H.pylori Rhesus Microbiome Analysis

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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

Odds ratios of variables based on H. pylori status
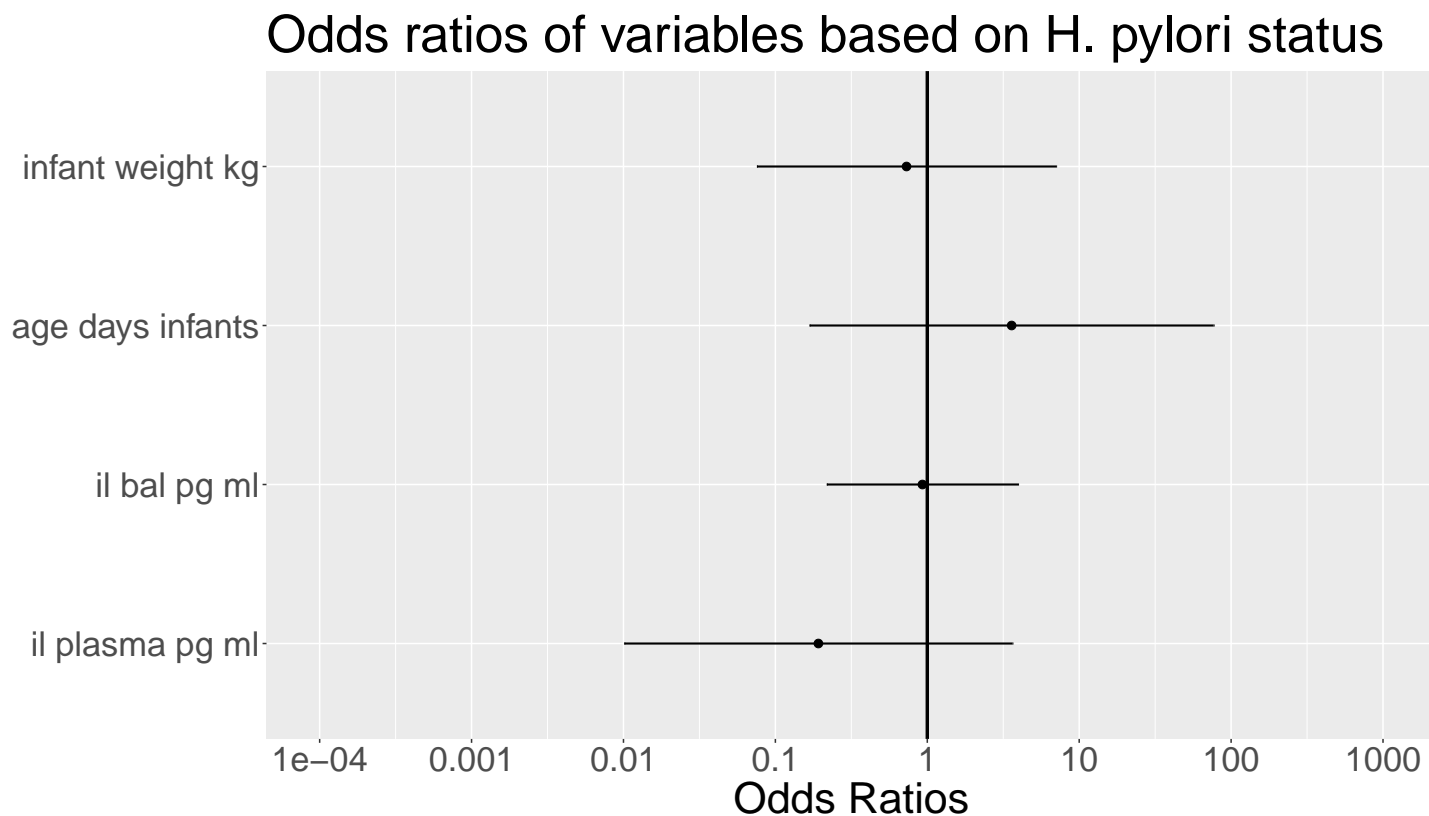
	OR	2.5 %	97.5 %	p
(Intercept)	0.018	0.000	110.146	0.410
infant_weight_kg	0.243	0.000	7254.525	0.786
age_days_infants	1.042	0.955	1.177	0.413
il_bal_pg.ml	0.993	0.852	1.158	0.921
il_plasma_pg.ml	0.996	0.985	1.001	0.271

H.pylori Il8 Pearson correlation

$R = -0.31, p = 0.45$
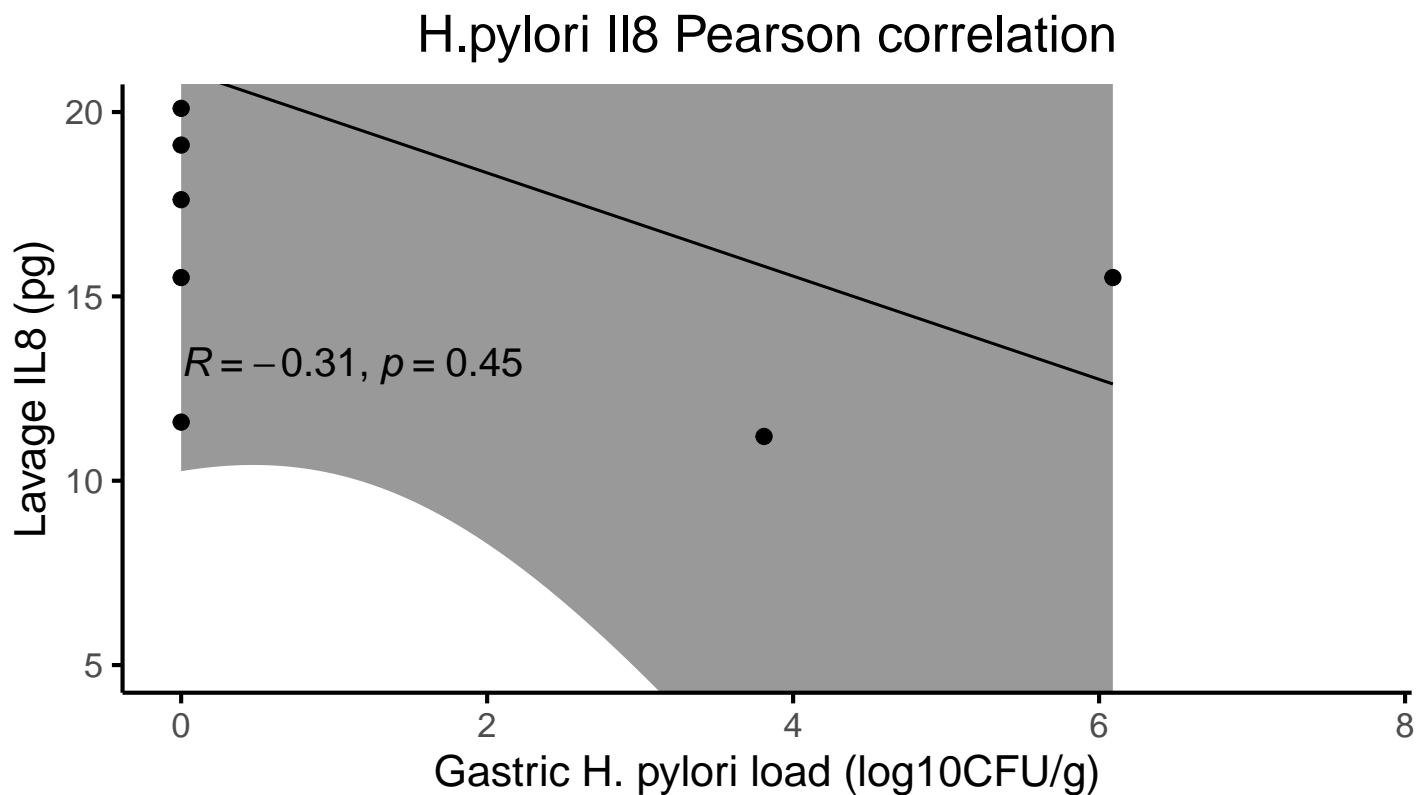
Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study
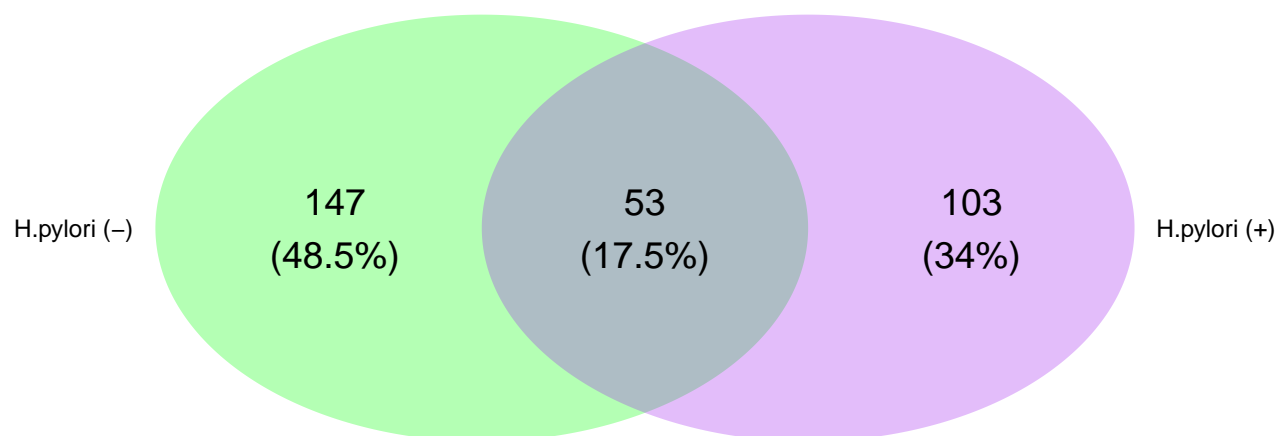
H.pylori plasma IL8 Pearson correlation

$R = 0.3, p = 0.32$
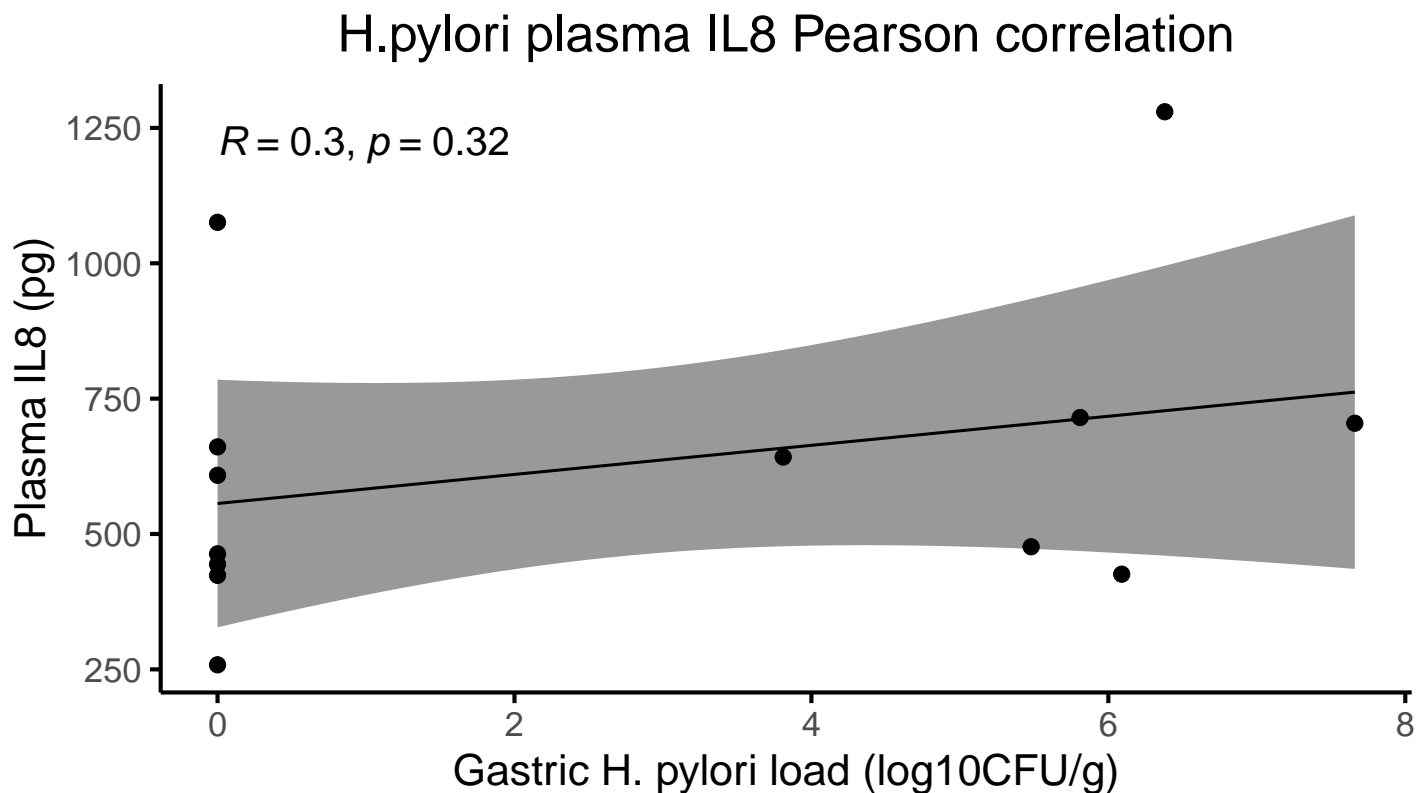
Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

