

# H.pylori Rhesus Microbiome Analysis

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## Data used in analysis

### Library

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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)  
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  library(questionr)  
  library(rmarkdown)  
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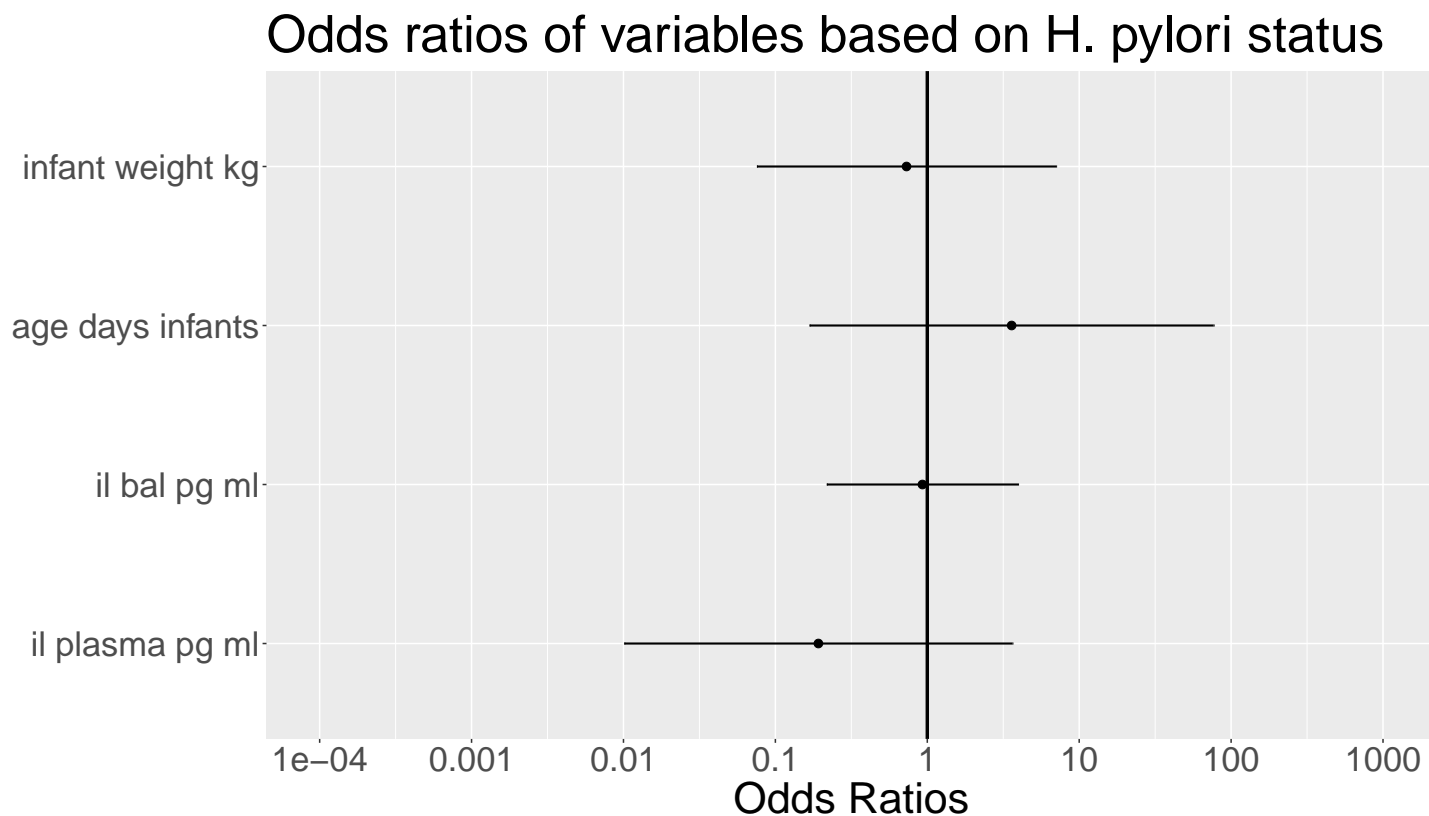
ASV counts the taxa table are linked below:

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

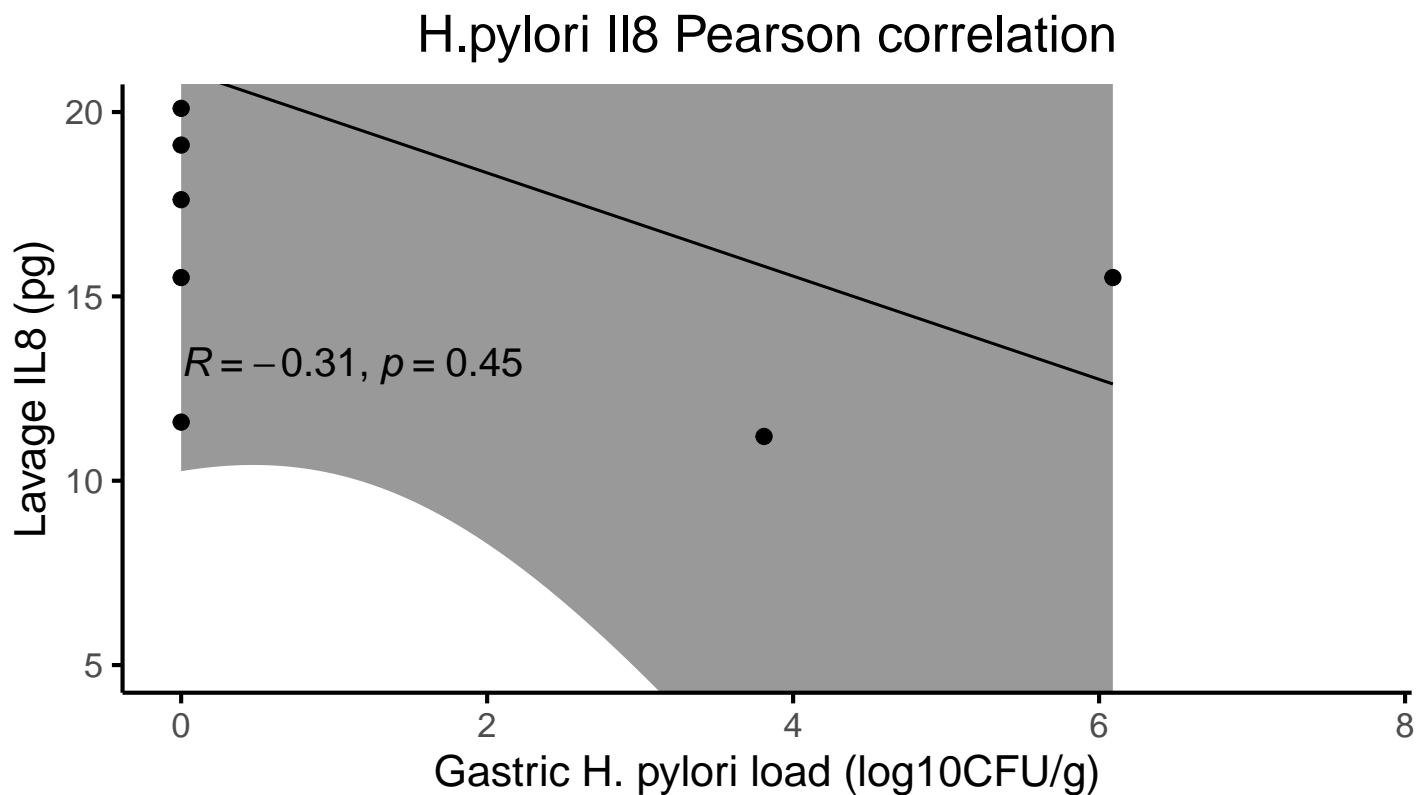


Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study

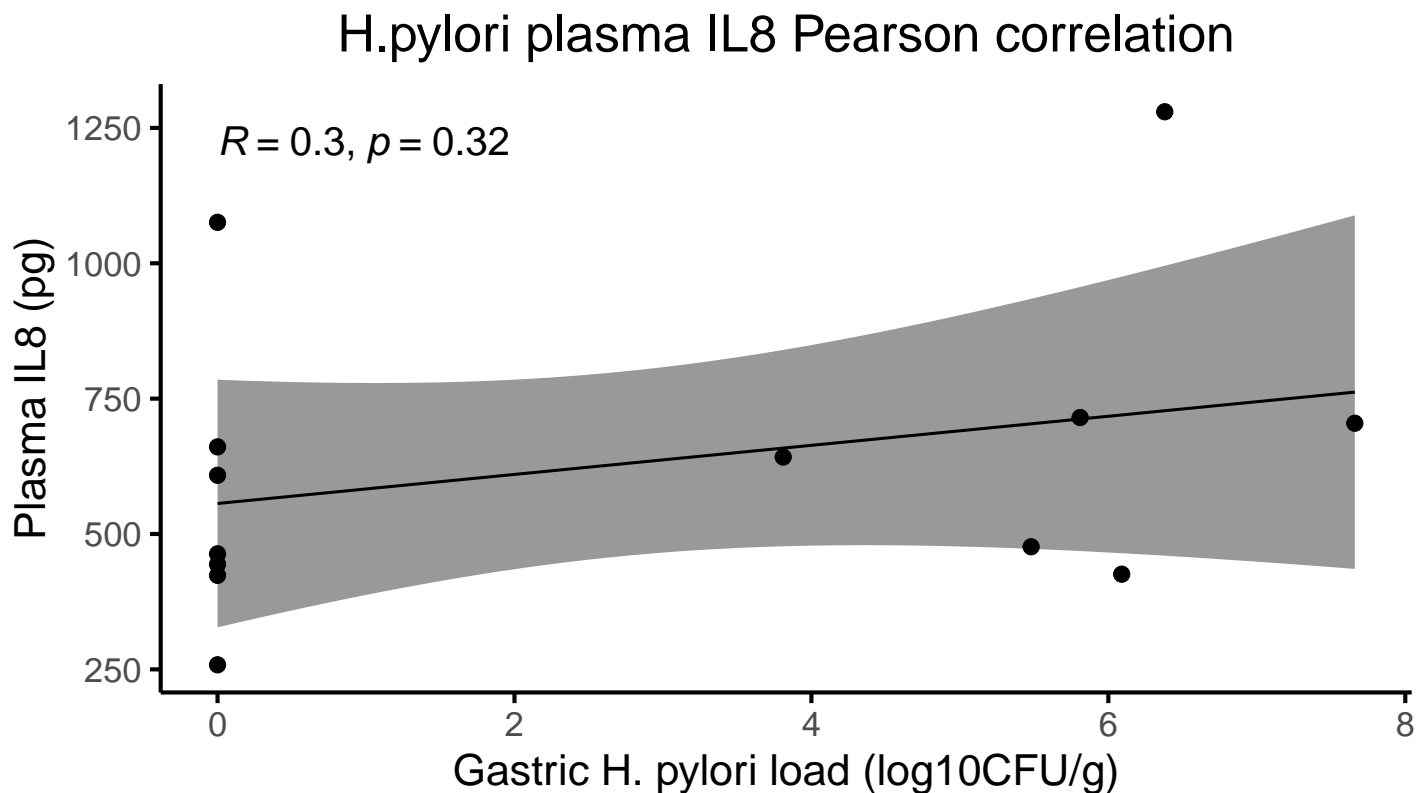
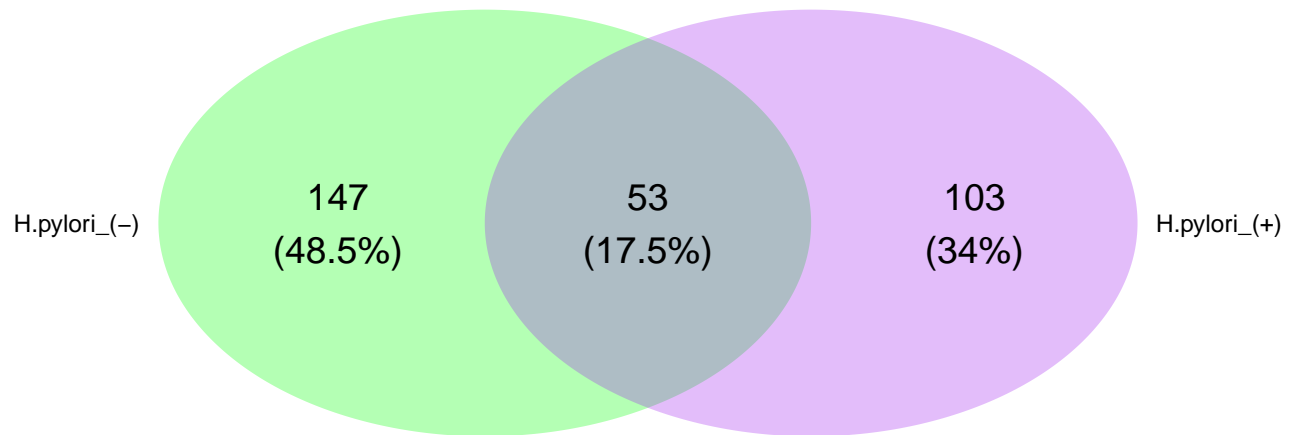


Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

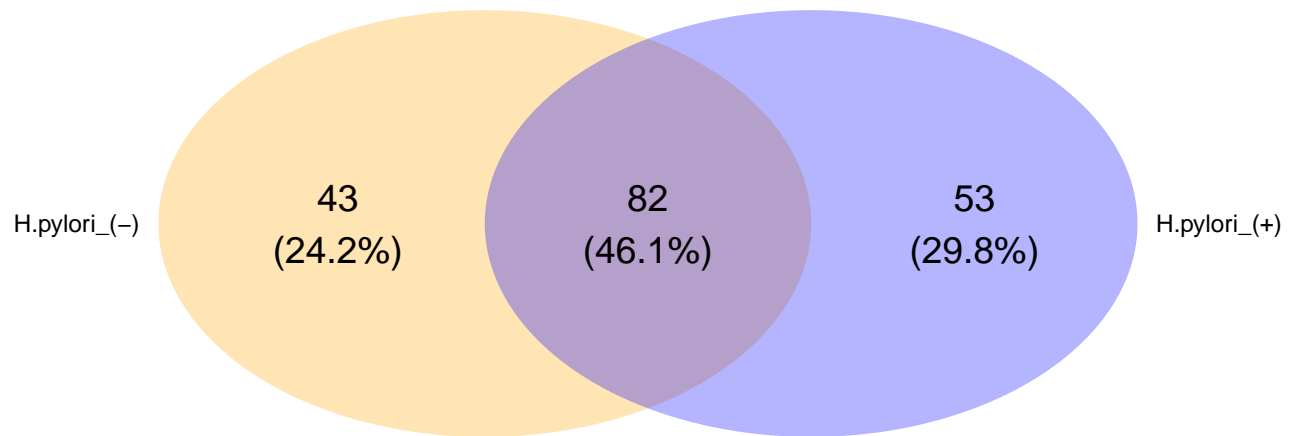
## Overlapping Taxa Between Sites and *H. pylori* Status

