

Supplement to: Camps-Massa P, Pérez-Mormeneu J, Guevara-Núñez D, Saiz-Escobedo L, Calatayud L, González-Díaz A, Sanllorente A, Vicens-Zygmunt V, Santos S, Morros R, Slavador-González B, Domínguez MA, Martí S. Gut microbiome shift in long COVID: impact of disease and montelukast treatment. J Glob Health. 2026;16:04164.

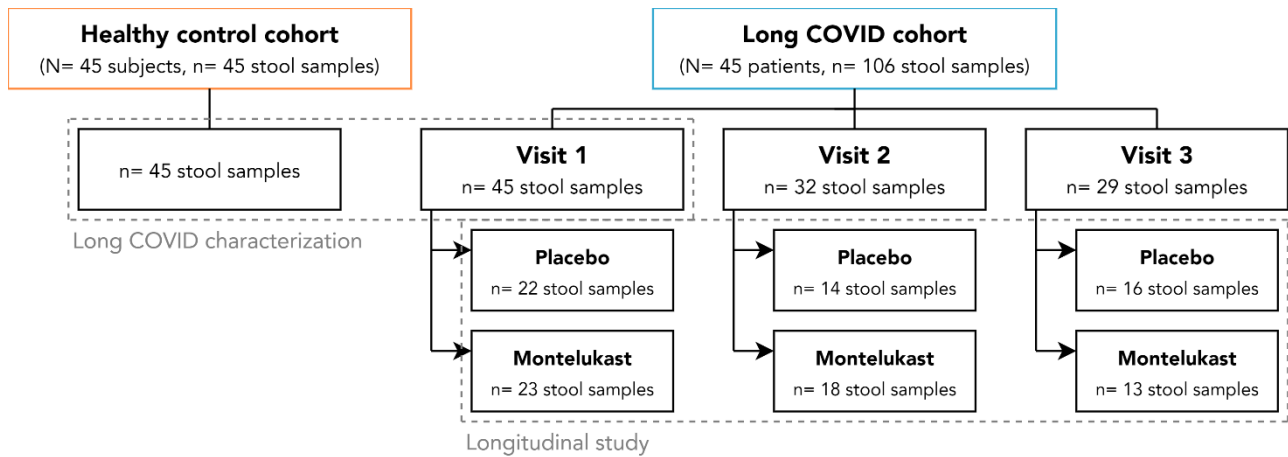


Figure S1. Flowchart of the clinical study. Stool samples from Long COVID patients were obtained at three time points: baseline (V1), 30 days post-treatment (V2), and one-year follow-up (V3). A cohort of healthy subjects was included as a control group for cross-sectional microbiome characterization.

Table S1. Age and sex distribution of the healthy control cohort and the Long-COVID patient cohort stratified by placebo or Montelukast treatment.

	Long-COVID (n = 45)	Placebo (n = 22)	Montelukast (n = 23)	Healthy controls (n = 45)
Female patients, n (%)	8 (17,8%)	5 (22,7%)	3 (13,0%)	8 (17,8%)
Age, median [IQR]	47 [41- 52]	49 [41,3-53,5]	46 [40,5-49,5]	44 [37-56]

