Supplementary Figures

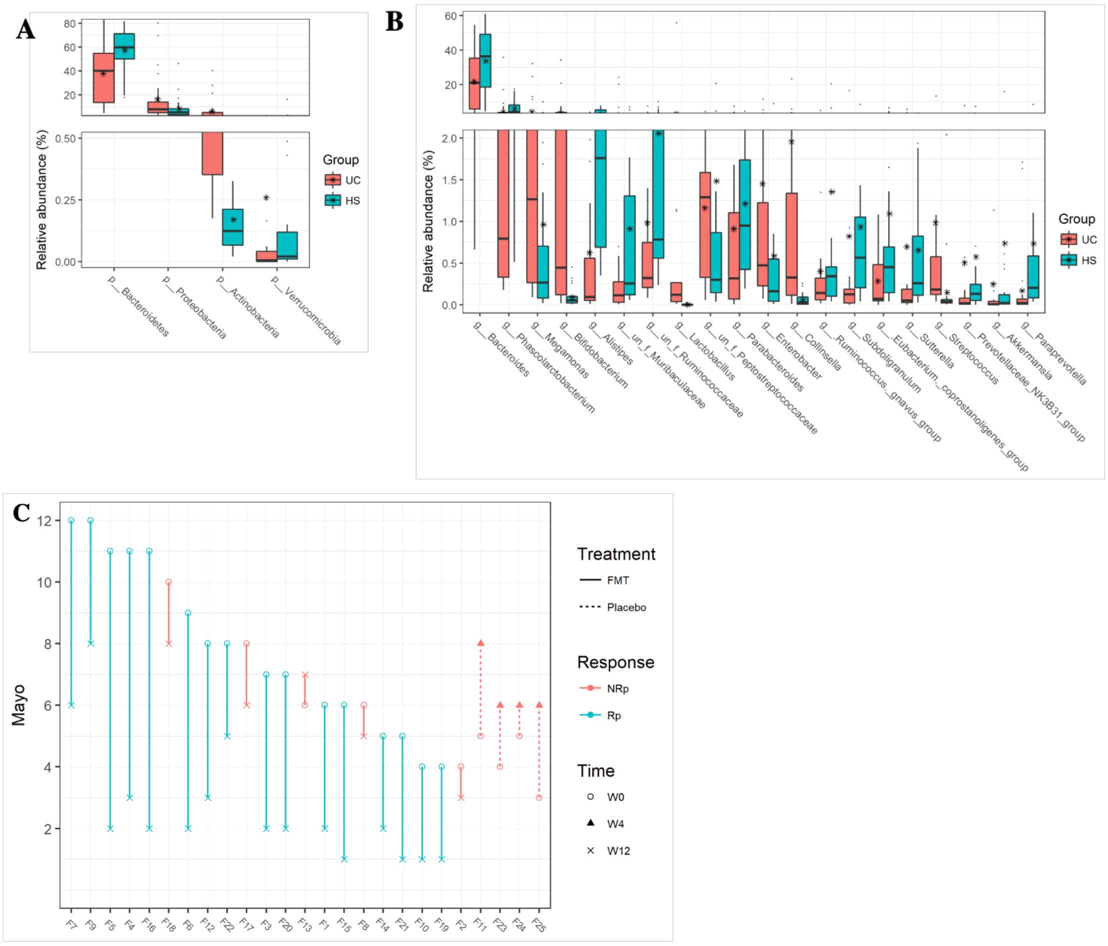

Fig S1 Differences in gut bacterial communities between UC and healthy subjects (HS), based on 16S V3-V4 sequencing data. (A) Phyla that were signicantly (P<0.05) differentiated bwteen UC and HS. (B) Top 20 of the genera that were signicantly (P<0.05) differentiated bwteen UC and HS.