Lavage overlapping taxa

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

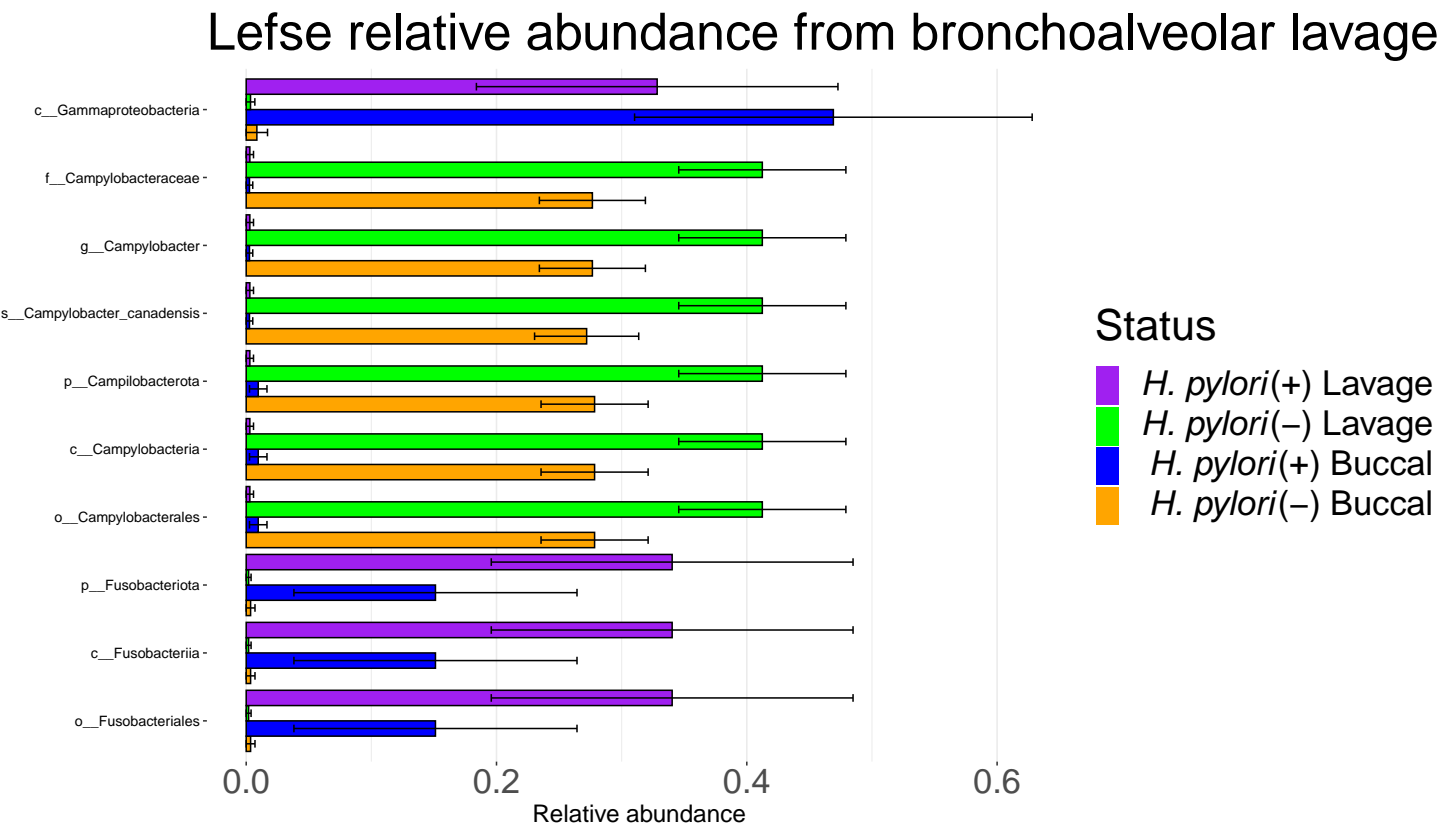# Overlapping taxa between H. pylori (+) and (−) in buccal cavity

H.pylori (−)

43
(24.2%)

82
(46.1%)

53
(29.8%)

H.pylori (+)
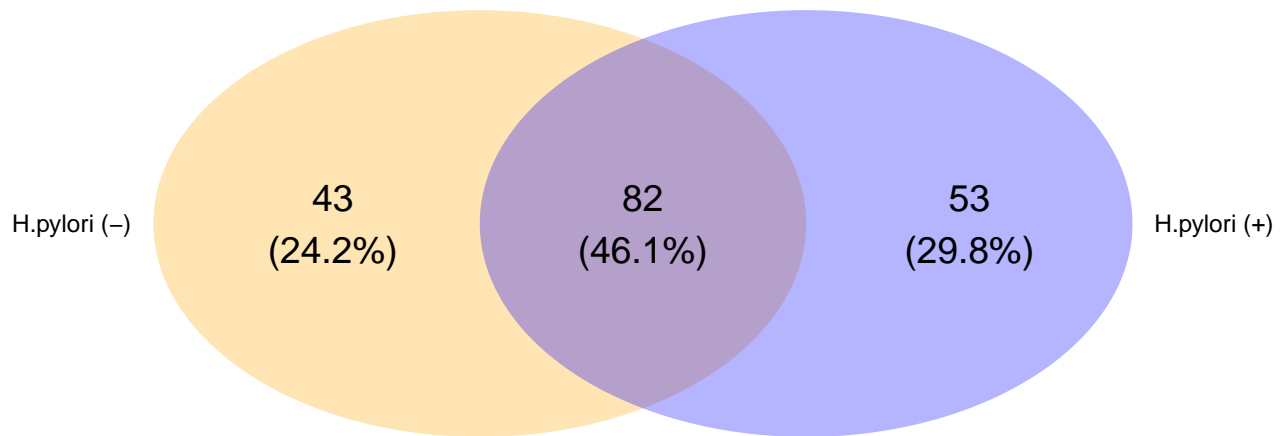
Lefse analysis and differential abundance for both sites

Lefse taxa from bronchoalveolar lavage and or

Status

- *H. pylori*(−) Buccal
- *H. pylori*(+) Buccal
- *H. pylori*(−) Lavage
- *H. pylori*(+) Lavage

LDA score

Relative abundance of differential taxa
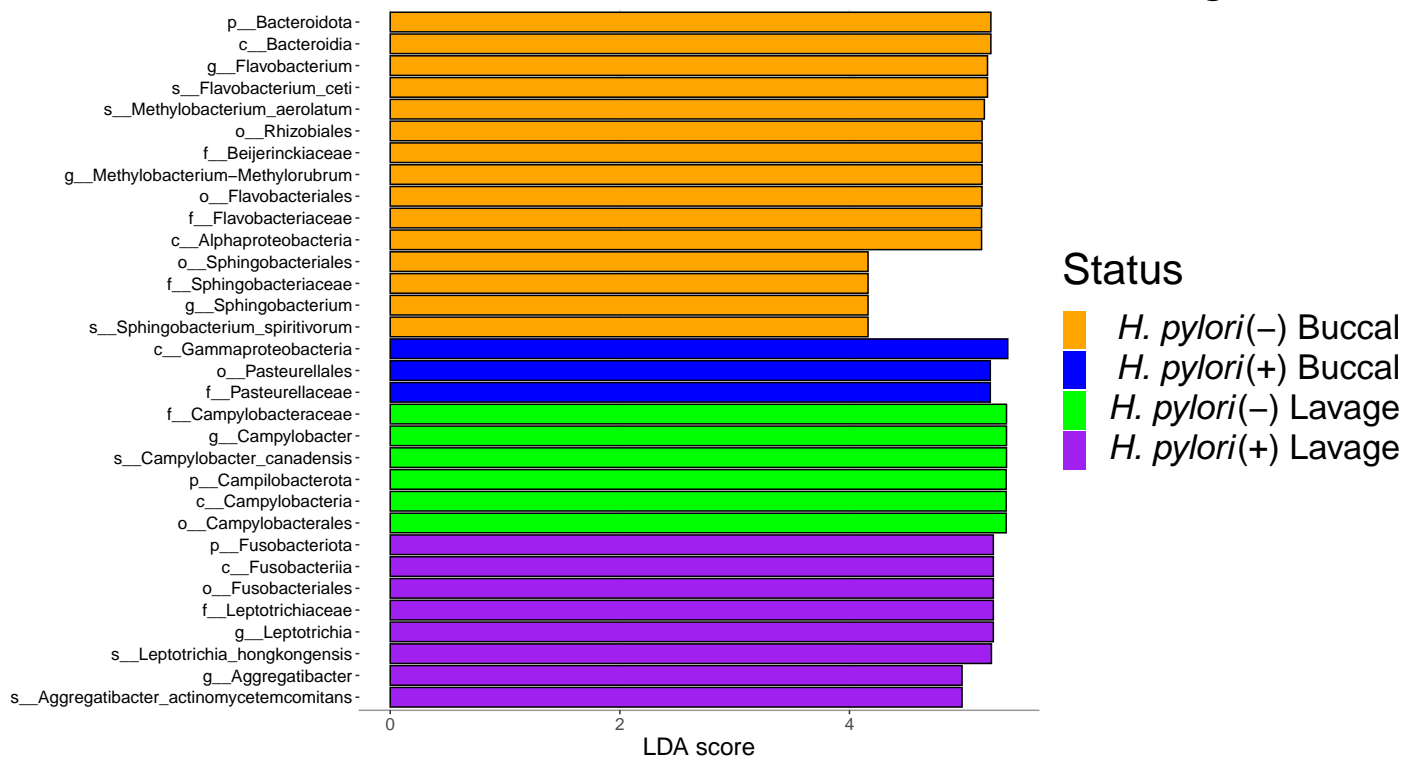
Lefse relative abundance from bronchoalveolar lavage

