

# 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)  
})
```

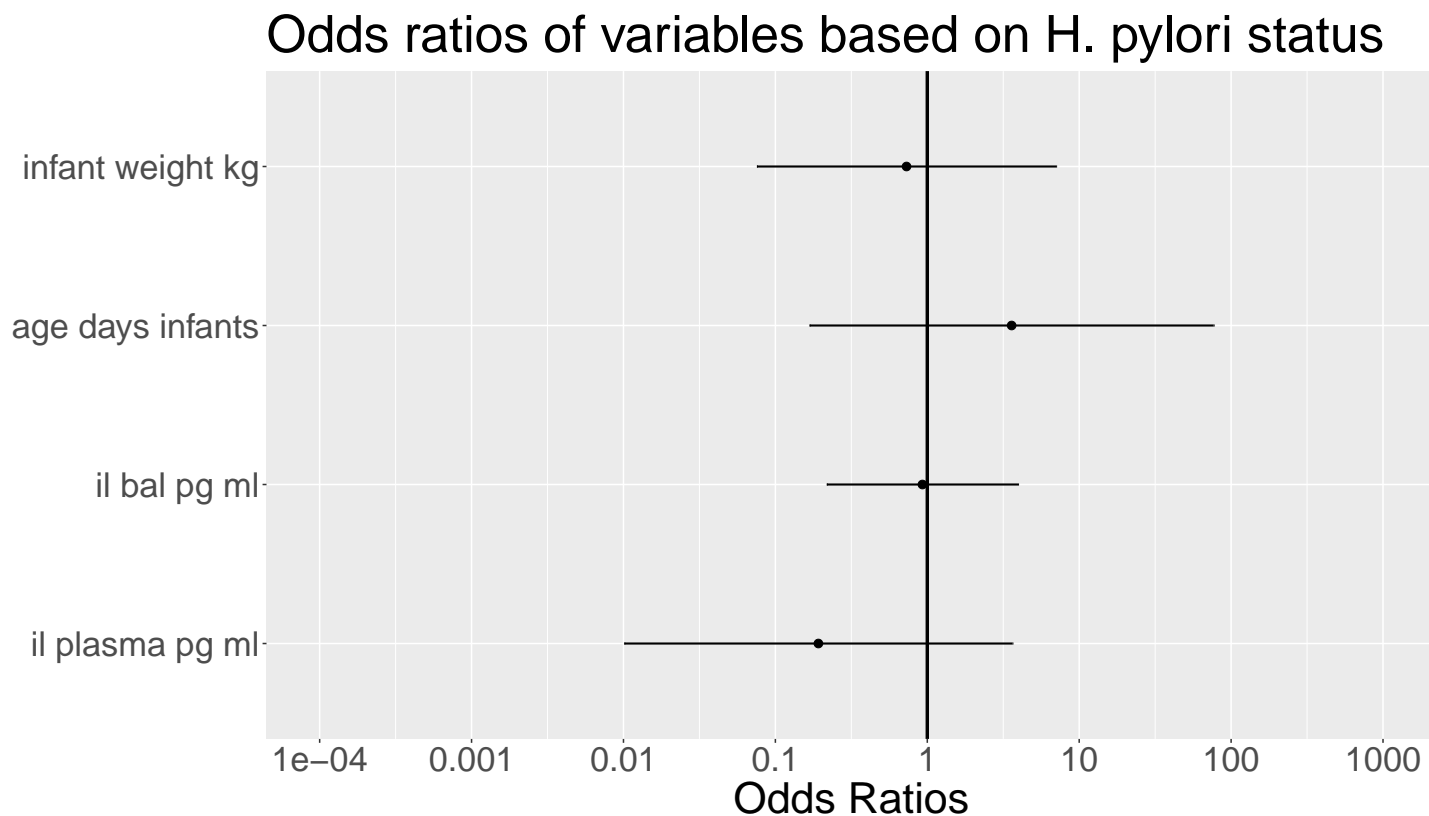
ASV counts the taxa table are linked below:

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_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	NA	463.376
LMiller_00458.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	NA	463.376
LMiller_00459.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	NA	258.416
LMiller_00459.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	NA	258.416
LMiller_00461.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	7.66	NA	704.550
LMiller_00461.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	7.66	NA	704.550
LMiller_00462.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	19.104	1075.626
LMiller_00462.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	19.104	1075.626
LMiller_00463.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	11.590	423.590
LMiller_00466.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	3.81	11.201	642.148
