

Figure S1. PCoA assessing beta diversity of the microbiome according to the participants (ID) enrolled. Axes correspond to principle coordinates displaying the maximum amount of variance (%) in the dataset. ($n = 9$ for all sample collections except for the final washout, $n = 7$, and inulin 2, $n = 8$).

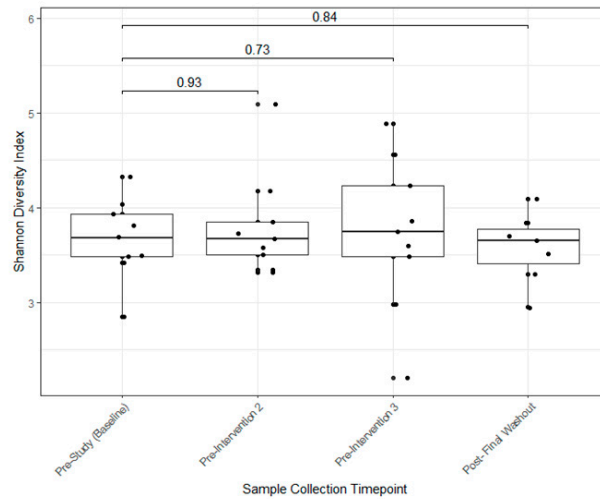


Figure S2. Alpha diversity measured by Shannon Diversity Index at Baseline, Pre-Intervention 2, Pre-Intervention 3, and Post-Final Washout. P -values are presented for paired t -test.

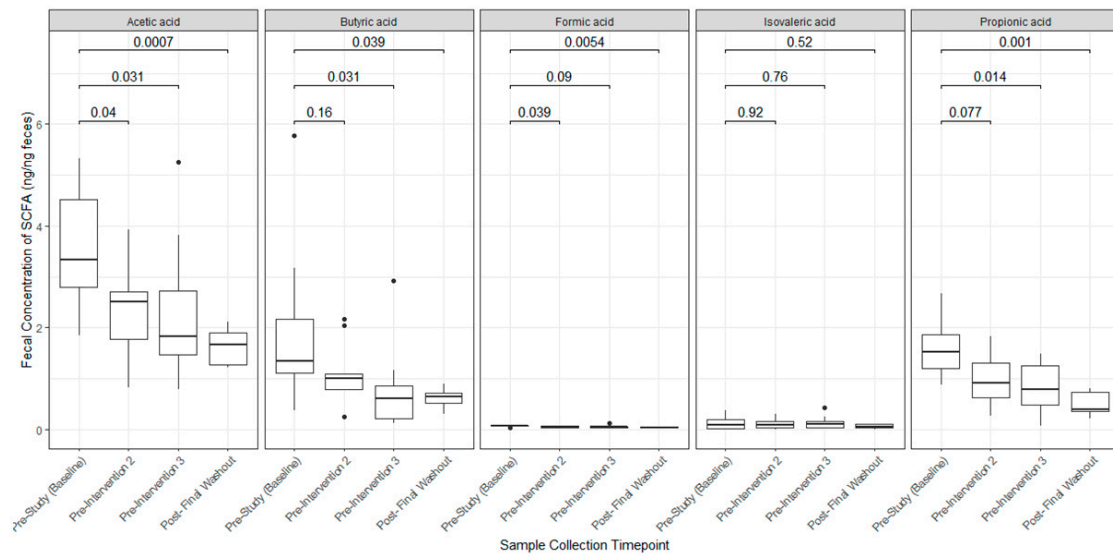


Figure S3. Short-Chain Fatty Acid (SCFA) concentrations (ng/ng feces) measured at Baseline, Pre-Intervention 2, Pre-Intervention 3, and Post-Final Washout. *P*-values are presented for paired *t*-test for the five SCFAs.

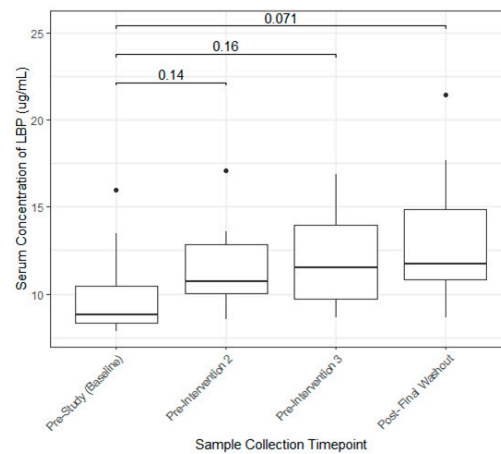


Figure S4. LBP concentrations (ug/mL) measured at Baseline, Pre-Intervention 2, Pre-Intervention 3, and Post-Final Washout. *P*-values are presented for paired *t*-test.

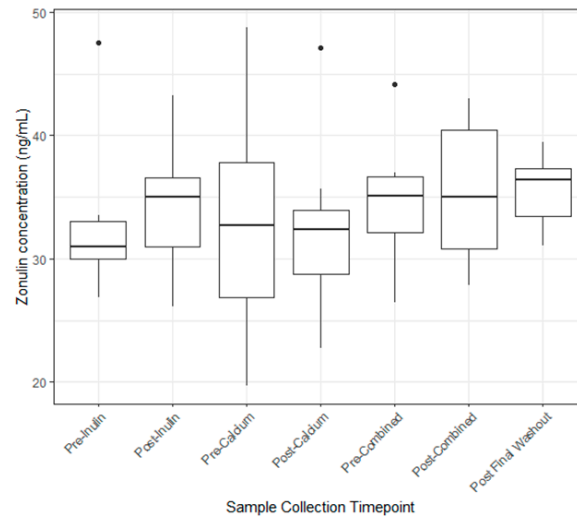


Figure S5. Zonulin concentrations (ng/mL) measured in serum at each sample collection time point. ($n = 9$ for all sample collections except for Post Final Washout, $n = 7$, and Post-Inulin, $n = 8$, and Post-Calcium, $n = 8$). No differences in concentration were noted (ANOVA, $p = 0.93$).