Lefse and differential abundance for bronchoalveolar lavage

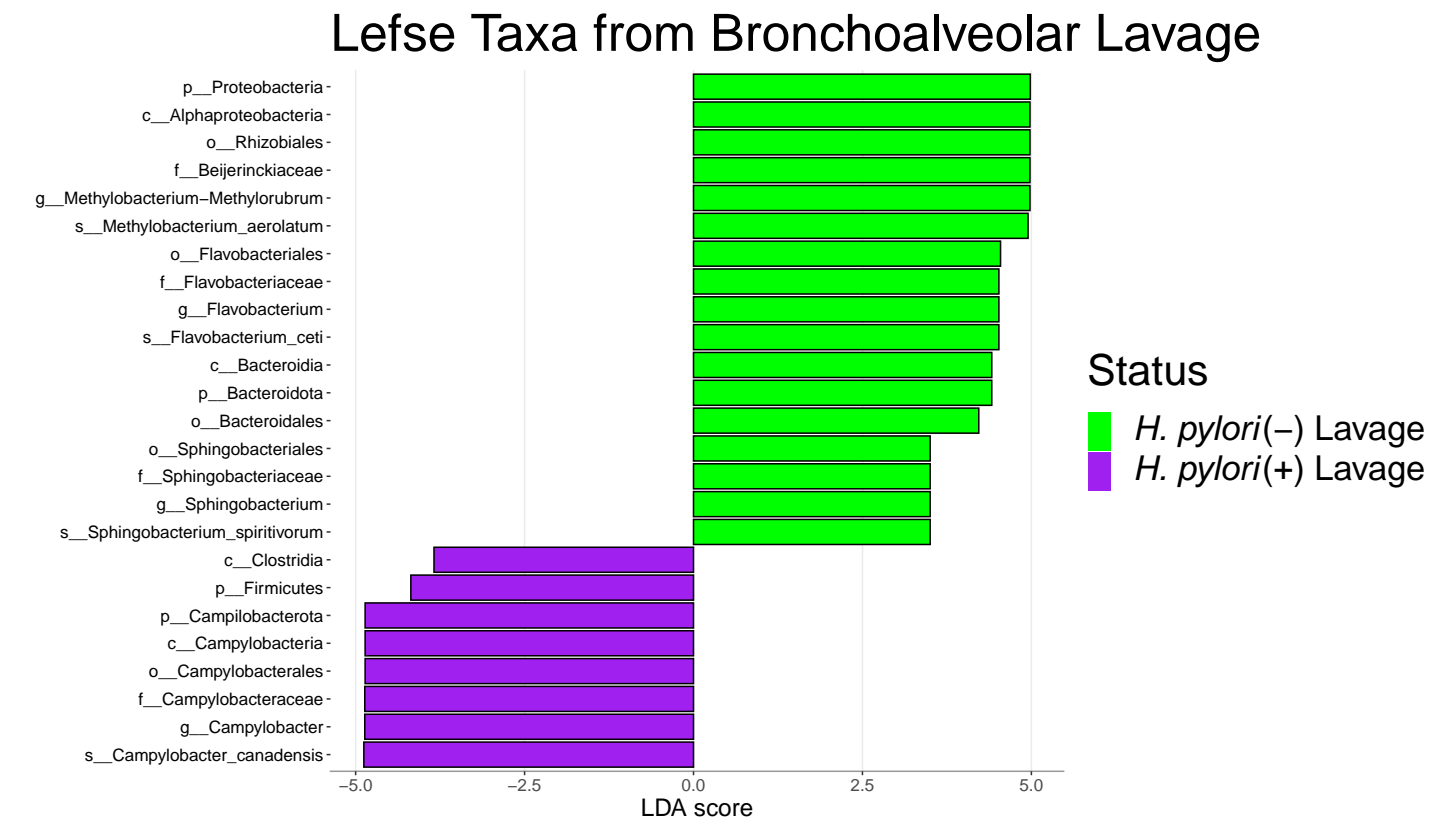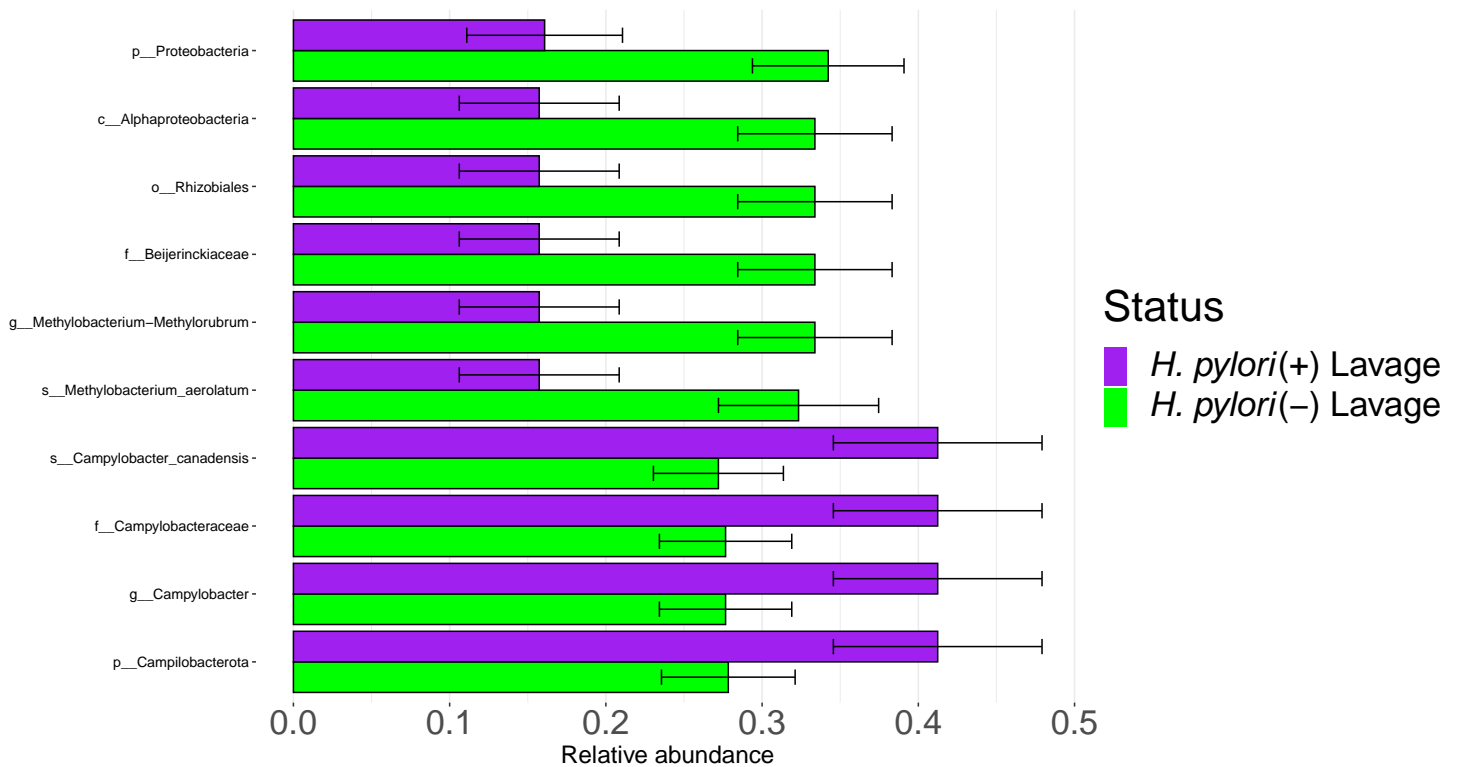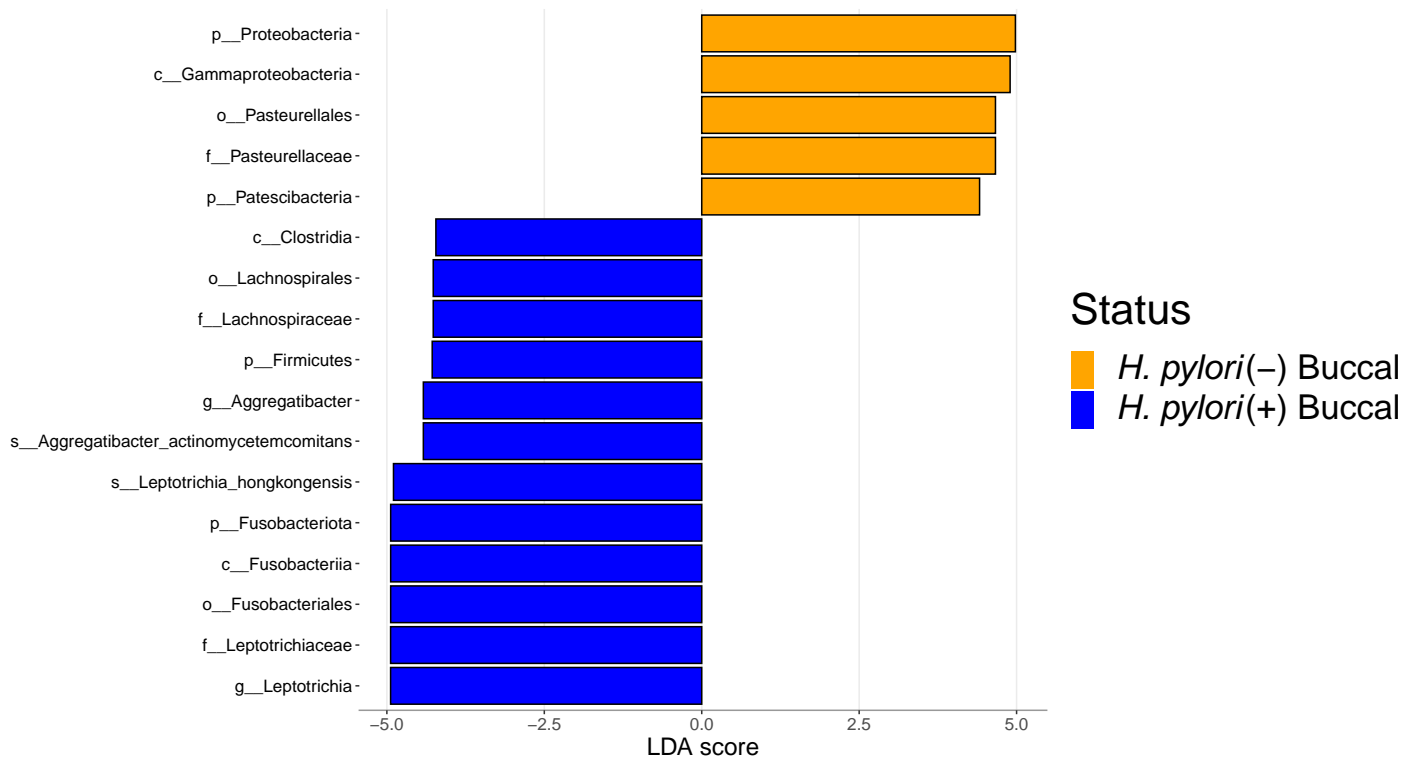# Lefse Taxa from Bronchoalveolar Lavage

Relative abundance of differential taxa

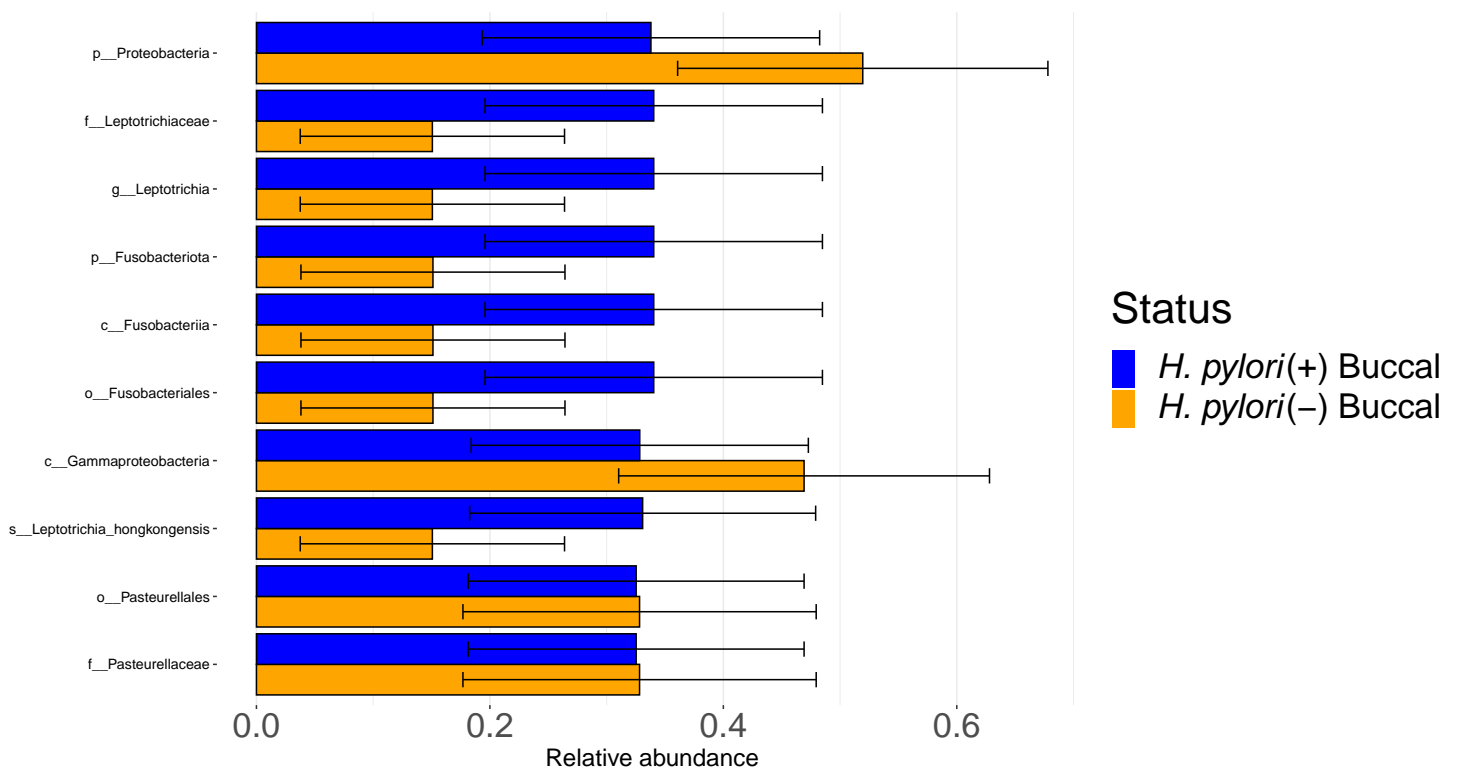## Lefse Relative Abundance from Bronchoalveolar Lav

Lefse and differential abundance for oral swabs

Lefse taxa from oral swabs

Relative abundance of differential taxa

Lefse relative abundance from oral swabs

Status

- ■ *H. pylori*(+) Buccal
- ■ *H. pylori*(−) Buccal
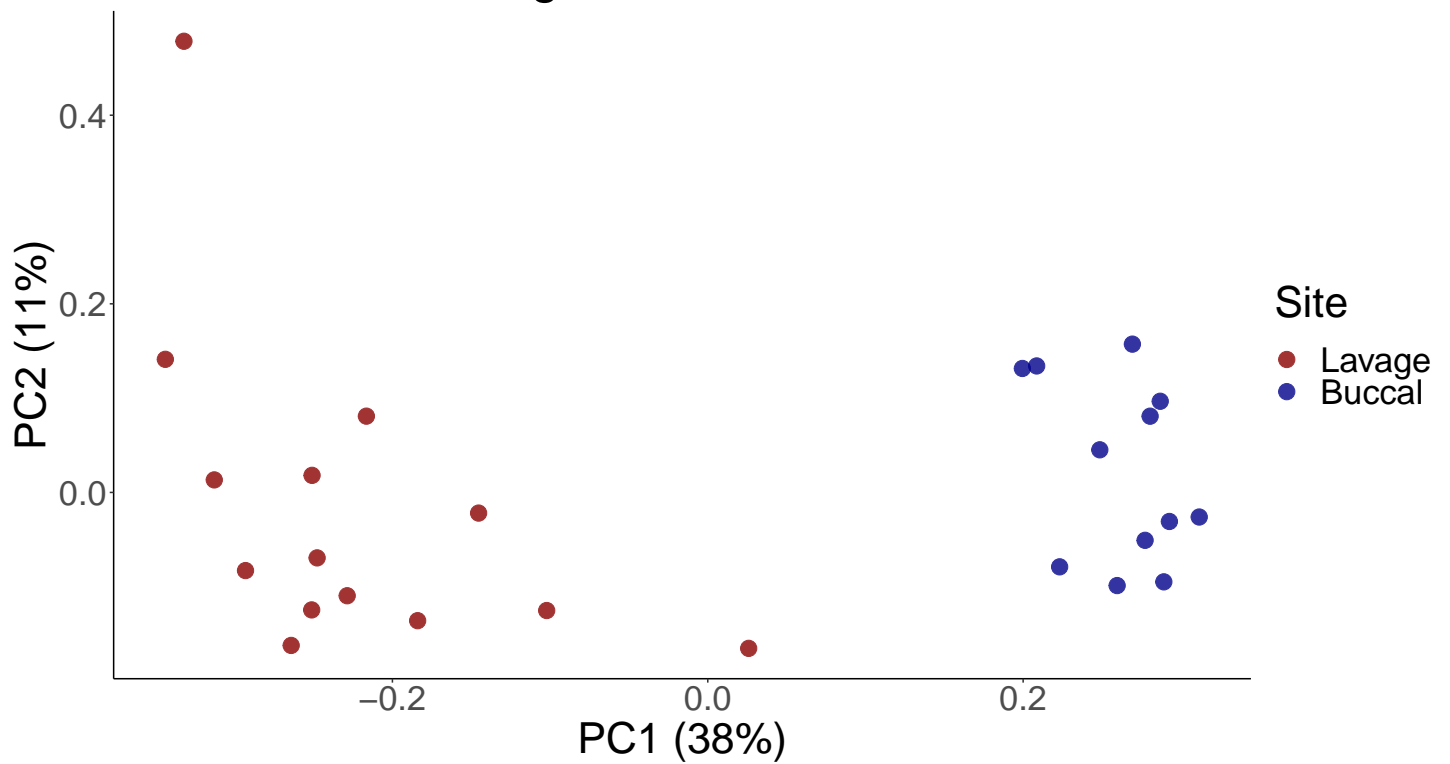
Beta diversity

