

SUPPLEMENTARY MATERIALS

Supplementary Table 1. Effects of live FMT on alpha diversity of the bacteriome

(A) Effects of live FMT at four weeks after the intervention

Diversity index	Coefficient for live FMT vs placebo	95% CI	P
Observed ASVs	25.1	11.5 to 38.6	0.00034
Chao1	26.8	12.9 to 40.8	0.00020
ACE	26.3	12.5 to 40.2	0.00021
Shannon	0.15	0.051 to 0.25	0.0033
Simpson	0.0056	-0.00024 to 0.011	0.061
InvSimpson	8.73	-0.64 to 18.1	0.069

(B) The long-term effects on alpha diversity measured at week ~32 by comparing subjects who received live FMT vs group C who received only placebo.

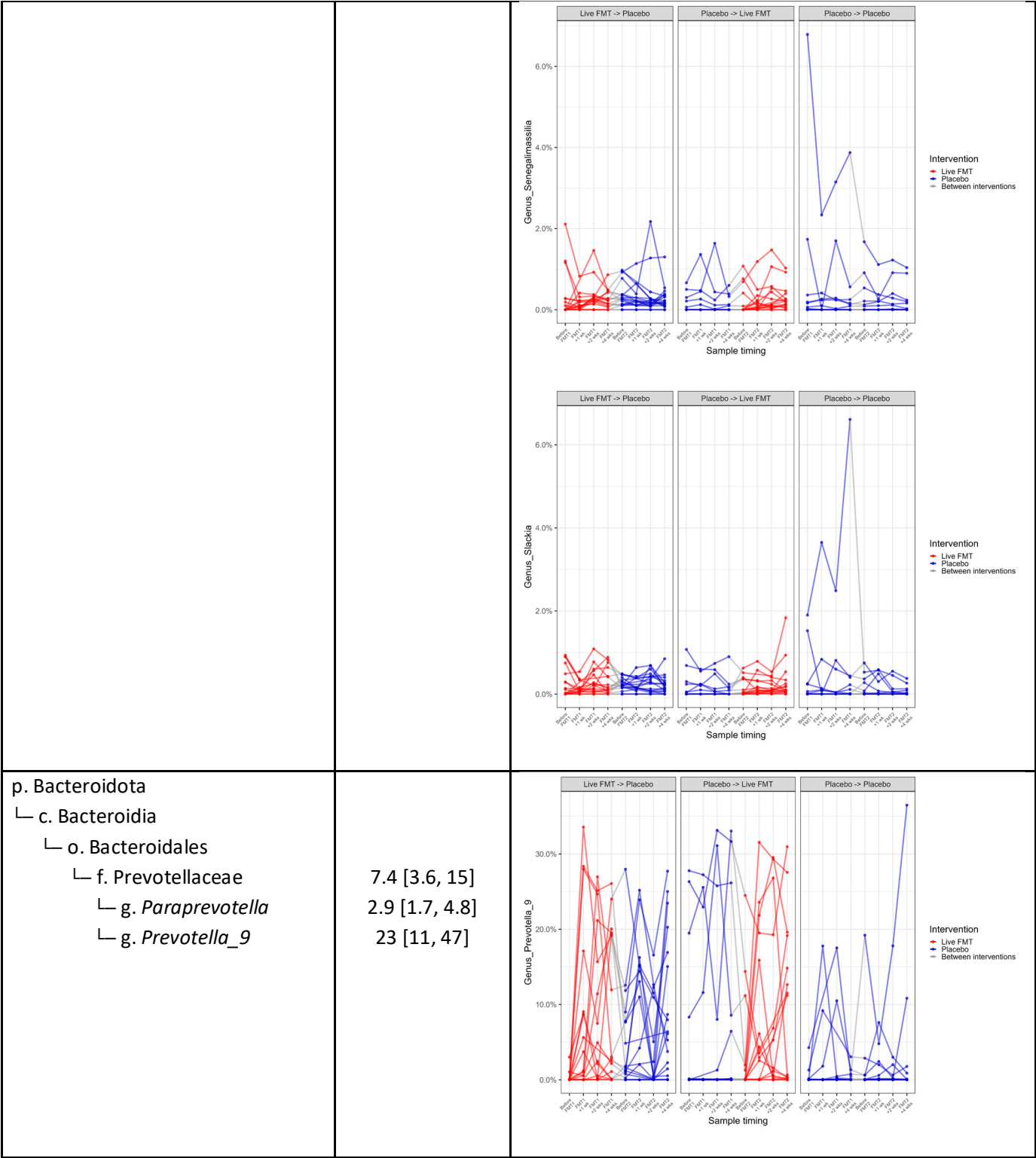
Model	Without adjustment for the bacteriome composition (its principal components)			With adjustment for the first three principal components of the bacteriome		
	Coefficient for live FMT	95% CI	P	Coefficient for live FMT	95% CI	P
Observed ASVs	12.5	-12.2 to 37.1	0.322	29.5	7.1 to 51.9	0.012
Chao1	15.4	-9.9 to 40.5	0.235	32.7	9.8 to 55.6	0.007
ACE	14.2	-10.9 to 39.2	0.268	31.0	8.1 to 53.9	0.010
Shannon	0.013	-0.165 to 0.191	0.887	0.152	-0.003 to 0.308	0.061
Simpson	0.001	-0.008 to 0.011	0.786	0.006	-0.002 to 0.015	0.169
InvSimpson	4.1	-11.0 to 19.1	0.599	10.5	-2.3 to 23.4	0.114