Lavage overlapping taxa

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

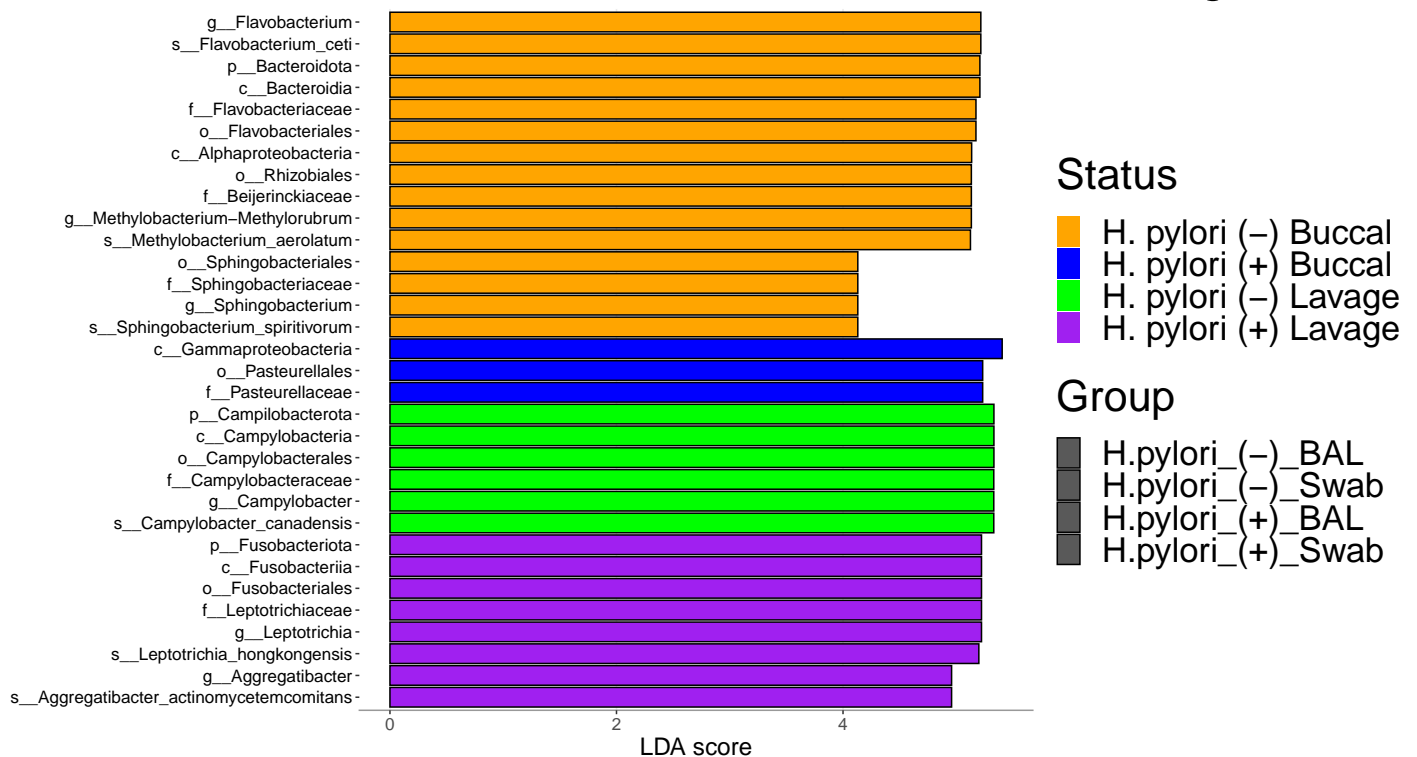


## Overlapping taxa between H. pylori (+) and (-) in buccal cavity

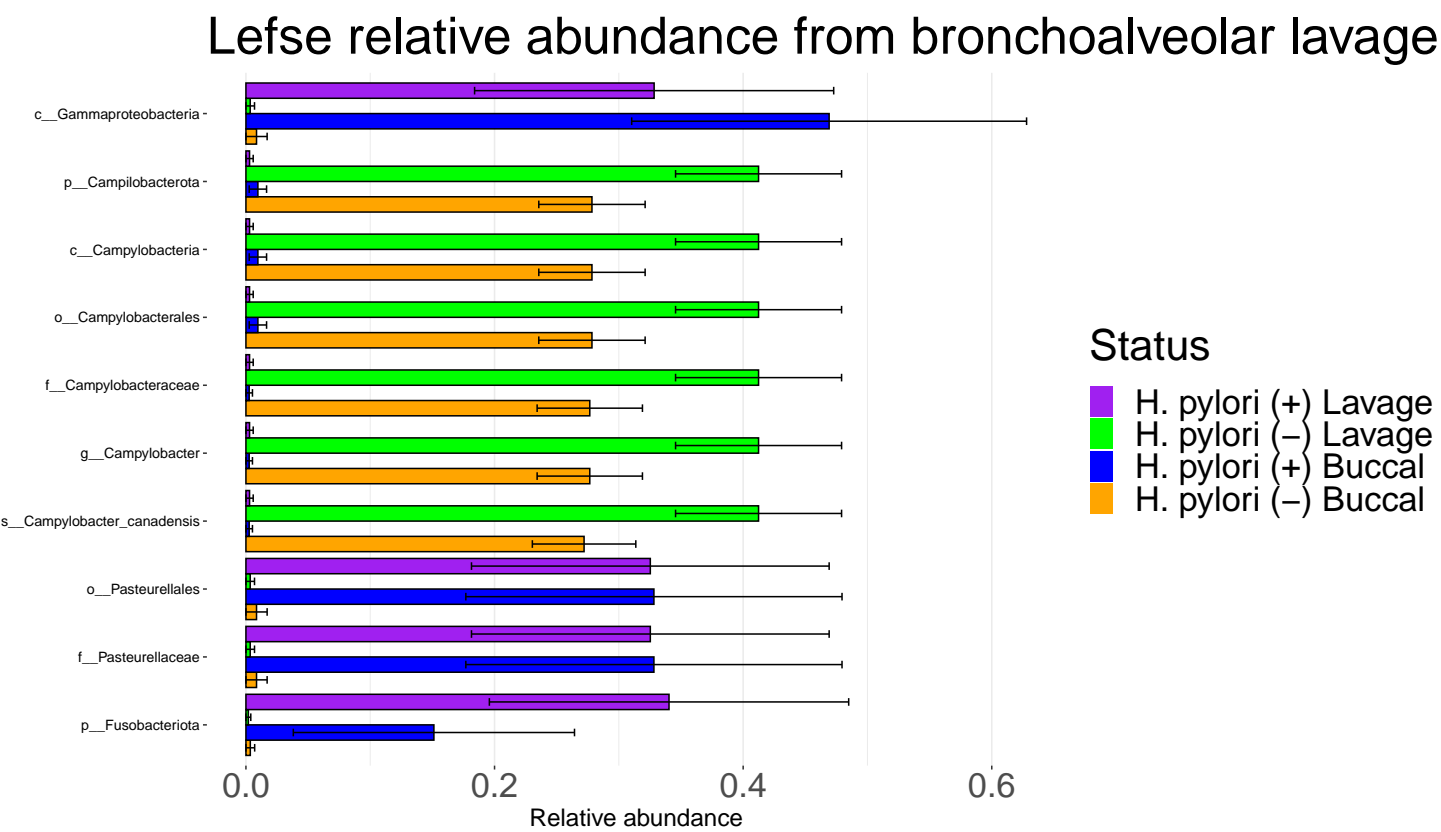


## Lefse analysis and differential abundance for both sites

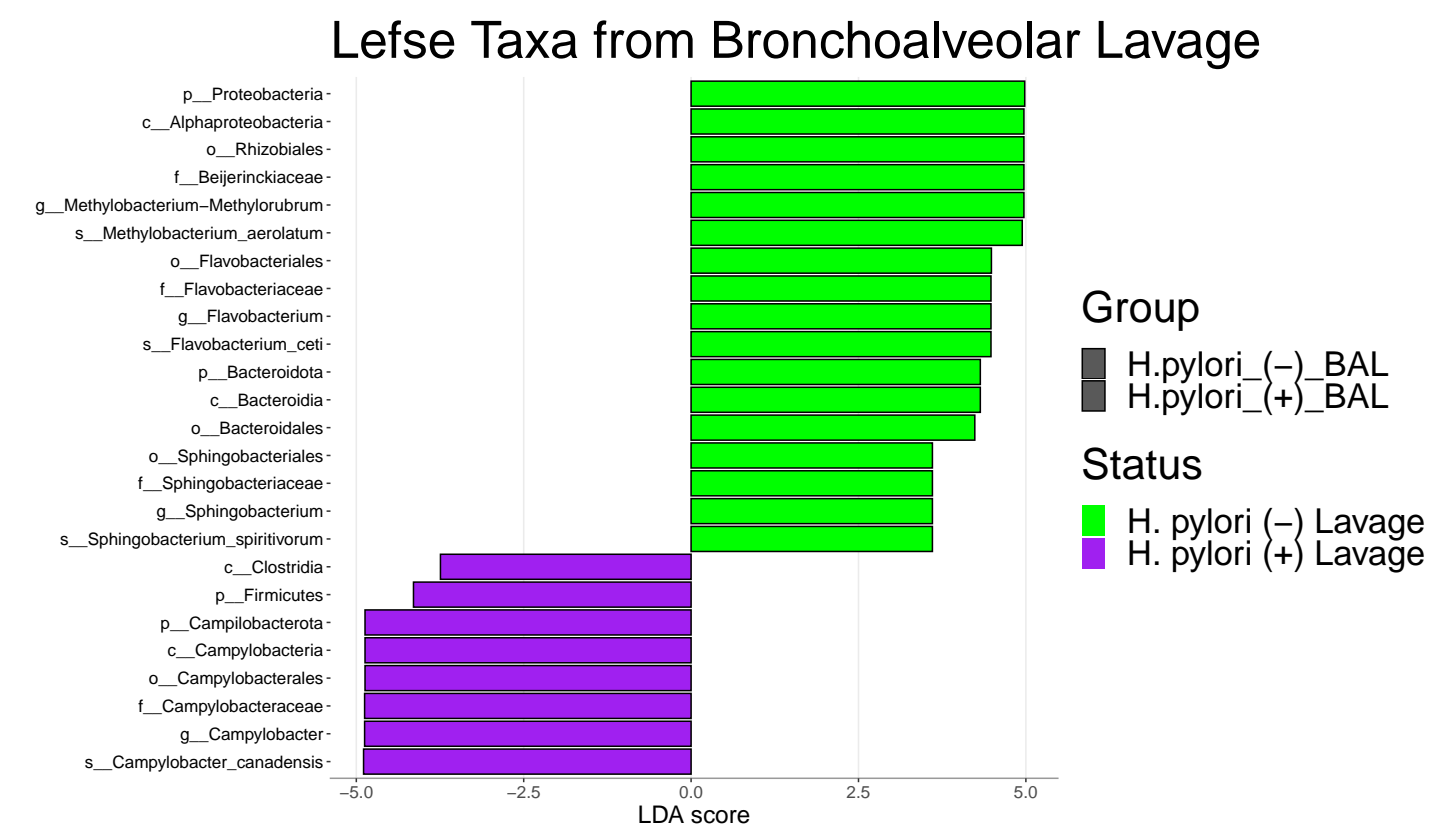
### Lefse taxa from bronchoalveolar lavage and or