LMiller_00466.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	3.81	11.201	642.148
LMiller_00467.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	6.09	15.511	425.782
LMiller_00467.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	6.09	15.511	425.782
LMiller_00468.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	15.511	660.911
LMiller_00468.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	15.511	660.911
LMiller_00469.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	6.38	NA	1279.789
LMiller_00469.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	6.38	NA	1279.789
LMiller_00473.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	20.100	608.508
LMiller_00473.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	20.100	608.508
LMiller_00474.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	44.699	443.989
LMiller_00476.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	5.48	NA	476.431
LMiller_00476.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	5.48	NA	476.431
LMiller_00477.BAL	H.pylori_(+)	BAL	H.pylori_(+)_BAL	Female	5.81	NA	715.056
LMiller_00477.Swab	H.pylori_(+)	Swab	H.pylori_(+)_Swab	Female	5.81	NA	715.056
LMiller_00481.BAL	H.pylori_(-)	BAL	H.pylori_(-)_BAL	Female	0.00	17.622	NA
LMiller_00481.Swab	H.pylori_(-)	Swab	H.pylori_(-)_Swab	Female	0.00	17.622	NA



	OR	2.5 %	97.5 %	p
(Intercept)	0.018	0.000	110.146	0.410
infant_weight_kg	0.243	0.000	7254.525	0.786
age_days_infants	1.042	0.955	1.177	0.413
il_bal_pg.ml	0.993	0.852	1.158	0.921
il_plasma_pg.ml	0.996	0.985	1.001	0.271

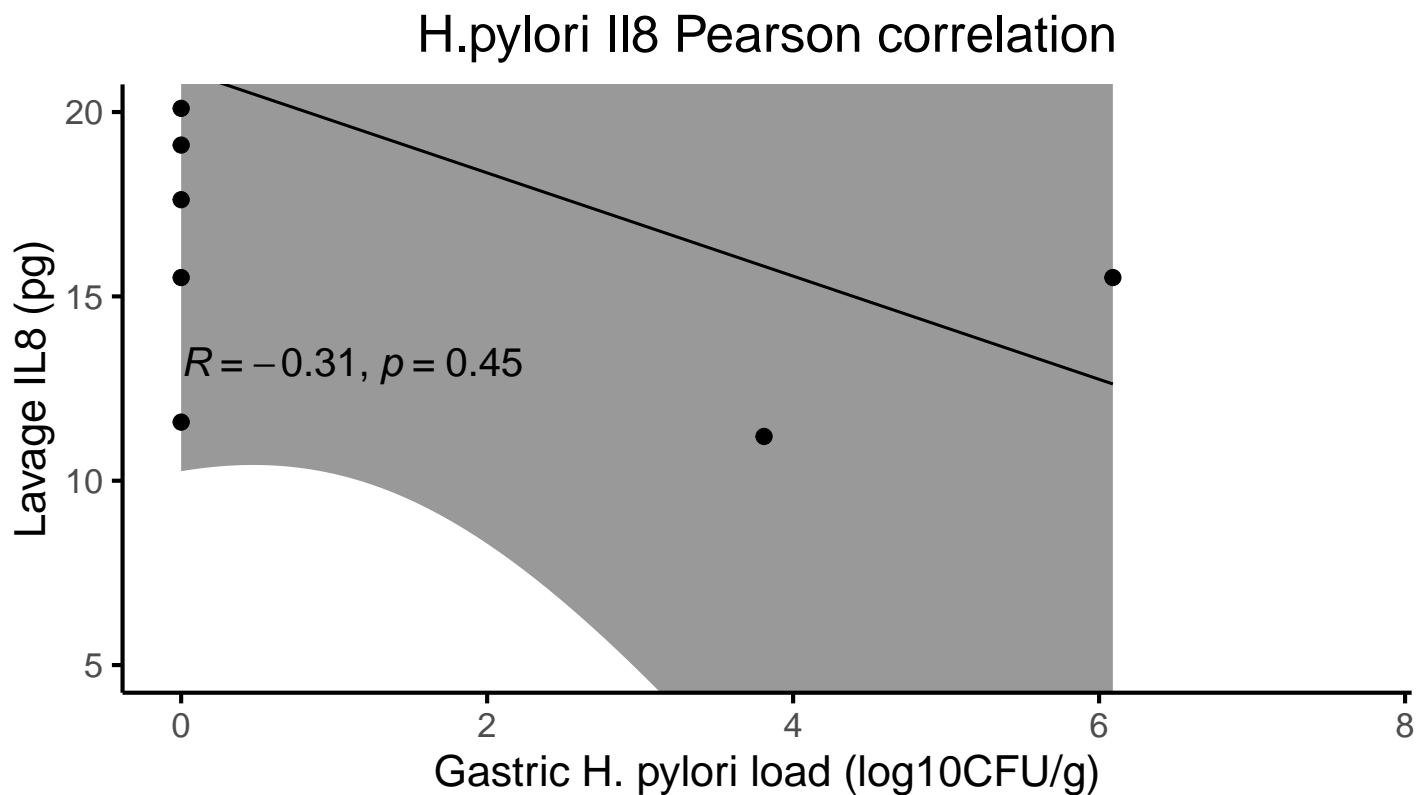


Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study

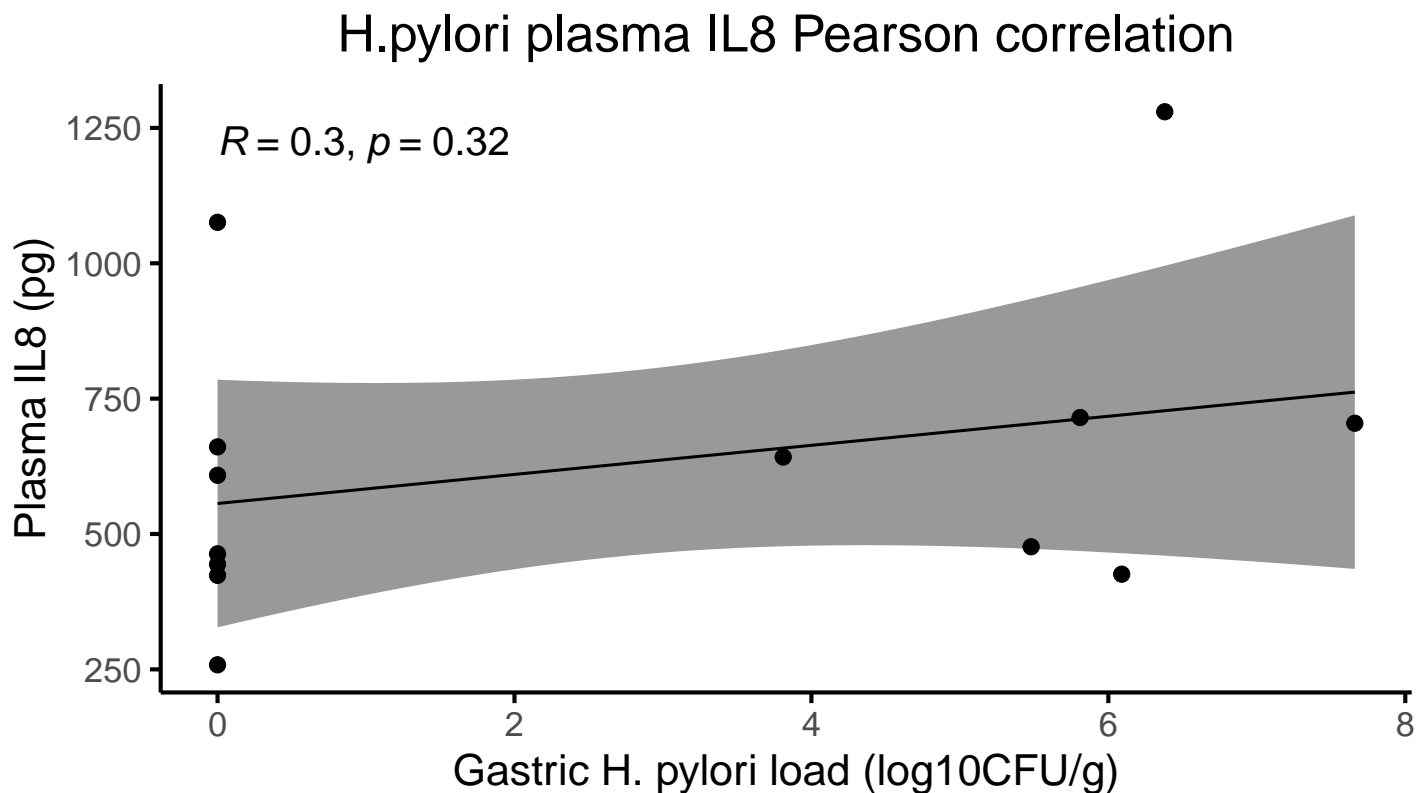
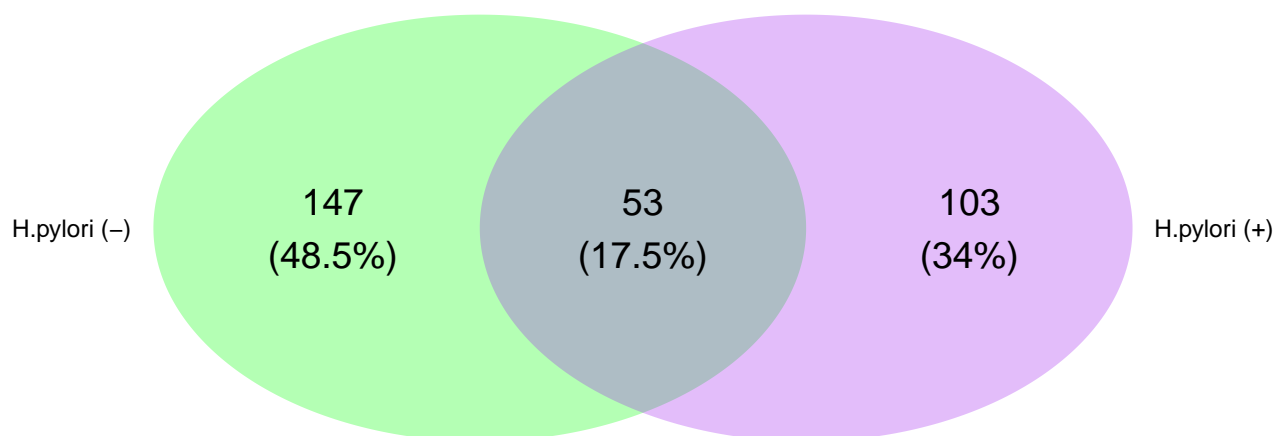


Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

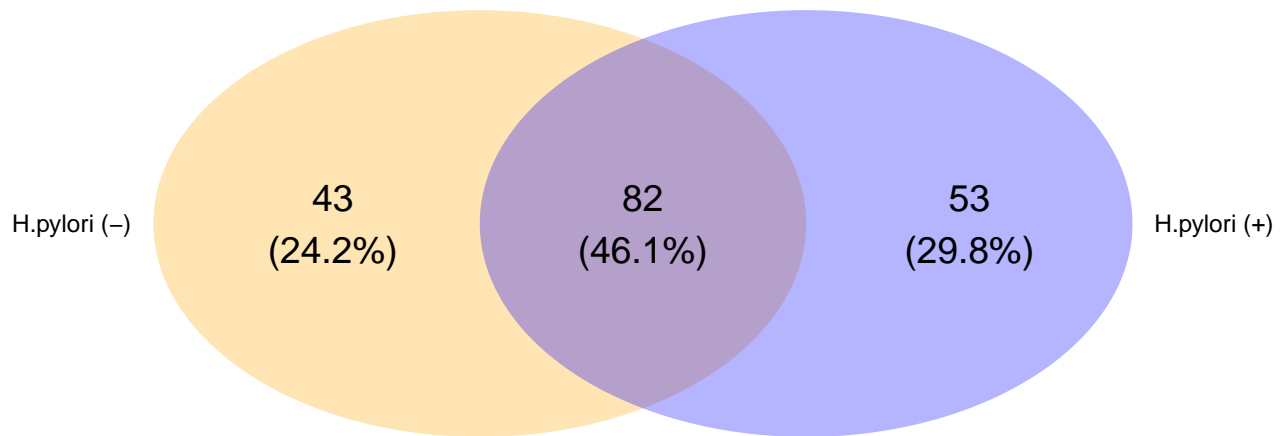
## Overlapping Taxa Between Sites and H. pylori Status

Lavage overlapping taxa

### Overlapping taxa between H. pylori (+) and (–) in lavage

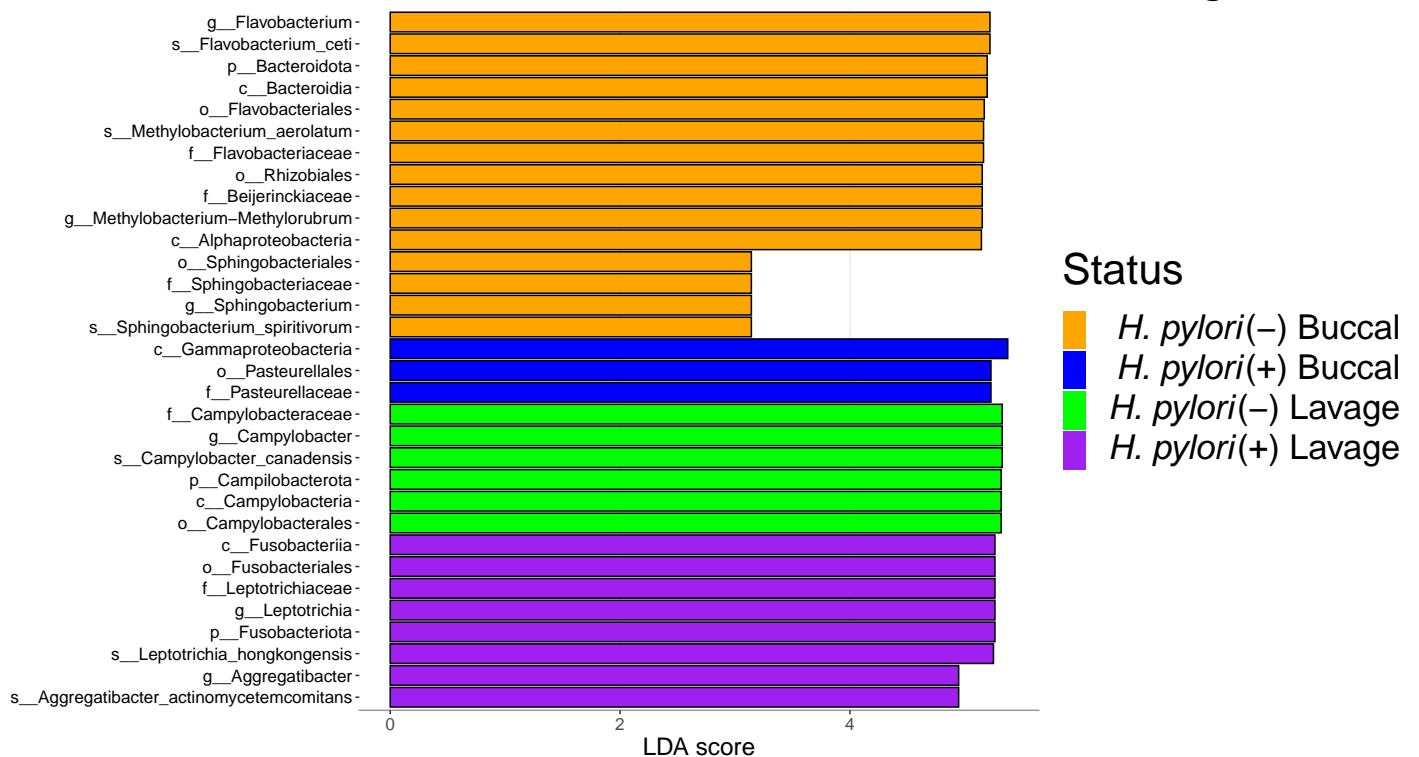


## Overlapping taxa between *H. pylori* (+) and (-) in buccal cavity



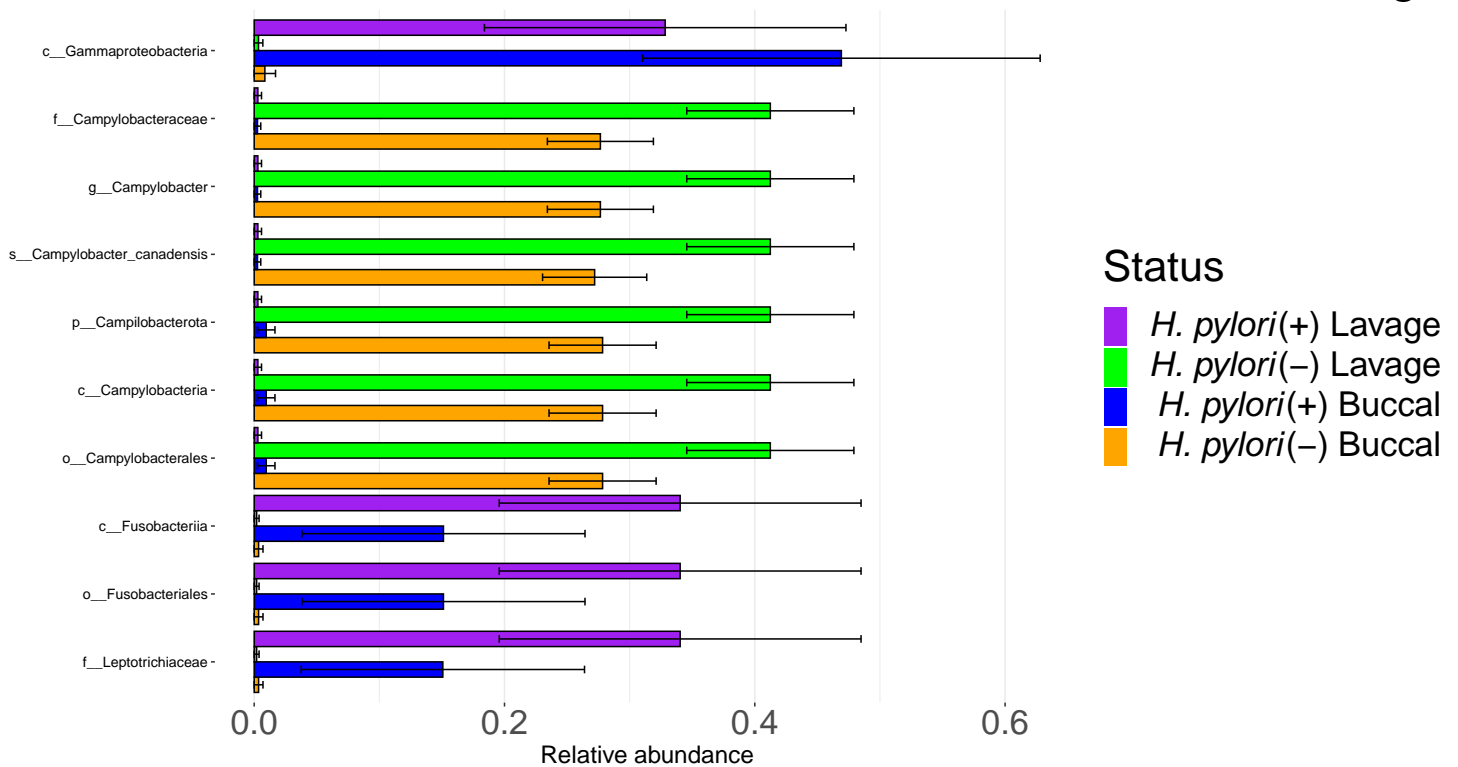
