

H.pylori Rhesus Microbiome Analysis

Noah Siegel

Data used in analysis

Library

```
suppressPackageStartupMessages({  
  library(sjPlot)  
  library(readxl)  
  library(phyloseq)  
  library(microbiome)  
  library(DESeq2)  
  library(qiime2R)  
  library(tidyverse)  
  library(tidyMicro)  
  library(kableExtra)  
  library(magrittr)  
  library(ggpubr)  
  library(microeco)  
  library(tidytree)  
  library(RColorBrewer)  
  library(questionr)  
  library(rmarkdown)  
  library(stringr)  
})
```

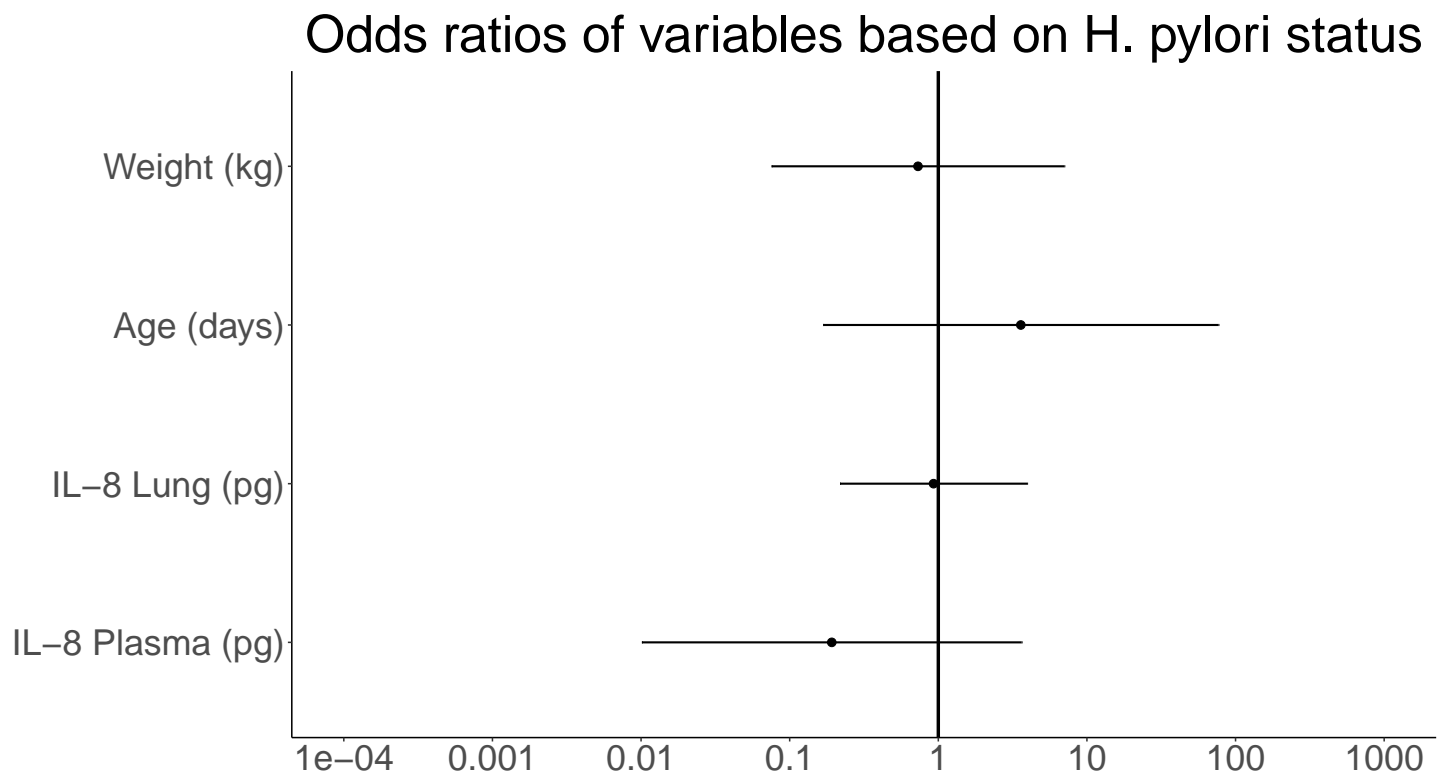
ASV counts the taxa table are linked below:

ASV counts

Taxa table

Table 1: H.pylori Metadata

SampleID	Treatment	site	Site_status	sex	log10_cfu.gm	IL8_Lavage	IL8_Plasma
LMiller_00458.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	NA	463.376
LMiller_00458.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	NA	463.376
LMiller_00459.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	NA	258.416
LMiller_00459.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	NA	258.416
LMiller_00461.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	7.66	NA	704.550
LMiller_00461.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	7.66	NA	704.550
LMiller_00462.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	19.104	1075.626
LMiller_00462.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	19.104	1075.626
LMiller_00463.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	11.590	423.590
LMiller_00466.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	3.81	11.201	642.148
LMiller_00466.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	3.81	11.201	642.148
LMiller_00467.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	6.09	15.511	425.782
LMiller_00467.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	6.09	15.511	425.782
LMiller_00468.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	15.511	660.911
LMiller_00468.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	15.511	660.911
LMiller_00469.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	6.38	NA	1279.789
LMiller_00469.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	6.38	NA	1279.789
LMiller_00473.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	20.100	608.508
LMiller_00473.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	20.100	608.508
LMiller_00474.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	44.699	443.989
LMiller_00476.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	5.48	NA	476.431
LMiller_00476.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	5.48	NA	476.431
LMiller_00477.BAL	H.pylori_(+)	Lung	H.pylori_(+)_Lung	Female	5.81	NA	715.056
LMiller_00477.Swab	H.pylori_(+)	Oral	H.pylori_(+)_Oral	Female	5.81	NA	715.056
LMiller_00481.BAL	H.pylori_(-)	Lung	H.pylori_(-)_Lung	Female	0.00	17.622	NA
LMiller_00481.Swab	H.pylori_(-)	Oral	H.pylori_(-)_Oral	Female	0.00	17.622	NA



	OR	2.5 %	97.5 %	p
(Intercept)	0.018	0.000	110.146	0.410
‘Weight (kg)’	0.243	0.000	7254.525	0.786
‘Age (days)’	1.042	0.955	1.177	0.413
‘IL-8 Lung (pg)’	0.993	0.852	1.158	0.921
‘IL-8 Plasma (pg)’	0.996	0.985	1.001	0.271

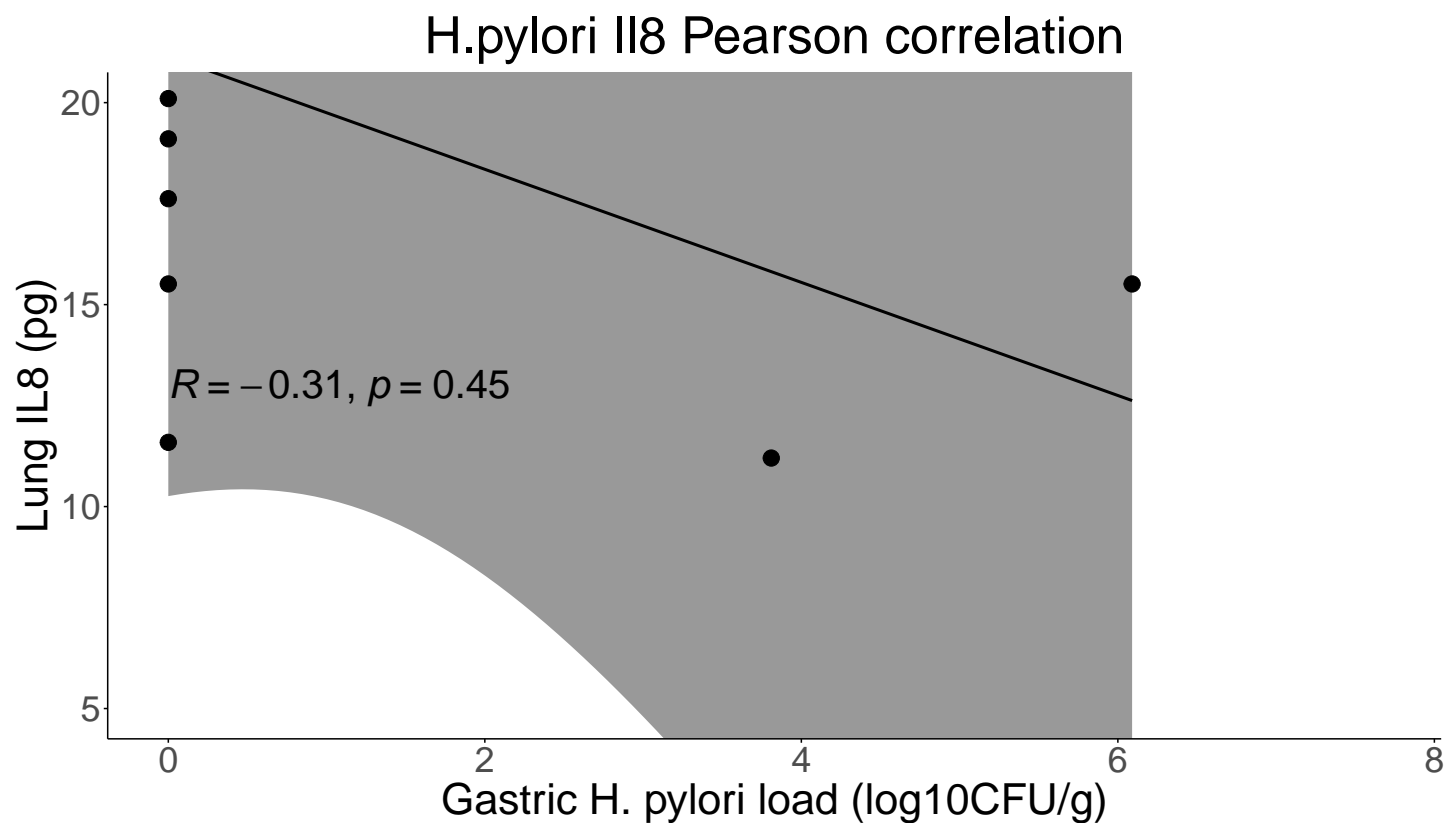


Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study

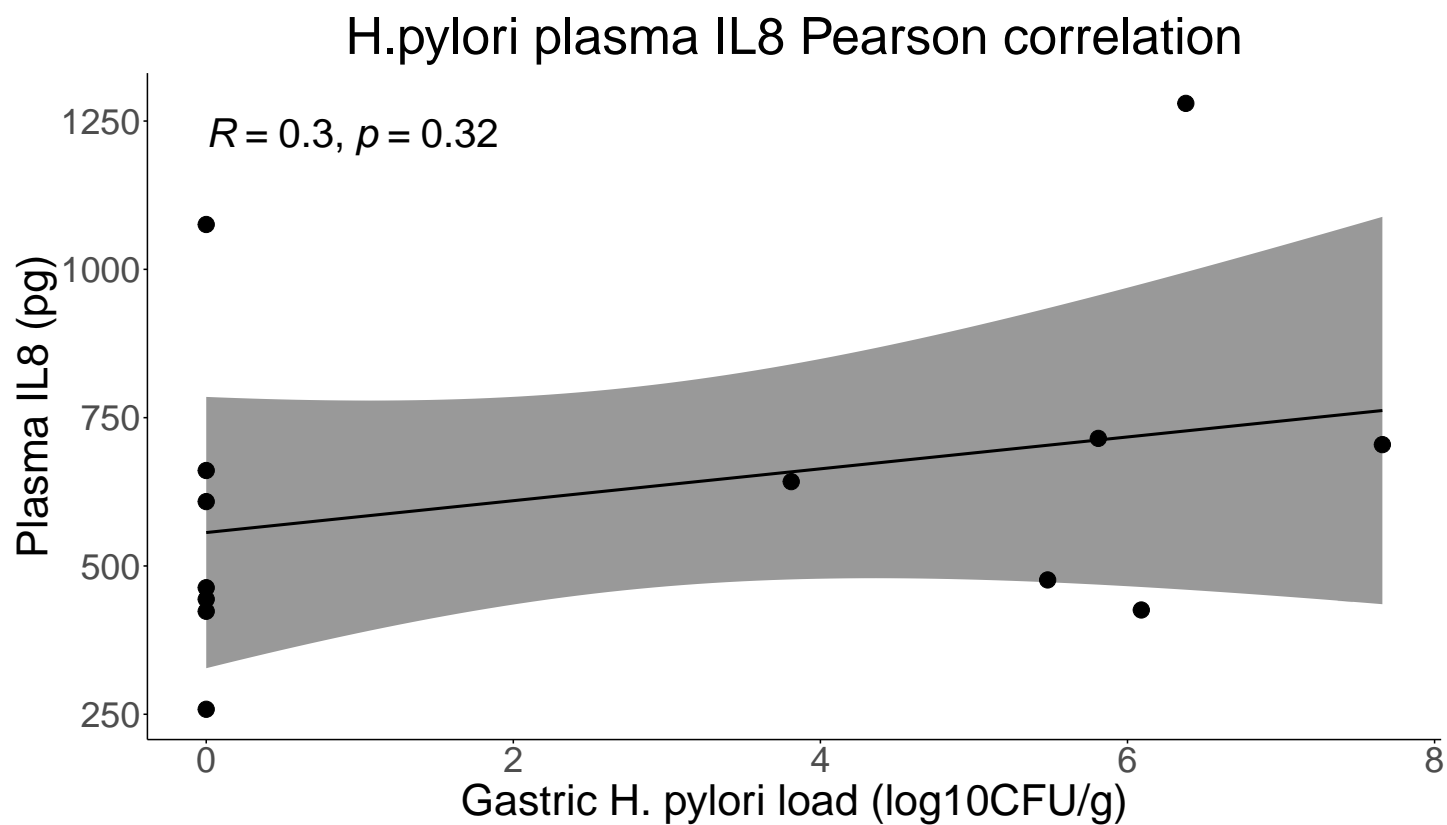
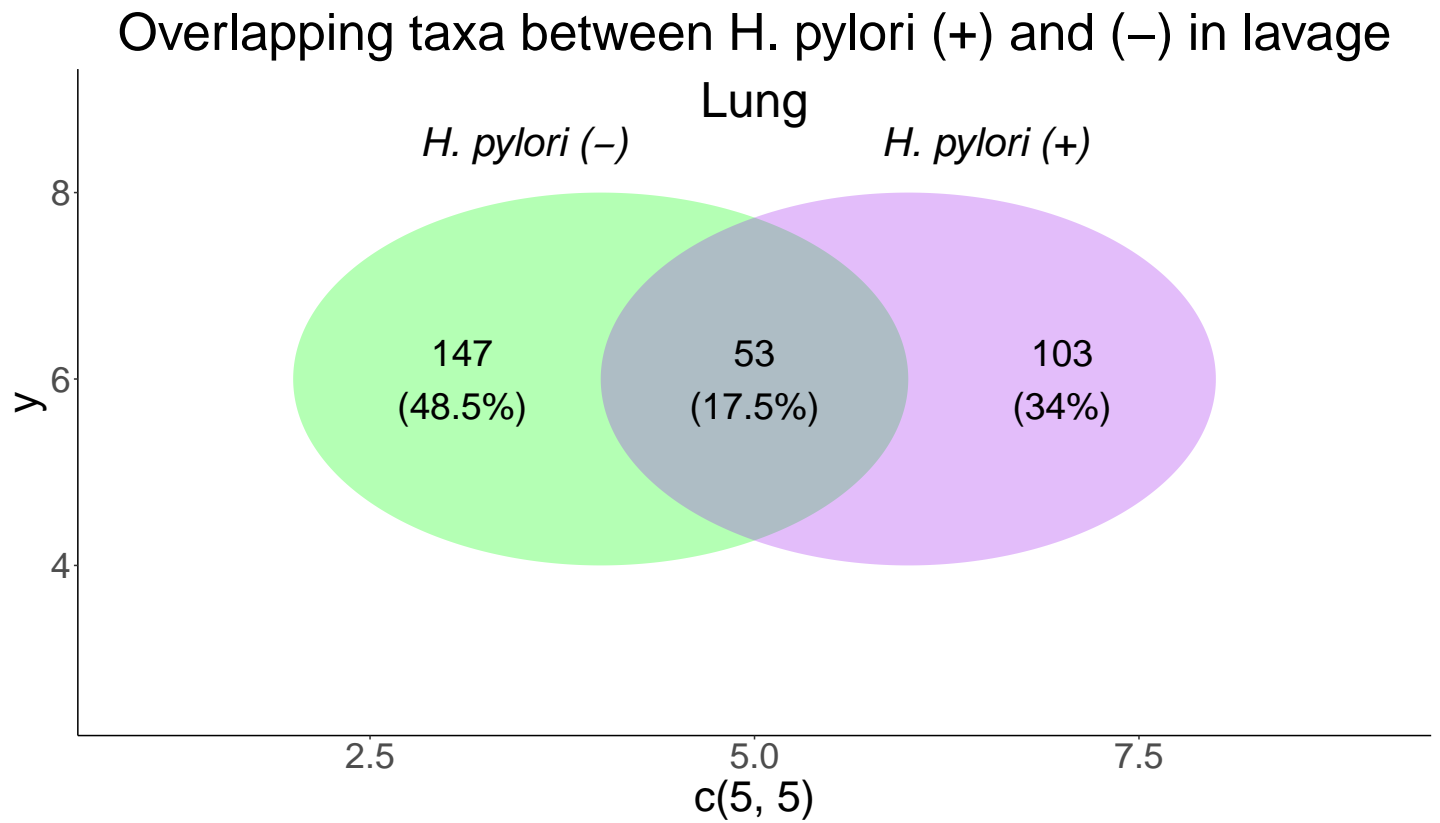