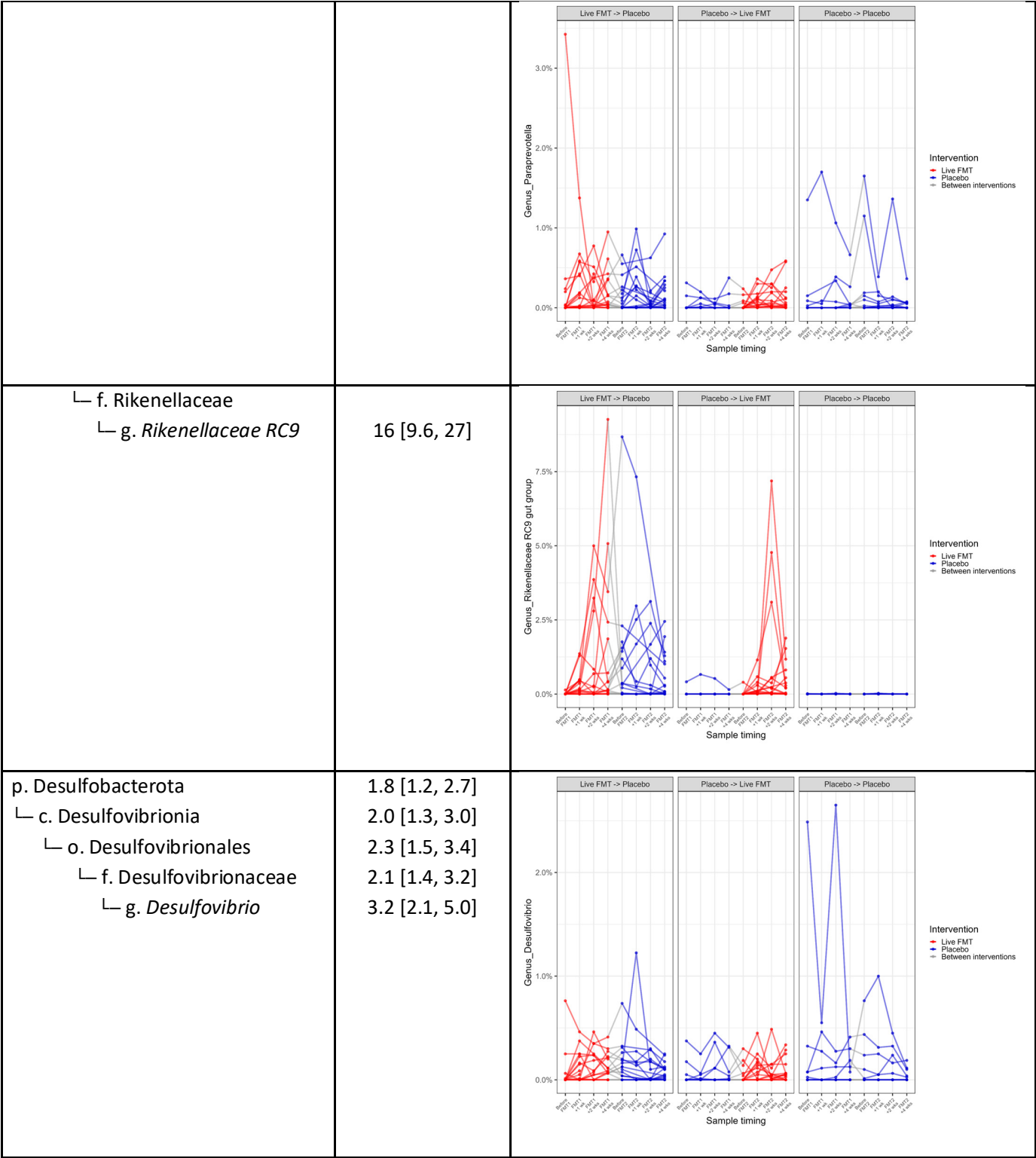
Supplementary Table 2. Bacterial taxa changing over time following live FMT.

