Supplementary File

Table S1. The estimated sequences in the control and treatment samples.

Sample Code	Input	Filtered	Input passed filter (%)	Denoised	Merged	Input merged (%)	Non-chimeric	Input non-chimeric (%)
Control								
SK11-1-pre	121964	45938	37.67	45832	45736	37.5	3912	3.21
SK12-1-pre	60050	23604	39.31	23481	23382	38.94	5800	9.66
SK16-1-pre	747785	275693	36.87	275051	272184	36.4	73782	9.87
SK19-1-pre	105407	36269	34.41	36086	35821	33.98	4502	4.27
SK9-1-pre	74450	26826	36.03	25109	22065	29.64	8785	11.8
SK11-1-post	76319	30849	40.42	30803	30710	40.24	8004	10.49
SK12-1-post	37546	13263	35.32	13076	12722	33.88	3868	10.3
SK16-1-post	35371	13096	37.02	12739	12124	34.28	2905	8.21
SK19-1-post	662518	241145	36.4	240707	240389	36.28	21824	3.29
SK9-1-post	436349	154647	35.44	154409	154066	35.31	37347	8.56
Treatment								
SK10-1-pre	325571	121197	37.23	120896	120224	36.93	18730	5.75
SK14-1-pre	34916	14121	40.44	14061	13872	39.73	2399	6.87
SK2-1-pre	375629	141506	37.67	141377	141032	37.55	25724	6.85
SK6-1-pre	136535	43500	31.86	43353	43111	31.58	4701	3.44
SK8-1-pre	173163	62751	36.24	62702	62606	36.15	14145	8.17
SK10-1-post	102889	38050	36.98	36588	34201	33.24	11901	11.57
SK14-1-post	42456	15704	36.99	15549	15452	36.4	4482	10.56
SK2-1-post	48527	19482	40.15	19468	19437	40.05	5430	11.19
SK6-1-post	81444	27892	34.25	24640	16355	20.08	12383	15.2
SK8-1-post	97459	34870	35.78	33928	32144	32.98	8997	9.23

Table S2. The statistical differences in the phylum, genus, and species level within the Cpre and Cpost samples (directions based on the RF%).

Taxonomy	Cpre (RF%)	Cpost (RF%)	Cpost Vs. Cpre (*p*-value)	Directions in Cpost samples
Phylum				
Proteobacteria	56.40	58.63	0.8927	Increased#
Firmicutes	11.22	14.85	0.5002	Increased#
Actinobacteriota	27.59	18.74	0.6858	Decreased#
Cyanobacteria	0.46	2.00	0.3452	Increased#
Planctomycetota	1.89	2.50	0.8927	Increased#
Bacteroidota	0.42	3.27	0.1736	Increased#
Verrucomicrobiota	2.02	0.02	0.2763	Decreased#
Genus				
Staphylococcus	15.53	15.85	0.5002	Increased#
Escherichia-Shigella	3.71	7.00	0.6858	Increased#
Cutibacterium	7.45	11.68	0.5002	Increased#
Lactobacillus	5.62	15.68	0.5002	Increased#
Sphingomonas	3.29	4.78	0.5862	Increased#
Enhydrobacter	7.26	5.32	0.6858	Decreased#
Micrococcus	13.71	8.02	1.0000	Decreased#
Corynebacterium	5.78	15.34	0.2249	Decreased#
Bacillus	14.04	1.76	0.6858	Decreased#
Gemmata	1.71	0	0.0897	Decreased#
Stenotrophomonas	20.30	7.94	0.4142	Decreased#
Kocuria	0.70	1.25	0.7855	Increased#
Streptococcus	0	3.71	0.0897	Increased#
Species				
E-Shigella sp.	4.65	7.06	0.6858	Increased#
C. tuberculostearicum	0.80	3.98	0.1736	Increased#

Note: Wilcoxon signed rank test $P \leq 0.05$; # - Statistically insignificant.

Table S3. The statistical differences in the phylum, genus, and species level within the Tpre and Tpost samples (directions based on the RF%).

