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Proton pump inhibitors affect the gut microbiome

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ABSTRACT

Background and aims Proton pump inhibitors (PPIs) are among the top 10 most widely used drugs in the world. PPI use has been associated with an increased risk of enteric infections, most notably *Clostridium difficile*. The gut microbiome plays an important role in enteric infections, by resisting or promoting colonisation by pathogens. In this study, we investigated the influence of PPI use on the gut microbiome.

Methods The gut microbiome composition of 1815 individuals, spanning three cohorts, was assessed by tag sequencing of the 16S rRNA gene. The difference in microbiota composition in PPI users versus non-users was analysed separately in each cohort, followed by a meta-analysis.

Results 211 of the participants were using PPIs at the moment of stool sampling. PPI use is associated with a significant decrease in Shannon's diversity and with changes in 20% of the bacterial taxa (false discovery rate <0.05). Multiple oral bacteria were over-represented in the faecal microbiome of PPI-users, including the genus *Rothia* ($p=9.8 \times 10^{-38}$). In PPI users we observed a significant increase in bacteria: genera *Enterococcus*, *Streptococcus*, *Staphylococcus* and the potentially pathogenic species *Escherichia coli*.

Conclusions The differences between PPI users and non-users observed in this study are consistently associated with changes towards a less healthy gut microbiome. These differences are in line with known changes that predispose to *C. difficile* infections and can potentially explain the increased risk of enteric infections in PPI users. On a population level, the effects of PPI are more prominent than the effects of antibiotics or other commonly used drugs.

BACKGROUND AND AIMS

Proton pump inhibitors (PPIs) are among the top 10 most widely used drugs in the world. In 2013, 7% of the population of the Netherlands used omeprazole. In the same year, esomeprazole was the second largest drug in terms of revenue in the USA.^{1–2} PPIs are used to treat GORD and to prevent gastric and duodenal ulcers.^{3–4} Of the general population, 25% report having heartburn at least once a month, explaining the large demand for PPIs.⁴ Nevertheless, PPIs are frequently prescribed or taken for long periods without evidence-based indication.^{5–6}

PPI use has been associated with increased risk of enteric infections.^{5–7–9} A meta-analysis of 23

Significance of this study**What is already known on this subject**

- Proton pump inhibitors (PPI) use is associated with increased risk of enteric infections, in particular with a 65% increase in incidence of *Clostridium difficile* infection.
- PPI is one of the most commonly used drugs.
- Changes in the gut microbiome can resist or promote the colonisation of enteric infections.

What are the new findings

- PPI use is associated with decreased bacterial richness and profound changes in the gut microbiome: 20% of the identified bacteria in this study showed significant deviation.
- Oral bacteria and potential pathogenic bacteria are increased in the gut microbiota of PPI users.
- On the population level we see more microbial alterations in the gut associated with PPI use than with antibiotics or other drug use.

How might it impact on clinical practice in the foreseeable future?

- Given the widespread use of PPI, the morbidity and mortality associated with enteric infections, and the increasing number of studies investigating the microbiome, healthcare practitioners and researchers should take into consideration the influence of PPI on the gut microbiome.

studies, comprising almost 300 000 patients, showed a 65% increase in the incidence of *Clostridium difficile*-associated diarrhoea among patients who used PPI.⁹ In healthcare-related settings, PPI use also increases the risk of recurrent *C. difficile* infections.⁵ Another meta-analysis of 11 280 patients, from six studies evaluating *Salmonella*, *Campylobacter* and other enteric infections, also found an increased risk due to acid suppression, with a greater association with PPI than with H₂-receptor antagonists.⁸ Recently, the Dutch National Institute for Public Health and the Environment noticed a marked increase in the occurrence of campylobacteriosis associated with increased PPI use in the Netherlands.⁷

The gut microbiome plays an important role in these enteric infections.^{10–13} Gut microbiota can

Table 1 Characteristics of the three independent cohorts in this study

	Cohort 1: Lifelines-DEEP (general population)		Cohort 2: patients with IBD UMCG		Cohort 3: IBS case-control study MUMC	
	PPI users (n=99) Average (SD)*	Non-PPI users (n=1075) Average (SD)*	PPI users (n=60) Average (SD)*	Non-PPI users (n=240) Average (SD)*	PPI users (n=52) Average (SD)*	Non-PPI users (n=289) Average (SD)*
Age	51.94 (13.59)	44.79 (13.58)	50.87 (14.49)	42.45 (14.57)	51.94 (14.27)	44.57 (18.24)
BMI	27.73 (5.10)	25.05 (4.03)	26.14 (5.53)	25.58 (4.72)	26.24 (4.10)	24.16 (4.11)
Gender (% male)	36.36	42.05	61.67	39.17	30.77	33.56
Reads per sample	48879 (43 001)	55 884 (40057)	51 081 (43 990)	52 970 (37787)	43 807 (28604)	65842 (119296)
Antibiotics (%)	2.02	1.02	31.67	16.67	0.00	1.73
IBD (%)	0.00	0.00	100.00	100.00	0.00	0.00
IBS (%)	34.34	25.77	0.00	0.00	90.38	49.48
Diarrhoea (%) (IBS-D and functional diarrhoea together)	7.07	4.47	–	–	28.4	17.3
Average bowel movements per day	1.36 (0.53)	1.38 (0.61)	–	–	1.60 (0.81)	1.92 (1.11)
Anti-TNF-a (%)	–	–	38.33	28.75	–	–
Mesalazine (%)	–	–	26.67	39.58	–	–
Methotrexate (%)	–	–	16.67	5.42	–	–
Steroids (%)	–	–	30.00	20.42	–	–
Thiopurines (%)	–	–	21.67	37.08	–	–

*Unless otherwise stated

IBD, Inflammatory Bowel Disease; IBS, Irritable Bowel Syndrome; SD, standard deviation, BMI, body mass index.

MUMC, Maastricht University Medical Center; PPI, proton pump inhibitor, TNF-a, tumour necrosis factor; UMCG, University Medical Center Groningen.

resist or promote the microbial colonisation of the gut by *C. difficile* and other enteric infections through several mechanisms that either directly inhibit bacterial growth or enhance the

immune system.^{10 11} Moreover, substituting the gut microbiota of patients with *C. difficile*-associated diarrhoea with a healthy microbiome through faecal transplantation has been proven to

Figure 1 PPI-associated statistically significant differences in the gut microbiome. Meta-analysis of three independent cohorts comprising 1815 faecal samples, showing a cladogram (circular hierarchical tree) of 92 significantly increased or decreased bacterial taxa in the gut microbiome of PPI users compared with non-users (FDR<0.05). Each dot represents a bacterial taxon. The two innermost dots represent the highest level of taxonomy in our data: the kingdoms Archaea and Bacteria (prokaryotes), followed outwards by the lower levels: phylum, class, order, family, genus and species. Red dots represent significantly increased taxa. Blue dots represent significantly decreased taxa. FDR, false discovery rate; PPI, proton pump inhibitor.

