Supplementary Materials:

Figure S1. Identified phyla from three fecal donors microbiota at 0, 12 and 24 h of fermentation for five prebiotic dietary fibers analyzed based on percent of sequence reads.

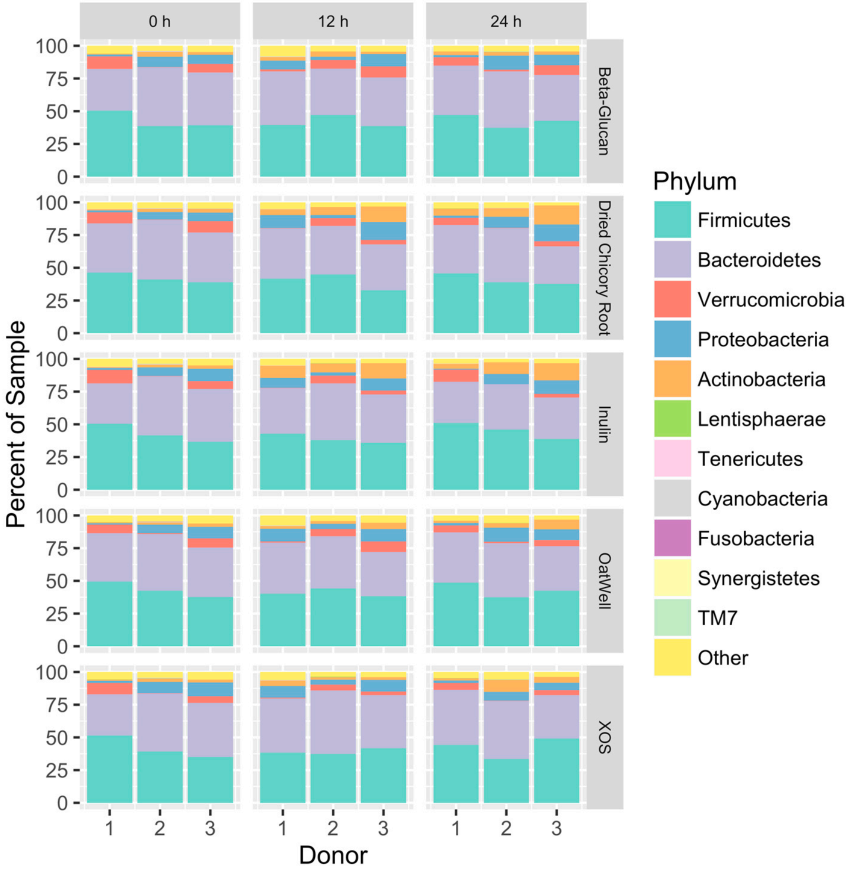

Figure S2. Identified abundant families for three fecal donors at 0, 12 and 24 h of fermentation for five prebiotic dietary fibers analyzed based on percent of sequence reads.

