Supplementary table 1. Baseline characteristics of study participants

Baseline characteristics	Anti-*H. pylori* treatment groups			*H. pylori* negative group		
	Successful eradication n=58	Failed treatment n=57	*P*[a]	n=49	*P*[b]	*P*[c]
Age, years (Mean ± SD)[d]	56.6 ± 9.2	56.2 ± 8.9	0.801	55.4 ± 8.1	0.447	0.603
Gender (%)[e]			0.043		0.260	0.002
Male	30 (51.7%)	40 (70.2%)		20 (40.8%)		
Female	28 (48.3%)	17 (29.8%)		29 (59.2%)		
BMI, kg/m^2 (Mean ± SD)[d]	26.3 ± 1.2	26.2 ± 1.3	0.739	23.5 ± 2.5	<0.001	<0.001
Smoking (%)[e]			0.720		0.015	0.035
No	41 (70.7%)	42 (73.7%)		44 (89.8%)		
Yes	17 (29.3%)	15 (26.3%)		5 (10.2%)		
Drinking (%)[e]			0.066		0.354	0.008
No	43 (74.1%)	33 (57.9%)		40 (81.6%)		
Yes	15 (25.9%)	24 (42.1%)		9 (18.4%)		
Antibiotics use (%)[e]			0.467		0.205	0.055
No	47 (81%)	43 (75.4%)		44 (89.8%)		
Yes	11 (19%)	14 (24.6%)		5 (10.2%)		
Gastric lesions (%)[f]			0.710		<0.001	<0.001
Normal/SG	5 (8.6%)	4 (7.0%)		26 (53.1%)		
CAG	25 (43.1%)	19 (33.4%)		9 (18.4%)		
IM/DYS	28 (48.3%)	30 (52.6%)		13 (26.5%)		
Missing	0 (0.0%)	4 (7.0%)		1 (2.0%)		

[a] Successful eradication group *v.s.* failed treatment group

[b] Successful eradication group *v.s. H. pylori* negative group

[c] Failed treatment group *v.s. H. pylori* negative group

[d] *t*-test

[e] χ^2 test

[f] Fisher's exact test

BMI, body mass index; CAG, chronic atrophic gastritis; DYS, dysplasia; *H. pylori*, *Helicobacter pylori*; IM, intestinal metaplasia; SG, superficial gastritis

Supplementary table 2. Significantly changed taxa after successful *H. pylori* eradication

Level	Taxa[a]	Alteration trend after eradication	Mean relative abundance before eradication	Mean relative abundance after eradication	Fold change[b]	q value[c]
Gastric biopsies						
Phylum	*p__Cyanobacteria/Chloroplast*	↑	0.99%	5.15%	5.18	0.023
Phylum	*p__Bacteroidetes*	↑	3.49%	17.83%	5.11	<0.001
Phylum	*p__Fusobacteria*	↑	0.82%	4.06%	4.98	<0.001
Phylum	*p__Actinobacteria*	↑	1.21%	6.02%	4.95	<0.001
Phylum	*p__Firmicutes*	↑	6.81%	28.35%	4.16	<0.001
Phylum	*p__unknown_ Bacteria*	↑	2.17%	8.06%	3.71	<0.001
Class	*c__Chloroplast*	↑	0.96%	5.11%	5.30	0.024
Class	*c__Bacteroidia*	↑	3.25%	16.73%	5.15	<0.001
Class	*c__Fusobacteriia*	↑	0.82%	4.06%	4.98	<0.001
Class	*c__Actinobacteria*	↑	1.21%	6.02%	4.95	<0.001
Class	*c__Negativicutes*	↑	0.74%	3.6%	4.86	<0.001
Class	*c__Clostridia*	↑	1.04%	4.82%	4.65	<0.001
Class	*c__Betaproteobacteria*	↑	2.03%	9.33%	4.59	<0.001
Class	*c__Bacilli*	↑	5.00%	19.76%	3.95	<0.001
Class	*c__unknown_ Bacteria*	↑	2.17%	8.06%	3.71	<0.001
Class	*c__Gammaproteobacteria*	↑	3.96%	7.39%	1.87	0.001
Order	*o__Bacillales*	↑	1.91%	12.37%	6.47	<0.001
Order	*o__Chloroplast*	↑	0.96%	5.11%	5.30	0.024
Order	*o__Bacteroidales*	↑	3.25%	16.73%	5.15	<0.001
Order	*o__Actinomycetales*	↑	1.10%	5.60%	5.08	<0.001
Order	*o__Fusobacteriales*	↑	0.82%	4.06%	4.98	<0.001
Order	*o__Selenomonadales*	↑	0.74%	3.60%	4.86	<0.001
Order	*o__Neisseriales*	↑	1.79%	8.56%	4.78	<0.001
Order	*o__Clostridiales*	↑	1.04%	4.82%	4.65	<0.001
Order	*o__unknown_ Bacteria*	↑	2.17%	8.06%	3.71	<0.001
Order	*o__Pasteurellales*	↑	1.93%	5.23%	2.71	<0.001
Order	*o__Lactobacillales*	↑	3.09%	7.40%	2.40	<0.001
Family	*f__Staphylococcaceae*	↑	1.58%	10.99%	6.97	<0.001
Family	*f__Corynebacteriaceae*	↑	0.38%	2.62%	6.83	<0.001
Family	*f__Fusobacteriaceae*	↑	0.51%	3.34%	6.56	<0.001
Family	*f__Bacteroidaceae*	↑	0.42%	2.28%	5.39	<0.001
Family	*f__Chloroplast*	↑	0.96%	5.11%	5.30	0.024
Family	*f__Porphyromonadaceae*	↑	0.58%	3.08%	5.30	<0.001
Family	*f__Prevotellaceae*	↑	2.12%	11.06%	5.22	<0.001
Family	*f__Lachnospiraceae*	↑	0.45%	2.32%	5.14	<0.001
Family	*f__Bacillales_Incertae Sedis XI*	↑	0.24%	1.18%	5.00	<0.001
Family	*f__Neisseriaceae*	↑	1.79%	8.56%	4.78	<0.001
Family	*f__Veillonellaceae*	↑	0.71%	3.29%	4.64	<0.001
Family	*f__Ruminococcaceae*	↑	0.25%	1.04%	4.17	<0.001
Family	*f__Streptococcaceae*	↑	1.62%	6.30%	3.88	<0.001
Family	*f__unknown_ Bacteria*	↑	2.17%	8.06%	3.71	<0.001
Family	*f__Micrococcaceae*	↑	0.41%	1.50%	3.63	<0.001
Family	*f__Pasteurellaceae*	↑	1.93%	5.23%	2.71	<0.001
Genus	*g__unknown_ Neisseriaceae*	↑	0.21%	1.88%	9.09	<0.001

