



**Supplementary Figure 1.** Alpha diversity indices difference between *H. pylori*-positive group and *H. pylori*-negative group. Ace (A) and Sobs (B) indices represent richness of community; Shannon (C) and Simpson (D) indices represent diversity of community; Heip (E) and Shannoneven (F) indices represent evenness of community. \*,  $p < 0.05$ .

**Supplementary Table 1** Bacterial taxa with significant different abundances between *H. pylori*-positive and *H. pylori*-negative groups

Bacterial taxa	<i>H. pylori</i> -positive		<i>H. pylori</i> -negative		p
	Relative abundance (%)	SD (%)	Relative abundance (%)	SD (%)	
<b>Genus level</b>					
<i>Sphingomonas</i>	0.00035	0.00146	0.00242	0.00361	***
<i>Bacillus</i>	0.00004	0.00032	0.00110	0.00249	**
<i>Streptomyces</i>	0.00013	0.00058	0.00126	0.00255	**
<i>Faecalibaculum</i>	0.00008	0.00045	0.00070	0.00152	**
<i>Acidothermus</i>	0	0	0.00093	0.00347	**
<i>norank_f__Lachnospiraceae</i>	1.25200	2.28000	2.00000	2.75700	**
<i>Pseudarthrobacter</i>	0.00008	0.00066	0.00048	0.00123	*
<i>Butyricimonas</i>	0.21410	0.21970	0.17080	0.28030	*
<i>Bradyrhizobium</i>	0.00021	0.00080	0.00094	0.00192	*
<i>Nitrospira</i>	0	0	0.00055	0.00205	*
<i>Phenylobacterium</i>	0	0	0.00044	0.00183	*
<i>H16</i>	0	0	0.00031	0.00106	*
<i>Mycobacterium</i>	0	0	0.00022	0.00071	*
<i>Ruminococcaceae UCG014</i>	0.25370	0.56220	0.38590	1.49400	*
<i>Ruminococcaceae UCG005</i>	0.33350	0.66570	0.33460	1.07300	*
<i>Howardella</i>	0.00738	0.02855	0	0	*
<i>Thiobacillus</i>	0.00006	0.00045	0.00274	0.00942	*
<i>norank_f__Peptococcaceae</i>	0.00622	0.01974	0.00125	0.00451	*
<i>Negativicoccus</i>	0.00004	0.00036	0.00044	0.00139	*
<i>Brevundimonas</i>	0.00008	0.00046	0.00081	0.00246	*
<i>Ruminococcaceae NK4A214 group</i>	0.26540	0.50280	0.15500	0.32670	*
<i>Eubacterium ventriosum group</i>	0.09885	0.15240	0.27500	0.73180	*
<b>Species level</b>					
<i>Sphingomonas sp.</i>	0.00013	0.00061	0.00218	0.00361	***
<i>Turicibacter sp.</i>	0.00008	0.00045	0.00102	0.00198	***
<i>Bacteroides plebeius</i>	5.81600	9.51500	4.09700	9.58600	***
<i>Bacillus niacini</i>	0.00004	0.00032	0.00110	0.00249	**
<i>Streptomyces sp.</i>	0.00013	0.00058	0.00126	0.00255	**
<i>Faecalibaculum sp.</i>	0.00008	0.00045	0.00070	0.00152	**
<i>Ruminiclostridium 9 sp.</i>	0.08016	0.07195	0.04239	0.04501	**
<i>Actinoallomurus sp.</i>	0	0	0.00093	0.00347	**
<i>Brevundimonas variabilis</i>	0	0	0.00074	0.00245	**
<i>Tyzzerella sp.</i>	0.04394	0.23520	0.09864	0.35680	**
<i>Clostridium sp. AT5</i>	0.46670	1.44800	1.03500	2.48300	*
<i>Clostridiaceae bacterium</i>	0.00008	0.00065	0.00146	0.00432	*
<i>BARN424CC10</i>					
<i>Candidatus Saccharibacteria bacterium</i>	0.00127	0.00478	0.00184	0.00256	*
<i>UB2523</i>					

