

Table S1. The effect of SCFP on Bacterial abundance in each level in rumen liquid fraction sampled on day 28 (RL28).

Item/Index ¹	CON	SCFP1	SCFP2		<i>P</i> value	
Phylum				SEM		
Order	Mean (%)			(%)	CON vs SCFP	SCFP 1 vs 2
Family						
Genus						
<i>Actinobacteria</i>	5.78	13.91	18.87	4.76	0.18	0.90
<i>Coriobacteriales</i>	3.74	12.53	18.35	4.10	0.08	0.68
<i>Coriobacteriaceae</i>	3.74	12.80	18.35	4.10	0.08	0.68
<i>Bifidobacteriales</i>	2.00	1.16	0.41	1.26	0.80	1.00
<i>Bifidobacteriaceae</i>	2.00	0.93	0.41	1.26	0.80	1.00
<i>Bifidobacterium</i>	1.25	0.80	0.41	0.87	1.00	1.00
<i>Bacteroidetes</i>	42.90	17.36	5.57	6.06	<0.001	0.36
<i>Bacteroidales</i>	42.84	19.92	5.50	6.03	0.004	0.36
<i>Prevotellaceae</i>	32.72	9.08	1.67	4.57	0.002	0.50
<i>Prevotella</i>	32.72	9.08	1.67	4.57	0.002	0.50
<i>[Paraprevotellaceae]</i>	0.80	0.18	0.07	0.28	0.16	1.00
<i>S24-7</i>	4.68	1.32	1.12	1.76	0.26	1.00
<i>Cyanobacteria</i>	0.27	0.61	0.63	0.18	0.26	1.00
<i>Firmicutes</i>	42.63	65.18	69.22	6.94	0.02	1.00
<i>Clostridiales</i>	39.89	54.12	64.47	5.32	0.02	0.52
<i>Lachnospiraceae</i>	19.22	31.69	48.81	6.95	0.06	0.20
<i>Butyrivibrio</i>	6.74	22.97	45.14	6.93	0.01	0.08
<i>Shuttleworthia</i>	4.59	0.19	0.13	1.32	0.38	1.00
<i>Roseburia</i>	0.35	0.11	0.07	0.15	0.40	1.00
<i>Ruminococcaceae</i>	3.33	8.05	5.01	3.10	0.81	0.96
<i>Ruminococcus</i>	0.85	1.29	1.17	0.59	1.00	1.00
<i>Oscillospira</i>	0.43	1.39	0.39	0.69	1.00	0.62
<i>Veillonellaceae</i>	5.15	1.30	1.49	2.31	0.42	1.00
<i>Dialister</i>	1.53	0.25	0.77	0.86	0.70	1.00
<i>Megasphaera</i>	2.03	0.16	0.06	1.03	0.30	1.00
<i>Succiniclasicum</i>	0.23	0.29	0.09	0.14	1.00	0.66
<i>Mogibacteriaceae</i>	0.10	0.34	0.75	0.14	0.06	0.12
<i>Mogibacterium</i>	0.02	0.24	0.60	0.13	0.06	0.12
<i>Erysipelotrichales</i>	2.69	8.22	4.52	2.85	0.50	0.50
<i>Erysipelotrichaceae</i>	2.69	9.17	4.52	2.85	0.50	0.50
<i>Bulleidia</i>	2.51	8.85	4.20	2.85	0.52	0.50

<i>Proteobacteria</i>	7.04	1.49	2.01	2.84	0.30	1.00
<i>Aeromonadales</i>	6.46	0.06	0.80	2.84	0.22	1.00
<i>Succinivibrionaceae</i>	6.46	0.06	0.80	2.84	0.22	1.00
<i>Succinivibrio</i>	6.43	0.04	0.73	2.83	0.22	1.00
<i>Pseudomonadales</i>	0.09	0.23	0.43	0.14	0.42	0.58
<i>Moraxellaceae</i>	0.08	0.21	0.43	0.14	0.42	0.56
<i>Spirochaetes</i>	0.60	0.02	0.02	0.17	0.04	1.00
<i>Sphaerochaetales</i>	0.60	0.02	0.02	0.17	0.04	1.00
<i>Sphaerochaetaceae</i>	0.60	0.02	0.02	0.17	0.04	1.00
<i>Sphaerochaeta</i>	0.60	0.02	0.02	0.17	0.04	1.00
<i>Tenericutes</i>	0.37	0.56	3.58	1.23	0.56	0.20
<i>RF39</i>	0.37	0.61	3.58	1.23	0.56	0.20

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 13 samples were used in RL28 analysis (CON: 4 samples, SCFP1: 5 samples, SCFP2: 4 samples).