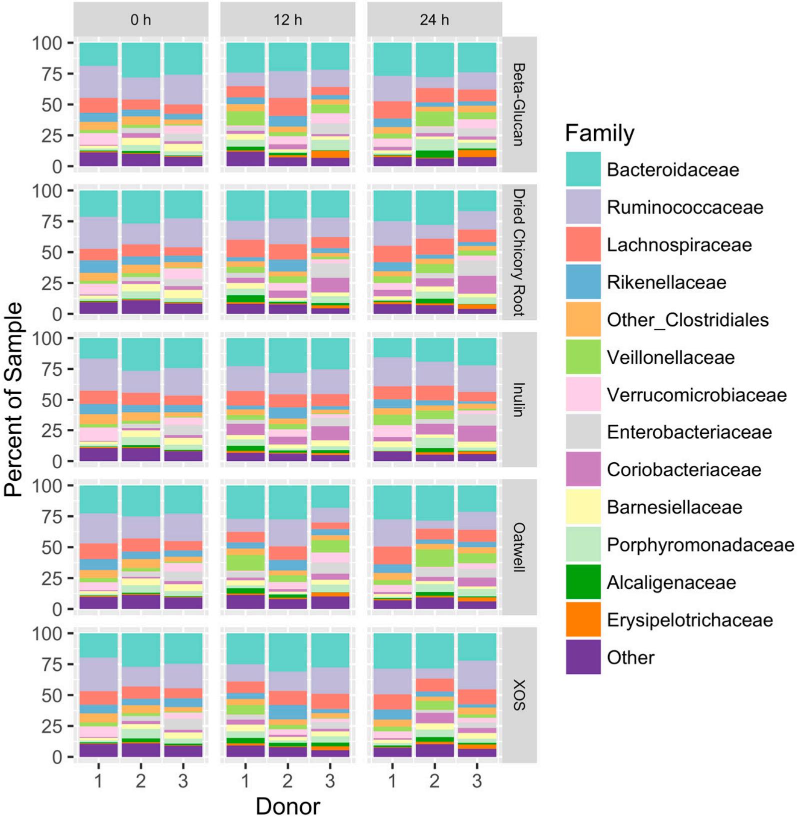

Figure S3. Identified abundant genera for three fecal donors at 0, 12 and 24 h of fermentation for five prebiotic dietary fibers analyzed based on percent of sequence reads.

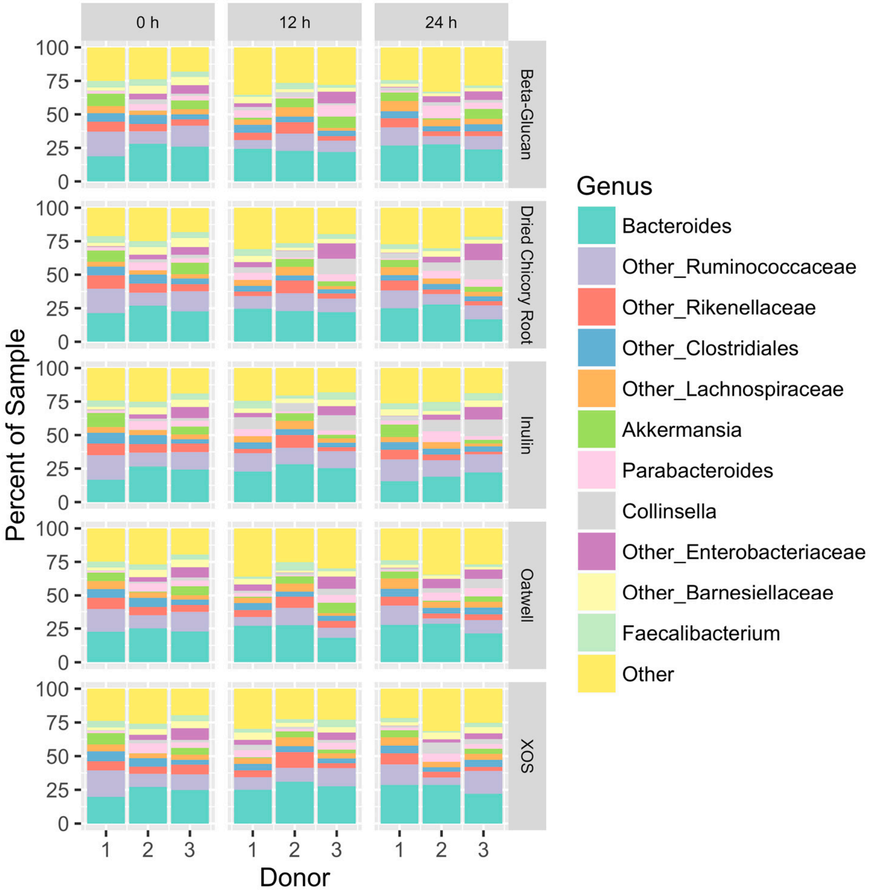

Figure S4. Six metrics of analysis for alpha-diversity among samples at 0, 12 and 24 h of analysis, grouped by donor for all five prebiotic dietary fibers analyzed.