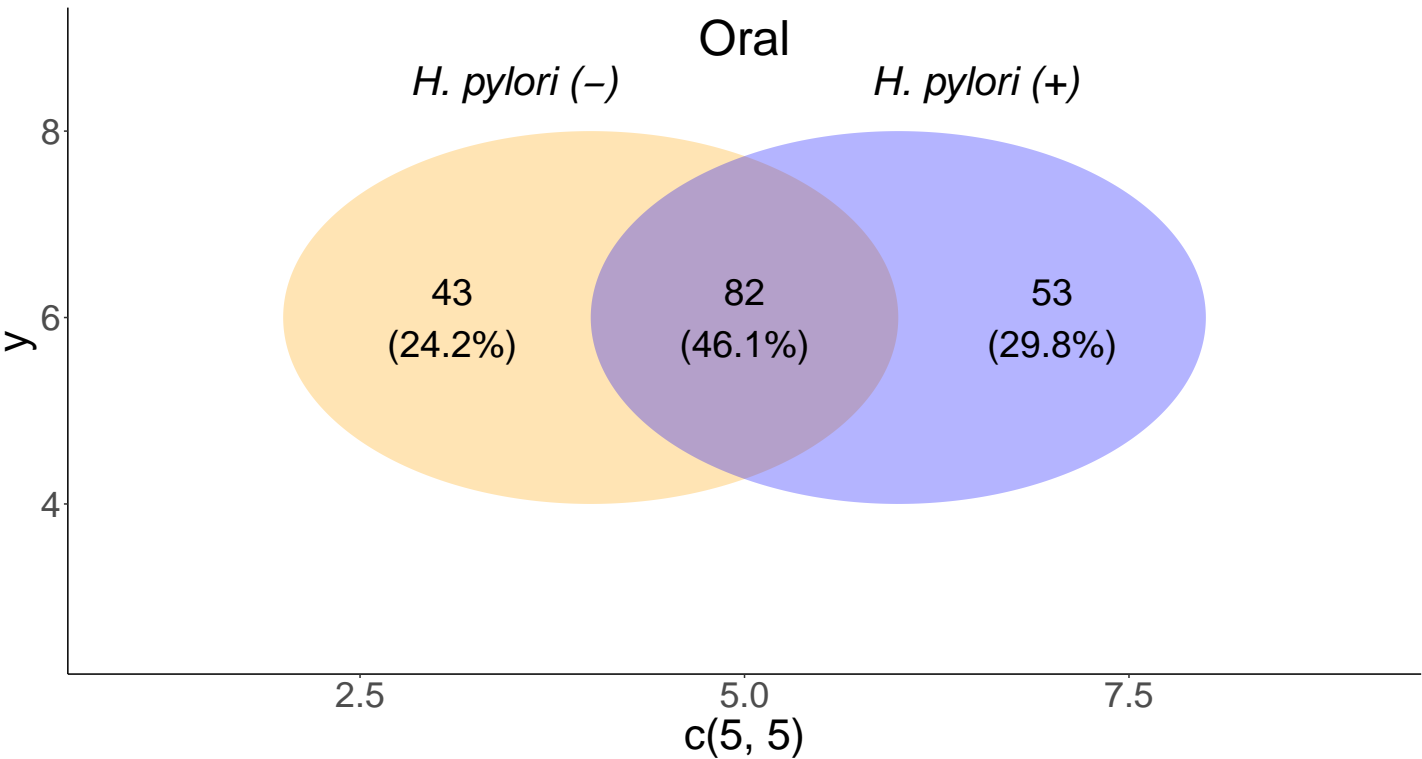
Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

Overlapping Taxa Between Sites and *H. pylori* Status

Lavage overlapping taxa

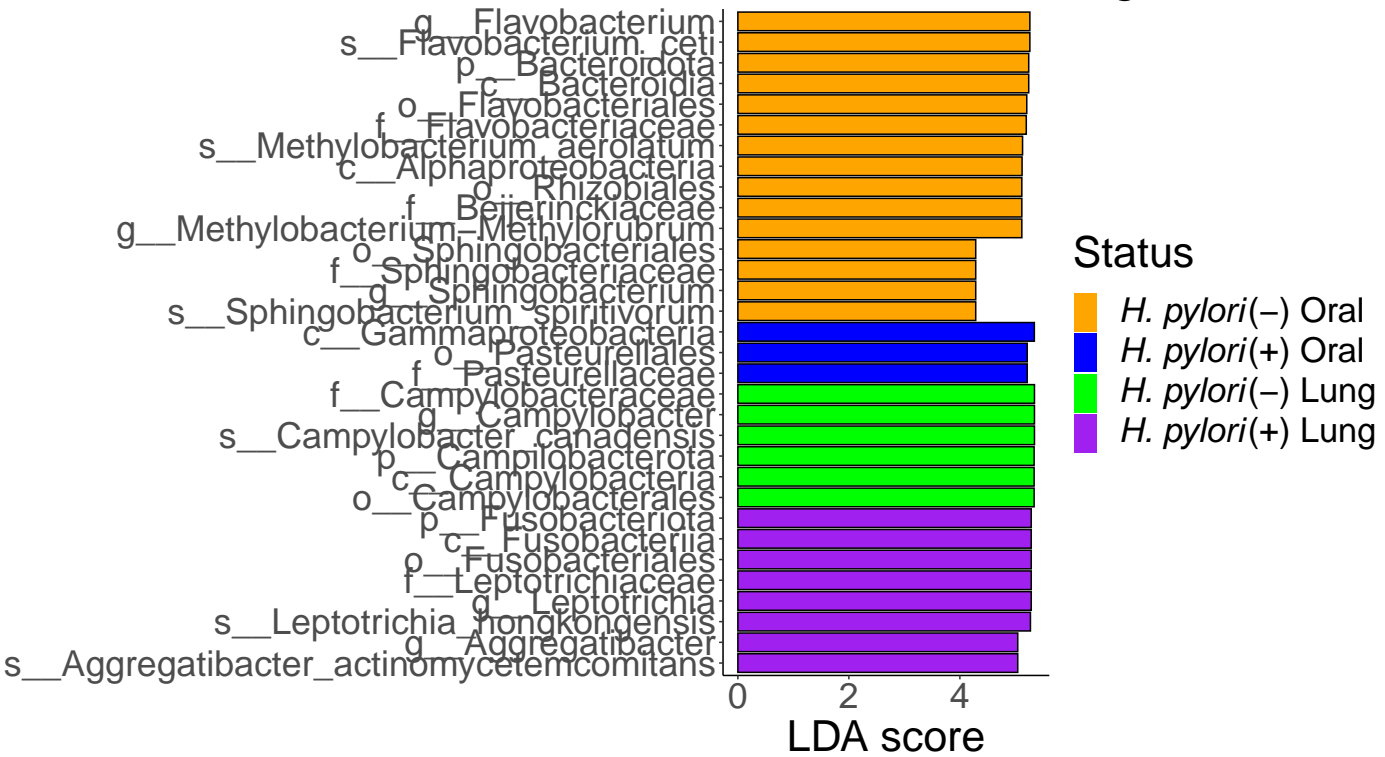


Overlapping taxa between *H. pylori* (+) and (–) in buccal cavity



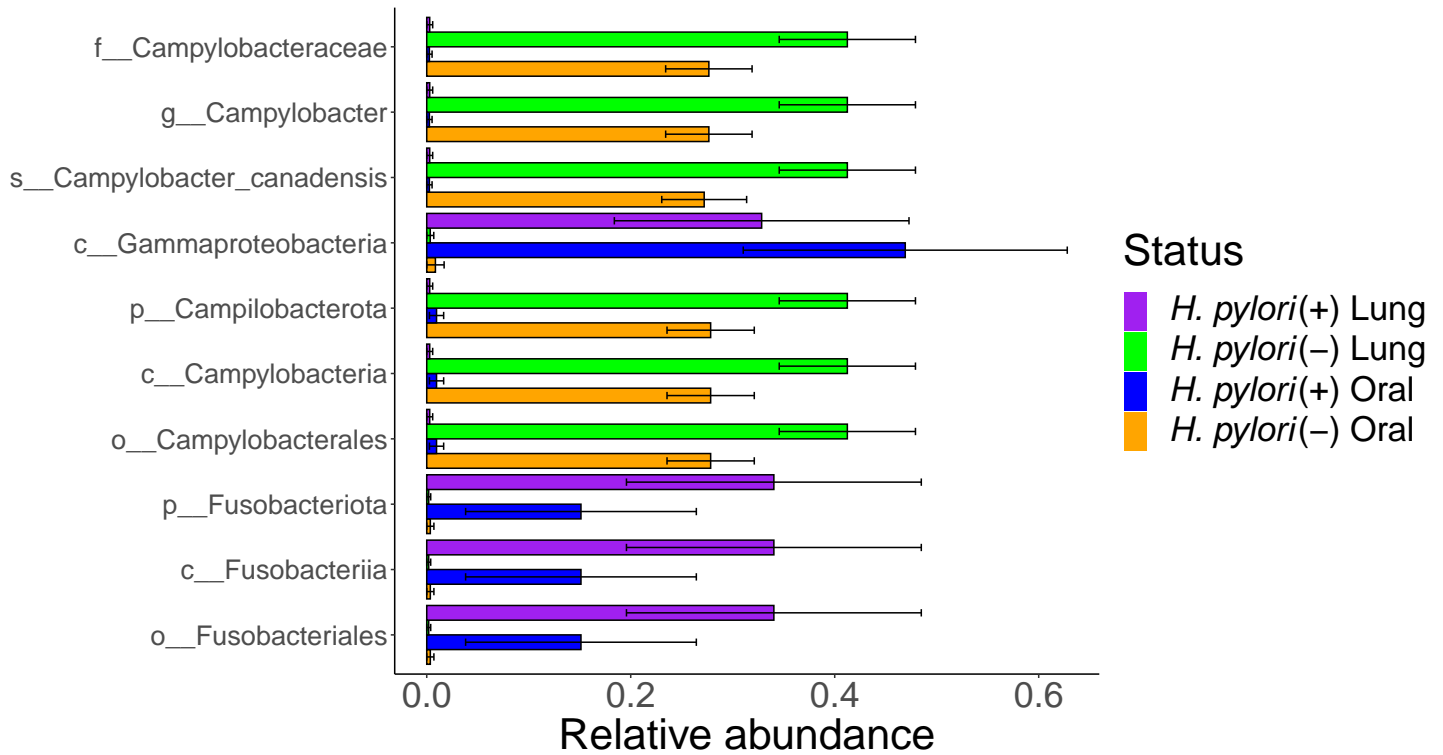
Lefse analysis and differential abundance for both sites

