

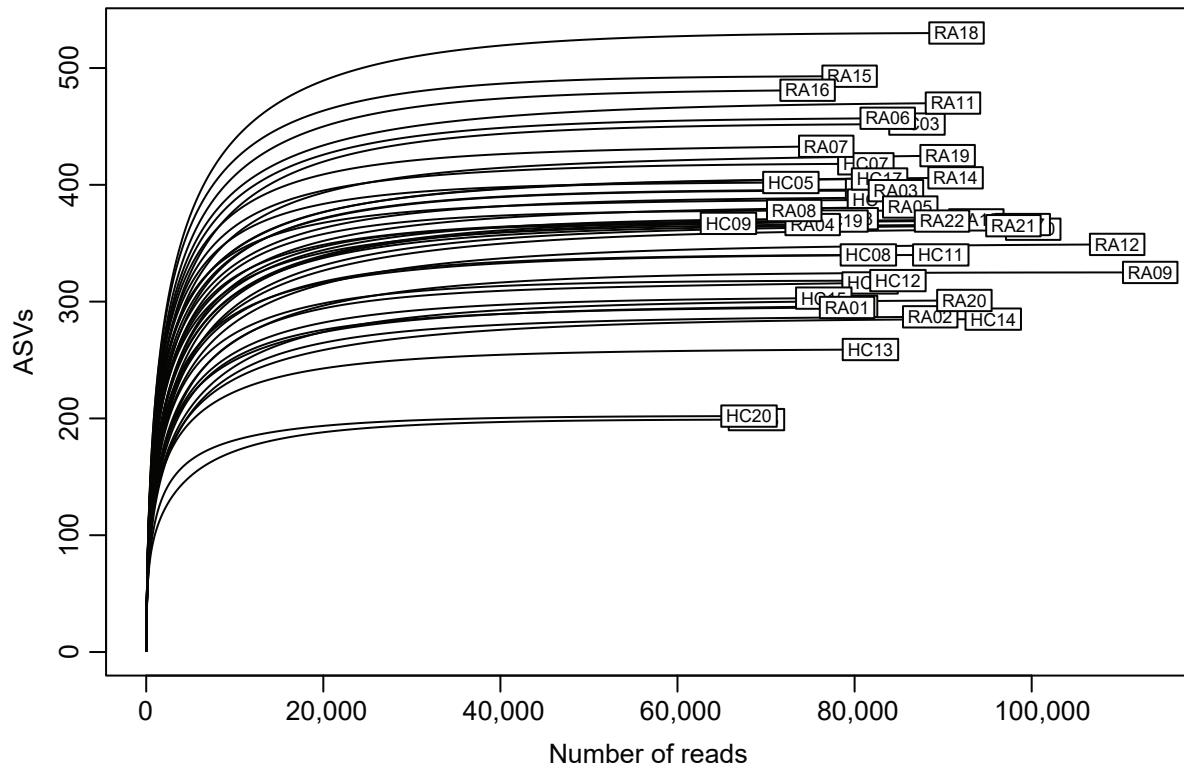


Figure S1. Rarefaction curves were plotted from the amplicon sequence variant (ASV) table for each sample. RA01-RA22, samples from patients with rheumatoid arthritis; HC01-HC20, samples from healthy controls.