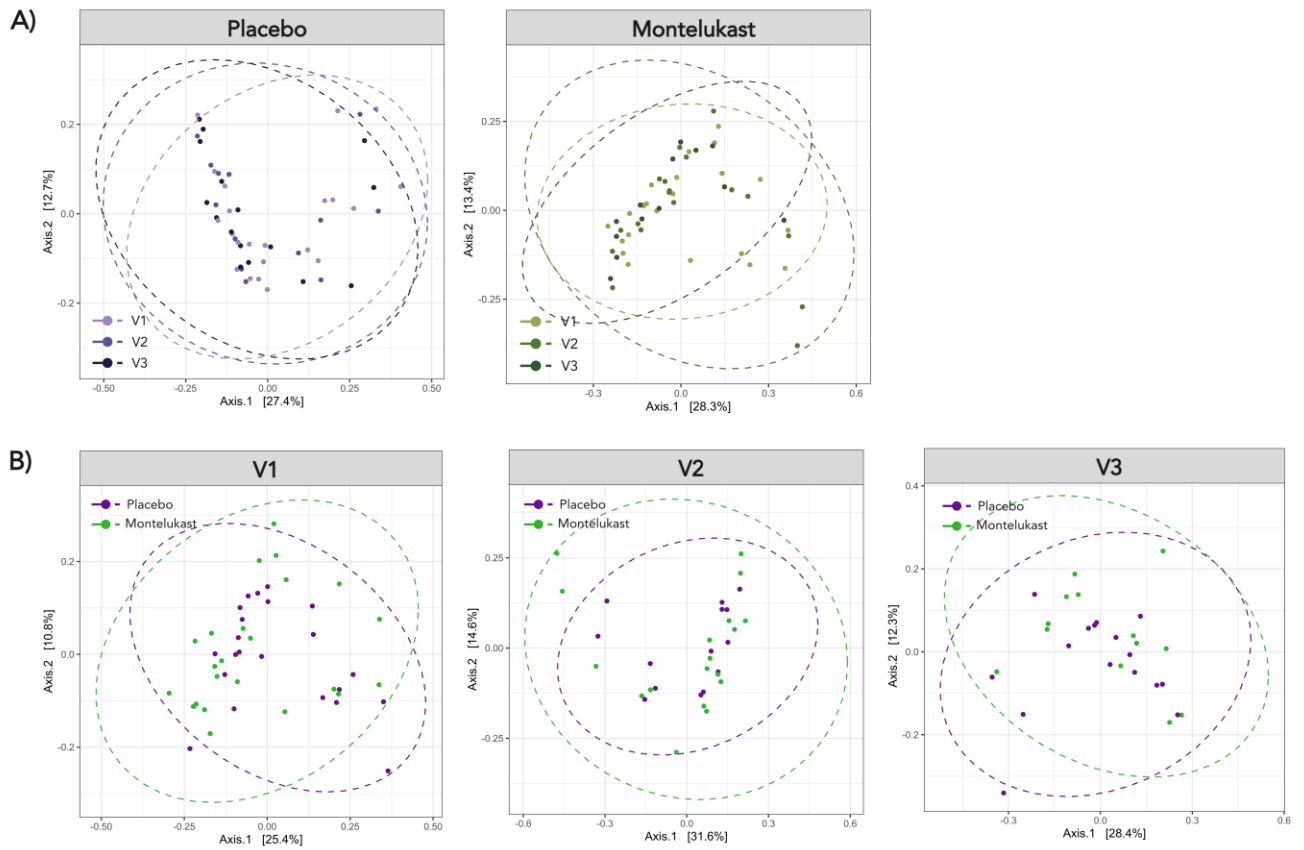


Figure S2. Longitudinal analysis of gut microbial diversity in Long COVID patients. A) Beta diversity (Bray-Curtis distance) across time points within the placebo and Montelukast groups. **B)** Beta diversity (Bray-Curtis distance) comparing the placebo and Montelukast groups at each individual time point.