Table S2. The effect of SCFP on Bacterial abundance in each level in rumen liquid fraction sampled on day 56 (RL56).

Item/Index ¹	CON	SCFP1	SCFP2	SEM	P value	
Phylum	Mean (%)			(%)	CON vs SCFP	SCFP 1 vs 2
Order						
Family						
Genus						
<i>Actinobacteria</i>	4.05	6.15	5.40	2.56	1.00	1.00
<i>Coriobacteriales</i>	4.03	6.00	5.32	2.55	1.00	1.00
<i>Coriobacteriaceae</i>	4.03	6.00	5.32	2.55	1.00	1.00
<i>Bacteroidetes</i>	44.73	29.34	43.96	9.77	1.00	0.62
<i>Bacteroidales</i>	44.73	29.34	43.96	9.77	1.00	0.62
<i>Prevotellaceae</i>	43.83	27.81	42.56	9.51	1.00	0.48
<i>Prevotella</i>	43.83	27.81	36.56	6.93	0.40	0.78
<i>S24-7</i>	0.30	0.14	0.30	0.15	1.00	0.92
<i>p-2534-18B5</i>	0.49	0.12	0.30	0.14	0.24	0.74
<i>Cyanobacteria</i>	0.33	0.37	0.22	0.14	1.00	0.90
<i>YS2</i>	0.27	0.32	0.10	0.13	1.00	0.58
<i>Fibrobacteres</i>	0.01	0.00	0.24	0.14	1.00	0.48
<i>Fibrobacterales</i>	0.01	0.00	0.24	0.14	1.00	0.48
<i>Fibrobacteraceae</i>	0.01	0.00	0.24	0.14	1.00	0.48
<i>Fibrobacter</i>	0.01	0.00	0.24	0.14	1.00	0.48
<i>Firmicutes</i>	43.27	57.20	48.06	9.69	0.90	1.00
<i>Clostridiales</i>	41.87	56.26	47.28	9.37	0.82	1.00
<i>Lachnospiraceae</i>	24.19	32.79	23.87	7.22	1.00	0.98
<i>Butyrivibrio</i>	10.74	20.93	20.84	4.62	0.20	1.00
<i>Shuttleworthia</i>	0.47	0.67	2.90	1.26	0.82	0.46
<i>Veillonellaceae</i>	7.47	7.92	7.34	2.12	1.00	1.00
<i>Dialister</i>	2.31	2.93	2.06	1.00	1.00	1.00
<i>Megasphaera</i>	0.14	0.85	0.25	0.23	0.34	0.20
<i>Succiniclasticum</i>	1.26	0.50	0.60	0.46	0.46	1.00
<i>Ruminococcaceae</i>	1.09	0.50	0.72	0.22	0.22	0.98
<i>Erysipelotrichales</i>	1.26	0.89	0.76	0.46	0.90	1.00
<i>Erysipelotrichaceae</i>	1.26	0.89	0.76	0.46	0.90	1.00
<i>Bulleidia</i>	0.61	0.61	0.56	0.24	1.00	1.00
<i>Sharpea</i>	0.62	0.22	0.12	0.32	0.56	1.00
<i>Proteobacteria</i>	6.80	6.33	1.52	3.31	0.98	0.64
<i>Aeromonadales</i>	5.57	5.81	0.96	3.38	1.00	0.66
<i>Succinivibrionaceae</i>	5.57	5.80	0.96	3.38	1.00	0.66
<i>Succinivibrio</i>	1.53	3.51	0.38	2.03	1.00	0.60

<i>Desulfovibrionales</i>	1.07	0.43	0.50	0.14	0.02	1.00
<i>Desulfovibrionaceae</i>	1.07	0.43	0.50	0.14	0.02	1.00
<i>Desulfovibrio</i>	1.07	0.43	0.47	0.15	0.02	1.00
<i>Tenericutes</i>	0.46	0.08	0.16	0.23	0.50	1.00
<i>RF39</i>	0.46	0.08	0.16	0.23	0.50	1.00

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 15 samples were used in RL56 analysis (CON: 5 samples, SCFP1: 5 samples, SCFP2: 5 samples).

Table S3. The effect of SCFP on Bacterial abundance in each level in rumen solid fraction sampled on day 56 (RS56).