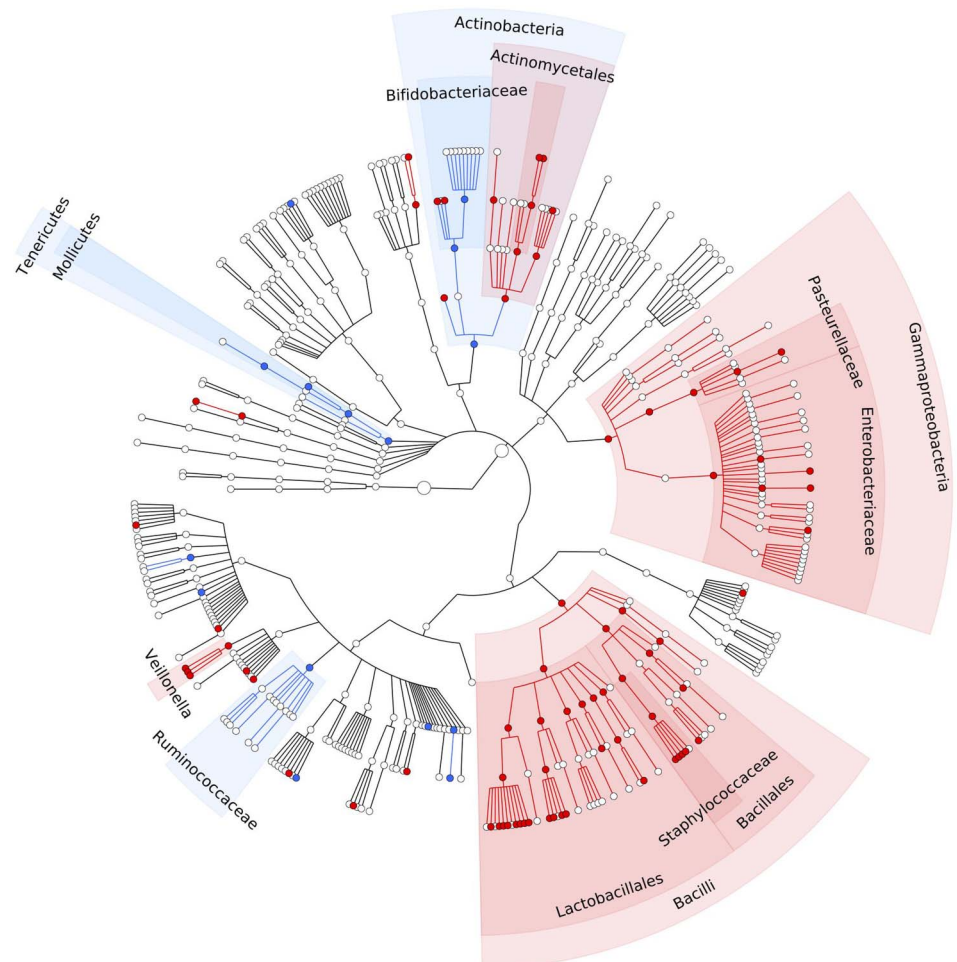
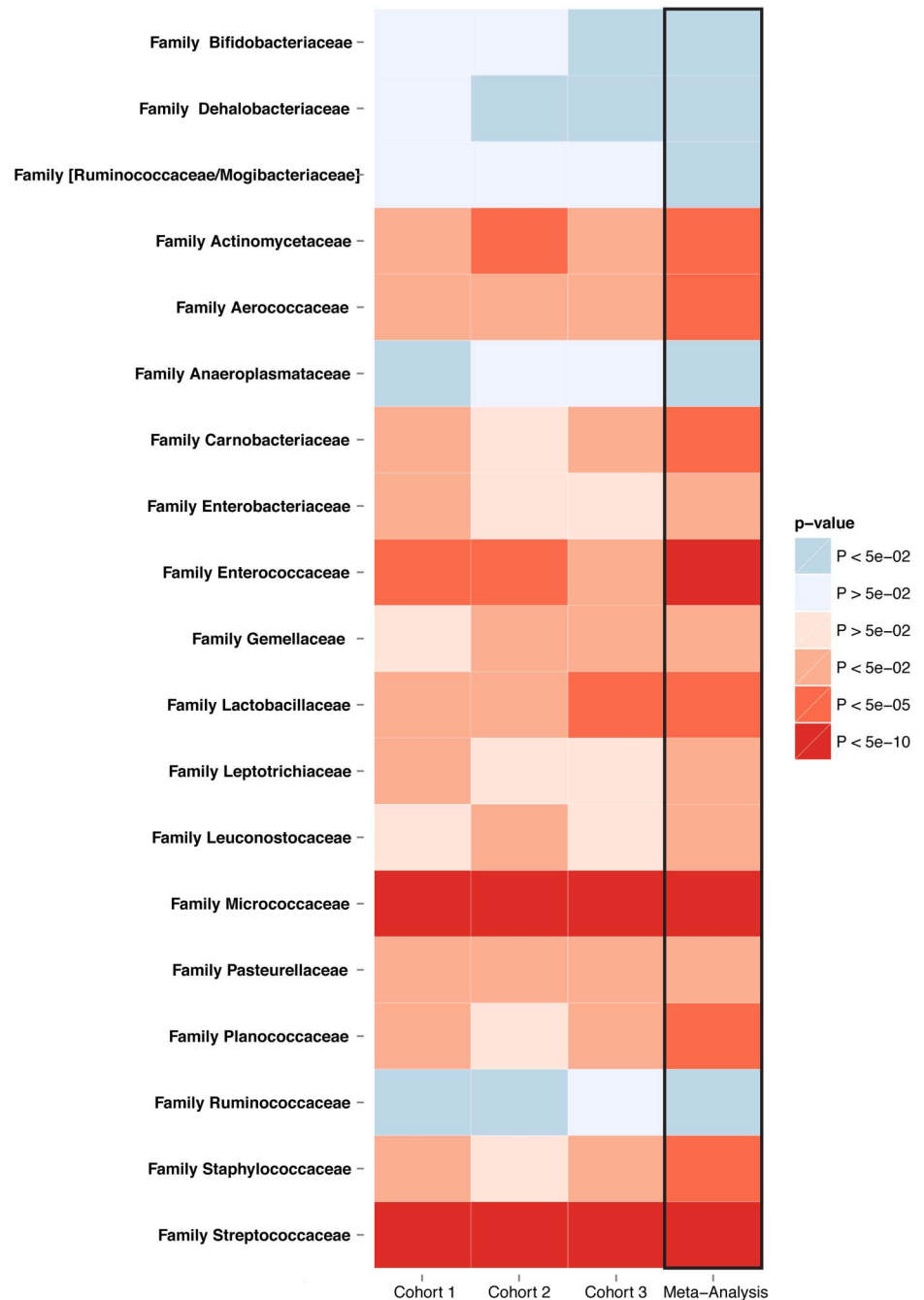


Figure 2 Significantly altered families in PPI users consistent in three cohorts. Meta-analysis of three independent cohorts comprising 1815 faecal samples. The heatmap shows 19 families significantly increased or decreased associated with PPI use in the gut microbiome for each cohort and for the meta-analysis (meta-analysis FDR<0.05). FDR, false discovery rate; PPI, proton pump inhibitor.



cure *C. difficile* infection.¹⁴ The increased incidence of enteric infections in PPI users and the importance of the gut microbiome composition in the development of these infections led us to investigate the influence of PPI use on the gut microbiome.

METHODS

Cohorts

We studied the effect of PPI use on the gut microbial composition in three independent cohorts from the Netherlands. These cohorts together comprise 1815 adult individuals, including healthy subjects and patients with GI diseases. Cohort 1 consists of 1174 individuals who participate in the general population study LifeLines-DEEP in the northern provinces of the Netherlands.¹⁵ Cohort 2 consists of 300 patients with IBD from

the department of Gastroenterology and Hepatology University Medical Center Groningen (UMCG), the Netherlands. Cohort 3 consists of 189 patients with IBS and 152 matched controls from Maastricht University Medical Center (MUMC), the Netherlands.

Medication use

Current medication use at the time of stool collection of Cohort 1 participants was extracted from a standardised questionnaire.¹⁶ Two medical doctors reviewed all the medication for 1174 participants. PPI use was scored if participants used omeprazole, esomeprazole, pantoprazole, lansoprazole, dexlansoprazole or rabeprazole. To exclude other possible drug effects on the gut microbiome, medication use was scored in eight categories, allowing for later correction of parameters or exclusion of

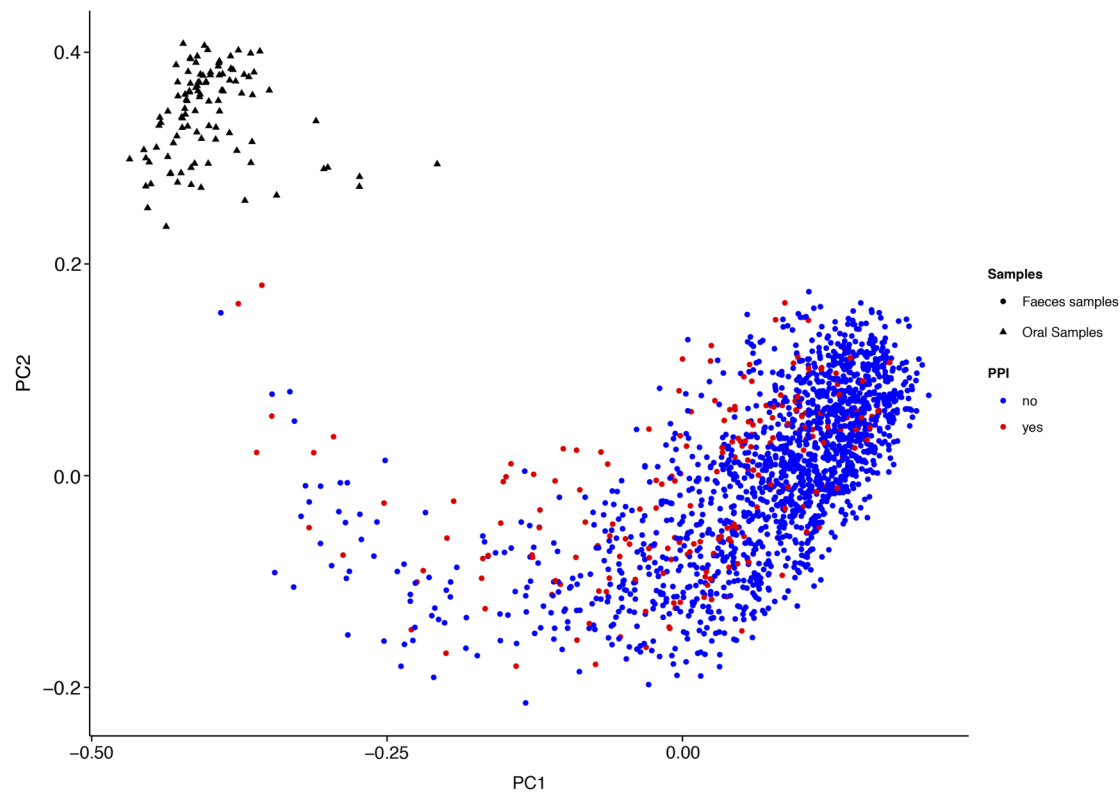


Figure 3 Principal coordinate analysis of 1815 gut microbiome samples and 116 oral microbiome samples. The gut microbiome of PPI users is significantly different from non-PPI users in the first coordinate (PCoA1: $p=1.39 \times 10^{-20}$, Wilcoxon test). For Principal Coordinate 1 there is a significant shift of the gut microbiome of PPI users towards the oral microbiome. PCoA, principal coordinate analysis; PPI, proton pump inhibitor.

certain participants. These categories were medication that: (1) changes bowel movement or stool frequency, (2) lowers triglyceride levels, (3) lowers cholesterol levels, (4) anti-diabetic medication (oral and insulin), (5) systemic anti-inflammatory medication (excluding NSAIDs), (6) topical anti-inflammatory medication, (7) systemic antibiotics, including antifungal and antimalarial medication, and (8) antidepressants including serotonin-specific reuptake inhibitors (SSRIs), serotonin-norepinephrine reuptake inhibitors (SNRIs), mirtazapine, and tricyclic antidepressants (TCAs). The definitions of these categories are described in the online supplementary appendix. Analysis of drugs used in Cohort 2 was based on the IBD-specific electronic patient record in the UMCG. Current PPI use, as well as current IBD medication (mesalazines, thiopurines, methotrexate, steroids, tumour necrosis factor (TNF)- α inhibitors and other biologicals) were scored at the time of sampling by the gastroenterologist treating the patient with IBD. Current PPI consumption in the IBS case-control Cohort 3 was based on self-reported questionnaires. Pseudonymised data for all three cohorts was provided to the researchers.

Gut complaints and other clinical characteristics

Information on age, gender and body mass index (BMI) was available for all three cohorts. In Cohort 1, gut complaints were investigated using an extensive questionnaire that included defecation frequency and the Bristol Stool Scale. Possible IBS and functional diarrhoea or constipation were determined using self-reported ROME III criteria. The patients with IBD in Cohort 2 were diagnosed based on accepted radiological, endoscopic and histopathological evaluation. All the IBD cases included in our

study fulfilled the clinical criteria for IBD. IBS in Cohort 3 was diagnosed by a gastroenterologist according to the ROME III criteria.