## Lefse analysis and differential abundance for both sites

### Lefse taxa from bronchoalveolar lavage and or



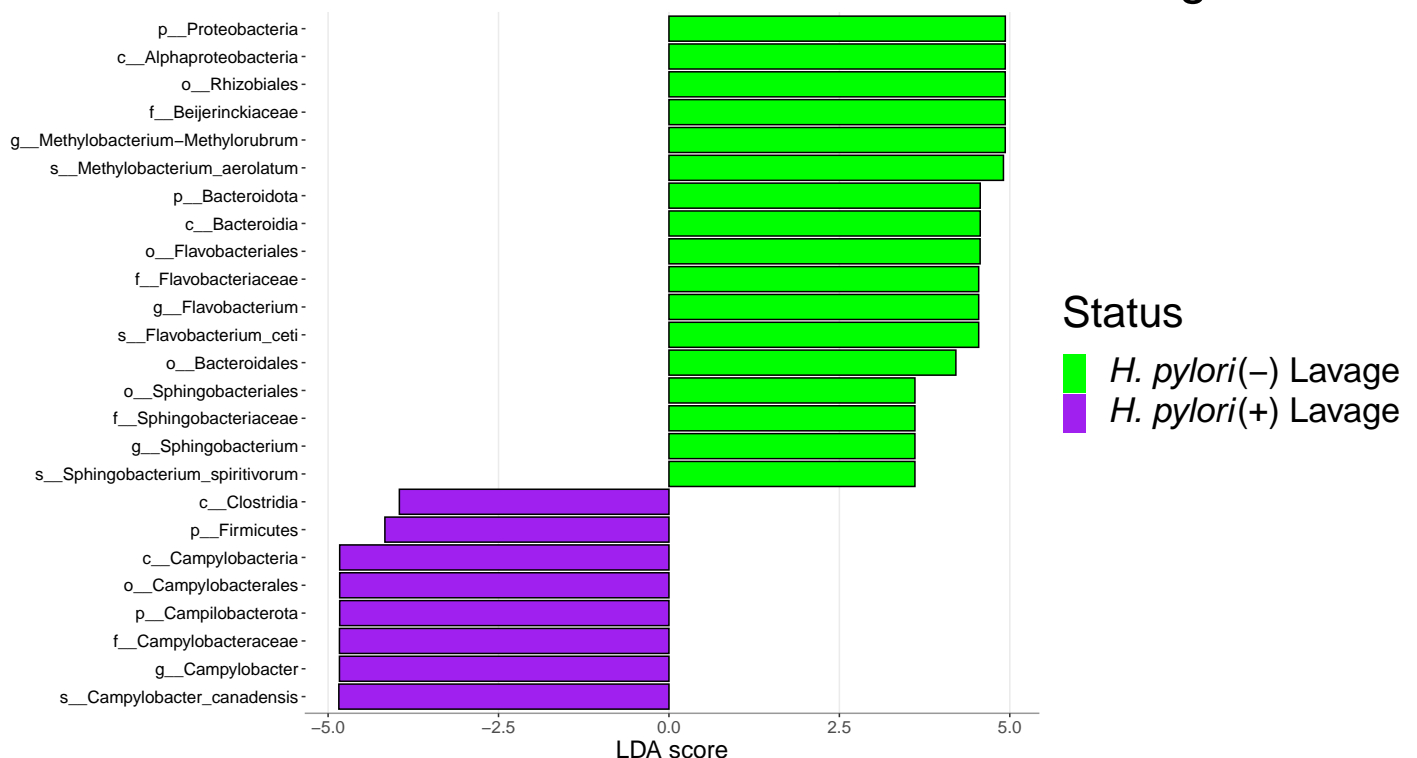
## Relative abundance of differential taxa

### Lefse relative abundance from bronchoalveolar lavage



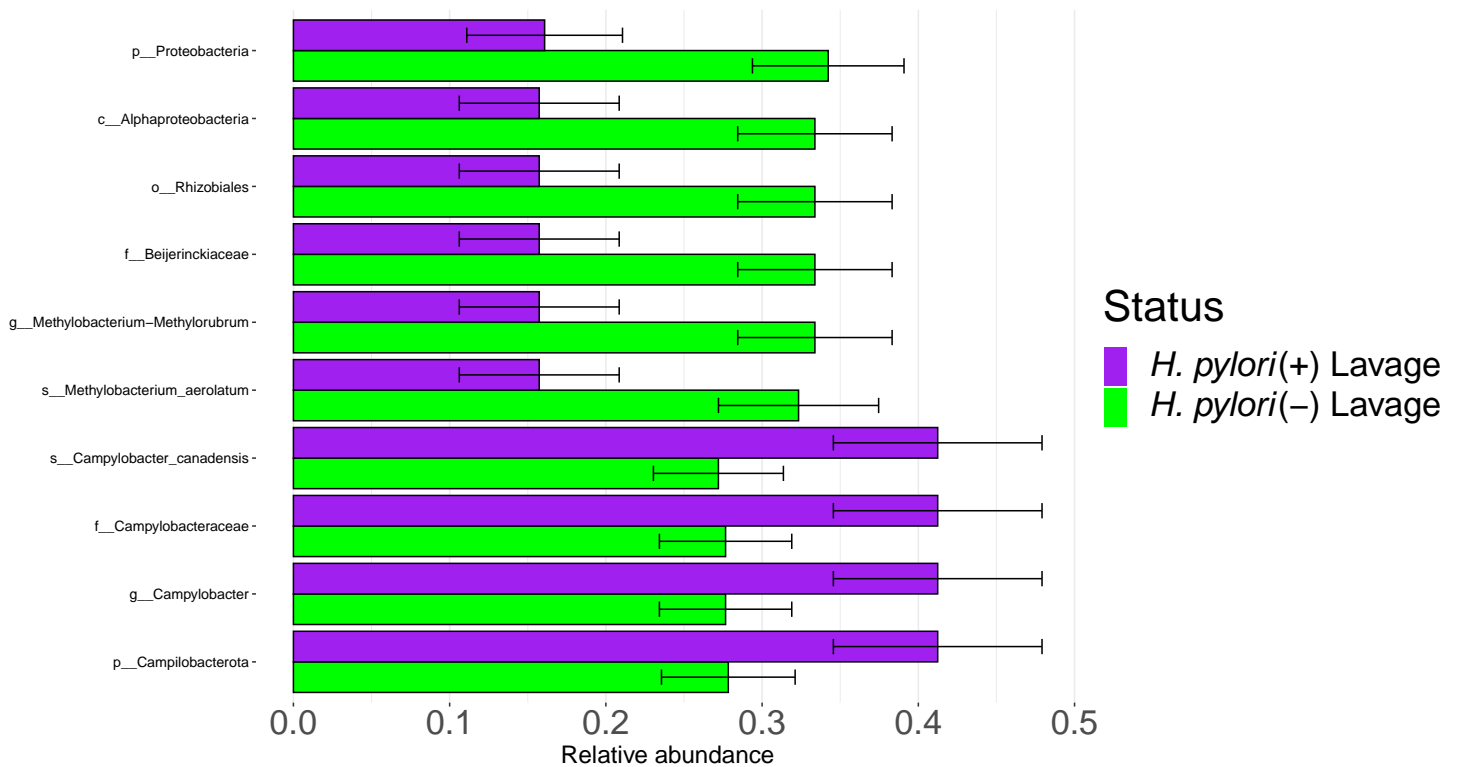
## Lefse and differential abundance for bronchoalveolar lavage

### Lefse Taxa from Bronchoalveolar Lavage



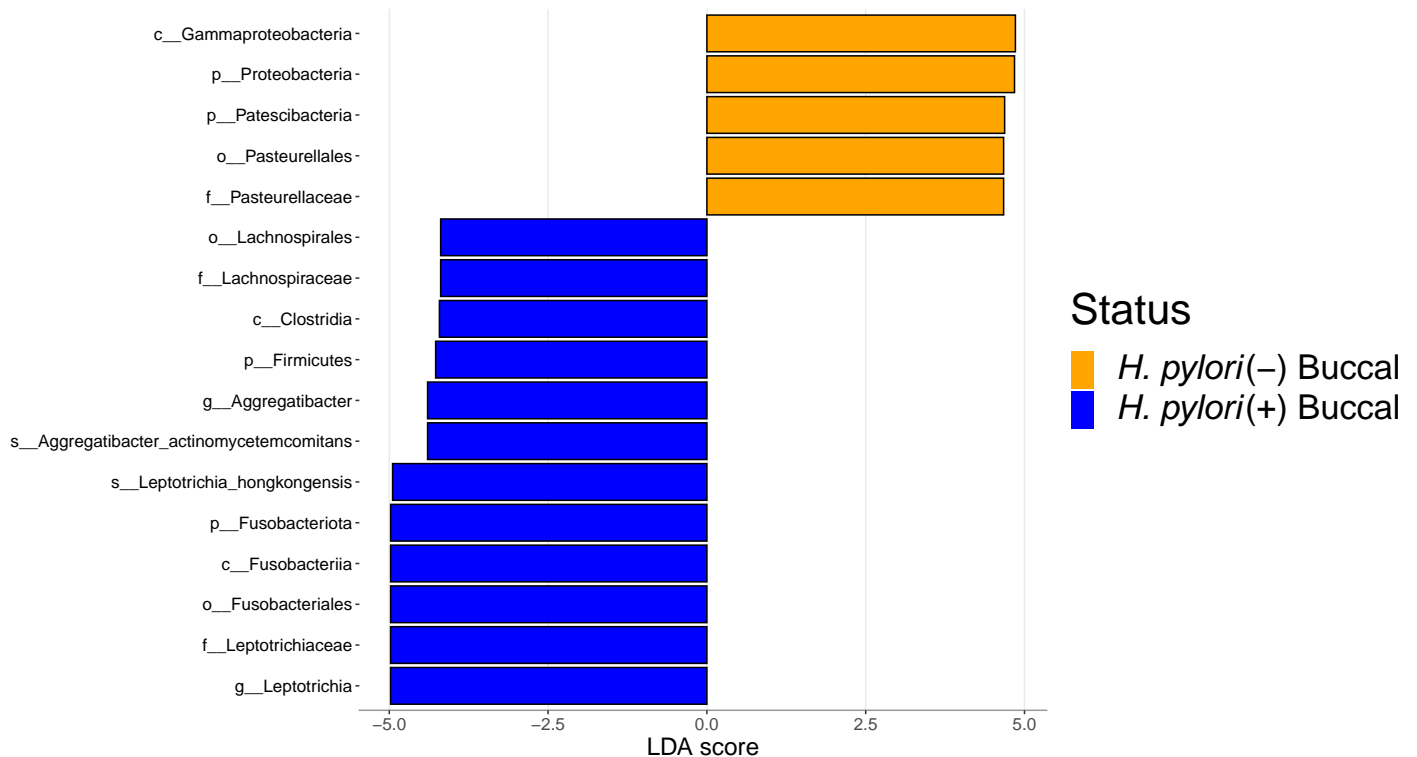
## Relative abundance of differential taxa

### Lefse Relative Abundance from Bronchoalveolar Lav



## Lefse and differential abundance for oral swabs

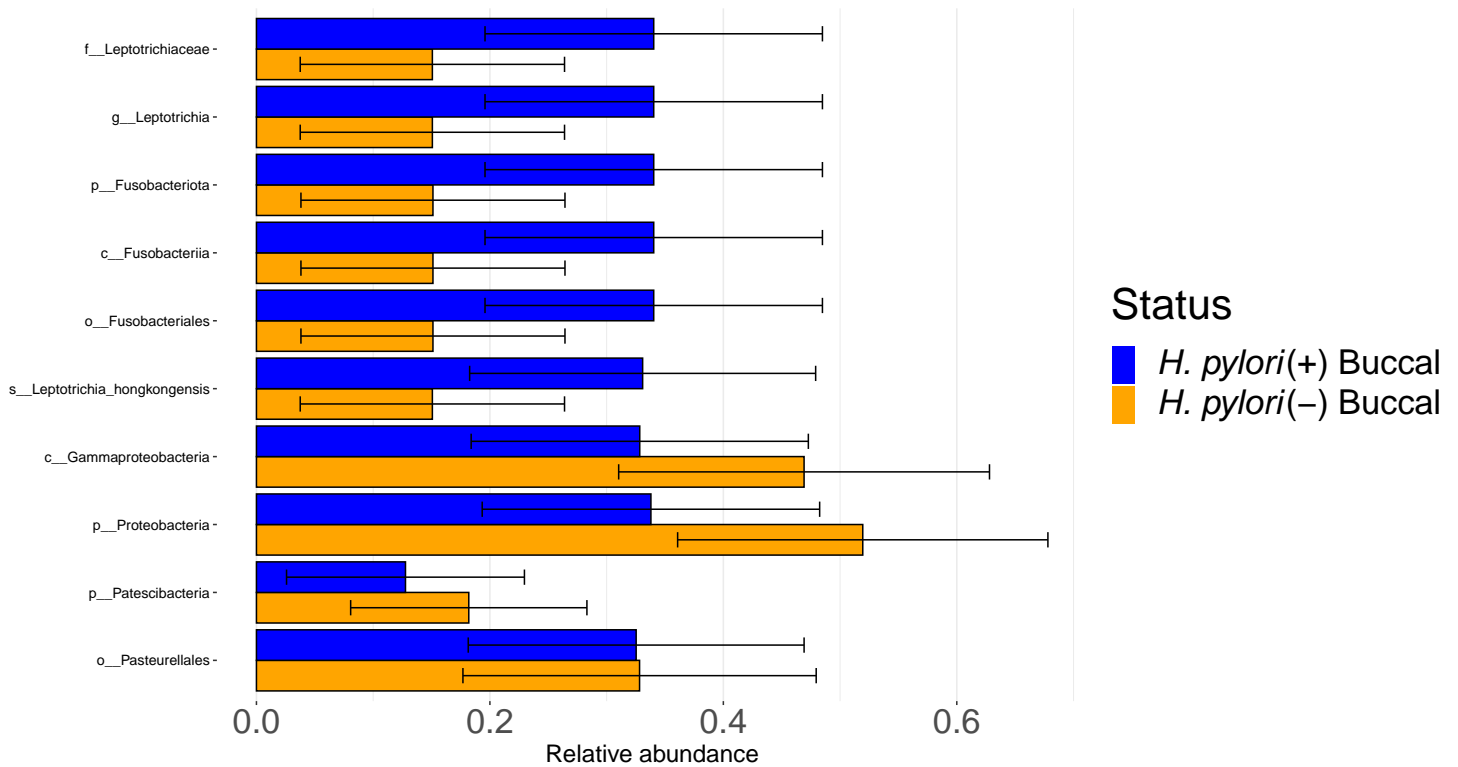
### Lefse taxa from oral swabs





## Relative abundance of differential taxa

### Lefse relative abundance from oral swabs

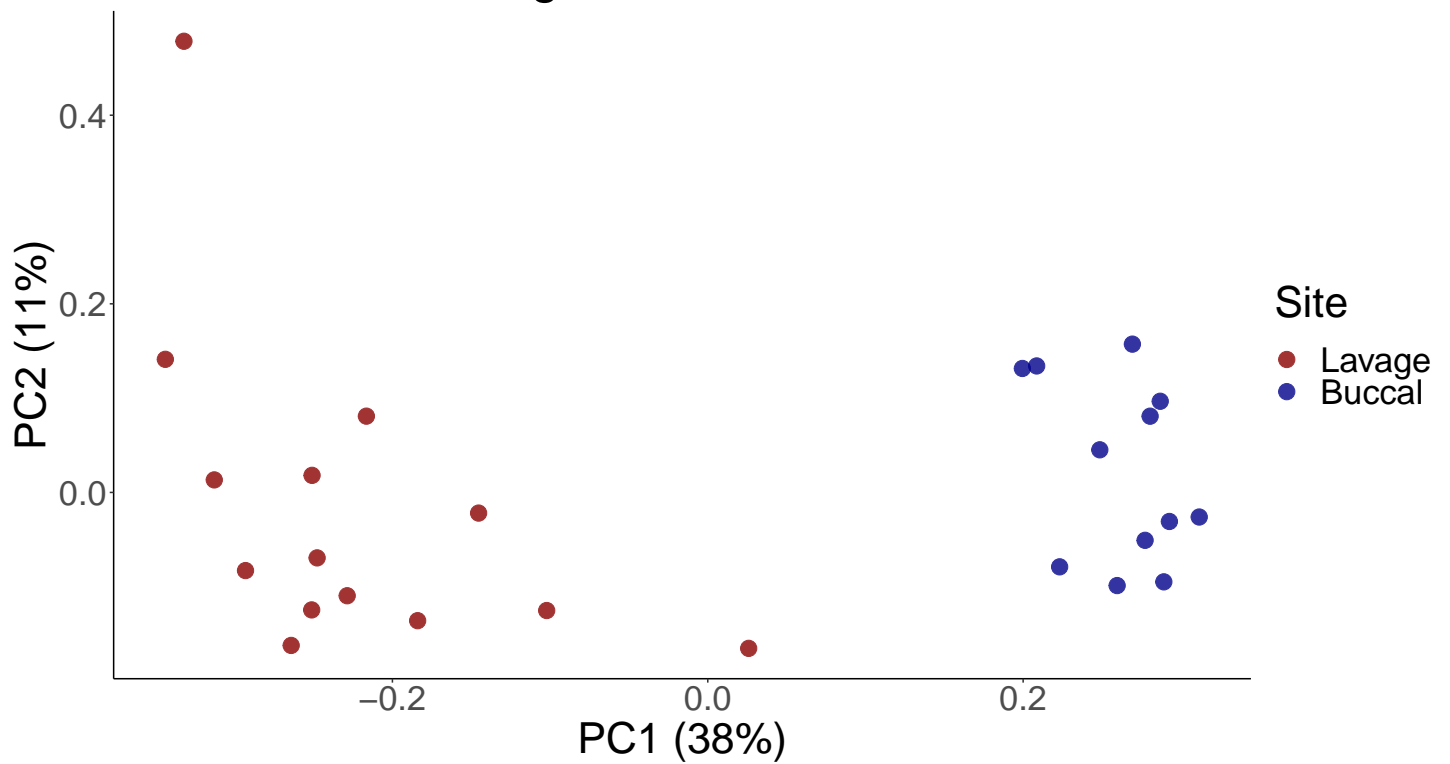


## Beta diversity

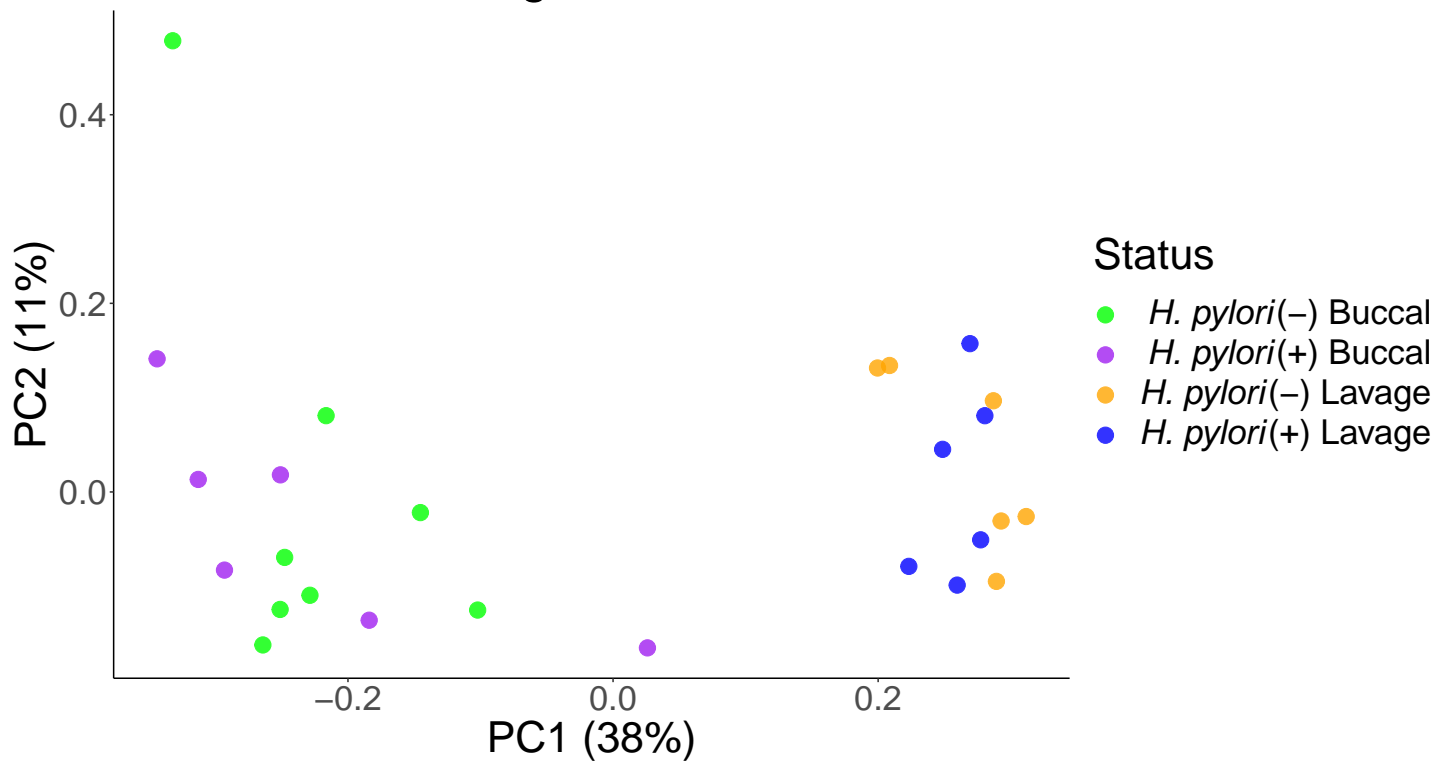
### Unweighted unifracs PCoA plots

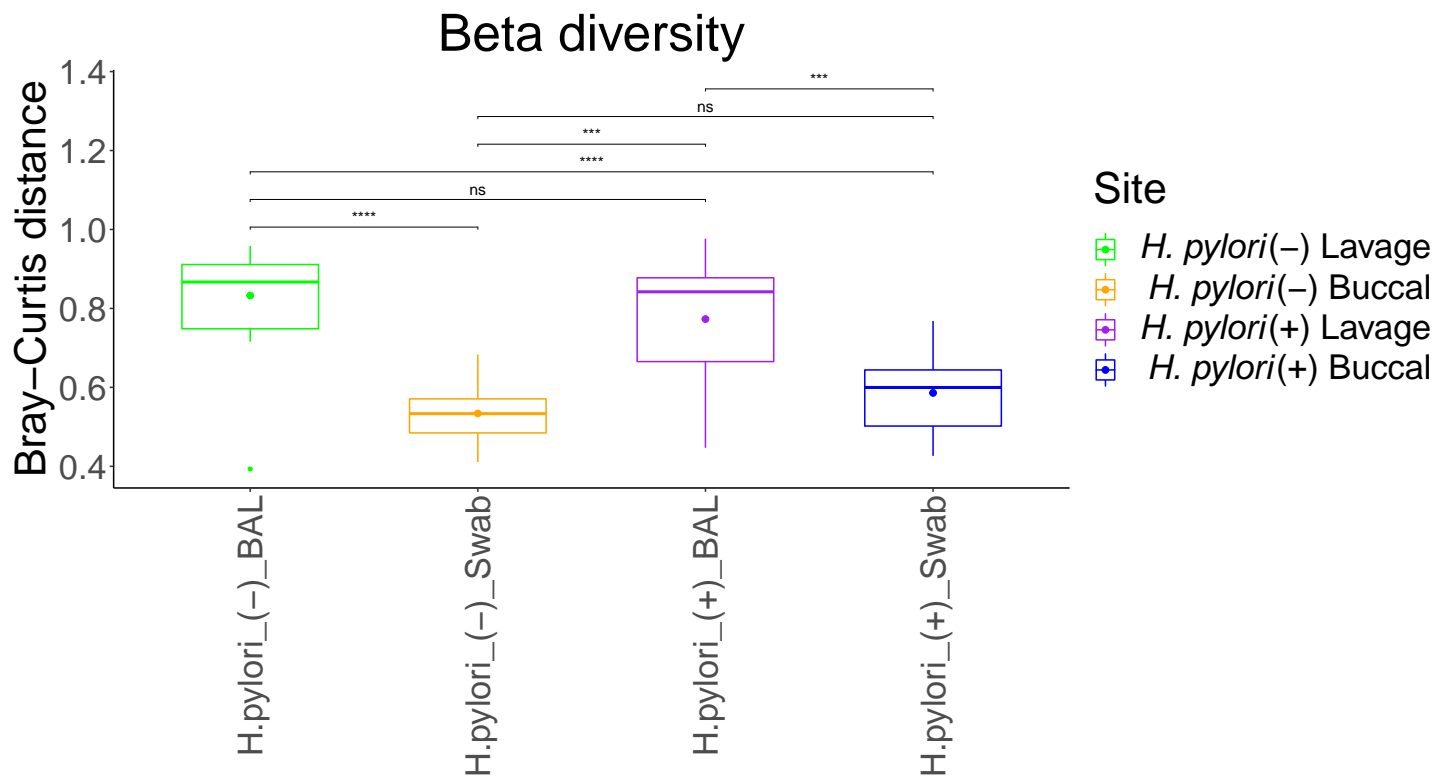