Lefse taxa from bronchoalveolar lavage and oral sites



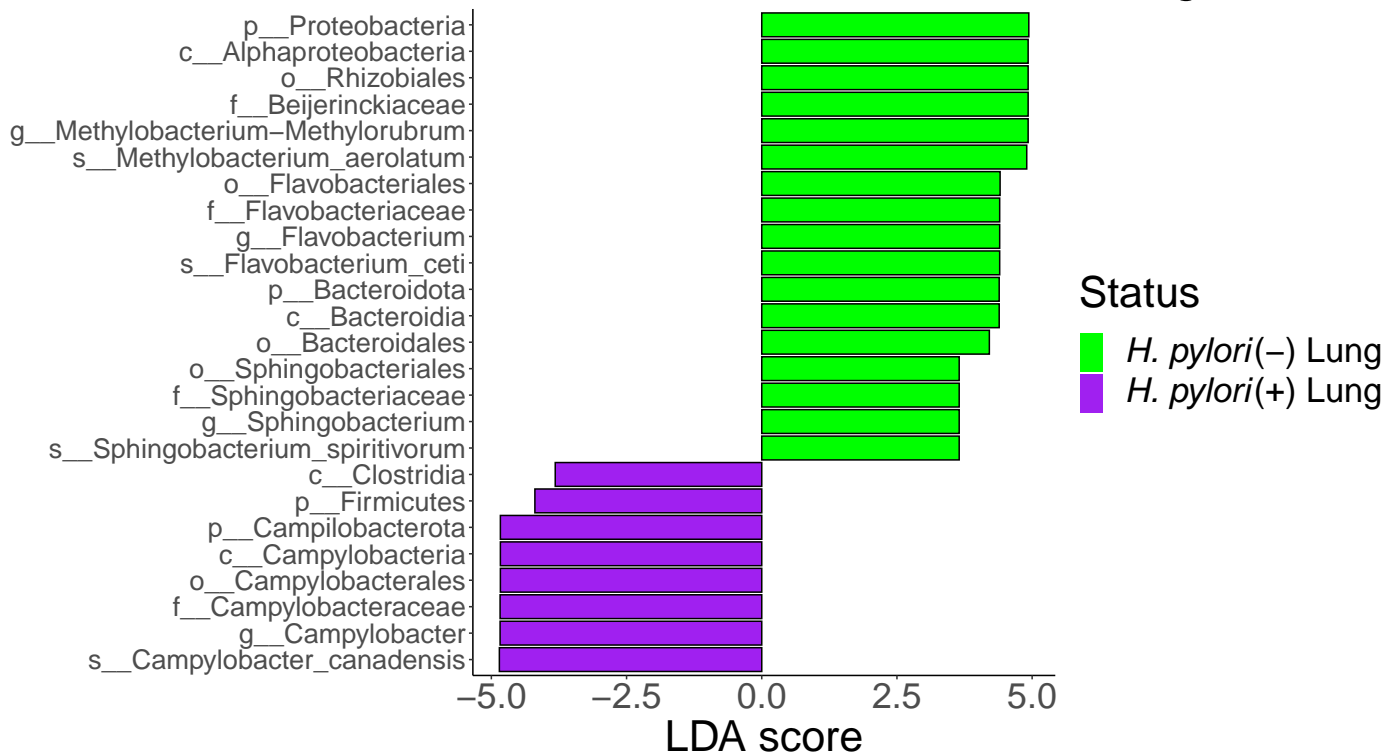
Relative abundance of differential taxa

False relative abundance from bronchoalveolar lavage and oral samples

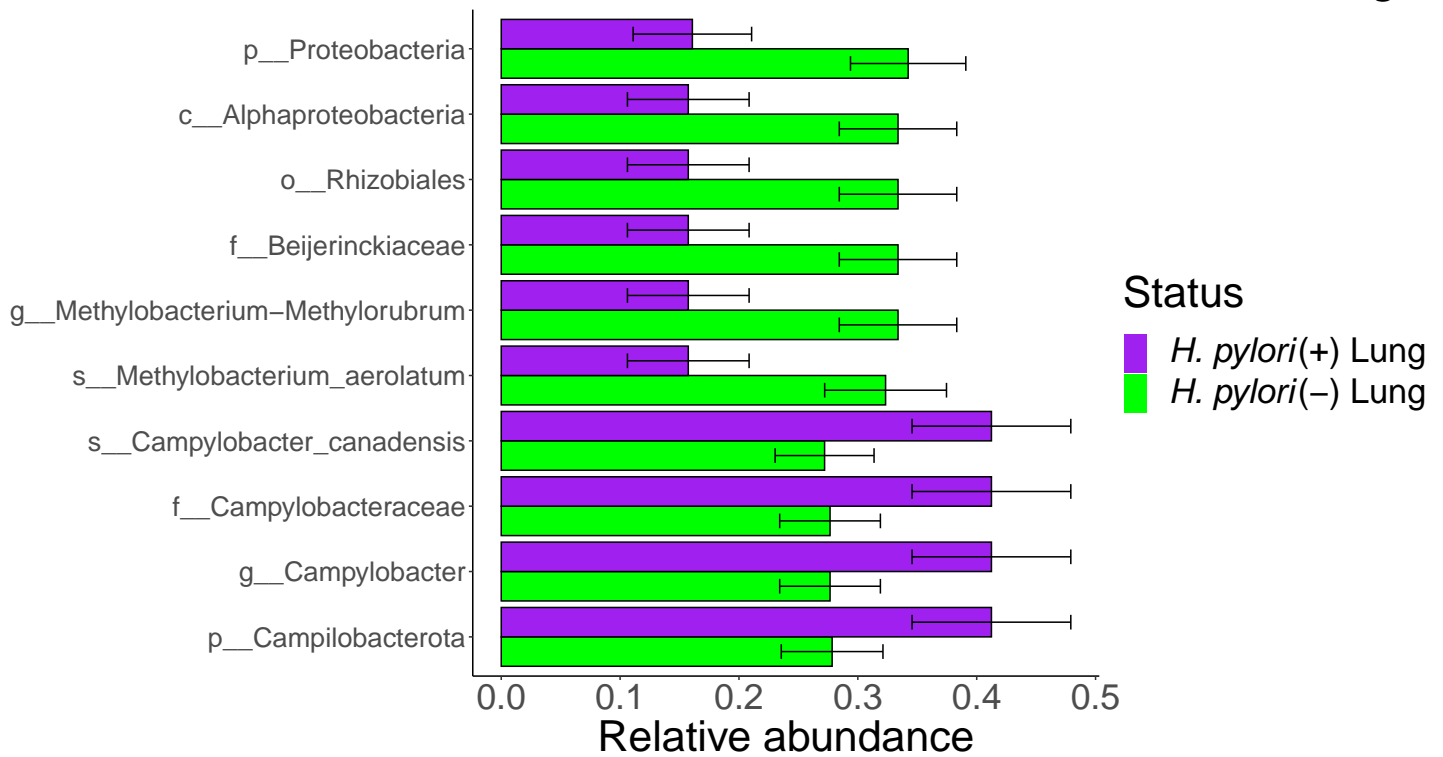


Lefse and differential abundance for bronchoalveolar lavage

Lefse Taxa from Bronchoalveolar Lavage

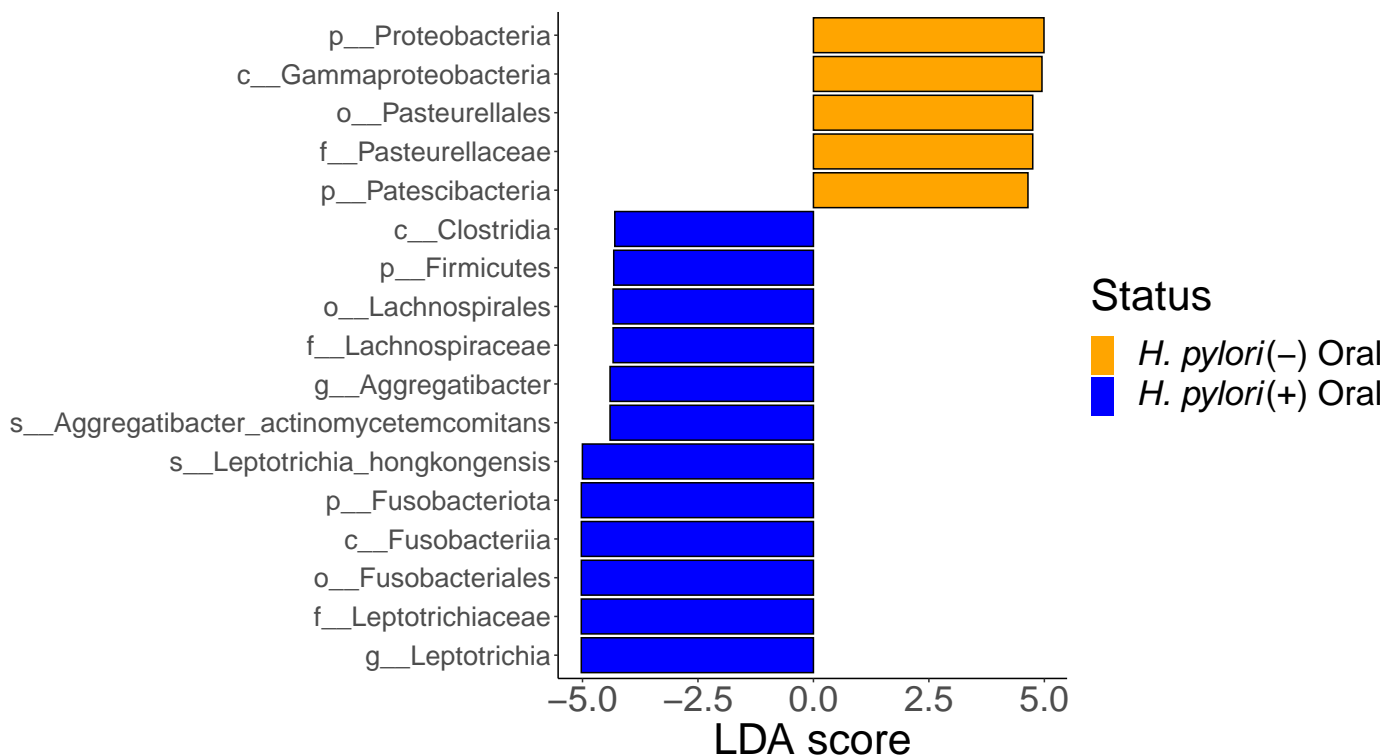


Lefse Relative Abundance from Bronchoalveolar Lavage



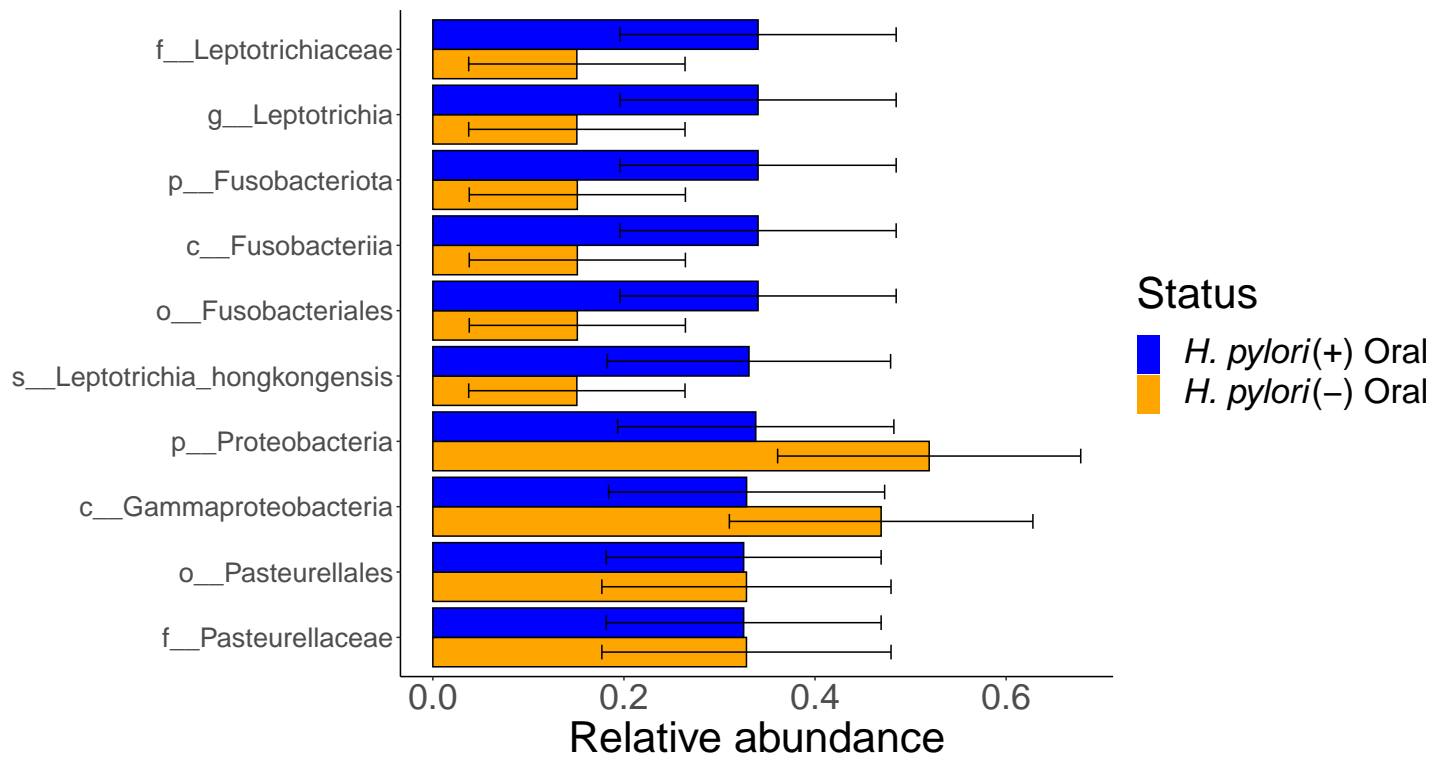
Lefse and differential abundance for oral swabs

Lefse taxa from oral swabs



Relative abundance of differential taxa

Lefse relative abundance from oral swabs

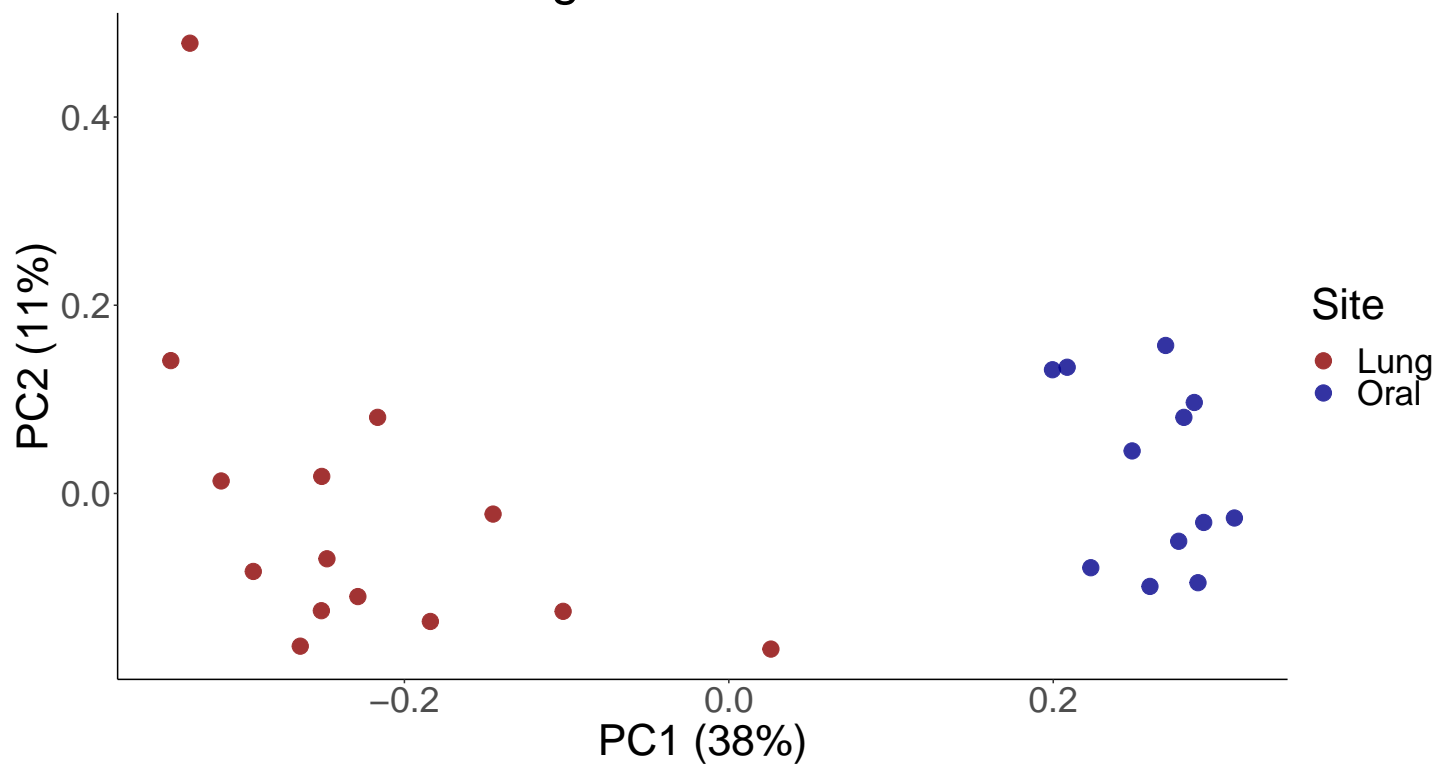


Beta diversity

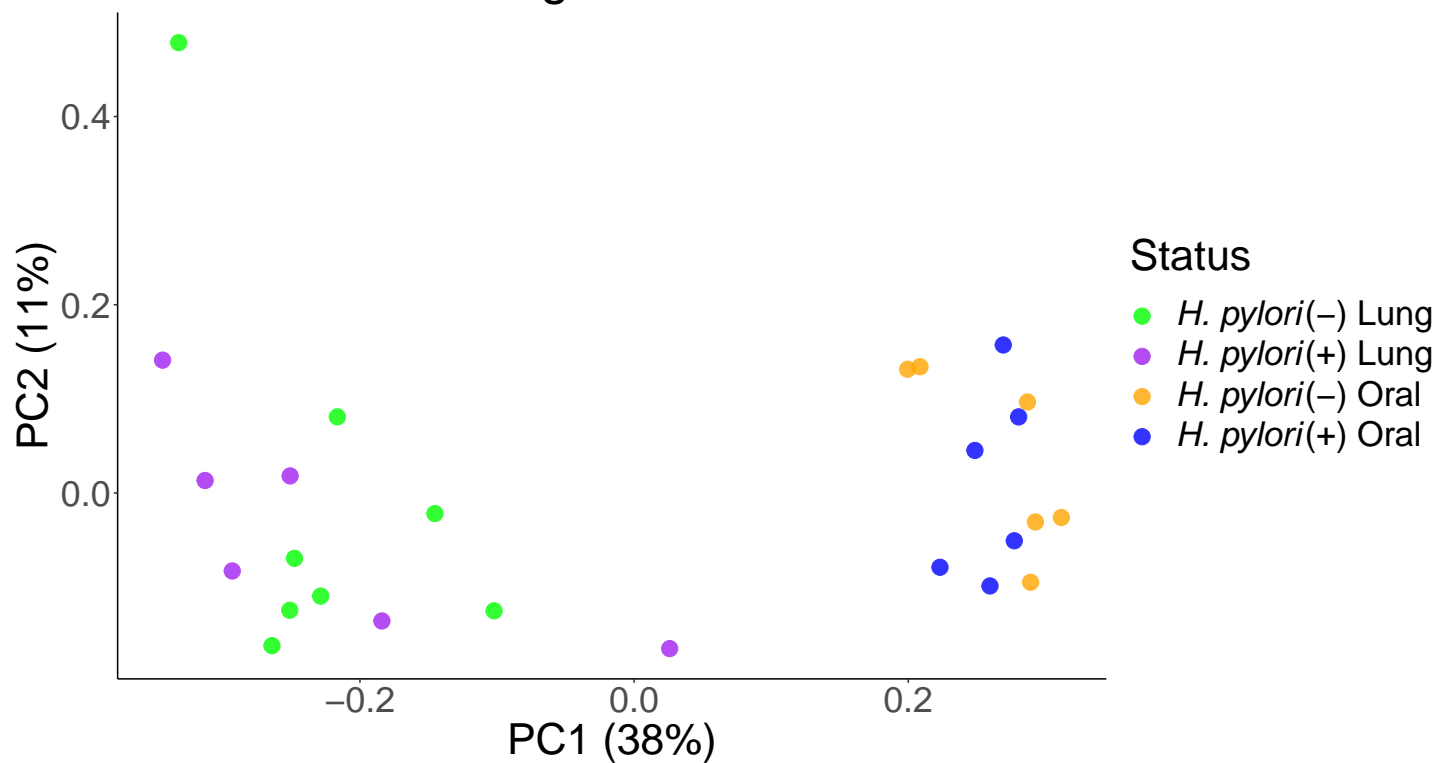
Unweighted unifracs PCoA plots

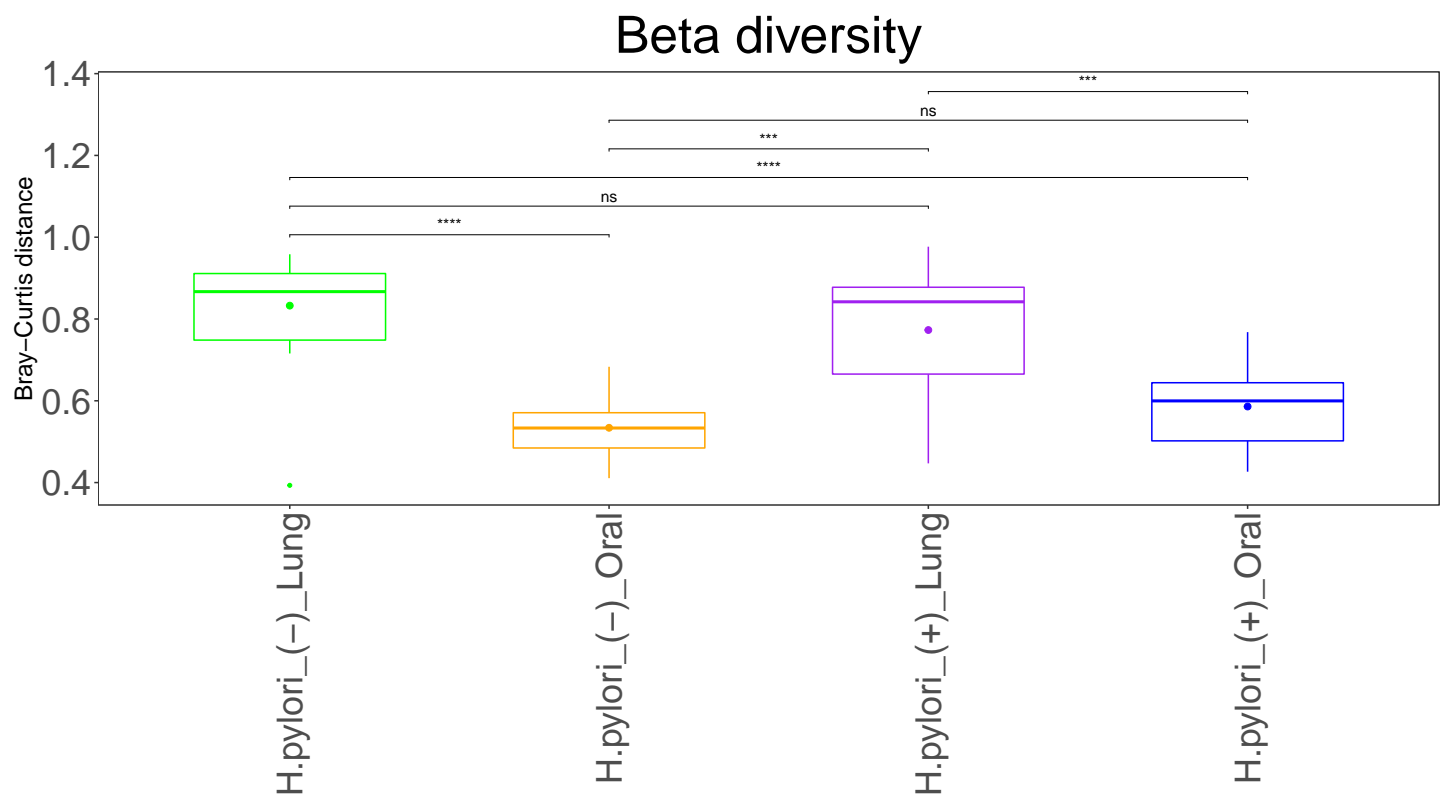
##	PC1	PC2	PC3	PC4	PC5	PC6	PC7
## 1	0.38311	0.1122317	0.08255574	0.05624649	0.04518453	0.04178459	0.03697168
##	PC8	PC9	PC10	PC11	PC12	PC13	PC14
## 1	0.03441675	0.0305229	0.0292508	0.02395872	0.0227312	0.01881898	0.01538496
##	PC15	PC16	PC17	PC18	PC19	PC20	
## 1	0.0140825	0.01226748	0.01155323	0.008776171	0.007488221	0.004824027	
##	PC21	PC22	PC23	PC24	PC25	PC26	
## 1	0.003528799	0.002630896	0.001679594	0	0	0	

