

**Table S1** Clinical characteristics of the patients and control

Characteristics	BT group (n=23)	CT group (n=19)	Healthy control (n=23)	P
Age (years)	11.2±1.7	11.2±2.1	8.7±2.0	<0.001***
Sex				
Male	21	15	13	0.02
Female	2	4	10	
BMI (kg/m <sup>2</sup> )	18.5±5.8	17.5±2.9	17.2±2.3	0.98
Eradication rate	90% (18/20)	93.3% (14/15)		
Ulcer heal rate	90% (18/20)	73.7% (14/19)		
Side effects				
Diarrhea	1	1		
Dark stool	5	0		
Nausea or vomit	0	3		
Rash	0	1		
Anorexia	0	1		
Headache	0	1		

Continuous data are presented as the mean ± standard deviation and categorical data as n (%). \*, 0.01≤P<0.05; \*\*\*, P<0.001. BMI, body mass index.

**Table S2** Alpha diversity comparison between baseline (week 0) and end of eradication therapy (week 2), baseline and 6 week post-eradication (week 6), and baseline and 1 year post-eradication (week 52) within each group

Alpha diversity	Week 0	Week 2	Week 6	Week 52	P value		
					week 0 vs. week 2	week 0 vs. week 6	week 0 vs. week 52
BT group							
Shannon	3.48±0.54	2.09±0.68	2.92±0.68	3.17±0.85	<0.001***	<0.001***	0.15
Chao 1	392.8±116.5	165.2±102.9	288.4±102.0	372.4±146.9	<0.001***	<0.001***	0.26
CT group							
Shannon	3.30±0.67	1.96±0.78	3.04±0.69	3.04±0.76	<0.001***	0.26	0.46
Chao 1	361.0±113.3	144.1±107.8	290.2±109.8	335.3±92.6	<0.001***	0.01*	0.46

Continuous data are presented as the mean ± standard deviation. \*, 0.01≤P<0.05; \*\*\*, P<0.001. BT, bismuth quadruple therapy; CT, concomitant therapy.

**Table S3** Comparison of the relative abundance of phyla between baseline (week 0) and end of eradication therapy (week 2), baseline and 6 week post-eradication (week 6), and baseline and 1 year post-eradication (week 52) within each group

Phylum	Mean relative abundance (%) ± SD (%)				P value		
	Week 0	Week 2	Week 6	Week 52	Week 0 vs. Week 2	Week 0 vs. Week 6	Week 0 vs. Week 52
BT group							
p__Firmicutes	47.37±18.33	19.42±18.60	42.72±19.24	39.55±18.45	<0.001***	0.45	0.21
p__Bacteroidetes	45.90±19.62	10.20±19.33	47.14±25.12	53.91±19.25	<0.001***	0.80	0.19
p__Proteobacteria	2.55±2.44	67.24±32.78	5.85±6.17	4.26±4.18	<0.001***	0.02*	0.10
p__Actinobacteria	3.21±5.06	2.88±7.67	2.52±5.48	1.61±1.21	0.03*	0.19	0.76
p__Fusobacteria	0.28±0.80	0.14±0.55	1.40±4.02	0.05±0.09	0.048*	0.73	1.00
CT group							
p__Firmicutes	44.69±18.84	17.25±14.43	41.19±19.43	38.47±17.53	<0.001***	0.50	0.39
p__Bacteroidetes	47.41±18.97	22.02±29.82	50.55±21.95	55.11±20.07	0.02*	0.40	0.35
p__Proteobacteria	2.60±2.87	57.83±34.19	5.40±6.30	2.20±2.99	<0.001***	0.11	0.18
p__Actinobacteria	2.50±2.68	2.73±5.74	1.55±3.00	3.12±4.53	0.04*	0.01*	0.91
p__Fusobacteria	2.03±7.33	4.94E-4±2.15E-3	0.92±3.57	0.45±1.18	0.02*	0.47	0.33

Continuous data are presented as the mean ± standard deviation. \*, 0.01 ≤ P < 0.05; \*\*\*, P < 0.001. The phyla with mean relative abundance > 1% were analysed. BT, bismuth quadruple therapy; CT, concomitant therapy.