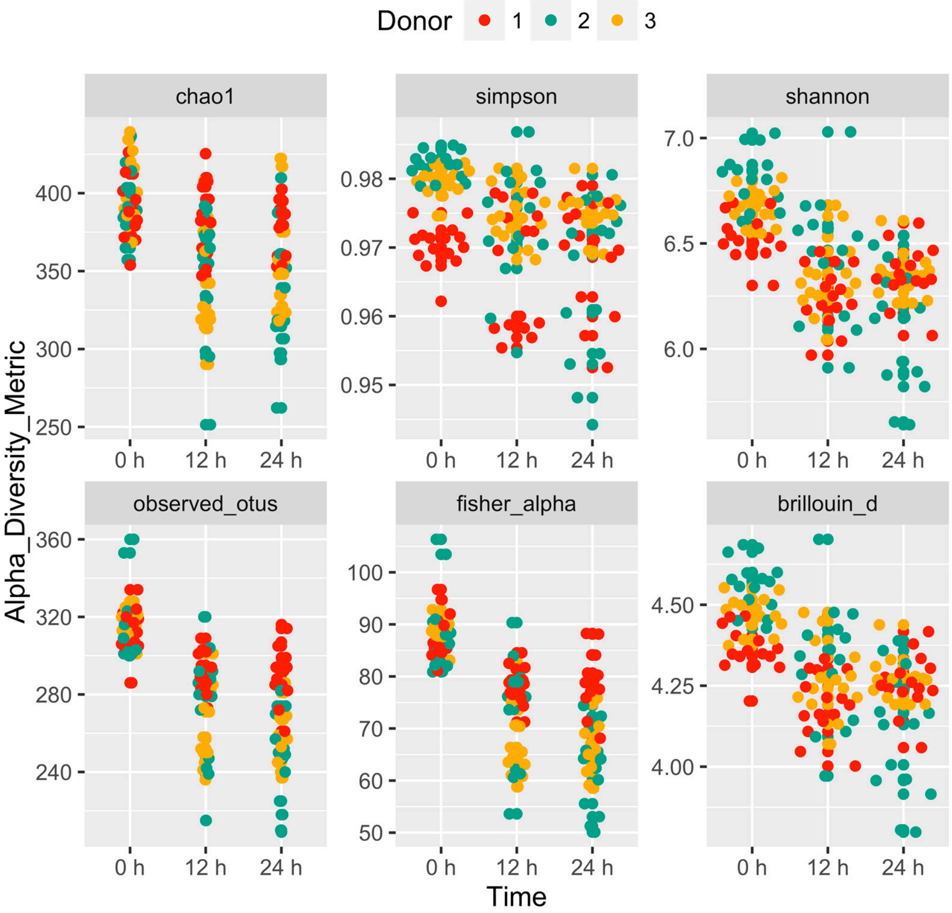

Figure S5. Six metrics of analysis for alpha-diversity among samples at 0, 12 and 24 h of analysis, grouped by treatment for all three fecal donors.