Unweighted unifrac PCoA

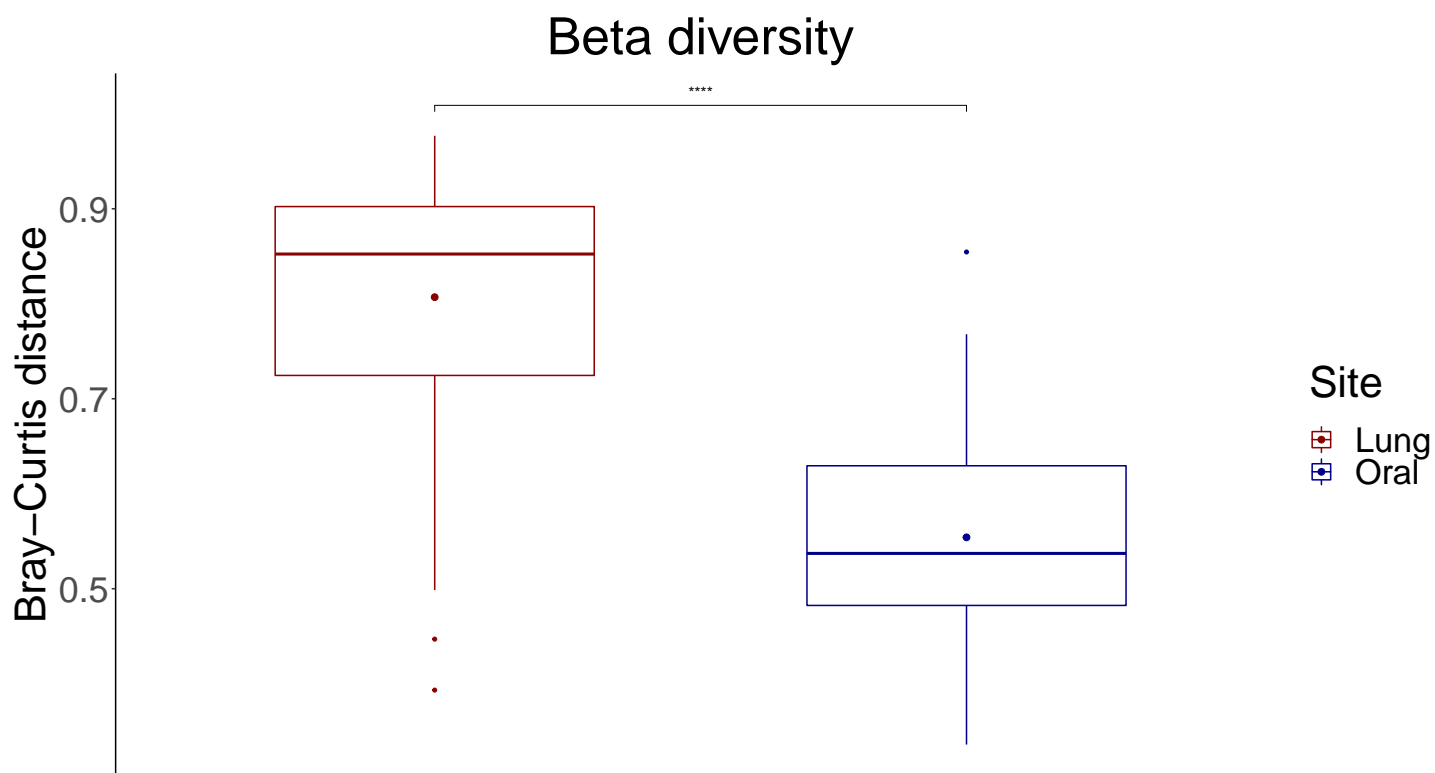


Status Unweighted unifrac PCoA



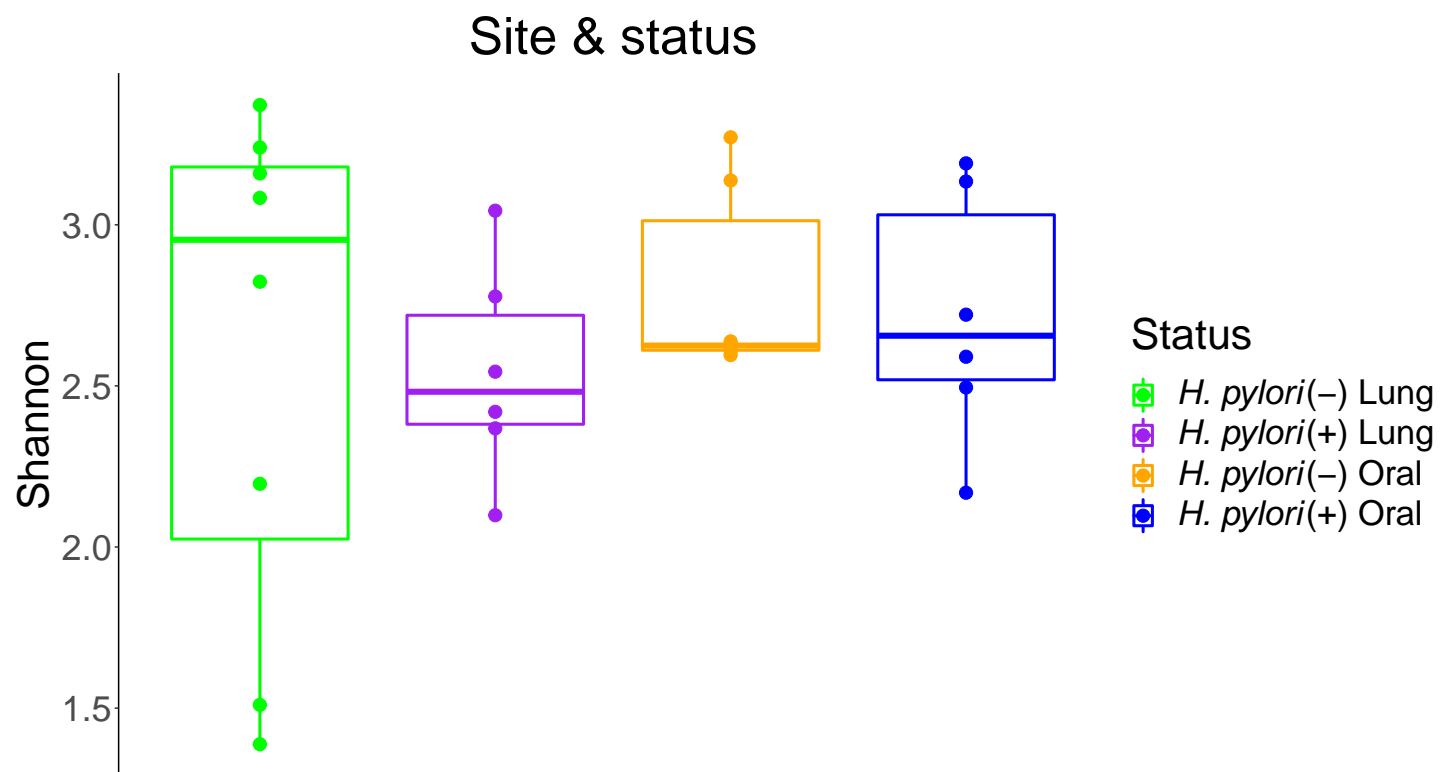


Bray-Curtis



Alpha Diversity

Shannon index by site and *H. pylori* status



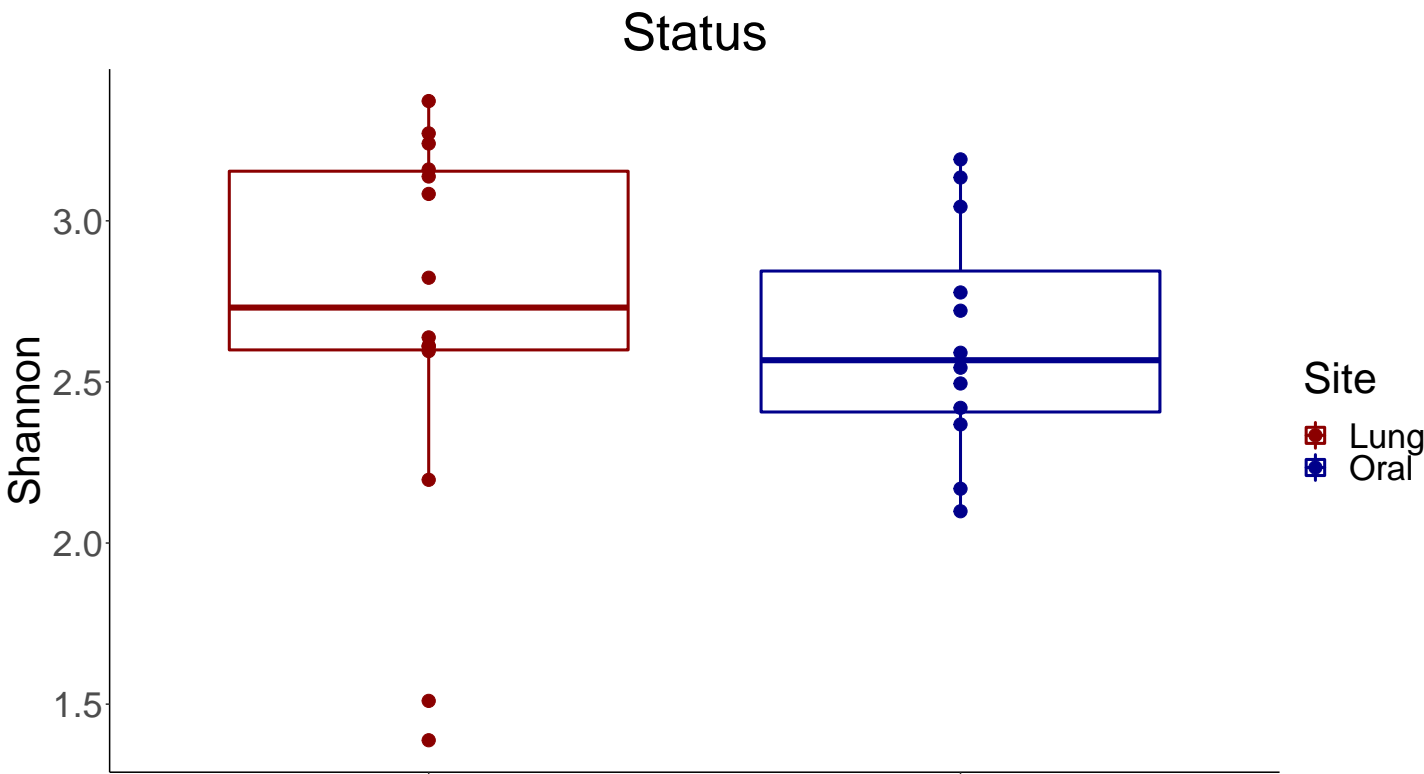
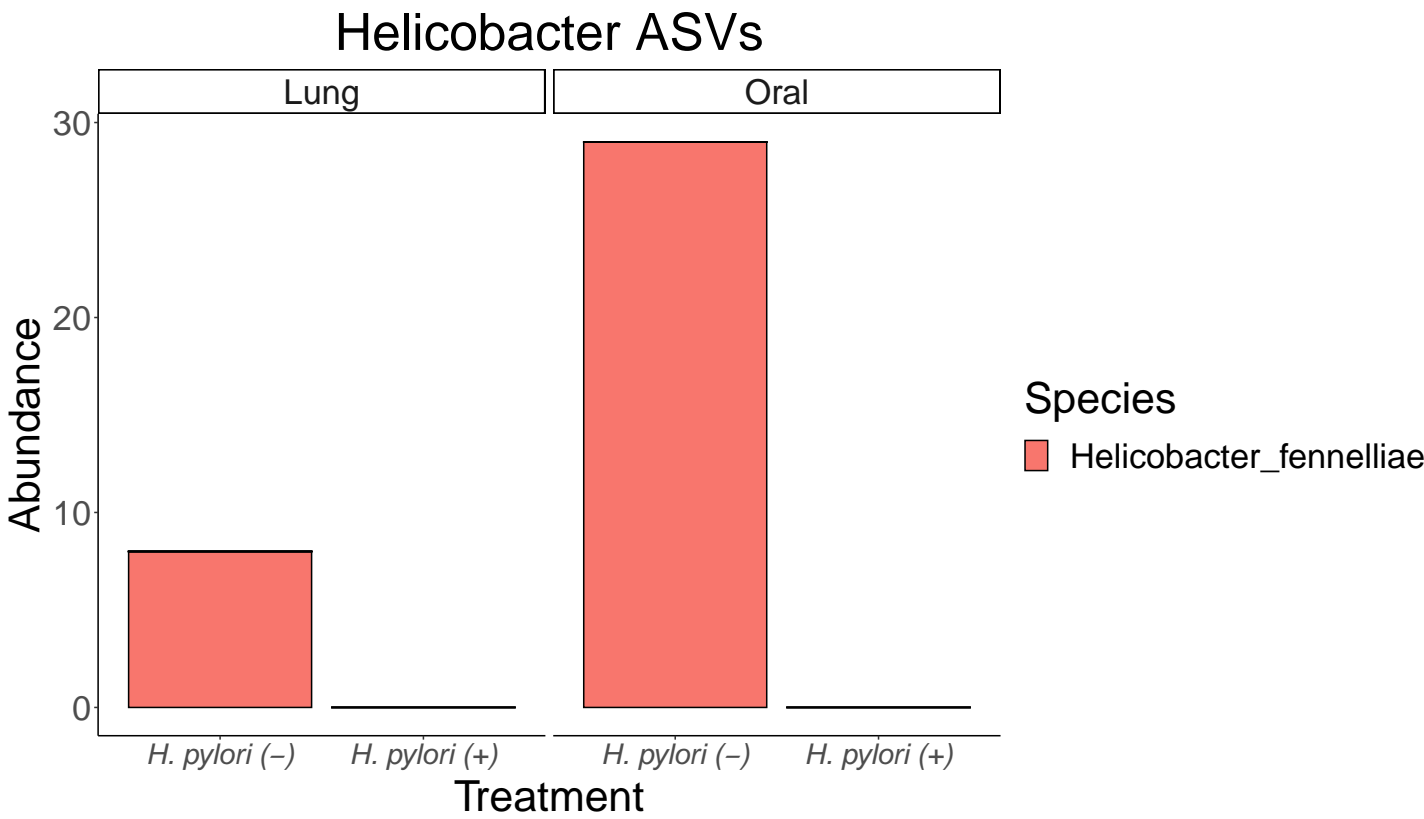


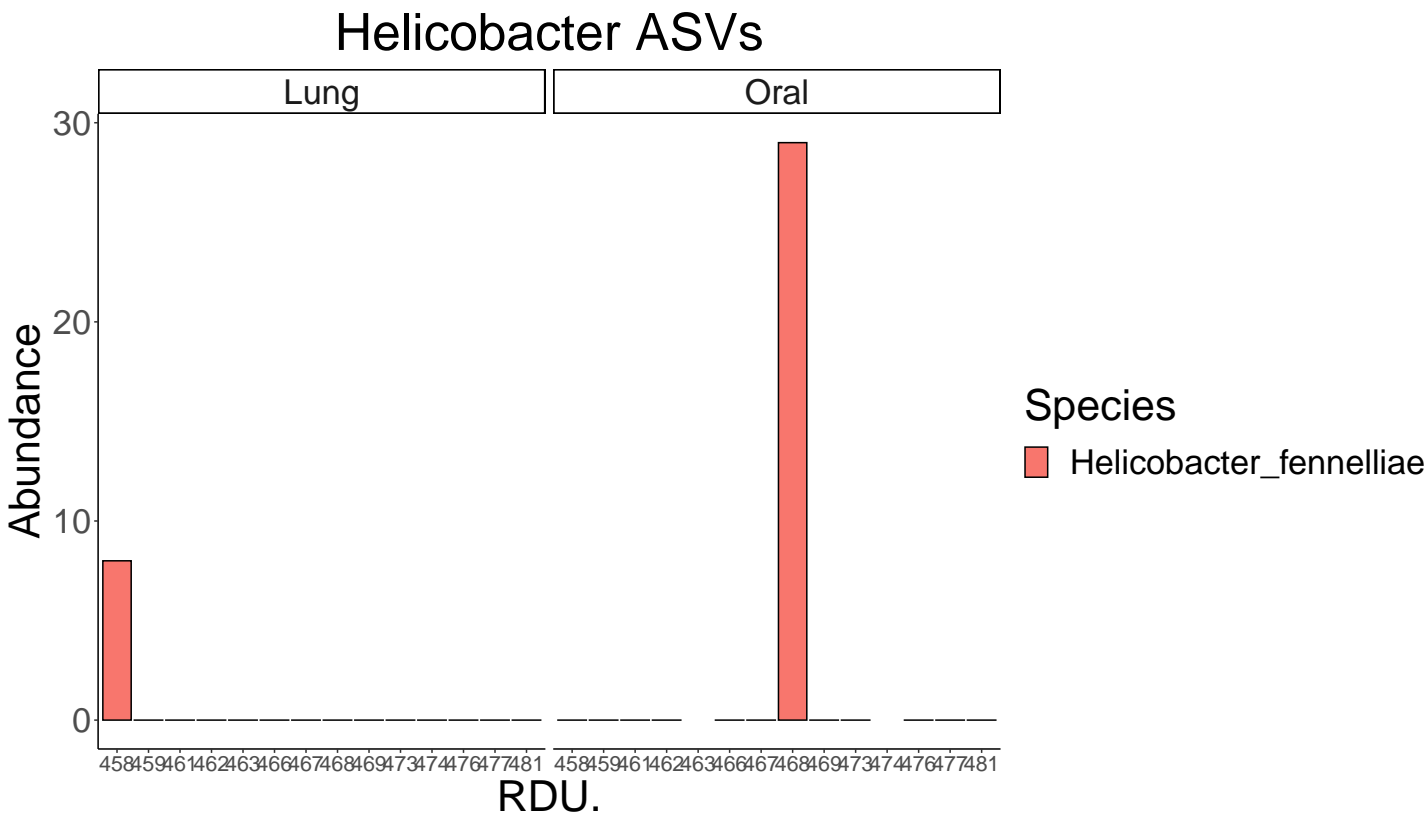
Table 2: All alpha diversity measurees

Groups	Measure	Test method	p.value	Significance
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Observed	KW	0.220	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Observed	KW	0.651	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Observed	KW	0.081	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Observed	KW	0.262	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Observed	KW	0.520	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Observed	KW	0.109	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Observed	KW	0.202	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Chao1	KW	0.220	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Chao1	KW	0.651	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Chao1	KW	0.081	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Chao1	KW	0.262	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Chao1	KW	0.520	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Chao1	KW	0.109	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Chao1	KW	0.202	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	ACE	KW	0.220	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	ACE	KW	0.651	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	ACE	KW	0.081	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	ACE	KW	0.262	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	ACE	KW	0.520	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	ACE	KW	0.109	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	ACE	KW	0.202	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Shannon	KW	0.439	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Shannon	KW	1.000	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Shannon	KW	0.796	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Shannon	KW	0.109	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Shannon	KW	0.337	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Shannon	KW	0.423	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Shannon	KW	0.540	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Simpson	KW	0.519	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Simpson	KW	0.699	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Simpson	KW	0.699	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Simpson	KW	0.109	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Simpson	KW	0.423	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Simpson	KW	0.262	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Simpson	KW	0.493	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	InvSimpson	KW	0.519	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	InvSimpson	KW	0.699	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	InvSimpson	KW	0.699	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	InvSimpson	KW	0.109	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	InvSimpson	KW	0.423	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	InvSimpson	KW	0.262	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	InvSimpson	KW	0.493	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Fisher	KW	0.606	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Fisher	KW	0.699	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Fisher	KW	0.796	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Fisher	KW	0.631	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Fisher	KW	0.631	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Fisher	KW	1.000	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Fisher	KW	0.927	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	Coverage	KW	NaN	NA
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	Coverage	KW	NaN	NA
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	Coverage	KW	NaN	NA
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	Coverage	KW	NaN	NA
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	Coverage	KW	NaN	NA
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Coverage	KW	NaN	NA
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	Coverage	KW	NaN	NA
H.pylori_(-)_Lung vs H.pylori_(-)_Oral	PD	KW	0.366	
H.pylori_(-)_Lung vs H.pylori_(+)_Lung	PD	KW	0.699	
H.pylori_(-)_Lung vs H.pylori_(+)_Oral	PD	KW	0.439	
H.pylori_(-)_Oral vs H.pylori_(+)_Lung	PD	KW	0.631	
H.pylori_(-)_Oral vs H.pylori_(+)_Oral	PD	KW	0.749	
H.pylori_(+)_Lung vs H.pylori_(+)_Oral	PD	KW	0.631	
H.pylori_(-)_Lung vs H.pylori_(-)_Oral vs H.pylori_(+)_Lung vs H.pylori_(+)_Oral	PD	KW	0.777	