Genus	*g__Staphylococcus*	↑	1.58%	10.99%	6.97	<0.001
Genus	*g__Corynebacterium*	↑	0.38%	2.61%	6.82	<0.001
Genus	*g__Fusobacterium*	↑	0.51%	3.34%	6.56	<0.001
Genus	*g__Bacteroides*	↑	0.42%	2.28%	5.39	<0.001
Genus	*g__Streptophyta*	↑	0.96%	5.10%	5.33	0.024
Genus	*g__unknown_ Prevotellaceae*	↑	0.41%	2.15%	5.28	<0.001
Genus	*g__Prevotella*	↑	1.38%	7.27%	5.27	<0.001
Genus	*g__Gemella*	↑	0.24%	1.18%	5.00	<0.001
Genus	*g__Porphyromonas*	↑	0.40%	1.96%	4.92	<0.001
Genus	*g__Alloprevotella*	↑	0.33%	1.64%	4.91	<0.001
Genus	*g__Veillonella*	↑	0.59%	2.56%	4.36	<0.001
Genus	*g__Neisseria*	↑	1.58%	6.68%	4.22	<0.001
Genus	*g__Streptococcus*	↑	1.59%	6.23%	3.92	<0.001
Genus	*g__Rothia*	↑	0.36%	1.35%	3.74	<0.001
Genus	*g__unknown_ Bacteria*	↑	2.17%	8.06%	3.71	<0.001
Genus	*g__Haemophilus*	↑	1.67%	4.24%	2.54	<0.001
Phylum	*p__Proteobacteria*	↓	83.92%	28.15%	0.34	<0.001
Class	*c__Epsilonproteobacteria*	↓	77.38%	10.11%	0.13	<0.001
Order	*o__Campylobacterales*	↓	77.38%	10.11%	0.13	<0.001
Family	*f__Helicobacteraceae*	↓	77.33%	9.67%	0.13	<0.001
Genus	*g__Helicobacter*	↓	77.33%	9.66%	0.12	<0.001
Stool samples						
Phylum	*p__Firmicutes*	↑	62.38%	70.13%	1.12	0.046
Class	*c__Clostridia*	↑	57.39%	65.55%	1.14	0.039
Order	*o__Bifidobacteriales*	↑	1.40%	2.60%	1.86	0.025
Order	*o__Clostridiales*	↑	57.11%	65.38%	1.14	0.038
Family	*f__Peptostreptococcaceae*	↑	0.71%	2.21%	3.10	0.025
Family	*f__Bifidobacteriaceae*	↑	1.40%	2.60%	1.86	0.025
Genus	*g__Anaerostipes*	↑	0.52%	1.83%	3.53	<0.001
Genus	*g__Escherichia/Shigella*	↑	0.63%	1.94%	3.09	0.039
Genus	*g__Clostridium XI*	↑	0.63%	1.92%	3.03	0.025
Genus	*g__Bifidobacterium*	↑	1.37%	2.54%	1.85	0.025
Genus	*g__Fusicatenibacter*	↑	0.97%	1.46%	1.51	0.039
Phylum	*p__Bacteroidetes*	↓	28.6%	18.95%	0.66	0.002
Class	*c__Bacteroidia*	↓	28.57%	18.88%	0.66	0.002
Order	*o__Bacteroidales*	↓	28.57%	18.88%	0.66	0.002
Family	*f__Rikenellaceae*	↓	1.07%	0.66%	0.62	0.025
Genus	*g__unknown_ Ruminococcaceae*	↓	3.71%	2.59%	0.70	0.048
Genus	*g__Alistipes*	↓	1.07%	0.66%	0.62	0.025

[a] The significantly changed taxa by successful eradication with mean relative abundances >1% were listed.

[b] The fold change was calculated as the ratio of the mean relative abundance after eradication to the mean relative abundance before eradication.

[c] Paired *t*-test after arcsine transformation of relative frequency and q values were used after adjustment for multiple comparison by the FDR.

Supplementary table 3. Significantly changed taxa after failed anti-*H. pylori* treatment

Level	Taxa	Alteration trend after treatment	Mean relative abundance before treatment	Mean relative abundance after treatment	Fold change[a]	q value[b]
Gastric biopsies						
None						
Stool samples						
Class	*c__Bacilli*	↑	0.41%	1.49%	3.64	0.037
Order	*o__Lactobacillales*	↑	0.41%	1.48%	3.63	0.037
Family	*f__Enterococcaceae*	↑	<0.01%	0.11%	40.18	0.025
Genus	*g__Lactococcus*	↑	<0.01%	0.02%	62.37	0.046
Genus	*g__Enterococcus*	↑	<0.01%	0.11%	40.18	0.025
Genus	*g__Raoultella*	↑	<0.01%	0.01%	14.64	0.025
Genus	*g__Anaerostipes*	↑	0.54%	1.41%	2.61	0.017
Genus	*g__Sutterella*	↓	0.54%	0.22%	0.41	0.046

[a] The fold change was calculated as the ratio of the mean relative abundance after treatment to the mean relative abundance before treatment.

[b] Paired *t*-test after arcsine transformation of relative frequency and q values were used after adjustment for multiple comparison by the FDR.

Supplementary table 4. Significant changes in predicted metabolic pathways after anti-*H. pylori* treatment in gastric biopsies

	Alteration trend after treatment	Mean relative frequency before treatment	Mean relative frequency after treatment	Fold change[a]	q value[b]
Successful eradication group					
ko04974 Protein digestion and absorption	↑	1.86E-04	1.36E-03	7.31	<0.001
ko04640 Hematopoietic cell lineage	↑	2.68E-05	1.91E-04	7.13	<0.001
ko00531 Glycosaminoglycan degradation	↑	1.40E-04	9.69E-04	6.91	<0.001
ko00604 Glycosphingolipid biosynthesis - ganglio series	↑	3.74E-05	2.51E-04	6.71	<0.001
ko04725 Cholinergic synapse	↑	4.39E-06	2.94E-05	6.71	<0.001
ko00563 Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	↑	3.56E-06	2.38E-05	6.68	<0.001
ko00944 Flavone and flavonol biosynthesis	↑	7.57E-06	5.02E-05	6.64	<0.001
ko00511 Other glycan degradation	↑	8.69E-04	5.69E-03	6.55	<0.001
ko04142 Lysosome	↑	1.77E-04	1.16E-03	6.55	<0.001
ko04064 NF-kappa B signaling pathway	↑	1.19E-08	7.80E-08	6.51	<0.001
ko05140 Leishmaniasis	↑	1.19E-08	7.80E-08	6.51	<0.001
ko00603 Glycosphingolipid biosynthesis - globo series	↑	7.41E-05	4.81E-04	6.49	<0.001
ko04614 Renin-angiotensin system	↑	4.76E-05	3.09E-04	6.48	<0.001
ko04960 Aldosterone-regulated sodium reabsorption	↑	5.36E-06	3.43E-05	6.40	<0.001
ko04970 Salivary secretion	↑	5.36E-06	3.43E-05	6.40	<0.001
ko04971 Gastric acid secretion	↑	5.36E-06	3.43E-05	6.40	<0.001
ko04961 Endocrine and other factor-regulated calcium reabsorption	↑	5.45E-06	3.45E-05	6.32	<0.001
ko04972 Pancreatic secretion	↑	5.64E-06	3.49E-05	6.20	<0.001
ko04973 Carbohydrate digestion and absorption	↑	1.20E-04	7.44E-04	6.19	<0.001
ko00940 Phenylpropanoid biosynthesis	↑	1.49E-04	9.07E-04	6.11	<0.001
ko00943 Isoflavonoid biosynthesis	↑	1.99E-06	1.21E-05	6.07	<0.001
ko03460 Fanconi anemia pathway	↑	4.48E-06	2.66E-05	5.93	<0.001
ko04930 Type II diabetes mellitus	↑	3.42E-05	1.98E-04	5.79	<0.001
ko00785 Lipoic acid metabolism	↑	2.52E-04	1.43E-03	5.69	<0.001
ko05202 Transcriptional misregulation in cancer	↑	2.47E-07	1.38E-06	5.60	<0.001
ko05203 Viral carcinogenesis	↑	3.69E-05	2.07E-04	5.60	<0.001
ko00121 Secondary bile acid biosynthesis	↑	3.12E-05	1.74E-04	5.57	<0.001
ko04370 VEGF signaling pathway	↑	4.89E-07	2.72E-06	5.57	<0.001
ko05143 African trypanosomiasis	↑	6.36E-05	3.52E-04	5.53	<0.001
ko04011 MAPK signaling pathway - yeast	↑	6.14E-05	3.38E-04	5.50	<0.001
ko00522 Biosynthesis of 12-, 14- and 16-membered macrolides	↑	3.39E-05	1.86E-04	5.48	<0.001
ko04920 Adipocytokine signaling pathway	↑	1.16E-04	6.35E-04	5.48	<0.001
ko00120 Primary bile acid biosynthesis	↑	3.70E-05	2.02E-04	5.46	<0.001
ko00941 Flavonoid biosynthesis	↑	7.47E-06	4.08E-05	5.45	<0.001
ko04976 Bile secretion	↑	1.05E-05	5.70E-05	5.44	<0.001
ko03022 Basal transcription factors	↑	1.96E-05	1.06E-04	5.43	<0.001
ko04622 RIG-I-like receptor signaling pathway	↑	2.03E-05	1.10E-04	5.40	<0.001
ko05219 Bladder cancer	↑	1.40E-05	7.51E-05	5.35	<0.001
ko05142 Chagas disease (American trypanosomiasis)	↑	3.40E-05	1.79E-04	5.26	<0.001
ko05100 Bacterial invasion of epithelial cells	↑	3.55E-04	1.85E-03	5.21	<0.001
ko02060 Phosphotransferase system (PTS)	↑	1.50E-03	7.67E-03	5.13	<0.001