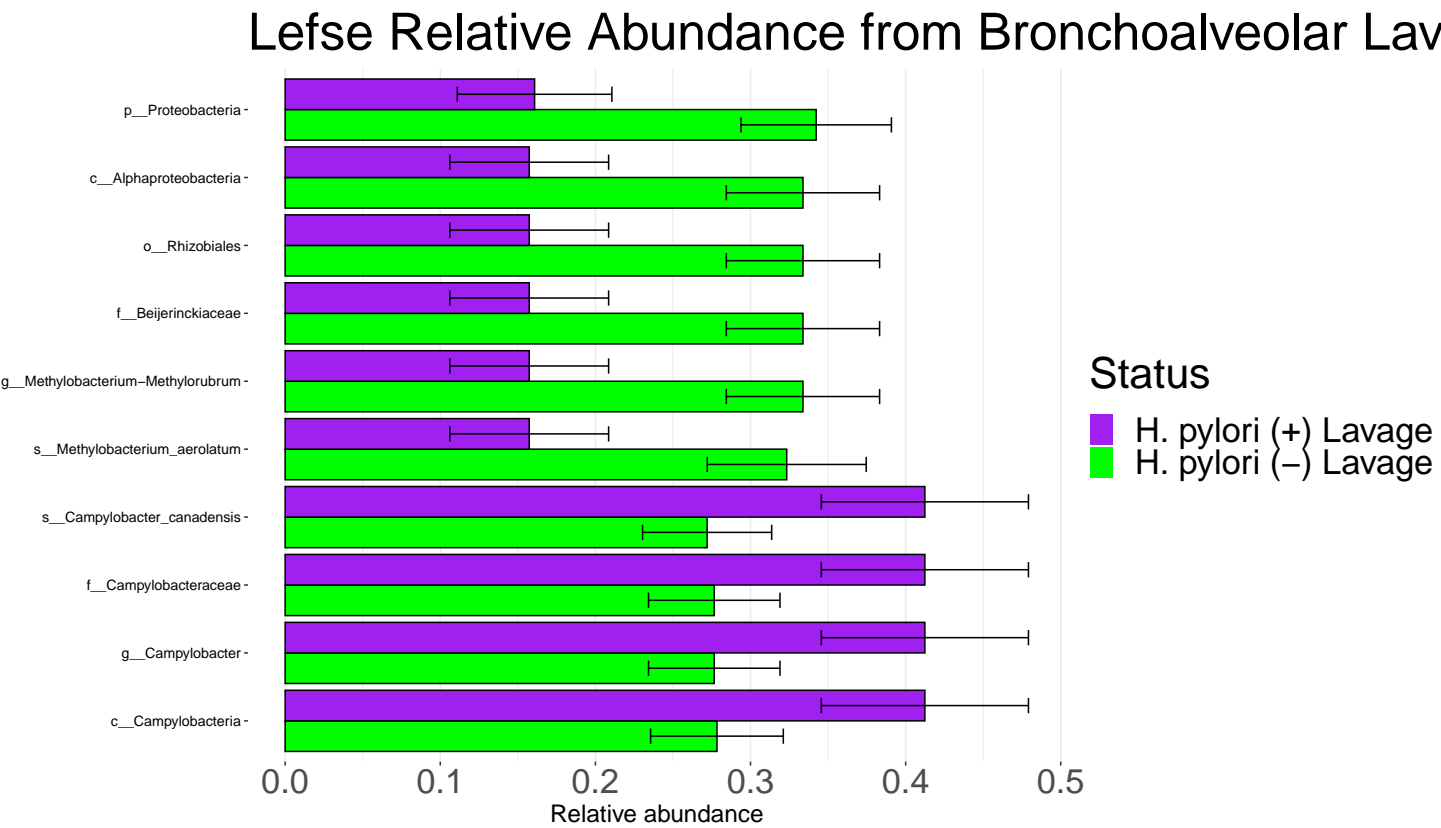
Relative abundance of differential taxa



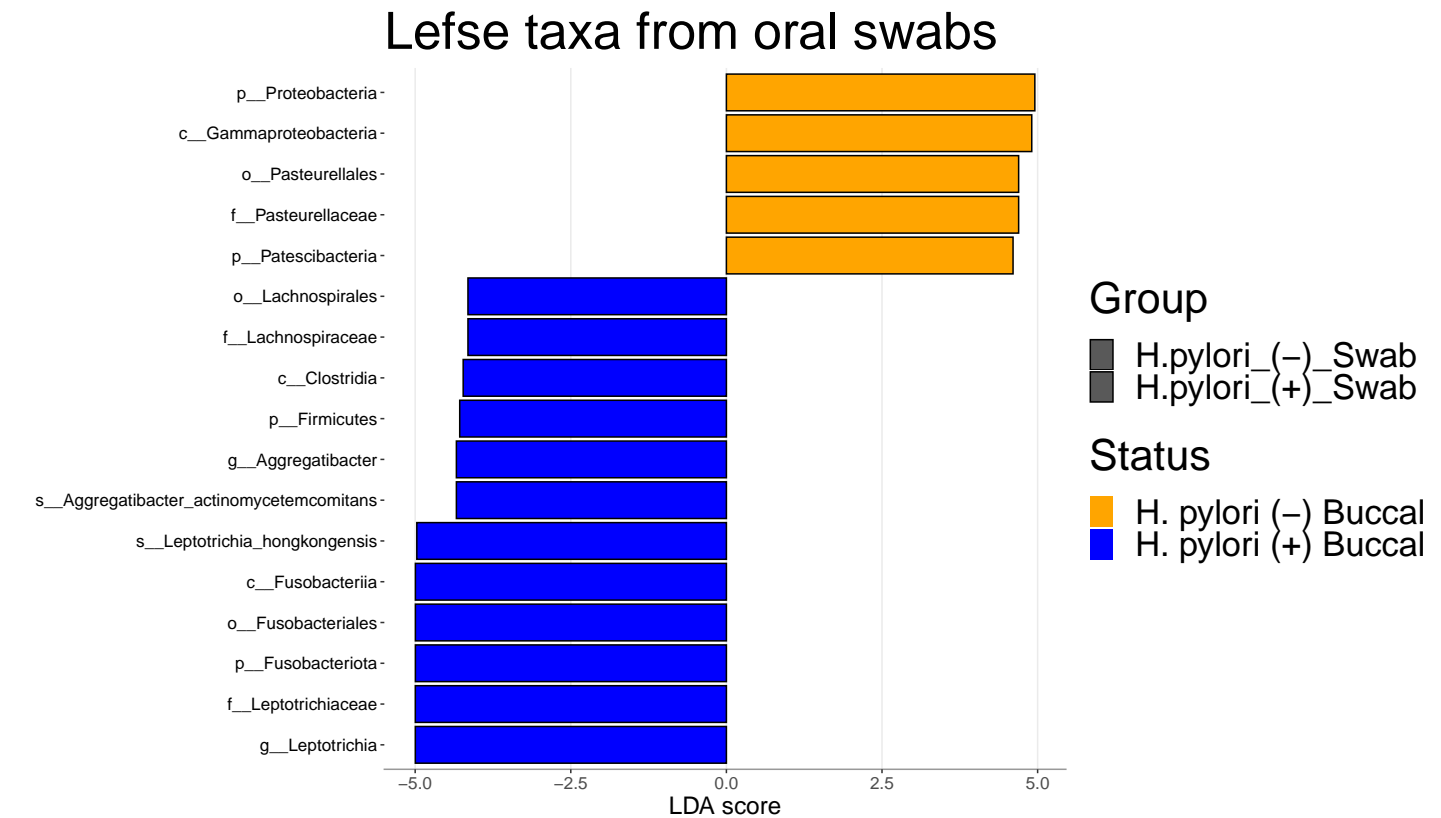
Lefse and differential abundance for bronchoalveolar lavage



Relative abundance of differential taxa



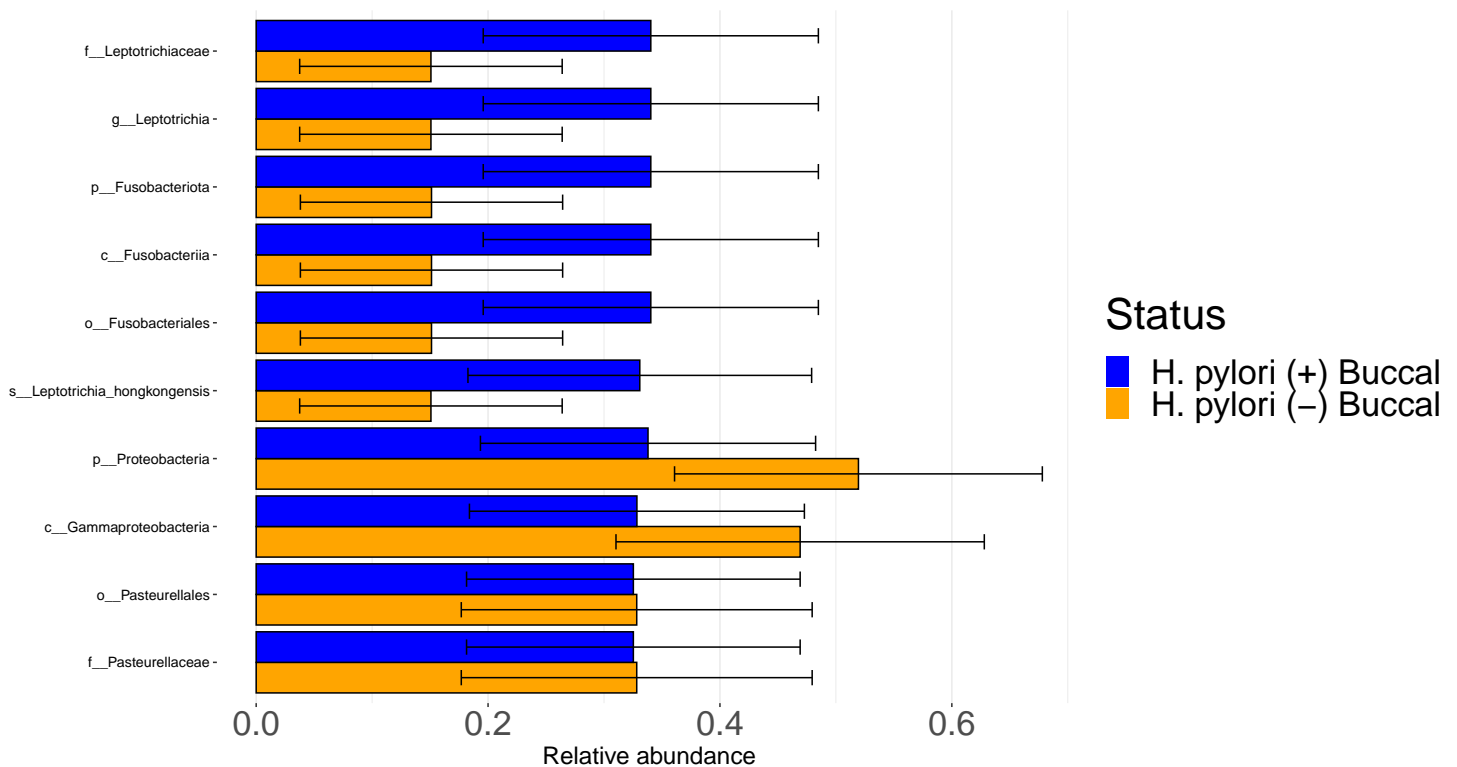
Lefse and differential abundance for oral swabs