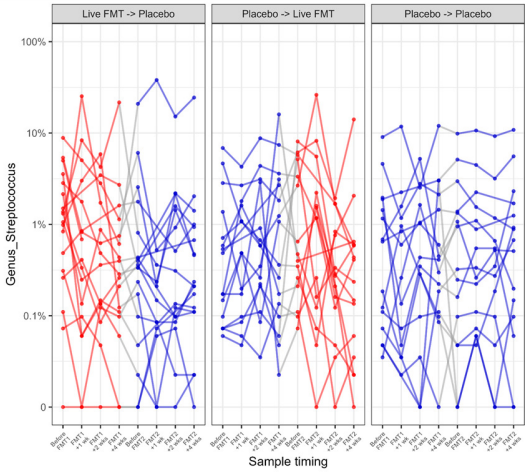
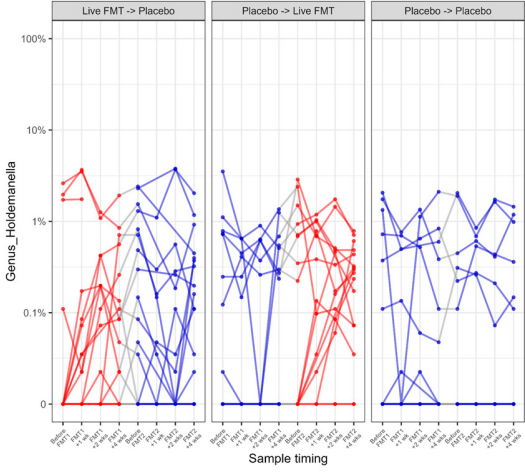
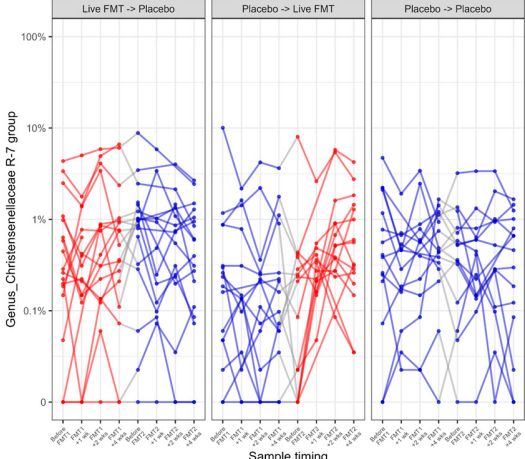
Red lines connect samples analysed before and after live FMT; blue lines connect samples taken while on placebo, while grey lines connect individual patients' samples between interventions.

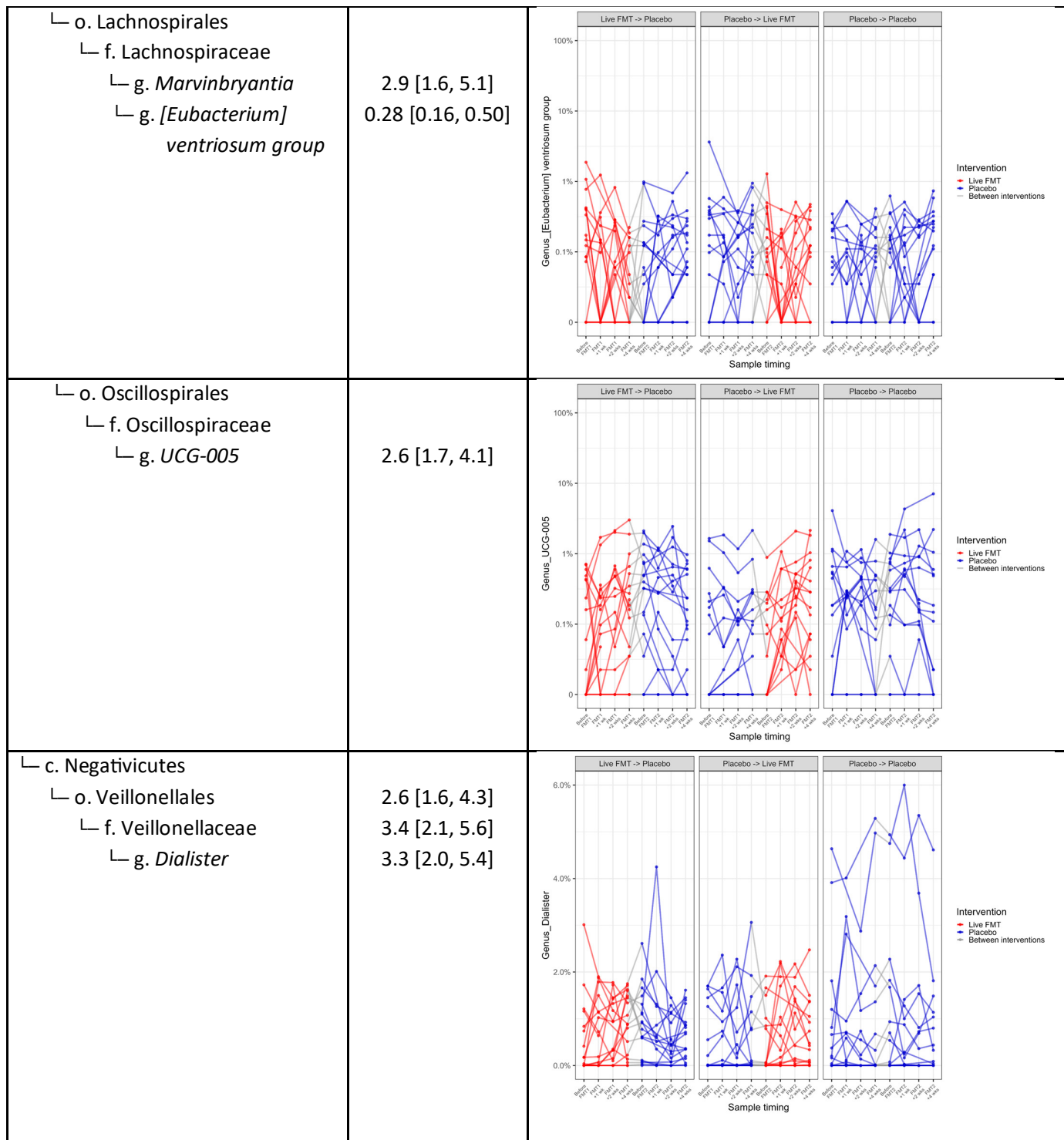
For details on the association, refer to **Table 6** in the main text.

