

**Table S7.** Relative abundance and *P-value* of intestinal microbial phyla (A), genera (B), and species (C) in 37 participants based on 16S rRNA analysis.

	Baseline	After	Washout	P-value	
				Baseline vs After	After vs Washout
Phylum level					
Proteobacteria	1.2%	1.1%	2.8%	0.077	0.341
Actinobacteria	7.77%	9.01%	5.85%	0.118	0.024
Bacteroidetes	5.30%	8.47%	5.93%	0.026	0.03
Firmicutes	85.5%	81.3%	84.9%	0.074	0.108
ETC (under 1% in average)	0.23%	0.14%	0.47%		
Genus level					
<i>Parabacteroides</i>		1.03%		5.60E-05	7.40E-05
<i>Prevotella</i>		1.10%		0.871	0.854
<i>Streptococcus</i>	1.74%	1.11%	1.21%	0.63	0.987
<i>Dorea</i>	2.04%	1.36%	2.00%	0.089	0.137
<i>Subdoligranulum</i>	1.62%	1.90%	1.69%	0.331	0.168
<i>Agathobacter</i>	2.33%	1.91%	2.34%	0.725	0.662
<i>Eubacterium_g5</i>	3.30%	2.93%	3.90%	0.189	0.008
<i>Fusicatenibacter</i>	4.06%	5.10%	3.72%	0.039	0.014
<i>Anaerostipes</i>	5.86%	5.43%	7.32%	0.6	0.089
<i>Bacteroides</i>	3.62%	5.55%	4.37%	0.143	0.155
<i>Bifidobacterium</i>	6.92%	8.36%	5.30%	0.099	0.017
<i>Faecalibacterium</i>	9.25%	13.76%	11.07%	0.009	0.165
<i>Blautia</i>	23.69%	19.28%	25.15%	0.116	0.005
<i>Lachnospiraceae_uc</i>	1.06%		1.02%	0.003	0.002
<i>Lactobacillus</i>	2.01%		1.68%	0.825	0.725
<i>Ruminococcus_g2</i>	1.64%	1.36%	1.69%	0.57	0.534
<i>Ruminococcus_g4</i>	1.53%	1.09%	1.54%	0.019	0.036
Species level					
<i>B. angulatum</i>		0.01%		0.196	0.195
<i>B. animalis</i>		0.18%		4.20E-13	2.00E-12

<i>B. longum</i>	0.47%	1.16%	0.44%	0.14	0.035
<i>B. pseudolongum</i>		0.01%		2.50E-08	6.50E-08
<i>L. paracasei</i>		0.01%		1.80E-07	2.00E-07
<i>L. plantarum</i>		0.01%		2.40E-04	2.30E-05

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