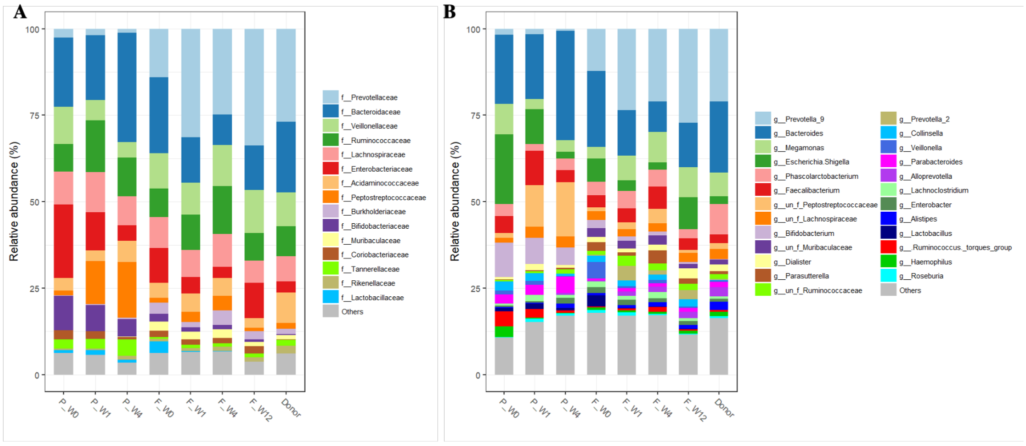

Fig S2 Alterations in gut bacterial communities of UC after treatment with FMT or placebo. (A) Relative abundances of the top 15 families (A) and top 25 genera in samples from patients treated with FMT or placebo, and donors.