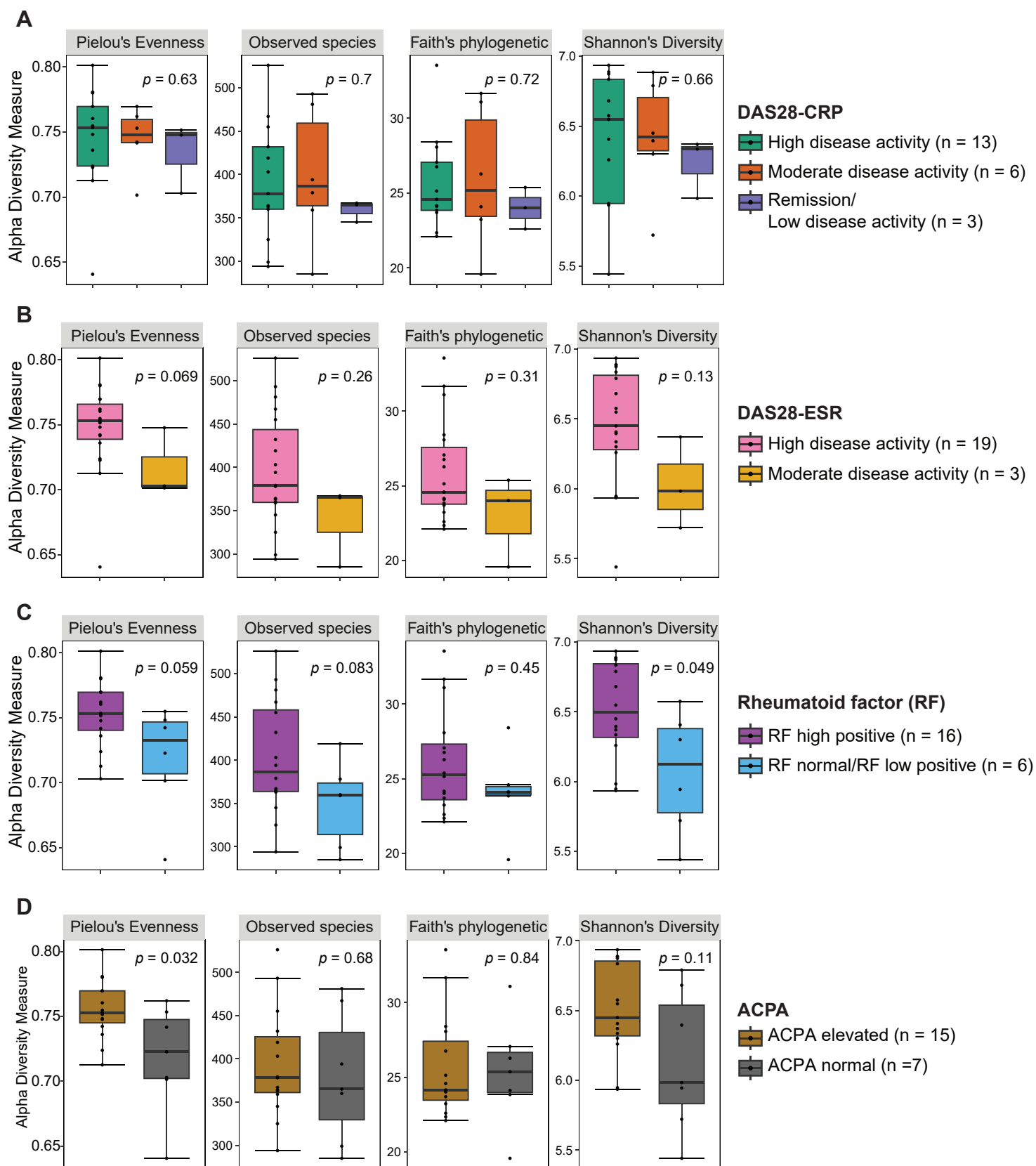


Figure S2. Alpha diversity of gut microbiota in patients with rheumatoid arthritis grouped using clinical indicators. A) Disease activity (high, moderate, low/remission) in function of the DAS28-CRP score. B) Disease activity (high, moderate) in function of the DAS28-ESR score. C) Concentration (high versus low/normal) of rheumatoid factor and D) of Anti-citrullinated protein antibodies (ACPA). *P* values were calculated with the Kruskal–Wallis test for the three DAS28-ESR subgroups, and with the Mann–Whitney U test for the other clinical indicators.