Item/Index ¹	CON	SCFP1	SCFP2	SEM	P value	
Phylum	Mean (%)			(%)	CON vs SCFP	SCFP 1 vs 2
Order						
Family						
Genus						
Actinobacteria	4.27	4.63	2.10	0.89	0.84	0.14
Coriobacteriales	4.27	4.60	2.09	0.89	0.84	0.14
Coriobacteriaceae	4.27	4.60	2.09	0.89	0.82	0.14
Bacteroidetes	44.26	40.90	47.26	5.01	1.00	0.74
Bacteroidales	44.26	40.89	47.26	5.01	1.00	0.78
Prevotellaceae	40.29	38.00	42.59	5.17	1.00	1.00
Prevotella	40.29	38.00	42.59	5.17	1.00	1.00
S24-7	1.23	0.47	0.46	0.35	0.20	1.00
Fibrobacteres	0.00	0.00	0.30	0.17	0.98	0.48
Fibrobacterales	0.00	0.00	0.30	0.17	0.98	0.48
Fibrobacteraceae	0.00	0.00	0.30	0.17	0.98	0.48
Fibrobacter	0.00	0.00	0.30	0.17	0.98	0.48
Firmicutes	50.02	52.52	48.54	4.93	1.00	1.00
Clostridiales	49.41	52.01	48.06	4.92	1.00	1.00
Lachnospiraceae	29.43	24.68	20.47	3.35	0.24	1.00
Butyrivibrio	19.49	14.45	12.44	3.16	0.28	1.00
Succinoclasticum	3.75	2.30	3.24	1.51	1.00	1.00
Veillonellaceae	12.59	16.34	21.10	3.17	0.28	0.62
Dialister	6.48	5.06	6.43	2.01	1.00	1.00
Acidaminococcus	0.50	0.76	0.86	0.22	0.54	1.00
Megasphaera	0.13	0.69	0.34	0.24	0.44	0.68
Shuttleworthia	0.12	2.03	0.10	0.77	0.66	0.20
Mitsuokella	0.09	0.29	0.20	0.11	0.54	1.00
Proteobacteria	0.84	1.37	1.22	0.68	1.00	1.00
Aeromonadales	0.51	1.09	1.03	0.68	1.00	1.00
Succinivibrionaceae	0.50	1.09	1.02	0.68	1.00	1.00
Succinivibrio	0.16	0.95	0.72	0.62	1.00	1.00

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 15 samples were used in RS56 analysis (CON: 5 samples, SCFP1: 5 samples, SCFP2: 5 samples).

Table S4. The effect of SCFP on Bacterial abundance in each level in duodenal content sampled on day 56 (DC56).

Item/Index ¹	CON	SCFP1	SCFP2		P value	
Phylum					CON	SCFP
Order					vs	1 vs 2
Family	Mean (%)				SCFP	
Genus						
Actinobacteria	5.88	4.34	5.29	3.20	1.00	1.00
Coriobacteriales	5.66	4.24	5.16	3.14	1.00	1.00
Coriobacteriaceae	5.66	4.24	5.16	3.14	1.00	1.00
Bacteroidetes	39.27	51.82	42.45	10.30	1.00	1.00
Bacteroidales	39.25	51.82	42.44	10.31	1.00	1.00
Prevotellaceae	37.85	51.13	41.53	10.40	1.00	1.00
Prevotella	37.85	51.13	41.53	10.40	1.00	1.00
S24-7	0.76	0.17	0.17	0.17	0.02	1.00
Cyanobacteria	0.53	0.68	0.70	0.18	1.00	1.00
YS2	0.38	0.48	0.30	0.15	1.00	0.84
Streptophyta	0.15	0.20	0.40	0.10	0.50	0.32
Firmicutes	47.86	34.74	44.94	8.37	0.90	0.82
Clostridiales	43.50	33.27	41.92	7.22	1.00	0.82
Lachnospiraceae	14.25	12.41	14.96	2.43	1.00	0.94
Butyrivibrio	5.55	5.43	6.05	1.49	1.00	1.00
Shuttleworthia	0.97	3.88	3.87	2.38	0.68	1.00
Veillonellaceae	12.26	11.71	13.13	3.28	1.00	1.00
Dialister	5.12	4.96	3.86	1.78	1.00	1.00
Megasphaera	1.59	2.02	4.45	2.19	1.00	0.90
Succiniclasicum	1.59	0.57	0.32	0.60	0.30	1.00
Acidaminococcus	0.98	0.57	0.73	0.25	0.62	1.00
Mitsuokella	0.28	0.27	0.38	0.17	1.00	1.00
Ruminococcaceae	6.61	1.41	3.63	2.28	0.34	1.00
Ruminococcus	0.51	0.05	0.14	0.17	0.14	1.00
Oscillospira	0.68	0.10	0.21	0.23	0.16	1.00
Mogibacteriaceae	0.62	0.12	0.31	0.25	0.42	1.00
Erysipelotrichales	4.06	1.42	2.95	1.54	0.68	1.00
Erysipelotrichaceae	4.06	1.42	2.95	1.54	0.68	1.00
Bulleidia	1.65	0.74	2.20	1.03	1.00	0.68
Sharpea	2.23	0.61	0.57	0.77	0.22	1.00
Proteobacteria	5.62	7.94	5.51	1.61	1.00	0.62
Aeromonadales	3.67	7.13	4.68	1.68	0.60	0.64
Succinivibrionaceae	3.66	7.13	4.67	1.68	0.60	0.64
Succinivibrio	0.72	2.51	0.83	0.78	0.68	0.32