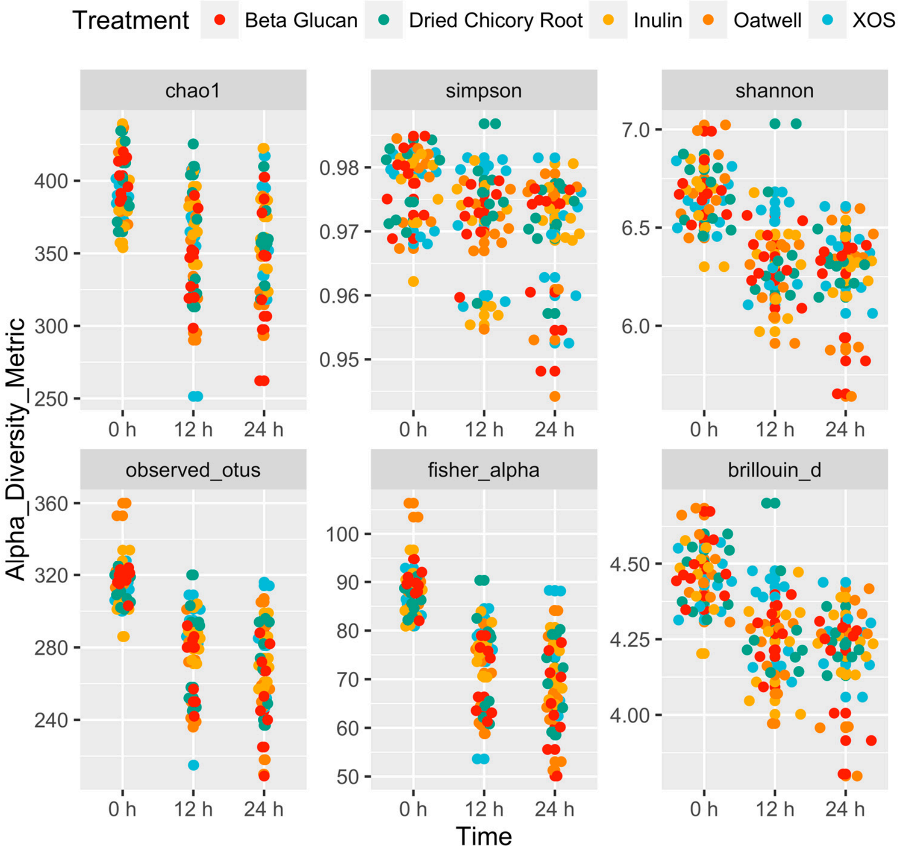

Figure S6. Bray-Curtis β-diversity principal component analysis of technical replicates among each treatment group between microbiota analysis of three fecal donors.