Stool and oral cavity mucus sample collection

A total of 1815 stool samples and 116 oral cavity mucus samples were collected. Cohorts 1 and 2 used identical protocols to collect the stool samples. Participants of cohort 1 and 2 were asked to collect one stool sample at home. Stool samples were frozen within 15 min after stool production in the participants' home freezer and remained frozen until DNA isolation. A research nurse visited all participants to collect the stool samples shortly after production and they were transported and stored at -80°C . Participants of cohort 3 were asked to bring a stool sample to the research facility within 24 h after stool production. These samples were immediately frozen upon arrival at -80°C .

Oral cavity mucus samples were collected from 116 additional healthy volunteers using buccal swabs.

DNA isolation and analysis of microbiota composition

Microbial DNA from stool samples was isolated with the Qiagen AllPrep DNA/RNA Mini Kit (cat. # 80204). DNA isolation from oral cavity swabs was performed using the UltraClean microbial DNA isolation kit (cat.# 12224) from MoBio Laboratories (Carlsbad, California, USA). To determine the bacterial composition of the stool and oral cavity mucus samples, sequencing of the variable region V4 of the 16S rRNA gene was performed using Illumina MiSeq. DNA isolation is described in the Methods section of the online supplementary appendix.

Table 2 Taxa and microbiome aspects associated with PPI use and increased risk of *C. difficile* infection

Taxa or microbiome aspect	Direction in PPI users that increases the risk of <i>C. difficile</i> infection	References of role on risk of <i>C. difficile</i> infection
α diversity	Reduced	Buffie et al ¹³ <i>Nature</i> . 2015 Chang et al ²⁷ <i>Journal of Infectious Diseases</i> . 2008 Antharam et al ²⁸ <i>Journal of Clinical Microbiology</i> . 2013
k_Bacteria	Decreased	Reeves et al ²⁶ <i>Gut Microbes</i> . 2011
p_Firmicutes		Antharam et al ²⁸ <i>Journal of Clinical Microbiology</i> . 2013.
c_Clostridia		Buffie et al. ¹³ <i>Nature</i> 2015 (Extended Figure 3d and 3e)
o_Clostridiales		Schubert et al ³¹ <i>Mbio</i> . 2014.
f_Ruminococcaceae		Rea et al ²⁹ <i>Journal of Clinical Microbiology</i> . 2011.
k_Bacteria	Decreased	Buffie et al ¹⁰ <i>Nature Reviews Immunology</i> . 2013
p_Actinobacteria		Rea et al ²⁹ <i>Journal of Clinical Microbiology</i> . 2011
c_Actinobacteria		Baines et al ³⁰ <i>Journal of Antimicrobial Chemotherapy</i> . 2013
o_Bifidobacteriales		
f_Bifidobacteriaceae		
g_Bifidobacterium		
k_Bacteria	Increased	Antharam et al ²⁸ <i>Journal of Clinical Microbiology</i> . 2013
p_Firmicutes		Schubert et al ³¹ <i>Mbio</i> . 2014
c_Bacilli		Rea et al ²⁹ <i>Journal of Clinical Microbiology</i> . 2011 (Figure 4)
o_Lactobacillales		Buffie et al ¹³ <i>Nature</i> . 2015 (Extended Figure 3d and 3e)
f_Enterococcaceae		Baines et al ³⁰ <i>Journal of Antimicrobial Chemotherapy</i> . 2013
g_Enterococcus		
k_Bacteria	Increased	Reeves et al ²⁶ <i>Gut Microbes</i> . 2011
p_Firmicutes		Antharam et al ²⁸ <i>Journal of Clinical Microbiology</i> . 2013
c_Bacilli		Rea et al ²⁹ <i>Journal of Clinical Microbiology</i> . 2012
o_Lactobacillales		Buffie et al ¹⁰ <i>Nature Reviews Immunology</i> . 2013
f_Lactobacillaceae,		Buffie et al ¹³ <i>Nature</i> . 2015
g_Lactobacillus,		
s_delbrueckii,		
s_plantarum		
and		
s_reuteri		
k_Bacteria	Increased	Antharam et al ²⁸ <i>The Journal of Clinical Microbiology</i> . 2013
p_Firmicutes		
c_Clostridia		
o_Clostridiales		
f_Veillonellaceae		
g_Veillonella		
k_Bacteria	Increased	Antharam et al ²⁸ <i>Journal of Clinical Microbiology</i> . 2013
p-Proteobacteria		Reeves et al ²⁶ <i>Gut Microbes</i> . 2011
c_Gammaproteobacteria		Schubert et al ³¹ <i>Mbio</i> . 2014
o_Enterobacteriales		
f_Enterobacteriaceae		
g_Escherichia		Peterfreund et al ³² <i>PLOS ONE</i> . 2012
s_coli		

PPI, proton pump inhibitor.

k_, kingdom; p_, phylum; c_, class; o_, order; f_, family; g_, genus; s_, species associations are in bold

Taxonomy determination

Bacterial taxonomy was determined by clustering the sequence reads with UCLUST (V1.2.22q) with a distance threshold of 97%, using Greengenes (V13.8) as the taxonomy reference database. Sequencing and the determination of taxonomy are described in the Methods section of the online supplementary appendix.

Statistical analysis

In each cohort, differentially abundant taxa in the gut microbiome between PPI users and non-PPI users were analysed using the multivariate statistical framework MaAsLin.¹⁷ MaAsLin performs boosted, additive, general linear models between meta-data and microbial abundance data. After running the association studies in the individual cohorts, we performed a meta-analysis of the three cohorts, using the weighted Z-score method. The Cochran's Q test was used to check for

heterogeneity. The significance cut-off for the Cochran's Q test was determined by Bonferroni correction for the 92 significant results: $p < 5.43 \times 10^{-4}$. Differences in richness (the number of species within a sample), principal coordinate analyses (PCoA) and Shannon diversity analysis were determined using the QIIME microbiome analysis software.¹⁸ The Wilcoxon test and Spearman's correlations were used to identify differences in Shannon's diversity and relations between the PCoA scores of PPI users and non-PPI users, while the χ^2 test, Fisher's exact test, Spearman's correlation and Wilcoxon-Mann-Whitney test (WMW test) were used to determine differences in age, gender, BMI, antibiotics use, and gut complaints between PPI users and non-users. In all the microbiome analyses, multiple test corrections were based on the false discovery rate (FDR). An FDR value of 0.05 was used as a statistically significant cut-off.

In addition to the PPI effect, we also tested the influence of other commonly used drugs in Cohort 1. Using MaAsLin with similar settings to those described above, we tested the microbial

changes associated with the use of other drugs, with and without correction for PPI, and the changes when including these common drugs as a correcting factor in the PPI versus non-PPI analysis.

Significant results were graphically represented in cladograms using GraPhlAn.¹⁹ More details on the statistical analysis can be found in the Methods section (see online supplementary appendix).

Correction for factors influencing the gut microbiota

Differentially abundant taxa were corrected for several parameters, which were identified by statistical analysis of cohort phenotypes or univariate MaAsLin runs and subsequently added as cofactors to the additive linear model. Analyses in the general population Cohort 1 were corrected for age, gender, BMI, antibiotics use, sequence read depth and ROME III diagnosis (IBS-Constipation (IBS-C), IBS-Diarrhoea (IBS-D), IBS-Mixed (IBS-M), IBS-Undetermined (IBS-U), functional bloating, functional constipation, functional diarrhoea or none). The analysis of patients with IBD in Cohort 2 was corrected for age, gender, BMI, antibiotics use, sequence read depth, diagnosis (Crohn's disease or UC) combined with disease location (colon, ileum or both) and IBD medication (use of mesalazines, steroids, thiopurines, methotrexate or anti-TNF antibodies). The analysis of the IBS case-control Cohort 3 was corrected for age, gender, BMI, sequence read depth and IBS status according to the ROME III criteria. In the meta-analysis, all microbiome data were corrected for age, gender, BMI, antibiotics use and sequence read depth.

RESULTS

PPI use is associated with older age and higher BMI

PPI were used by 211 (11.6%) of the 1815 participants: 8.4% of the general population (Cohort 1), 20.0% of the patients with IBD (Cohort 2) and 15.2% of the participants of case-control Cohort 3. Women use PPI more often than men: 9.2% versus 7.4%, albeit this was not statistically significant ($p=0.61$, χ^2 test). PPI users were generally older: 51.6 (SD 13.4) years of age versus 44.4 (SD 14.7) years of age ($p=2.50 \times 10^{-11}$ WMW test) and have a higher BMI of 26.9 (SD 5.0) versus 24.9 (SD 4.2) for non-users ($p=1.89 \times 10^{-8}$, WMW test). Antibiotics were concomitantly used by 2% of the 99 PPI users of Cohort 1 and 33% of the 60 PPI users of Cohort 2. There was no overlap between PPI users and antibiotics users in Cohort 3. Based on our data, we included age, gender, BMI and antibiotics as cofactors in the microbiome analyses. Table 1 provides an overview of the characteristics per cohort and the use of PPI.

Composition of the gut microbiota

The predominant phylum in each cohort was Firmicutes with abundances of 76.7%, 73.8% and 77.4% in Cohorts 1, 2 and 3, respectively. Information on the composition of the gut microbiome for all three cohorts and on all taxonomic levels is provided in online supplementary figures S1, S2 and table S1. Independent of PPI use, the overall high-level bacterial composition of the gut was homogeneous in all three cohorts (by phylum, class and order level, Spearman's correlations: $r>0.94$; $p<1.6 \times 10^{-13}$).

Reduced diversity of the gut microbiome associated with PPI use

In all three cohorts we identified a lower species richness and lower Shannon diversity, although not significant (Cohort 1, $p=0.85$; Cohort 2, $p=0.16$; Cohort 3, $p=0.53$), however in combined analysis of all three data sets we identified, moderate

but significant decrease in gut α diversity of PPI users was observed in the meta-analysis of all 1815 gut microbiome samples: Shannon index ($p=0.01$) and species richness ($p=0.02$) (see online supplementary figures S3 and S4).

Meta-analysis: differences in gut microbiome associated with PPI use

The meta-analysis across all three cohorts showed statistically significant alterations in 92 of the 460 bacterial taxa abundance (FDR<0.05). These changes are depicted in a cladogram in figure 1 and in a heatmap in figure 2, and in online supplementary figure S5. Details of each taxon, including the individual direction, coefficient, p value and FDR for each cohort, as well as the meta-analysis, are provided in online supplementary tables S2 and S3. Cochran's Q test was used to check for heterogeneity. None of the 92 reported associations were significantly heterogeneous at the Bonferroni corrected p value cut-off ($p<5.43 \times 10^{-4}$) (see online supplementary table S2).