Taxonomy	Tpre (RF%)	Tpost (RF%)	Post Vs. Pre (*p*-value)	Directions in Tpost samples
Phylum				
Proteobacteria	63.73	51.71	0.5002	Decreased#
Actinobacteriota	25.18	9.74	0.0796	Decreased#
Cyanobacteria	0.92	0.32	0.5862	Decreased#
Firmicutes	6.66	7.65	0.5002	Increased#
Acidobacteriota	0.61	2.88	0.2763	Increased#
Bacteroidota	1.25	3.73	0.5862	Increased#
Planctomycetota	0.22	6.54	0.0568	Increased#
Verrucomicrobiota	1.17	2.33	0.3961	Increased#
Desulfobacterota	0	2.98	0.0897	ND
Myxococcota	0.09	0.48	0.2763	Increased#
Chloroflexi	0.01	7.25	0.0568	Increased#
Armatimonadota	0	0.76	0.0897	ND
Gemmatimonadota	0	0.56	0.0897	ND
Spirochaetota	0	1.57	0.0897	ND
Patescibacteria	0.03	0.88	0.1736	Increased#
Nitrospirota	0	0.36	0.0897	ND
Genus				
Ochrobactrum	0.01	38.43	0.1736	Increased#
Micrococcus	4.55	0	0.0568	Uprooted#
Enhydrobacter	3.07	0	0.0568	Uprooted#
Cutibacterium	7.74	0	0.0431	Uprooted*
Xanthomonas	14.77	0	0.0568	Uprooted#
Corynebacterium	10.63	0.02	0.0431	Decreased*
Staphylococcus	2.98	0	0.0568	Uprooted#
Mycobacterium	0.62	2.33	0.3452	Increased#
Sphingomonas	1.37	0.23	0.0568	Decreased#
Roseomonas	1.11	0	0.0897	Uprooted#
Paracoccus	0.38	0	0.0568	Uprooted#
Finegoldia	0.69	0	0.0568	Uprooted#
Kocuria	0.58	0	0.0897	Uprooted#
Microbacterium	0.62	0.52	0.7773	Decreased#
Chryseobacterium	1.24	0	0.0897	Uprooted#
Haemophilus	0.30	0	0.0897	Uprooted#
Acinetobacter	0.67	0	0.0431	Uprooted*
Allorhizobium	0.58	0	0.0897	Uprooted#
Pla1_lineage	0	1.32	0.0897	ND
Streptomyces	0	1.83	0.0897	ND
JG30-KF-CM45	0	2.59%	0.0897	ND
Pseudomonas	0.76	0.71	0.7773	Decreased#
Neochlamydia	0	1.84	0.0897	ND
WD2101	0	3.25	0.0568	ND
Treponema	0	1.39	0.0897	ND
Stenotrophomonas	0.07	0.62	0.0897	Increased#
Pseudogracilibacillus	0	0.45	0.0897	ND
Bacillus	0.06	4.35	0.1736	Increased#

Ruminiclostridium	0	1.48	0.0897	ND
67-14	0	2.97	0.0568	ND
Lysinibacillus	0	0.52	0.0897	ND
Paenibacillus	0.02	0.79	0.0568	Increased[#]
Aquisphaera	0	0.82	0.0897	ND
Bryobacter	0	0.99	0.0897	ND
IMCC26256	0	0.65	0.0897	ND
Nitrospira	0	0.83	0.0897	ND
Mesorhizobium	0	1.10	0.0897	ND
TK10	0	0.50	0.0897	ND
Legionella	0	0.66	0.0897	ND
SJA-28	0	0.63	0.0897	ND
SC-I-84	0	0.42	0.0897	ND
Anaeromyxobacter	0	1.00	0.0897	ND
Species				
C. tuberculostearicum	4.35	0	0.0897	Uprooted[#]
S. acidaminiphila	0	0.70	0.0897	ND

Note: * - Statistically significant - Wilcoxon signed rank test $P \leq 0.05$; [#] - Statistically insignificant; ND - Newly developed.

Table S4. The statistical differences in the phylum, genus, and species level between control and treatment groups.

Taxonomy	**C_{diff} Vs. T_{diff} (*p*-value)**
Phylum	
Proteobacteria	0.9168[#]
Firmicutes	0.6015[#]
Actinobacteriota	0.6015[#]
Cyanobacteria	0.3472[#]
Planctomycetota	0.1172[#]
Bacteroidota	0.6752[#]
Proteobacteria	0.9168[#]
Firmicutes	0.6015[#]
Genus	
Bacillus	0.3472[#]

Note: Wilcoxon signed rank test $P \leq 0.05$; [#] - Statistically not significant