##	PC1	PC2	PC3	PC4	PC5	PC6	PC7
## 1	0.38311	0.1122317	0.08255574	0.05624649	0.04518453	0.04178459	0.03697168
##	PC8	PC9	PC10	PC11	PC12	PC13	PC14
## 1	0.03441675	0.0305229	0.0292508	0.02395872	0.0227312	0.01881898	0.01538496
##	PC15	PC16	PC17	PC18	PC19	PC20	
## 1	0.0140825	0.01226748	0.01155323	0.008776171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

# Unweighted unifrac PCoA

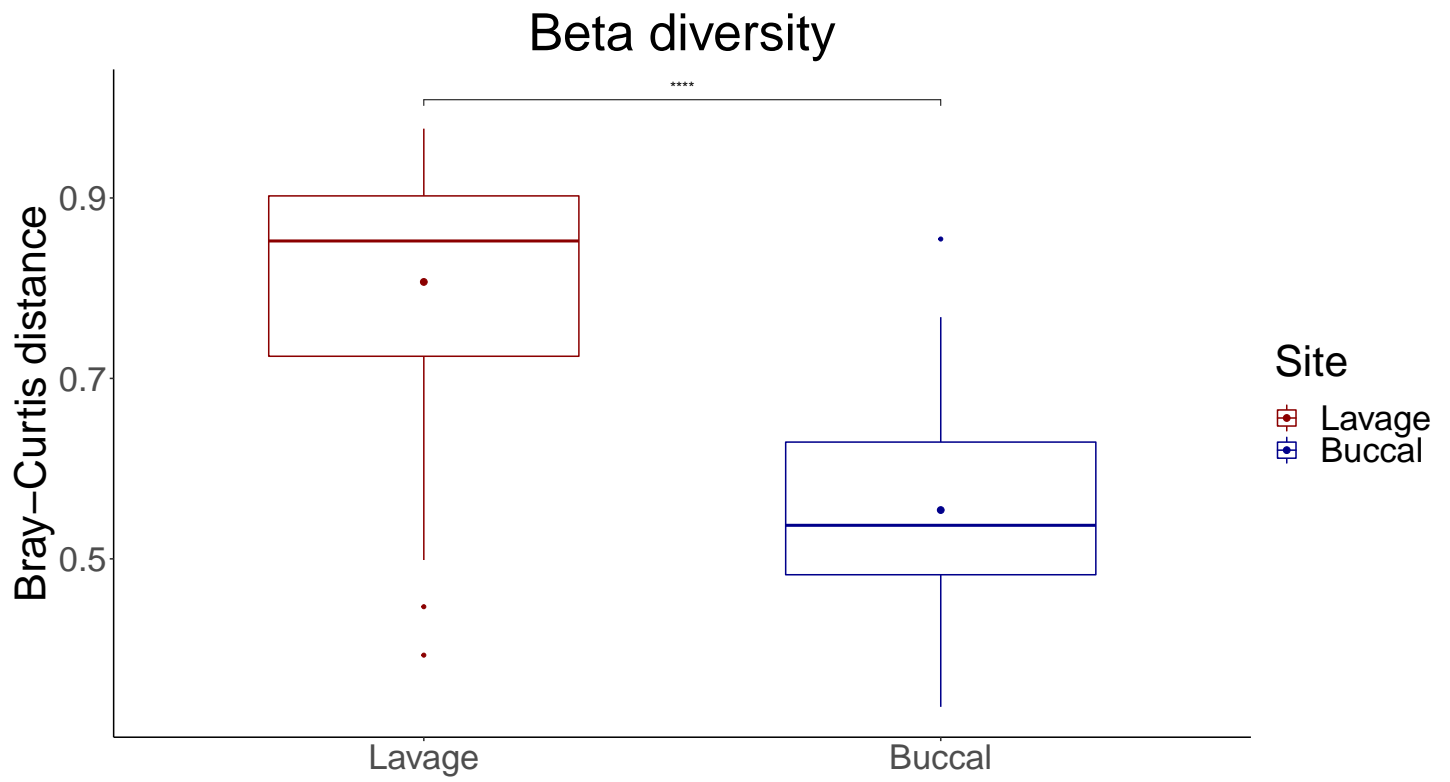


# Status Unweighted unifrac PCoA



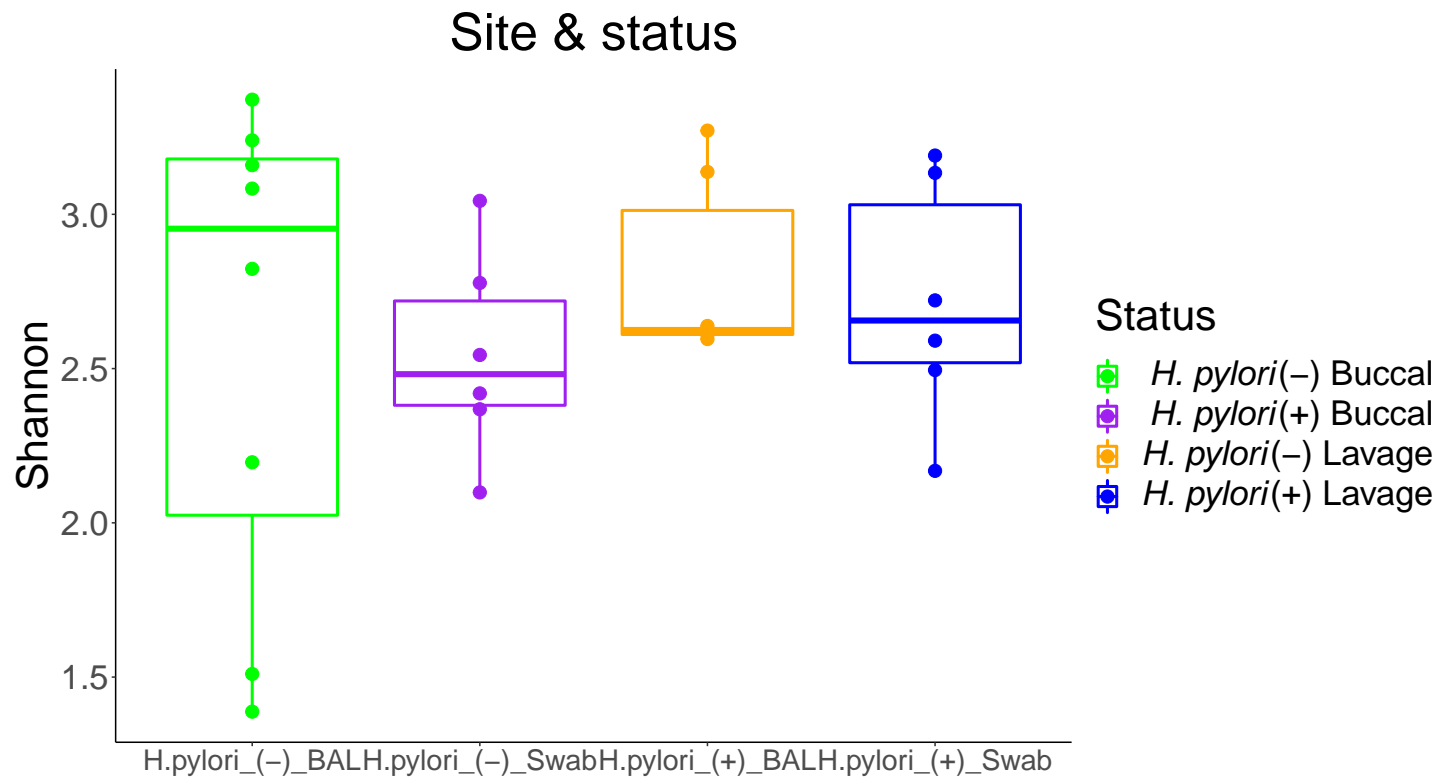


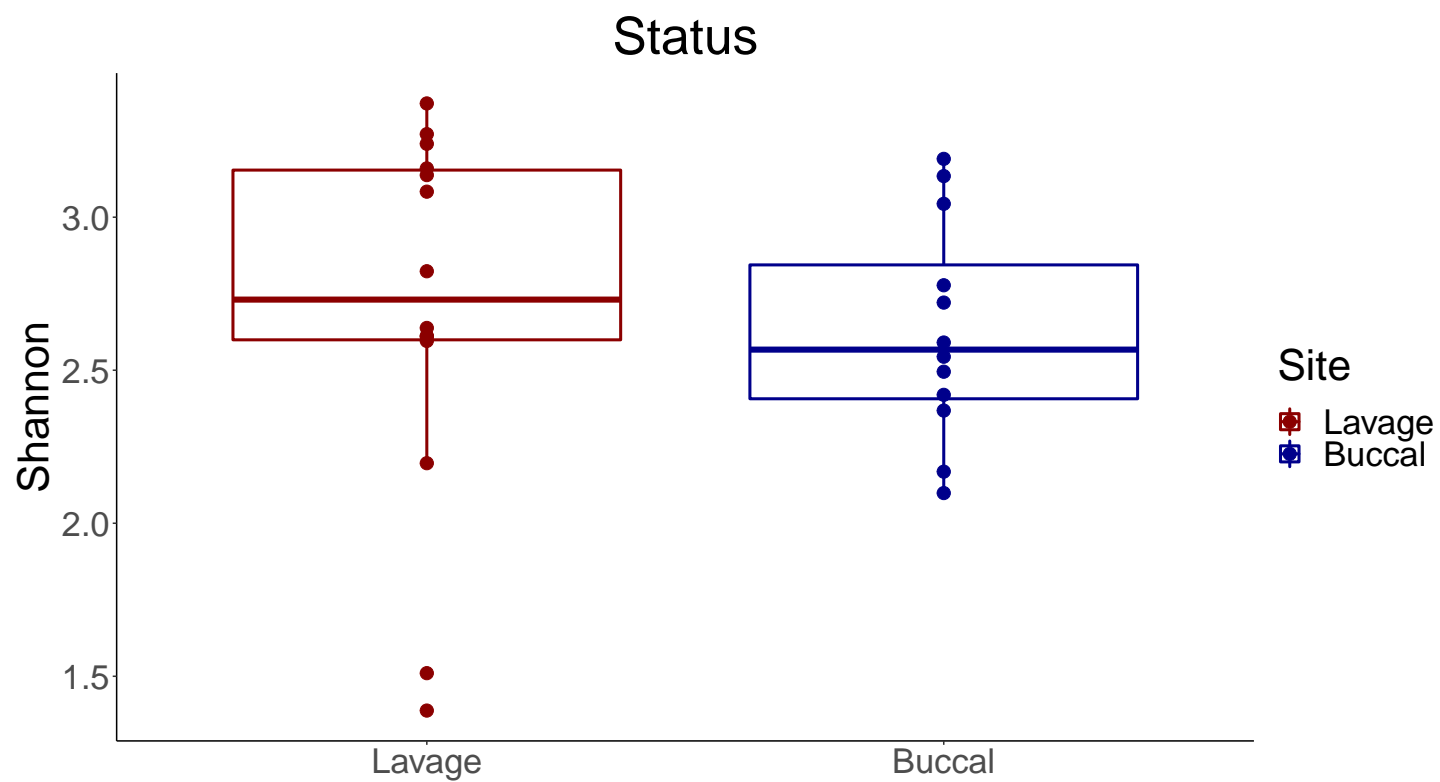
Bray-Curtis



## Alpha Diversity

Shannon index by site and *H. pylori* status



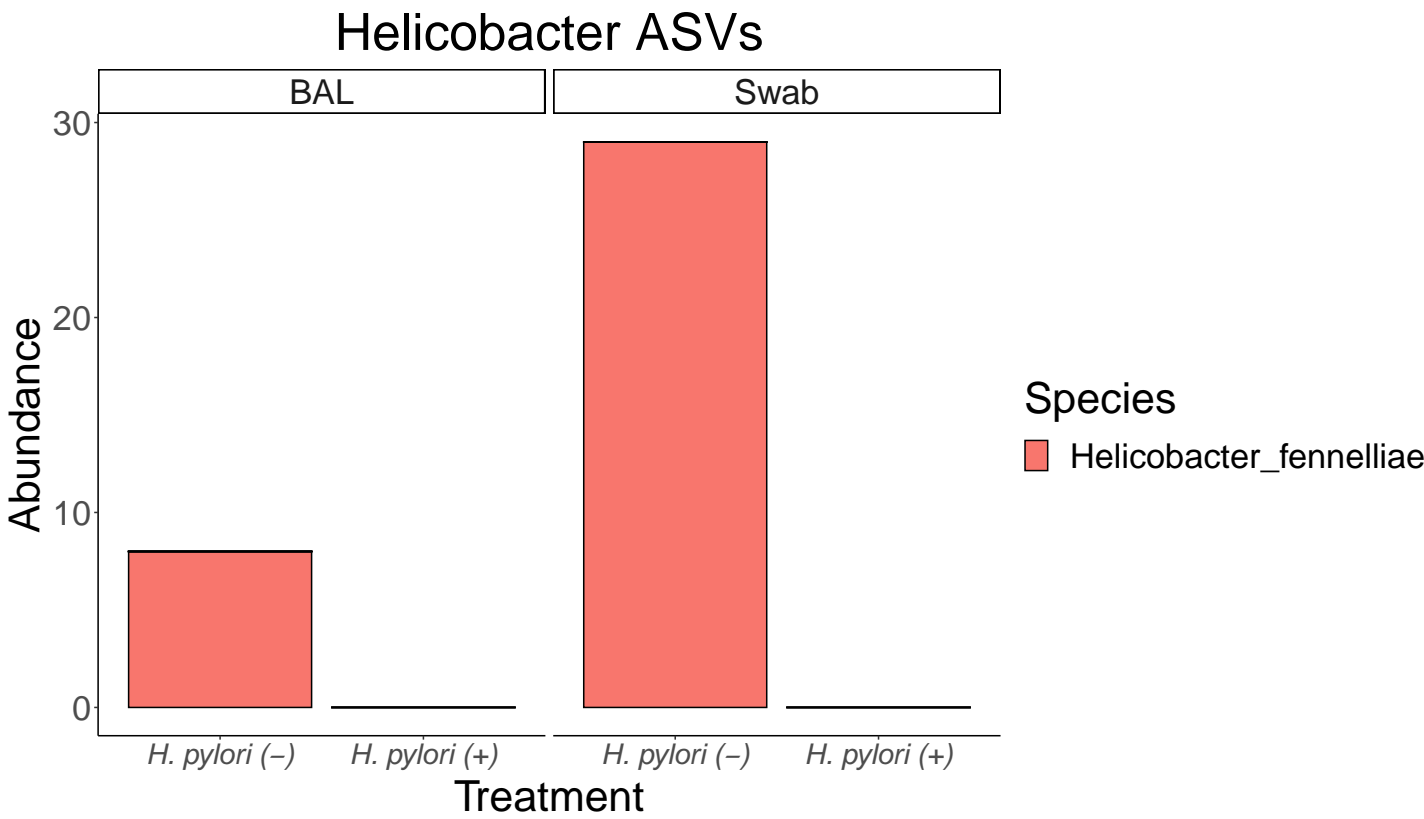


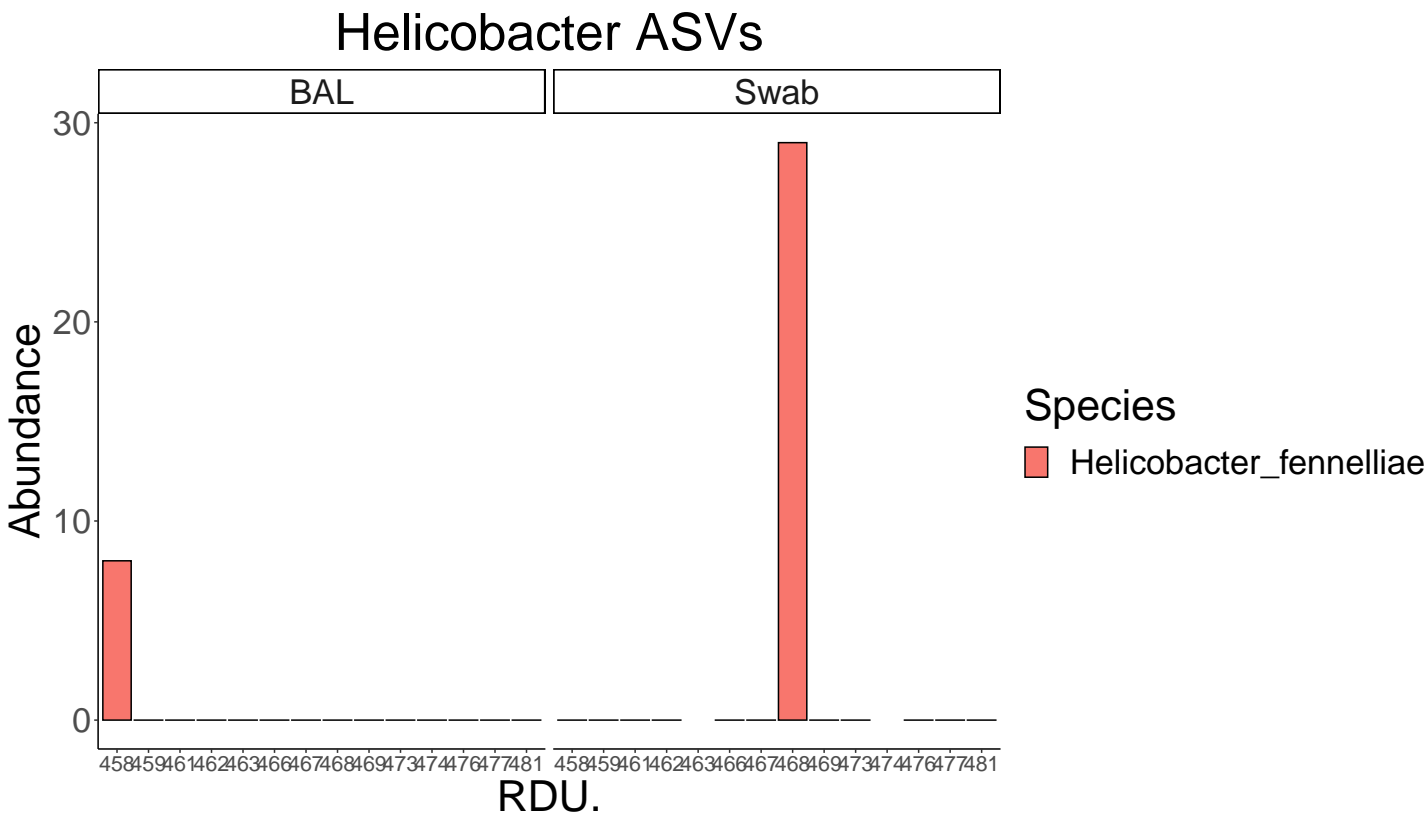
**Table 2:** All alpha diversity measurees

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

Helicobacter positive respiratory samples

Helicobacter positive samples separated by site







Taxa barplots

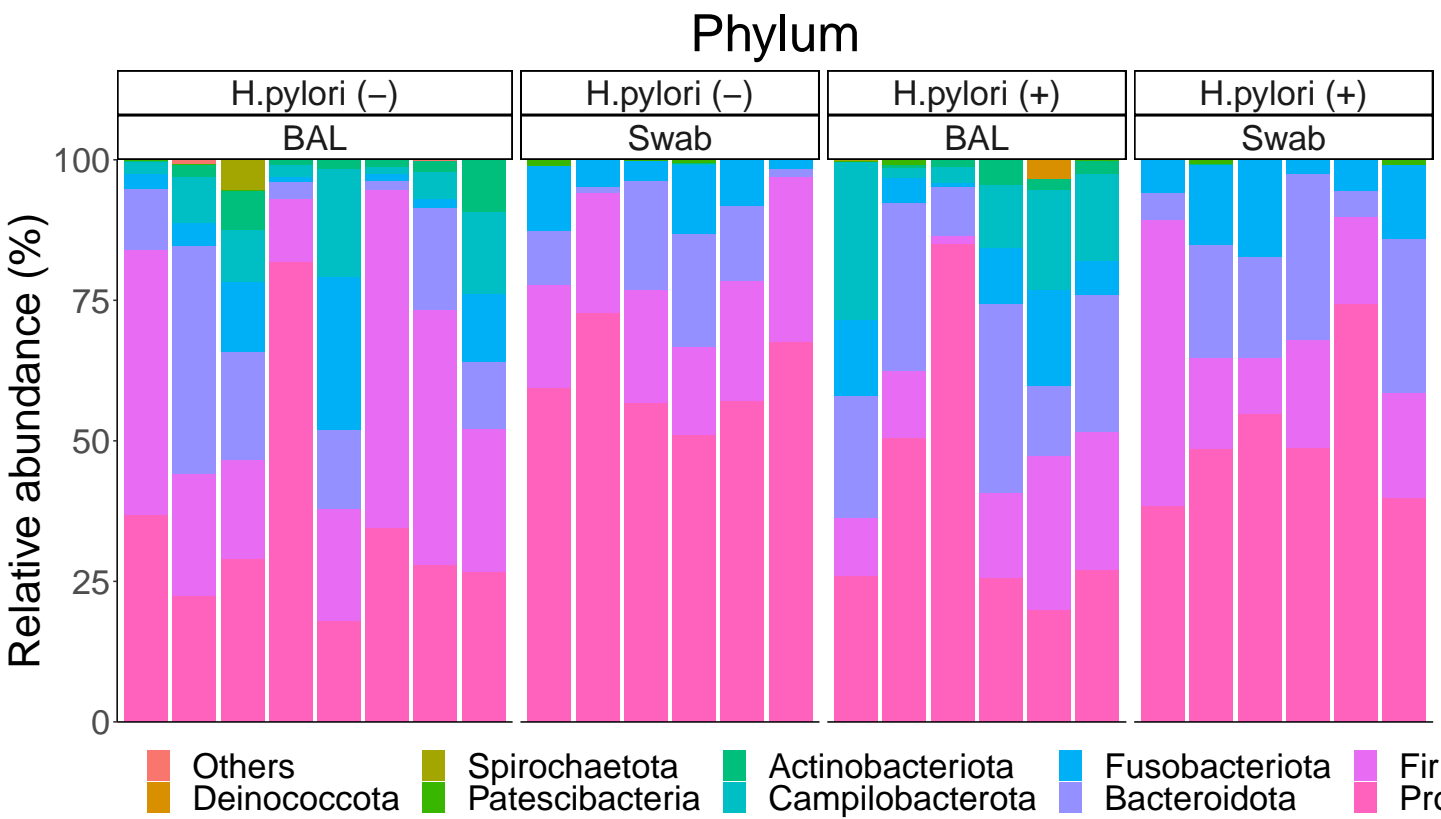


Figure 3: Microbiota Composition at Phylum level.

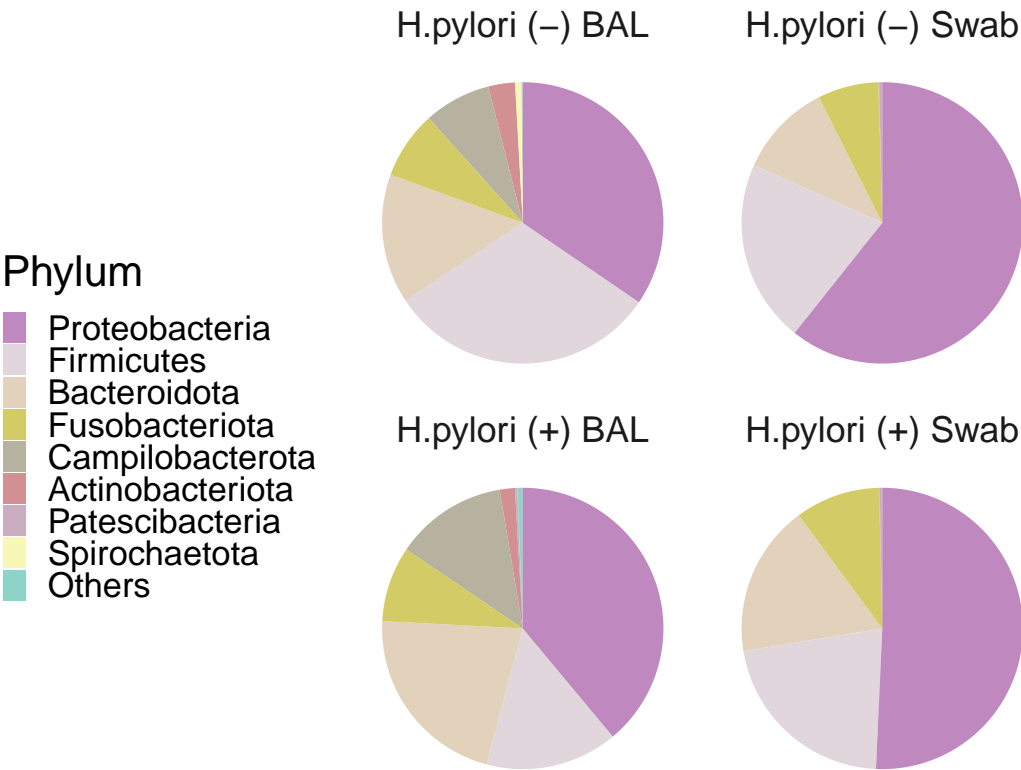
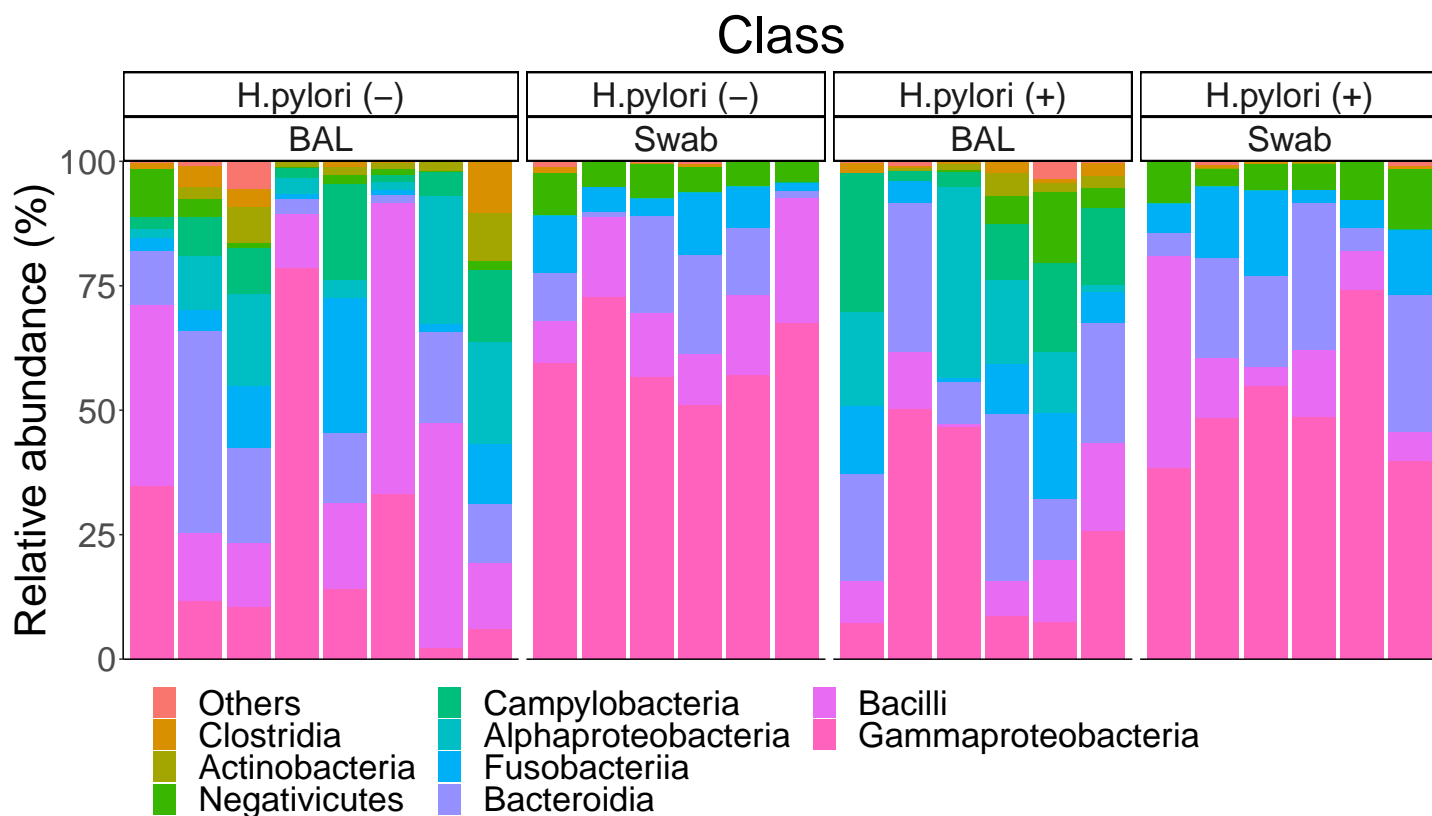


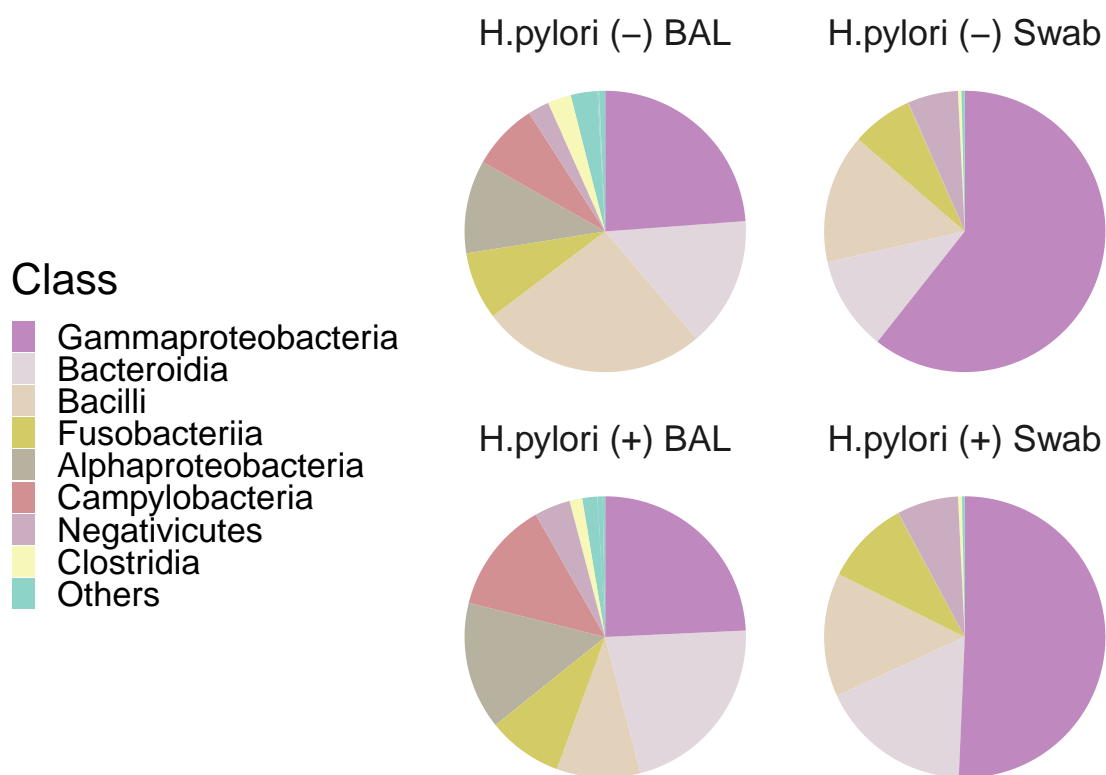
Figure 4: Microbiota Composition at Phylum level.