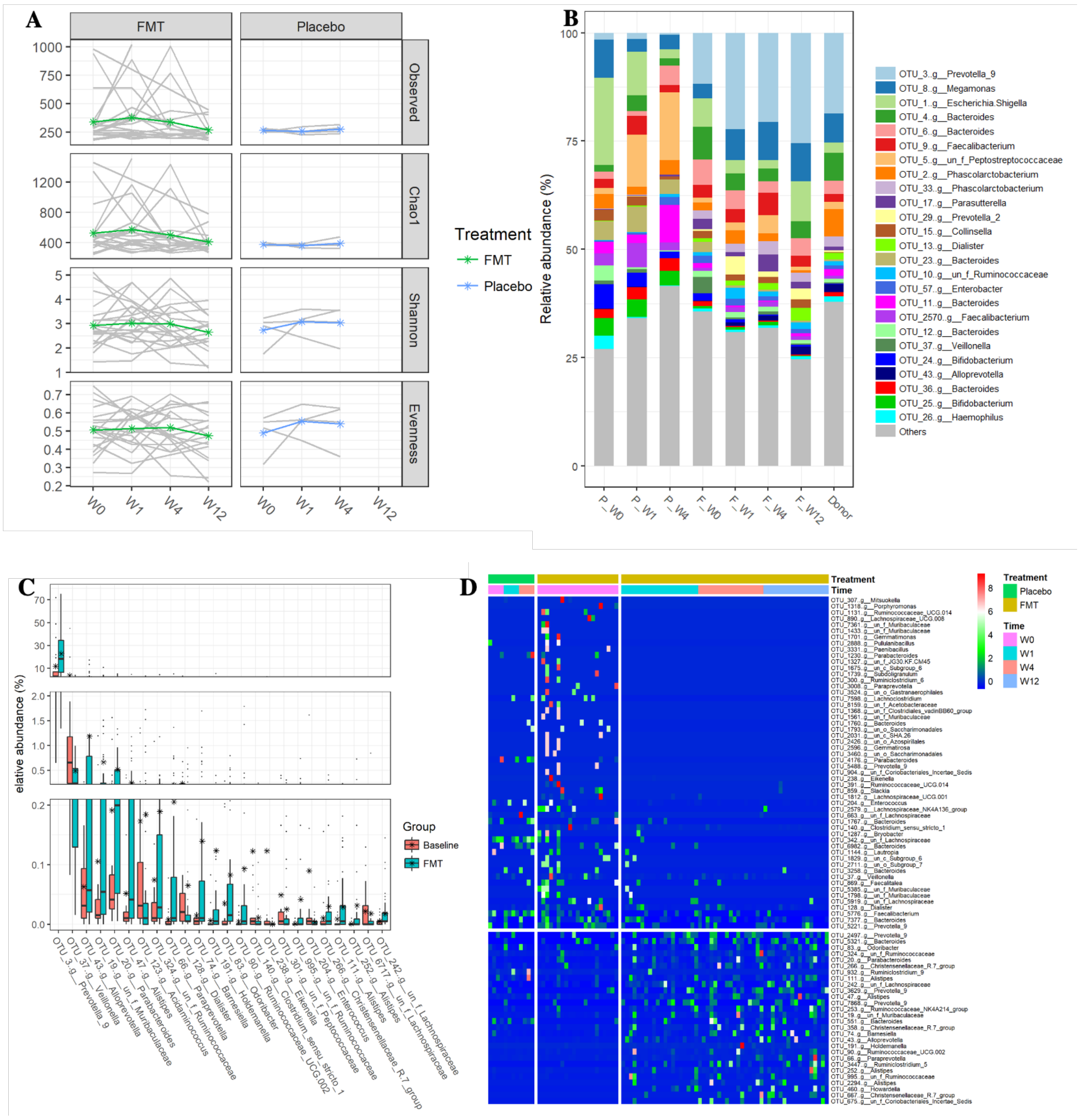

Fig S3 Alterations in gut bacterial communities (OTU level) of UC after treatment with FMT or placebo. (A) Changes of alpha-diversity indexes estimated by richness (Observed OTUs, Chao1), Shannon, and Pielow evenness of each individual over time. The star indicate the mean value of each timepoint. (B) Relative abundances of the top 25 OTUs in samples from patients treated with FMT or placebo, and donors. (C) The predominat OTUs (relative abundance > 0.01%) that were signicantly (P<0.05) differentiated between baseline and after FMT. The star indicate the mean value of the group. (D) Heatmap of OTUs that were signicantly (P<0.05) differentiated between baseline and after FMT and possessed FC>2 or FC<0.5 in samples from patients treated with FMT or placebo.