<i>Desulfovibrionales</i>	0.77	0.39	0.49	0.23	0.54	1.00
<i>Desulfovibrionaceae</i>	0.77	0.39	0.49	0.23	0.54	1.00
<i>Desulfovibrio</i>	0.75	0.39	0.48	0.23	0.60	1.00
<i>Pseudomonadales</i>	0.38	0.05	0.03	0.10	0.04	1.00
<i>Tenericutes</i>	0.17	0.09	0.69	0.39	1.00	0.60
<i>RF39</i>	0.16	0.09	0.68	0.39	1.00	0.60
<i>Acidobacteria</i>	0.001	0	0	<0.001	0.08	1.00
<i>Chloroflexi</i>	0.004	0.001	0.001	0.001	0.16	1.00
<i>Deferribacteres</i>	0.002	0	0	<0.001	0.20	1.00
<i>Elusimicrobia</i>	0.002	0.000	0.001	<0.001	0.24	1.00
<i>Nitrospirae</i>	0.004	0	0	0.00	0.06	1.00
<i>Spirochaetes</i>	0.02	0.01	0.01	0.004	0.10	1.00
<i>TM7</i>	0.017	0.002	0.004	0.01	0.20	1.00

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 15 samples were used in DC56 analysis (CON: 5 samples, SCFP1: 5 samples, SCFP2: 5 samples).

Table S5. The effect of SCFP on Bacterial abundance in each level in cecal content sampled on day 56 (CC56).

Item/Index ¹	CON	SCFP1	SCFP2		P value	
Phylum				SEM		
Order					CON	SCFP
Family	Mean (%)			(%)	vs	1 vs 2
Genus					SCFP	
<i>Actinobacteria</i>	5.14	8.05	3.55	2.17	1.00	0.34
<i>Coriobacteriales</i>	5.04	7.99	3.50	2.17	1.00	0.34
<i>Coriobacteriaceae</i>	5.04	7.99	3.50	2.17	1.00	1.00
<i>Bacteroidetes</i>	21.43	22.21	23.31	3.92	1.00	1.00
<i>Bacteroidales</i>	21.43	22.21	23.31	3.92	1.00	1.00
<i>S24-7</i>	11.52	8.51	8.36	2.98	0.82	1.00
<i>Prevotellaceae</i>	1.51	2.66	2.36	0.91	0.78	1.00
<i>Prevotella</i>	1.45	2.53	2.27	0.84	0.76	1.00
<i>Bacteroidaceae</i>	1.03	1.39	1.88	0.42	0.52	0.84
<i>Bacteroides</i>	1.02	1.38	1.84	0.41	0.54	0.90
<i>Porphyromonadaceae</i>	0.77	0.84	1.04	0.24	1.00	1.00
<i>Parabacteroides</i>	0.77	0.84	1.04	0.24	1.00	1.00
<i>[Odoribacteraceae]</i>	0.22	0.28	0.45	0.11	0.62	0.58
<i>Odoribacter</i>	0.19	0.20	0.42	0.11	0.80	0.34
<i>[Paraprevotellaceae]</i>	0.31	0.60	0.53	0.13	0.30	1.00
<i>Firmicutes</i>	65.25	64.16	66.63	3.98	1.00	1.00
<i>Clostridiales</i>	61.84	63.26	63.97	3.66	1.00	1.00
<i>Ruminococcaceae</i>	26.41	34.76	32.25	3.50	0.24	1.00
<i>Ruminococcus</i>	4.15	12.32	7.85	3.26	0.32	0.70
<i>Oscillospira</i>	0.57	1.02	1.23	0.17	0.04	0.80
<i>Faecalibacterium</i>	0.67	0.52	1.26	0.63	1.00	0.84
<i>Lachnospiraceae</i>	12.35	8.59	8.75	1.30	0.08	1.00
<i>Dorea</i>	1.90	1.98	1.66	0.78	1.00	1.00
<i>Blautia</i>	1.84	0.76	0.79	0.44	0.14	01.00
<i>Coproccoccus</i>	0.25	0.63	0.45	0.23	0.60	1.00
<i>Clostridiaceae</i>	2.10	1.72	1.88	0.48	1.00	1.00
<i>Clostridium</i>	1.23	0.77	0.87	0.29	0.54	1.00
<i>Mogibacteriaceae</i>	1.34	0.43	0.46	0.29	0.06	1.00
<i>Mogibacterium</i>	0.75	0.22	0.24	0.14	0.02	1.00
<i>Veillonellaceae</i>	0.77	0.31	0.42	0.42	0.88	1.00
<i>Phascolarctobacterium</i>	0.38	0.21	0.40	0.24	1.00	1.00
<i>Anaerovibrio</i>	0.25	0.05	0.01	0.13	0.38	1.00
<i>Erysipelotrichales</i>	2.39	0.86	2.66	0.86	1.00	0.34
<i>Erysipelotrichaceae</i>	2.39	0.86	2.66	0.86	1.00	0.34
<i>p-75-a5</i>	1.46	0.54	2.19	0.71	1.00	0.26