**Table 3:** Phylum Average Relative Abundance

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



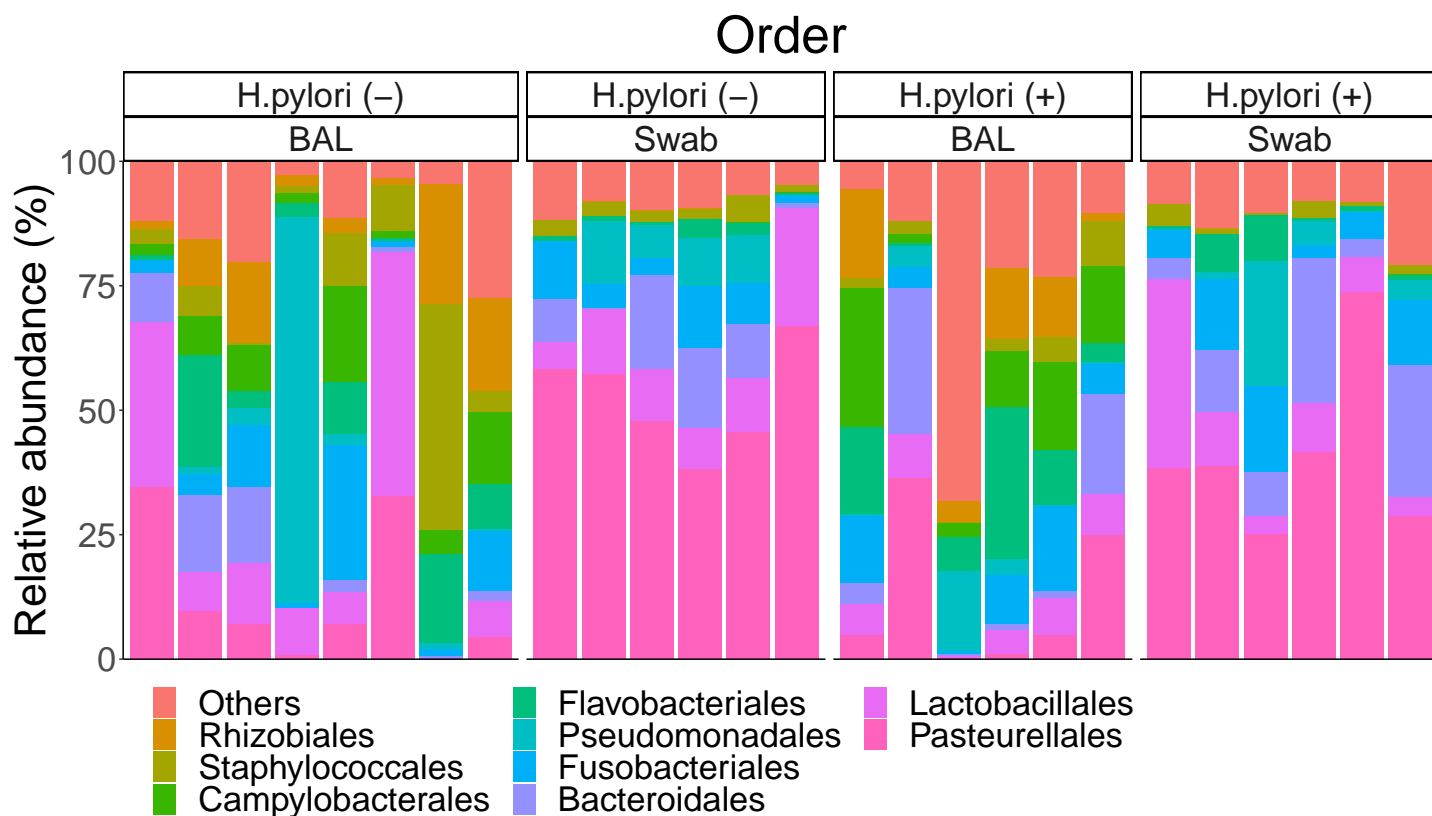
**Figure 5:** Microbiota Composition at Class level.



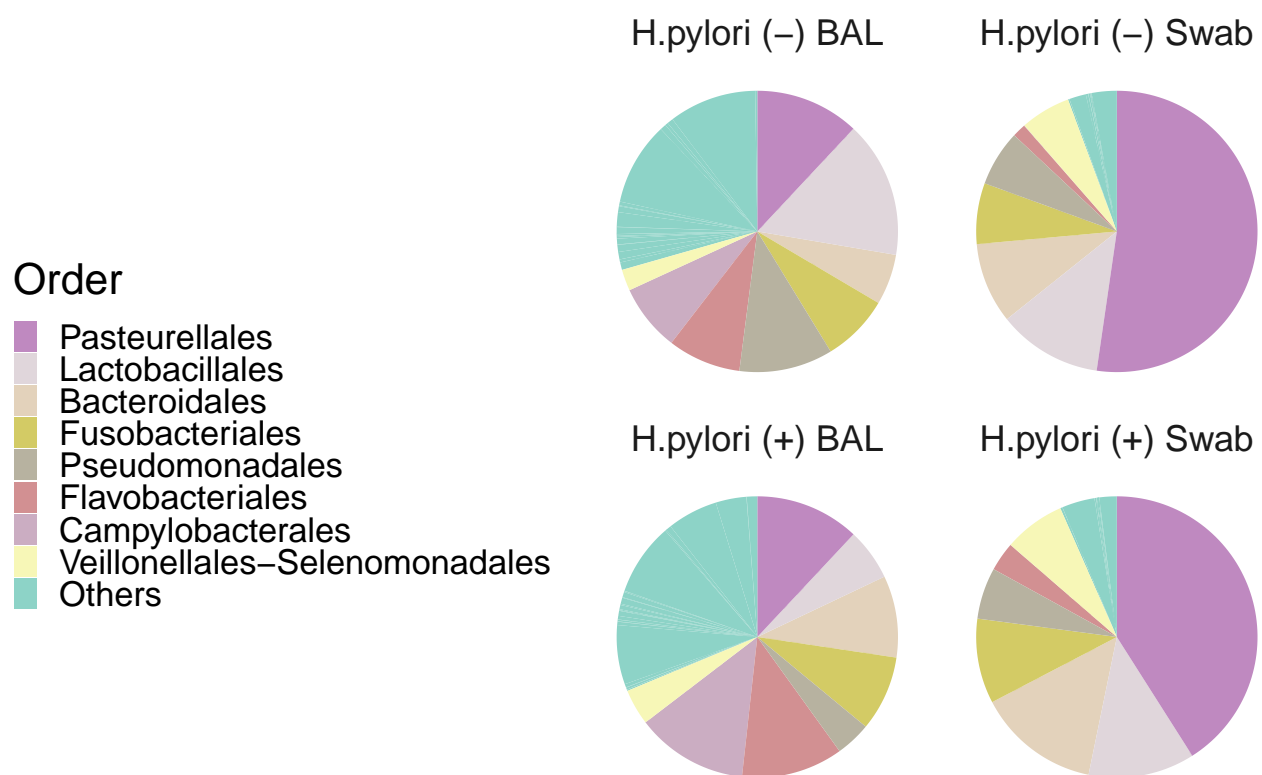
**Figure 6:** Microbiota Composition at Class level.

**Table 4:** Class Average Relative Abundance

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



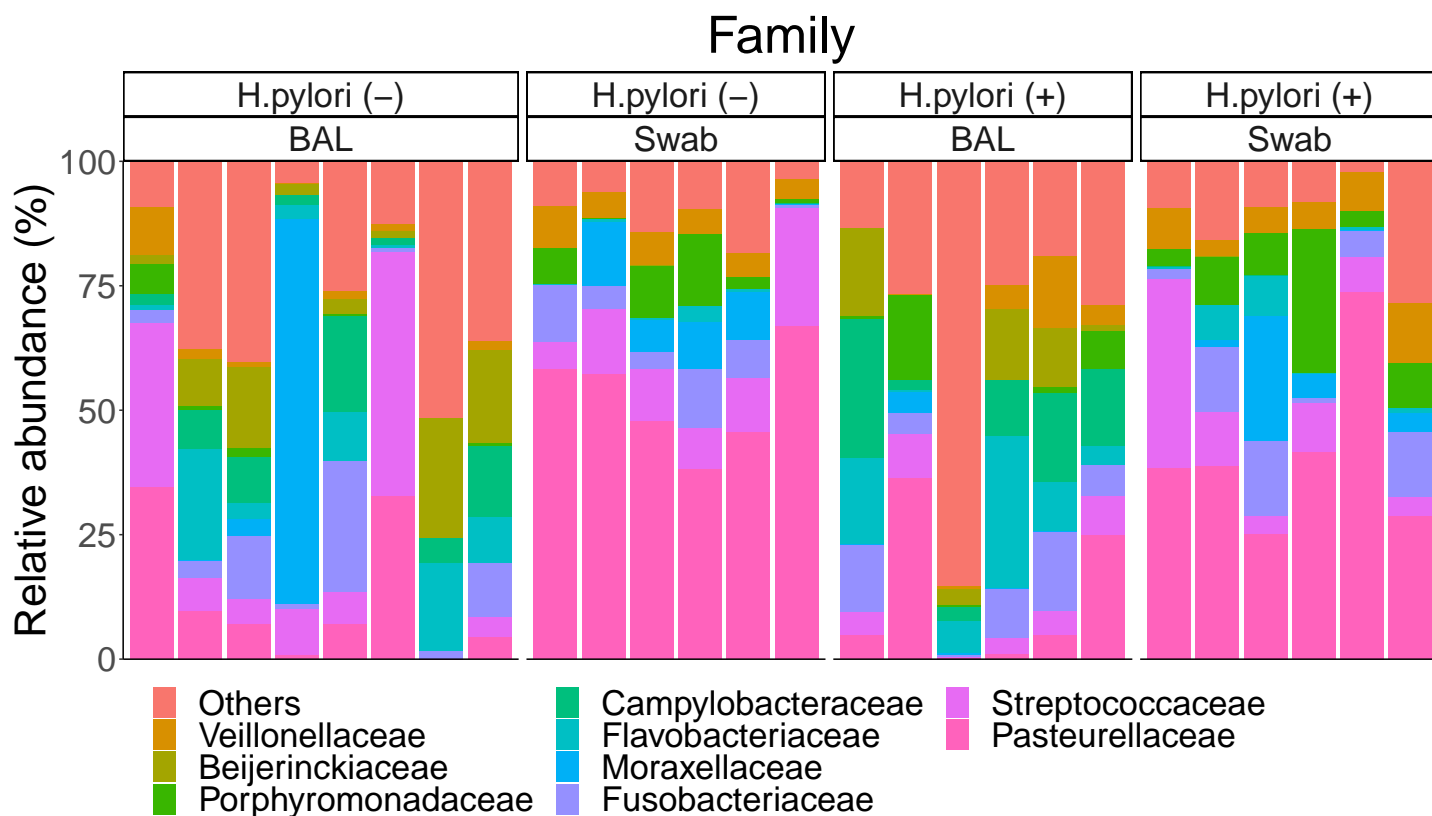
**Figure 7:** Microbiota Composition at Order level.



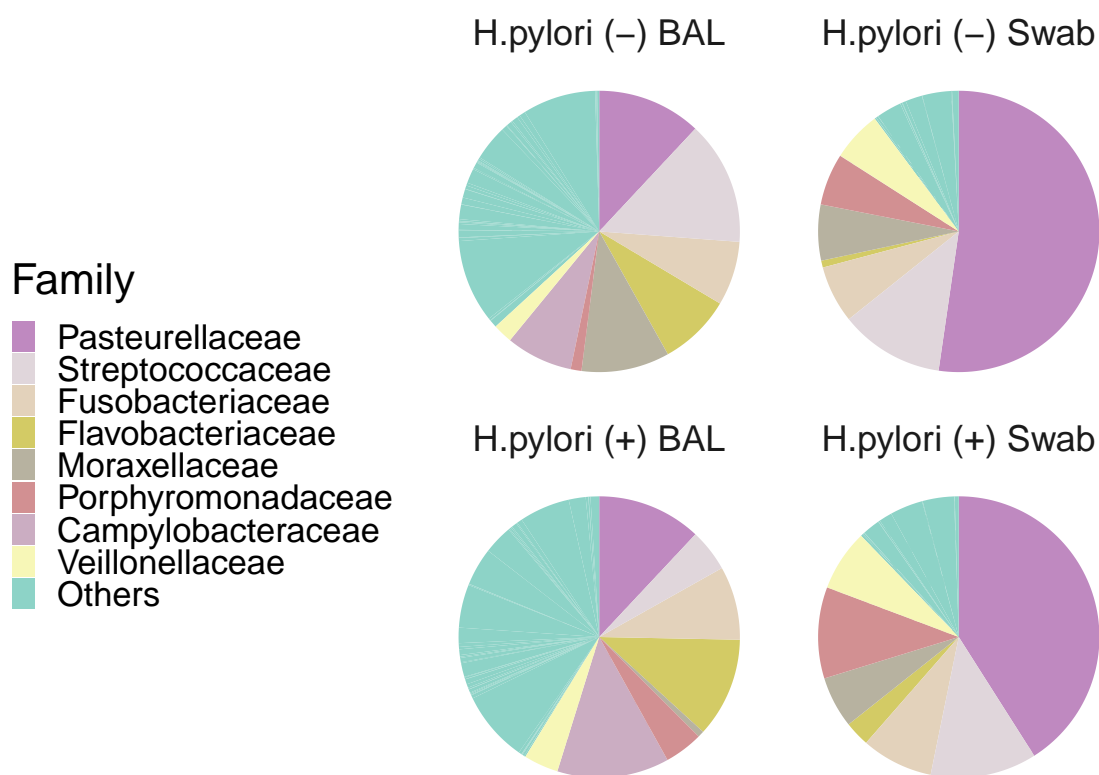
**Figure 8:** Microbiota Composition at Order level.

**Table 5:** Order Average Relative Abundance

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



**Figure 9:** Microbiota Composition at Family level.

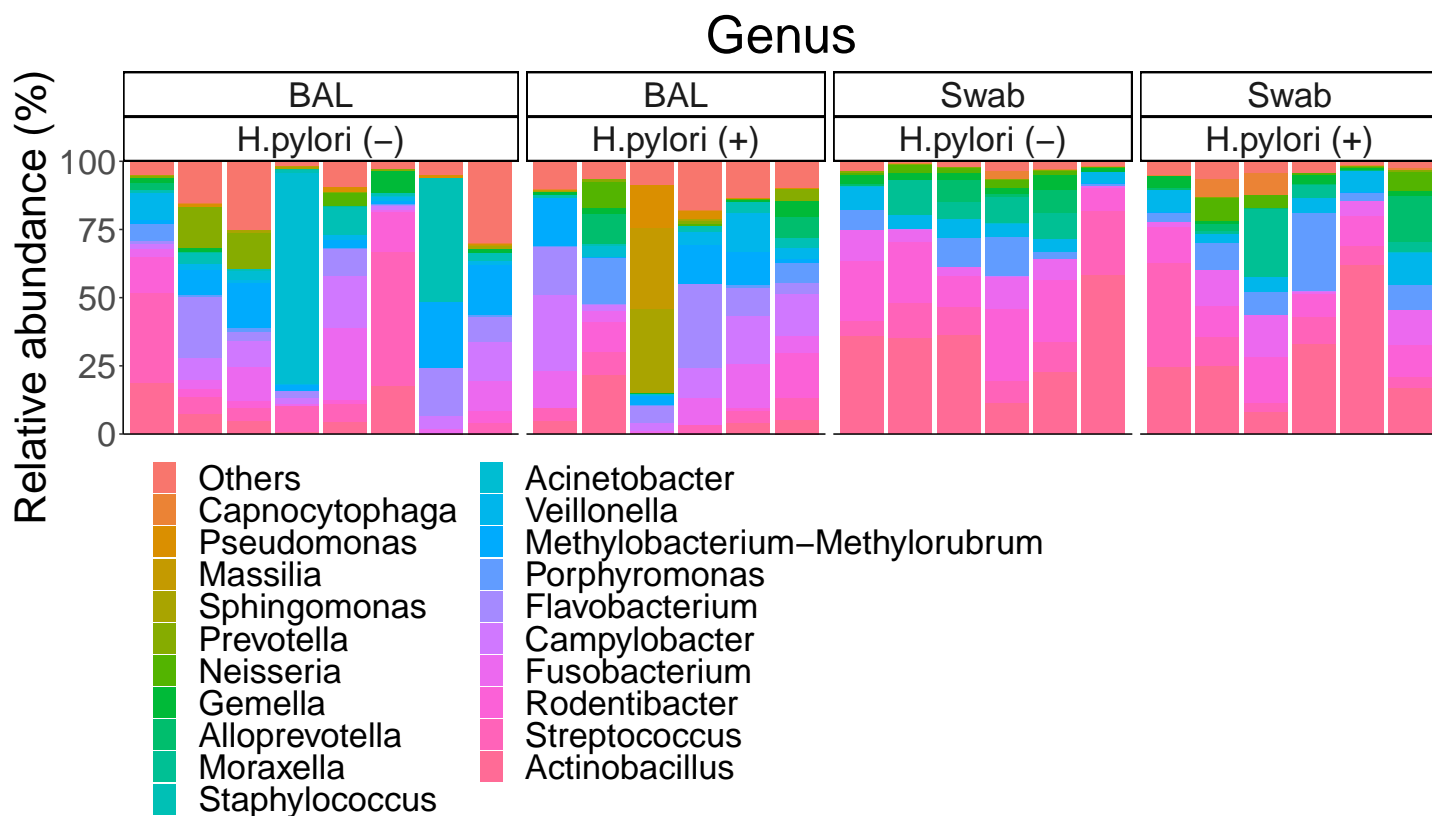