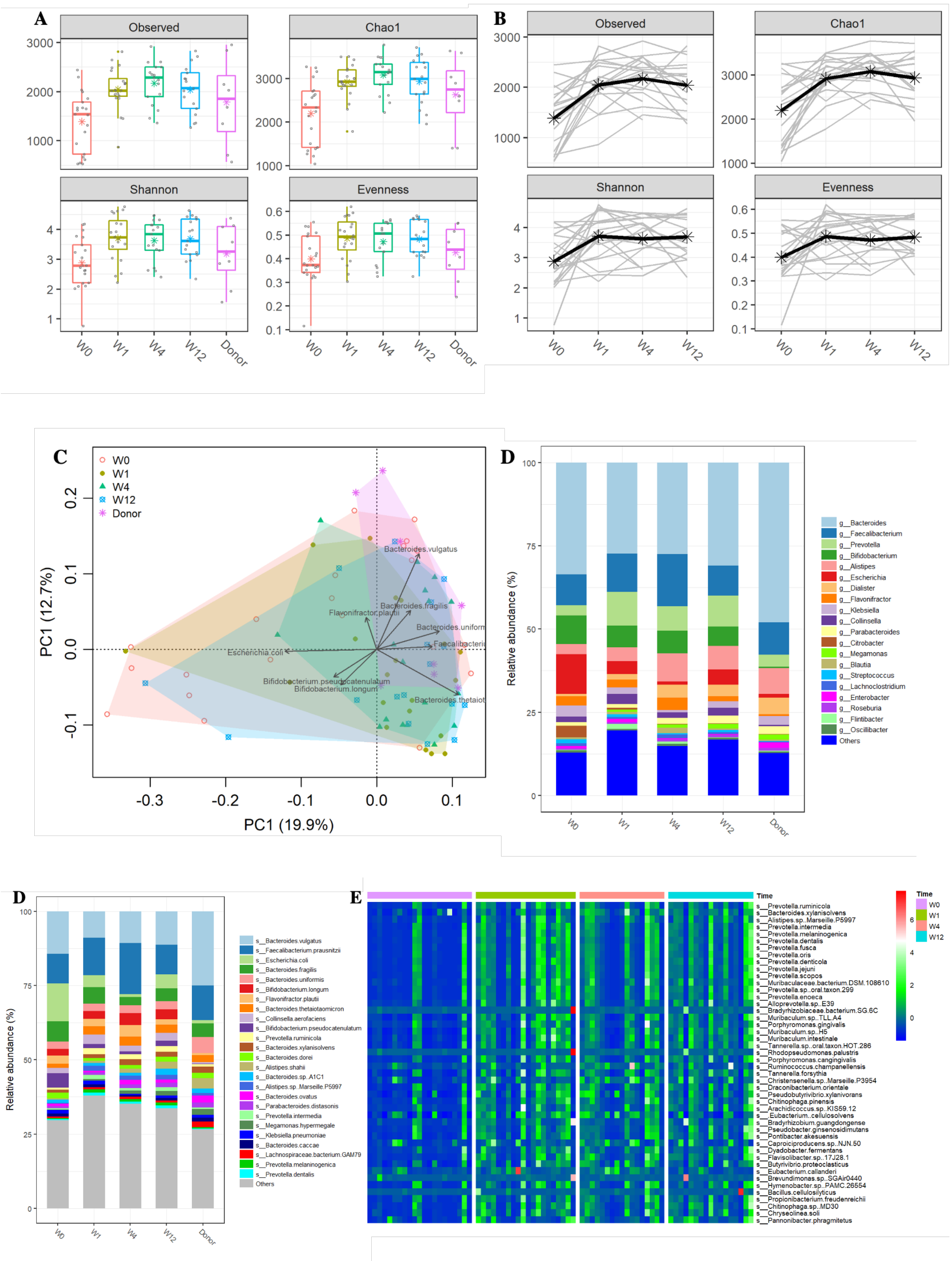

Fig S4 Alterations in gut microbial communities (metagenomics) of UC after treatment with FMT. (A) Changes of alpha-diversity indexes estimated by richness (Observed OTUs, Chao1), Shannon, and Pielow evenness of each timepoint (A) and each individual over time (B). The star indicate the mean value of each timepoint. (C) Differences in gut microbial community structures among UC patients at baseline, at other time points during follow-up visit, and donors, assessed by PCA of euclidean distance of specicies abundances. Data were Hellinger-transformed. Top 10 species were fitted to PCA with significance of P<0.05. (D) Relative abundances of the top 20 genera in samples from patients treated with FMT and donors.