Taxon	Fold change associated with live FMT [95% CI]	Abundance plot of the respective genera
p. Actinobacteriota c. Coriobacteriia o. Coriobacteriales f. Coriobacteriaceae g. <i>Collinsella</i>	2.3 [1.5, 3.5]	
f. Eggerthellaceae g. <i>Enterorhabdus</i> g. <i>Senegalimassilia</i> g. <i>Slackia</i>	2.7 [1.7, 4.1] 4.2 [2.8, 6.3] 2.6 [1.7, 3.8]	

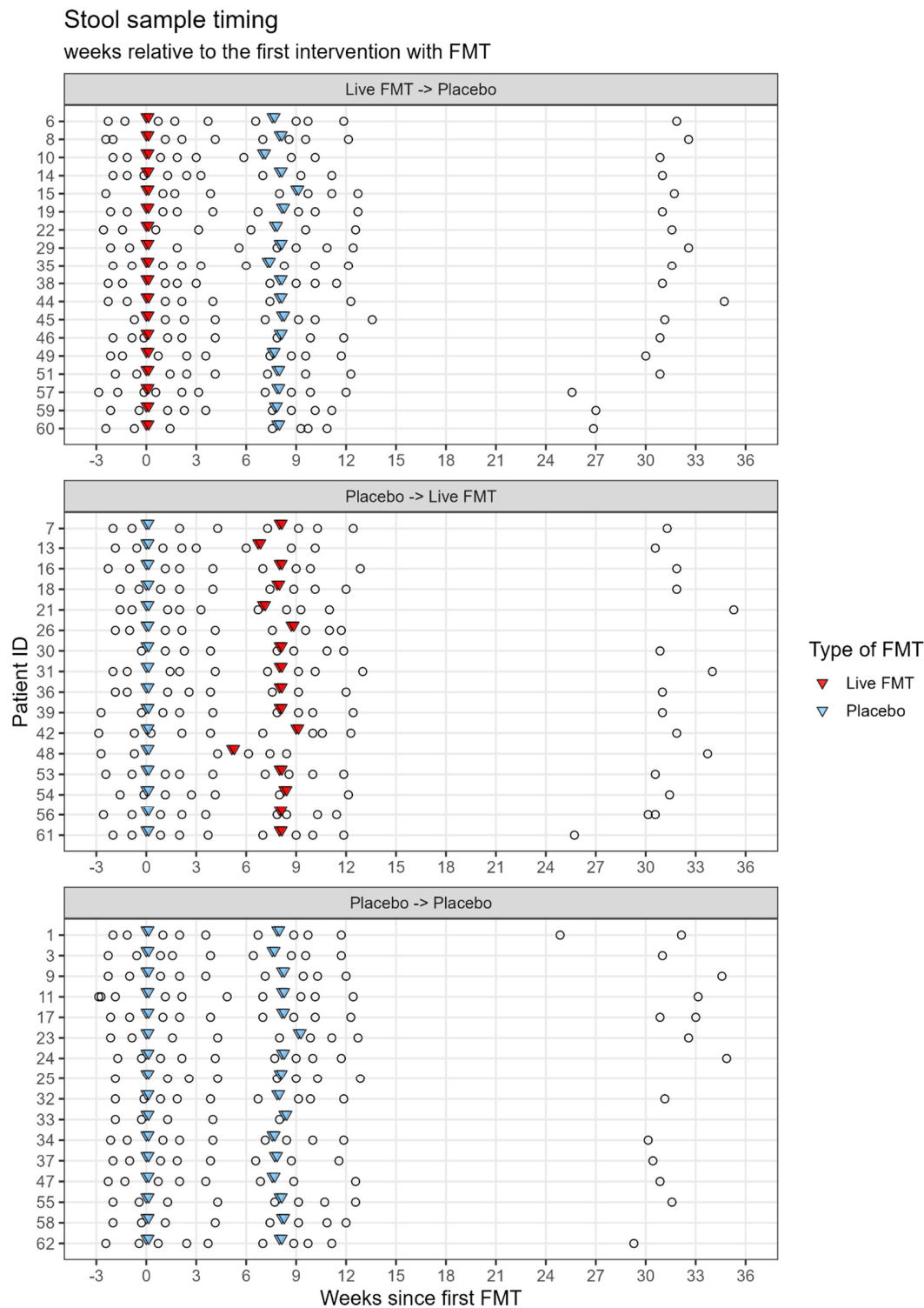




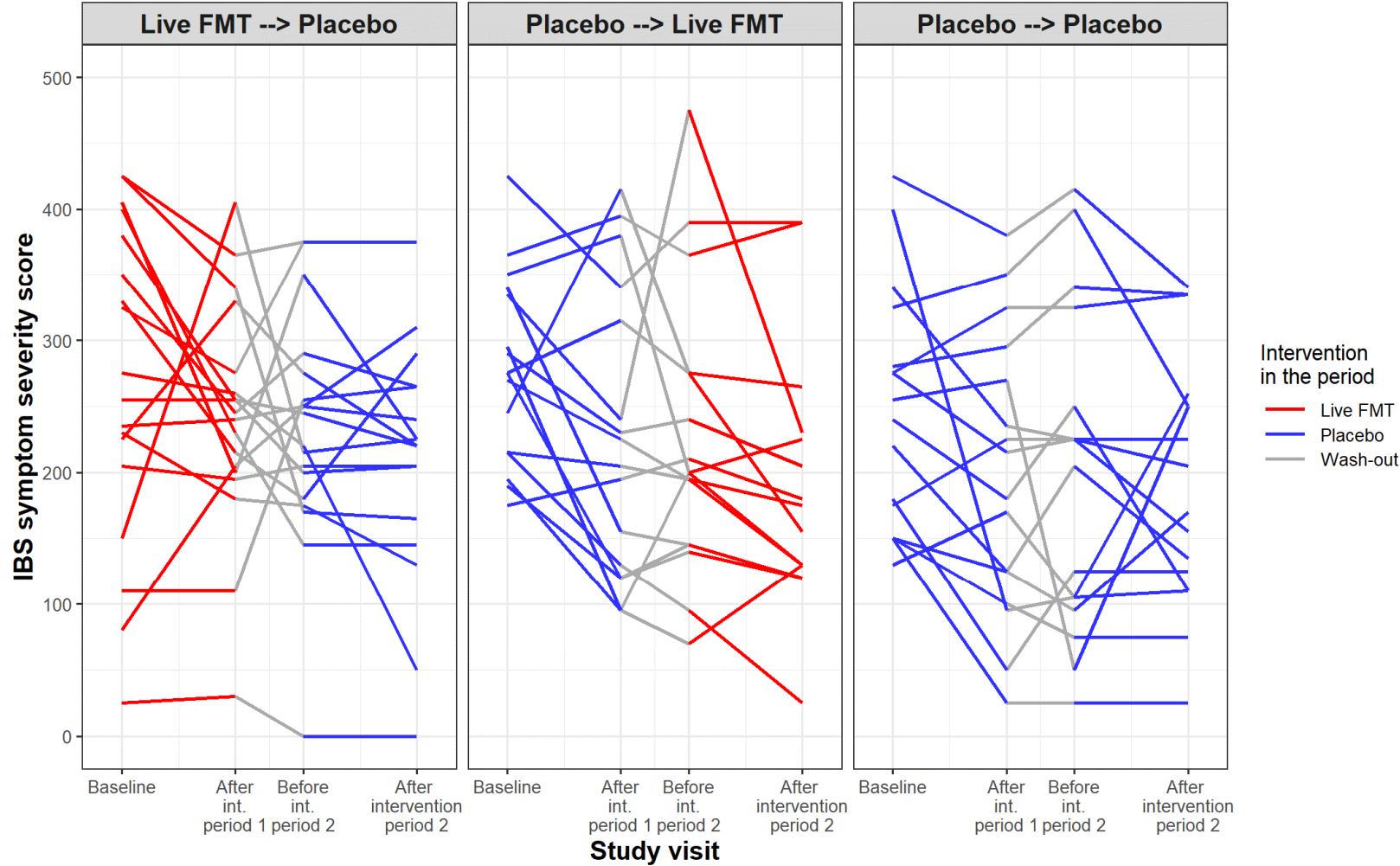
p. Firmicutes c. Bacilli o. Lactobacillales f. Streptococcaceae g. <i>Streptococcus</i>	0.33 [0.19, 0.59] 0.30 [0.17, 0.53] 0.36 [0.21, 0.63]	 Genus Streptococcus Sample timing Intervention - Live FMT - Placebo - Between interventions
o. Erysipelotrichales f. Erysipelotrichaceae g. <i>Holdemanella</i>	2.9 [1.7, 4.9] 2.7 [1.7, 4.3]	 Genus Holdemanella Sample timing Intervention - Live FMT - Placebo - Between interventions
c. Clostridia o. Christensenellales f. Christensenellaceae g. Christensenellaceae R-7 group	2.6 [1.6, 4.0] 2.6 [1.7, 4.0] 2.8 [1.8, 4.4]	 Genus Christensenellaceae R-7 group Sample timing Intervention - Live FMT - Placebo - Between interventions