ko05222 Small cell lung cancer	↑	1.42E-06	7.21E-06	5.08	<0.001
ko05145 Toxoplasmosis	↑	8.17E-07	4.14E-06	5.07	<0.001
ko00909 Sesquiterpenoid and triterpenoid biosynthesis	↑	2.28E-05	1.15E-04	5.06	<0.001
ko00600 Sphingolipid metabolism	↑	3.63E-04	1.82E-03	5.00	<0.001
ko01054 Nonribosomal peptide structures	↑	3.56E-04	1.77E-03	4.99	<0.001
ko05150 Staphylococcus aureus infection	↑	6.23E-04	3.07E-03	4.94	<0.001
ko00311 Penicillin and cephalosporin biosynthesis	↑	1.39E-04	6.79E-04	4.89	<0.001
ko04916 Melanogenesis	↑	4.90E-07	2.40E-06	4.89	<0.001
ko00100 Steroid biosynthesis	↑	4.12E-06	2.00E-05	4.86	<0.001
ko01057 Biosynthesis of type II polyketide products	↑	1.43E-05	6.94E-05	4.85	<0.001
ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	↑	2.96E-05	1.43E-04	4.83	<0.001
ko04512 ECM-receptor interaction	↑	1.96E-06	9.46E-06	4.82	<0.001
ko04510 Focal adhesion	↑	1.97E-06	9.46E-06	4.80	<0.001
ko05410 Hypertrophic cardiomyopathy (HCM)	↑	2.93E-06	1.38E-05	4.73	<0.001
ko04113 Meiosis - yeast	↑	1.23E-04	5.81E-04	4.72	<0.001
ko00472 D-Arginine and D-ornithine metabolism	↑	7.44E-06	3.47E-05	4.66	<0.001
ko04020 Calcium signaling pathway	↑	1.25E-06	5.82E-06	4.65	<0.001
ko05110 Vibrio cholerae infection	↑	3.55E-05	1.65E-04	4.65	<0.001
ko00364 Fluorobenzoate degradation	↑	3.50E-05	1.59E-04	4.53	<0.001
ko03320 PPAR signaling pathway	↑	2.39E-04	1.08E-03	4.53	<0.001
ko00980 Metabolism of xenobiotics by cytochrome P450	↑	8.92E-05	4.03E-04	4.52	<0.001
ko04310 Wnt signaling pathway	↑	8.44E-07	3.80E-06	4.49	<0.001
ko04330 Notch signaling pathway	↑	8.44E-07	3.80E-06	4.49	<0.001
ko05220 Chronic myeloid leukemia	↑	8.44E-07	3.80E-06	4.49	<0.001
ko00982 Drug metabolism - cytochrome P450	↑	9.03E-05	4.06E-04	4.49	<0.001
ko04666 Fc gamma R-mediated phagocytosis	↑	2.50E-06	1.11E-05	4.44	<0.001
ko00965 Betalain biosynthesis	↑	1.34E-06	5.93E-06	4.43	<0.001
ko00312 beta-Lactam resistance	↑	1.49E-04	6.55E-04	4.41	<0.001
ko00984 Steroid degradation	↑	5.52E-05	2.41E-04	4.36	<0.001
ko00232 Caffeine metabolism	↑	7.48E-06	3.25E-05	4.35	<0.001
ko04728 Dopaminergic synapse	↑	2.14E-06	9.17E-06	4.29	<0.001
ko05030 Cocaine addiction	↑	1.68E-06	7.19E-06	4.28	<0.001
ko05031 Amphetamine addiction	↑	1.69E-06	7.19E-06	4.25	<0.001
ko05204 Chemical carcinogenesis	↑	5.18E-05	2.19E-04	4.23	<0.001
ko00053 Ascorbate and aldarate metabolism	↑	4.78E-04	2.02E-03	4.23	<0.001
ko00361 Chlorocyclohexane and chlorobenzene degradation	↑	1.47E-04	6.17E-04	4.20	<0.001
ko04726 Serotonergic synapse	↑	1.86E-06	7.82E-06	4.20	<0.001
ko05034 Alcoholism	↑	4.28E-06	1.79E-05	4.19	<0.001
ko04144 Endocytosis	↑	2.00E-06	8.34E-06	4.17	<0.001
ko04912 GnRH signaling pathway	↑	2.00E-06	8.34E-06	4.17	<0.001
ko00660 C5-Branched dibasic acid metabolism	↑	4.00E-04	1.67E-03	4.16	<0.001
ko05020 Prion diseases	↑	7.61E-06	3.12E-05	4.10	<0.001
ko00500 Starch and sucrose metabolism	↑	4.23E-03	1.73E-02	4.08	<0.001
ko05133 Pertussis	↑	1.50E-03	5.93E-03	3.94	<0.001
ko00510 N-Glycan biosynthesis	↑	2.95E-04	1.16E-03	3.94	<0.001
ko01053 Biosynthesis of siderophore group nonribosomal peptides	↑	3.22E-04	1.24E-03	3.86	<0.001
ko00523 Polyketide sugar unit biosynthesis	↑	3.73E-04	1.44E-03	3.86	<0.001
ko00902 Monoterpenoid biosynthesis	↑	2.37E-06	9.02E-06	3.81	<0.001