## Relative abundance of differential taxa

### Lefse relative abundance from oral swabs

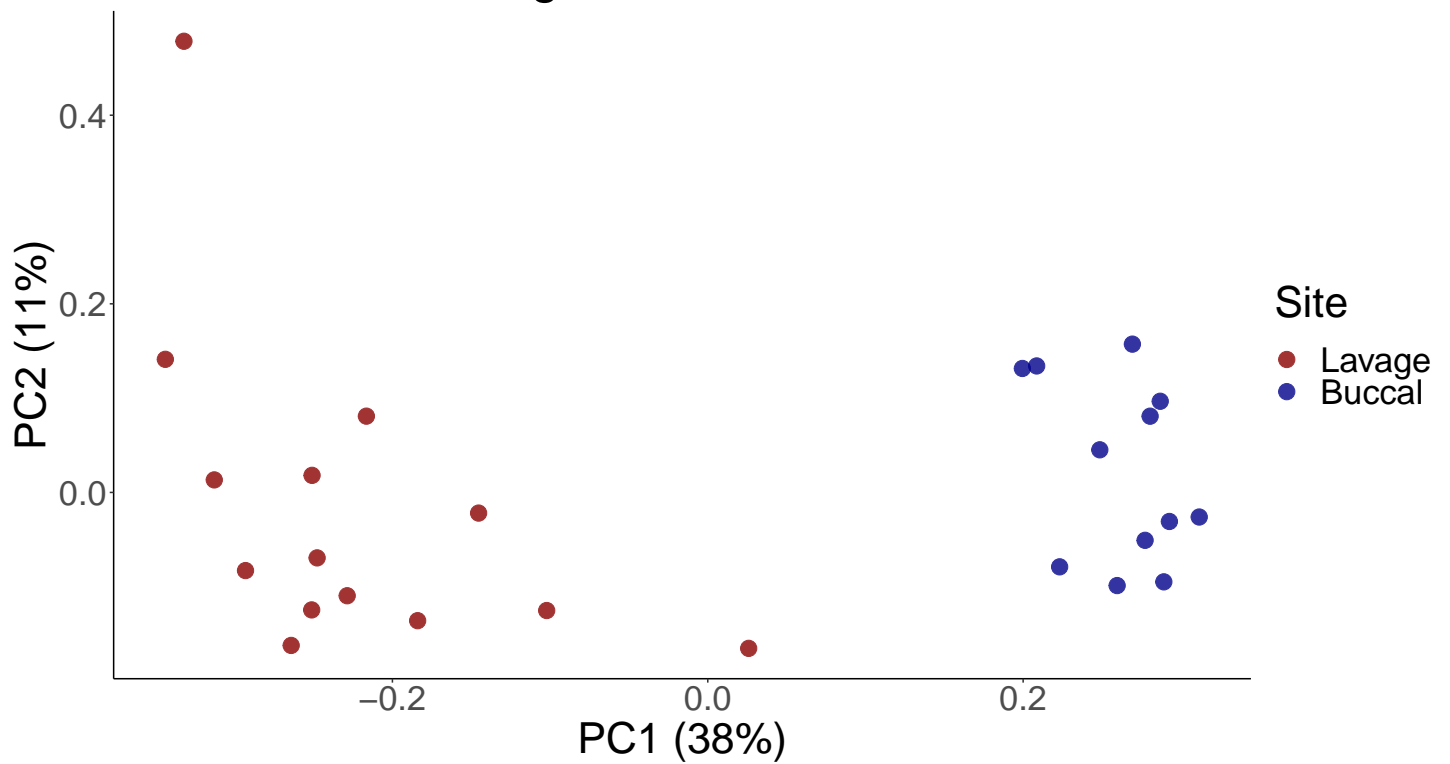


## Beta diversity

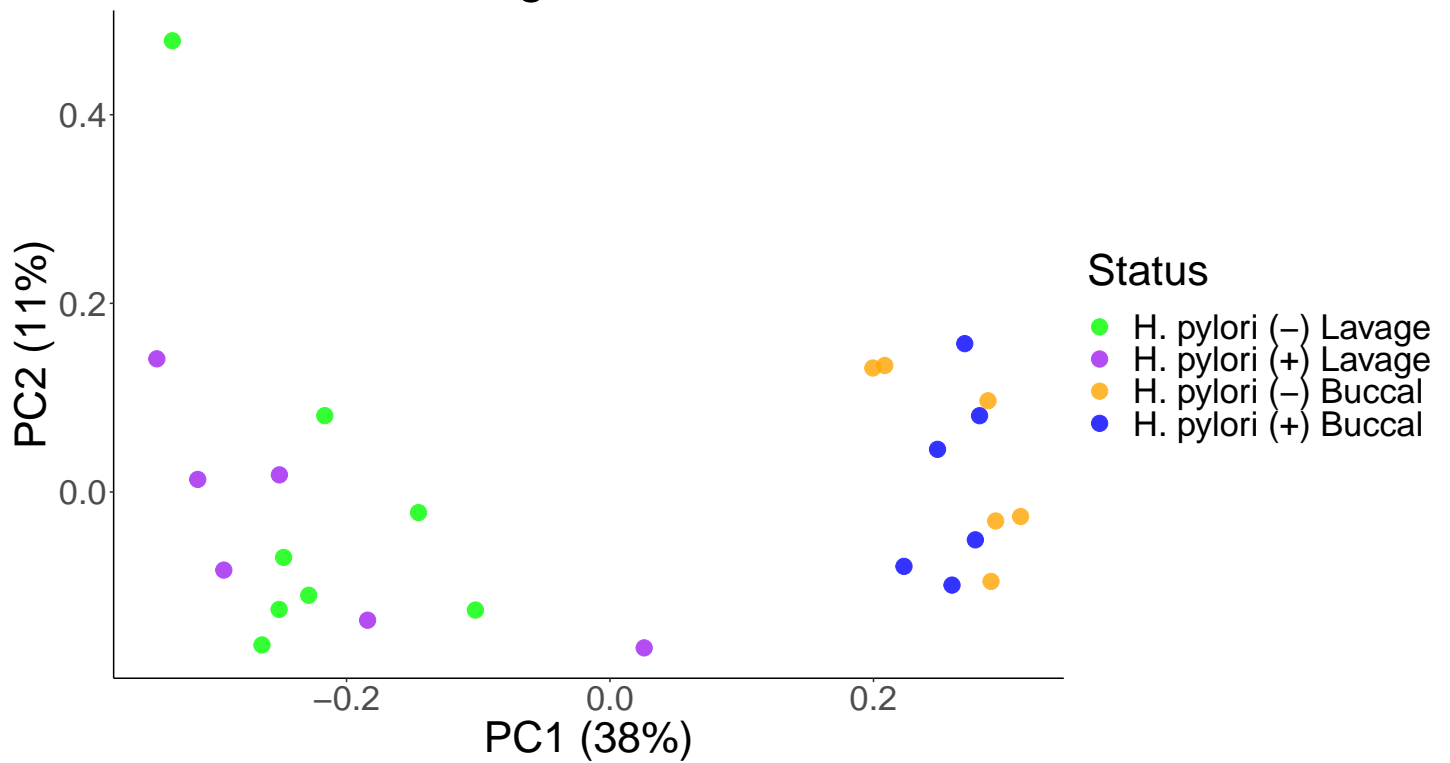
### Unweighted unifracs PCoA plots

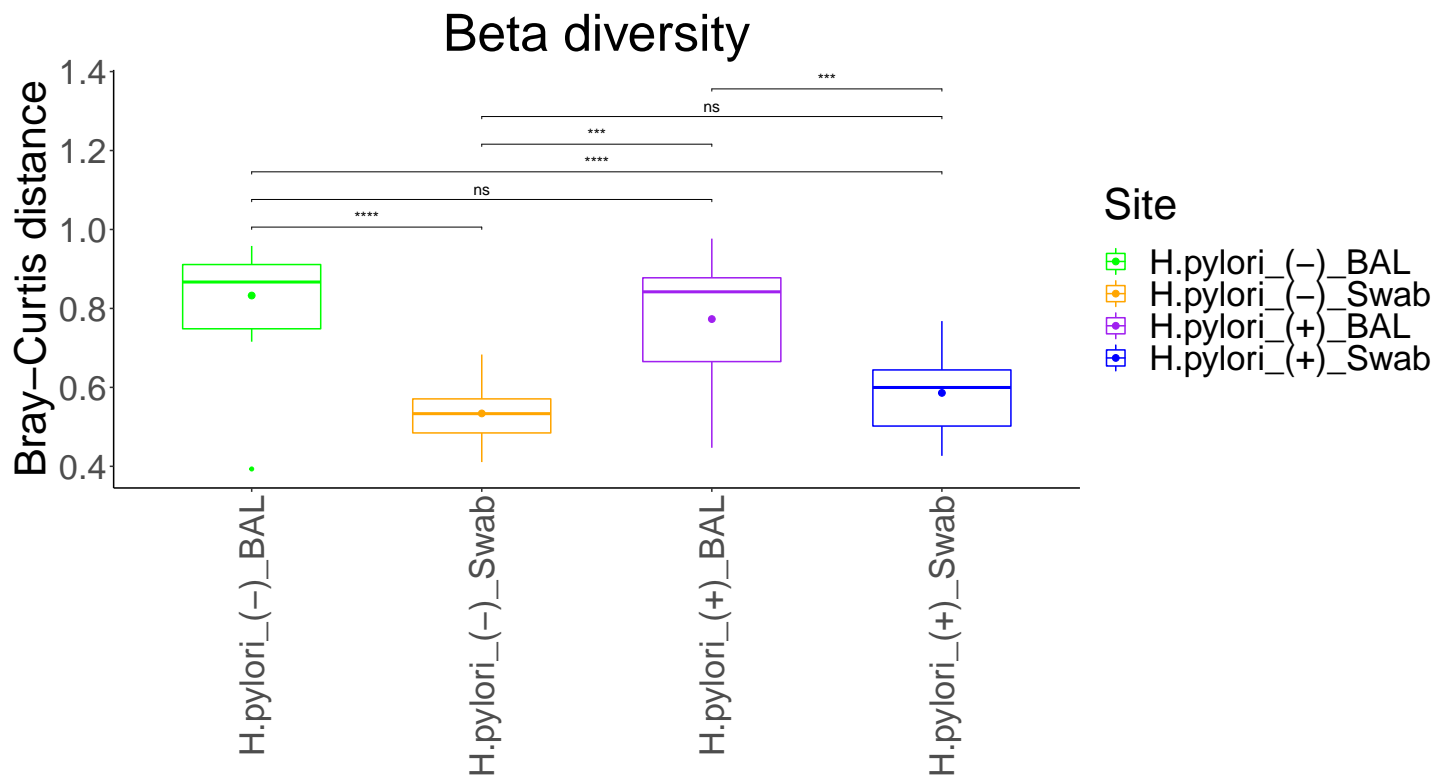
##	PC1	PC2	PC3	PC4	PC5	PC6	PC7
## 1	0.38311	0.1122317	0.08255574	0.05624649	0.04518453	0.04178459	0.03697168
##	PC8	PC9	PC10	PC11	PC12	PC13	PC14
## 1	0.03441675	0.0305229	0.0292508	0.02395872	0.0227312	0.01881898	0.01538496
##	PC15	PC16	PC17	PC18	PC19	PC20	
## 1	0.0140825	0.01226748	0.01155323	0.008776171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