Supplementary Figure 1: Participants and their stool samples



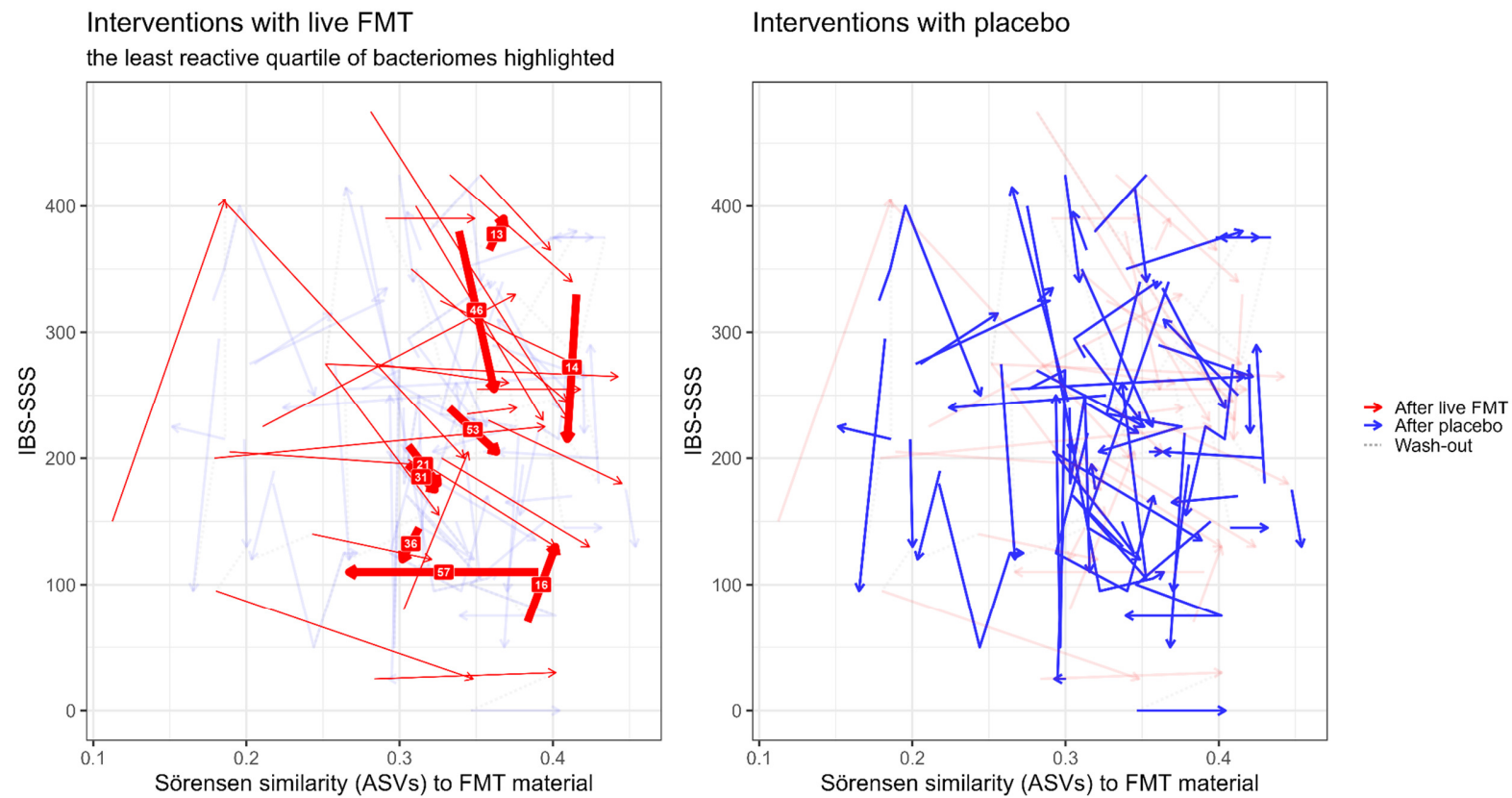
Supplementary Figure 2. Individual data on IBS symptom severity scores by allocation