Helicobacter positive respiratory samples

Helicobacter positive samples separated by site





Taxa barplots

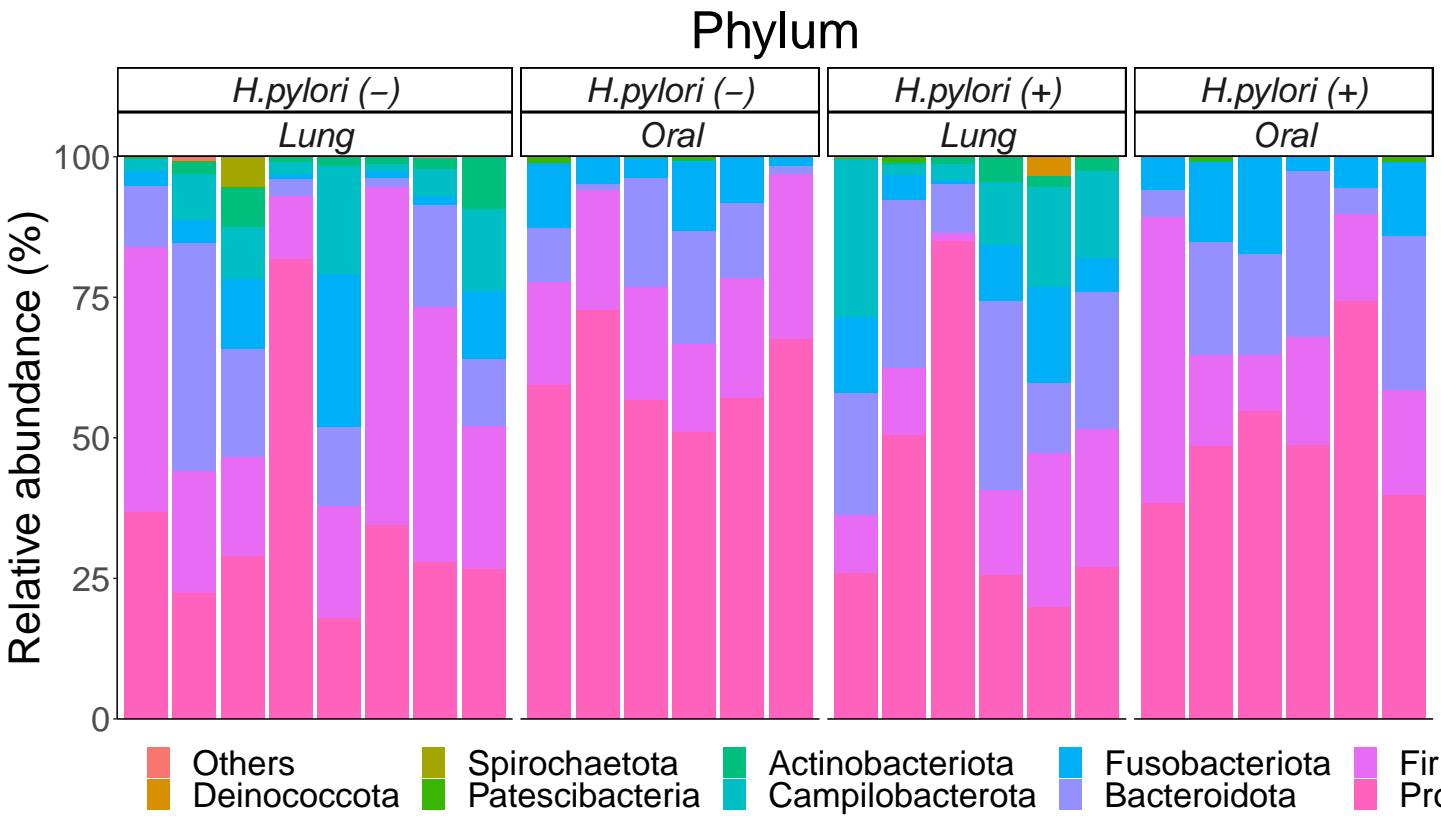


Figure 3: Microbiota Composition at Phylum level.

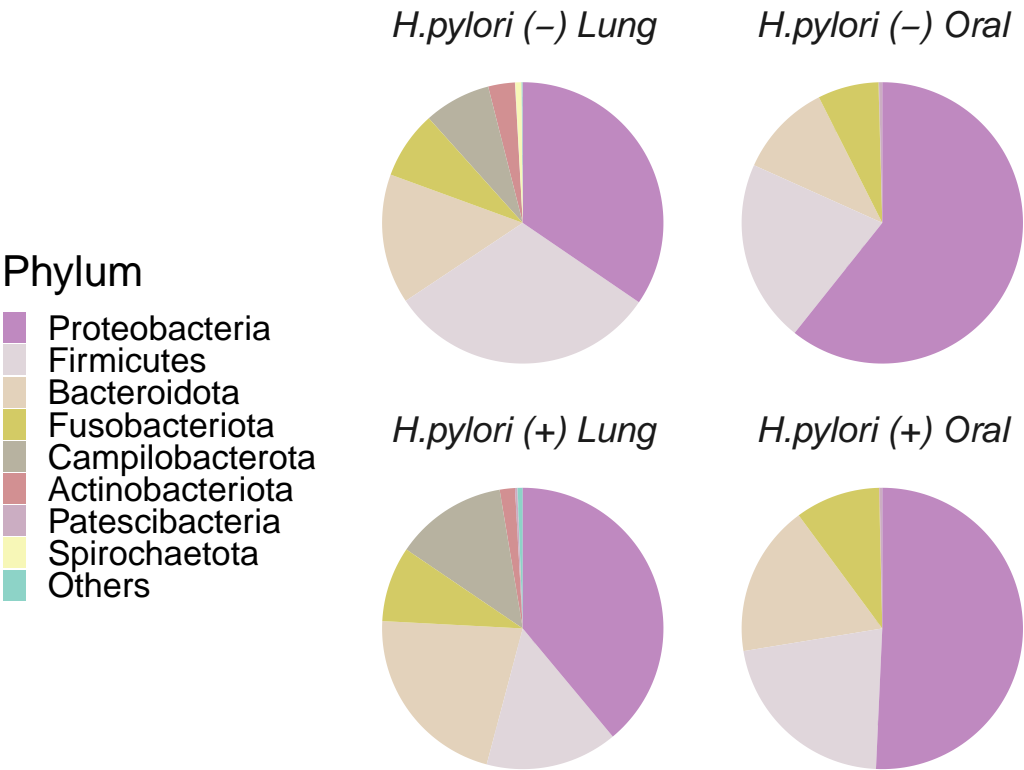


Figure 4: Microbiota Composition at Phylum level.

Table 3: Phylum Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Acidobacteriota	H.pylori (+) Lung	0.1%
Actinobacteriota	H.pylori (-) Lung	3.1%
Actinobacteriota	H.pylori (+) Lung	1.8%
Actinobacteriota	H.pylori (+) Oral	0.1%
Actinobacteriota	H.pylori (-) Oral	0%
Bacteroidota	H.pylori (+) Lung	21.7%
Bacteroidota	H.pylori (+) Oral	17.4%
Bacteroidota	H.pylori (-) Lung	14.9%
Bacteroidota	H.pylori (-) Oral	10.8%
Campilobacterota	H.pylori (+) Lung	12.9%
Campilobacterota	H.pylori (-) Lung	7.7%
Campilobacterota	H.pylori (-) Oral	0%
Deinococcota	H.pylori (+) Lung	0.6%
Desulfobacterota	H.pylori (-) Lung	0.1%
Firmicutes	H.pylori (-) Lung	31.1%
Firmicutes	H.pylori (+) Oral	21.7%
Firmicutes	H.pylori (-) Oral	21%
Firmicutes	H.pylori (+) Lung	15.2%
Fusobacteriota	H.pylori (+) Oral	9.8%
Fusobacteriota	H.pylori (+) Lung	8.6%
Fusobacteriota	H.pylori (-) Lung	7.8%
Fusobacteriota	H.pylori (-) Oral	7%
Latescibacterota	H.pylori (-) Lung	0%
Patescibacteria	H.pylori (-) Oral	0.4%
Patescibacteria	H.pylori (+) Oral	0.3%
Patescibacteria	H.pylori (+) Lung	0.3%
Patescibacteria	H.pylori (-) Lung	0%
Proteobacteria	H.pylori (-) Oral	60.7%
Proteobacteria	H.pylori (+) Oral	50.7%
Proteobacteria	H.pylori (+) Lung	38.9%
Proteobacteria	H.pylori (-) Lung	34.5%
Spirochaetota	H.pylori (-) Lung	0.7%

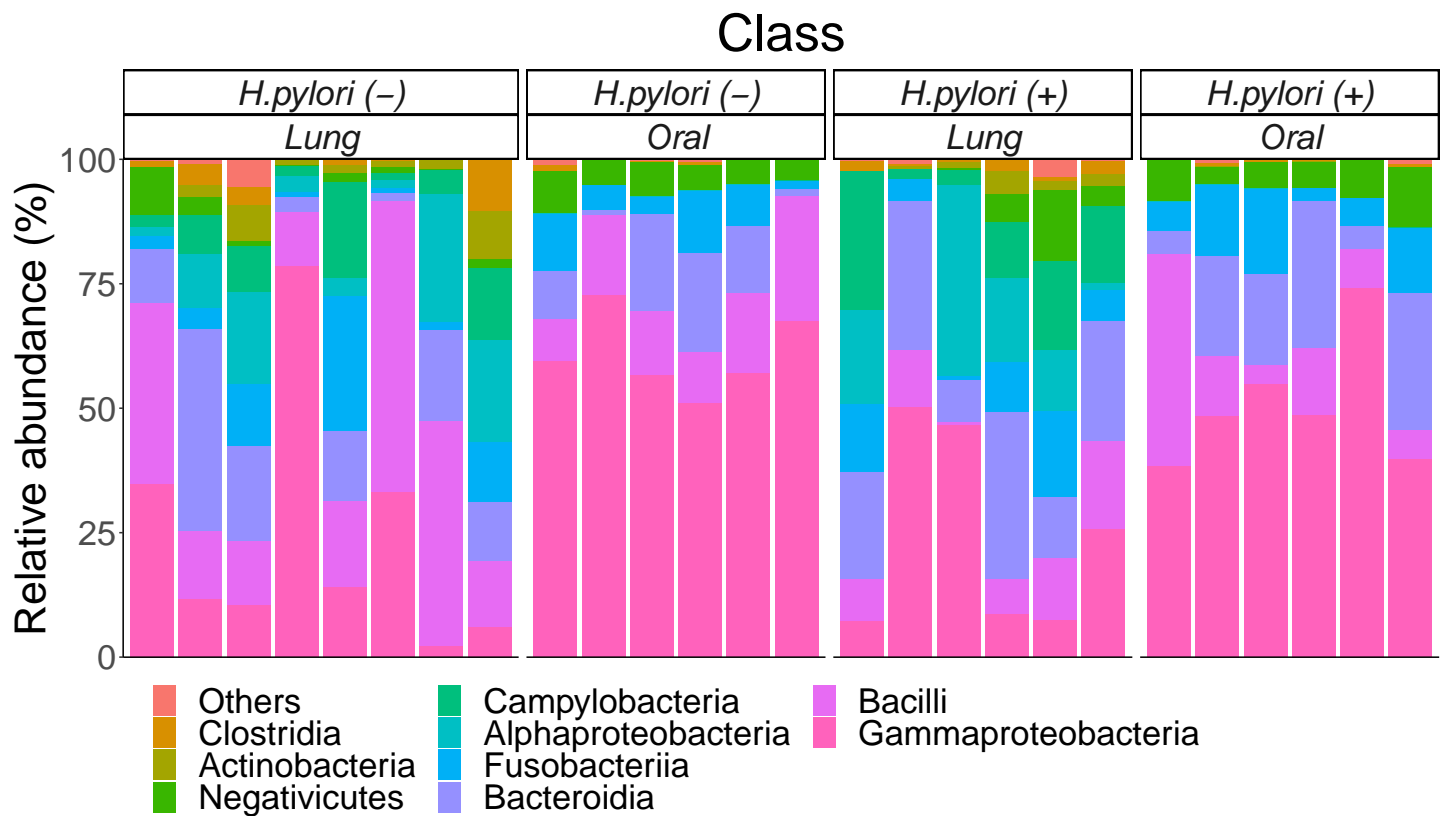


Figure 5: Microbiota Composition at Class level.

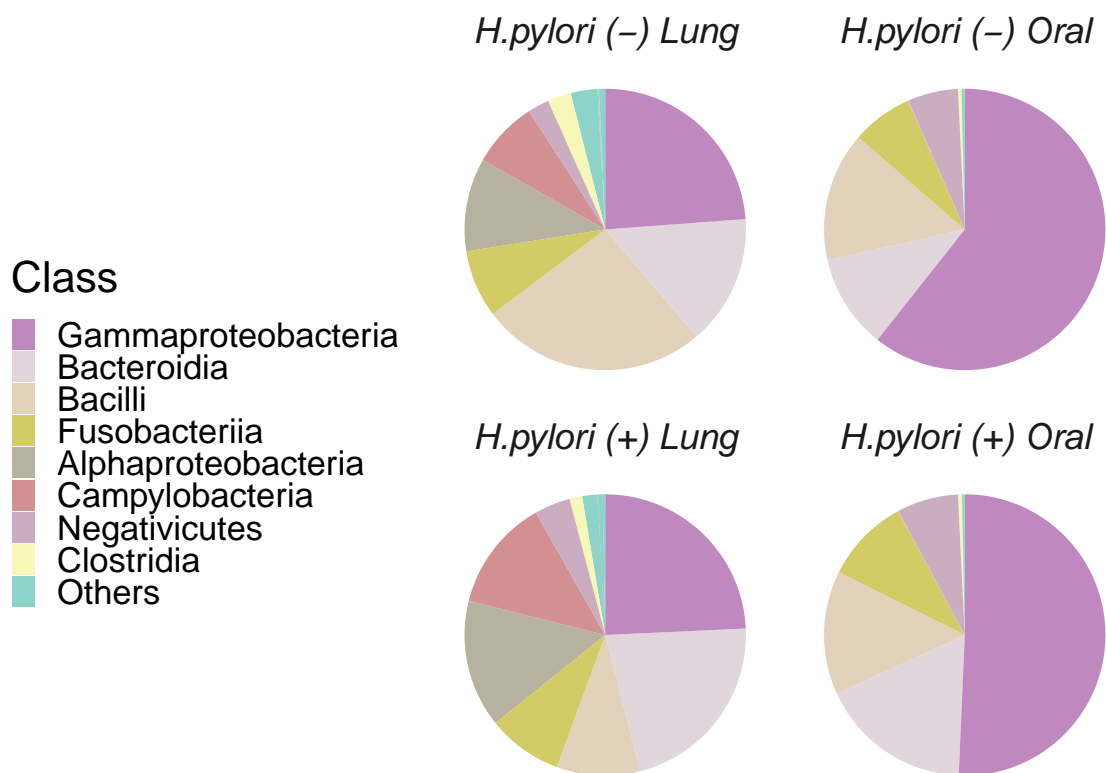


Figure 6: Microbiota Composition at Class level.