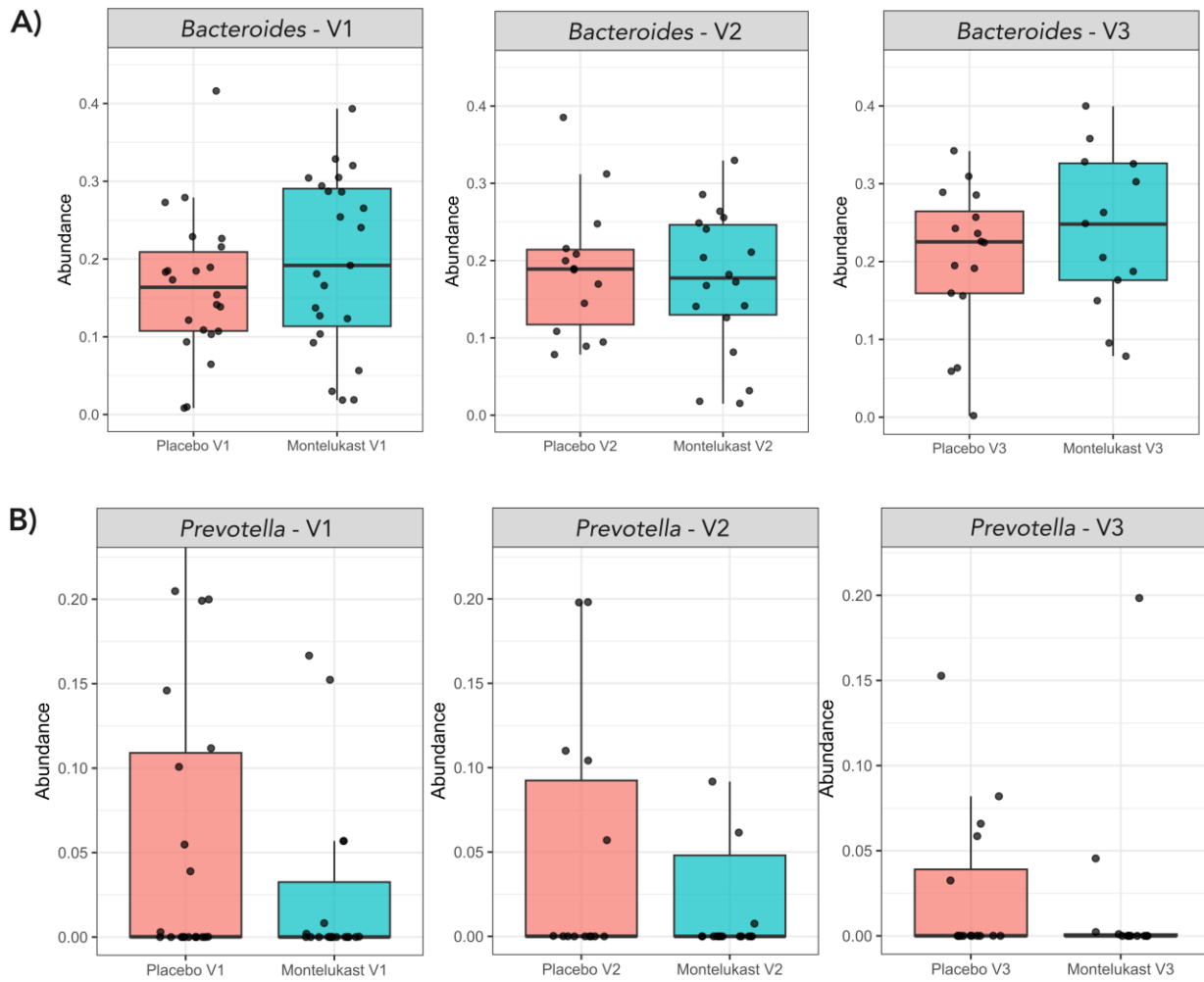


Figure S3. Longitudinal fluctuation in relative abundance of *Bacteroides* and *Prevotella* in the gut microbiome. A) Relative abundance of *Bacteroides* and **B)** relative abundance of *Prevotella* across the three study visits: V1 (before treatment), V2 (after completing the 30-day treatment), and V3 (one year after baseline) for both treatment groups.

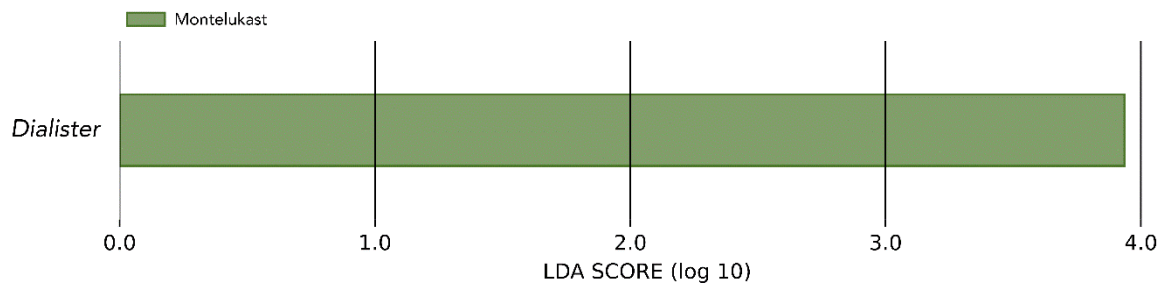


Figure S4. Differentially enriched taxa in Long COVID patients following Montelukast treatment. LEfSe analysis at the genus level comparing the placebo and Montelukast groups at Visit 2 (30 days post-treatment). Taxa are identified based on the Linear Discriminant Analysis (LDA) score.

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