**Unweighted unifrac 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
```
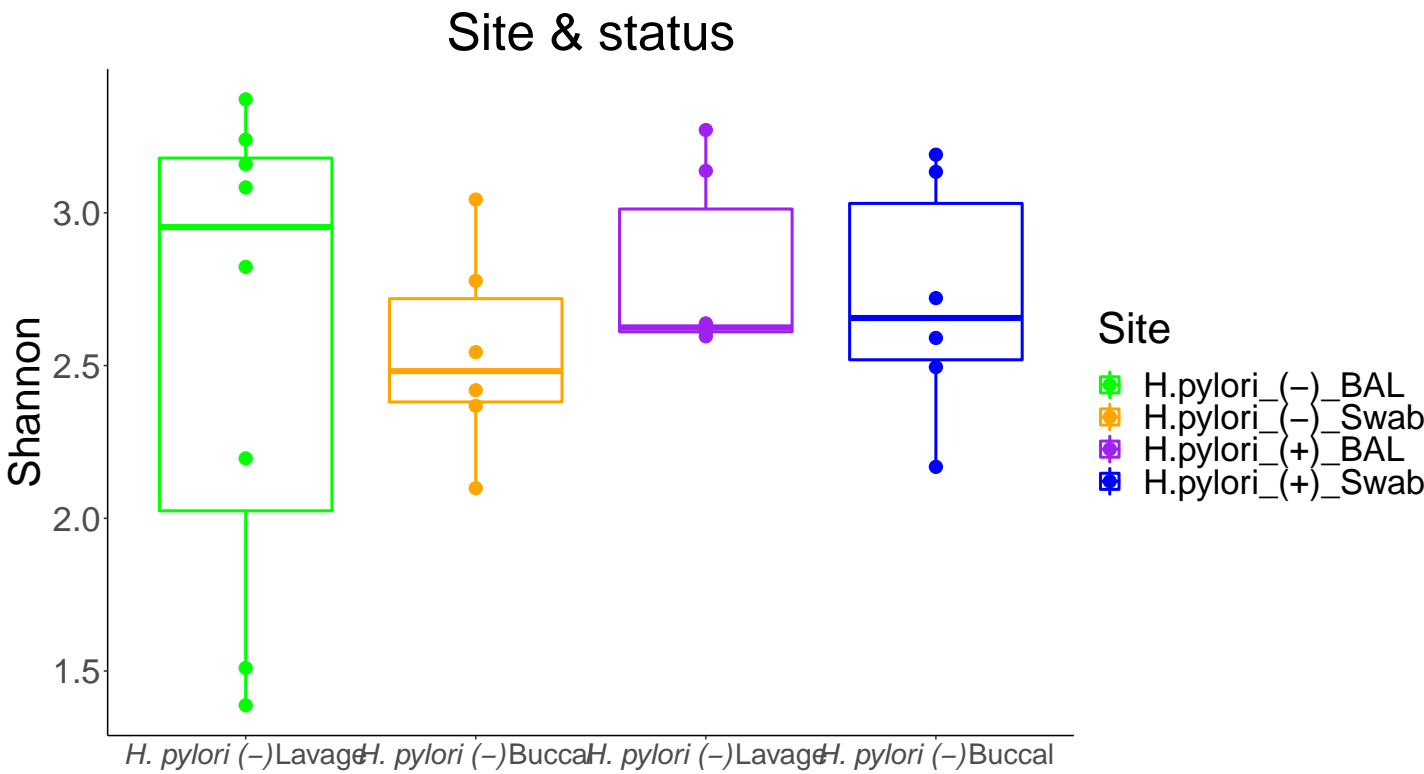
Unweighted unifrac PCoA

Status Unweighted unifrac PCoA

Beta diversity

Bray-Curtis
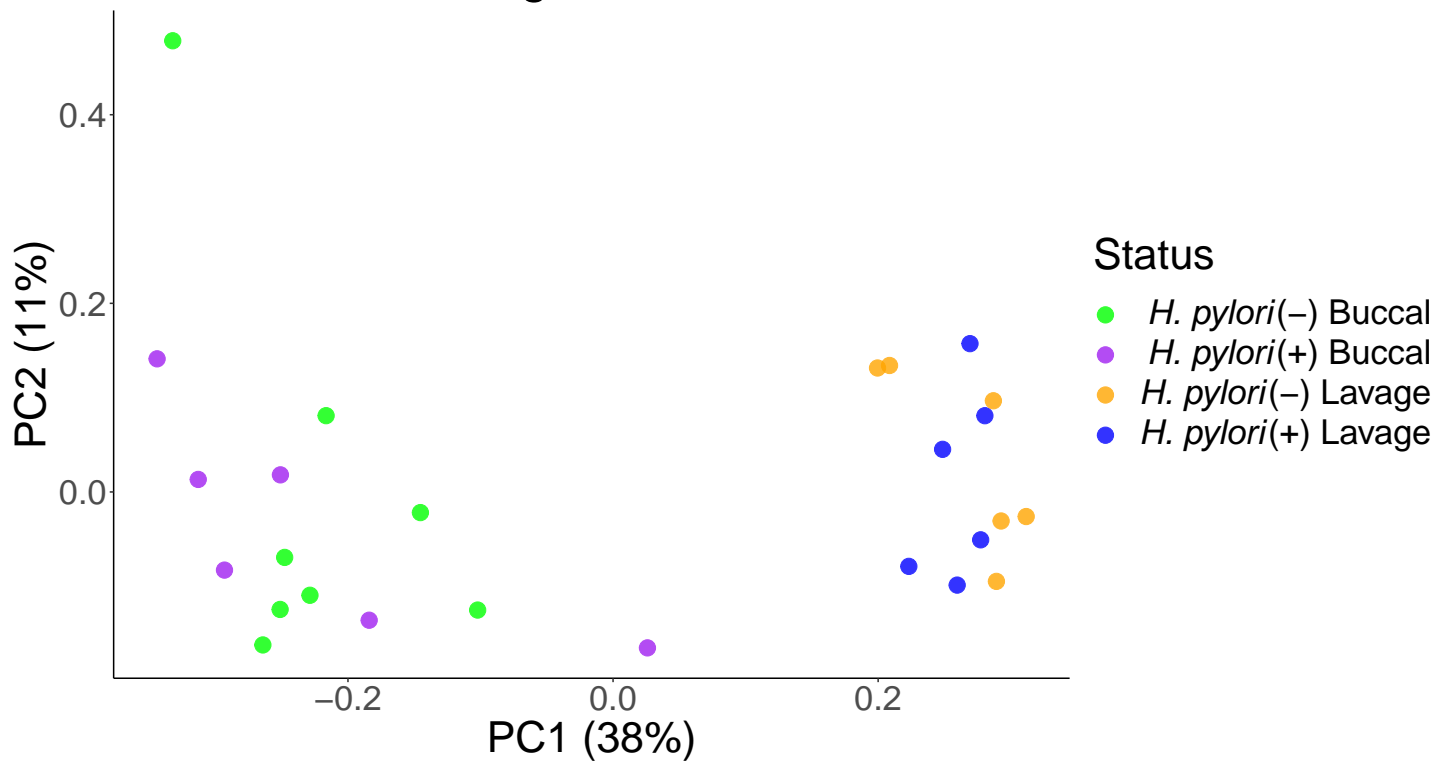
Alpha Diversity

Shannon index by site and H. pylori status

Site & status

Status
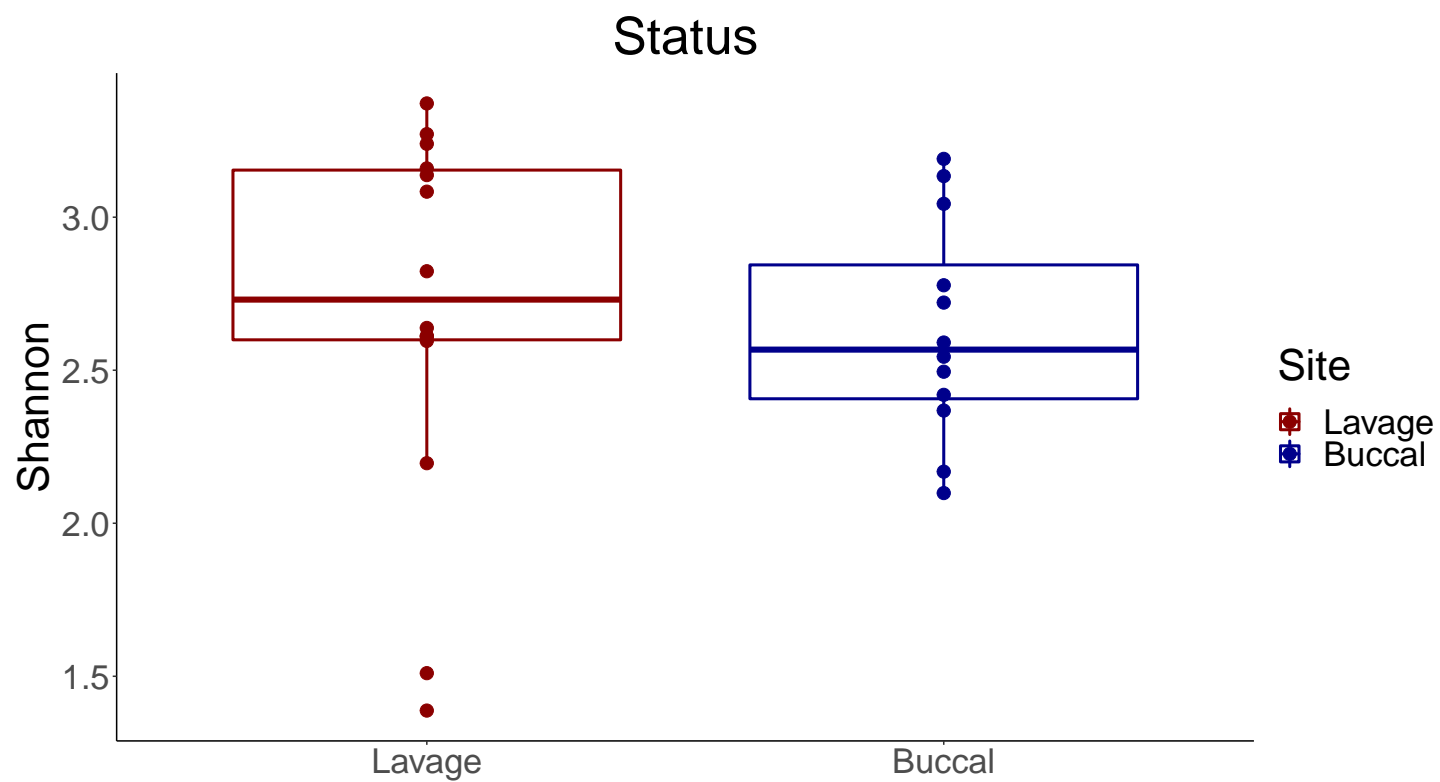
Table 2: All alpha diversity measurees

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

Helicobacter ASVs
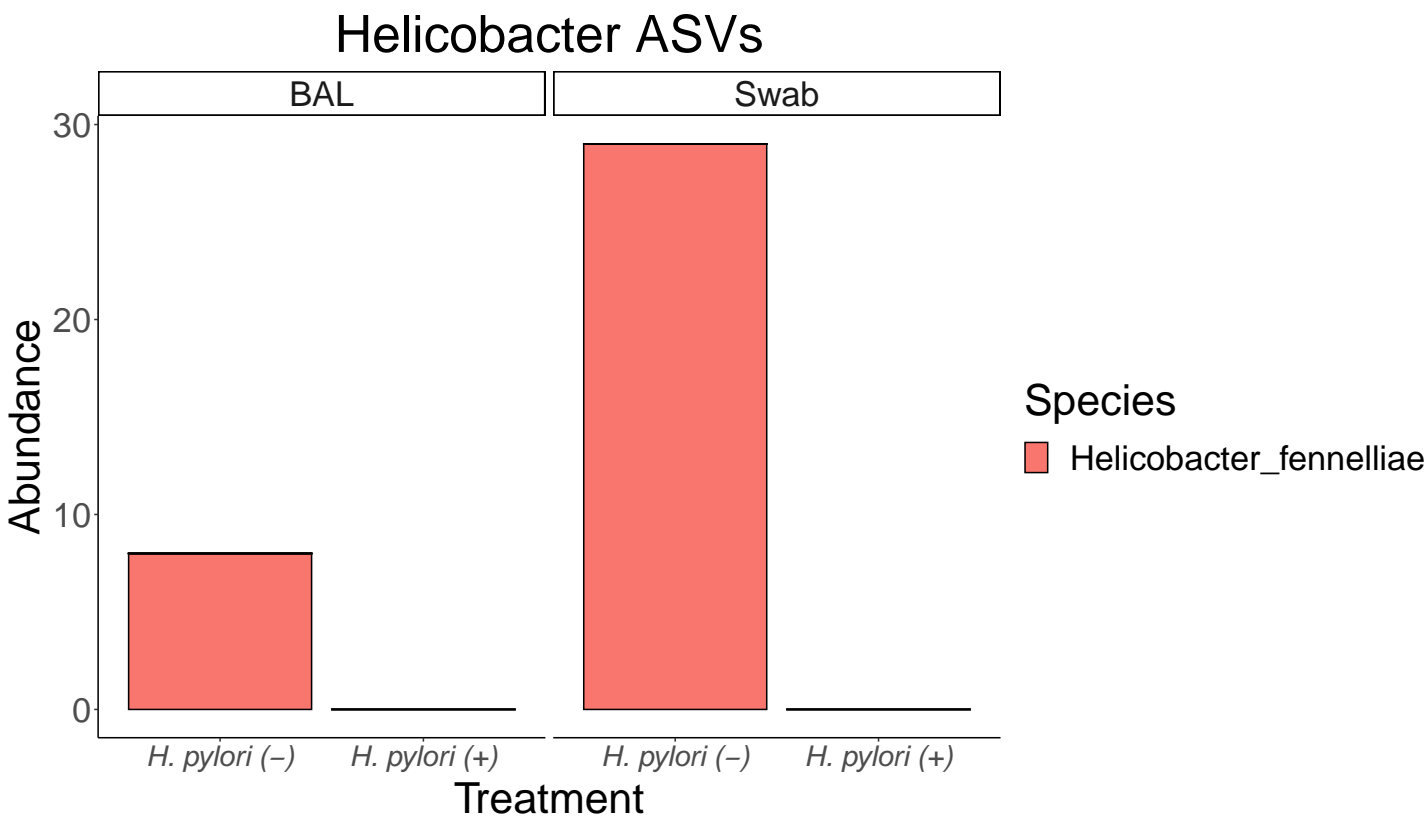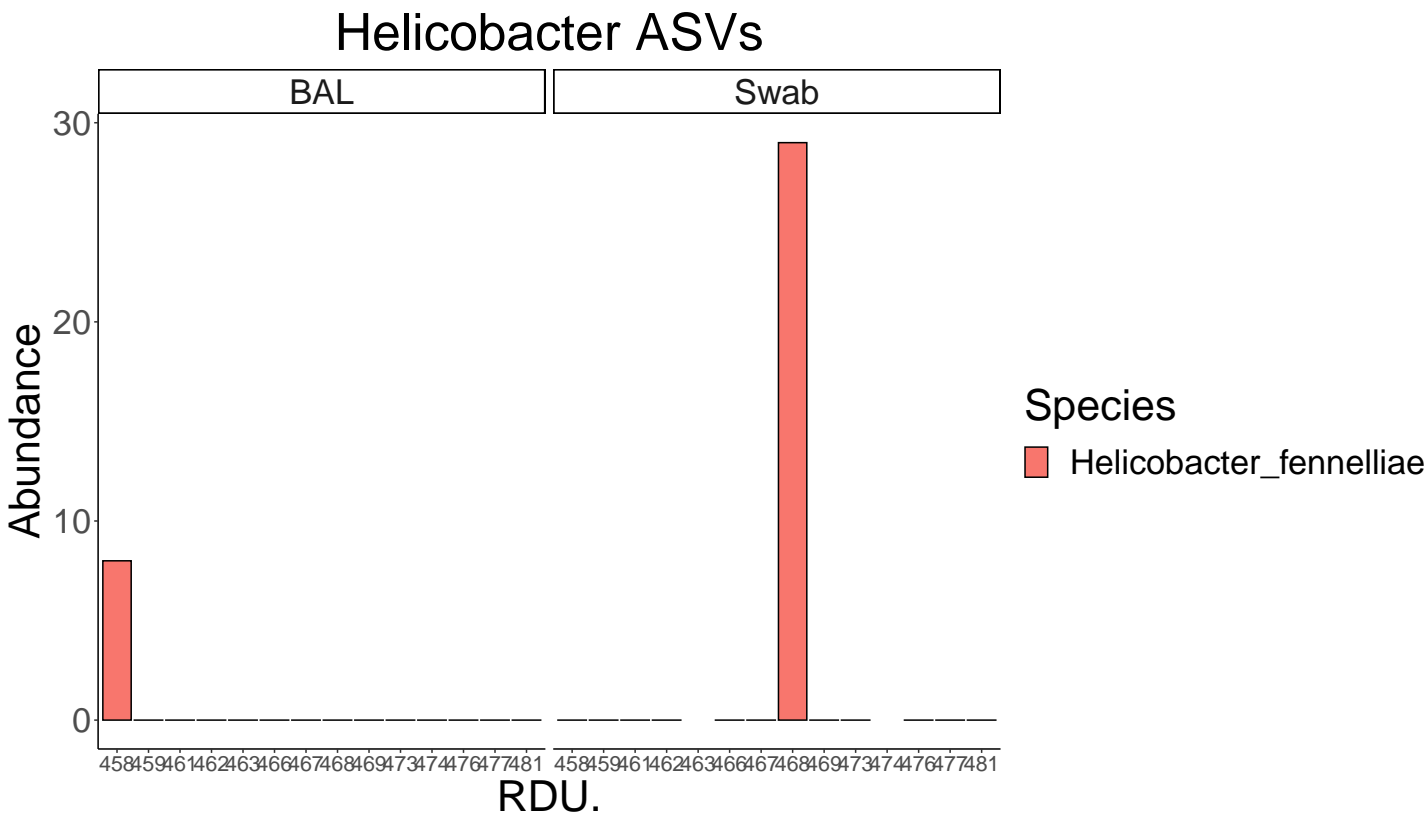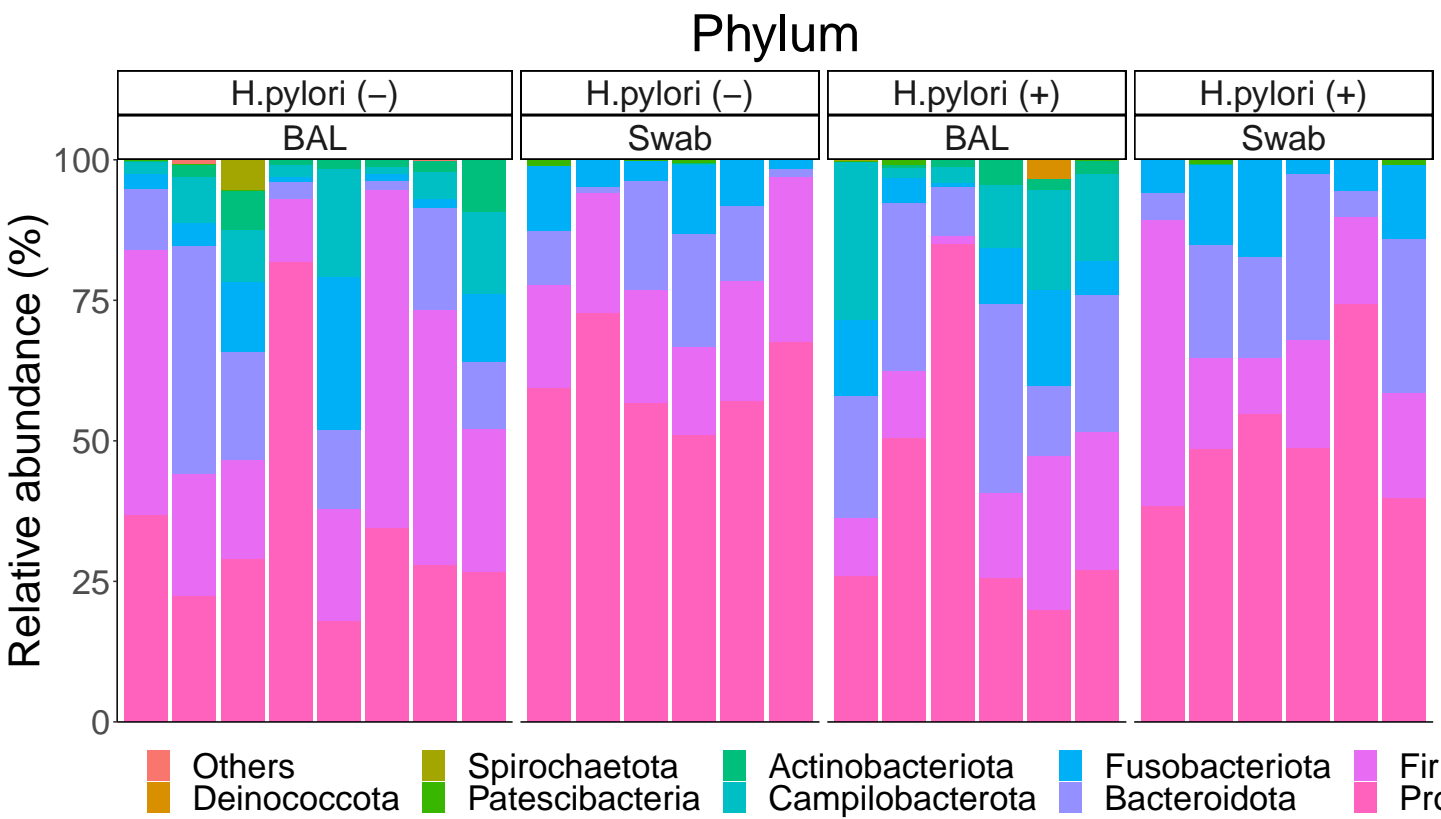
Taxa barplots

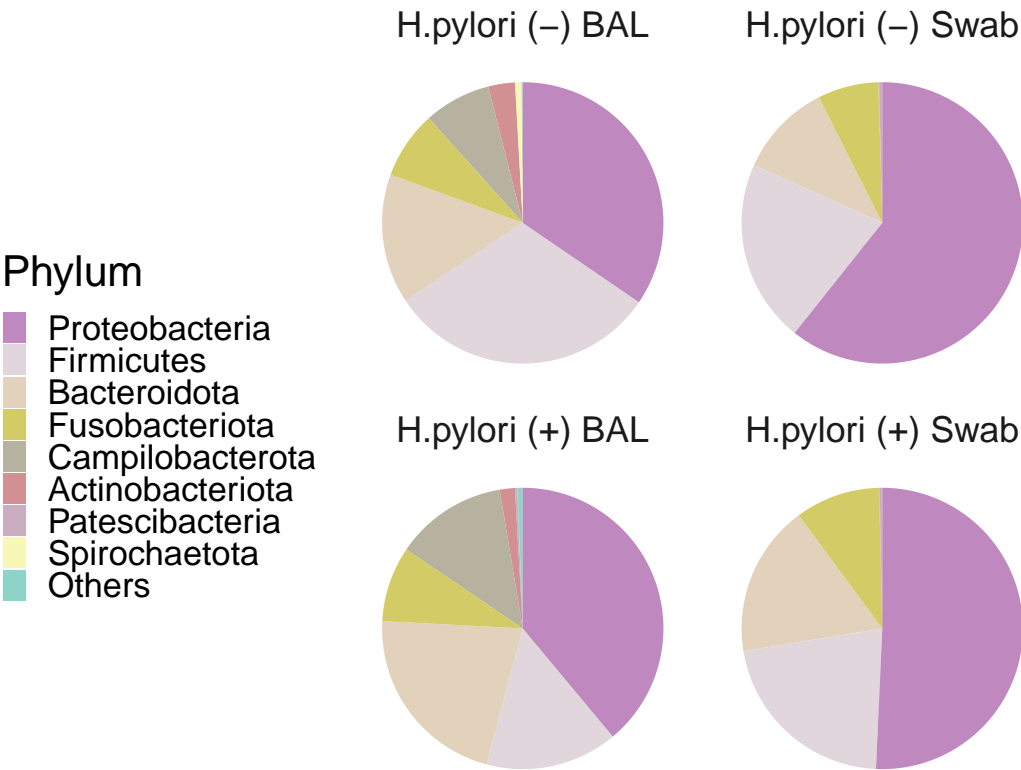**Figure 3:** Microbiota Composition at Phylum level.

Figure 4: Microbiota Composition at Phylum level.

Table 3: Phylum Average Relative Abundance

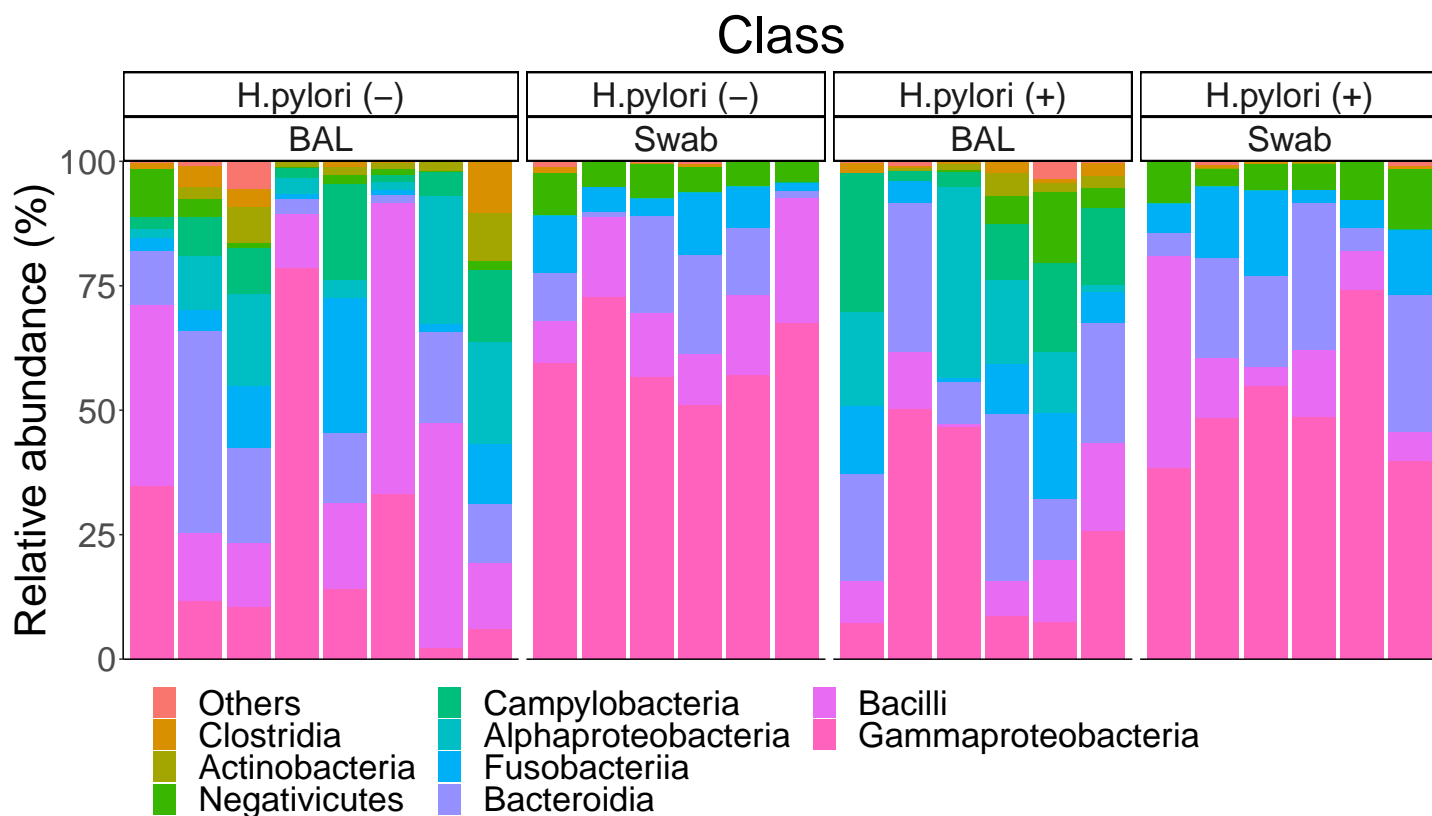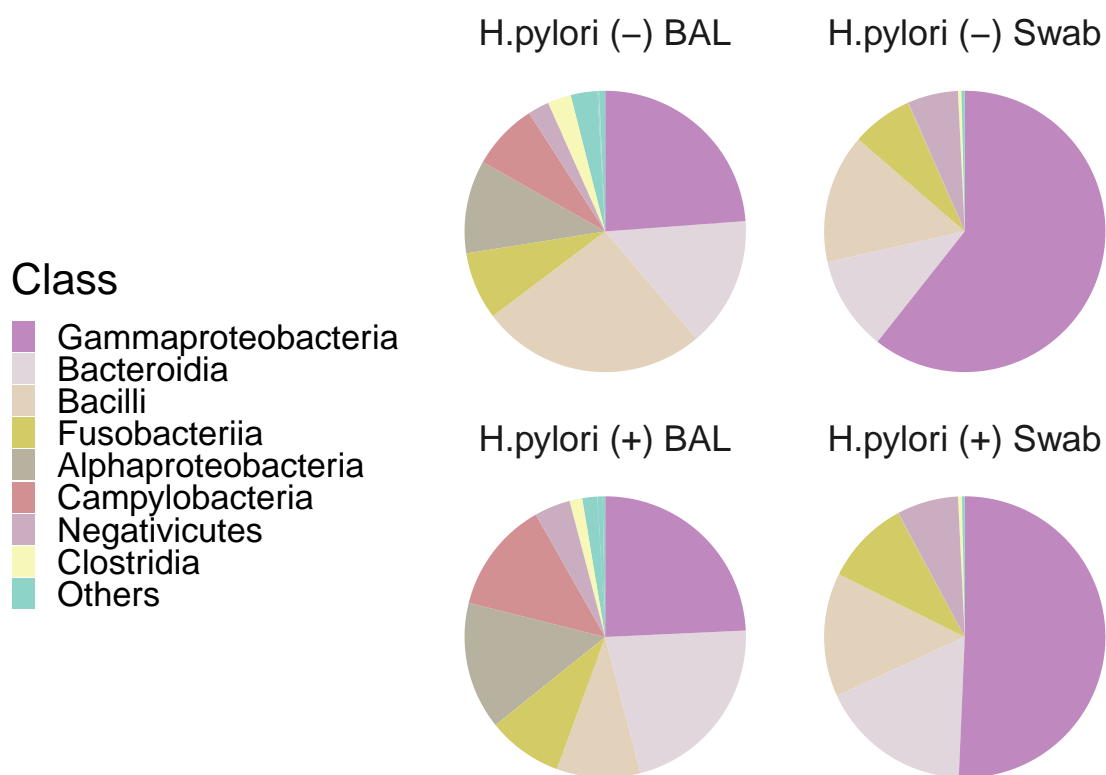| Taxonomy	Sample	Average Percent Abundance
Acidobacteriota	H.pylori (+) BAL	0.1%