Table 4: Class Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Actinobacteria	H.pylori (-) Lung	3.1%
Actinobacteria	H.pylori (+) Lung	1.7%
Alphaproteobacteria	H.pylori (+) Lung	14.7%
Alphaproteobacteria	H.pylori (-) Lung	10.7%
Bacilli	H.pylori (-) Lung	26%
Bacilli	H.pylori (-) Oral	14.9%
Bacilli	H.pylori (+) Oral	14.2%
Bacilli	H.pylori (+) Lung	9.6%
Bacteroidia	H.pylori (+) Lung	21.7%
Bacteroidia	H.pylori (+) Oral	17.4%
Bacteroidia	H.pylori (-) Lung	14.9%
Bacteroidia	H.pylori (-) Oral	10.8%
Campylobacteria	H.pylori (+) Lung	12.9%
Campylobacteria	H.pylori (-) Lung	7.7%
Clostridia	H.pylori (-) Lung	2.7%
Clostridia	H.pylori (+) Lung	1.5%
Clostridia	H.pylori (+) Oral	0.4%
Clostridia	H.pylori (-) Oral	0.4%
Deinococci	H.pylori (+) Lung	0.6%
Fusobacteriia	H.pylori (+) Oral	9.8%
Fusobacteriia	H.pylori (+) Lung	8.6%
Fusobacteriia	H.pylori (-) Lung	7.8%
Fusobacteriia	H.pylori (-) Oral	7%
Gammaproteobacteria	H.pylori (-) Oral	60.7%
Gammaproteobacteria	H.pylori (+) Oral	50.7%
Gammaproteobacteria	H.pylori (+) Lung	24.3%
Gammaproteobacteria	H.pylori (-) Lung	23.8%
Negativicutes	H.pylori (+) Oral	7.1%
Negativicutes	H.pylori (-) Oral	5.8%
Negativicutes	H.pylori (+) Lung	4.1%
Negativicutes	H.pylori (-) Lung	2.4%
Spirochaetia	H.pylori (-) Lung	0.7%

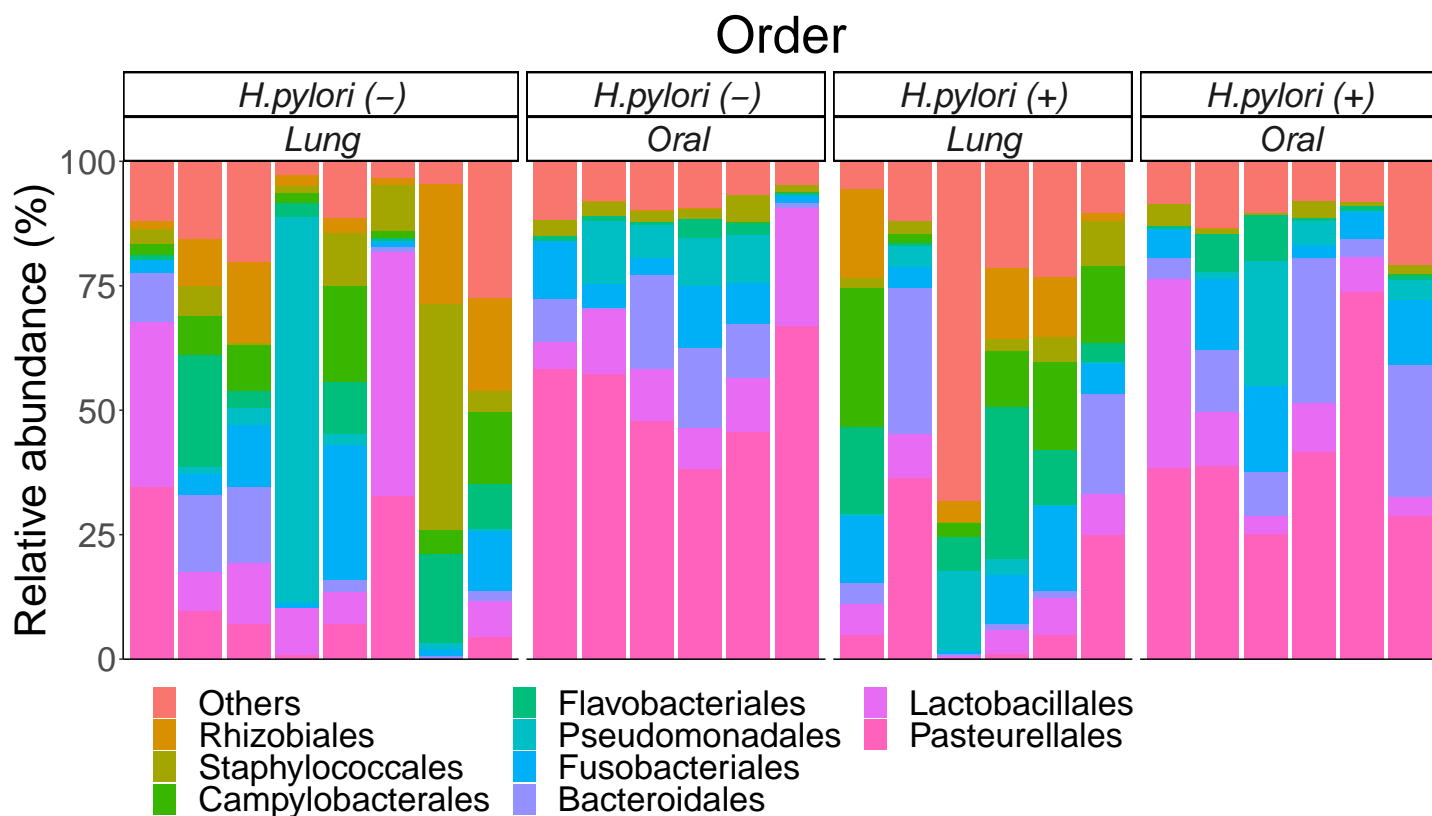


Figure 7: Microbiota Composition at Order level.

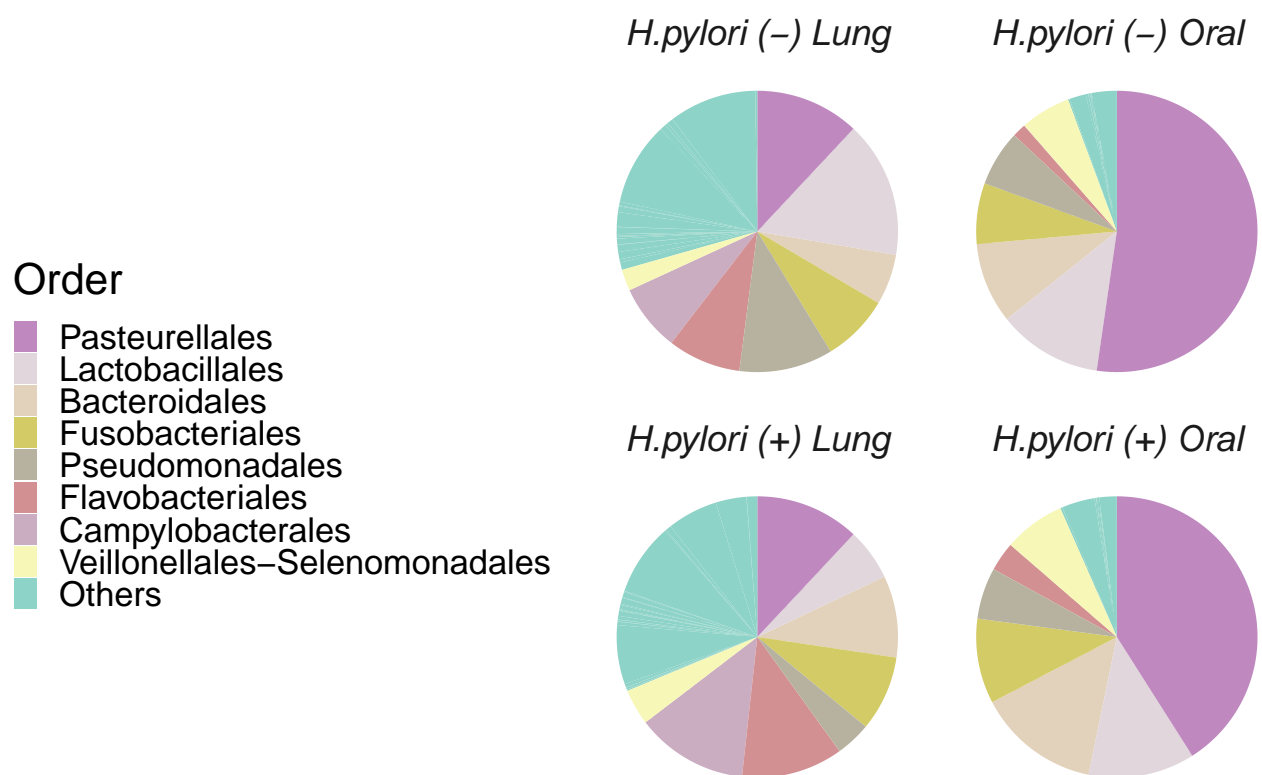


Figure 8: Microbiota Composition at Order level.

Table 5: Order Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Bacteroidales	H.pylori (+) Oral	14.1%
Bacteroidales	H.pylori (+) Lung	9.4%
Bacteroidales	H.pylori (-) Oral	9.3%
Bacteroidales	H.pylori (-) Lung	5.8%
Burkholderiales	H.pylori (+) Lung	6.8%
Campylobacteriales	H.pylori (+) Lung	12.9%
Campylobacteriales	H.pylori (-) Lung	7.7%
Flavobacteriales	H.pylori (+) Lung	11.7%
Flavobacteriales	H.pylori (-) Lung	8.4%
Fusobacteriales	H.pylori (+) Oral	9.8%
Fusobacteriales	H.pylori (+) Lung	8.6%
Fusobacteriales	H.pylori (-) Lung	7.8%
Fusobacteriales	H.pylori (-) Oral	7%
Lactobacillales	H.pylori (-) Lung	15.7%
Lactobacillales	H.pylori (+) Oral	12.2%
Lactobacillales	H.pylori (-) Oral	12%
Lactobacillales	H.pylori (+) Lung	6%
Pasteurellales	H.pylori (-) Oral	52.3%
Pasteurellales	H.pylori (+) Oral	41%
Pasteurellales	H.pylori (+) Lung	12%
Pasteurellales	H.pylori (-) Lung	12%
Pseudomonadales	H.pylori (-) Lung	10.8%
Pseudomonadales	H.pylori (-) Oral	6.4%
Pseudomonadales	H.pylori (+) Oral	5.9%
Pseudomonadales	H.pylori (+) Lung	4.1%
Rhizobiales	H.pylori (-) Lung	9.6%
Rhizobiales	H.pylori (+) Lung	8.3%
Sphingomonadales	H.pylori (+) Lung	5.8%
Staphylococcales	H.pylori (-) Lung	10.1%
Veillonellales-Selenomonadales	H.pylori (+) Oral	7.1%
Veillonellales-Selenomonadales	H.pylori (-) Oral	5.8%
Veillonellales-Selenomonadales	H.pylori (+) Lung	4.1%

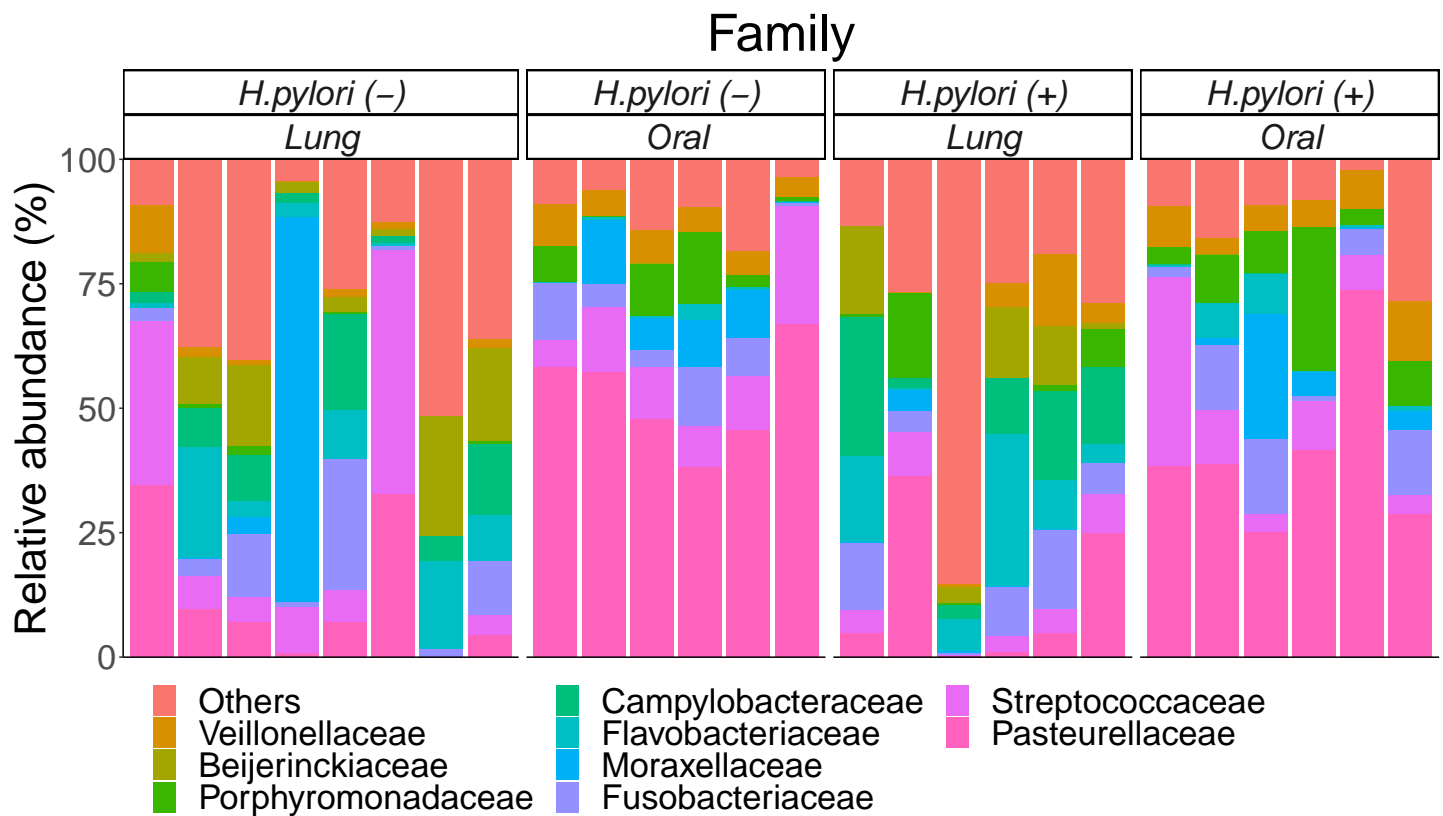


Figure 9: Microbiota Composition at Family level.

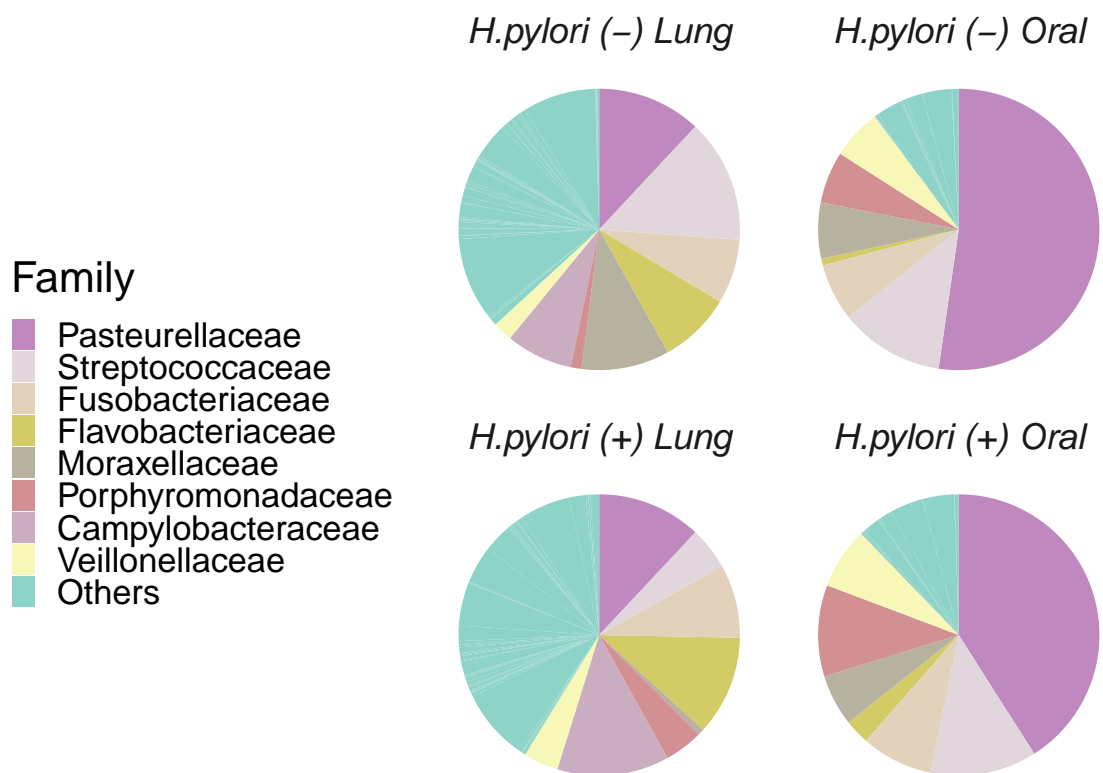


Figure 10: Microbiota Composition at Family level.