ko03450 Non-homologous end-joining	↑	2.95E-05	1.11E-04	3.77	<0.001
ko05210 Colorectal cancer	↑	5.38E-07	2.00E-06	3.73	<0.001
ko05416 Viral myocarditis	↑	5.38E-07	2.00E-06	3.73	<0.001
ko00331 Clavulanic acid biosynthesis	↑	4.96E-07	1.83E-06	3.69	<0.001
ko00906 Carotenoid biosynthesis	↑	1.97E-04	7.01E-04	3.55	<0.001
ko04610 Complement and coagulation cascades	↑	2.73E-06	9.45E-06	3.46	<0.001
ko05131 Shigellosis	↑	4.32E-05	1.45E-04	3.35	<0.001
ko00830 Retinol metabolism	↑	1.10E-04	3.62E-04	3.29	<0.001
ko00071 Fatty acid metabolism	↑	6.18E-04	2.02E-03	3.27	<0.001
ko00281 Geraniol degradation	↑	4.59E-04	1.47E-03	3.21	<0.001
ko00901 Indole alkaloid biosynthesis	↑	9.15E-07	2.91E-06	3.18	<0.001
ko01056 Biosynthesis of type II polyketide backbone	↑	8.57E-06	2.70E-05	3.15	<0.001
ko05322 Systemic lupus erythematosus	↑	2.03E-06	6.38E-06	3.14	<0.001
ko00626 Naphthalene degradation	↑	3.71E-04	1.15E-03	3.10	<0.001
ko00040 Pentose and glucuronate interconversions	↑	1.64E-03	4.72E-03	2.88	<0.001
ko05130 Pathogenic Escherichia coli infection	↑	1.81E-05	5.09E-05	2.81	<0.001
ko00052 Galactose metabolism	↑	3.08E-03	8.32E-03	2.70	<0.001
ko00351 DDT degradation	↑	1.98E-05	5.27E-05	2.66	<0.001
ko01055 Biosynthesis of vancomycin group antibiotics	↑	1.93E-04	5.02E-04	2.60	<0.001
ko04910 Insulin signaling pathway	↑	3.72E-04	9.67E-04	2.60	<0.001
ko00521 Streptomycin biosynthesis	↑	9.45E-04	2.44E-03	2.58	<0.001
ko05168 Herpes simplex infection	↑	9.50E-07	2.40E-06	2.53	<0.001
ko00960 Tropane, piperidine and pyridine alkaloid biosynthesis	↑	3.36E-04	8.49E-04	2.52	<0.001
ko00363 Bisphenol degradation	↑	7.02E-04	1.70E-03	2.42	<0.001
ko00627 Aminobenzoate degradation	↑	1.28E-03	3.08E-03	2.41	<0.001
ko00140 Steroid hormone biosynthesis	↑	2.19E-04	5.21E-04	2.38	<0.001
ko00562 Inositol phosphate metabolism	↑	8.30E-04	1.97E-03	2.37	<0.001
ko05032 Morphine addiction	↑	1.13E-05	2.68E-05	2.37	<0.001
ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate	↑	1.01E-04	2.26E-04	2.25	<0.001
ko00601 Glycosphingolipid biosynthesis - lacto and neolacto series	↑	2.56E-05	5.71E-05	2.23	<0.001
ko00591 Linoleic acid metabolism	↑	4.70E-04	1.03E-03	2.19	<0.001
ko04080 Neuroactive ligand-receptor interaction	↑	2.98E-07	6.41E-07	2.15	<0.001
ko00565 Ether lipid metabolism	↑	9.03E-05	1.92E-04	2.13	<0.001
ko03050 Proteasome	↑	3.79E-05	8.00E-05	2.11	<0.001
ko00903 Limonene and pinene degradation	↑	7.62E-04	1.60E-03	2.11	<0.001
ko00362 Benzoate degradation	↑	1.62E-03	3.37E-03	2.08	<0.001
ko03040 Spliceosome	↑	1.13E-05	2.27E-05	2.01	<0.001
ko00650 Butanoate metabolism	↑	3.16E-03	6.19E-03	1.96	<0.001
ko00290 Valine, leucine and isoleucine biosynthesis	↑	2.26E-03	4.35E-03	1.93	<0.001
ko00920 Sulfur metabolism	↑	1.84E-03	3.52E-03	1.92	<0.001
ko04723 Retrograde endocannabinoid signaling	↑	6.30E-05	1.17E-04	1.85	<0.001
ko03013 RNA transport	↑	1.32E-03	2.24E-03	1.70	<0.001
ko00360 Phenylalanine metabolism	↑	2.36E-03	3.98E-03	1.69	<0.001
ko00625 Chloroalkane and chloroalkene degradation	↑	1.31E-03	2.05E-03	1.56	<0.001
ko00622 Xylene degradation	↑	2.40E-04	3.72E-04	1.55	<0.001
ko00621 Dioxin degradation	↑	2.19E-04	3.39E-04	1.54	<0.001
ko00340 Histidine metabolism	↑	5.44E-03	8.05E-03	1.48	<0.001
ko00010 Glycolysis / Gluconeogenesis	↑	6.89E-03	1.00E-02	1.45	<0.001

ko02010 ABC transporters	↑	5.74E-02	8.12E-02	1.41	<0.001
ko00670 One carbon pool by folate	↑	3.95E-03	5.58E-03	1.41	<0.001
ko00310 Lysine degradation	↑	2.77E-03	3.91E-03	1.41	<0.001
ko04141 Protein processing in endoplasmic reticulum	↑	4.08E-04	5.62E-04	1.38	<0.001
ko05111 Vibrio cholerae pathogenic cycle	↑	2.14E-03	2.93E-03	1.37	<0.001
ko00460 Cyanoamino acid metabolism	↑	1.42E-03	1.91E-03	1.35	<0.001
ko00051 Fructose and mannose metabolism	↑	1.13E-02	1.52E-02	1.35	<0.001
ko00280 Valine, leucine and isoleucine degradation	↑	3.04E-03	4.08E-03	1.34	<0.001
ko00440 Phosphonate and phosphinate metabolism	↑	9.07E-04	1.21E-03	1.34	<0.001
ko00710 Carbon fixation in photosynthetic organisms	↑	3.42E-03	4.57E-03	1.33	<0.001
ko05132 Salmonella infection	↑	1.05E-03	1.39E-03	1.33	<0.001
ko04621 NOD-like receptor signaling pathway	↑	3.61E-04	4.77E-04	1.32	<0.001
ko00524 Butirosin and neomycin biosynthesis	↑	2.18E-04	2.87E-04	1.31	<0.001
ko00473 D-Alanine metabolism	↑	2.44E-03	3.09E-03	1.27	<0.001
ko04514 Cell adhesion molecules (CAMs)	↑	6.60E-09	8.37E-09	1.27	<0.001
ko05412 Arrhythmogenic right ventricular cardiomyopathy (ARVC)	↑	6.60E-09	8.37E-09	1.27	<0.001
ko05414 Dilated cardiomyopathy	↑	6.60E-09	8.37E-09	1.27	<0.001
ko01051 Biosynthesis of ansamycins	↑	9.85E-04	1.23E-03	1.25	<0.001
ko00950 Isoquinoline alkaloid biosynthesis	↑	1.86E-04	2.31E-04	1.25	<0.001
ko01040 Biosynthesis of unsaturated fatty acids	↑	1.16E-03	1.41E-03	1.22	<0.001
ko00260 Glycine, serine and threonine metabolism	↑	1.06E-02	1.27E-02	1.20	<0.001
ko00983 Drug metabolism - other enzymes	↑	3.16E-03	3.78E-03	1.20	<0.001
ko00760 Nicotinate and nicotinamide metabolism	↑	7.07E-03	8.23E-03	1.16	<0.001
ko00196 Photosynthesis - antenna proteins	↑	4.84E-07	5.61E-07	1.16	<0.001
ko00230 Purine metabolism	↑	3.39E-02	3.92E-02	1.16	<0.001
ko00640 Propanoate metabolism	↑	3.85E-03	4.42E-03	1.15	<0.001
ko00620 Pyruvate metabolism	↑	1.09E-02	1.25E-02	1.15	<0.001
ko05340 Primary immunodeficiency	↑	4.72E-04	5.38E-04	1.14	<0.001
ko00480 Glutathione metabolism	↑	6.48E-03	7.33E-03	1.13	<0.001
ko02020 Two-component system	↑	4.35E-02	4.91E-02	1.13	<0.001
ko04724 Glutamatergic synapse	↑	2.94E-04	3.30E-04	1.12	<0.001
ko00350 Tyrosine metabolism	↑	4.58E-03	5.14E-03	1.12	<0.001
ko04964 Proximal tubule bicarbonate reclamation	↑	1.15E-04	1.28E-04	1.11	<0.001
ko00450 Selenocompound metabolism	↑	4.87E-03	5.39E-03	1.11	<0.001
ko03008 Ribosome biogenesis in eukaryotes	↑	8.24E-04	9.10E-04	1.10	<0.001
ko00730 Thiamine metabolism	↑	6.65E-03	7.32E-03	1.10	<0.001
ko00520 Amino sugar and nucleotide sugar metabolism	↑	2.01E-02	2.21E-02	1.10	<0.001
ko04978 Mineral absorption	↑	3.27E-04	3.60E-04	1.10	<0.001
ko00550 Peptidoglycan biosynthesis	↑	1.71E-02	1.87E-02	1.10	<0.001
ko00561 Glycerolipid metabolism	↑	5.19E-03	5.68E-03	1.09	<0.001
ko03440 Homologous recombination	↑	1.56E-02	1.70E-02	1.09	<0.001
ko00380 Tryptophan metabolism	↑	1.29E-03	1.40E-03	1.09	<0.001
ko00720 Carbon fixation pathways in prokaryotes	↑	8.78E-03	9.44E-03	1.08	<0.001
ko00860 Porphyrin and chlorophyll metabolism	↑	1.69E-02	1.80E-02	1.07	<0.001
ko00908 Zeatin biosynthesis	↑	1.11E-03	1.18E-03	1.06	<0.001
ko00020 Citrate cycle (TCA cycle)	↑	5.72E-03	6.05E-03	1.06	<0.001
ko04146 Peroxisome	↑	1.78E-03	1.88E-03	1.06	<0.001
ko03018 RNA degradation	↑	1.51E-02	1.58E-02	1.05	<0.001
ko00250 Alanine, aspartate and glutamate metabolism	↑	1.18E-02	1.23E-02	1.04	<0.001