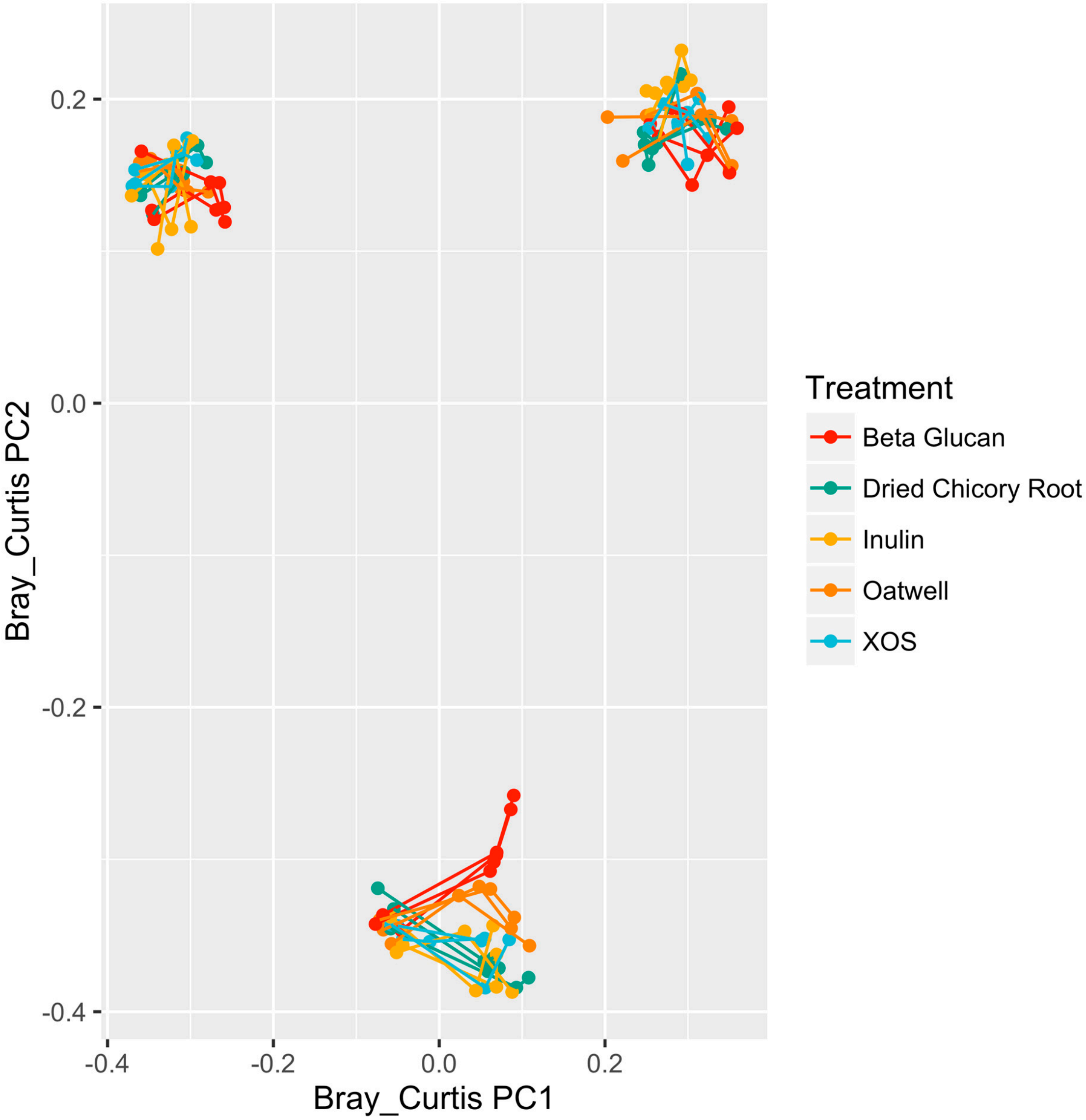

Figure S7. Bray-Curtis β-diversity principal component analysis among microbiota of three fecal donors at 0, 12 and 24 h of analysis.