Table 6: Family Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Beijerinckiaceae	H.pylori (-) Lung	9.5%
Beijerinckiaceae	H.pylori (+) Lung	8.1%
Campylobacteraceae	H.pylori (+) Lung	12.9%
Campylobacteraceae	H.pylori (-) Lung	7.7%
Flavobacteriaceae	H.pylori (+) Lung	11.5%
Flavobacteriaceae	H.pylori (-) Lung	8.3%
Fusobacteriaceae	H.pylori (+) Lung	8.5%
Fusobacteriaceae	H.pylori (+) Oral	8.2%
Fusobacteriaceae	H.pylori (-) Lung	7.4%
Fusobacteriaceae	H.pylori (-) Oral	6.6%
Moraxellaceae	H.pylori (-) Lung	10.1%
Moraxellaceae	H.pylori (-) Oral	6.4%
Moraxellaceae	H.pylori (+) Oral	5.9%
Oxalobacteraceae	H.pylori (+) Lung	5%
Pasteurellaceae	H.pylori (-) Oral	52.3%
Pasteurellaceae	H.pylori (+) Oral	41%
Pasteurellaceae	H.pylori (+) Lung	12%
Pasteurellaceae	H.pylori (-) Lung	12%
Porphyromonadaceae	H.pylori (+) Oral	10.5%
Porphyromonadaceae	H.pylori (-) Oral	5.9%
Porphyromonadaceae	H.pylori (+) Lung	4.4%
Prevotellaceae	H.pylori (+) Lung	4.3%
Prevotellaceae	H.pylori (-) Lung	4.1%
Sphingomonadaceae	H.pylori (+) Lung	5.8%
Staphylococcaceae	H.pylori (-) Lung	8.4%
Streptococcaceae	H.pylori (-) Lung	14.2%
Streptococcaceae	H.pylori (+) Oral	12.2%
Streptococcaceae	H.pylori (-) Oral	12%
Streptococcaceae	H.pylori (+) Lung	4.9%
Veillonellaceae	H.pylori (+) Oral	7%
Veillonellaceae	H.pylori (-) Oral	5.8%
Veillonellaceae	H.pylori (+) Lung	4%

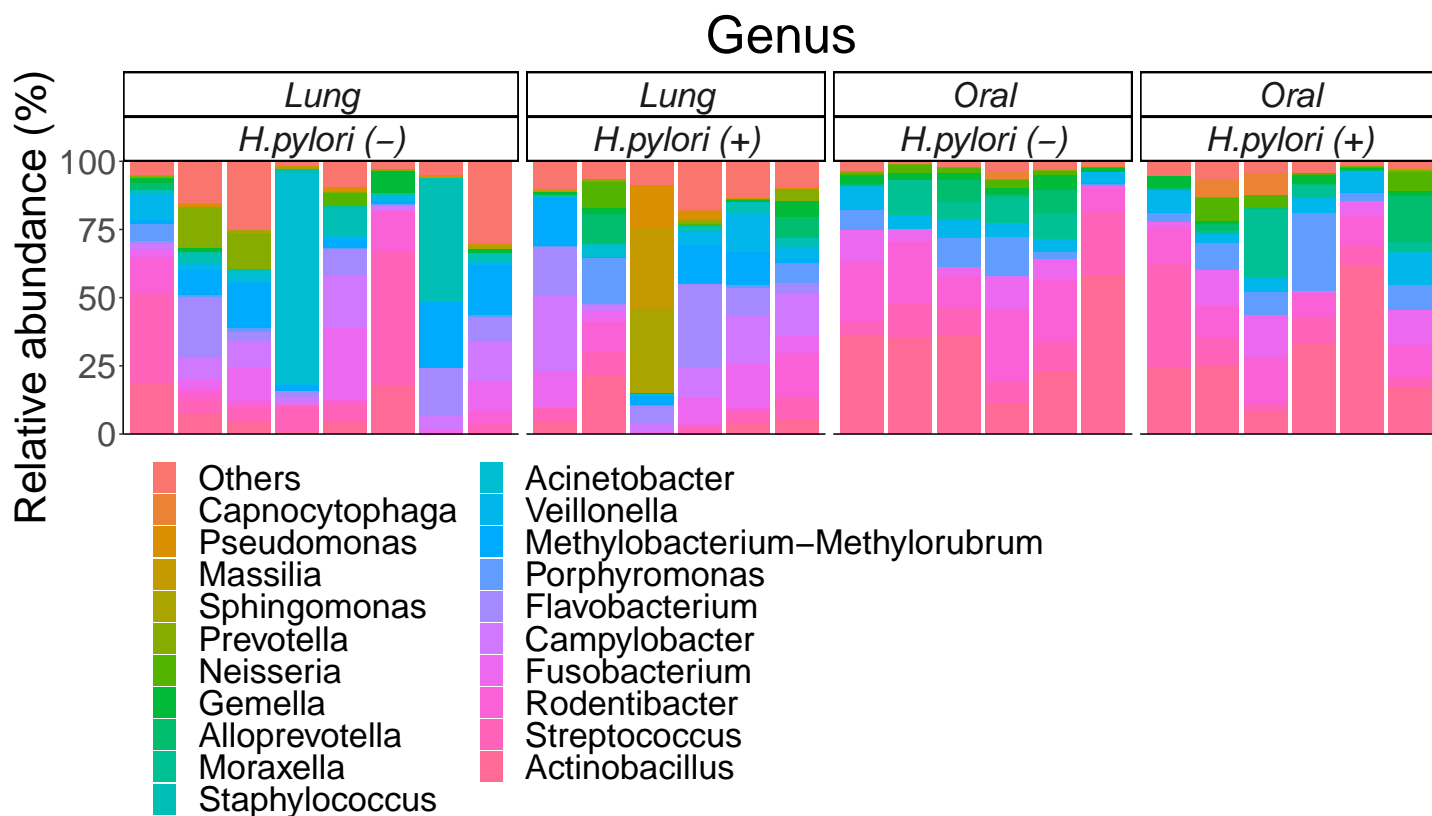


Figure 11: Microbiota Composition at Genus level.

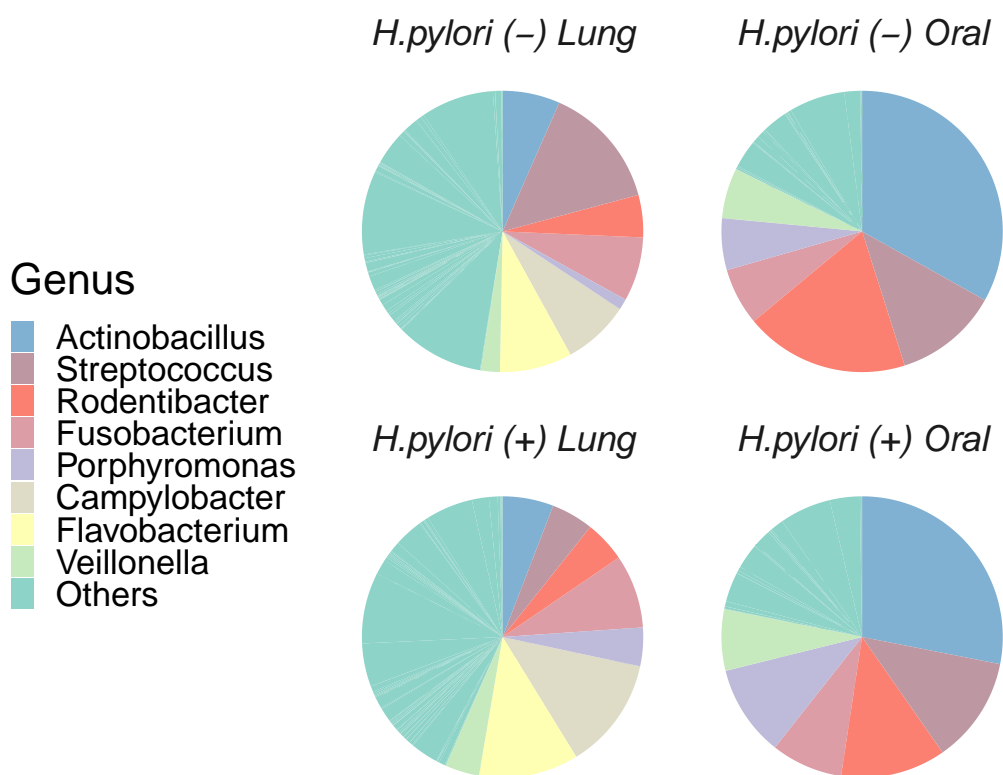


Figure 12: Microbiota Composition at Genus level.

Table 7: Genus Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Acinetobacter	H.pylori (-) Lung	10.1%
Actinobacillus	H.pylori (-) Oral	33.1%
Actinobacillus	H.pylori (+) Oral	28.1%
Actinobacillus	H.pylori (-) Lung	6.6%
Actinobacillus	H.pylori (+) Lung	5.9%
Campylobacter	H.pylori (+) Lung	12.9%
Campylobacter	H.pylori (-) Lung	7.7%
Flavobacterium	H.pylori (+) Lung	11.5%
Flavobacterium	H.pylori (-) Lung	8.3%
Fusobacterium	H.pylori (+) Lung	8.5%
Fusobacterium	H.pylori (+) Oral	8.2%
Fusobacterium	H.pylori (-) Lung	7.4%
Fusobacterium	H.pylori (-) Oral	6.6%
Massilia	H.pylori (+) Lung	4.9%
Methylobacterium-Methylobacterium	H.pylori (-) Lung	9.5%
Methylobacterium-Methylobacterium	H.pylori (+) Lung	8.1%
Moraxella	H.pylori (-) Oral	6.4%
Moraxella	H.pylori (+) Oral	5.9%
Porphyromonas	H.pylori (+) Oral	10.5%
Porphyromonas	H.pylori (-) Oral	5.9%
Rodentibacter	H.pylori (-) Oral	18.9%
Rodentibacter	H.pylori (+) Oral	12.1%
Rodentibacter	H.pylori (-) Lung	4.9%
Rodentibacter	H.pylori (+) Lung	4.7%
Sphingomonas	H.pylori (+) Lung	5.4%
Staphylococcus	H.pylori (-) Lung	8.4%
Streptococcus	H.pylori (-) Lung	14.2%
Streptococcus	H.pylori (+) Oral	12.2%
Streptococcus	H.pylori (-) Oral	12%
Streptococcus	H.pylori (+) Lung	4.9%
Veillonella	H.pylori (+) Oral	7%
Veillonella	H.pylori (-) Oral	5.8%

Genera correlation with IL8 concentration (Serum and BAL)

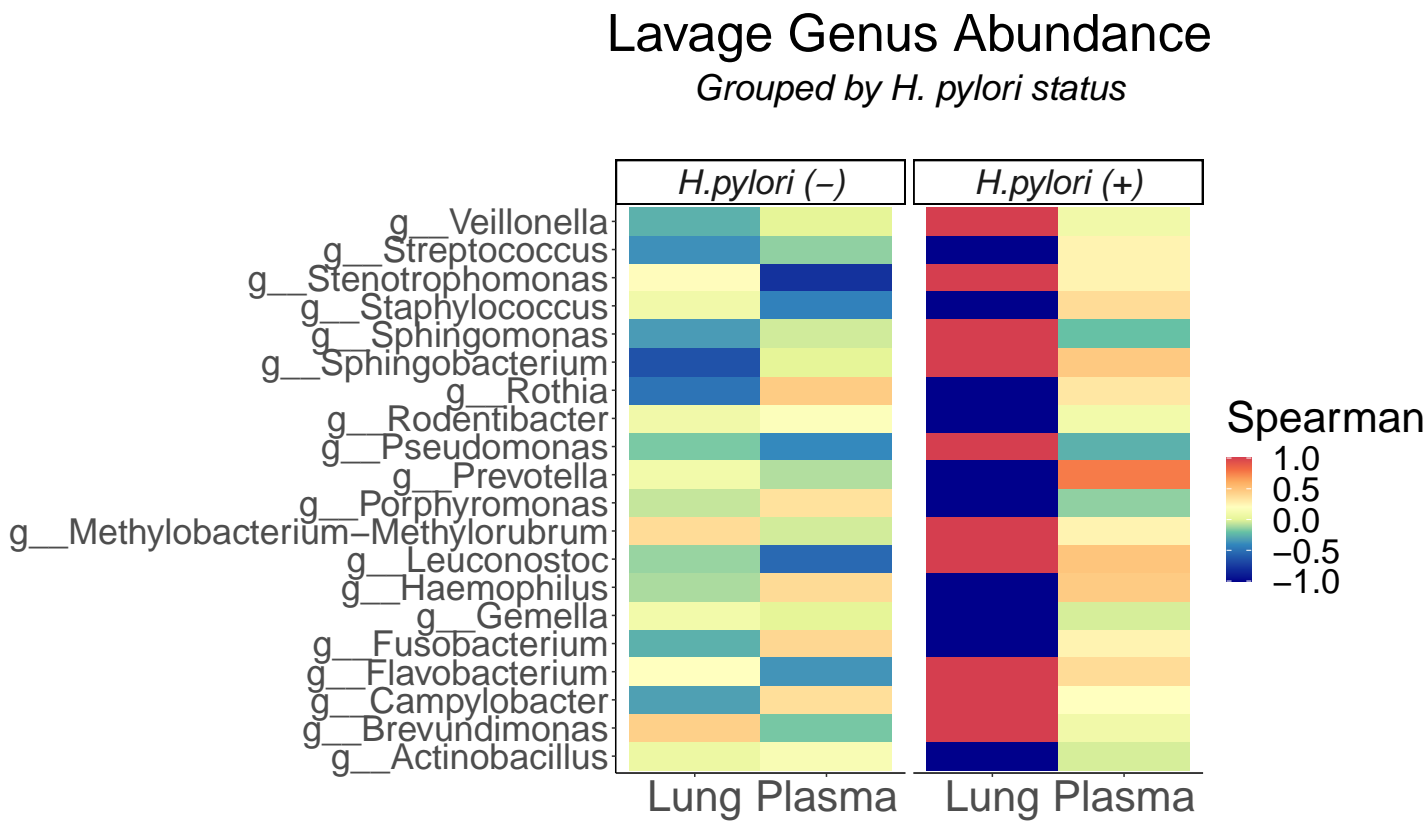


Figure 13: IL8 and lavage genus abundance Spearman correlations separated by *H. pylori* status

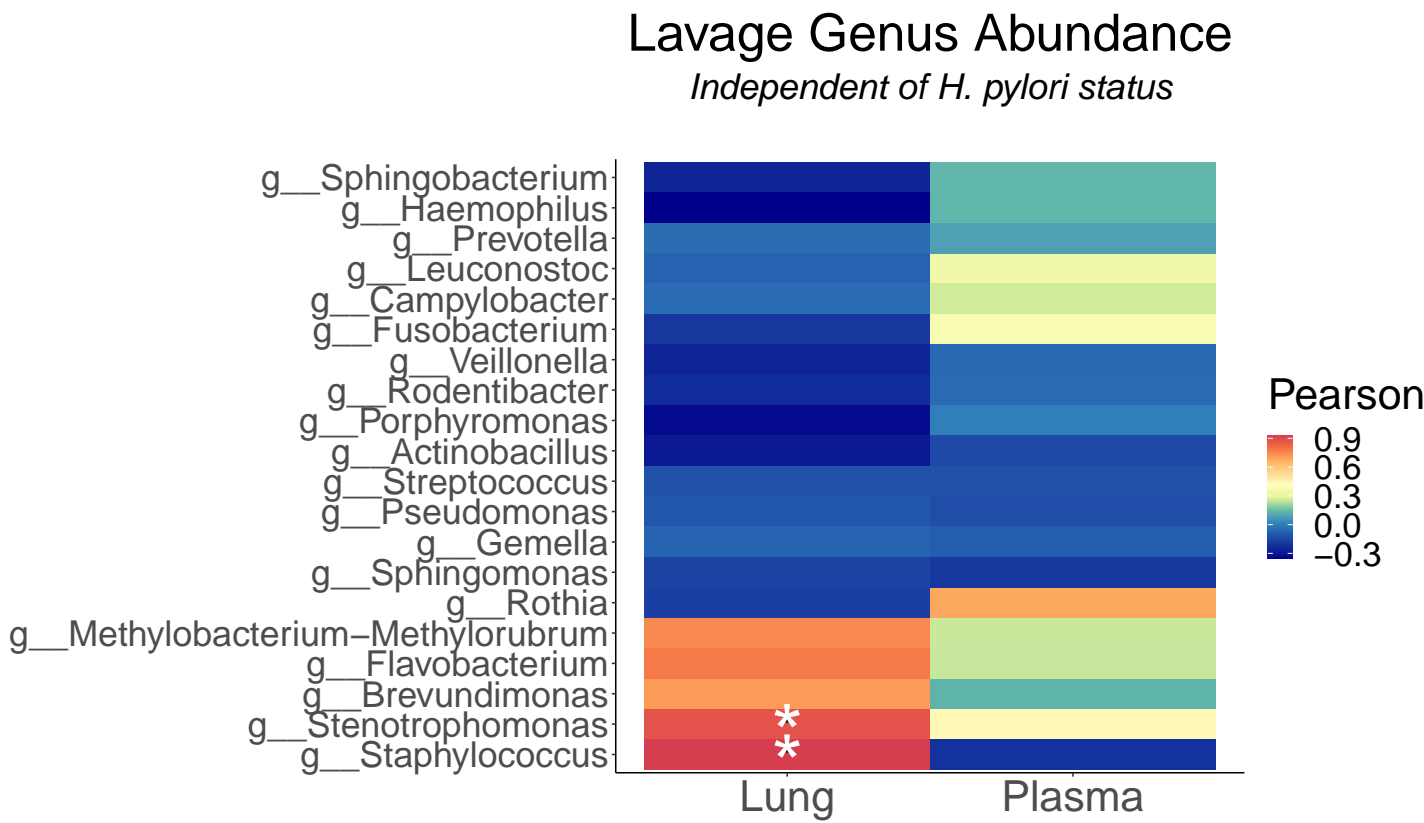


Figure 14: IL8 and lavage genus abundance Spearman correlations independent of *H. pylori* status

Lavage Alpha Diversity

Independent of H. pylori status

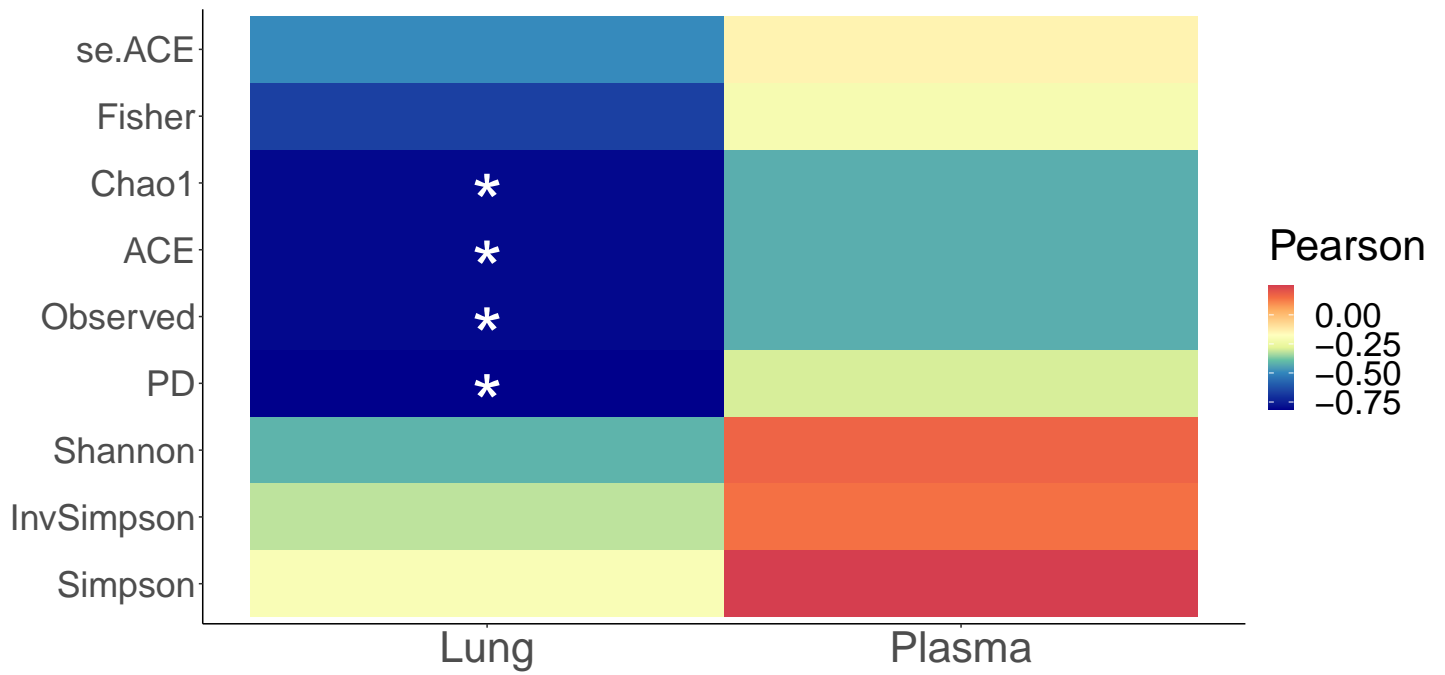


Figure 15: IL8 and lavage alpha diversity Spearman correlations independent of H. pylori status.