The overall difference of the gut microbiome associated with PPI use was also observed in the PCoA of all the data sets together (figure 3 and see online supplementary figure S6). The same PCoA with separate colours for each cohort has been added in online supplementary figure S7. Notably, we observed statistically significant differences between PPI users and non-users in two principal coordinates (PCoA1: $p=1.39 \times 10^{-20}$, PCoA3: $p=0.0004$, Wilcoxon test).

Similar changes in three independent cohorts were associated with PPI use

The order Actinomycetales, families *Streptococcaceae*, *Micrococcaceae*, genus *Rothia* and species *Lactobacillus salivarius* were increased in participants using PPI in each cohort. None of the individual cohorts contained any significantly decreased taxa (FDR<0.05). In the general population (Cohort 1), 41 of the 829 bacterial taxa were significantly increased, including the class Gammaproteobacteria, the family *Enterococcaceae* and the genera *Streptococcus*, *Veillonella* and *Enterococcus* (FDR<0.05) (see online supplementary table S4). In patients with IBD (Cohort 2), PPI use was associated with an increase of 12 of the 667 bacterial taxa, including the family *Lactobacillaceae* as well as the genera *Streptococcus* and *Lactobacillus* (FDR<0.05) (see online supplementary table S5). In IBS case-control Cohort 3, 18 of the 624 taxa were significantly increased, including the order Lactobacillales (FDR<0.05) (see online supplementary table S6).

Oral cavity bacteria are more abundant in the gut microbiome of PPI users

We hypothesised that the changes in the gut microbiome associated with PPI use are caused by reduced acidity of the stomach and the subsequent survival of more bacteria that are ingested with food and oral mucus. Indeed, some of the statistically significantly increased bacteria in PPI users (eg, *Rothia dentocariosa*, *Rothia mucilaginosa*, the genera *Scardovia* and *Actinomyces* and the family *Micrococcaceae*) are typically found in the oral microbiome.²⁰ By analysing 116 oral microbiome samples from participants in Cohort 1, we could compare the overall composition of bacteria in the oral microbiome with the composition of the gut microbiome. We observed a statistically significant shift in Principal Coordinate 1 in the gut microbiome samples of the PPI users towards the oral samples, compared with non-PPI users ($p=1.39 \times 10^{-20}$, Wilcoxon test) (figure 3). In online supplementary figure S8, the over-representation of oral cavity bacteria in the guts of PPI users is depicted in a cladogram.

PPI use is independent of bowel movement frequency and stool consistency

Some of the significantly increased taxa were more abundant in the small intestine.¹¹ To ensure that the changes observed in microbiota composition were not due to diarrhoea and/or more frequent bowel movements, we checked in our general population whether clinical symptoms of diarrhoea were more often present in PPI users. Neither diarrhoeal complaints (IBS-D and functional diarrhoea, $p=0.22$, Fisher's exact test), stool consistency as defined by the Bristol Stool Scale ($r=0.027$, $p=0.36$, Spearman's correlation) nor the defecation frequency ($r=-0.001$, $p=0.98$, Spearman's correlation) of the participants in Cohort 1 were related to PPI use.

PPI, ANTIBIOTICS AND OTHER COMMONLY USED DRUGS

In Cohort 1, 16 taxa were associated with antibiotics and other commonly used drug categories besides PPI (see online supplementary table S7). After correction for PPI use, only six taxa remained associated with certain drugs: statins, fibrates and drugs that change bowel movements. All 92 alterations in bacterial taxa associated with PPI use remained statistically significant if we correct the microbiome analyses for antibiotics and other commonly used drugs.

CONCLUSIONS

We show that PPI use is consistently associated with profound changes in the gut microbiome. In our study, these changes were more prominent than changes associated with either antibiotics or other commonly used drugs. While PPIs have proven to be useful in the prevention and treatment of ulcers and GORD, they have also been associated with an increased risk of *C. difficile*, *Salmonella* spp, *Shigella* spp, *Campylobacter* spp, and other enteric infections.^{4 5 7-9} The increased risk of acquiring one of these enteric infections is likely due to changes in the PPI user's gut microbiome. Gut microbiota can resist or promote colonisation of *C. difficile* and other enteric infections through mechanisms that either directly inhibit bacterial growth or enhance the immune system.¹⁰⁻¹³ In the case of *C. difficile*, spores might be able to germinate more easily because of metabolites synthesised by certain gut bacteria.^{12 13}

We hypothesised that PPIs change the gut microbiome through their direct effect on stomach acid. This acidity forms one of the main defenses against the bacterial influx that accompanies ingesting food and oral mucus. PPIs reduce the acidity of the stomach, allowing more bacteria to survive this barrier. We have shown here that species in the oral microbiome are more abundant in the gut microbiome of PPI users. Moreover, a study looking into the effect of PPIs on the oesophageal and gastric microbiome in oesophagitis and Barrett's oesophagus showed similar bacterial taxa associated with PPI use, including increased levels of *Enterobacteriaceae*, *Micrococcaceae*, *Actinomycetaceae* and *Erysipelotrichaceae*.²¹ Gastric bypass surgery compromises the stomach acid barrier and leads to gut microbiome changes similar to the PPI-associated alterations in this study, thereby supporting our hypothesis.²²

We looked at the role of the gut microbiome in *C. difficile* infections, which cause 12.1% of all nosocomial infections and were responsible for half a million infections and associated with 29 000 deaths in the USA in 2011.^{23 24} Virulent strains of *C. difficile* can only colonise a susceptible gut, after which toxins are produced and spores are shed. This leads to a wide spectrum of symptoms varying from mild diarrhoea to fulminant relapsing diarrhoea and pseudomembranous colitis.²⁵

Recent human, animal and in vitro studies show an overlap between the specific alterations in the gut microbiota associated with PPI use found in this study and bacterial changes that lead to increased susceptibility to *C. difficile*. The reduced α diversity in PPI-users is associated with increased susceptibility to *C. difficile* infection.^{13 27 28} The PPI-associated decreases of the family *Ruminococcaceae* and the genus *Bifidobacterium*, as well as the PPI-associated increases of the class *Gammaproteobacteria*, the families *Enterobacteriaceae*, *Enterococcaceae*, *Lactobacillaceae* and the genera *Enterococcus* and *Veillonella*, have been consistently linked to increased susceptibility to *C. difficile* infection (table 2).^{10 13 26-32}

The *Ruminococcaceae* family is significantly decreased in patients with *C. difficile* and enriched in healthy controls.^{28 29 31} Moreover, mice that have been treated with a mixture of antibiotics that do not become clinically ill after a challenge with *C. difficile* have higher levels of *Ruminococcaceae*.²⁶ Within the *Ruminococcaceae* family, the *Faecalibacterium* genus was significantly increased in patients who recovered from *C. difficile* illness, whereas it was severely decreased in patients with *C. difficile* with active disease.³¹ Last, a decreased *Ruminococcus torques* operational taxonomic unit (OTU) was significantly associated with *C. difficile* infection in another study, although their OTU picking was done using a different reference database and associations were performed using OTU level, making direct comparisons with our study difficult.¹³

Species of the *Bifidobacterium* genus: *Bifidobacterium longum*, *Bifidobacterium lactis*, *Bifidobacterium pseudocatenulatum*, *Bifidobacterium breve*, *Bifidobacterium pseudolongum*, *Bifidobacterium adolescentis* and *Bifidobacterium animalis lactis* have been shown to inhibit or prevent *C. difficile* infection.¹⁰ The administration of antibiotics that enhance the susceptibility to *C. difficile* in an in vitro model of the gut also significantly reduce the genus *Bifidobacterium*.³⁰ Moreover, active *C. difficile* diarrhoea is associated with decreased *Bifidobacteria* in elderly patients.²⁹

The class *Gammaproteobacteria* and the family *Enterobacteriaceae* are significantly increased in PPI users. *Gammaproteobacteria* are enriched in patients with *C. difficile* compared with healthy controls.²⁸ Within the class *Gammaproteobacteria*, the family *Enterobacteriaceae* dominate the murine gut microbiome after administration of clindamycin. Those mice that became clinically ill after the administration of an antibiotic cocktail containing clindamycin and a *C. difficile* challenge, had profoundly increased levels of *Enterobacteriaceae* in their gut microbiome, while mice that did not become clinically ill had a gut microbiome that predominantly consisted of Firmicutes.²⁶ The family *Enterobacteriaceae* is also increased in hamsters that were treated with clindamycin and subsequently infected with *C. difficile*.³²

The *Enterococcus* genus, which is also more abundant in PPI users, is significantly enriched in *C. difficile*-infected patients compared with healthy controls.^{28 31} An *Enterococcus faecalis* OTU and an *Enterococcus avium* OTU are significantly associated with increased susceptibility to *C. difficile* infections in mice.¹³ Moreover, an *Enterococcus avium* OTU is also significantly associated with *C. difficile* in humans.¹³ The administration of the antibiotic ceftriaxone led to an increase in the genus *Enterococcus* and enhanced the susceptibility to *C. difficile* in an in vitro model of the gut.³⁰

The increased abundance of the family *Lactobacillaceae* in PPI users was associated with increased risk of *C. difficile* infection in several studies. Mice treated with a cocktail of antibiotics (consisting of kanamycin, gentamycin, colistin, metronidazole

and vancomycin), cefoperazone or a combination of clindamycin and cefoperazone have higher levels of *Lactobacillaceae* in their gut.²⁶ Mice treated with cefoperazone and clindamycin that developed *C. difficile* infection after being challenged with the pathogen also had a higher level of *Lactobacillaceae*.²⁶ Within the *Lactobacillaceae* family, the *Lactobacillus* genus is significantly enriched in patients with *C. difficile* infection compared with healthy controls.²⁸ *Lactobacillus spp* in the gut microbiome are also associated with active *C. difficile* diarrhoea in patients.²⁹ In contrast to these studies, the *Lactobacillus* species *Lactobacillus delbrueckii*, *Lactobacillus plantarum* and a *Lactobacillus reuteri* OTU increased colonisation resistance to *C. difficile*.^{10 13} However, in concordance with increased risk, a *Lactobacillus johnsonii* OTU enhanced *C. difficile* infection.¹³

Last, the *Veillonella* genus that is increased in PPI users is significantly enriched in patients with *C. difficile* compared with healthy controls.²⁸

The prevention of healthcare-associated *C. difficile* infections is a priority in the USA and reduction targets for 2020 have been established.^{5 33} A recent study looking into the effect of PPI on the risk of developing recurrent *C. difficile* infections found that of 191 PPI users admitted to a hospital, only 47.1% had an evidence-based indication for PPI use.⁵ Moreover, PPI use was discontinued in only 0.6% of the cases.⁵ The US Food and Drug Administration already recommends limiting PPI use to a minimum dose and duration.³⁴ Despite these recommendations, PPIs are still often overprescribed.^{5 6} The risk of unnecessary antibiotics use is already addressed.³⁵ However, limiting the unnecessary use of PPI should also be considered in preventing *C. difficile* and other enteric infections.