**Table S4** Alpha diversity comparison between BT group, CT group and healthy control group at baseline (week 0), end of eradication therapy (week 2), 6 week post-eradication (week 6), and 1 year post-eradication (week 52)

Alpha diversity	BT group	CT group	HC group	P value		
				BT/CT	BT/HC	CT/HC
Week 0						
Shannon	3.48±0.54	3.30±0.67	3.35±0.53	0.63	0.52	0.92
Chao1	392.8±116.5	361.0±113.3	375.5±112.2	0.39	0.58	0.87
Week 2						
Shannon	2.09±0.68	1.96±0.78	3.35±0.53	0.32	<0.001***	<0.001***
Chao1	165.2±102.9	144.1±107.8	375.5±112.2	0.23	<0.001***	<0.001***
Week 6						
Shannon	2.92±0.68	3.04±0.69	3.35±0.53	0.65	0.02*	0.09
Chao1	288.4±102.1	290.2±109.8	375.5±112.2	0.94	0.008**	0.02*
Week 52						
Shannon	3.17±0.85	3.03±0.76	3.35±0.53	0.59	0.57	0.25
Chao1	372.4±146.9	335.3±92.6	375.5±112.2	0.51	0.93	0.31

Continuous data are presented as the mean ± standard deviation. \*, 0.01 ≤ P < 0.05; \*\*, 0.001 ≤ P < 0.01; \*\*\*, P < 0.001. BT, bismuth quadruple therapy; CT, concomitant therapy; HC, healthy control.

**Table S5** Comparison of the relative abundance of different phyla among the three group at baseline (week 0), end of eradication therapy (week 2), 6 week post-eradication (week 6), and 1 year post-eradication (week 52)

Phylum	Mean relative abundance (%) $\pm$ SD (%)			P value		
	BT group	CT group	HC group	BT/CT	BT/HC	CT/HC
<b>Week 0</b>						
p__Firmicutes	47.37 $\pm$ 18.33	44.69 $\pm$ 18.84	46.10 $\pm$ 15.07	0.88	0.97	0.97
p__Bacteroidetes	45.90 $\pm$ 19.62	47.41 $\pm$ 18.97	45.51 $\pm$ 15.26	0.96	1.00	0.94
p__Actinobacteria	3.21 $\pm$ 5.06	2.50 $\pm$ 2.68	5.41 $\pm$ 13.07	0.96	0.68	0.54
p__Proteobacteria	2.55 $\pm$ 2.44	2.60 $\pm$ 2.87	2.41 $\pm$ 1.82	1.00	0.98	0.97
p__Fusobacteria	0.28 $\pm$ 0.80	2.03 $\pm$ 7.33	0.14 $\pm$ 0.42	0.37	0.99	0.32
<b>Week 2</b>						
p__Proteobacteria	67.24 $\pm$ 32.78	57.83 $\pm$ 34.19	2.41 $\pm$ 1.82	0.53	<0.001***	<0.001***
p__Bacteroidetes	10.20 $\pm$ 19.33	22.02 $\pm$ 29.82	45.51 $\pm$ 15.26	0.22	<0.001***	0.004**
p__Firmicutes	19.42 $\pm$ 18.60	17.25 $\pm$ 14.43	46.10 $\pm$ 15.07	0.91	<0.001***	<0.001***
p__Actinobacteria	2.88 $\pm$ 7.67	2.73 $\pm$ 5.74	5.41 $\pm$ 13.07	1.00	0.67	0.67
p__Desulfobacterota	0.04 $\pm$ 0.11	0.10 $\pm$ 0.40	0.21 $\pm$ 0.29	0.77	0.12	0.47
<b>Week 6</b>						
p__Bacteroidetes	47.14 $\pm$ 25.12	50.55 $\pm$ 21.95	45.51 $\pm$ 15.26	0.87	0.97	0.74
p__Firmicutes	42.72 $\pm$ 19.24	41.19 $\pm$ 19.43	46.10 $\pm$ 15.07	0.96	0.82	0.68
p__Proteobacteria	5.85 $\pm$ 6.17	5.40 $\pm$ 6.30	2.41 $\pm$ 1.82	0.96	0.08	0.18
p__Actinobacteria	2.52 $\pm$ 5.48	1.55 $\pm$ 3.00	5.41 $\pm$ 13.07	0.94	0.53	0.36
p__Fusobacteria	1.40 $\pm$ 4.02	0.92 $\pm$ 3.57	0.14 $\pm$ 0.42	0.88	0.39	0.72
<b>Week 52</b>						
p__Bacteroidetes	53.91 $\pm$ 19.25	55.11 $\pm$ 20.07	45.51 $\pm$ 15.26	0.98	0.35	0.29
p__Firmicutes	39.55 $\pm$ 18.45	38.47 $\pm$ 17.53	46.10 $\pm$ 15.07	0.98	0.48	0.42
p__Proteobacteria	4.26 $\pm$ 4.18	2.20 $\pm$ 2.99	2.41 $\pm$ 1.82	0.18	0.17	0.98
p__Actinobacteria	1.61 $\pm$ 1.21	3.12 $\pm$ 4.53	5.41 $\pm$ 13.07	0.90	0.42	0.75
p__Desulfobacterota	0.17 $\pm$ 0.19	0.49 $\pm$ 0.94	0.21 $\pm$ 0.29	0.27	0.97	0.31