Buccal Cavity Genus Abundance

Grouped by *H. pylori* status

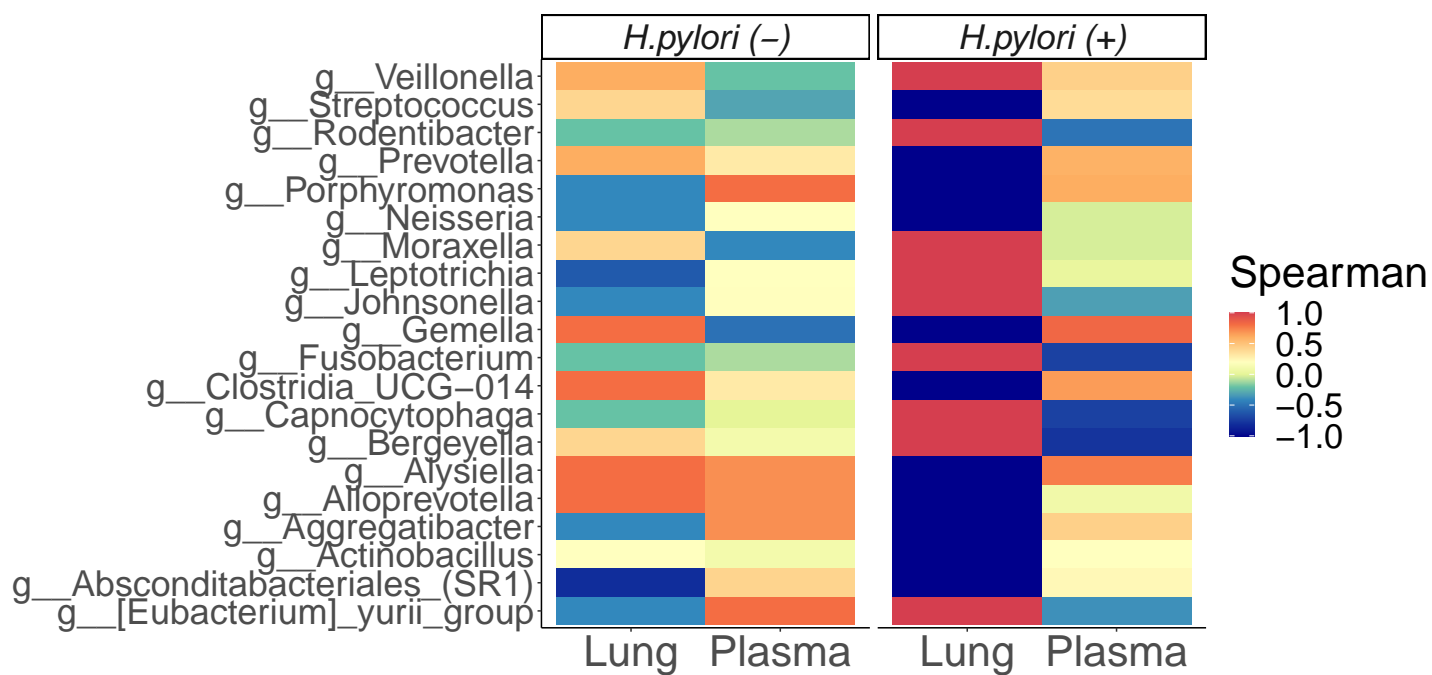


Figure 16: IL8 and Buccal genus abundance Spearman correlations separated by *H. pylori* status

Buccal Cavity Genus Abundance

Independent of H. pylori status

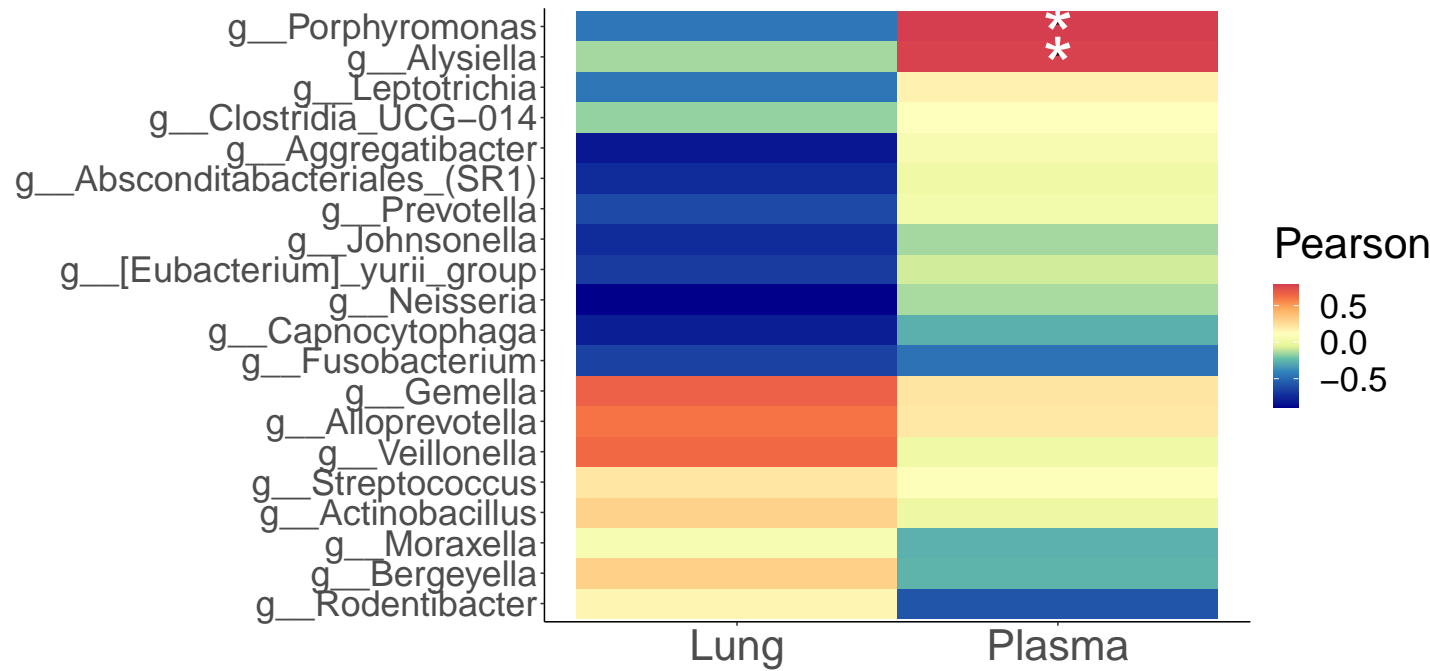


Figure 17: IL8 and Buccal genus abundance Spearman correlations independent of H. pylori status

Buccal Cavity Alpha Diversity

Independent of H. pylori status

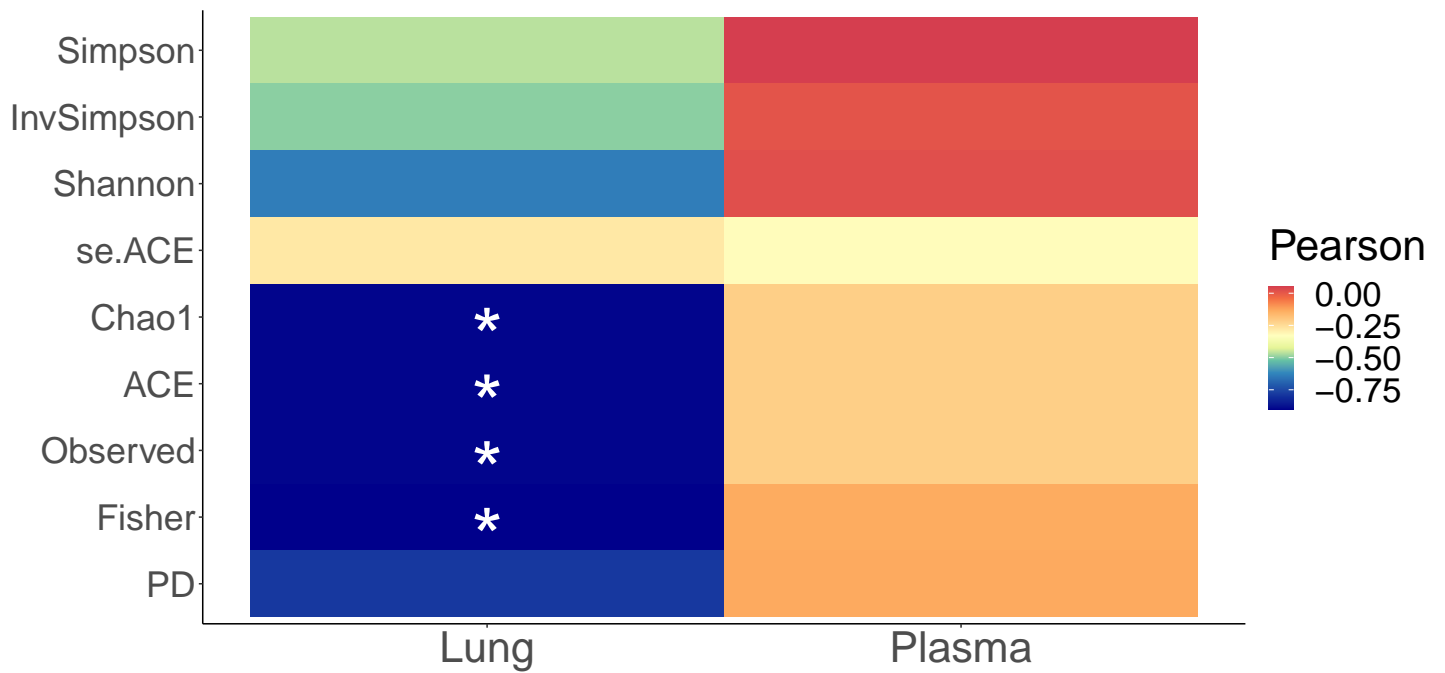


Figure 18: IL8 and Buccal alpha diversity Spearman correlations independent of H. pylori status

Record session information

```
## R version 4.1.3 (2022-03-10)
## Platform: x86_64-conda-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.6 LTS
##
## Matrix products: default
## BLAS/LAPACK: /srv/conda/envs/notebook/lib/libopenblas-r0.3.20.so
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats4      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##
## other attached packages:
##  [1] rmarkdown_2.14          questionr_0.7.7
##  [3] RColorBrewer_1.1-3      tidytree_0.3.9
##  [5] microeco_0.3.2          ggpubr_0.4.0
##  [7] magrittr_2.0.3          kableExtra_1.3.4
##  [9] tidyMicro_1.48          forcats_0.5.1
## [11] stringr_1.4.0           dplyr_1.0.9
## [13] purrr_0.3.4             readr_2.1.2
## [15] tidyr_1.2.0             tibble_3.1.7
## [17] tidyverse_1.3.1         qiime2R_0.99.6
## [19] DESeq2_1.34.0           SummarizedExperiment_1.24.0
## [21] Biobase_2.54.0          MatrixGenerics_1.6.0
## [23] matrixStats_0.62.0      GenomicRanges_1.46.1
## [25] GenomeInfoDb_1.30.0     IRanges_2.28.0
## [27] S4Vectors_0.32.3        BiocGenerics_0.40.0
## [29] microbiome_1.16.0       ggplot2_3.3.6
## [31] phyloseq_1.38.0         readxl_1.4.0
## [33] sjPlot_2.8.10
##
## loaded via a namespace (and not attached):
##  [1] estimability_1.3        bit64_4.0.5            knitr_1.39
##  [4] DelayedArray_0.20.0     data.table_1.14.2      rpart_4.1.16
##  [7] KEGGREST_1.34.0         RCurl_1.98-1.7         generics_0.1.2
## [10] timeSeries_3062.100     RSQlite_2.2.8          VGAM_1.1-8
## [13] bit_4.0.4               tzdb_0.3.0            webshot_0.5.3
## [16] xml2_1.3.3              lubridate_1.8.0        httpuv_1.6.5
## [19] assertthat_0.2.1        xfun_0.31              fBasics_3042.89.1
## [22] hms_1.1.1               evaluate_0.15          promises_1.2.0.1
## [25] fansi_1.0.3             dbplyr_2.2.0          igraph_1.3.1
## [28] DBI_1.1.2               geneplotter_1.72.0     htmlwidgets_1.6.2
## [31] ellipsis_0.3.2          backports_1.4.1        insight_0.17.1
## [34] permute_0.9-7           picante_1.8.2          annotate_1.72.0
## [37] vctrs_0.4.1             sjlabelled_1.2.0       abind_1.4-5
## [40] cachem_1.0.6            withr_2.5.0            checkmate_2.2.0
## [43] emmeans_1.7.4-1         vegan_2.6-2            svglite_2.1.0
## [46] cluster_2.1.3           ape_5.6-2             lazyeval_0.2.2
## [49] crayon_1.5.1            genefilter_1.76.0      pkgconfig_2.0.3
## [52] zCompositions_1.4.0-1   labeling_0.4.2         nlme_3.1-157
## [55] nnet_7.3-17             rlang_1.0.2            spatial_7.3-15
```

## [58] lifecycle_1.0.1	miniUI_0.1.1.1	modelr_0.1.8
## [61] randomForest_4.7-1.1	cellranger_1.1.0	datawizard_0.4.1
## [64] Matrix_1.4-1	carData_3.0-5	Rhdf5lib_1.16.0
## [67] boot_1.3-28	reprex_2.0.1	base64enc_0.1-3
## [70] png_0.1-7	viridisLite_0.4.0	stabledist_0.7-1
## [73] parameters_0.18.1	bitops_1.0-7	rhdf5filters_1.6.0
## [76] Biostrings_2.62.0	blob_1.2.3	GUniFrac_1.6
## [79] rstatix_0.7.0	ggeffects_1.1.2	ggsignif_0.6.3
## [82] scales_1.2.0	memoise_2.0.1	plyr_1.8.7
## [85] zlibbioc_1.40.0	compiler_4.1.3	tinytex_0.39
## [88] clue_0.3-60	lme4_1.1-29	cli_3.6.1
## [91] ade4_1.7-19	XVector_0.34.0	htmlTable_2.4.1
## [94] Formula_1.2-5	MASS_7.3-57	mgcv_1.8-40
## [97] tidyselect_1.1.2	stringi_1.7.6	highr_0.9
## [100] yaml_2.3.5	locfit_1.5-9.5	ggrepel_0.9.1
## [103] grid_4.1.3	tools_4.1.3	parallel_4.1.3
## [106] rstudioapi_0.13	foreach_1.5.2	foreign_0.8-82
## [109] statip_0.2.3	gridExtra_2.3	scatterplot3d_0.3-44
## [112] farver_2.1.0	Rtsne_0.16	stable_1.1.6
## [115] digest_0.6.29	shiny_1.7.1	Rcpp_1.0.8.3
## [118] car_3.0-13	broom_0.8.0	performance_0.9.0
## [121] later_1.2.0	httr_1.4.3	AnnotationDbi_1.56.1
## [124] effectsize_0.7.0	sjstats_0.18.1	colorspace_2.0-3
## [127] rvest_1.0.2	XML_3.99-0.10	fs_1.5.2
## [130] modeest_2.4.0	truncnorm_1.0-9	splines_4.1.3
## [133] yulab.utils_0.0.4	rmutil_1.1.9	statmod_1.4.36
## [136] multtest_2.50.0	systemfonts_1.0.4	xtable_1.8-4
## [139] jsonlite_1.8.0	nloptr_2.0.3	timeDate_3043.102
## [142] R6_2.5.1	Hmisc_5.1-0	NADA_1.6-1.1
## [145] pillar_1.7.0	htmltools_0.5.5	mime_0.12
## [148] glue_1.6.2	fastmap_1.1.0	minqa_1.2.4
## [151] DT_0.23	BiocParallel_1.28.3	codetools_0.2-18
## [154] mvtnorm_1.1-3	utf8_1.2.2	lattice_0.20-45
## [157] survival_3.3-1	biomformat_1.22.0	munsell_0.5.0
## [160] rhdf5_2.38.0	GenomeInfoDbData_1.2.7	iterators_1.0.14
## [163] labelled_2.9.1	sjmisc_2.8.9	haven_2.5.0
## [166] reshape2_1.4.4	gtable_0.3.0	bayestestR_0.12.1