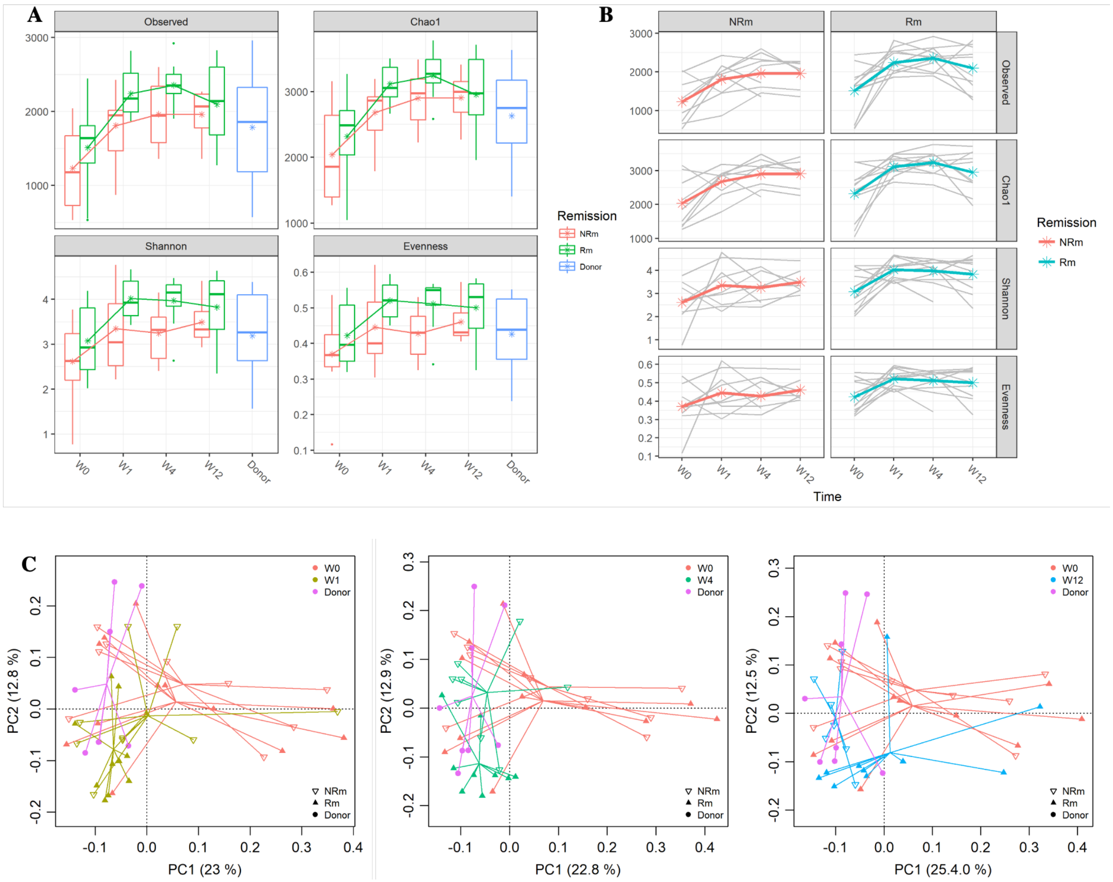

Fig S5 Changes in gut microbial communities (metagenomics) associated with Rm and NRm after FMT. Alpha-diversity of Rm, NRm, and donor samples, estimated by richness (Observed species, Chao1), Shannon, and Pielow evenness at each timepoint (A) and of each individual over time (B) . The black line indicates significant (P<0.05) differences between the two groups covered by the line. (C) Differences in gut microbial community structures of Rm, NRm, and donors between the baseline and the other time point during follow-up after FMT, by PCA based on euclidean distance of species abundances. Data were Hellinger-transformed. More significance test results were recorded in Table S2.

