

## SUPPLEMENTARY TABLES

Table S1 Phylum-level microbiota alterations in Colon cancer mucosa and tumor samples compared to Control mucosa at colonoscopy

Phylum	Relative Abundance (%)			Colon cancer Mucosa vs. Control p value (FDR)	Colon cancer Tumor vs. Control p value (FDR)
	Control (n=14)	Colon cancer Mucosa (n=12)	Colon cancer Tumor (n=12)		
Fusobacteria	0.26 ± 0.63	1.5 ± 2.3	7.9 ± 8.0	0.002 ( <b>0.008</b> )	<0.001 ( <b>0.003</b> )
Euryarchaeota	0.01 ± 0.04	0.43 ± 0.53	0.25 ± 0.33	0.001 ( <b>0.008</b> )	0.002 ( <b>0.01</b> )
Tenericutes	0.01 ± 0.02	0.19 ± 0.37	0.16 ± 0.39	0.02 ( <b>0.05</b> )	0.02 ( <b>0.05</b> )
Bacteroidetes	16 ± 17	25 ± 9.7	21 ± 9.8	0.02 ( <b>0.05</b> )	-
Spirochaetes	0.00 ± 0.00	0.02 ± 0.06	0.44 ± 1.4	-	0.02 (0.06)

Data are presented as mean ± SD. Wilcoxon rank sum test comparing Colon cancer mucosa or tumor vs. Control mucosa. Only p values ≤0.05 are shown. Bold values indicate FDR≤0.05. FDR, false discovery rate (Benjamini-Hochberg).

Table S2 Microbiota alterations in Colon cancer compared to Control fecal samples at colonoscopy

Taxon	Relative Abundance (%)		p value (FDR)
	Control Fecal (n=21)	Colon cancer Fecal (n=14)	
Phylum			
Tenericutes	0.26 ± 0.66	0.13 ± 0.47	0.003 ( <b>0.03</b> )
Genus			
<i>Clostridiaceae</i> spp.	1.8 ± 2.6	2.8 ± 3.4	<0.001( <b>0.008</b> )
<i>Dorea</i>	0.91 ± 0.57	1.4 ± 0.76	<0.001 ( <b>0.01</b> )
<i>Roseburia</i>	1.2 ± 1.3	0.35 ± 0.37	0.001 ( <b>0.03</b> )
<i>Peptostreptococcus</i>	0.00 ± 0.00	0.33 ± 0.51	0.002 ( <b>0.03</b> )
<i>Dialister</i>	0.68 ± 1.1	1.9 ± 3.5	0.01 (0.1)
[Mogibacteriaceae] spp.	0.17 ± 0.09	0.26 ± 0.13	0.03 (0.3)
<i>Parvimonas</i>	0.00 ± 0.00	0.54 ± 1.1	0.03 (0.3)
<i>Bulleidia</i>	0.01 ± 0.01	0.15 ± 0.19	0.05 (0.3)
<i>RF39</i> spp.	0.08 ± 0.38	0.44 ± 0.77	0.05 (0.3)

Data are presented as mean ± SD. Wilcoxon rank sum test comparing Colon cancer fecal samples (prior to probiotic intervention) vs. Control fecal samples. Only p values ≤0.05 are shown. Bold values indicate FDR≤0.05.

FDR, false discovery rate (Benjamini-Hochberg).

Table S3 Microbiota alterations in tumor samples at colonoscopy compared to surgery for Colon cancer patients

Genus	Relative Abundance (%)		p value (FDR)
	Tumor Colonoscopy n=12	Tumor Surgery n=12	
<i>Peptostreptococcaceae</i> spp.	0.02 ± 0.03	0.22 ± 0.30	0.01 (0.3)
<i>Marinomonas</i>	0.40 ± 0.52	0.03 ± 0.09	0.01 (0.3)
<i>Turicibacter</i>	0.01 ± 0.02	0.32 ± 0.47	0.02 (0.3)
<i>Veillonella</i>	1.8 ± 5.7	0.46 ± 1.4	0.02 (0.3)
<i>Sutterella</i>	0.50 ± 0.47	1.3 ± 1.3	0.02 (0.3)
Unclassified <i>Vibrionaceae</i>	0.34 ± 0.41	0.02 ± 0.06	0.05 (0.5)

Data are presented as mean ± SD. Wilcoxon rank sum test comparing Colon cancer tumor samples at colonoscopy vs. surgery. Only p values ≤0.05 are shown.  
FDR, false discovery rate (Benjamini-Hochberg).

Table S4 Phylum-level microbiota alterations with probiotic intervention in Colon cancer patients at surgery

Phylum	Effect of probiotic	Relative Abundance, %		p value (FDR)
		No Probiotic (n=6-7)	Probiotic (n=7-8)	
Fecal				
Firmicutes	increase	63 ± 12	77 ± 4.9	0.002 ( <b>0.01</b> )
Fusobacteria	decrease	0.83 ± 0.89	0.03 ± 0.05	0.01 (0.06)
Mucosa				
Proteobacteria	decrease	6.4 ± 3.0	3.1 ± 2.3	0.03 (0.4)

Data are presented as mean ± SD. Wilcoxon rank sum test comparing No Probiotic with Probiotic groups for each sample type. Only p values ≤0.05 are shown. Bold values indicate FDR≤0.05. FDR, false discovery rate (Benjamini-Hochberg).