ko00770 Pantothenate and CoA biosynthesis	↓	7.84E-03	7.72E-03	0.99	<0.001
ko04070 Phosphatidylinositol signaling system	↓	7.66E-04	7.48E-04	0.98	<0.001
ko00061 Fatty acid biosynthesis	↓	7.87E-03	7.60E-03	0.97	<0.001
ko00240 Pyrimidine metabolism	↓	3.04E-02	2.94E-02	0.97	<0.001
ko00910 Nitrogen metabolism	↓	1.64E-02	1.57E-02	0.96	<0.001
ko05152 Tuberculosis	↓	1.95E-03	1.85E-03	0.95	<0.001
ko04626 Plant-pathogen interaction	↓	2.90E-03	2.75E-03	0.95	<0.001
ko00750 Vitamin B6 metabolism	↓	3.84E-03	3.62E-03	0.94	<0.001
ko00642 Ethylbenzene degradation	↓	1.09E-03	1.03E-03	0.94	<0.001
ko00930 Caprolactam degradation	↓	6.22E-04	5.88E-04	0.94	<0.001
ko00564 Glycerophospholipid metabolism	↓	1.04E-02	9.83E-03	0.94	<0.001
ko00130 Ubiquinone and other terpenoid-quinone biosynthesis	↓	6.94E-03	6.54E-03	0.94	<0.001
ko00401 Novobiocin biosynthesis	↓	8.05E-04	7.57E-04	0.94	<0.001
ko00680 Methane metabolism	↓	1.29E-02	1.20E-02	0.94	<0.001
ko00630 Glyoxylate and dicarboxylate metabolism	↓	9.50E-03	8.84E-03	0.93	<0.001
ko05010 Alzheimers disease	↓	1.19E-03	1.09E-03	0.91	<0.001
ko03030 DNA replication	↓	8.94E-03	8.13E-03	0.91	<0.001
ko00643 Styrene degradation	↓	4.73E-04	4.28E-04	0.90	<0.001
ko03420 Nucleotide excision repair	↓	1.58E-02	1.43E-02	0.90	<0.001
ko00072 Synthesis and degradation of ketone bodies	↓	4.93E-04	4.39E-04	0.89	<0.001
ko00270 Cysteine and methionine metabolism	↓	1.44E-02	1.27E-02	0.88	<0.001
ko00300 Lysine biosynthesis	↓	1.23E-02	1.08E-02	0.88	<0.001
ko00330 Arginine and proline metabolism	↓	1.91E-02	1.67E-02	0.88	<0.001
ko03060 Protein export	↓	9.61E-03	8.36E-03	0.87	<0.001
ko04940 Type I diabetes mellitus	↓	5.26E-04	4.56E-04	0.87	<0.001
ko00970 Aminoacyl-tRNA biosynthesis	↓	4.65E-02	3.98E-02	0.86	<0.001
ko03010 Ribosome	↓	2.87E-02	2.45E-02	0.85	<0.001
ko00471 D-Glutamine and D-glutamate metabolism	↓	2.83E-03	2.39E-03	0.84	<0.001
ko00900 Terpenoid backbone biosynthesis	↓	1.32E-02	1.11E-02	0.84	<0.001
ko00190 Oxidative phosphorylation	↓	1.89E-02	1.56E-02	0.83	<0.001
ko00430 Taurine and hypotaurine metabolism	↓	1.84E-03	1.50E-03	0.82	<0.001
ko00195 Photosynthesis	↓	4.11E-03	3.26E-03	0.79	<0.001
ko00740 Riboflavin metabolism	↓	6.16E-03	4.88E-03	0.79	<0.001
ko03020 RNA polymerase	↓	3.71E-03	2.91E-03	0.78	<0.001
ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	↓	1.69E-02	1.29E-02	0.77	<0.001
ko04112 Cell cycle - Caulobacter	↓	1.92E-02	1.45E-02	0.76	<0.001
ko00780 Biotin metabolism	↓	8.37E-03	6.17E-03	0.74	<0.001
ko04122 Sulfur relay system	↓	6.75E-03	4.96E-03	0.73	<0.001
ko00790 Folate biosynthesis	↓	1.02E-02	7.46E-03	0.73	<0.001
ko00062 Fatty acid elongation	↓	2.95E-05	2.17E-05	0.73	<0.001
ko00624 Polycyclic aromatic hydrocarbon degradation	↓	3.78E-03	2.64E-03	0.70	<0.001
ko05146 Amoebiasis	↓	5.08E-04	3.44E-04	0.68	<0.001
ko00253 Tetracycline biosynthesis	↓	7.15E-04	4.48E-04	0.63	<0.001
ko00791 Atrazine degradation	↓	1.58E-03	9.82E-04	0.62	<0.001
ko04210 Apoptosis	↓	9.42E-04	5.70E-04	0.61	<0.001
ko05200 Pathways in cancer	↓	7.33E-04	4.35E-04	0.59	<0.001
ko05211 Renal cell carcinoma	↓	4.16E-04	2.45E-04	0.59	<0.001
ko04721 Synaptic vesicle cycle	↓	2.26E-05	1.31E-05	0.58	<0.001
ko04962 Vasopressin-regulated water reabsorption	↓	2.26E-05	1.31E-05	0.58	<0.001

ko05215 Prostate cancer	↓	3.15E-04	1.82E-04	0.58	<0.001
ko04612 Antigen processing and presentation	↓	3.14E-04	1.78E-04	0.57	<0.001
ko04914 Progesterone-mediated oocyte maturation	↓	3.14E-04	1.78E-04	0.57	<0.001
ko00540 Lipopolysaccharide biosynthesis	↓	2.05E-02	1.17E-02	0.57	<0.001
ko05016 Huntingtons disease	↓	8.81E-04	4.87E-04	0.55	<0.001
ko03070 Bacterial secretion system	↓	2.82E-02	1.54E-02	0.55	<0.001
ko00633 Nitrotoluene degradation	↓	3.60E-03	1.82E-03	0.50	<0.001
ko02030 Bacterial chemotaxis	↓	1.21E-02	6.05E-03	0.50	<0.001
ko05134 Legionellosis	↓	6.87E-03	3.43E-03	0.50	<0.001
ko05012 Parkinsons disease	↓	4.10E-04	1.93E-04	0.47	<0.001
ko05014 Amyotrophic lateral sclerosis (ALS)	↓	5.73E-04	2.61E-04	0.46	<0.001
ko03015 mRNA surveillance pathway	↓	8.27E-05	3.49E-05	0.42	<0.001
ko04115 p53 signaling pathway	↓	1.11E-05	4.57E-06	0.41	<0.001
ko04260 Cardiac muscle contraction	↓	3.47E-04	1.37E-04	0.39	<0.001
ko00592 alpha-Linolenic acid metabolism	↓	6.43E-04	2.23E-04	0.35	<0.001
ko02040 Flagellar assembly	↓	3.32E-02	9.38E-03	0.28	<0.001
ko05120 Epithelial cell signaling in Helicobacter pylori infection	↓	6.01E-02	1.28E-02	0.21	<0.001
ko04975 Fat digestion and absorption	↓	2.97E-05	5.76E-06	0.19	<0.001
Failed treatment group					
None					

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[a] The fold change was calculated as the ratio of the mean relative frequency after treatment to the mean relative frequency before treatment.

