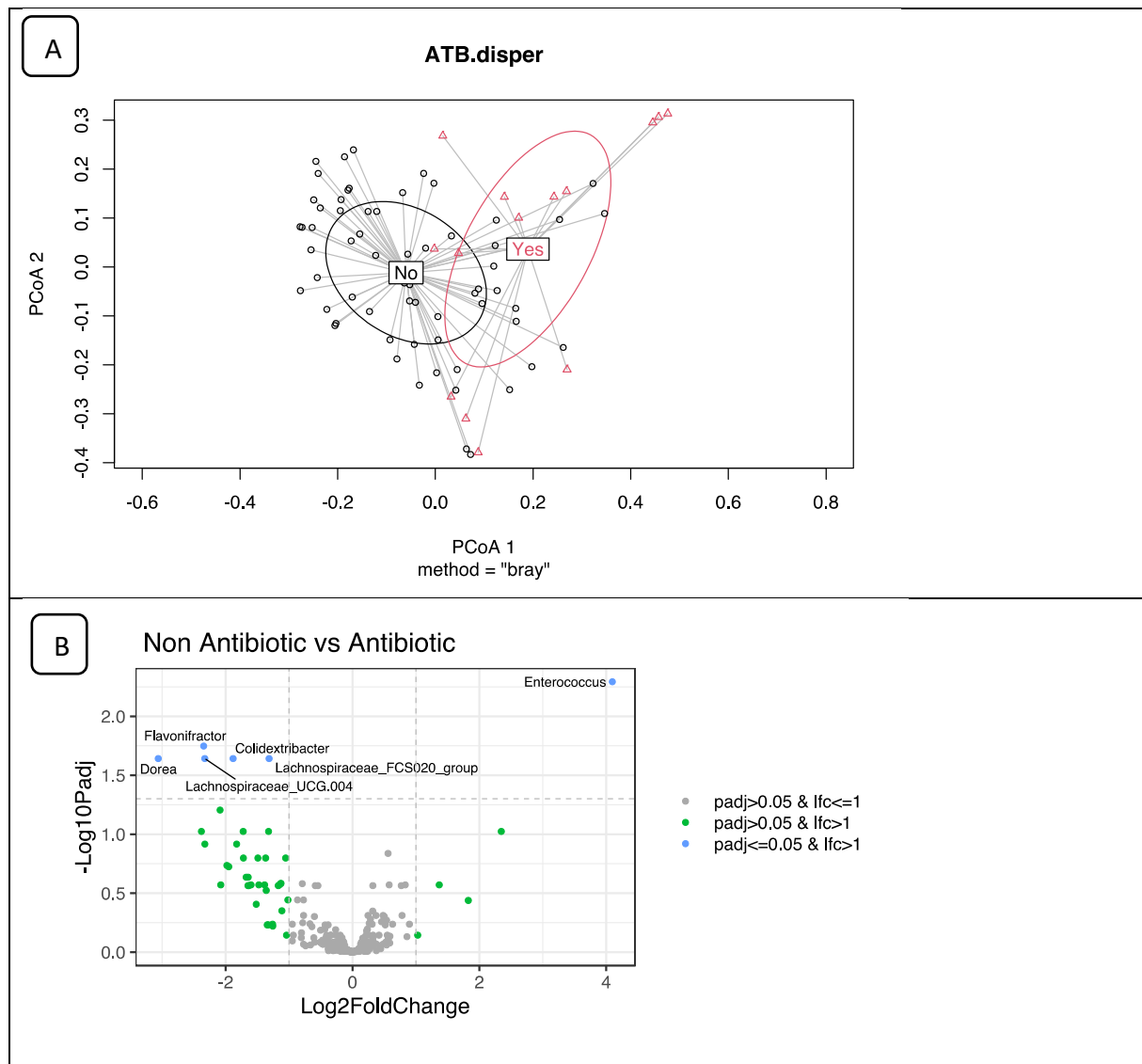


Figure S6 – Antibiotic effect on bacterial microbiota

- (A) Analysis of β -diversity using betadisper in Rstudio v4.2.2. Betadisper analyzed beta-dispersion on the basis of Bray-Curtis dissimilarity matrix. Dissimilarity (beta dispersion) between groups was assessed using the Adonis₂ test. No-antibiotic used group is represented in black, Antibiotic group is represented in red (P value = 0.01331)
- (B) Linear model for differential abundance in Rstudio v4.2. (linDA) using antibiotic used and patients as variable. Here a representation of log₂fold change of the antibiotic used group between non antibiotic group. Two thresholds are present: the first one is fixed at $-\log_{10}(padj > 0.05)$ and the second one is fixed at -1 and +1 log₂fold change. The grey dots are the genera with $padj > 0.05$ and with an effect size ≤ 1 ; the green dots are the genera with $padj > 0.05$ and with an effect size > 1 and the blue dots are the genera with $padj \leq 0.05$ and with an effect size ≤ 1 .