Continuous data are presented as the mean  $\pm$  standard deviation. \*\*,  $0.001 \leq P < 0.01$ ; \*\*\*,  $P < 0.001$ . BT, bismuth quadruple therapy; CT, concomitant therapy; HC, healthy control.

**Table S6** Comparison of the relative abundance of different genera among the three group at baseline (week 0), end of eradication therapy (week 2), 6 week post-eradication (week 6), and 1 year post-eradication (week 52)

Genus	Mean relative abundance (%) $\pm$ SD (%)			P value		
	BT group	CT group	HC group	BT/CT	BT/HC	CT/HC
<b>Week 0</b>						
g__Bacteroides	29.89 $\pm$ 20.37	23.74 $\pm$ 20.41	37.85 $\pm$ 18.52	0.61	0.40	0.08
g__Prevotella	11.19 $\pm$ 22.64	20.00 $\pm$ 29.08	3.45 $\pm$ 12.74	0.44	0.50	0.06
g__Faecalibacterium	8.07 $\pm$ 5.82	9.73 $\pm$ 7.31	12.42 $\pm$ 9.55	0.79	0.17	0.54
g__unclassified_f__Lachnospiraceae	4.66 $\pm$ 4.76	4.34 $\pm$ 3.81	5.16 $\pm$ 4.91	0.97	0.93	0.84
g__Blautia	5.22 $\pm$ 6.76	4.43 $\pm$ 6.24	3.23 $\pm$ 2.87	0.90	0.48	0.78
g__Bifidobacterium	2.50 $\pm$ 4.06	1.90 $\pm$ 2.24	3.65 $\pm$ 6.34	0.92	0.70	0.48
g__Subdoligranulum	2.12 $\pm$ 2.54	1.91 $\pm$ 2.28	1.56 $\pm$ 2.12	0.96	0.72	0.89
g__Megamonas	1.75 $\pm$ 3.82	1.05 $\pm$ 2.11	1.75 $\pm$ 4.49	0.83	1.00	0.83
g__Alistipes	2.13 $\pm$ 3.47	1.36 $\pm$ 2.33	1.06 $\pm$ 1.60	0.64	0.39	0.93
g__Phascolarctobacterium	0.97 $\pm$ 1.60	1.33 $\pm$ 2.20	2.17 $\pm$ 3.19	0.89	0.25	0.54
g__Parabacteroides	1.41 $\pm$ 1.37	0.99 $\pm$ 0.81	1.06 $\pm$ 1.10	0.50	0.59	0.98
g__Eubacterium_hallii_group	1.78 $\pm$ 3.31	1.04 $\pm$ 0.94	0.65 $\pm$ 0.73	0.53	0.19	0.83
g__Ruminococcus	1.10 $\pm$ 1.39	1.13 $\pm$ 1.98	1.05 $\pm$ 1.62	1.00	0.99	0.99
g__Lachnoclostridium	1.09 $\pm$ 1.73	1.34 $\pm$ 2.83	0.47 $\pm$ 0.42	0.91	0.53	0.33
g__Collinsella	0.54 $\pm$ 1.18	0.49 $\pm$ 0.75	1.61 $\pm$ 7.11	1.00	0.70	0.71
g__Parasutterella	0.73 $\pm$ 0.83	0.54 $\pm$ 0.87	1.36 $\pm$ 1.66	0.88	0.22	0.10
g__Fusicatenibacter	0.86 $\pm$ 0.98	0.61 $\pm$ 0.66	1.12 $\pm$ 1.37	0.75	0.72	0.31
g__Ruminococcus_torques_group	0.94 $\pm$ 1.09	0.76 $\pm$ 1.11	0.77 $\pm$ 1.18	0.88	0.89	1.00