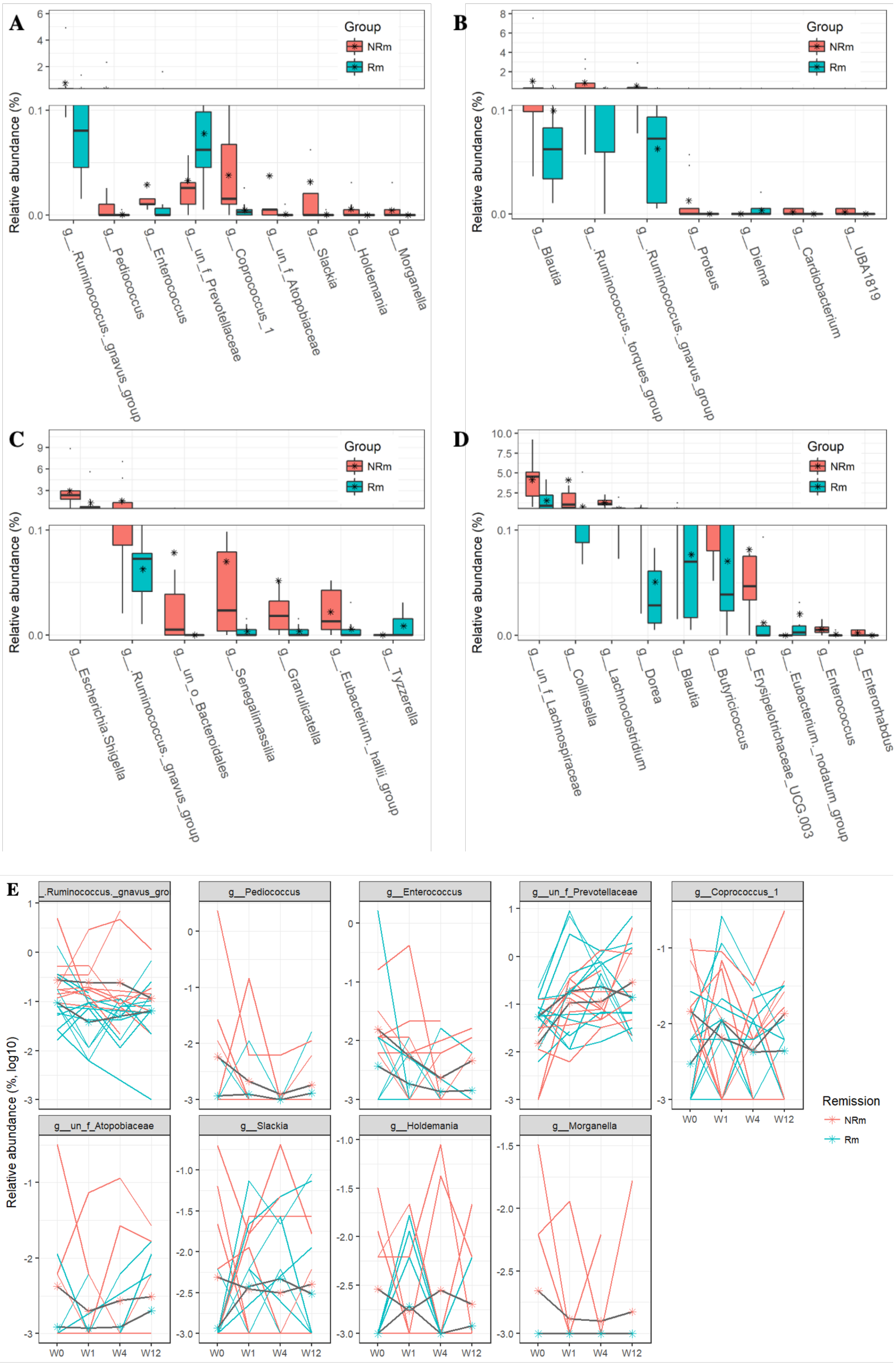

Fig S6 Relative abundances of the bacterial genera significantly different between Rm and NRm at W0 (A), W1(B), W4 (C), W12 (D). (E) Relative abundances of the bacterial genera significantly different between W0_Rm and W0_NRm over time.

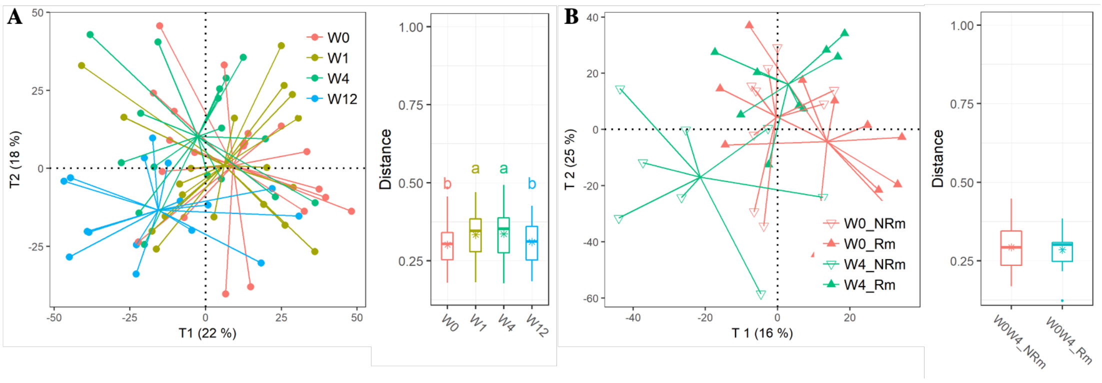

Fig S7 Metabolic profiles in negative ion model associated with clinical remission. (A) PLS_DA analysis of metabolomic profiles by time points (left panel) and Euclidean distances of samples within the same time points (right panel). (B) PLS_DA analysis of metabolomic profiles at Week 0 and Week 4 after FMT with achieving clinical remission or not achieving clinical remission (left panel), as well as Euclidean distances of patients between Week 0 and Week 4 (right panel).