**Figure 10:** Microbiota Composition at Family level.

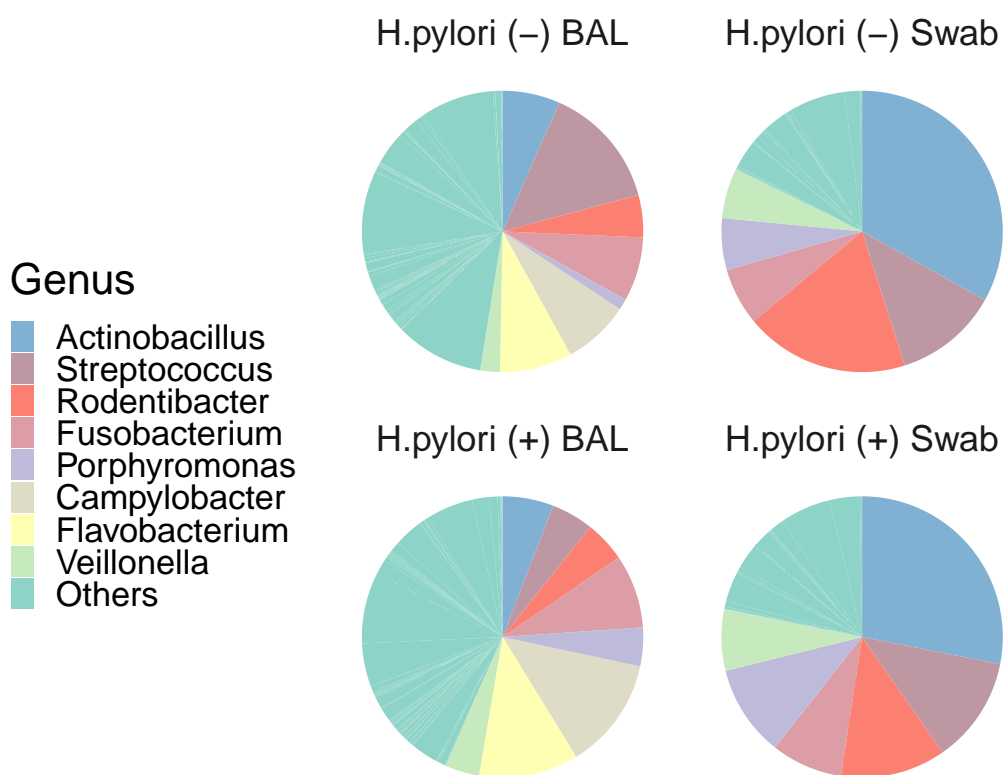
**Table 6:** Family Average Relative Abundance

Taxonomy	Sample	Average Percent Abundance
Beijerinckiaceae	H.pylori (-) BAL	9.5%
Beijerinckiaceae	H.pylori (+) BAL	8.1%
Campylobacteraceae	H.pylori (+) BAL	12.9%
Campylobacteraceae	H.pylori (-) BAL	7.7%
Flavobacteriaceae	H.pylori (+) BAL	11.5%
Flavobacteriaceae	H.pylori (-) BAL	8.3%
Fusobacteriaceae	H.pylori (+) BAL	8.5%
Fusobacteriaceae	H.pylori (+) Swab	8.2%
Fusobacteriaceae	H.pylori (-) BAL	7.4%
Fusobacteriaceae	H.pylori (-) Swab	6.6%
Moraxellaceae	H.pylori (-) BAL	10.1%
Moraxellaceae	H.pylori (-) Swab	6.4%
Moraxellaceae	H.pylori (+) Swab	5.9%
Oxalobacteraceae	H.pylori (+) BAL	5%
Pasteurellaceae	H.pylori (-) Swab	52.3%
Pasteurellaceae	H.pylori (+) Swab	41%
Pasteurellaceae	H.pylori (+) BAL	12%
Pasteurellaceae	H.pylori (-) BAL	12%
Porphyromonadaceae	H.pylori (+) Swab	10.5%
Porphyromonadaceae	H.pylori (-) Swab	5.9%
Porphyromonadaceae	H.pylori (+) BAL	4.4%
Prevotellaceae	H.pylori (+) BAL	4.3%
Prevotellaceae	H.pylori (-) BAL	4.1%
Sphingomonadaceae	H.pylori (+) BAL	5.8%
Staphylococcaceae	H.pylori (-) BAL	8.4%
Streptococcaceae	H.pylori (-) BAL	14.2%
Streptococcaceae	H.pylori (+) Swab	12.2%
Streptococcaceae	H.pylori (-) Swab	12%
Streptococcaceae	H.pylori (+) BAL	4.9%
Veillonellaceae	H.pylori (+) Swab	7%
Veillonellaceae	H.pylori (-) Swab	5.8%
Veillonellaceae	H.pylori (+) BAL	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 (-) BAL	10.1%
Actinobacillus	H.pylori (-) Swab	33.1%
Actinobacillus	H.pylori (+) Swab	28.1%
Actinobacillus	H.pylori (-) BAL	6.6%
Actinobacillus	H.pylori (+) BAL	5.9%
Campylobacter	H.pylori (+) BAL	12.9%
Campylobacter	H.pylori (-) BAL	7.7%
Flavobacterium	H.pylori (+) BAL	11.5%
Flavobacterium	H.pylori (-) BAL	8.3%
Fusobacterium	H.pylori (+) BAL	8.5%
Fusobacterium	H.pylori (+) Swab	8.2%
Fusobacterium	H.pylori (-) BAL	7.4%
Fusobacterium	H.pylori (-) Swab	6.6%
Massilia	H.pylori (+) BAL	4.9%
Methylobacterium-Methylobacterium	H.pylori (-) BAL	9.5%
Methylobacterium-Methylobacterium	H.pylori (+) BAL	8.1%
Moraxella	H.pylori (-) Swab	6.4%
Moraxella	H.pylori (+) Swab	5.9%
Porphyromonas	H.pylori (+) Swab	10.5%
Porphyromonas	H.pylori (-) Swab	5.9%
Rodentibacter	H.pylori (-) Swab	18.9%
Rodentibacter	H.pylori (+) Swab	12.1%
Rodentibacter	H.pylori (-) BAL	4.9%
Rodentibacter	H.pylori (+) BAL	4.7%
Sphingomonas	H.pylori (+) BAL	5.4%
Staphylococcus	H.pylori (-) BAL	8.4%
Streptococcus	H.pylori (-) BAL	14.2%
Streptococcus	H.pylori (+) Swab	12.2%
Streptococcus	H.pylori (-) Swab	12%
Streptococcus	H.pylori (+) BAL	4.9%
Veillonella	H.pylori (+) Swab	7%
Veillonella	H.pylori (-) Swab	5.8%

Genera correlation with IL8 concentration (Serum and BAL)

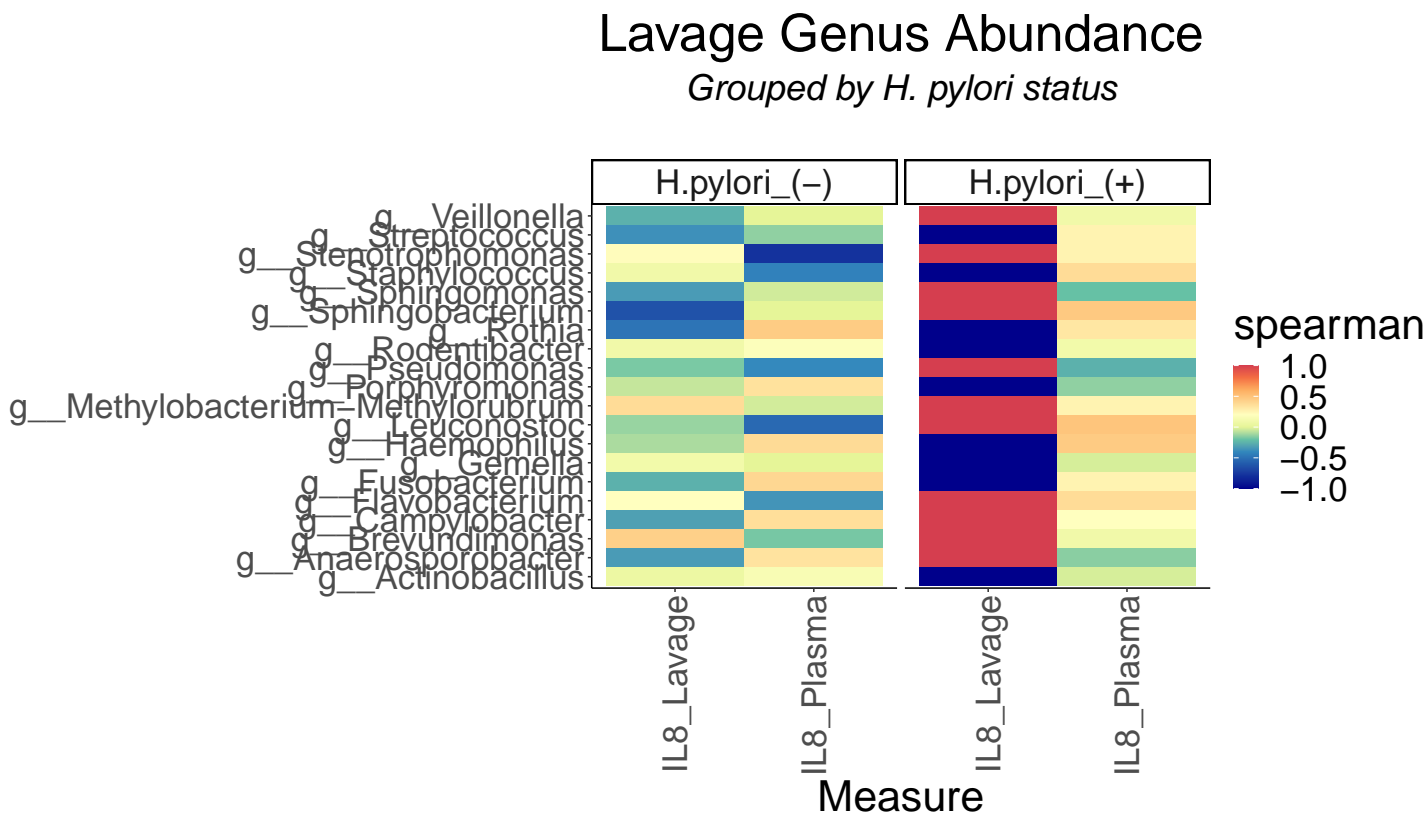


Figure 13: IL8 and lavage genus abundance Spearman correlations separated by *H. pylori* status

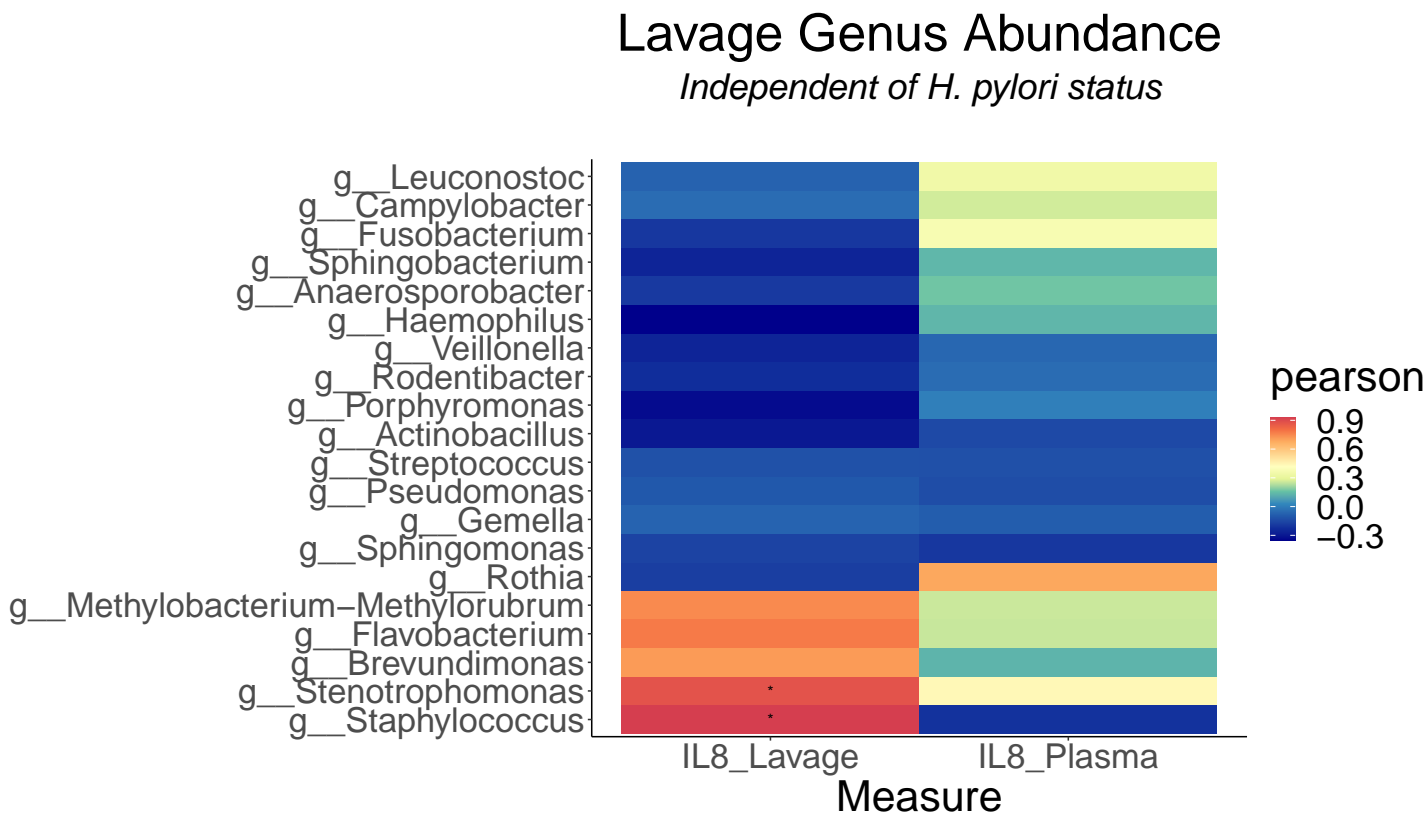
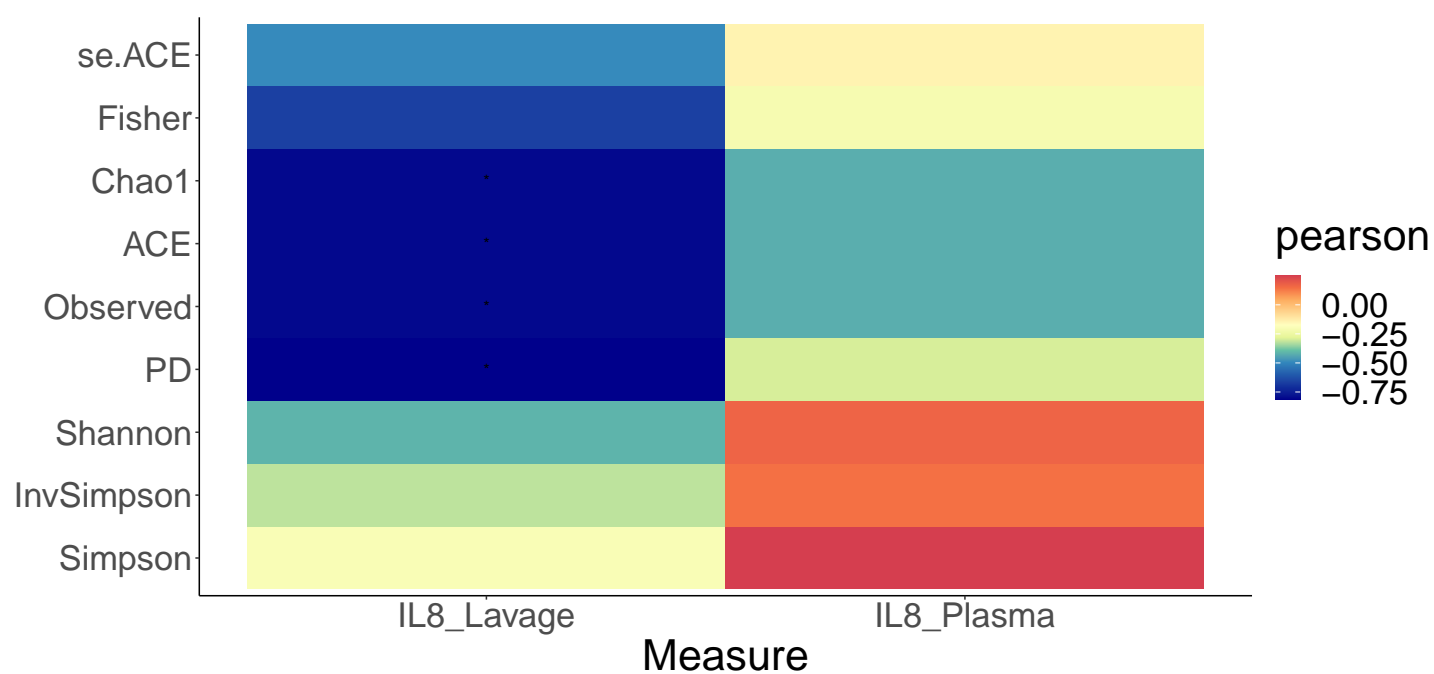


Figure 14: IL8 and lavage genus abundance Spearman correlations independent of *H. pylori* status