g__norank_f__Eubacterium_coprostanoligenes_group	0.96 $\pm$ 1.91	1.07 $\pm$ 1.98	0.43 $\pm$ 0.76	0.97	0.55	0.45
g__Fusobacterium	0.27 $\pm$ 0.81	2.03 $\pm$ 7.33	0.14 $\pm$ 0.42	0.37	0.99	0.32
<b>Week 2</b>						
g__Escherichia-Shigella	31.03 $\pm$ 19.52	33.36 $\pm$ 32.63	0.31 $\pm$ 0.52	0.94	<0.001***	<0.001***
g__Bacteroides	6.01 $\pm$ 13.76	13.59 $\pm$ 24.34	37.85 $\pm$ 18.52	0.44	<0.001***	<0.001***
g__Klebsiella	26.23 $\pm$ 21.54	14.70 $\pm$ 19.48	0.06 $\pm$ 0.18	0.09	<0.001***	0.02*
g__Faecalibacterium	0.67 $\pm$ 2.02	2.72 $\pm$ 4.92	12.42 $\pm$ 9.55	0.59	<0.001***	<0.001***
g__Prevotella	3.58 $\pm$ 14.01	6.75 $\pm$ 19.43	3.45 $\pm$ 12.74	0.80	1.00	0.79
g__Enterococcus	5.28 $\pm$ 9.24	3.78 $\pm$ 7.99	0.01 $\pm$ 0.03	0.79	0.04*	0.23
g__Bifidobacterium	2.63 $\pm$ 7.73	2.57 $\pm$ 5.75	3.65 $\pm$ 6.34	1.00	0.88	0.88
g__unclassified_f__Enterobacteriaceae	2.98 $\pm$ 2.89	5.06 $\pm$ 14.67	0.01 $\pm$ 0.03	0.71	0.47	0.14
g__Streptococcus	2.61 $\pm$ 4.22	4.05 $\pm$ 7.17	0.14 $\pm$ 0.28	0.61	0.20	0.03*
g__unclassified_f__Lachnospiraceae	0.83 $\pm$ 2.56	0.41 $\pm$ 0.70	5.16 $\pm$ 4.91	0.92	<0.001***	<0.001***
g__Blautia	0.60 $\pm$ 1.87	0.71 $\pm$ 1.76	3.23 $\pm$ 2.87	0.99	<0.001***	0.003**
g__Parasutterella	1.34 $\pm$ 5.50	1.73 $\pm$ 4.32	1.36 $\pm$ 1.66	0.96	1.00	0.96
g__Veillonella	3.21 $\pm$ 6.90	0.46 $\pm$ 1.28	0.18 $\pm$ 0.42	0.11	0.06	0.98
g__Megamonas	0.47 $\pm$ 1.55	0.78 $\pm$ 2.85	1.75 $\pm$ 4.49	0.95	0.41	0.63
g__Parabacteroides	0.30 $\pm$ 0.67	1.58 $\pm$ 4.61	1.06 $\pm$ 1.10	0.29	0.61	0.81
g__Sutterella	1.39 $\pm$ 6.13	0.72 $\pm$ 2.11	0.50 $\pm$ 0.84	0.86	0.73	0.98
g__Phascolarctobacterium	0.10 $\pm$ 0.37	0.08 $\pm$ 0.32	2.17 $\pm$ 3.19	1.00	0.002**	0.004**
g__Ruminococcus_gnavus_group	0.64 $\pm$ 1.86	0.46 $\pm$ 1.81	1.22 $\pm$ 2.00	0.95	0.58	0.43
g__Subdoligranulum	0.06 $\pm$ 0.22	0.36 $\pm$ 1.18	1.56 $\pm$ 2.12	0.80	0.003**	0.03*
g__Eubacterium_eligens_group	0.53 $\pm$ 2.16	0.47 $\pm$ 1.97	0.81 $\pm$ 1.74	1.00	0.89	0.85

**Table S6** (continued)

Table S6 (continued)