The microbiome is being intensively studied in various diseases and conditions including IBD, IBS, obesity, old age, non-alcoholic steatohepatitis and non-alcoholic fatty liver disease (NAFLD).³⁶ PPI users are over-represented in these groups as they more likely to have GI complaints or experience GORD, either due to their health condition or their associated lifestyle. Prominent microbiome studies looking into obesity, IBD and NAFLD include results that researchers have contributed to the condition under study, but we show they are also associated with PPI use.^{17 37} It could well be that some of the observed effects should rather have been attributed to the use of PPI. Future microbiome studies in humans should therefore always take the effect of PPI on the gut microbiome into account.

This paper reports the largest study to date investigating the influence of PPI on the gut microbiome. The profound alterations seen in the gut microbiome could be linked to the increased risk of *C. difficile* and other enteric infections. Given the widespread use of PPI, the morbidity and mortality associated with enteric infections, and the increasing number of studies investigating the microbiome, healthcare practitioners and microbiome researchers should be fully aware of the influence of PPI on the gut microbiome.

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Contributors AZ, RKW, CW and DJ designed the study. FI, EFT, SAJ, ZM, LV, MCC and GD acquired the data; FI, MJB and AVV analysed and interpreted the data; FI drafted the manuscript; MJB and AVV performed the statistical analysis; AZ, RKW, CW, DJ, GD, LF, JF, HJM and RJX critically revised the manuscript; AZ, RKW, CW, DJ, LF and JF obtained funding; AZ, RKW, CW and DJ supervised the study.

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REFERENCES

- 1 The Dutch Foundation for Pharmaceutical Statistics (SFK). Data and Facts on 2013. 2014.
- 2 Drugs.com. Top 100 sales in the United States in 2013. 2013.
- 3 Olbe L, Carlsson E, Lindberg P. A proton-pump inhibitor expedition: the case histories of omeprazole and esomeprazole. *Nat Rev Drug Discov* 2003;2:132–9.
- 4 Moayyedi P, Talley NJ. Gastro-oesophageal reflux disease. *Lancet* 2006;367:2086–100.
- 5 McDonald EG, Milligan J, Frenette C, et al. Continuous proton pump inhibitor therapy and the associated risk of recurrent clostridium difficile infection. *JAMA Intern Med* 2015;175:784–91.
- 6 Kelly OB, Dillane C, Patchett SE, et al. The Inappropriate prescription of oral proton pump inhibitors in the hospital setting: a prospective cross-sectional study. *Dig Dis Sci* 2015;60:2280–6.
- 7 Bouwknegt M, Pelt W Van, Kubbinga ME, et al. Potential association between the recent increase in campylobacteriosis incidence in the Netherlands and proton-pump inhibitor use—an ecological study. *Eurosurveillance* 2014;19:1–6.
- 8 Leonard J, Marshall JK, Moayyedi P. Systematic review of the risk of enteric infection in patients taking acid suppression. *Am J Gastroenterol* 2007;102:2047–56.
- 9 Janarthanan S, Ditah I, Adler DG, et al. Clostridium difficile-Associated Diarrhea and Proton Pump Inhibitor Therapy: a Meta-Analysis. *Am J Gastroenterol* 2012;107:1001–10.
- 10 Buffie CG, Pamer EG. Microbiota-mediated colonization resistance against intestinal pathogens. *Nat Rev Immunol* 2013;13:790–801.
- 11 Kamada N, Chen GY, Inohara N, et al. Control of pathogens and pathobionts by the gut microbiota. *Nat Immunol* 2013;14:685–90.
- 12 Britton RA, Young VB. Role of the intestinal microbiota in resistance to colonization by *Clostridium difficile*. *Gastroenterology* 2014;146:1547–53.
- 13 Buffie CG, Bucci V, Stein RR, et al. Precision microbiome reconstitution restores bile acid mediated resistance to *Clostridium difficile*. *Nature* 2014;517:205–8.
- 14 Van Nood E, Vriee A, Nieuwdorp M, et al. Duodenal infusion of donor feces for recurrent *Clostridium difficile*. *N Engl J Med* 2013;368:407–15.
- 15 Tigchelaar EF, Zernakova A, Dekens JA. Cohort profile: Lifelines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. *BMJ Open* 2015;5:e006772.
- 16 Scholtens S, Smidt N, Swertz M a., et al. Cohort Profile: Lifelines, a three-generation cohort study and biobank. *Int J Epidemiol* 2015;44:1172–80.
- 17 Morgan XC, Tickle TL, Sokol H, et al. Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biol* 2012;13:R79.
- 18 Caporaso JG, Kuczynski J, Stombaugh J, et al. Correspondence QIIME allows analysis of high-throughput community sequencing data Intensity

- normalization improves color calling in SOLiD sequencing. *Nat Publ Gr* 2010;7:335–6.
- 19 Asnicar F, Weingart G, Tickle TL, *et al.* Compact graphical representation of phylogenetic data and metadata with GraPhlAn. *PeerJ* 2015;3:e1029.
 - 20 Segata N, Haake S, Mannon P, *et al.* Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples. *Genome Biol* 2012;13:R42.
 - 21 Amir I, Konikoff FM, Oppenheim M, *et al.* Gastric microbiota is altered in oesophagitis and Barrett's oesophagus and further modified by proton pump inhibitors. *Environ Microbiol* 2014;16:2905–14.
 - 22 Zhang H, DiBaise JK, Zuccolo a, *et al.* Human gut microbiota in obesity and after gastric bypass. *Proc Natl Acad Sci USA* 2009;106:2365–70.
 - 23 Lessa FC, Mu Y, Bamberg WM, *et al.* Burden of Clostridium difficile Infection in the United States. *N Engl J Med* 2015;372:825–34.
 - 24 Magill SS, Edwards JR, Bamberg W, *et al.* Multistate point-prevalence survey of health care-associated infections. *N Engl J Med* 2014;370:1198–208.
 - 25 Rupnik M, Wilcox MH, Gerding DN. Clostridium difficile infection: new developments in epidemiology and pathogenesis. *Nat Rev Microbiol* 2009;7:526–36.
 - 26 Reeves AE, Theriot CM, Bergin IL, *et al.* The interplay between microbiome dynamics and pathogen dynamics in a murine model of Clostridium difficile infection. *Gut Microbes* 2011;2:145–58.
 - 27 Chang JY, Antonopoulos DA, Kalra A, *et al.* Decreased diversity of the fecal Microbiome in recurrent Clostridium difficile-associated diarrhea. *J Infect Dis* 2008;197:435–8.
 - 28 Antharam VC, Li EC, Ishmael A, *et al.* Intestinal dysbiosis and depletion of butyrogenic bacteria in Clostridium difficile infection and nosocomial diarrhea. *J Clin Microbiol* 2013;51:2884–92.
 - 29 Rea MC, O'Sullivan O, Shanahan F, *et al.* Clostridium difficile carriage in elderly subjects and associated changes in the intestinal microbiota. *J Clin Microbiol* 2012;50:867–75.
 - 30 Baines SD, Crowther GS, Todhunter SL, *et al* F and MHW. Mixed infection by Clostridium difficile in an in vitro model of the human gut. *J Antimicrob Chemother* 2013;68:1139–43.
 - 31 Schubert AM, Rogers M a M, Ring C, *et al.* Microbiome data distinguish patients with clostridium difficile infection and non- C. difficile -associated diarrhea from healthy. *MBio* 2014;5:e01021–14.
 - 32 Peterfreund GL, Vandivier LE, Sinha R, *et al.* Succession in the Gut Microbiome following Antibiotic and Antibody Therapies for Clostridium difficile. *PLoS ONE* 2012;7.
 - 33 Department H and HS. Request for Comments on the Proposed 2020 Targets for the National Action Plan To Prevent Health Care-Associated Infections: Road Map To Elimination (Phase I: Acute Care Hospital) Measures. 2014. <https://www.federalregister.gov/articles/2014/02/25/2014-04069/request-for-comments-on-the-proposed-2020-targets-for-the-national-action-plan-to-prevent-health>
 - 34 U.S. Food and Drug Administration. FDA Drug Safety Communication: Clostridium difficile-associated diarrhea can be associated with stomach acid drugs known as proton pump inhibitors (PPIs). 2012. <http://www.fda.gov/drugs/drugsafety/ucm290510.htm>
 - 35 Blaser M. Antibiotic overuse: Stop the killing of beneficial bacteria. *Nature* 2011;476:393–4.
 - 36 Mehal WZ. The Gordian Knot of dysbiosis, obesity and NAFLD. *Nat Rev Gastroenterol Hepatol* 2013;10:637–44.
 - 37 Goodrich JK, Waters JL, Poole AC, *et al.* Human Genetics Shape the Gut Microbiome. *Cell* 2014;159:789–99.