# Lavage Alpha Diversity

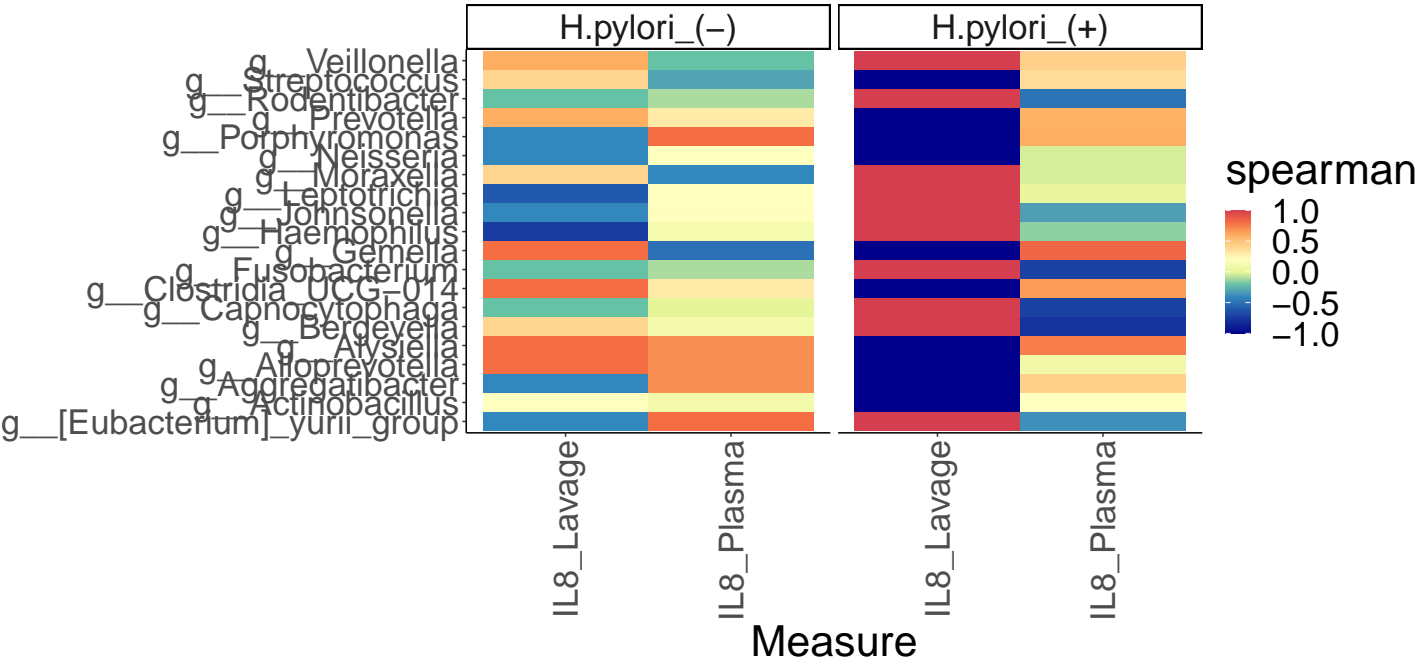
*Independent of H. pylori status*



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

# Buccal Cavity Genus Abundance

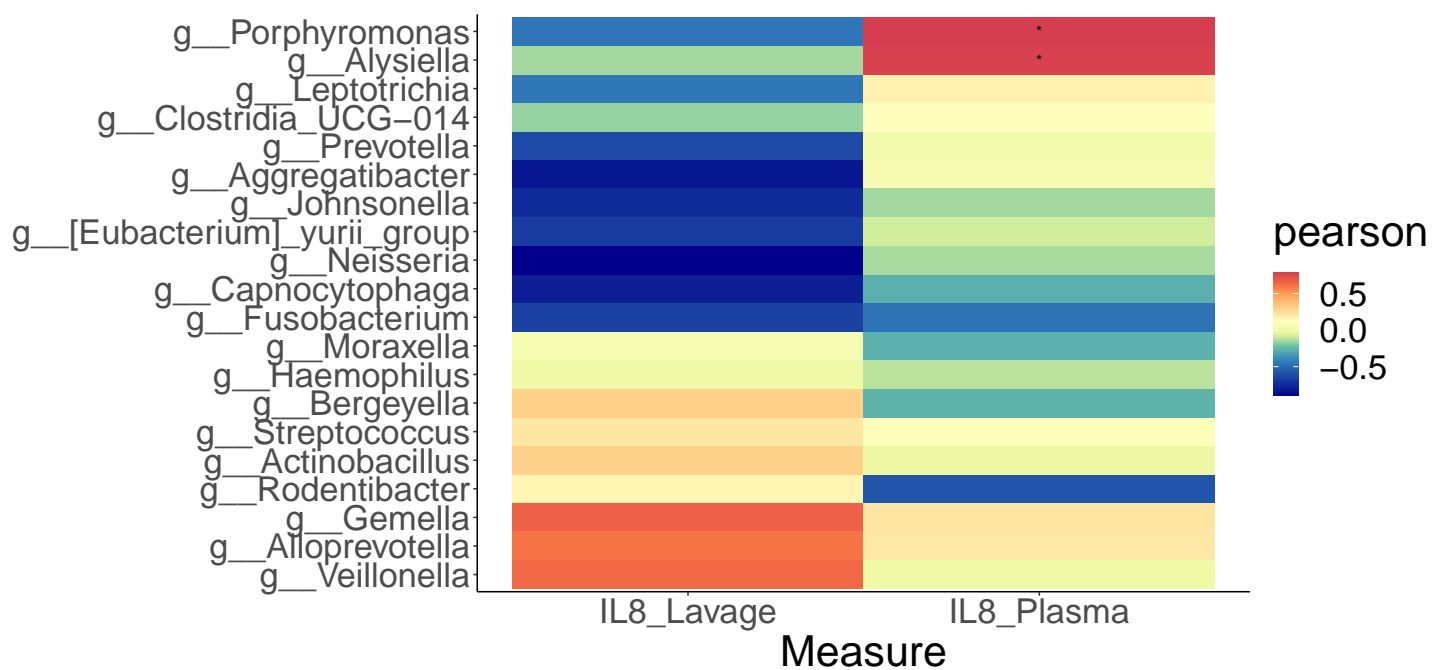
Grouped by *H. pylori* status



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

# Buccal Cavity Genus Abundance

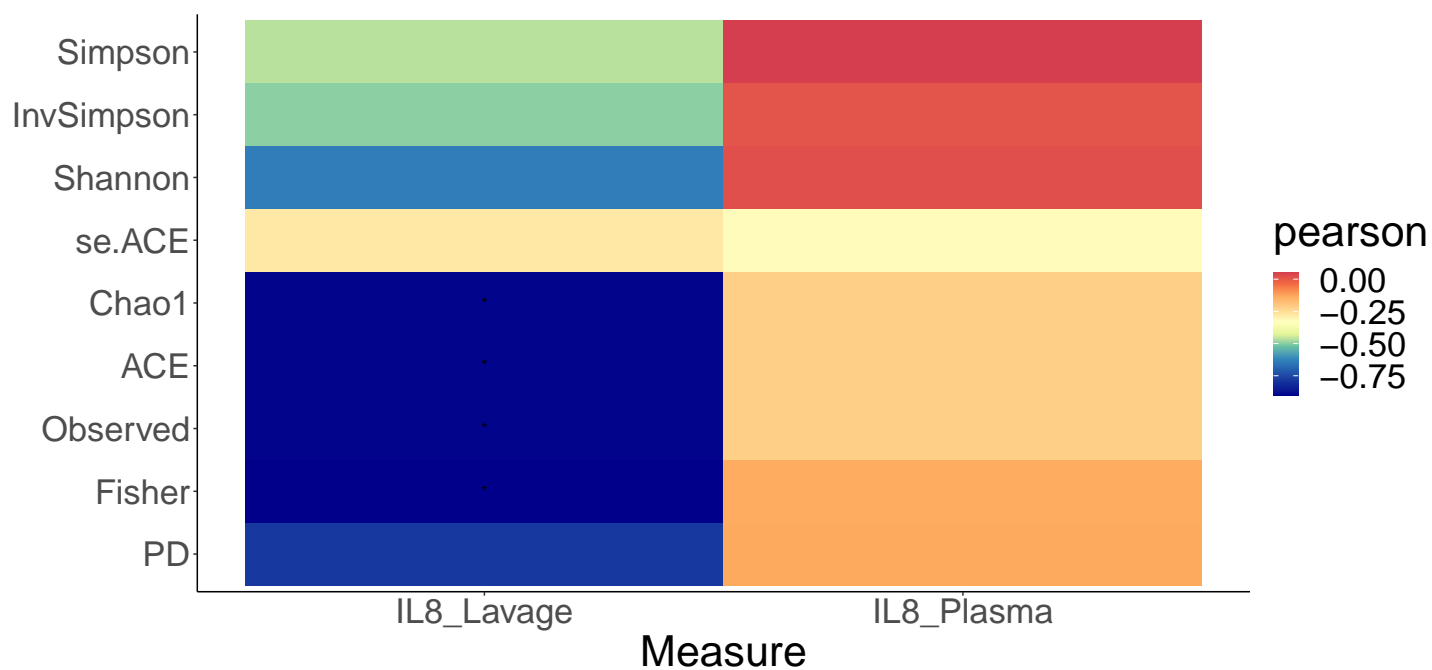
*Independent of H. pylori status*



**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_1.1-7
## [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_1.5.4
## [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] deldir_1.0-6            vctrs_0.4.1           sjlabelled_1.2.0
## [40] abind_1.4-5             cachem_1.0.6           withr_2.5.0
## [43] checkmate_2.1.0         emmeans_1.7.4-1        vegan_2.6-2
## [46] svglite_2.1.0           cluster_2.1.3          ape_5.6-2
## [49] lazyeval_0.2.2          crayon_1.5.1           genefilter_1.76.0
## [52] pkgconfig_2.0.3         zCompositions_1.4.0-1  labeling_0.4.2
## [55] nlme_3.1-157            nnet_7.3-17            rlang_1.0.2
```



## [58] spatial_7.3-15	lifecycle_1.0.1	miniUI_0.1.1.1
## [61] modelr_0.1.8	randomForest_4.7-1.1	cellranger_1.1.0
## [64] datawizard_0.4.1	Matrix_1.4-1	carData_3.0-5
## [67] Rhdf5lib_1.16.0	boot_1.3-28	reprex_2.0.1
## [70] base64enc_0.1-3	png_0.1-7	viridisLite_0.4.0
## [73] stabledist_0.7-1	parameters_0.18.1	bitops_1.0-7
## [76] rhdf5filters_1.6.0	Biostrings_2.62.0	blob_1.2.3
## [79] GUniFrac_1.6	jpeg_0.1-9	rstatix_0.7.0
## [82] ggeffects_1.1.2	ggsignif_0.6.3	scales_1.2.0
## [85] memoise_2.0.1	plyr_1.8.7	zlibbioc_1.40.0
## [88] compiler_4.1.3	tinytex_0.39	clue_0.3-60
## [91] lme4_1.1-29	cli_3.3.0	ade4_1.7-19
## [94] XVector_0.34.0	htmlTable_2.4.1	Formula_1.2-4
## [97] MASS_7.3-57	mgcv_1.8-40	tidyselect_1.1.2
## [100] stringi_1.7.6	highr_0.9	yaml_2.3.5
## [103] locfit_1.5-9.5	latticeExtra_0.6-30	ggrepel_0.9.1
## [106] grid_4.1.3	tools_4.1.3	parallel_4.1.3
## [109] rstudioapi_0.13	foreach_1.5.2	foreign_0.8-82
## [112] statip_0.2.3	gridExtra_2.3	scatterplot3d_0.3-42
## [115] farver_2.1.0	Rtsne_0.16	stable_1.1.6
## [118] digest_0.6.29	shiny_1.7.1	Rcpp_1.0.8.3
## [121] car_3.0-13	broom_0.8.0	performance_0.9.0
## [124] later_1.2.0	httr_1.4.3	AnnotationDbi_1.56.1
## [127] effectsize_0.7.0	sjstats_0.18.1	colorspace_2.0-3
## [130] rvest_1.0.2	XML_3.99-0.10	fs_1.5.2
## [133] modeest_2.4.0	truncnorm_1.0-8	splines_4.1.3
## [136] yulab.utils_0.0.4	rmutil_1.1.9	statmod_1.4.36
## [139] multtest_2.50.0	systemfonts_1.0.4	xtable_1.8-4
## [142] jsonlite_1.8.0	nloptr_2.0.3	timeDate_3043.102
## [145] R6_2.5.1	Hmisc_4.7-1	NADA_1.6-1.1
## [148] pillar_1.7.0	htmltools_0.5.2	mime_0.12
## [151] glue_1.6.2	fastmap_1.1.0	minqa_1.2.4
## [154] DT_0.23	BiocParallel_1.28.3	codetools_0.2-18
## [157] mvtnorm_1.1-3	utf8_1.2.2	lattice_0.20-45
## [160] interp_1.1-3	survival_3.3-1	biomformat_1.22.0
## [163] munsell_0.5.0	rhdf5_2.38.0	GenomeInfoDbData_1.2.7
## [166] iterators_1.0.14	labelled_2.9.1	sjmisc_2.8.9
## [169] haven_2.5.0	reshape2_1.4.4	gtable_0.3.0
## [172] bayestestR_0.12.1		