Actinobacteriota	H.pylori (-) BAL	3.1%
Actinobacteriota	H.pylori (+) BAL	1.8%
Actinobacteriota	H.pylori (+) Swab	0.1%
Actinobacteriota	H.pylori (-) Swab	0%
Bacteroidota	H.pylori (+) BAL	21.7%
Bacteroidota	H.pylori (+) Swab	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

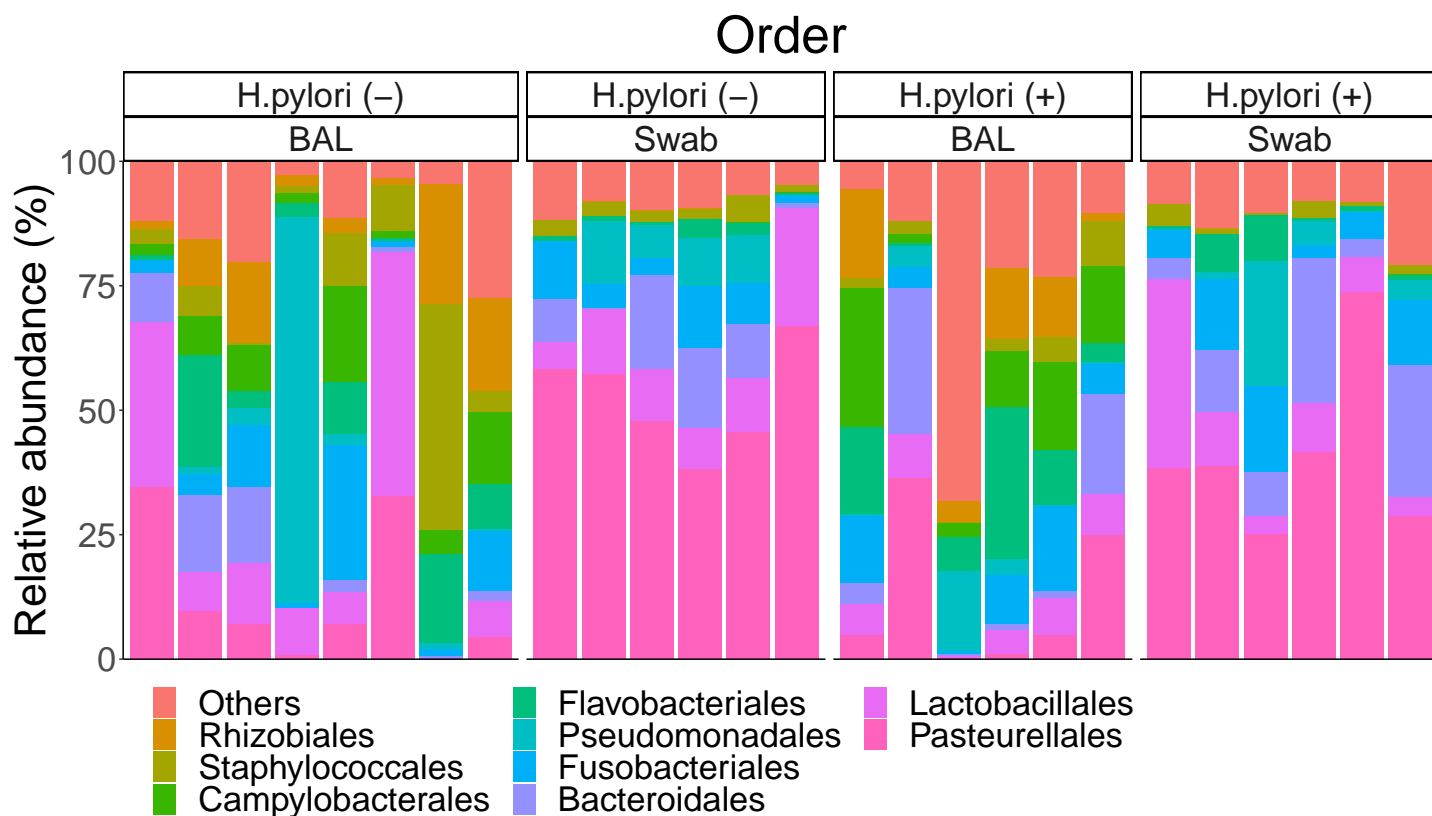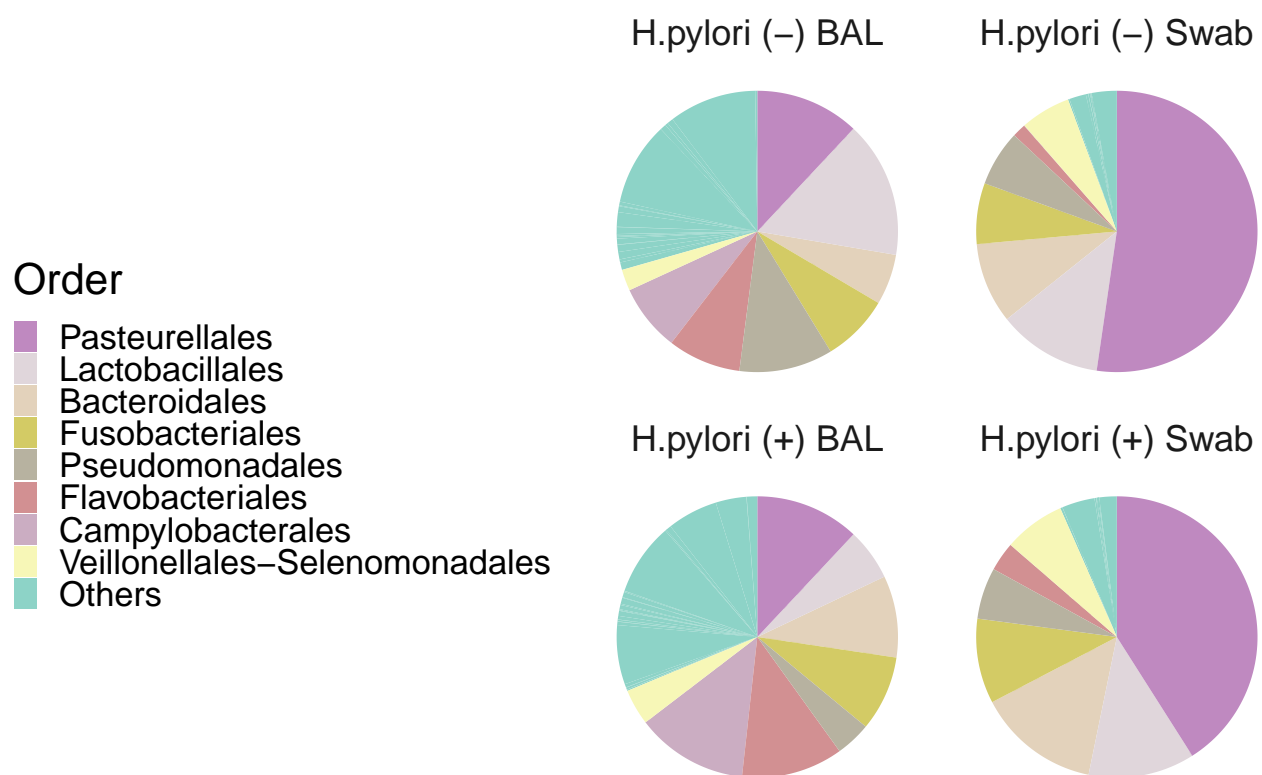| Taxonomy	Sample	Average Percent Abundance
Actinobacteria	H.pylori (-) BAL	3.1%
Actinobacteria	H.pylori (+) BAL	1.7%
Alphaproteobacteria	H.pylori (+) BAL	14.7%
Alphaproteobacteria	H.pylori (-) BAL	10.7%
Bacilli	H.pylori (-) BAL	26%
Bacilli	H.pylori (-) Swab	14.9%
Bacilli	H.pylori (+) Swab	14.2%
Bacilli	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

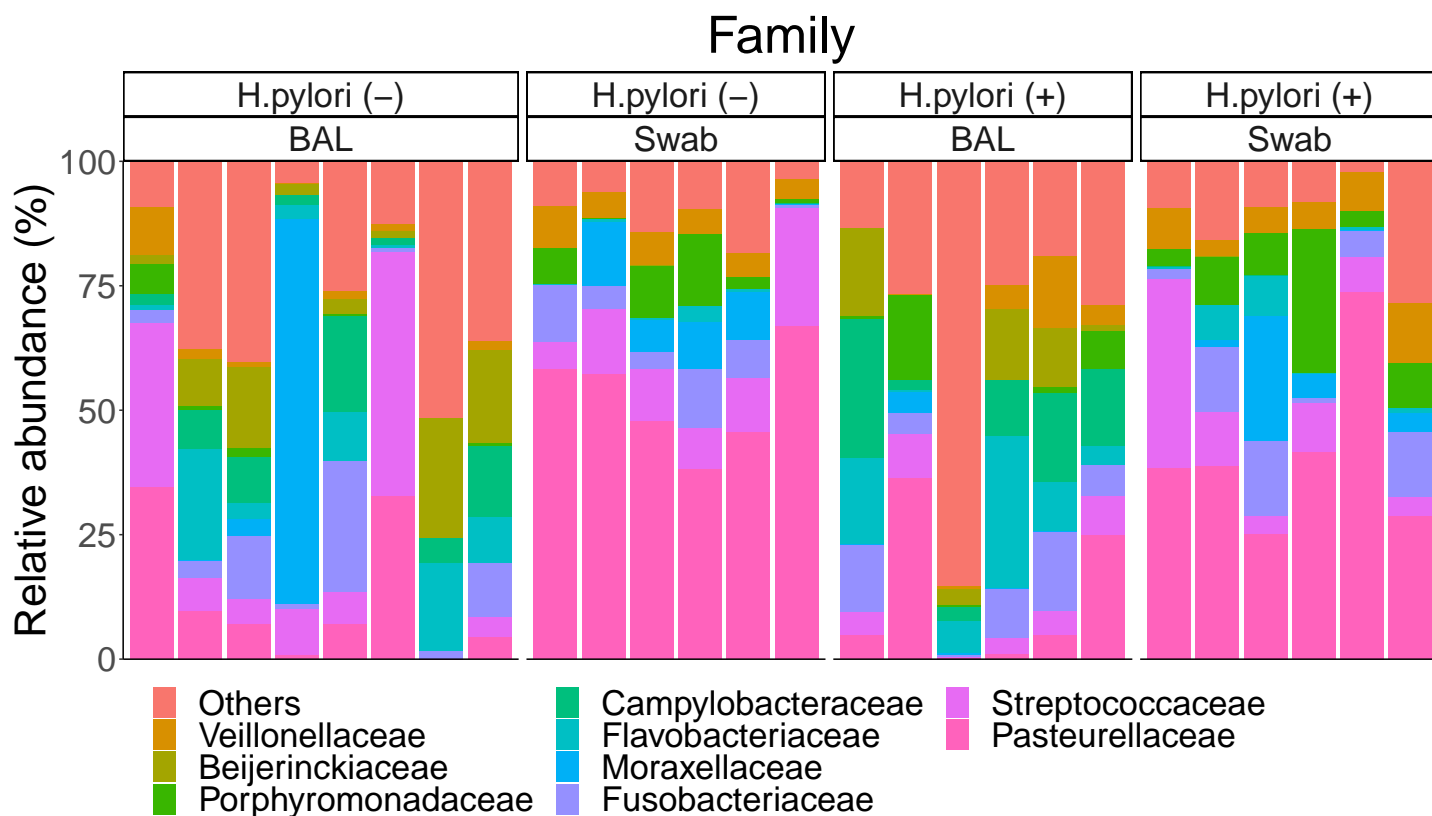| Taxonomy	Sample	Average Percent Abundance
Bacteroidales	H.pylori (+) Swab	14.1%
Bacteroidales	H.pylori (+) BAL	9.4%
Bacteroidales	H.pylori (-) Swab	9.3%
Bacteroidales	H.pylori (-) BAL	5.8%
Burkholderiales	H.pylori (+) BAL	6.8%