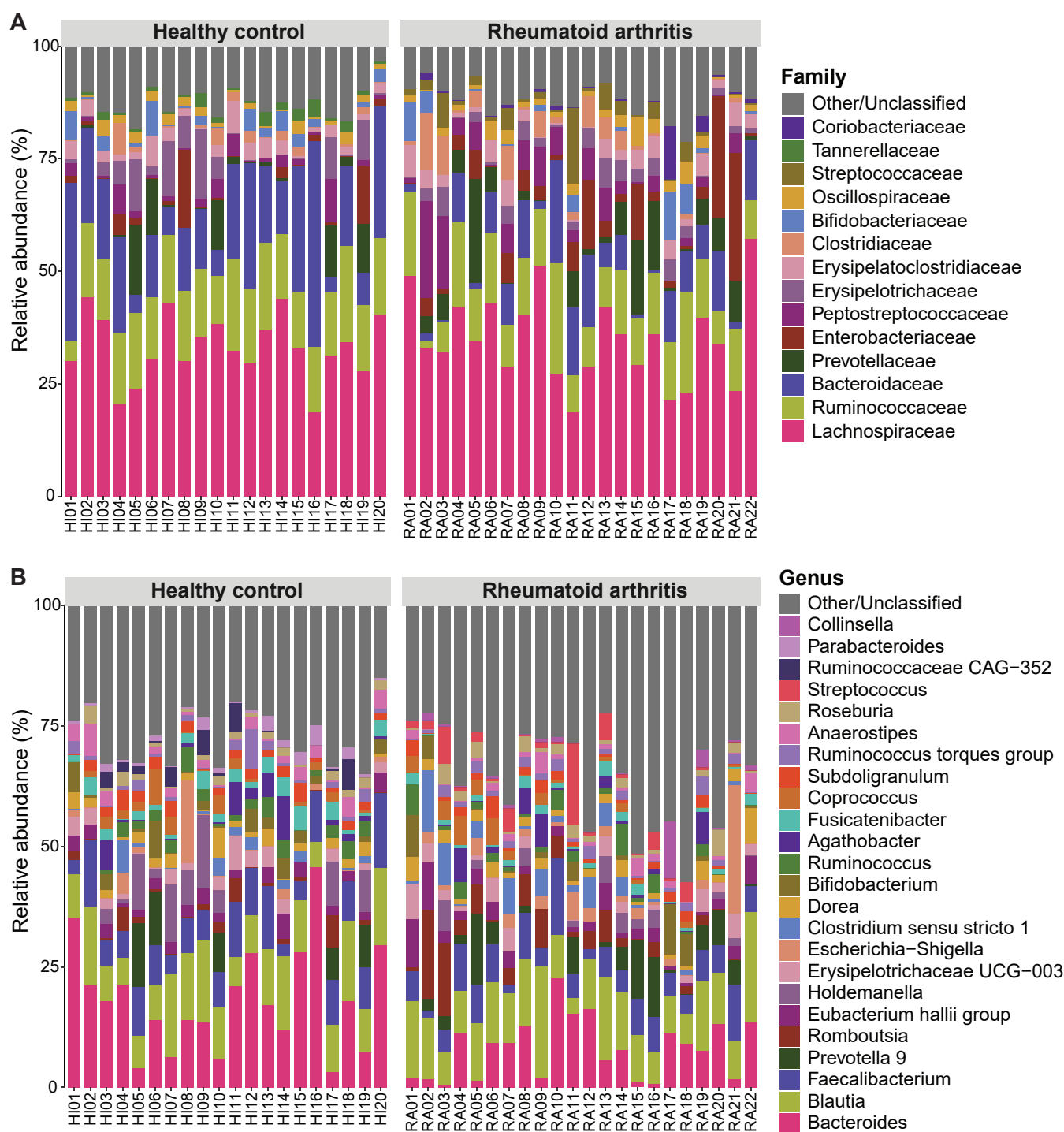


Figure S3. Gut microbial communities at the family (A) and genus (B) levels in patients with rheumatoid arthritis and healthy controls. Other/Unclassified, families/genera representing <1% of the relative abundance and unclassified taxa. HI, healthy control; RA, patient with rheumatoid arthritis.



Figure S4. Phyla and families with significantly different abundances between patients with rheumatoid arthritis (RA) and healthy controls (HC) using either the Mann–Whitney U test or ANCOM-BC2 (nominal p values < 0.05). Violet, taxa enriched in the RA group; green, taxa enriched in the HC group.