[b] Paired *t*-test after arcsine transformation of relative frequency and q values were used after adjustment for multiple comparison by the FDR.

Supplementary table 5. Significant changes in predicted metabolic pathways after anti-*H. pylori* treatment in stool samples

	Alteration trend after treatment	Mean relative frequency before treatment	Mean relative frequency after treatment	Fold change[a]	q value[b]
Successful eradication group					
ko05145 Toxoplasmosis	↑	1.18E-06	2.01E-06	1.71	0.033
ko00062 Fatty acid elongation	↑	6.25E-06	9.73E-06	1.56	<0.001
ko05160 Hepatitis C	↑	1.35E-07	1.96E-07	1.45	0.036
ko05162 Measles	↑	1.35E-07	1.96E-07	1.45	0.036
ko01057 Biosynthesis of type II polyketide products	↑	2.38E-05	3.00E-05	1.26	0.003
ko03040 Spliceosome	↑	2.70E-05	3.37E-05	1.25	0.025
ko03450 Non-homologous end-joining	↑	5.92E-05	7.15E-05	1.21	0.015
ko05034 Alcoholism	↑	6.25E-06	7.50E-06	1.20	0.037
ko05100 Bacterial invasion of epithelial cells	↑	1.03E-03	1.23E-03	1.19	0.049
ko05143 African trypanosomiasis	↑	4.41E-04	5.25E-04	1.19	<0.001
ko05150 Staphylococcus aureus infection	↑	1.17E-03	1.38E-03	1.17	0.022
ko00984 Steroid degradation	↑	6.76E-05	7.87E-05	1.16	0.042
ko00253 Tetracycline biosynthesis	↑	2.05E-04	2.36E-04	1.15	0.017
ko00072 Synthesis and degradation of ketone bodies	↑	2.02E-04	2.31E-04	1.14	0.016
ko02010 ABC transporters	↑	7.78E-02	8.57E-02	1.10	0.006
ko00791 Atrazine degradation	↑	6.00E-04	6.54E-04	1.09	0.032
ko00473 D-Alanine metabolism	↑	3.84E-03	4.17E-03	1.08	0.006
ko04910 Insulin signaling pathway	↑	1.66E-03	1.78E-03	1.07	0.017
ko00450 Selenocompound metabolism	↑	5.18E-03	5.42E-03	1.05	0.009
ko00401 Novobiocin biosynthesis	↑	7.18E-04	7.49E-04	1.04	0.022
ko00030 Pentose phosphate pathway	↑	7.77E-03	8.00E-03	1.03	0.019
ko00400 Phenylalanine, tyrosine and tryptophan biosynthesis	↑	1.26E-02	1.29E-02	1.03	0.010
ko00620 Pyruvate metabolism	↓	1.06E-02	1.04E-02	0.98	0.025
ko00190 Oxidative phosphorylation	↓	1.62E-02	1.58E-02	0.97	0.015
ko00260 Glycine, serine and threonine metabolism	↓	1.20E-02	1.17E-02	0.97	0.010
ko00650 Butanoate metabolism	↓	5.67E-03	5.47E-03	0.96	0.019
ko00591 Linoleic acid metabolism	↓	1.13E-03	1.09E-03	0.96	0.026
ko00910 Nitrogen metabolism	↓	1.47E-02	1.41E-02	0.96	0.027
ko00520 Amino sugar and nucleotide sugar metabolism	↓	2.86E-02	2.73E-02	0.95	0.015
ko05200 Pathways in cancer	↓	3.76E-04	3.58E-04	0.95	0.048
ko04727 GABAergic synapse	↓	5.44E-04	5.16E-04	0.95	0.036
ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate	↓	4.22E-04	3.98E-04	0.94	0.042
ko00051 Fructose and mannose metabolism	↓	1.98E-02	1.87E-02	0.94	0.006
ko00020 Citrate cycle (TCA cycle)	↓	4.73E-03	4.45E-03	0.94	0.044
ko00430 Taurine and hypotaurine metabolism	↓	8.73E-04	8.18E-04	0.94	0.025
ko00280 Valine, leucine and isoleucine degradation	↓	2.79E-03	2.61E-03	0.94	0.030
ko00521 Streptomycin biosynthesis	↓	3.37E-03	3.14E-03	0.93	0.009
ko00780 Biotin metabolism	↓	4.90E-03	4.55E-03	0.93	0.031
ko00523 Polyketide sugar unit biosynthesis	↓	2.36E-03	2.19E-03	0.93	0.006
ko04612 Antigen processing and presentation	↓	2.21E-04	2.05E-04	0.93	0.026
ko04914 Progesterone-mediated oocyte maturation	↓	2.21E-04	2.05E-04	0.93	0.026
ko01055 Biosynthesis of vancomycin group antibiotics	↓	7.05E-04	6.55E-04	0.93	0.006
ko00311 Penicillin and cephalosporin biosynthesis	↓	5.33E-04	4.93E-04	0.92	0.025

ko04621 NOD-like receptor signaling pathway	↓	5.70E-04	5.17E-04	0.91	0.034
ko05215 Prostate cancer	↓	2.48E-04	2.25E-04	0.91	0.010
ko00130 Ubiquinone and other terpenoid-quinone biosynthesis	↓	4.48E-03	4.05E-03	0.90	0.033
ko00460 Cyanoamino acid metabolism	↓	3.05E-03	2.75E-03	0.90	0.019
ko00440 Phosphonate and phosphinate metabolism	↓	1.07E-03	9.63E-04	0.90	0.036
ko00511 Other glycan degradation	↓	1.11E-02	9.87E-03	0.89	0.032
ko00600 Sphingolipid metabolism	↓	4.88E-03	4.33E-03	0.89	0.047
ko00940 Phenylpropanoid biosynthesis	↓	2.28E-03	2.02E-03	0.89	0.032
ko04964 Proximal tubule bicarbonate reclamation	↓	8.54E-05	7.57E-05	0.89	0.030
ko00830 Retinol metabolism	↓	2.63E-04	2.32E-04	0.88	0.032
ko00785 Lipoic acid metabolism	↓	1.33E-03	1.14E-03	0.86	0.022
ko04113 Meiosis - yeast	↓	1.08E-03	9.09E-04	0.84	0.020
ko00590 Arachidonic acid metabolism	↓	3.26E-04	2.75E-04	0.84	0.017
ko04210 Apoptosis	↓	7.53E-04	6.24E-04	0.83	0.001
ko00540 Lipopolysaccharide biosynthesis	↓	6.99E-03	5.77E-03	0.83	0.014
ko04974 Protein digestion and absorption	↓	2.19E-03	1.80E-03	0.82	0.034
ko00364 Fluorobenzoate degradation	↓	5.94E-05	4.86E-05	0.82	0.038
ko04142 Lysosome	↓	2.97E-03	2.43E-03	0.82	0.026
ko04723 Retrograde endocannabinoid signaling	↓	1.63E-04	1.32E-04	0.81	0.048
ko00604 Glycosphingolipid biosynthesis - ganglio series	↓	5.90E-04	4.75E-04	0.80	0.015
ko04310 Wnt signaling pathway	↓	3.61E-06	2.90E-06	0.80	0.001
ko04330 Notch signaling pathway	↓	3.61E-06	2.90E-06	0.80	0.001
ko05220 Chronic myeloid leukemia	↓	3.61E-06	2.90E-06	0.80	0.001
ko05410 Hypertrophic cardiomyopathy (HCM)	↓	9.99E-06	7.86E-06	0.79	0.009
ko00531 Glycosaminoglycan degradation	↓	2.48E-03	1.94E-03	0.78	0.009
ko00140 Steroid hormone biosynthesis	↓	8.71E-04	6.81E-04	0.78	0.019
ko05322 Systemic lupus erythematosus	↓	1.43E-05	1.06E-05	0.74	0.036
ko03015 mRNA surveillance pathway	↓	4.13E-05	2.98E-05	0.72	0.006
Failed treatment group					
ko00902 Monoterpenoid biosynthesis	↑	7.01E-08	2.88E-07	4.11	0.006
ko04916 Melanogenesis	↑	6.66E-09	2.28E-08	3.38	0.018
ko00513 Various types of N-glycan biosynthesis	↑	8.99E-06	2.11E-05	2.35	0.032
ko05210 Colorectal cancer	↑	1.07E-07	2.37E-07	2.21	0.032
ko05416 Viral myocarditis	↑	1.07E-07	2.37E-07	2.21	0.032
ko05110 Vibrio cholerae infection	↑	6.68E-06	1.24E-05	1.85	0.049
ko00909 Sesquiterpenoid and triterpenoid biosynthesis	↑	3.48E-06	6.03E-06	1.73	0.032
ko00901 Indole alkaloid biosynthesis	↑	3.17E-07	5.28E-07	1.66	0.036
ko04115 p53 signaling pathway	↑	4.89E-07	8.10E-07	1.66	0.032
ko05145 Toxoplasmosis	↑	8.90E-07	1.46E-06	1.64	0.024
ko05168 Herpes simplex infection	↑	2.65E-07	4.06E-07	1.53	0.032
ko00592 alpha-Linolenic acid metabolism	↑	3.89E-05	5.80E-05	1.49	0.019
ko00062 Fatty acid elongation	↑	5.52E-06	7.62E-06	1.38	0.020
ko05014 Amyotrophic lateral sclerosis (ALS)	↑	4.60E-05	6.31E-05	1.37	0.040
ko00984 Steroid degradation	↑	5.67E-05	7.58E-05	1.34	0.018
ko04512 ECM-receptor interaction	↑	5.65E-06	7.52E-06	1.33	0.024
ko04510 Focal adhesion	↑	5.66E-06	7.52E-06	1.33	0.024
ko05100 Bacterial invasion of epithelial cells	↑	9.71E-04	1.28E-03	1.31	0.022
ko00643 Styrene degradation	↑	8.89E-05	1.11E-04	1.25	0.026
ko00351 DDT degradation	↑	2.48E-05	3.09E-05	1.24	0.019