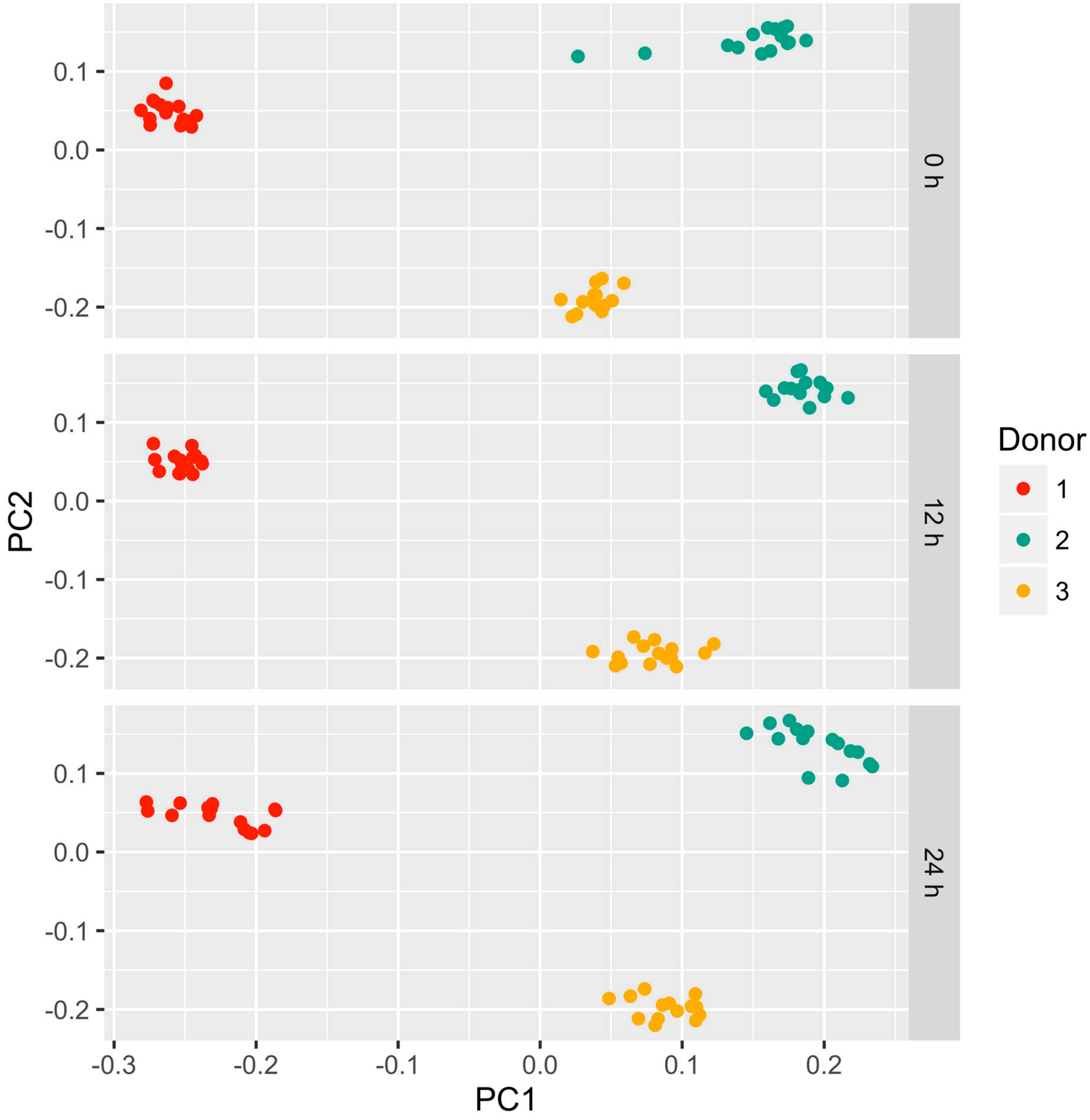

Figure S8. Variations in abundant phyla among three donors analyzed.

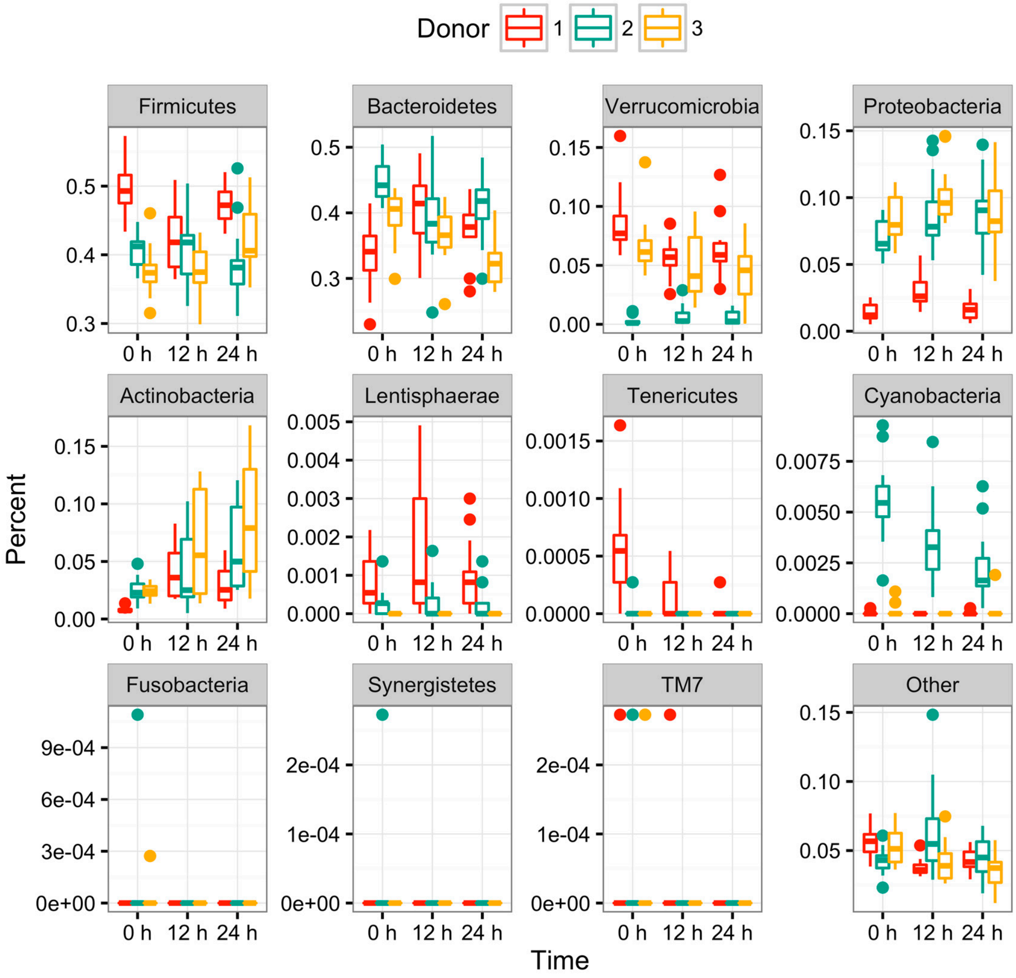

Figure S9. Variations in treatment groups and pooled donors analyzed.