<i>Pseudarthrobacter sp.</i>	0.00008	0.00066	0.00048	0.00123	*
<i>Bradyrhizobium elkanii</i>	0.00021	0.00081	0.00094	0.00192	*
<i>Ruminococcaceae UCG002 sp.</i>	0.65870	0.95600	0.47780	0.90500	*
<i>Corynebacterium 1 sp.</i>	0	0	0.00064	0.00260	*
<i>Nitrospira sp.</i>	0	0	0.00055	0.00205	*
<i>Phenylobacterium sp.</i>	0	0	0.00044	0.00183	*
<i>H16 sp.</i>	0	0	0.00031	0.00106	*
<i>Mycobacterium sp.</i>	0	0	0.00022	0.00071	*
<i>Fusobacterium varium</i>	0.11590	0.55820	0.44550	1.15100	*
<i>Christensenellaceae R7 group sp.</i>	0.02437	0.09125	0.00077	0.00456	*
<i>Parabacteroides merdae</i>	0.81990	1.36300	0.49420	0.87060	*
<i>Ruminococcaceae NK4A214 group sp.</i>	0.23890	0.44090	0.14630	0.32000	*
<i>s__uncultured bacterium_g__Christensenellaceae R7 group</i>	0.01041	0.02602	0.01091	0.06126	*
<i>Bacteroides coprophilus</i>	0.85670	3.08100	0.13160	0.55570	*
<i>Thiobacillus sp.</i>	0.00006	0.00045	0.00274	0.00942	*
<i>Ruminococcaceae bacterium AM2</i>	0.00004	0.00032	0.00252	0.00949	*
<i>Butyricimonas sp.</i>	0.08892	0.13000	0.08087	0.18670	*
<i>Actinomyces odontolyticus</i>	0.00793	0.02408	0.01229	0.02331	*
<i>Ruminococcaceae UCG002 sp.</i>	0.88270	1.65500	0.85900	2.04900	*
<i>Negativicoccus succinicivorans</i>	0.00004	0.00036	0.00044	0.00139	*
<i>Eubacterium ramulus</i>	0.12710	0.21130	0.06727	0.14220	*
<i>Bacteroides ovatus</i>	1.22900	2.13700	1.98100	2.53200	*
<i>Desulfovibrio desulfuricans</i>	0.00052	0.00416	0.00203	0.00712	*
<i>Butyricimonas virosa</i>	0.08962	0.16270	0.07544	0.16310	*
<i>Parabacteroides goldsteinii</i>	0.07594	0.22490	0.05321	0.20390	*

\*, p value<0.05; \*\*, p value<0.01; \*\*\*, p value<0.001.

**Supplementary Table 2** GSRS (gastrointestinal symptom rating scale) scores on day 0 and day 56

Variable	Group A (n=32)			Group B (n=31)		
	Day 0	Day 56	P	Day 0	Day 56	P
Abdominal pains	0.44±0.10	0.53±0.13	0.366	0.42±0.11	0.16±0.07	<0.05
Abdominal distension	0.75±0.11	0.22±0.07	<0.05	0.84±0.14	0.32±0.11	<0.05
Borborygmus	0.53±0.12	0.38±0.09	0.132	0.52±0.12	0.29±0.11	0.052
Increased flatus	0.44±0.12	0.25±0.09	0.130	0.65±0.15	0.29±0.11	<0.05
Increased passage of stools	0.06±0.04	0.13±0.06	0.414	0.13±0.10	0.26±0.12	<0.05
Decreased passage of stools	0.09±0.05	0.03±0.03	0.317	0.26±0.13	0.06±0.05	0.131
Loose stools	0.34±0.10	0.25±0.09	0.467	0.61±0.13	0.55±0.15	0.592
Hard Stools	0.28±0.10	0.38±0.13	0.366	0.39±0.14	0.10±0.05	<0.05
Urgent need for defecation	0.34±0.11	0.31±0.10	0.822	0.55±0.14	0.39±0.13	0.132
Feeling of incomplete evacuation	0.59±0.13	0.28±0.09	<0.05	0.68±0.13	0.32±0.09	<0.05
Eructation	0.66±0.12	0.16±0.07	<0.05	0.94±0.17	0.39±0.10	<0.05
Acid regurgitation	0.66±0.12	0.16±0.07	<0.05	0.26±0.09	0.03±0.03	<0.05
Heartburn	0.41±0.11	0.19±0.07	<0.05	0.35±0.10	0.10±0.07	<0.05
Nausea and vomiting	0.41±0.12	0.19±0.07	0.052	0.29±0.11	0.16±0.07	0.206
Sucking sensations in the epigastrium	0.34±0.12	0.28±0.10	0.658	0.45±0.11	0.13±0.10	<0.05
Total score	6.34±0.79	3.72±0.54	<0.05	7.32±0.69	3.55±0.56	<0.05

Data are presented as the mean ± standard error (SE). The p values are for differences of gastrointestinal symptom rating scale scores between day 0 and day 56 in each group (Wilcoxon signed rank test).

**Supplementary Table 3** Bristol stool scale score change after eradication therapy of *H. pylori*

	Group A			Group B		
	Day 0	Day 56	P	Day 0	Day 56	P
Score-4	0.719±0.142	0.547±0.155	0.254	0.790±0.137	0.419±0.129	<0.05

Data are presented as the mean  $\pm$  standard error (SE). Group A, *H. pylori*-infected patients with bismuth-containing quadruple therapy; Group B, *H. pylori*-infected patients with bismuth-containing quadruple therapy supplemented with *C. butyricum*.

**Supplementary Table 4** Adverse effects and compliance of different eradication regimens

	<b>Group A (n=32)</b>	<b>Group B (n=31)</b>	<b>P</b>
Any adverse effects	13(40.6%)	7(22.6%)	0.124
Skin rash	4(12.5%)	2(6.5%)	0.698
Pruritus	4(12.5%)	2(6.5%)	0.698
Headache	0(0.0%)	0(0.0%)	
Dizziness	3(9.4%)	3(9.7%)	1.000
Fever	3(9.4%)	1(3.2%)	0.628
Bitter taste	5(15.6%)	5(16.1%)	1.000
Hepatic and renal dysfunction	0(0.0%)	0(0.0%)	
Poor compliance	3(9.4%)	0(0.0%)	0.248

Group A, *H. pylori*-infected patients with bismuth-containing quadruple therapy; Group B, *H. pylori*-infected patients with bismuth-containing quadruple therapy supplemented with *C. butyricum*.