Genus	Mean relative abundance (%) ± SD (%)			P value		
	BT group	CT group	HC group	BT/CT	BT/HC	CT/HC
Week 6						
g__Bacteroides	29.83±26.19	31.72±22.75	37.85±18.52	0.96	0.49	0.69
g__Prevotella	14.07±25.87	13.52±26.60	3.45±12.74	1.00	0.28	0.35
g__Faecalibacterium	9.84±10.46	7.51±8.55	12.42±9.55	0.74	0.66	0.26
g__Blautia	6.08±7.47	2.97±3.43	3.23±2.87	0.16	0.18	0.99
g__unclassified_f__Lachnospiraceae	4.17±3.59	2.70±2.91	5.16±4.91	0.49	0.70	0.14
g__Ruminococcus_gnavus_group	1.61±2.39	4.24±8.44	1.22±2.00	0.23	0.97	0.15
g__Bifidobacterium	2.35±5.53	1.01±1.66	3.65±6.34	0.70	0.69	0.25
g__Megamonas	1.81±5.87	1.65±3.94	1.75±4.49	0.99	1.00	1.00
g__Parasutterella	1.73±3.25	1.28±2.90	1.36±1.66	0.86	0.90	1.00
g__Parabacteroides	1.32±2.14	1.94±2.70	1.06±1.10	0.62	0.91	0.39
g__Escherichia-Shigella	2.07±4.81	1.46±3.95	0.31±0.52	0.86	0.26	0.59
g__Lachnoclostridium	1.03±1.23	2.02±4.87	0.47±0.42	0.51	0.79	0.20
g__Alistipes	0.50±1.16	1.90±2.68	1.06±1.60	0.06	0.60	0.35
g__Fusicatenibacter	0.99±1.96	1.26±3.55	1.12±1.37	0.94	0.98	0.98
g__Phascolarctobacterium	0.21±0.40	0.67±1.08	2.17±3.19	0.76	0.006**	0.06
g__Ruminococcus_torques_group	0.97±1.17	1.04±1.41	0.77±1.18	0.98	0.87	0.79
g__Sutterella	1.13±2.69	1.11±1.91	0.50±0.84	1.00	0.55	0.60
g__Subdoligranulum	0.45±0.88	0.72±1.23	1.56±2.12	0.85	0.05	0.21
g__Veillonella	1.07±1.90	1.45±1.98	0.18±0.42	0.74	0.17	0.04*
g__Fusobacterium	1.40±4.02	0.92±3.57	0.14±0.42	0.88	0.39	0.72
Week 52						
g__Bacteroides	36.08±25.19	30.41±23.01	37.85±18.52	0.78	0.97	0.61
g__Prevotella	14.07±27.65	20.35±33.28	3.45±12.74	0.78	0.40	0.13
g__Faecalibacterium	5.89±4.37	7.74±4.28	12.42±9.55	0.77	0.02*	0.16
g__unclassified_f__Lachnospiraceae	4.97±5.16	3.40±2.77	5.16±4.91	0.64	0.99	0.52
g__Blautia	3.03±2.18	4.71±4.71	3.23±2.87	0.37	0.98	0.42
g__Bifidobacterium	0.96±1.24	2.68±4.23	3.65±6.34	0.61	0.22	0.83
g__Megamonas	0.96±2.41	3.96±9.43	1.75±4.49	0.36	0.91	0.53
g__Parabacteroides	1.10±1.09	2.34±3.01	1.06±1.10	0.17	1.00	0.12
g__Parasutterella	1.99±2.80	0.83±2.15	1.36±1.66	0.35	0.67	0.78
g__Subdoligranulum	0.97±1.04	1.22±1.46	1.56±2.12	0.92	0.55	0.83
g__Alistipes	1.74±3.12	0.83±1.93	1.06±1.60	0.55	0.65	0.96
g__Phascolarctobacterium	0.36±0.54	0.91±1.42	2.17±3.19	0.80	0.049*	0.26
g__Fusicatenibacter	0.79±0.59	1.15±1.02	1.12±1.37	0.66	0.63	1.00
g__UCG-002	0.87±2.14	1.45±3.82	0.72±0.80	0.79	0.98	0.65
g__Ruminococcus	1.42±2.17	0.27±0.38	1.05±1.62	0.16	0.77	0.38
g__Ruminococcus_gnavus_group	0.55±1.45	0.82±1.06	1.22±2.00	0.90	0.44	0.77
g__Lachnospira	1.13±2.24	0.62±0.77	0.78±0.58	0.58	0.73	0.94
g__Collinsella	0.49±0.47	0.36±0.55	1.61±7.11	1.00	0.76	0.74
g__Roseburia	1.18±2.18	0.66±1.16	0.59±0.97	0.63	0.47	0.99
g__Ruminococcus_torques_group	0.91±1.00	0.53±0.61	0.77±1.18	0.58	0.91	0.78

Continuous data are presented as the mean ± standard deviation (SD). \*, 0.01≤P<0.05; \*\*, 0.001≤P<0.01; \*\*\*, P<0.001. BT, bismuth quadruple therapy; CT, concomitant therapy; HC, healthy control.