ko00380 Tryptophan metabolism	↑	3.94E-04	4.82E-04	1.22	0.027
ko05222 Small cell lung cancer	↑	4.21E-06	5.01E-06	1.19	0.029
ko00253 Tetracycline biosynthesis	↑	1.89E-04	2.22E-04	1.17	0.018
ko05016 Huntingtons disease	↑	2.02E-04	2.33E-04	1.15	0.036
ko00072 Synthesis and degradation of ketone bodies	↑	1.84E-04	2.11E-04	1.15	0.024
ko00791 Atrazine degradation	↑	5.84E-04	6.49E-04	1.11	0.027
ko00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis	↑	5.62E-05	6.21E-05	1.10	0.033
ko00361 Chlorocyclohexane and chlorobenzene degradation	↑	3.67E-04	4.01E-04	1.10	0.019
ko01040 Biosynthesis of unsaturated fatty acids	↑	7.93E-04	8.66E-04	1.09	0.032
ko00626 Naphthalene degradation	↑	8.33E-04	8.93E-04	1.07	0.027
ko00450 Selenocompound metabolism	↑	5.09E-03	5.40E-03	1.06	0.019
ko00030 Pentose phosphate pathway	↑	7.47E-03	7.87E-03	1.05	0.019
ko00564 Glycerophospholipid metabolism	↑	8.47E-03	8.79E-03	1.04	0.032
ko00627 Aminobenzoate degradation	↑	2.38E-03	2.43E-03	1.02	0.044
ko00500 Starch and sucrose metabolism	↓	3.04E-02	2.91E-02	0.96	0.027
ko00051 Fructose and mannose metabolism	↓	2.02E-02	1.91E-02	0.95	0.019
ko01055 Biosynthesis of vancomycin group antibiotics	↓	7.10E-04	6.72E-04	0.95	0.032
ko00521 Streptomycin biosynthesis	↓	3.39E-03	3.19E-03	0.94	0.032
ko04724 Glutamatergic synapse	↓	4.98E-04	4.68E-04	0.94	0.032
ko00523 Polyketide sugar unit biosynthesis	↓	2.36E-03	2.21E-03	0.94	0.027
ko00532 Glycosaminoglycan biosynthesis - chondroitin sulfate	↓	4.23E-04	3.95E-04	0.93	0.049
ko04973 Carbohydrate digestion and absorption	↓	1.20E-03	1.09E-03	0.91	0.027
ko04978 Mineral absorption	↓	3.34E-04	3.04E-04	0.91	0.032
ko04210 Apoptosis	↓	7.87E-04	6.95E-04	0.88	0.032
ko04310 Wnt signaling pathway	↓	3.97E-06	3.45E-06	0.87	0.032
ko04330 Notch signaling pathway	↓	3.97E-06	3.45E-06	0.87	0.032
ko05220 Chronic myeloid leukemia	↓	3.97E-06	3.45E-06	0.87	0.032
ko03015 mRNA surveillance pathway	↓	4.53E-05	3.54E-05	0.78	0.020

[a] The fold change was calculated as the ratio of the mean relative frequency after treatment to the mean relative frequency before treatment.

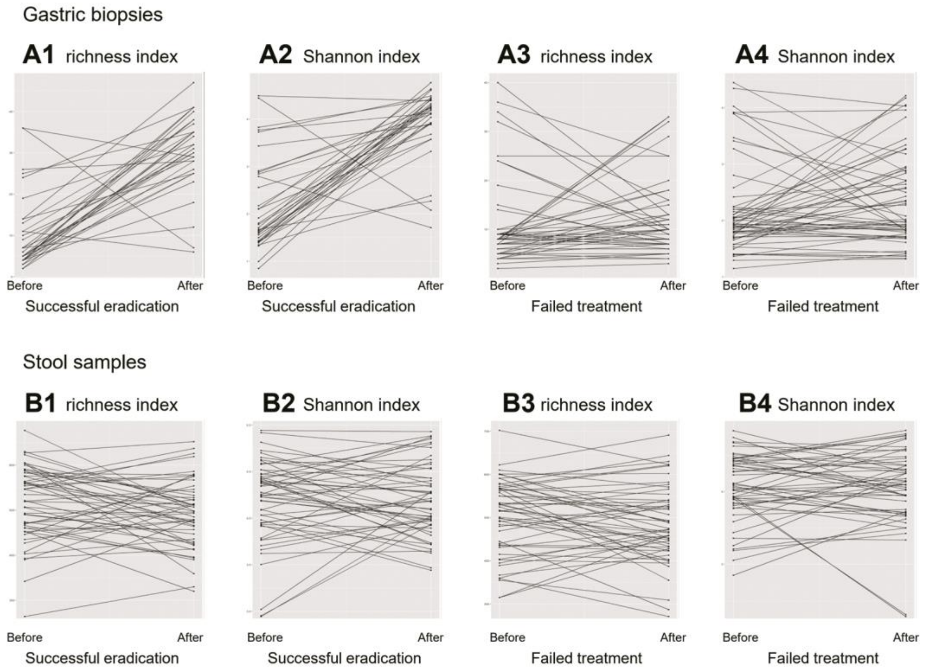
[b] Paired *t*-test after arcsine transformation of relative frequency and q values were used after adjustment for multiple comparison by the FDR.