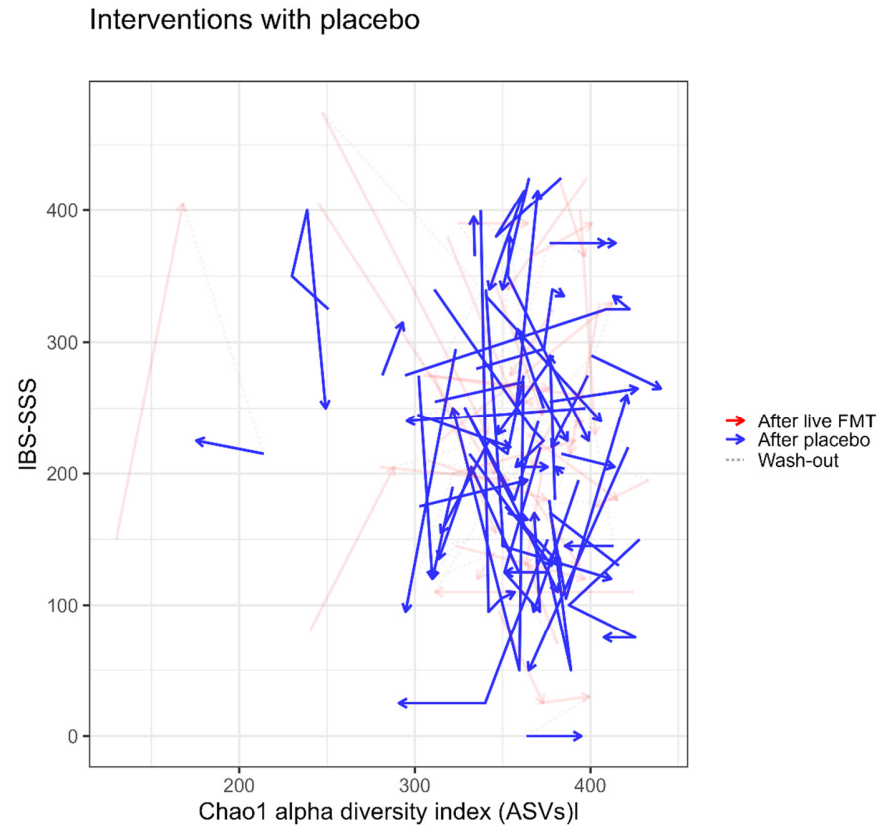
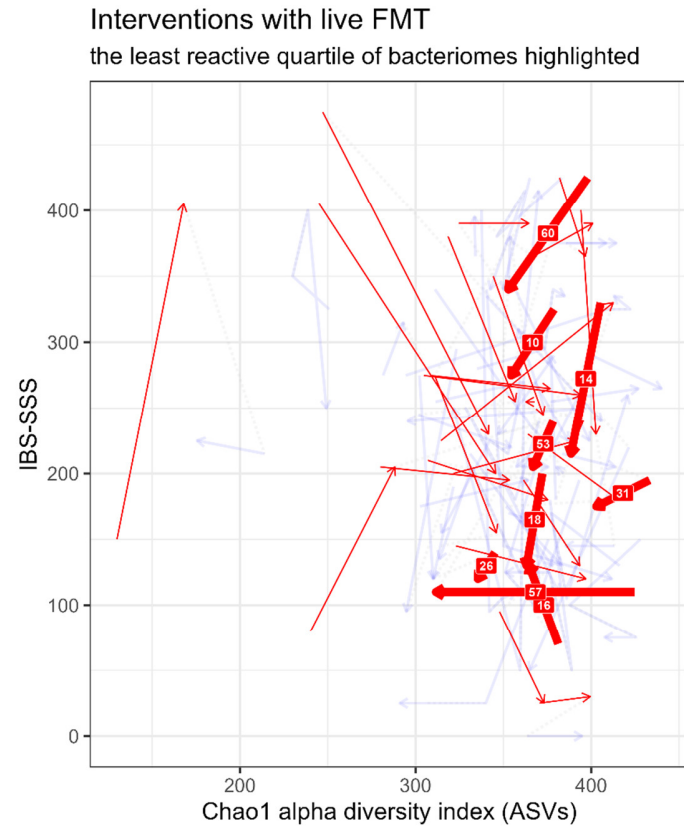
Supplementary Figure 3. Responses to FMT: changes in IBS-SSS against the changes of the bacteriome

Thicker red arrows show patients falling within the lowest quartile of microbiome response to live FMT. Numeric labels are patient codes.

(A) Patients unresponsive in the similarity of the microbiome to the FMT material

