

Supplemental Material

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Item S2 Supplemental Figures -3-

Item S1: Supplemental Tables

Supplemental Table S1: Bacterial taxa, by relative abundance at end of intervention.

Taxonomy	Abundance Placebo (mean \pm SD)	Abundance Synbiotics (mean \pm SD)	Fold Change	FDR	P-value (clr)
Phylum					
Actinobacteria	4.6 \pm 5.1	3.3 \pm 3.5	-1.4	0.061	0.011
Euryarchaeota	0.097 \pm 0.25	0.086 \pm 0.16	-1.1	0.061	0.0079
Family					
Streptococcaceae	1.3 \pm 2.8	0.3 \pm 0.34	-4.3	0.065	0.0014
Methanobacteriaceae	0.097 \pm 0.25	0.086 \pm 0.16	-1.1	0.11	0.0049
Bifidobacteriaceae	2.3 \pm 4.0	2.5 \pm 3.3	1.1	0.21	0.014
CAG-272	0.04 \pm 0.091	0.024 \pm 0.06	-1.7	0.41	0.037
Genus					
Streptococcus	1.3 \pm 2.8	0.3 \pm 0.34	-4.3	0.20	0.0015
Methanobrevibacter_A	0.097 \pm 0.25	0.086 \pm 0.16	-1.1	0.32	0.006
Ruminiclostridium_C	0.35 \pm 0.5	0.21 \pm 0.26	-1.7	0.32	0.0073
Bifidobacterium	2.3 \pm 4.0	2.5 \pm 3.3	1.1	0.43	0.013
Eubacterium_G	0.033 \pm 0.064	0.034 \pm 0.068	1	0.56	0.022
CAG-226	0.1 \pm 0.26	0.11 \pm 0.32	1.1	0.56	0.034
Intestinimonas	0.022 \pm 0.079	0.059 \pm 0.15	2.7	0.56	0.038
Species					
s_Bifidobacterium animalis	0.55 \pm 2.7	1.3 \pm 2.8	2.4	0.04	0.00017
s_Bacteroides cellulosilyticus	0.49 \pm 1.6	0.28 \pm 1.1	-1.7	0.47	0.0039
s_Blautia MIC1901	0.039 \pm 0.12	0.093 \pm 0.19	2.4	0.47	0.0084
s_Ruminiclostridium_C MIC856	0.35 \pm 0.5	0.2 \pm 0.27	-1.7	0.47	0.009
s_Duodenibacillus MIC4494	0.22 \pm 1.1	0.24 \pm 0.74	1.1	0.47	0.013
s_Streptococcus thermophilus	0.21 \pm 0.89	0.22 \pm 0.33	1	0.47	0.015
s_Subdoligranulum MIC5784	0.055 \pm 0.14	0.13 \pm 0.23	2.4	0.47	0.018
s_Alistipes senegalensis	0.014 \pm 0.039	0.011 \pm 0.036	-1.3	0.47	0.019
s_Acidaminococcus intestini	0.039 \pm 0.2	0.034 \pm 0.1	-1.1	0.47	0.019
s_Eubacterium_E hallii	0.38 \pm 0.5	0.095 \pm 0.18	-4	0.47	0.023
s_Bacteroides_B vulgatus	1.7 \pm 2.6	3.5 \pm 4.0	2.1	0.47	0.024
s_Prevotella MIC849	0.55 \pm 1.0	0.071 \pm 0.21	-7.7	0.47	0.026
s_CAG-312 MIC3688	0.0056 \pm 0.021	0.028 \pm 0.097	5	0.47	0.026
s_Methanobrevibacter_A smithii	0.06 \pm 0.17	0.071 \pm 0.15	1.2	0.47	0.028
s_CAG-226 MIC3942	0.1 \pm 0.26	0.11 \pm 0.32	1.1	0.53	0.036
s_Alistipes MIC3765	0.038 \pm 0.087	0.24 \pm 0.69	6.3	0.53	0.036
s_Butyricimonas MIC1139	0.0023 \pm 0.013	0.013 \pm 0.028	5.7	0.53	0.042
s_CAG-103 MIC5000	0.25 \pm 0.61	0.11 \pm 0.35	-2.3	0.53	0.044
s_Ruthenibacterium lactatiformans	0.85 \pm 2.0	0.065 \pm 0.19	-13	0.53	0.049
s_CAG-103 MIC465	0.0073 \pm 0.04	0.075 \pm 0.14	10	0.53	0.049

Item S2: Supplemental Figure Legends

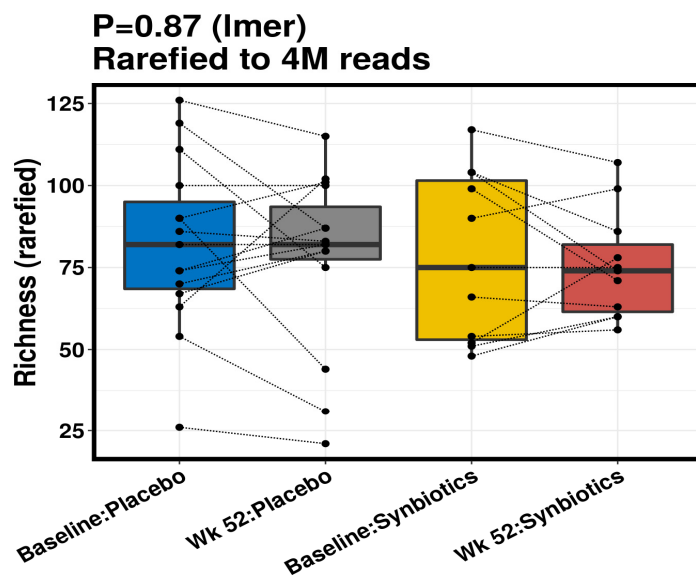
Supplemental Figure S1: A) Richness of the gastrointestinal microbiota, by species.