Supplementary table 6. Associations of differential gastric genera after *H. pylori* eradication with gastric lesions

Differential gastric genera	**Normal/SG** n=32	**CAG** n=42			**IM/DYS** n=61		
	Median of relative abundance (Interquartile range)	Median of relative abundance (Interquartile range)	OR (95% CI)[a]	*P*	Median of relative abundance (Interquartile range)	OR (95% CI)[a]	*P*
g__Alloprevotella	**0.90% (0.19%-2.78%)**	**0.09% (0.03%-0.68%)**	**0.60 (0.39-0.92)**	**0.019**	**0.11% (0.02%-0.58%)**	**0.71 (0.51-0.98)**	**0.037**
g__Bacteroides	0.33% (0.11%-0.66%)	0.13% (0.03%-0.50%)	0.40 (0.13-1.25)	0.115	0.15% (0.05%-0.63%)	0.95 (0.74-1.22)	0.700
g__Corynebacterium	0.15% (0.03%-0.25%)	0.04% (0.01%-0.24%)	0.87 (0.62-1.24)	0.453	0.04% (0.02%-0.22%)	0.83 (0.53-1.30)	0.424
g__Fusobacterium	**1.95% (0.47%-4.39%)**	**0.18% (0.08%-0.86%)**	**0.58 (0.41-0.82)**	**0.002**	**0.28% (0.07%-1.2%)**	**0.68 (0.52-0.88)**	**0.004**
g__Gemella	0.53% (0.11%-0.89%)	0.09% (0.02%-0.50%)	0.49 (0.22-1.11)	0.088	0.12% (0.03%-0.55%)	0.61 (0.29-1.30)	0.201
g__Haemophilus	3.81% (0.86%-6.88%)	0.47% (0.08%-1.76%)	0.83 (0.73-0.96)	0.009	0.65% (0.08%-2.53%)	0.91 (0.82-1.01)	0.064
g__Helicobacter	**2.26% (0.76%-16.01%)**	**90.09% (24.85%-96.62%)**	**1.03 (1.02-1.05)**	**<0.001**	**86.66% (29.47%-96.53%)**	**1.03 (1.01-1.04)**	**<0.001**
g__Neisseria	**5.80% (0.98%-12.02%)**	**0.42% (0.13%-3.71%)**	**0.89 (0.82-0.97)**	**0.006**	**0.72% (0.14%-3.07%)**	**0.85 (0.77-0.94)**	**0.001**
g__Porphyromonas	**1.65% (0.36%-3.04%)**	**0.19% (0.04%-0.73%)**	**0.63 (0.46-0.87)**	**0.005**	**0.23% (0.06%-0.9%)**	**0.58 (0.41-0.82)**	**0.002**
g__Prevotella	**3.62% (1.57%-6.85%)**	**0.48% (0.17%-2.13%)**	**0.81 (0.69-0.95)**	**0.009**	**0.42% (0.15%-1.79%)**	**0.80 (0.68-0.93)**	**0.004**
g__Rothia	**1.25% (0.34%-2.38%)**	**0.09% (0.02%-0.62%)**	**0.40 (0.22-0.73)**	**0.003**	**0.16% (0.04%-0.92%)**	**0.44 (0.28-0.71)**	**<0.001**
g__Staphylococcus	0.15% (0.03%-0.24%)	0.04% (0.01%-0.26%)	1.53 (0.64-3.67)	0.337	0.04% (0.01%-0.18%)	1.24 (0.80-1.90)	0.336
g__Streptococcus	3.67% (1.64%-7.59%)	0.49% (0.13%-3.38%)	0.79 (0.67-0.93)	0.004	1.00% (0.17%-2.79%)	0.93 (0.86-1.02)	0.110
g__Streptophyta	0.41% (0.05%-1.25%)	0.05% (0.01%-0.52%)	0.88 (0.74-1.06)	0.191	0.32% (0.05%-0.84%)	0.96 (0.92-1.00)	0.072
g__unknown_ Bacteria	**11.43% (3.39%-17.94%)**	**0.88% (0.33%-3.8%)**	**0.94 (0.89-0.99)**	**0.020**	**0.94% (0.43%-6.78%)**	**0.95 (0.90-0.99)**	**0.025**
g__unknown_ Neisseriaceae	0.12% (0.03%-0.29%)	0.03% (0.00%-0.13%)	0.28 (0.05-1.73)	0.171	0.01% (0.00%-0.14%)	0.85 (0.25-2.86)	0.789
g__unknown_ Prevotellaceae	**1.32% (0.49%-2.17%)**	**0.14% (0.05%-0.8%)**	**0.54 (0.34-0.86)**	**0.009**	**0.13% (0.03%-0.59%)**	**0.64 (0.42-0.97)**	**0.034**
g__Veillonella	**0.96% (0.21%-2.23%)**	**0.22% (0.04%-1.00%)**	**0.47 (0.28-0.79)**	**0.005**	**0.33% (0.06%-0.86%)**	**0.63 (0.42-0.95)**	**0.028**

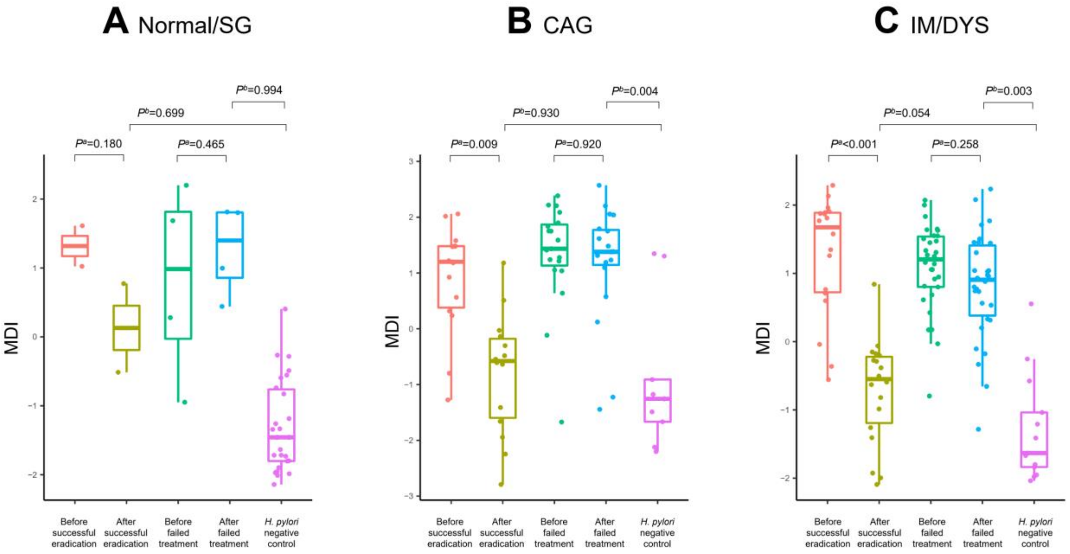
[a] Unconditional logistic regression adjusted for age and sex.

CAG, chronic atrophic gastritis; CI, confidence interval; DYS, dysplasia; IM, intestinal metaplasia; OR, odds ratio; SG, superficial gastritis



Supplementary figure 1. The trends in gastrointestinal microbial diversity before and after anti-*H. pylori* treatment

Paired plots showing alteration trends in (**A1**) gastric richness index before and after successful eradication; (**A2**) gastric Shannon index before and after successful eradication; (**A3**) gastric richness index before and after failed treatment; (**A4**) gastric Shannon index before and after failed treatment; (**B1**) fecal richness index before and after successful eradication; (**B2**) fecal Shannon index before and after successful eradication; (**B3**) fecal richness index before and after failed treatment; (**B4**) fecal Shannon index before and after failed treatment.



Supplementary figure 2. Changes of gastric MDI after anti-*H. pylori* treatment by baseline gastric lesion

Box plots showing decreased gastric MDI following successful eradication compared to that of baseline in groups of baseline (**A**) normal/SG, (**B**) CAG, and (**C**) IM/DYS.

[a]Wilcoxon signed-rank test

[b]Logistic regression adjusted for age and sex

SG, superficial gastritis; CAG, chronic atrophic gastritis; IM, intestinal metaplasia; DYS, dysplasia; MDI, microbial dysbiosis index