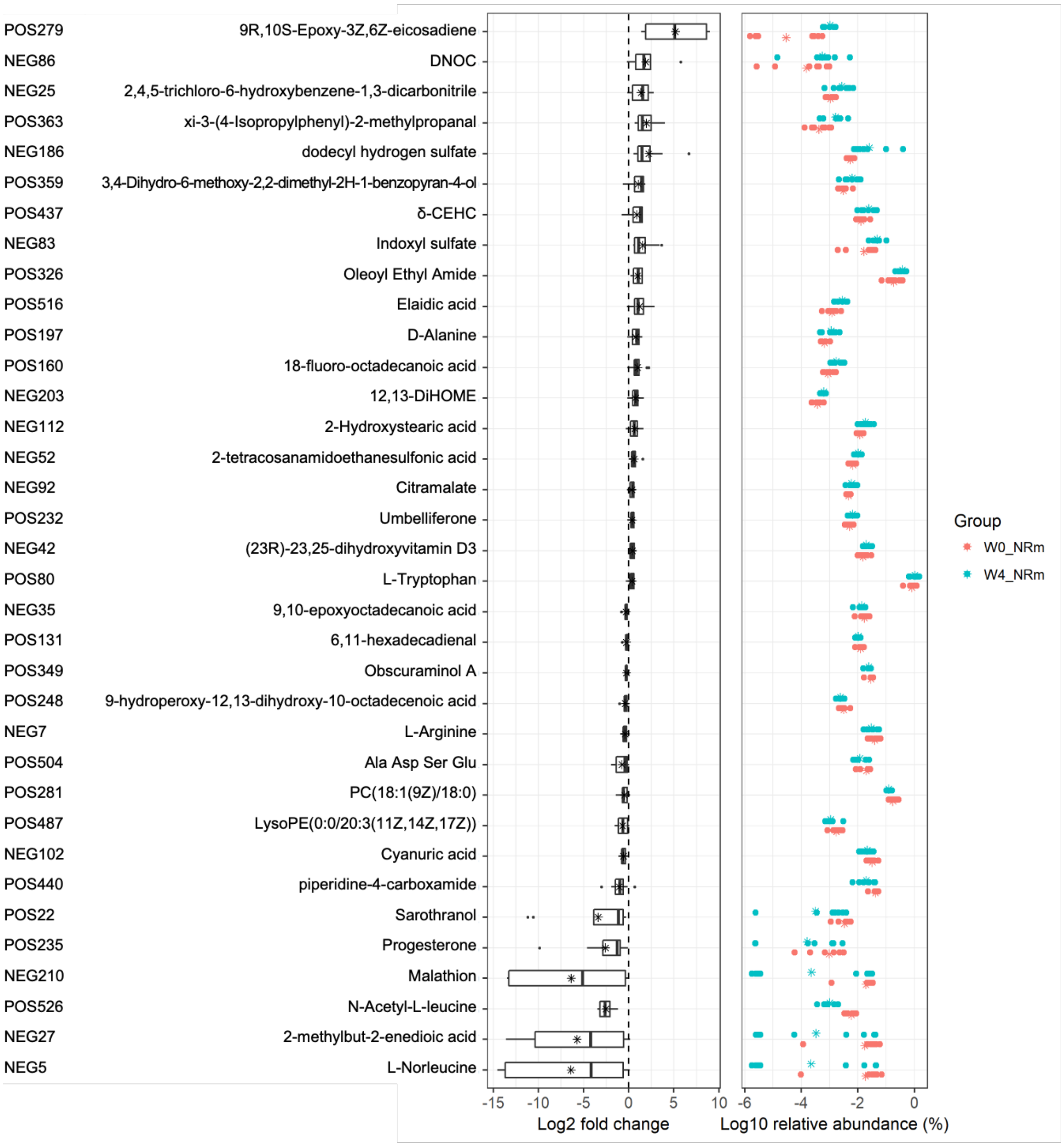

Fig S8 Metabolites that were significantly decreased or increased uniquely in W4_NRm compared with W0_NRm group (namely, not significantly differentiated in W4_Rm vs W0_Rm), were filtered by VIP score >1, and were structurally identified in databases.

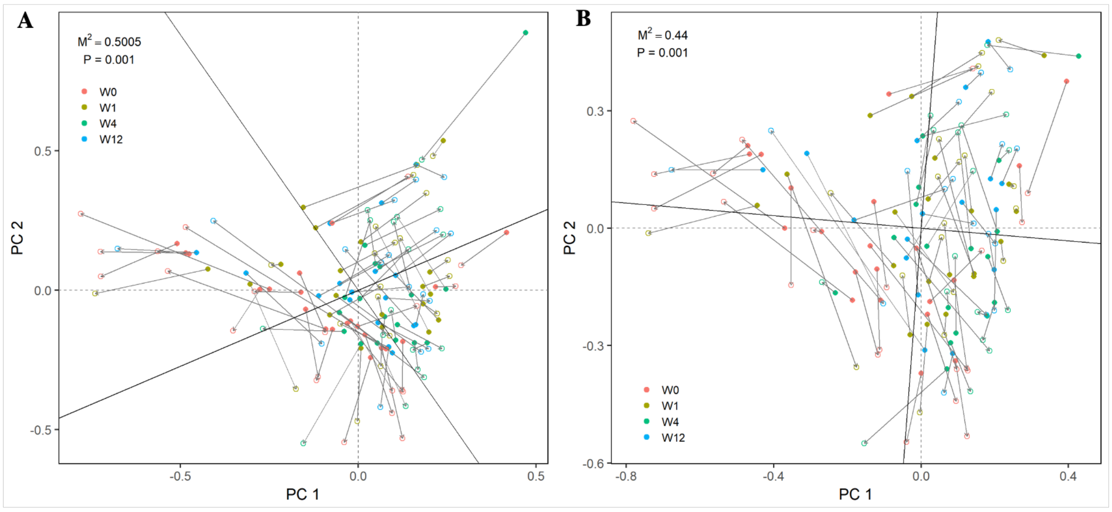