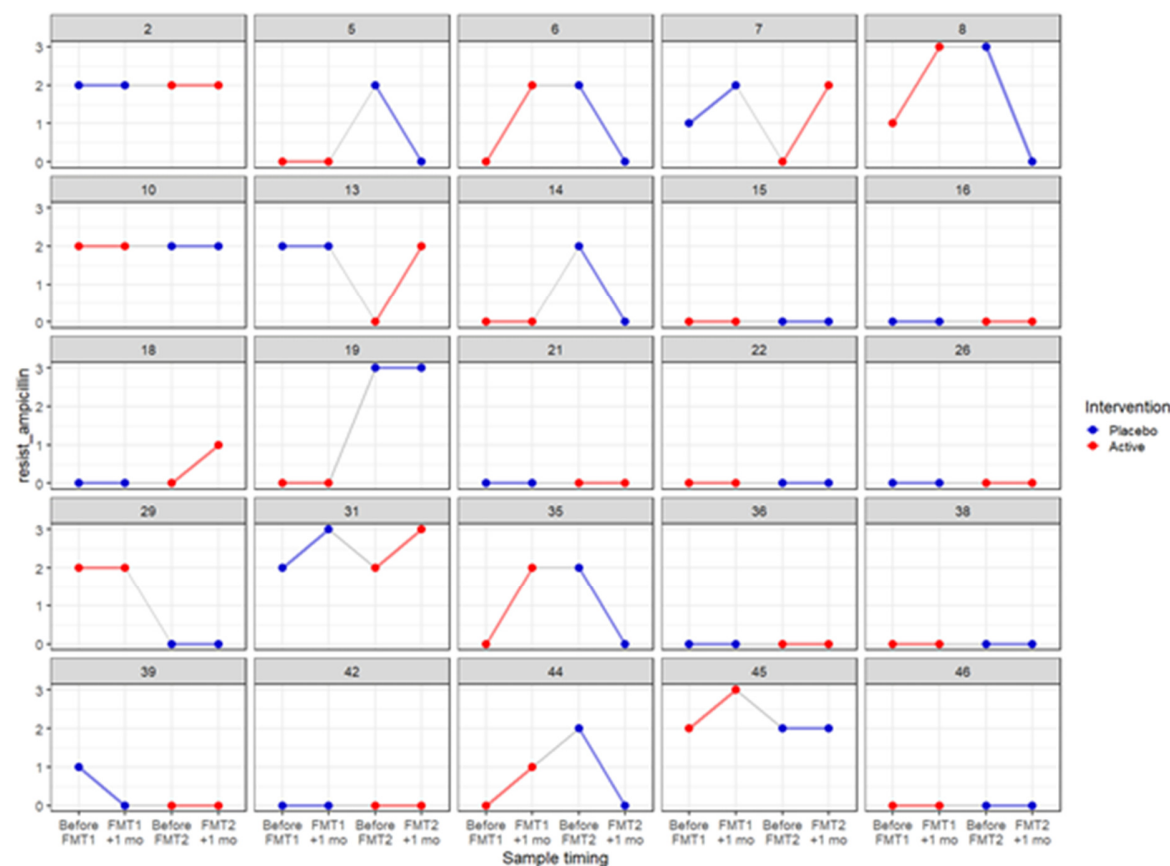


(B) Patients unresponsive in the alpha diversity of the microbiome

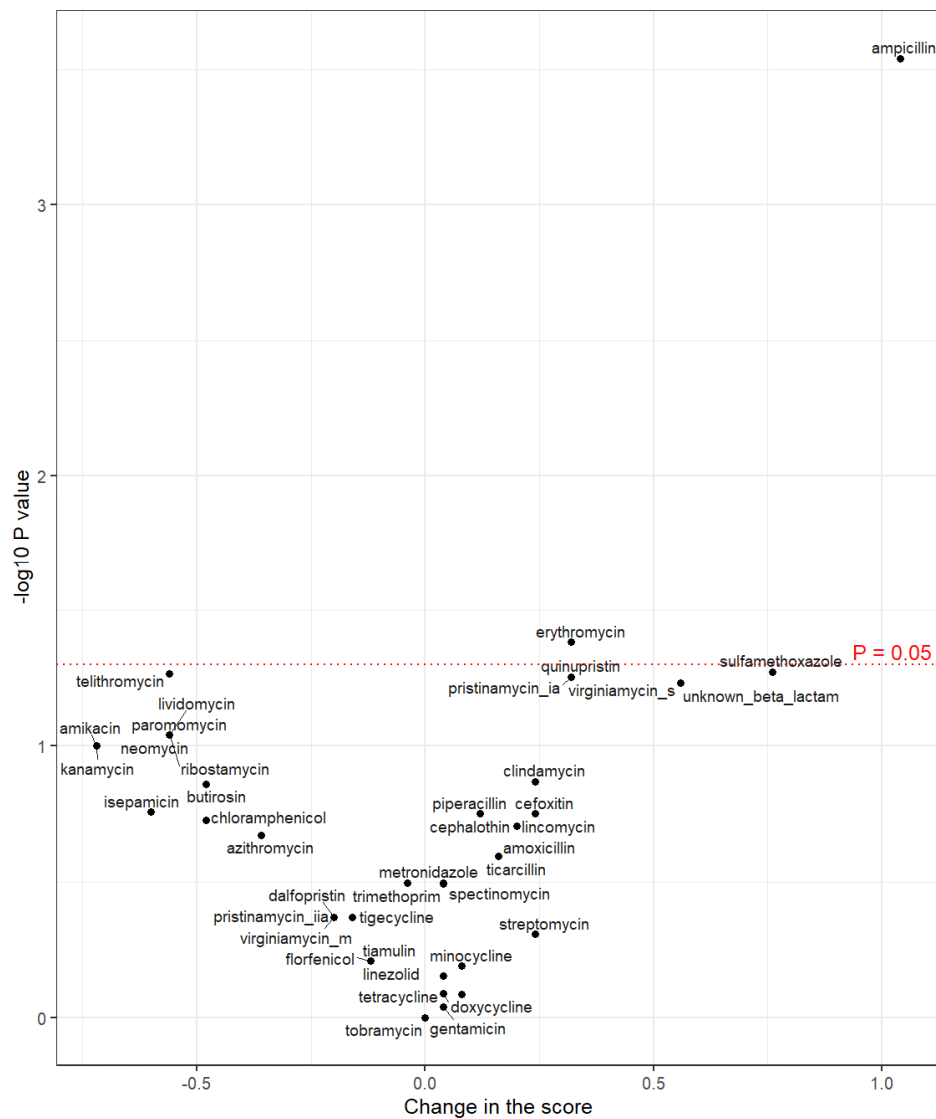


Supplementary Figure 4. The match scores to ampicillin AR genes in the metagenomic substudy

One pane is one study participant. Ampicillin was the only antibiotic for which AR gene scores changed in association with the live FMT. Blue segments are samples before and after placebo, whereas red segments are samples before and after live FMT.



Supplementary Figure 5. The association of changes in the AR gene resistance scores with the administration of live FMT.



Coefficients are the change in the score associated with live FMT, together with P values, they come from a mixed-effects model that tested the difference in AR gene score between FMT with live microbiota and placebo (details in Methods). Only the ampicillin AR gene score was associated with administering the live FMT. Nominal uncorrected P value of 0.05 indicated by the dotted line.