<i>Lactobacillales</i>	0.99	0.01	0.001	0.55	0.34	1.00
<i>Streptococcaceae</i>	0.63	0.004	<0.001	0.35	0.36	1.00
<i>Streptococcus</i>	0.62	0.004	<0.001	0.35	0.36	1.00
<i>Lactobacillaceae</i>	0.37	0.01	0.001	0.19	0.30	1.00
<i>Lactobacillus</i>	0.37	0.005	0.001	0.19	0.30	1.00
<i>Tenericutes</i>	7.43	4.98	5.59	1.27	0.38	1.00
<i>RF39</i>	7.38	4.90	5.51	1.27	0.38	1.00
<i>Chloroflexi</i>	0	0.001	0.001	<0.001	0.26	1.00
<i>Elusimicrobia</i>	0.01	0.01	0.00	0.003	1.00	0.14
<i>Planctomycetes</i>	0.004	0.001	0	0.002	0.20	1.00
<i>Spirochaetes</i>	0.03	0.01	0.04	0.01	1.00	0.50

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 15 samples were used in CC56 analysis (CON: 5 samples, SCFP1: 5 samples, SCFP2: 5 samples).

Table S6. The effect of SCFP on Bacterial abundance in each level in rectal content sampled on day 56 (RC56).

Item/Index ¹	CON	SCFP1	SCFP2	SEM	P value	
Phylum	Mean (%)			SEM (%)	CON	SCFP
Order					vs	1 vs 2
Family					SCFP	
Genus						
<i>Actinobacteria</i>	5.98	6.32	2.83	1.73	1.00	0.36
<i>Coriobacteriales</i>	5.87	6.26	2.79	1.72	1.00	0.36
<i>Coriobacteriaceae</i>	5.87	6.26	2.79	1.72	1.00	0.36
<i>Bacteroidetes</i>	22.75	20.99	26.23	4.50	1.00	0.86
<i>Bacteroidales</i>	22.74	20.99	26.22	4.50	1.00	0.86
<i>S24-7</i>	12.21	6.86	9.49	2.86	0.54	1.00
<i>Prevotellaceae</i>	1.71	2.86	2.95	1.01	0.70	0.95
<i>Prevotella</i>	1.63	2.69	2.83	0.94	0.70	1.00
<i>Bacteroidaceae</i>	0.83	1.31	1.81	0.35	0.24	0.68
<i>Bacteroides</i>	0.83	1.31	1.78	0.35	0.24	0.72
<i>Porphyromonadaceae</i>	0.76	0.79	0.96	0.20	1.00	1.00
<i>Parabacteroides</i>	0.76	0.79	0.96	0.20	1.00	1.00
[<i>Paraprevotellaceae</i>]	0.32	0.64	0.52	0.13	0.24	1.00
<i>Firmicutes</i>	63.57	67.58	65.88	4.29	1.00	1.00
<i>Clostridiales</i>	60.27	66.78	63.65	4.06	1.00	1.00
<i>Ruminococcaceae</i>	26.05	38.15	33.48	4.06	0.14	0.86
<i>Ruminococcus</i>	3.46	12.60	8.52	2.97	0.14	0.70
<i>Oscillospira</i>	0.59	1.23	1.29	0.17	0.02	1.00
<i>Faecalibacterium</i>	0.27	0.46	1.40	0.63	0.82	0.62
<i>Lachnospiraceae</i>	13.09	9.14	9.31	1.22	0.04	1.00
<i>Dorea</i>	1.71	2.36	1.63	0.77	1.00	1.00
<i>Blautia</i>	1.25	0.80	0.79	0.29	0.48	1.00
<i>Coproccoccus</i>	0.37	0.54	0.57	0.16	0.68	1.00
<i>Clostridiaceae</i>	2.00	2.00	2.16	0.58	1.00	1.00
<i>Clostridium</i>	0.95	0.72	0.92	0.24	1.00	1.00
<i>Mogibacteriaceae</i>	1.31	0.45	0.35	0.24	0.02	1.00
<i>Mogibacterium</i>	0.67	0.19	0.13	0.10	0.002	1.00
<i>Veillonellaceae</i>	0.07	0.29	0.45	0.17	0.32	0.98
<i>Erysipelotrichales</i>	2.27	0.74	2.22	0.80	0.88	0.44
<i>Erysipelotrichaceae</i>	2.27	0.74	2.22	0.80	0.88	0.44
<i>p-75-a5</i>	1.38	0.44	1.81	0.67	1.00	0.34
<i>Lactobacillales</i>	1.00	0.02	0.003	0.52	0.30	1.00
<i>Streptococcaceae</i>	0.61	0.01	0.001	0.33	0.30	1.00
<i>Streptococcus</i>	0.61	0.005	0.001	0.32	0.30	1.00