# Unweighted unifrac PCoA

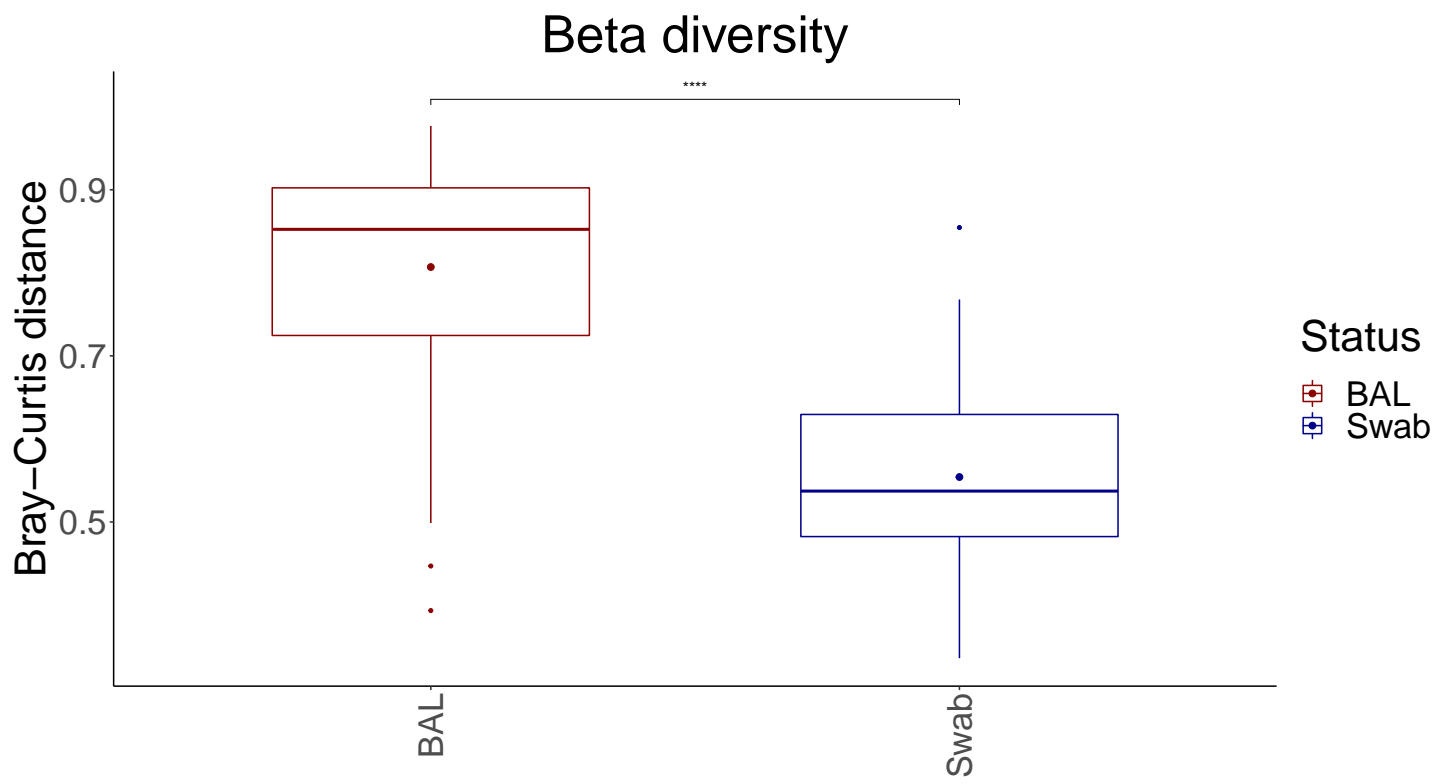


# Status Unweighted unifrac PCoA



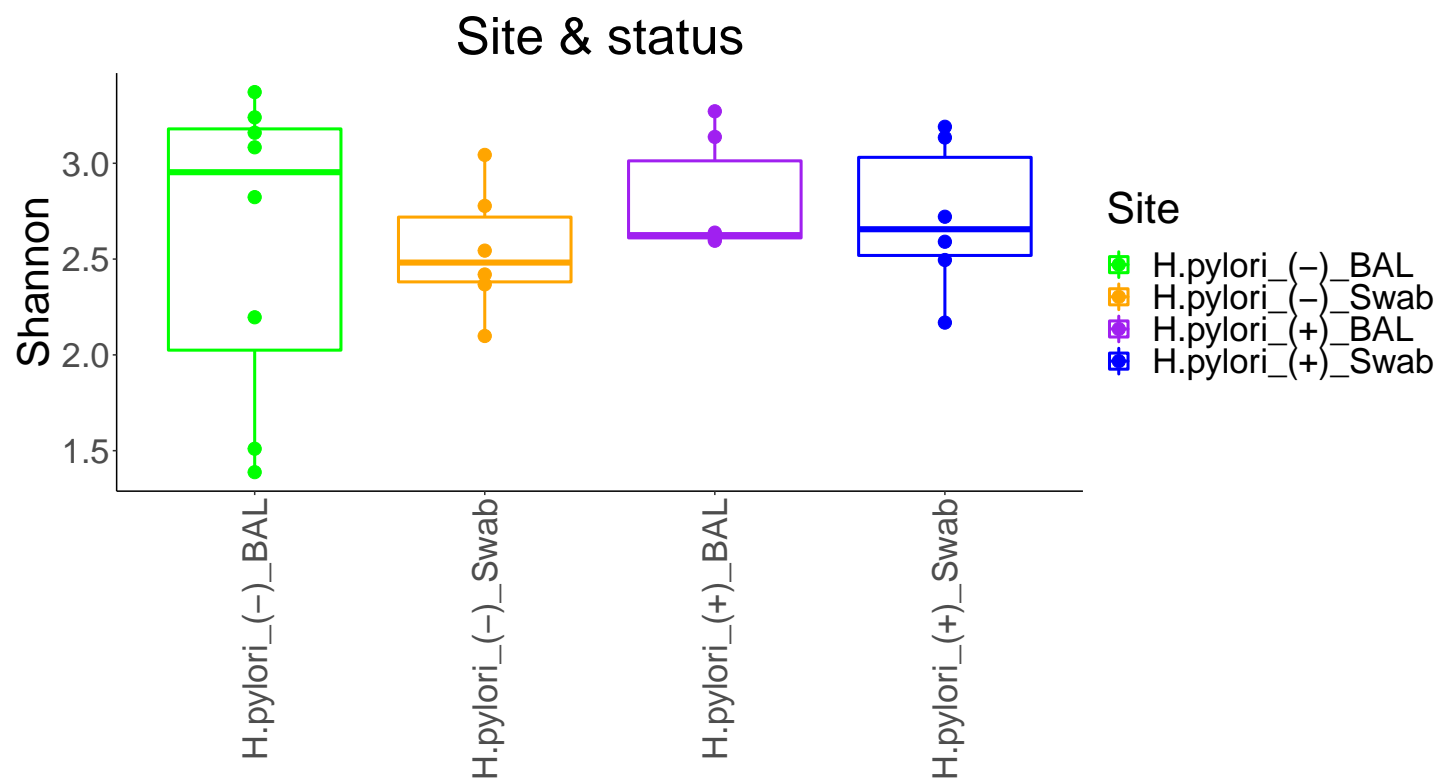


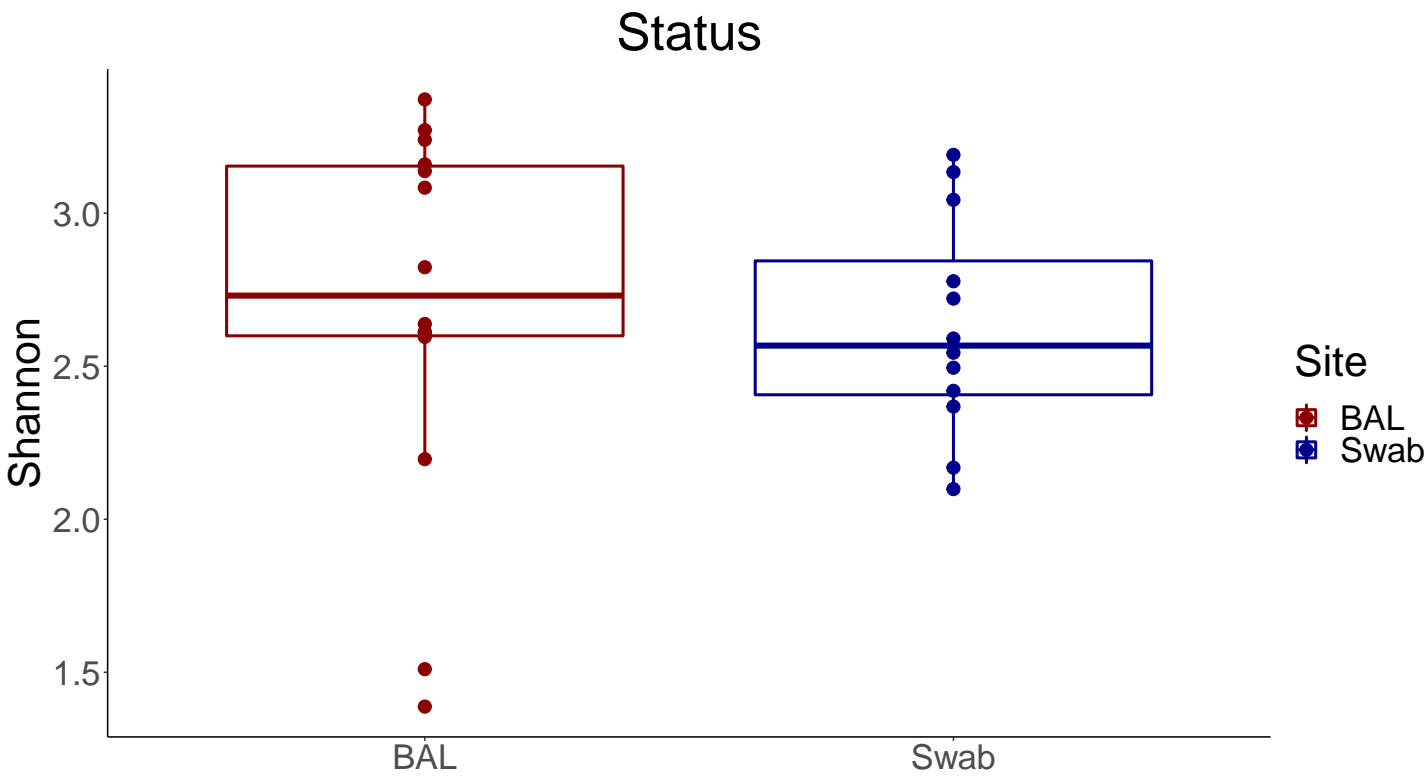
Bray-Curtis



## Alpha Diversity

Shannon index by site and H. pylori status



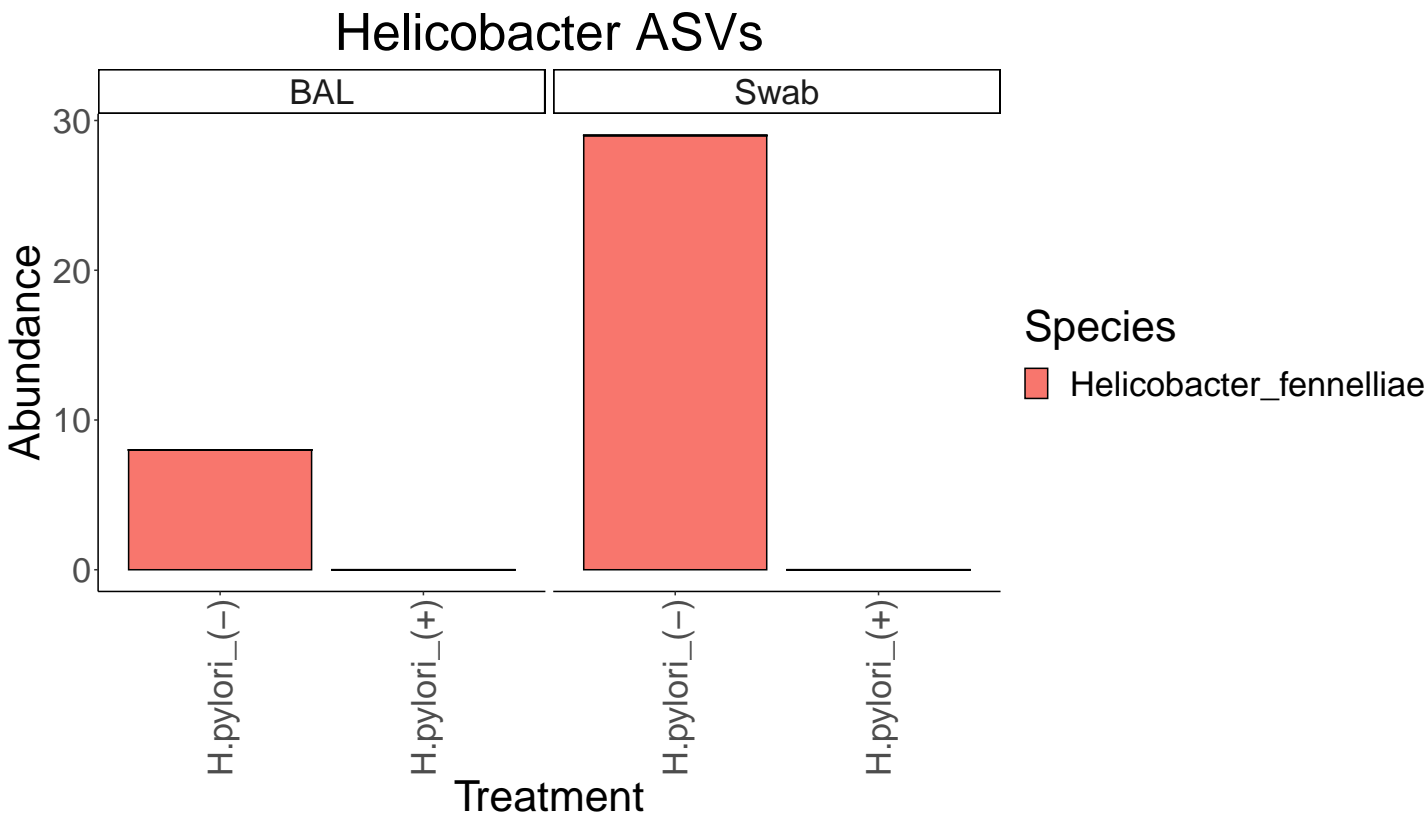


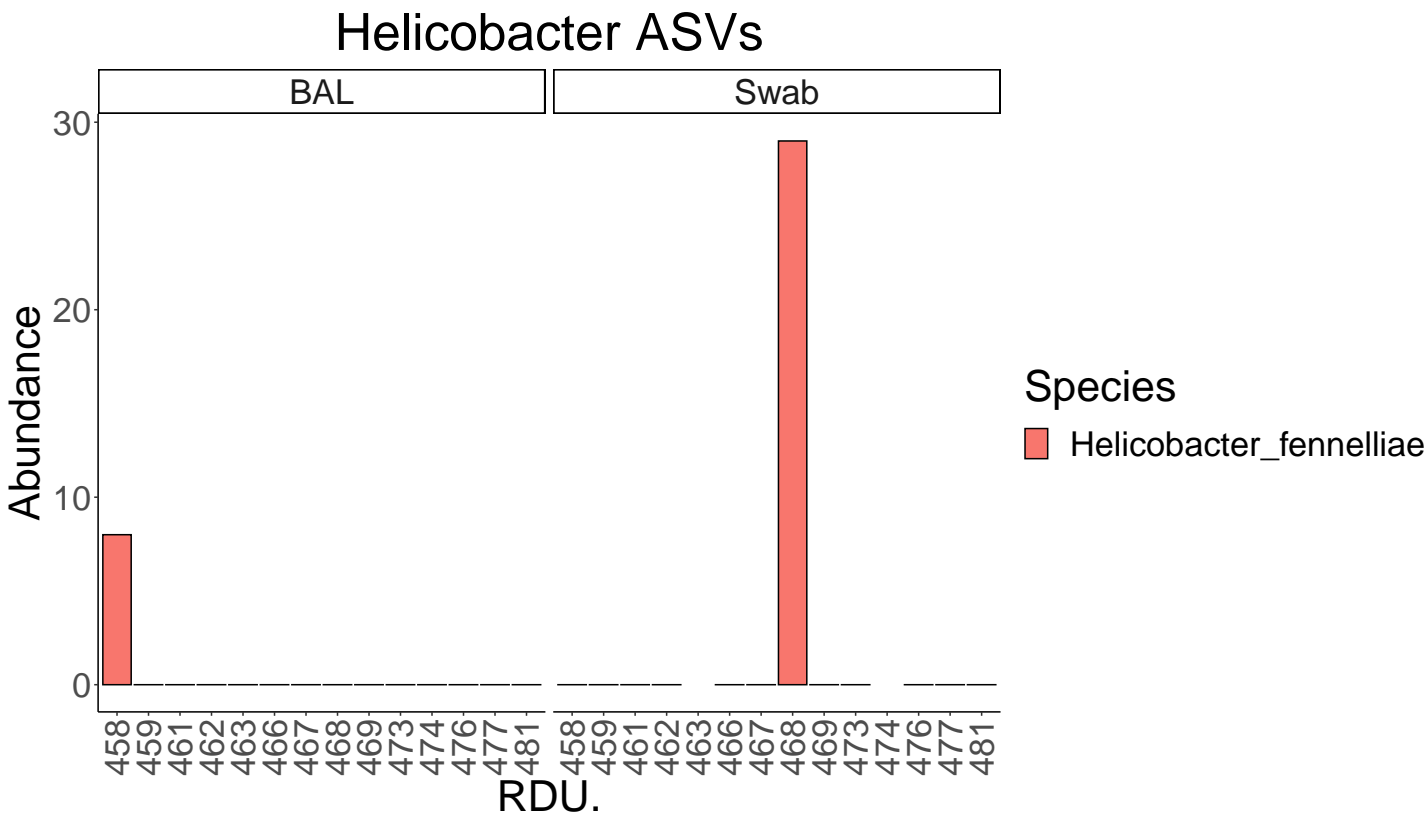
**Table 2:** All alpha diversity measurees

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

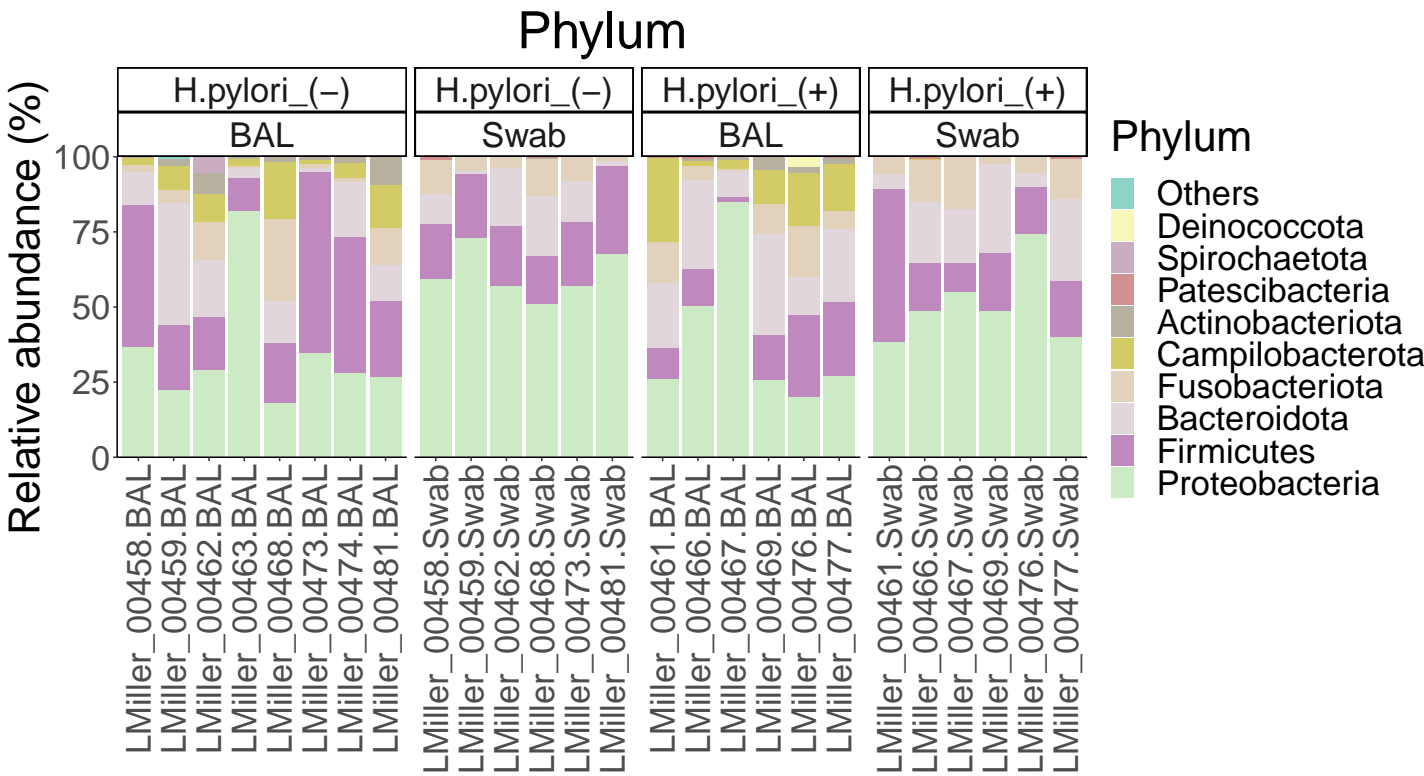


Figure 3: Microbiota Composition at Phylum level.