Supplementary Appendix

Proton Pump Inhibitors Affect the Gut

Microbiome

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Supplementary Methods

Cohorts

Cohort 1: General Population; LifeLines-DEEP

LifeLines-DEEP is a sub-cohort of LifeLines: a multi-disciplinary prospective population-based study that examines health and health-related behaviors of 167,729 participants in the North of The Netherlands.¹ A subset of approximately 1,500 LifeLines participants also takes part in LifeLines-DEEP.² These participants are examined more thoroughly, specifically with respect to molecular data. This allows for more in-depth investigation of the genetic and phenotypic variation. Additional biological materials as well as additional information on environmental factors are collected. For a subset of 116 LifeLines participants, oral microbiome data is available as well. Consumption of PPI was obtained from questionnaire data. Analysis of gut complaints and presence of Irritable Bowel Syndrome (IBS) in LifeLines-DEEP cohort were defined according to the Rome III criteria.³ The 116 LifeLines-DEEP participants from which oral microbiome samples were collected, were used to compare the gut microbiome compositions to oral composition

Cohort 2: IBD patients; Gastroenterology UMCG

The Groningen IBD Microbiome Cohort consists of more than 309 IBD patients from the Gastroenterology and Hepatology department of the University Medical Center Groningen. Stool samples are collected from these patients.

Cohort 3: IBS Case-Control

In Cohort 3, 193 IBS patients, between 18 and 75 years of age, were diagnosed by their general practitioner using the ROME III criteria.³ Patients were recruited via the outpatient gastroenterology clinic of the MUMC+ (Maastricht University Medical Center, a secondary and tertiary referral centre) and via general practitioners in the area of Maastricht. Medical history was taken and GI endoscopy with biopsies, abdominal imaging and/or blood, breath and fecal analyses were performed to exclude organic disease, if indicated. Patients with a history of abdominal surgery, except appendectomy, laparoscopic cholecystectomy and hysterectomy, were excluded. Patients were assigned to IBS subtypes based on predominant bowel habits according to the ROME III criteria: diarrhea (IBS-D), constipation (IBS-C), mixed stool pattern (IBS-M) and unspecified subtype (IBS-U). Age and sex matched healthy controls (HC, n=152) were enrolled via public advertising. A brief medical history was taken to exclude the presence of previous or current GI disorders or complaints. All study participants gave written informed consent prior to inclusion, and completed questionnaires regarding demographic characteristics and lifestyle factors. A 14-day end-of-day GI symptom diary was completed, addressing symptoms GI complaints and medication information.

PPI definition

The PPI users were defined as users of: Omeprazol (Lozec), Esomeprazol (Nexium), Pantoprazol (Pantozol). In cohort 1 (LifeLines-Deep) the information of drugs usage was extracted from standardized questionnaire. In cohort 2 (IBD) drug analysis was performed

based on electronic patient's record. PPI consumption in IBS case-control cohort was performed based on self-reported questionnaires.

Definition of other drug groups (% of users in cohort 1)

(1) medication that changes bowel movement or stool frequency (2.8%)

- a. Opiates (can cause severe constipation)
- b. Laxatives

(2) lowers triglycerides levels (0.2%)

- a. Fibrates

(3) lowers cholesterol levels (3.6%)

- a. Statins

(4) anti-diabetic medication (both oral and insulin) (1.2%)

- a. Insulin
- b. Biguanides
- c. Sulfonylureas
- d. α -glucosidase Inhibitors
- e. Dipeptidyl Peptidase-IV Inhibitors
- f. Glinides
- g. Thiazolidinediones

(5) systemic anti-inflammatory medication (does not include NSAIDs)(0.6%)

- a. Thiopurines
- b. Methotrexate
- c. TNF-alpha inhibitors

- d. Steroids
- (6) topical anti-inflammatory medication (4.1%)
- a. steroid cream, steroid nose drops or steroid nose spray
- (7) systemic antibiotics, including antifungal and antimalarial medication (1.1%)
- (8) antidepressants (3.2%)
- a. SSRIs
 - b. SNRIs
 - c. Mirtazapine
 - d. Tricyclic antidepressants

Fecal sample collection

Fecal samples in all three cohorts were collected at home and immediately stored at -20°C. After transport on dry ice, all samples were stored at -80°C. Aliquots were made and DNA was isolated with the AllPrep DNA/RNA Mini Kit (Qiagen; cat. # 80204). Isolated DNA was sequenced at the Broad institute as described below.

Oral sample collection

Oral cavity samples were collected using sterilized cotton swabs. The cotton swabs were placed directly in tubes containing 300 µl MicroBead solution and stored at -80 °C before DNA extraction. DNA isolation from oral swabs was performed using the UltraClean microbial DNA isolation kit (cat.# 12224) from MoBio Laboratories, Carlsbad, CA. Isolated DNA was stored at -20 °C and sequenced at the Broad institute as described below.

Sequencing

Illumina MiSeq paired end sequencing was used to determine the bacterial composition of the fecal and oral samples. Hyper-variable region V4 was selected using forward primer 515F [GTGCCAGCMGCCGCGGTAA] and reverse primer 806R [GGACTACHVGGGTWTCTAAT]. We used custom scripts to remove the primer sequences and align the paired end reads. Details on the process can be found in Gevers et al⁴.

OTU-picking

The operational taxonomic unit (OTU) formation was performed using the QIIME reference optimal picking, which uses UCLUST⁵ (version 1.2.22q) to perform the clustering at 97% similarity. As a reference database we used a primer-specific version of the full Greengenes 13.8⁶. Using TaxMan⁷, we created the primer-specific reference database containing only reference entries that matched the selected primers. During this process we restricted probe-reference mismatches to a maximum of 25%. The 16S regions that were captured by our primers, including the primer sequences, were extracted from the full 16S sequences. For each of the unique 16S sequences present in the reference database after primer selection, we determined the shared taxonomic label of the original sequences. This overlapping part of the taxonomy was used as the taxonomic label of the sequence. This process is based on work described in Bonder et al.⁸ and Brandt et al.⁷.

Statistical analysis

QIIME⁹ was used for exploratory analysis on the microbiome datasets, gathering basic statistics, Shannon index, richness calculation and PCoA creation. PCoA metrics were

calculated using the Bray-Curtis dissimilarity statistic implemented in QIIME. Both alpha and beta diversity were calculated in a single rarefaction of the abundance table, setting the read depth at 10,000 reads. Differences in diversity, PCoA scores and other factors associated to PPI differences were performed using the Wilcoxon test, the Spearman correlation, Fischer exact test and the chi-squared test as implemented in R¹⁰.

In the PCoA analysis, we compared the PPI group to the non-PPI group in terms of their scores on the first three components using a Wilcoxon test. After the test we compared the group averages to determine the direction of the shift.

To identify differentially abundant taxa between the PPI users and the non-PPI users we used MaAsLin¹¹. In the analysis performed in MaAsLin we did not test individual OTUs, instead we focused on the most detailed taxonomic label each OTU represented. Using QIIMETOMAASLIN¹² tool we aggregated the OTUs if the taxonomic label was identical, moreover if multiple OTUs represented a higher order taxa we added this higher order taxa to the analysis. In this process we compress 60.000 OTUs to 1450 separate taxonomic units. We removed taxa from the tests if they were not present in at least 1% of our samples. During the conversion from OTU to taxonomies, QIIMETOMAASLIN transformed the microbiome data to percentages after which these percentages were arcsin square root transformed. This transforms the percentages into a normal distribution.

MaAsLin uses a boosted, additive general linear model to discriminate between groups of data. We used two different MaAsLin runs, correcting for different factors. We forced the cofactors: age, gender, BMI, read-depth and antibiotic usage and turned off the automatic filtering of input taxonomies. We did not remove any taxonomic inputs during the analysis to enable the meta-analysis.

GraphAn was used to represent the significant results from the MaAsLin analysis in cladograms.

Meta-analysis

The individual analyses were combined in a meta-analysis. For the meta-analysis a weighted Z-score approach was used. The individual P-values derived from the tests were transformed to Z-scores and the direction was taken from the coefficient of the test. The Z-scores were weighted according to the sample size and combined in a meta Z-score, this was subsequently transformed in a meta P-value.

Multiple testing correction

For correction for multiple testing in individual analyses and in meta-analysis we used the Q-value calculated using the R¹⁰ Q-value package¹³. The Q-value is the minimal false discovery rate at which a test may be called significant. A Q-value of 0.05 was used as the cut-off point for significance.