B) Diversity of gastrointestinal microbiota, by species.

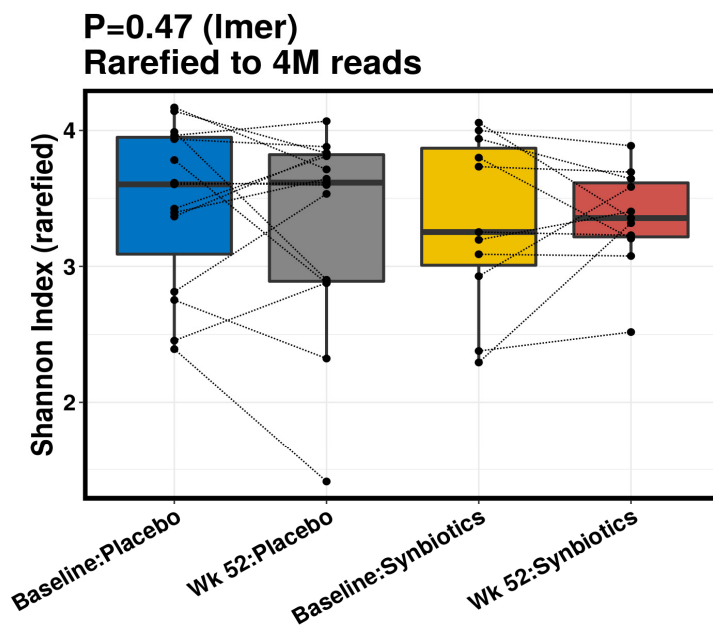
Supplemental Figure S2: Redundancy analysis (RDA) of gut microbiome composition by condition.

Supplemental Figure S3: Functional groups of the gastrointestinal microbiota differentiating between participants after placebo or synbiotic supplementation as identified by sparse Partial Least Squares Discriminant Analysis (sPLS-DA).

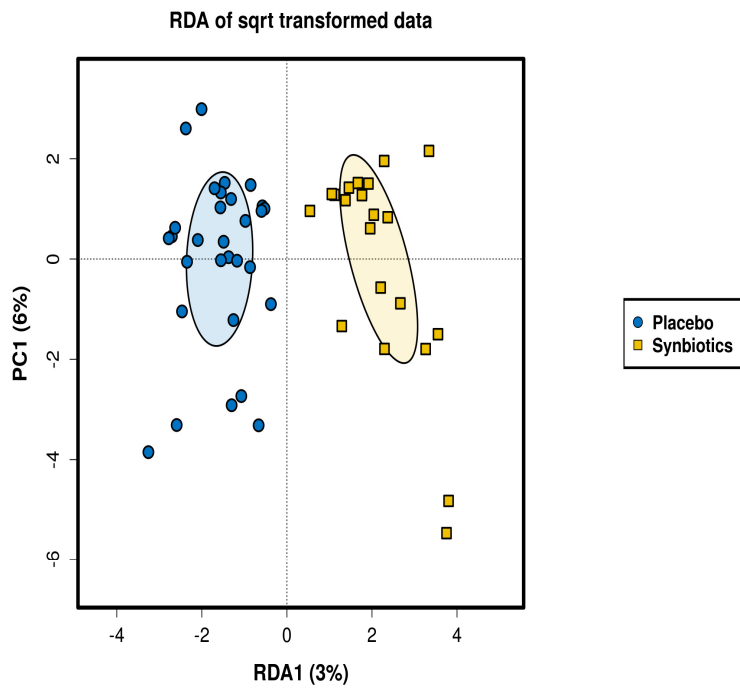
Supplemental Figure S1A



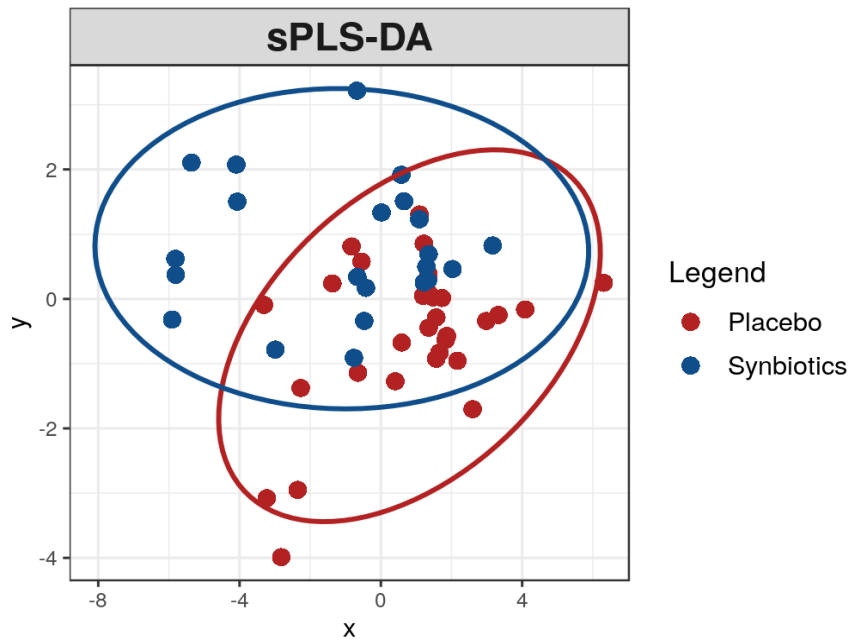
Supplemental Figure S1B



Supplemental Figure S2



Supplemental Figure S3



sPLS-DA