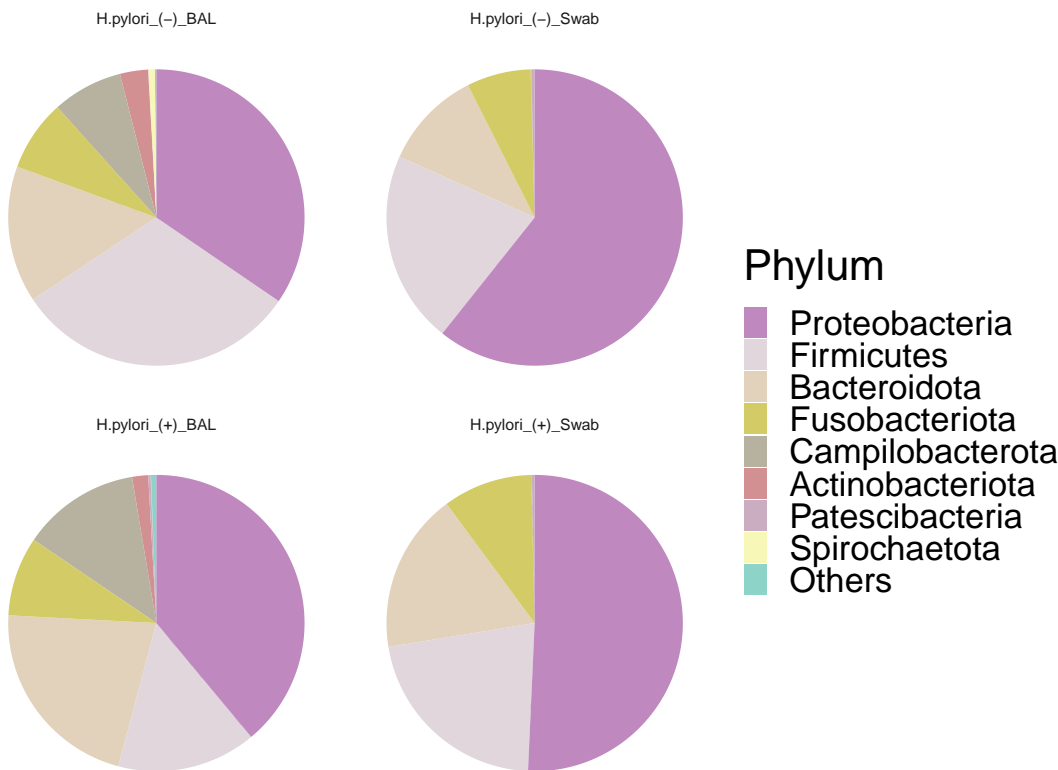
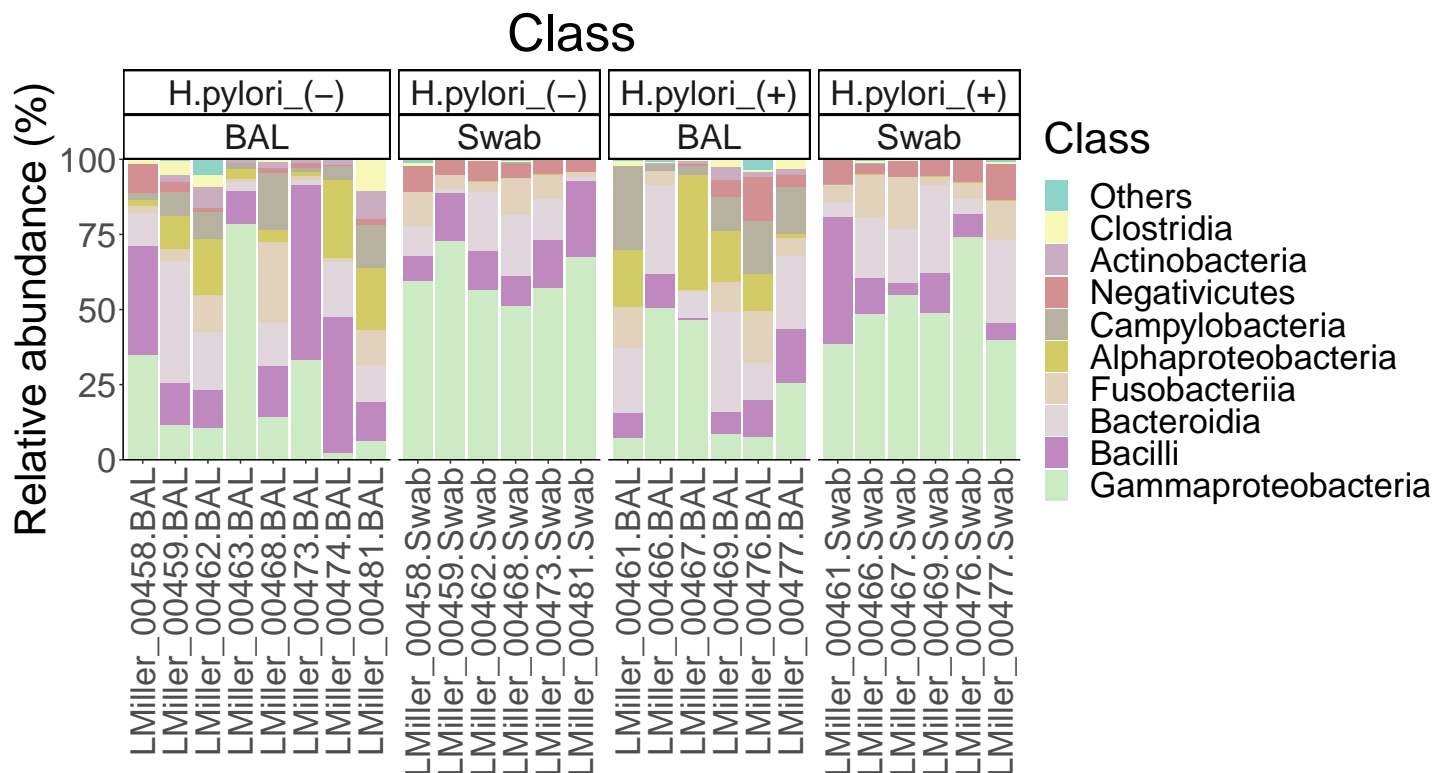


Figure 4: Microbiota Composition at Phylum level.

**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%



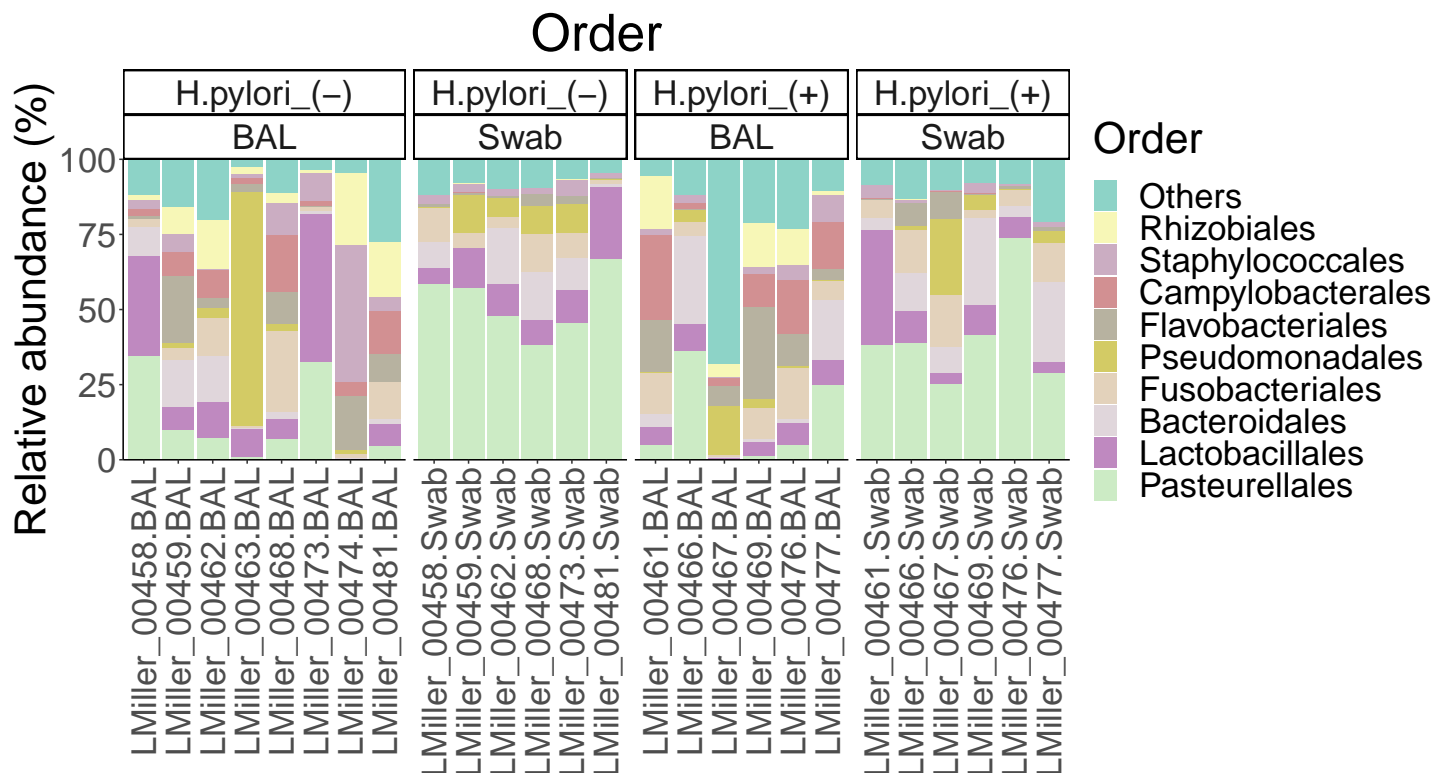
**Figure 5:** Microbiota Composition at Class level.



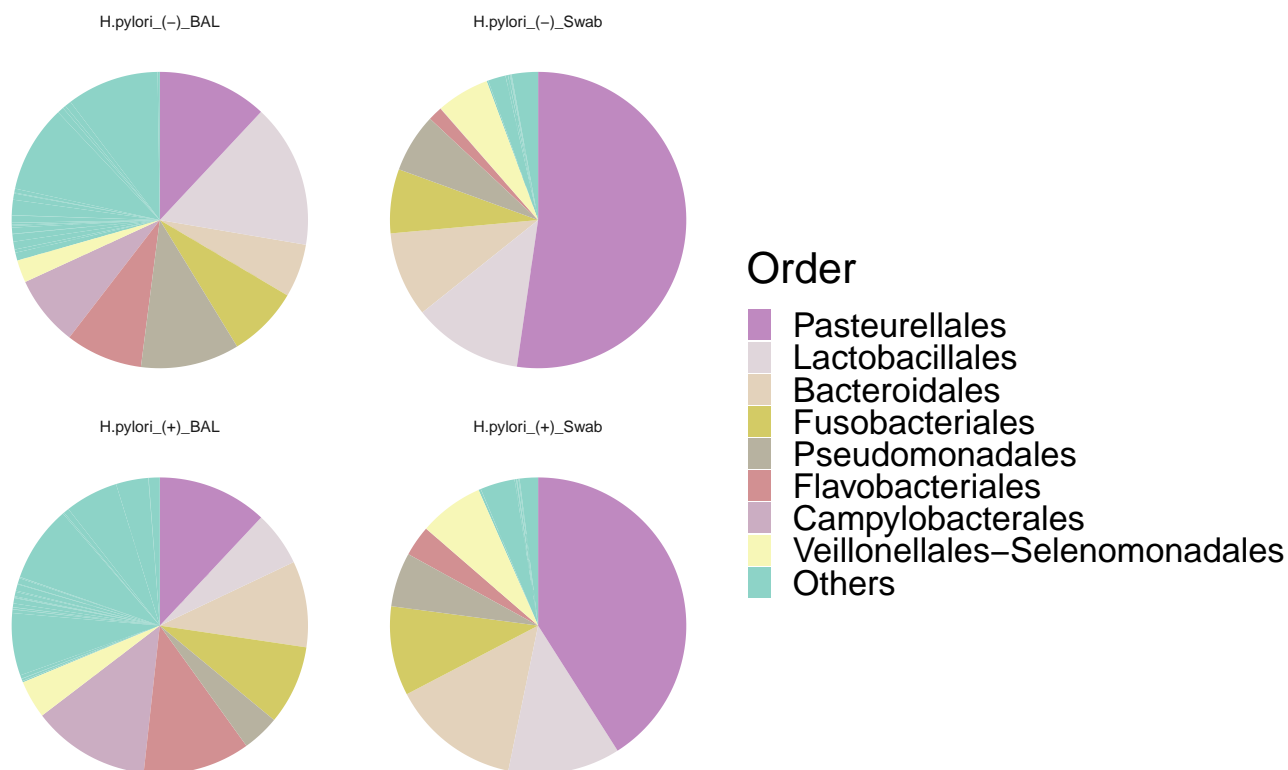
**Figure 6:** Microbiota Composition at Class level.

**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%



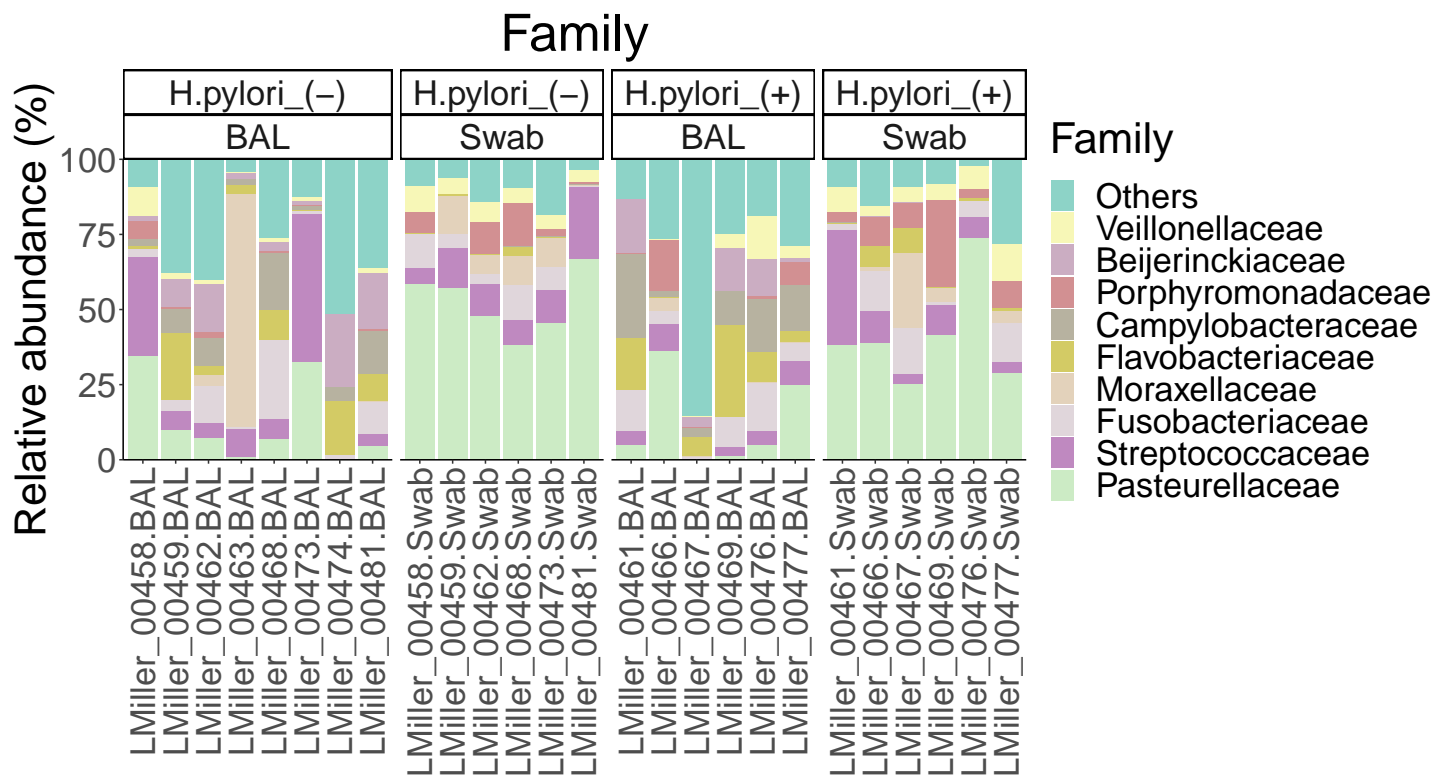
**Figure 7:** Microbiota Composition at Order level.