References

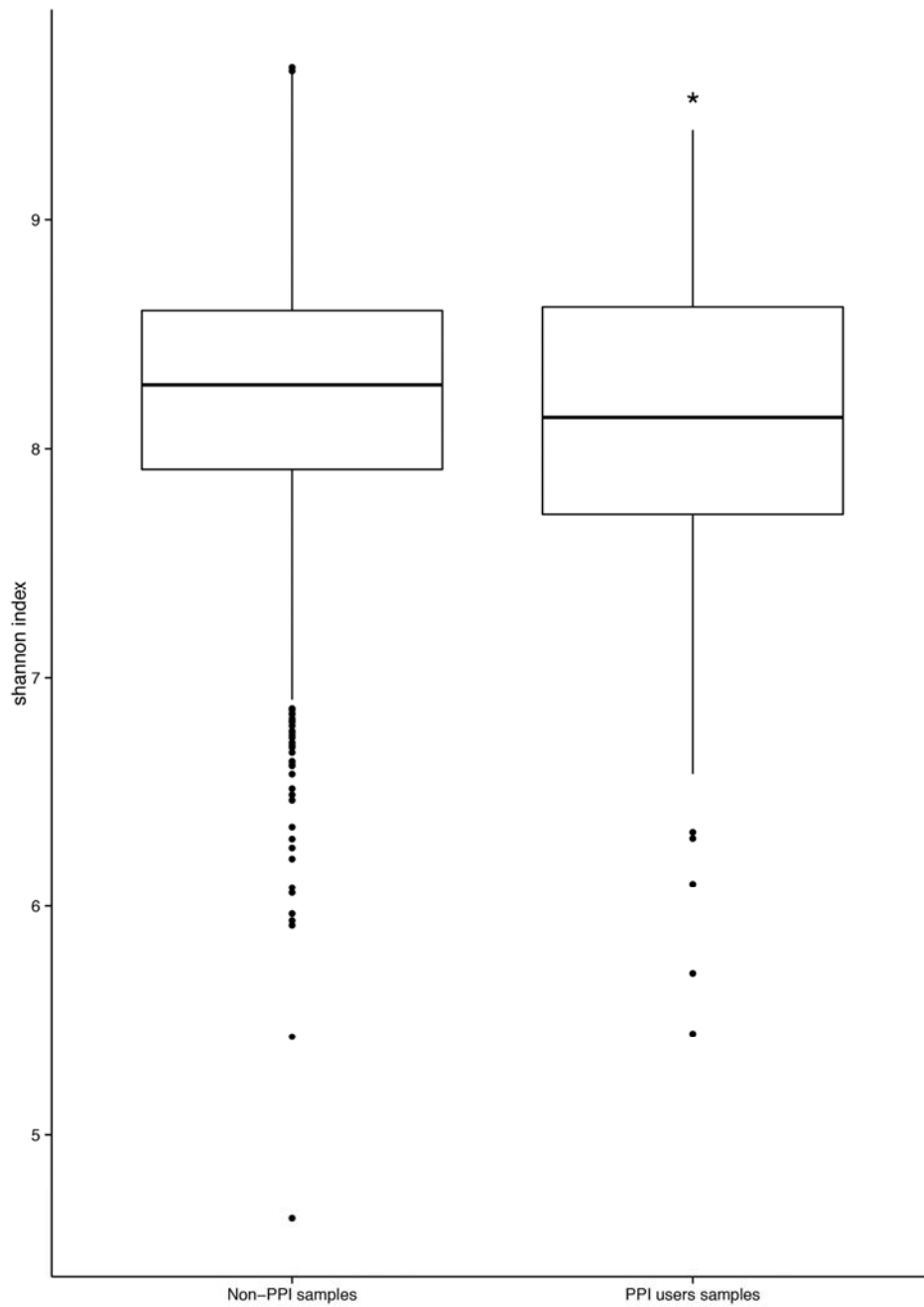
1. Scholtens S, Smidt N, Swertz M a., et al. Cohort Profile: LifeLines, a three-generation cohort study and biobank. *Int J Epidemiol* 2014;1–9.
2. Tigchelaar EF, Zhernakova A, Dekens JAM, et al. An introduction to LifeLines DEEP: study design and baseline characteristics. 2014.
3. Drossman DA, Dumitrascu DL. Rome III: New standard for functional gastrointestinal disorders. *J Gastrointest Liver Dis* 2006;15(3):237–41.
4. Gevers D, Kugathasan S, Denson LA, et al. The Treatment-Naive Microbiome in New-Onset Crohn’s Disease. *Cell Host Microbe*. 2014 Mar 12;15(3):382-92
5. Edgar RC. Search and clustering orders of magnitude faster than BLAST. *Bioinformatics* 2010;26:2460–1.
6. DeSantis TZ, Hugenholtz P, Larsen N, et al. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* 2006;72(7):5069–72.
7. Brandt BW, Bonder MJ, Huse SM, Zaura E. TaxMan: a server to trim rRNA reference databases and inspect taxonomic coverage. *Nucleic Acids Res* 2012;40:W82–7.
8. Bonder MJ, Abeln S, Zaura E, Brandt BW. Comparing clustering and pre-processing in taxonomy analysis. *Bioinformatics* 2012;28(22):2891–7.
9. Caporaso JG, Kuczynski J, Stombaugh J, et al. QIIME allows analysis of high-throughput community sequencing data. *Nat. Methods*. 2010;7:335–6.
10. R Development Core Team RFFSC. R: A Language and Environment for Statistical Computing. *R Found. Stat. Comput.* 2008;1:2673.
<http://www.r-project.org>
11. Tickle T, Waldron L, Yiren L, Huttenhower C. MaAsLin: Multivariate association of microbial communities with rich metadata in high-dimensional studies.
<https://bitbucket.org/biobakery/maaslin>
12. Tickle T. QIIMEToMaAsLin. 2013; <https://bitbucket.org/biobakery/qiimetomaaslin>
13. Dabney A, Storey JD. qvalue: Q-value estimation for false discovery rate control.
<http://qvalue.princeton.edu/>

Supplementary Tables

1. Supplementary Table S1: Taxonomic comparison of cohort 1,2 and 3. Comparison of the taxonomic distributions in the datasets, including PPI status.
 - a. File: SupplementaryTableS1_barplots_L2-L_IBD_LLD_MIBS_PPI.xlsx
2. Supplementary Table S2: Outcome meta-analysis: All bacterial taxa
 - a. File: SupplementaryTableS2_MetaAnalysis.xlsx
3. Supplementary Table S3: Outcome meta-analysis: Annotation
 - a. File: SupplementaryTableS6_MetaAnalysis_Sorted_Significantonly.xlsx
4. Supplementary Table S4: MaAsLin results: Cohort 1 LifeLines DEEP
 - a. File: SupplementaryTableS4_Cohort1_MaAsLin_PPI.xlsx
5. Supplementary Table S5: MaAsLin results: Cohort 2 IBD UMCG
 - a. File: SupplementaryTableS5_Cohort2_MaAsLin_PPI.xlsx
6. Supplementary Table S6: MaAsLin results: Cohort 3 IBS MUMC
 - a. File: SupplementaryTableS6_Cohort3_MaAsLin_PPI.xlsx
7. Supplementary Table S7: Cohort 1 medication influencing the microbiome
 - a. File: SupplementaryTableS7_Cohort1_FullMedicationCheck.xlsx

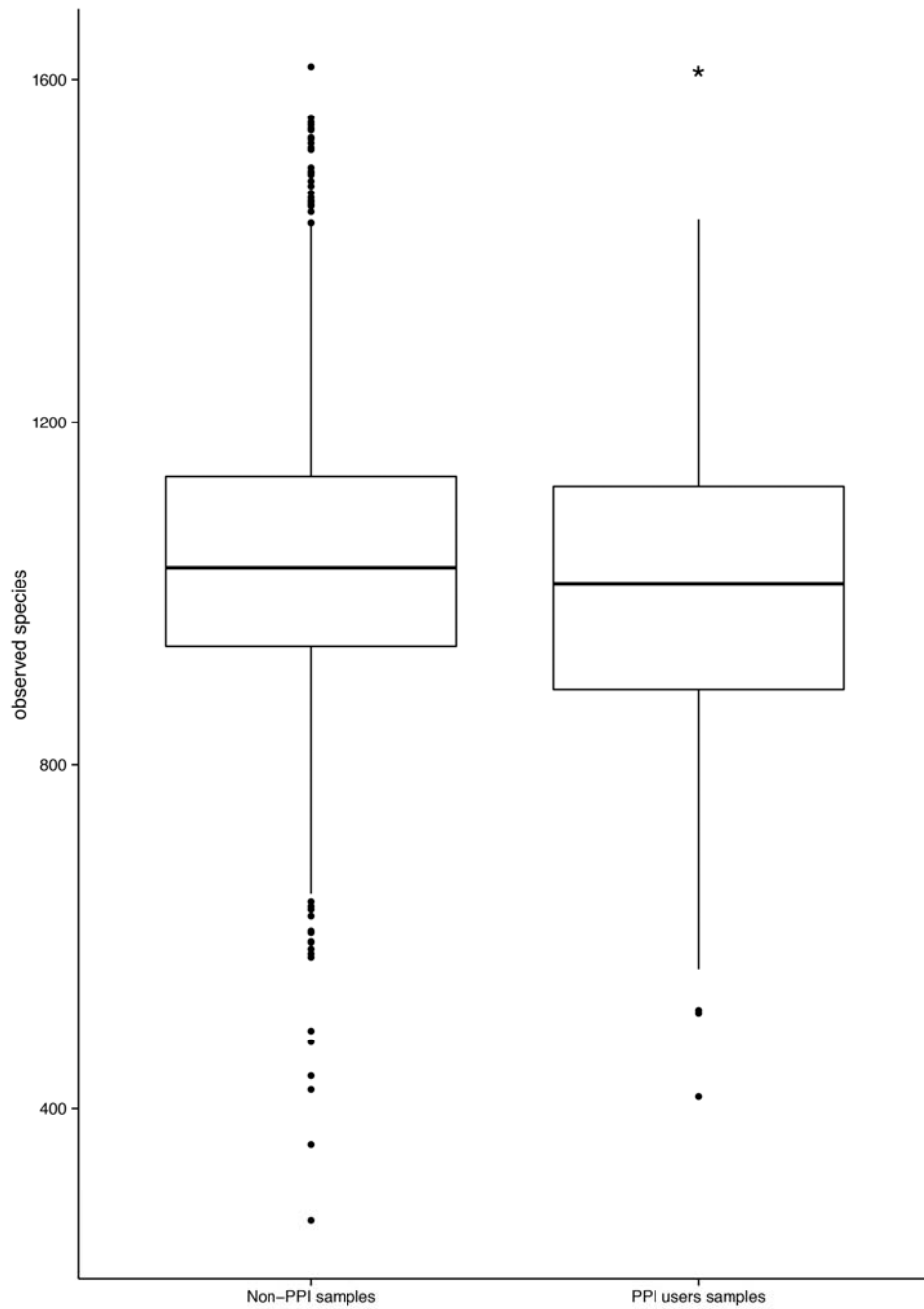
Supplementary Figure S3:

Shannon diversity: Gut microbiome diversity is significantly diminished in PPI users. ($p = 0.01$)