<i>Lactobacillaceae</i>	0.38	0.01	0.002	0.19	0.28	1.00
<i>Lactobacillus</i>	0.38	0.01	0.002	0.19	0.28	1.00
<i>Tenericutes</i>	6.85	4.48	4.18	1.18	0.22	1.00
<i>RF39</i>	6.80	4.41	4.11	1.18	0.20	1.00
<i>Cyanobacteria</i>	0.21	0.15	0.08	0.04	0.16	0.50
<i>Elusimicrobia</i>	0.01	0.02	0.003	0.002	0.88	0.02
<i>Planctomycetes</i>	0.002	0.001	0	<0.001	0.42	0.48
<i>Proteobacteria</i>	0.31	0.14	0.20	0.10	0.56	1.00
<i>Spirochaetes</i>	0.03	0.01	0.05	0.02	1.00	0.14
<i>TM7</i>	0.001	0	0	<0.001	0.08	1.00

¹Only predominant bacteria (abundance $\geq 1\%$ in at least one sample) were compared in Phylum, Order, Family and genus level. 15 samples were used in RC56 analysis (CON: 5 samples, SCFP1: 5 samples, SCFP2: 5 samples).

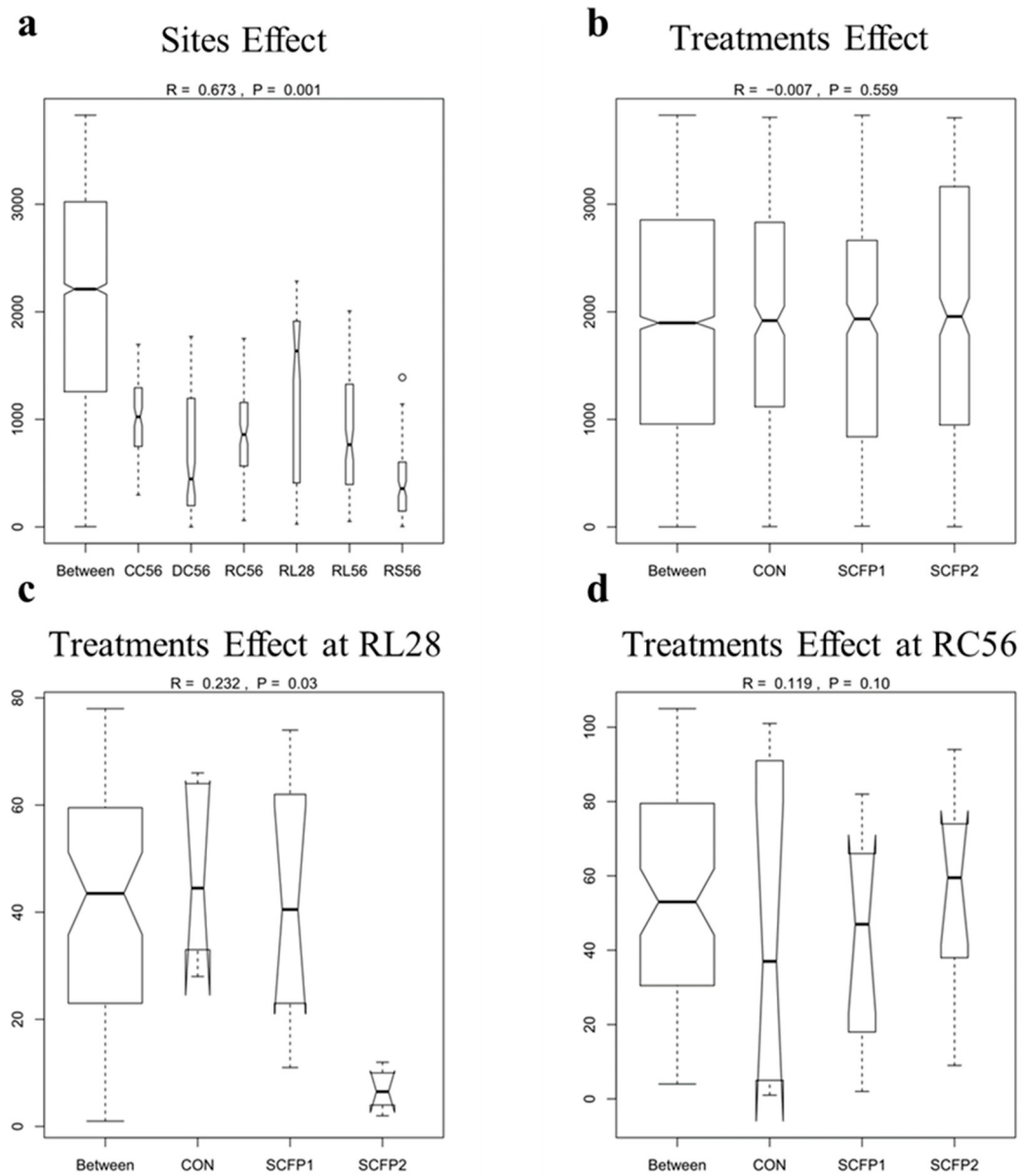


Figure S1. ANOSIM analysis were performed at sites (a) and treatments in GITs (b), RL28. (c), and RC56 (d).