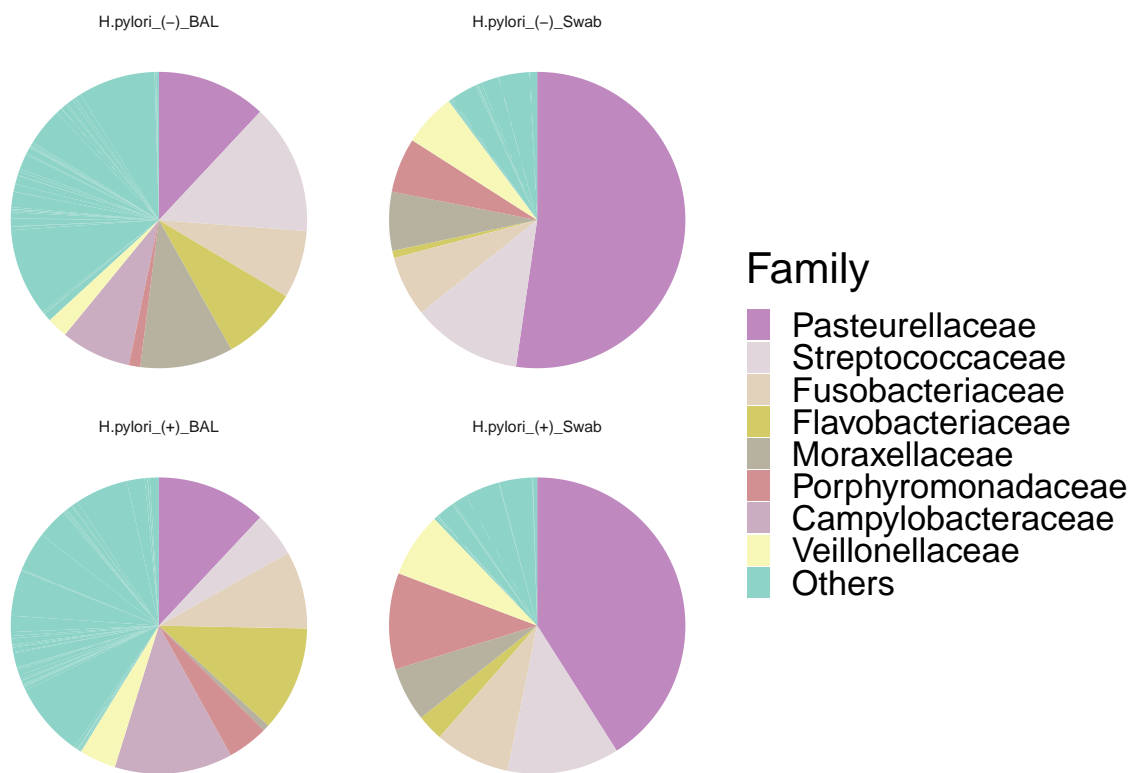
**Figure 8:** Microbiota Composition at Order level.

**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%
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%



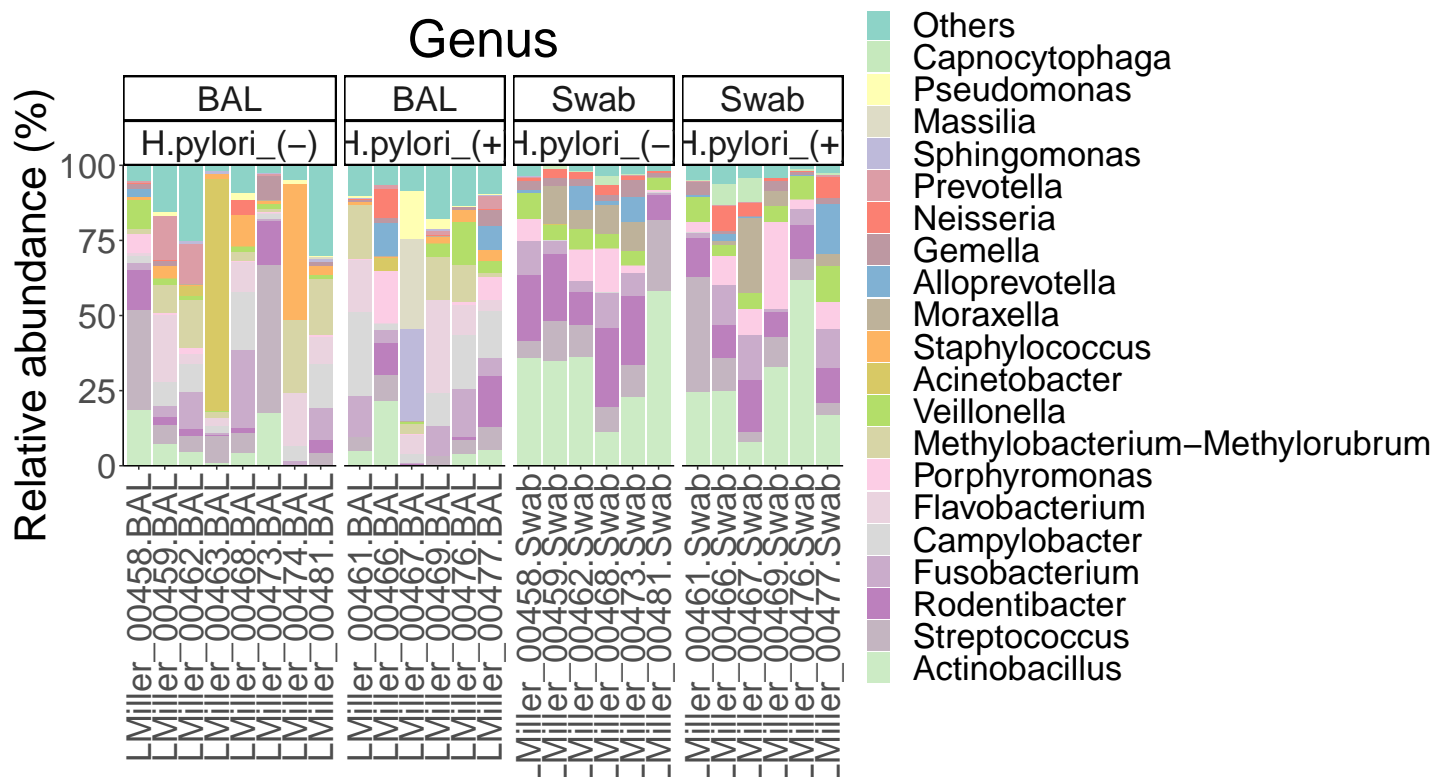


Figure 11: Microbiota Composition at Genus level.

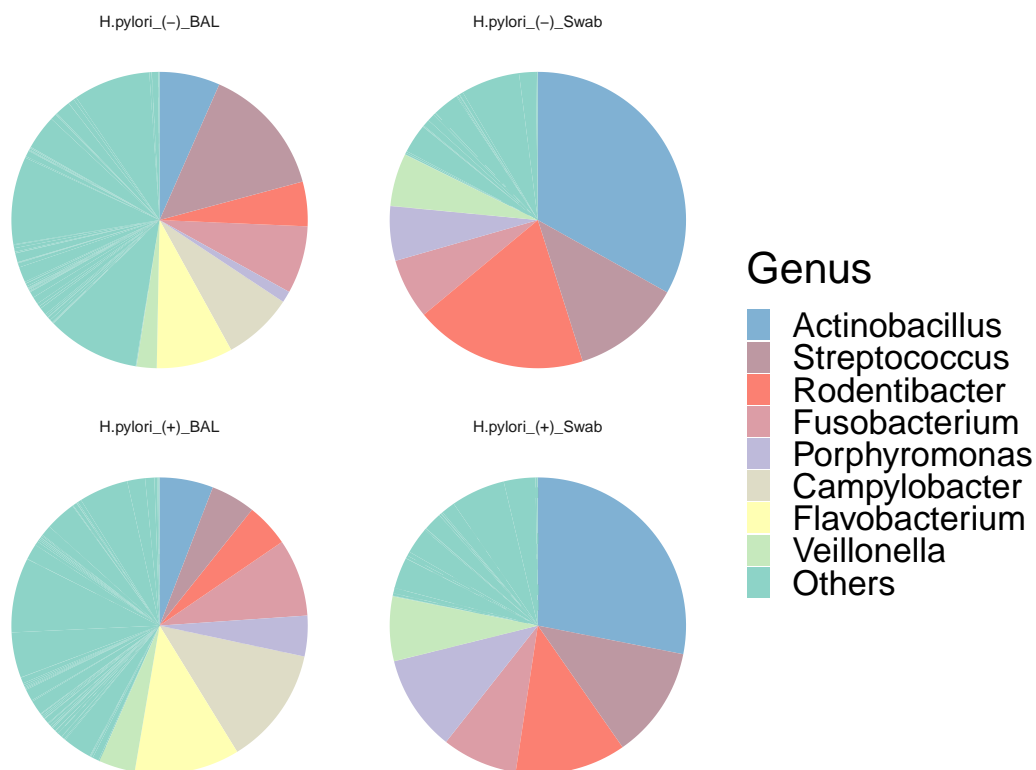


Figure 12: Microbiota Composition at Genus level.

**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-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)

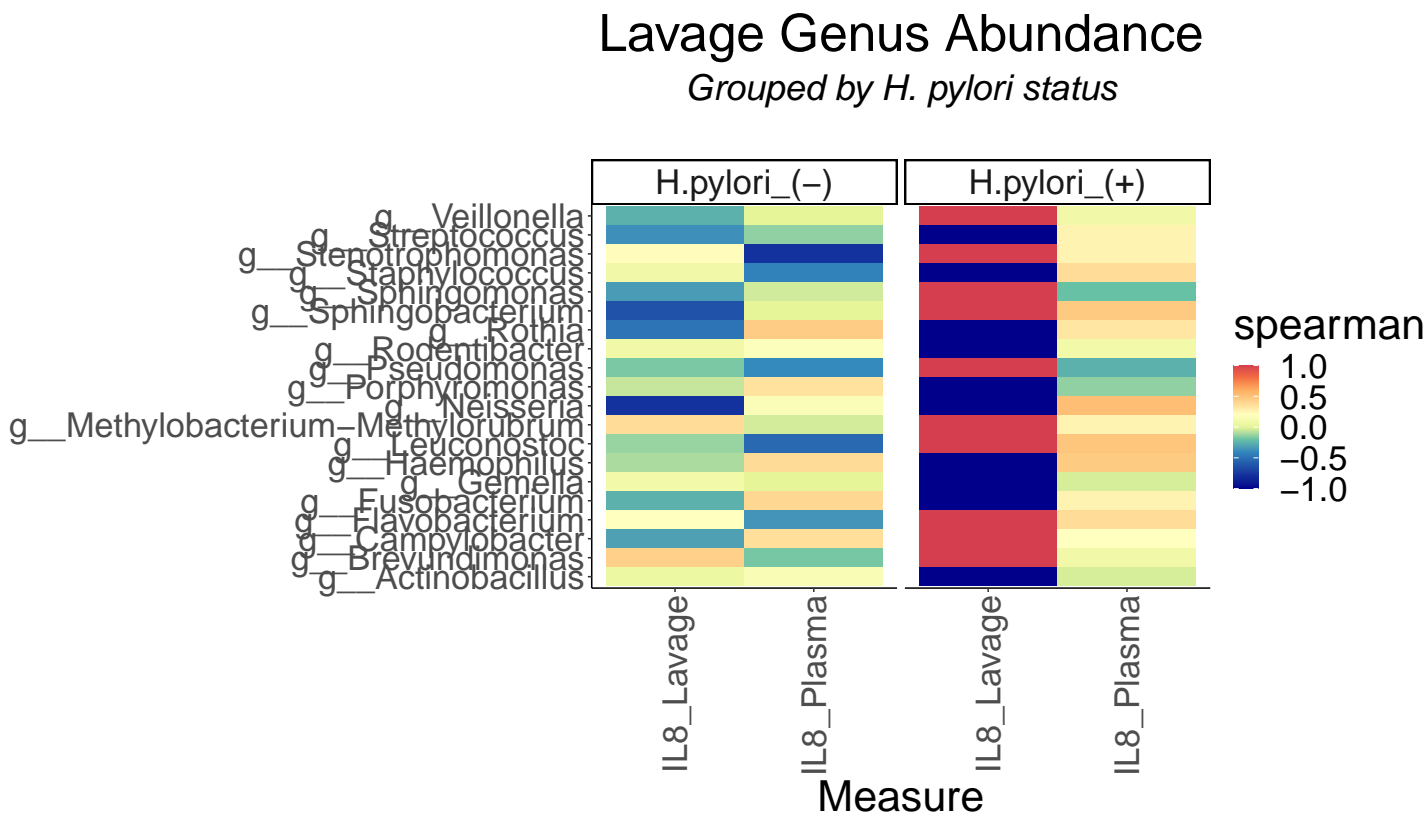


Figure 13: IL8 and lavage genus abundance Spearman correlations separated by *H. pylori* status