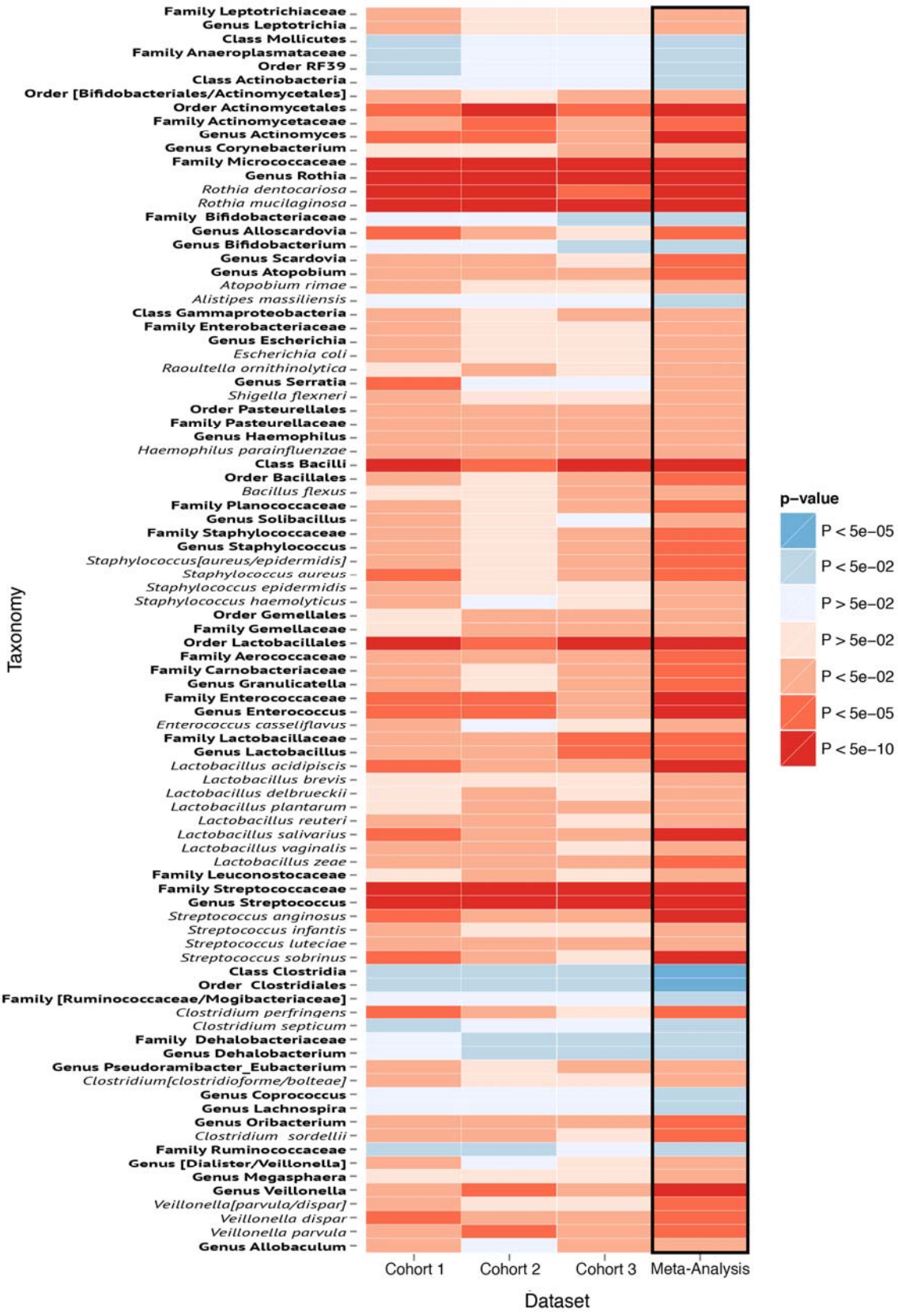
Supplementary Figure S4:

Richness: gut microbiome of PPI-users contains significantly less observed species. ($p = 0.02$)



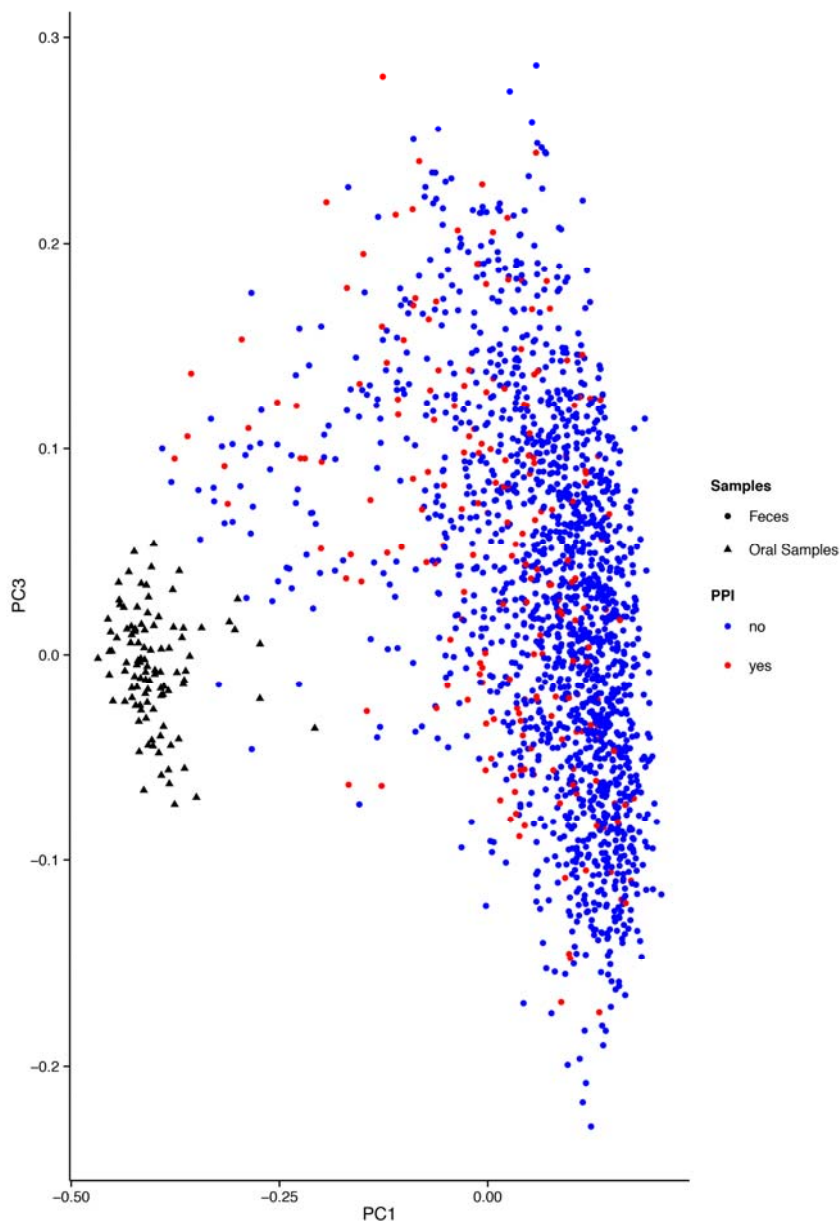
Supplementary Figure S5:

Significantly altered taxa in PPI users is consistent in three cohorts. Meta-analysis of three independent cohorts comprising 1815 fecal samples. The heatmap shows 92 significantly increased or decreased taxa associated with PPI use in the gut microbiome for each cohort and for the meta-analysis (meta-analysis FDR < 0.05).



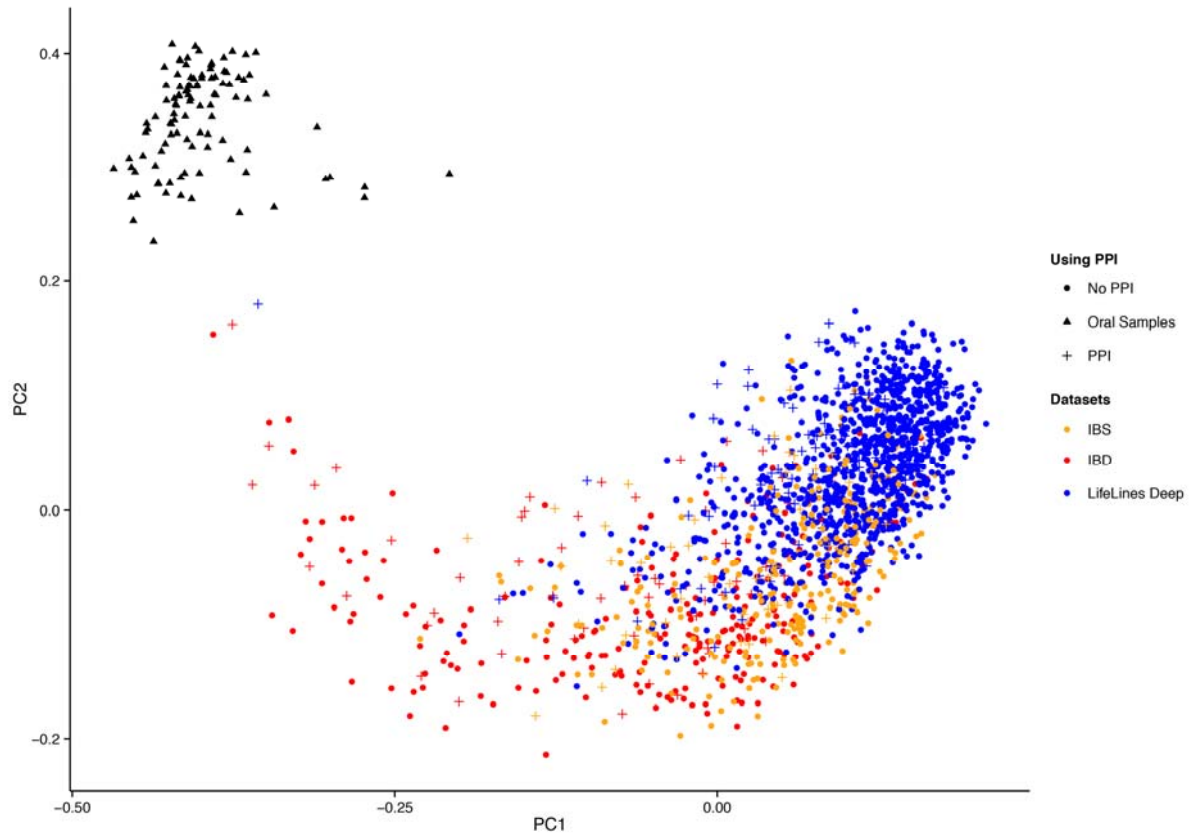
Supplementary Figure S6:

Principal Coordinate Analysis: The gut microbiome of PPI users (red dots) is significantly different to non-PPI users (blue dots) in the first coordinate (PCoA1: $P = 1.39 \times 10^{-20}$, Wilcoxon test) and third coordinate (PCoA3: $P = 0.0004$, Wilcoxon test).



Supplementary Figure S7:

PCoA with separate colors for the individual cohorts. The gut microbiome of PPI users was significantly closer to the oral microbiome.



Supplementary Figure S8:

Cladogram of PPI-associated changes in the gut microbiome. Red dots represent significantly increased bacterial taxa. Blue dots represent significantly decreased bacterial taxa ($q < 0.05$). Yellow areas represent bacterial taxa of the gut microbiome that are more abundantly present in the oral microbiome.