Campylobacterales	H.pylori (+) BAL	12.9%
Campylobacterales	H.pylori (-) 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%

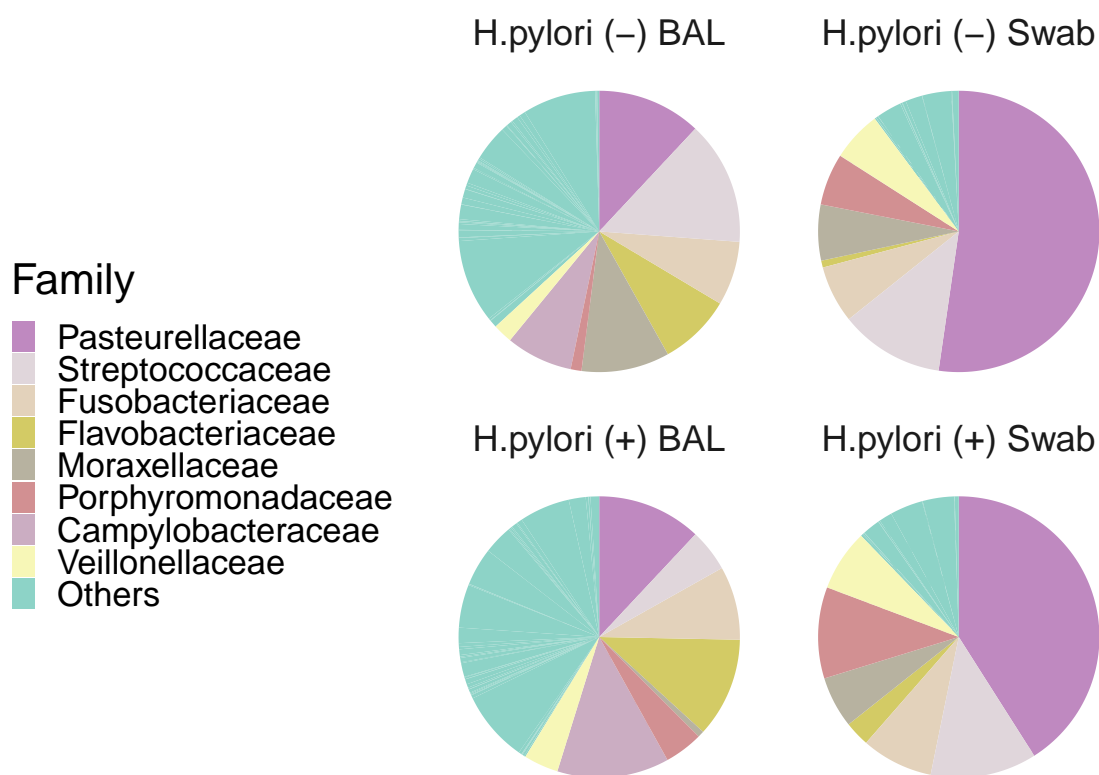**Figure 9:** Microbiota Composition at Family level.

Figure 10: Microbiota Composition at Family level.

Table 6: Family Average Relative Abundance

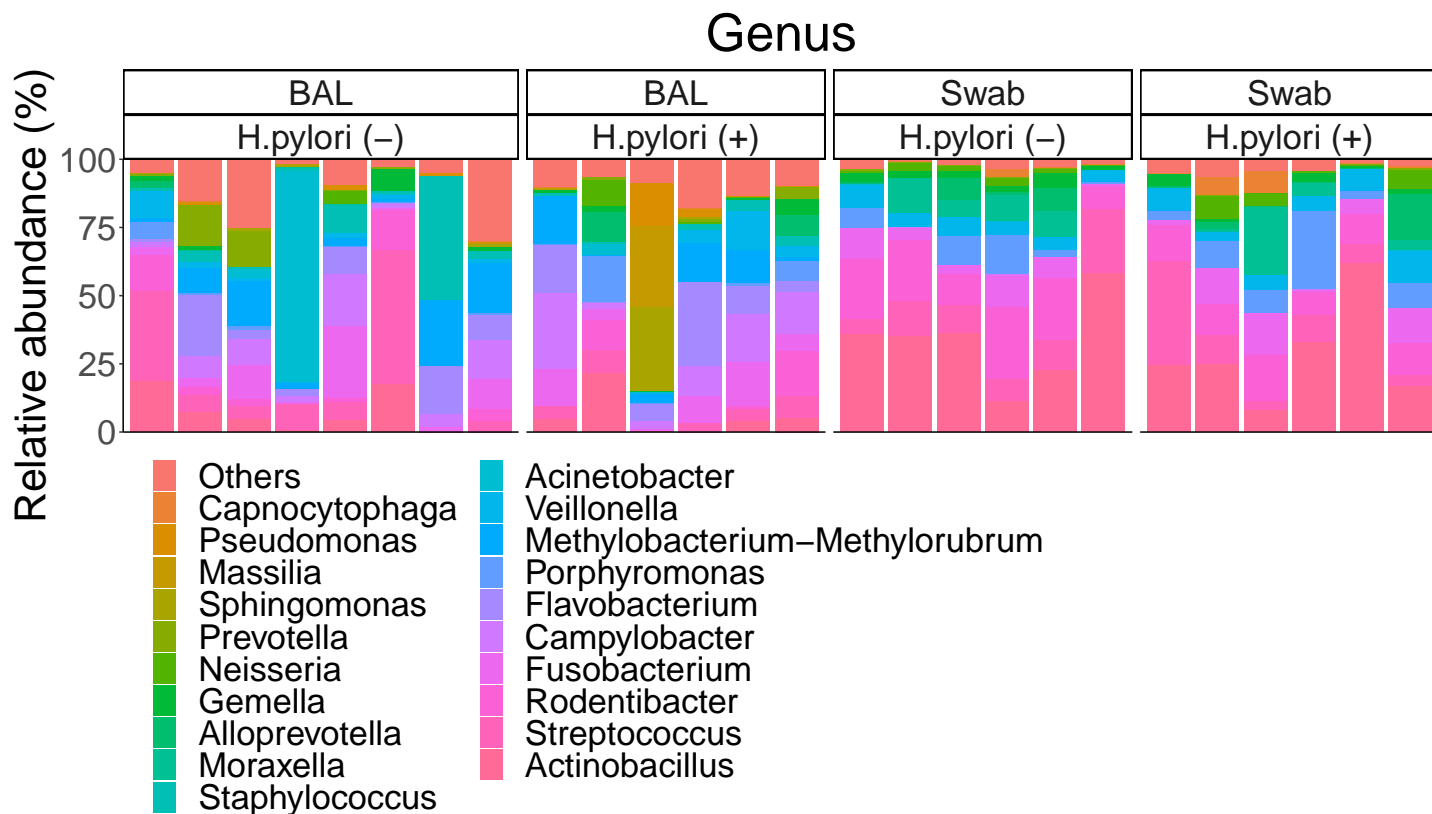| Taxonomy	Sample	Average Percent Abundance
Beijerinckiaceae	H.pylori (-) BAL	9.5%
Beijerinckiaceae	H.pylori (+) BAL	8.1%
Campylobacteraceae	H.pylori (+) BAL	12.9%
Campylobacteraceae	H.pylori (-) BAL	7.7%
Flavobacteriaceae	H.pylori (+) BAL	11.5%
Flavobacteriaceae	H.pylori (-) BAL	8.3%
Fusobacteriaceae	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%

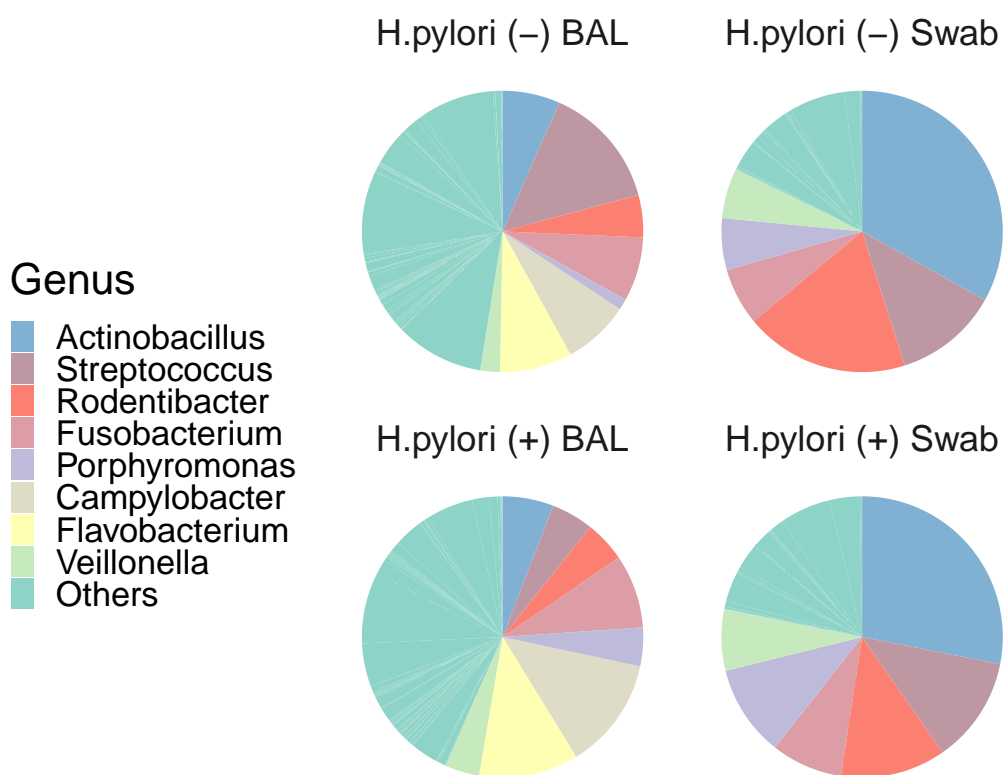**Figure 11:** Microbiota Composition at Genus level.

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-Methylorubrum	H.pylori (-) BAL	9.5%
Methylobacterium-Methylorubrum	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%