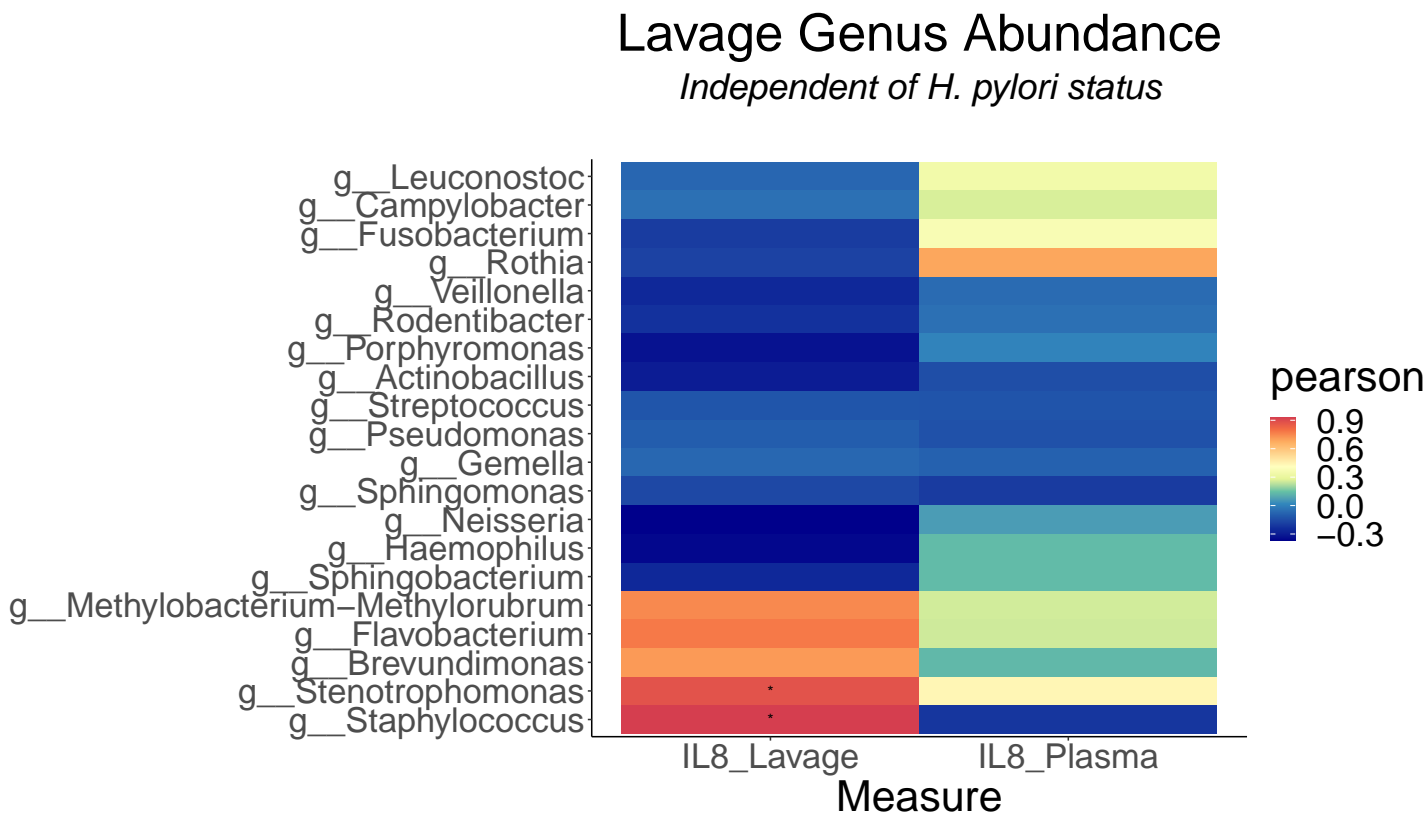
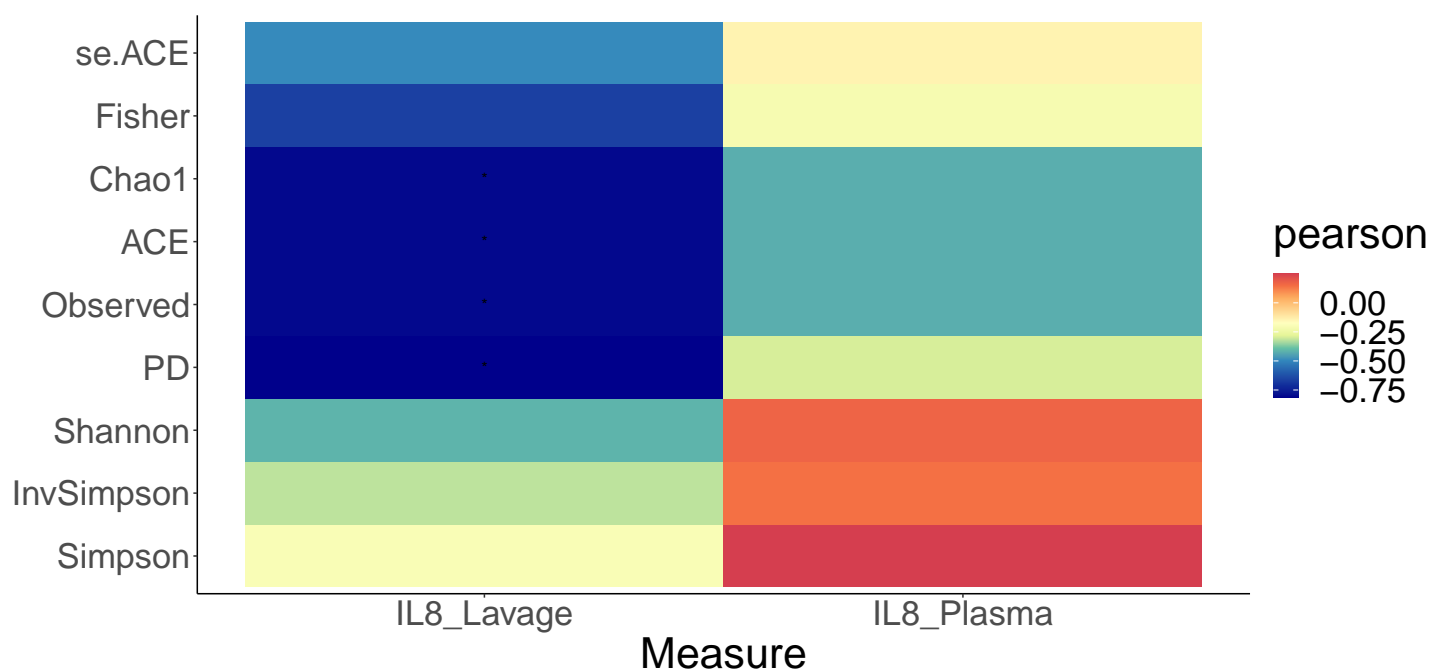


Figure 14: IL8 and lavage genus abundance Spearman correlations independent of *H. pylori* status

# Lavage Alpha Diversity

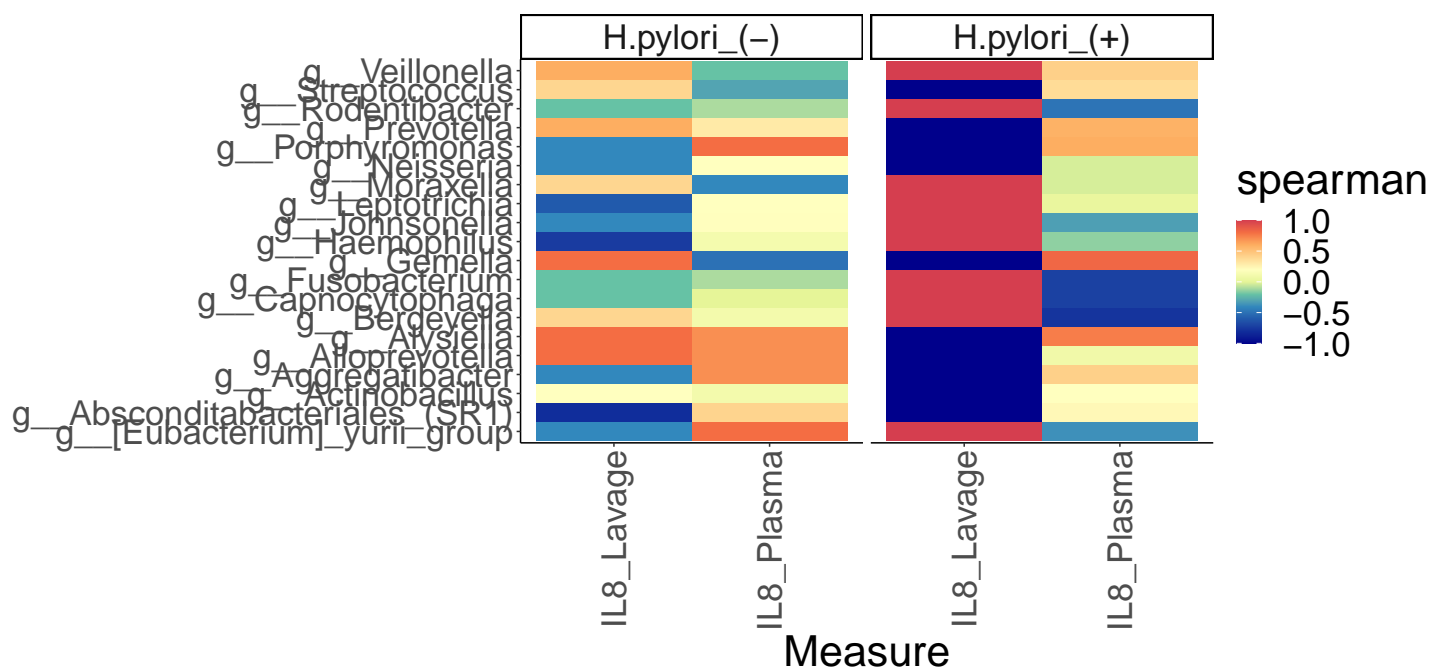
*Independent of H. pylori status*



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

# Buccal Cavity Genus Abundance

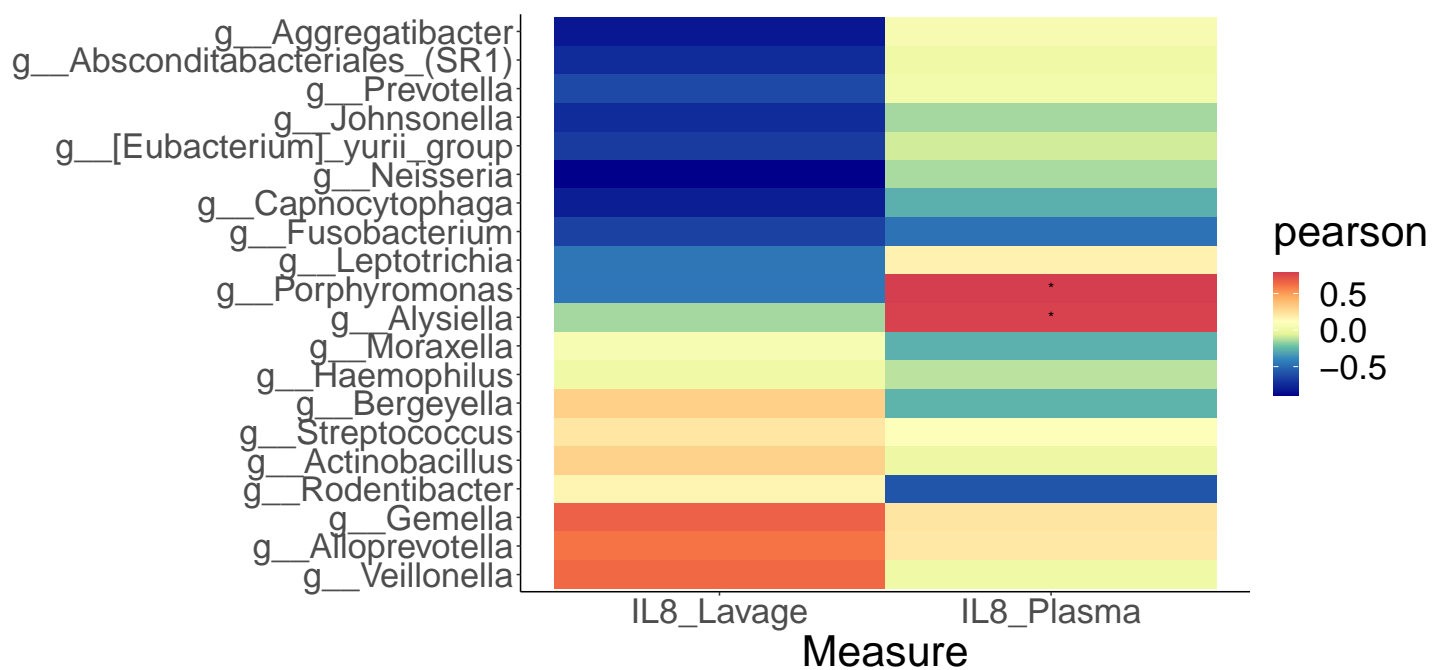
Grouped by *H. pylori* status



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

# Buccal Cavity Genus Abundance

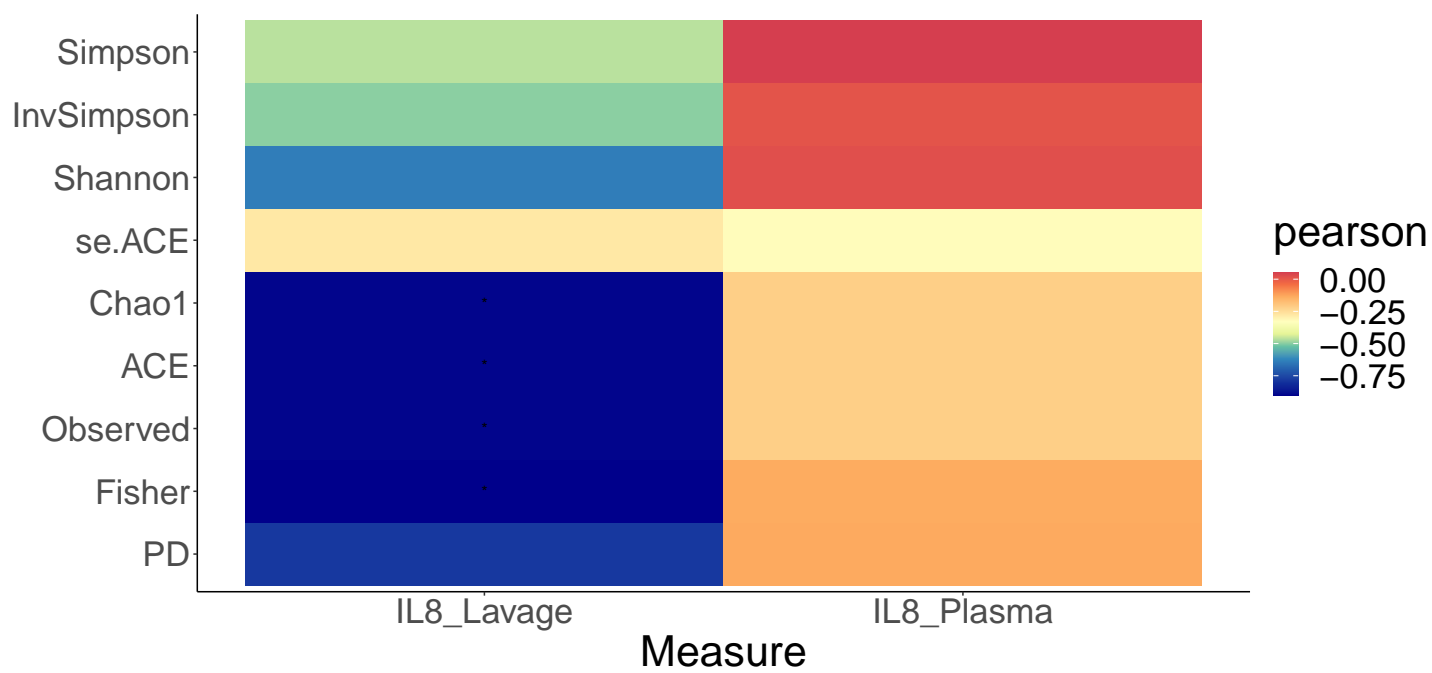
*Independent of H. pylori status*



**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

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## 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
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##  [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
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##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
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## 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
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## [31] phyloseq_1.38.0            readxl_1.4.0
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