Fig S9 Inter-omic correlations between gut microbial species and functional features, by Procrustes analysis of gut microbial species and KEGG modules (A) and MetaCyc pathways (B).

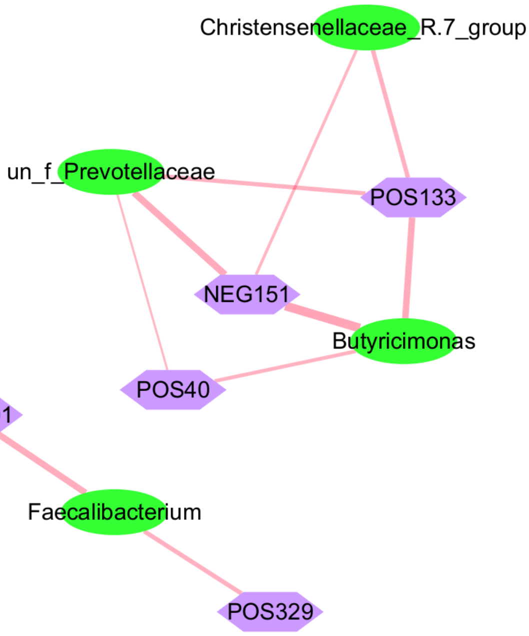

Fig S10 Correlations between gut microbial species from 16S V4 and metabolites.