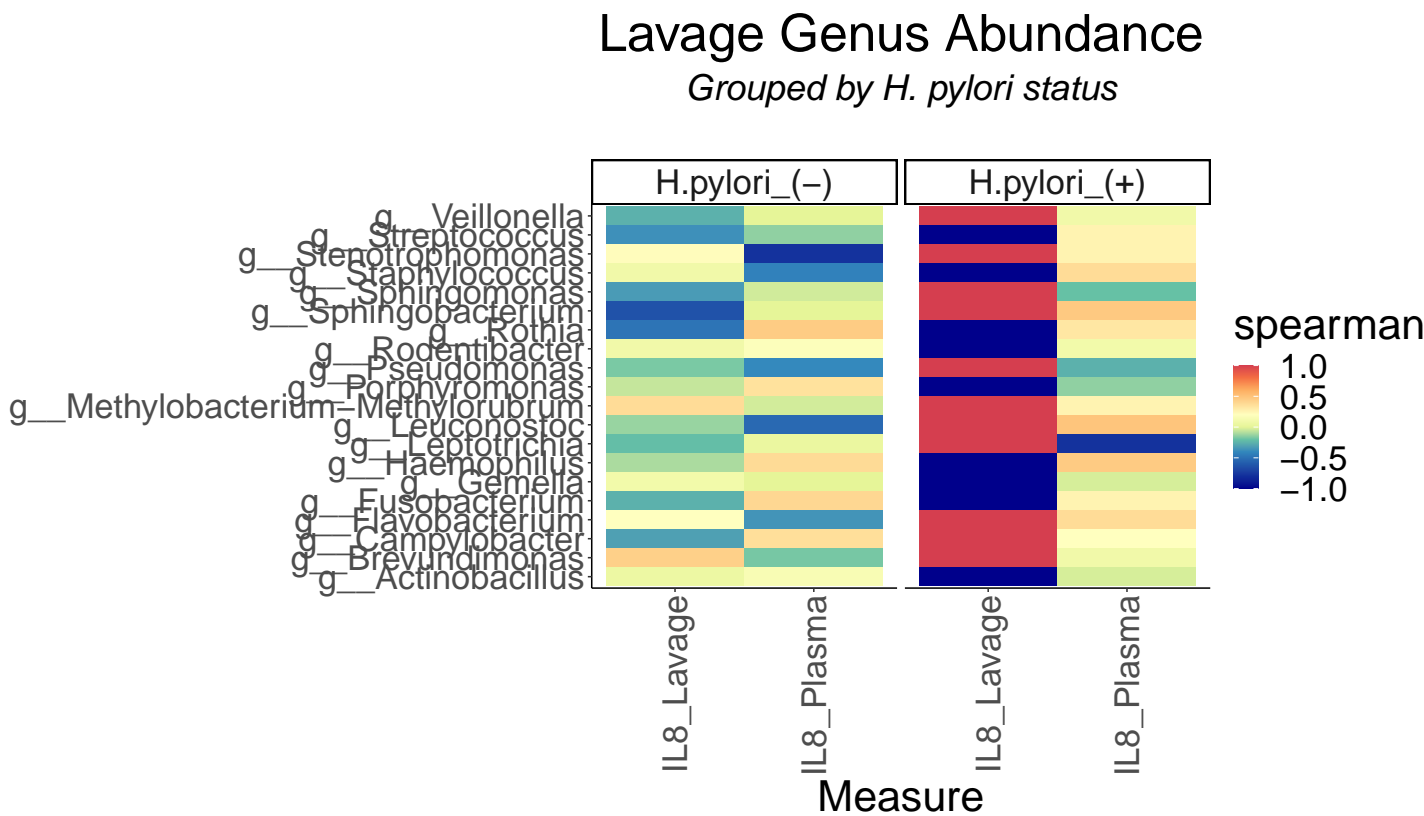# Genera correlation with Il8 concentration (Serum and BAL)

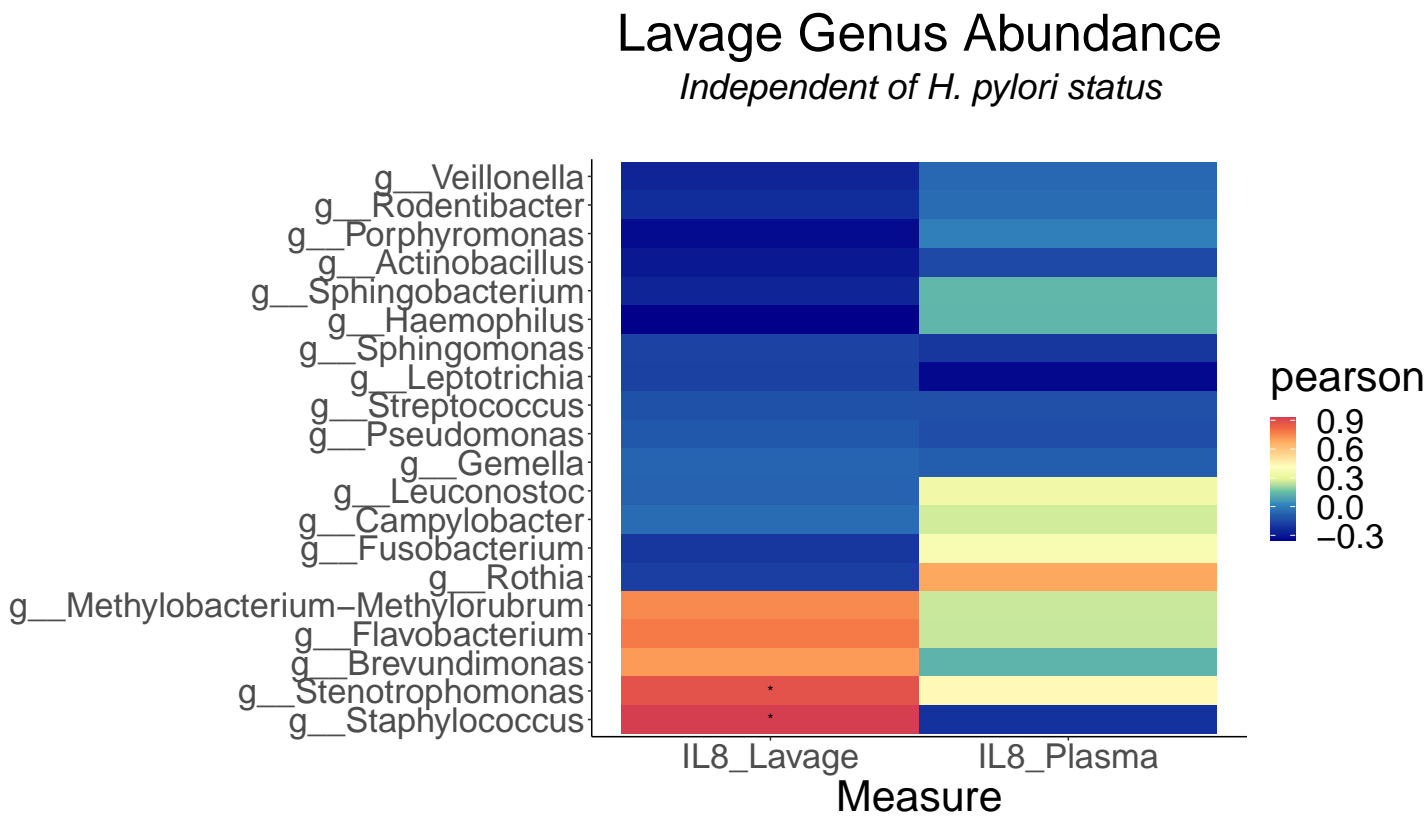**Figure 13:** IL8 and lavage genus abundance Spearman correlations separated by H. pylori status

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

Figure 15: IL8 and lavage alpha diversity Spearman correlations inpendent of H. pylori status.
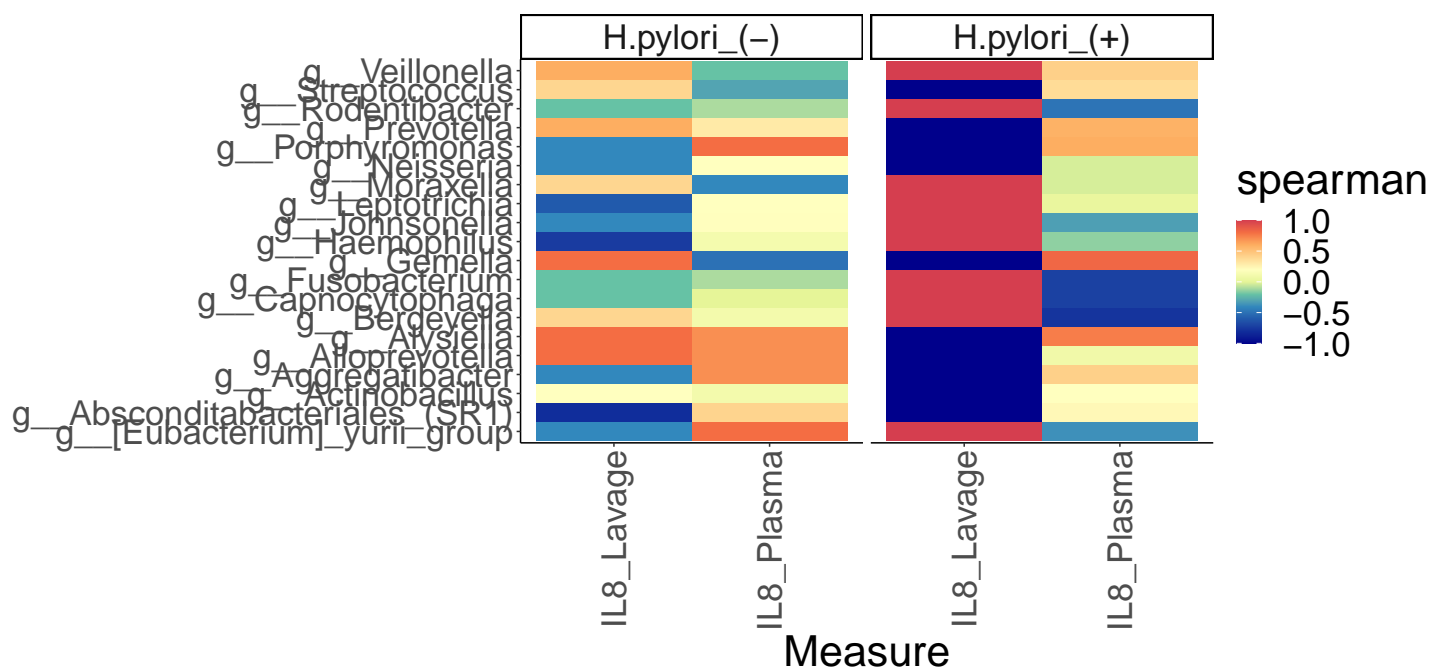
Figure 16: IL8 and Buccal genus abundance Spearman correlations separated by H. pylori status
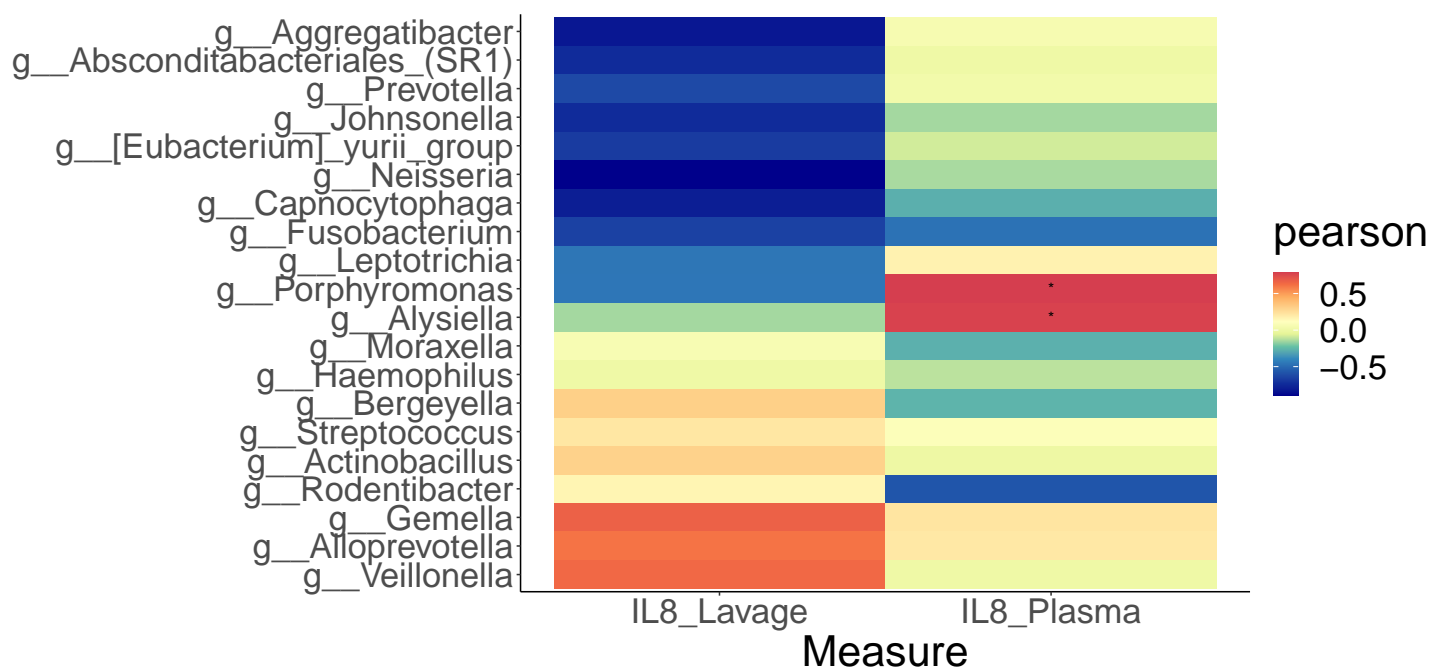
Figure 17: IL8 and Buccal genus abundance Spearman correlations independent of H. pylori status
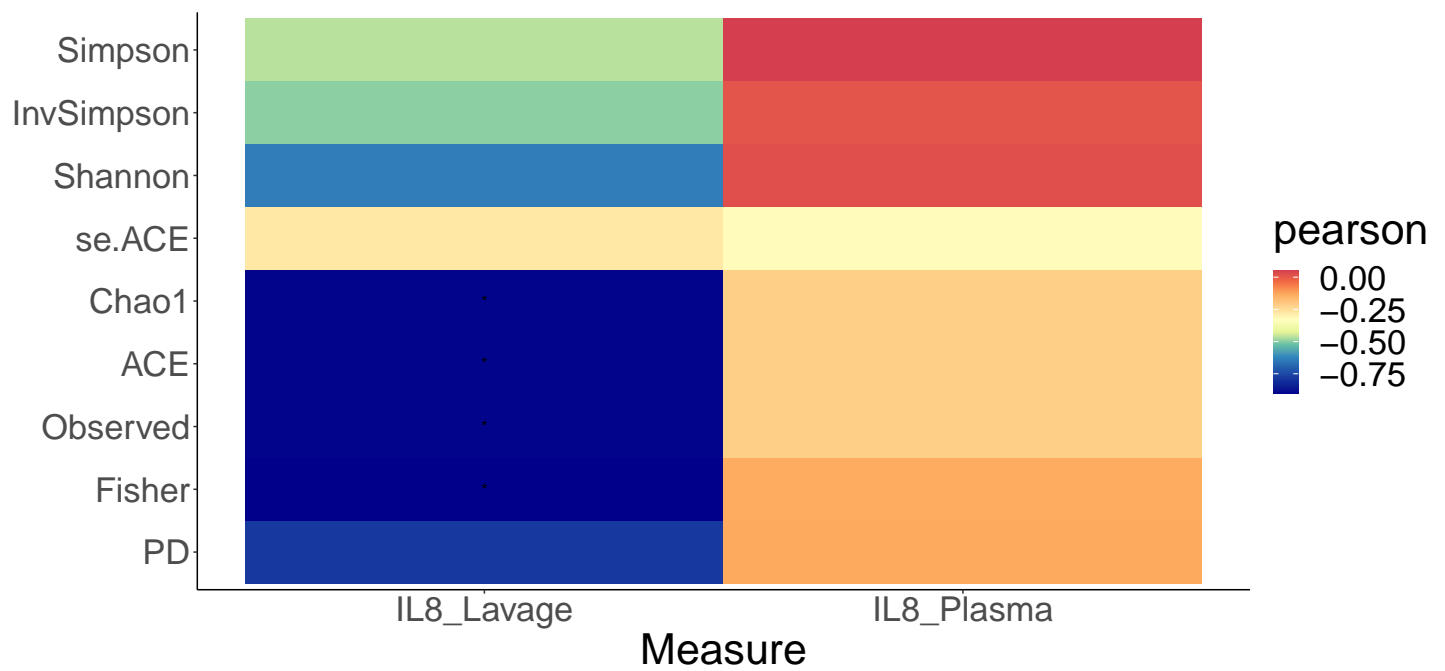
Figure 18: IL8 and Buccal alpha diversity Spearman correlations independent of H. pylori status

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/libopenblasp-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
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## [19] DESeq2_1.34.0          SummarizedExperiment_1.24.0
## [21] Biobase_2.54.0         MatrixGenerics_1.6.0
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## [25] GenomeInfoDb_1.30.0    IRanges_2.28.0
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## [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
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##  [37] deldir_1.0-6        vctrs_0.4.1         sjlabelled_1.2.0
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##  [46] svglite_2.1.0       cluster_2.1.3       ape_5.6-2
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##  [52] pkgconfig_2.0.3     zCompositions_1.4.0-1 labeling_0.4.2
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##  [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
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## [169] haven_2.5.0            reshape2_1.4.4         gtable_0.3.0
## [172] bayestestR_0.12.1
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