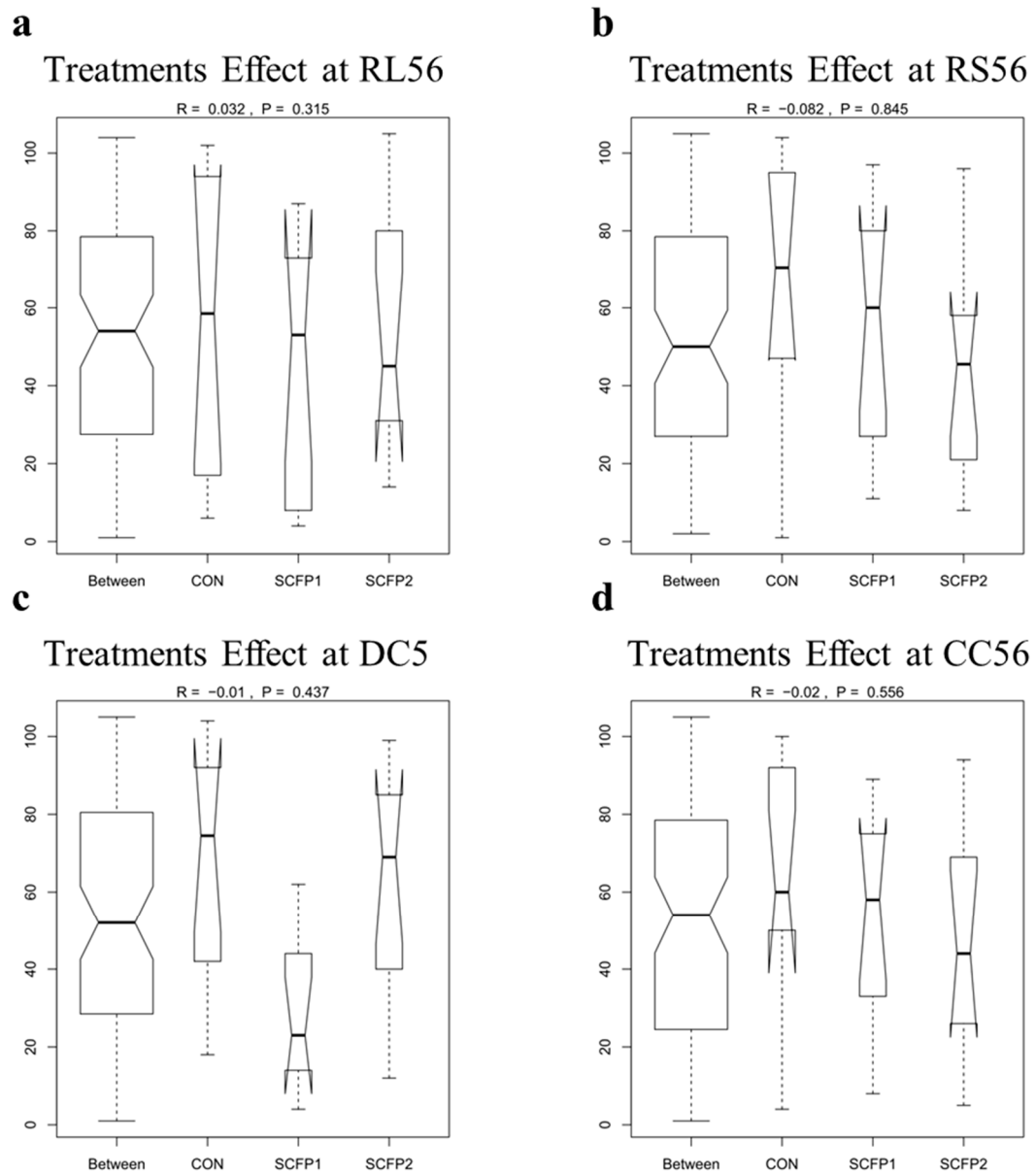


Figure S2. ANOSIM analysis were performed among treatments in RL56 (a), RS56 (b), DC56 (c) and CC56 (d).

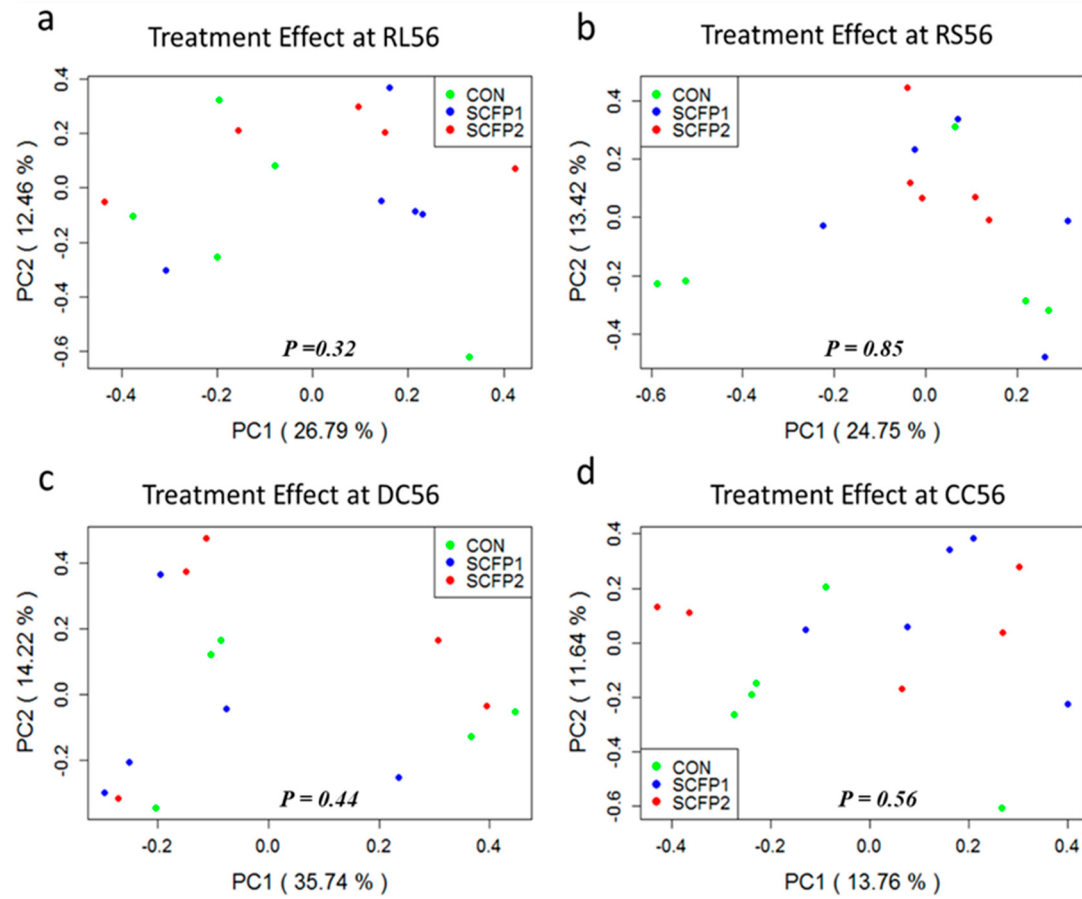


Figure S3. Separation of samples based on phylogenetic information using PCoA plot. (a), treatment separation in RL56. (b), treatment separation in RS56. (c), treatment separation in DC56. (d), treatment separation in CC56.