

H.pylori Rhesus Microbiome Analysis

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Data used in analysis

Library

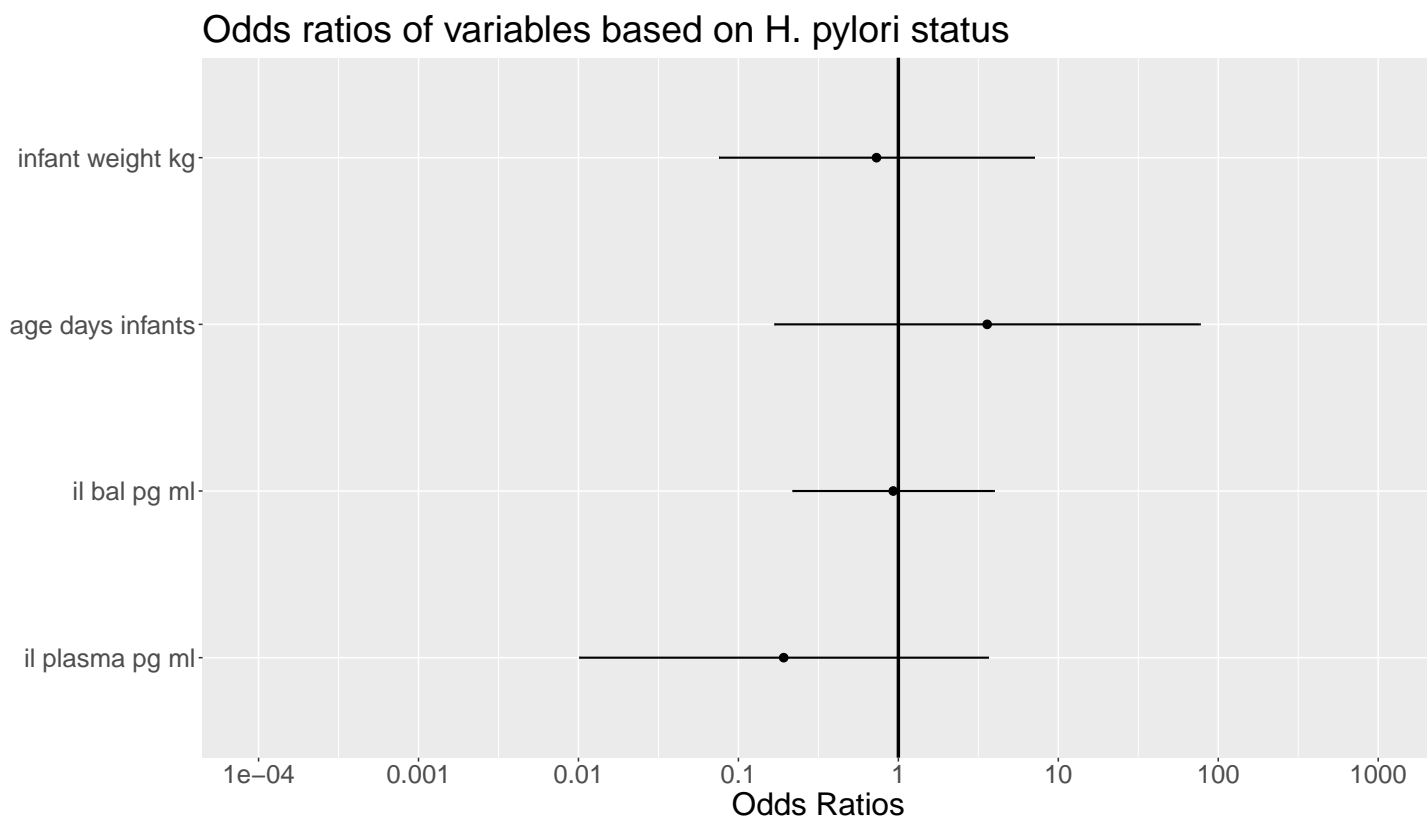
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ASV counts Taxa table

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

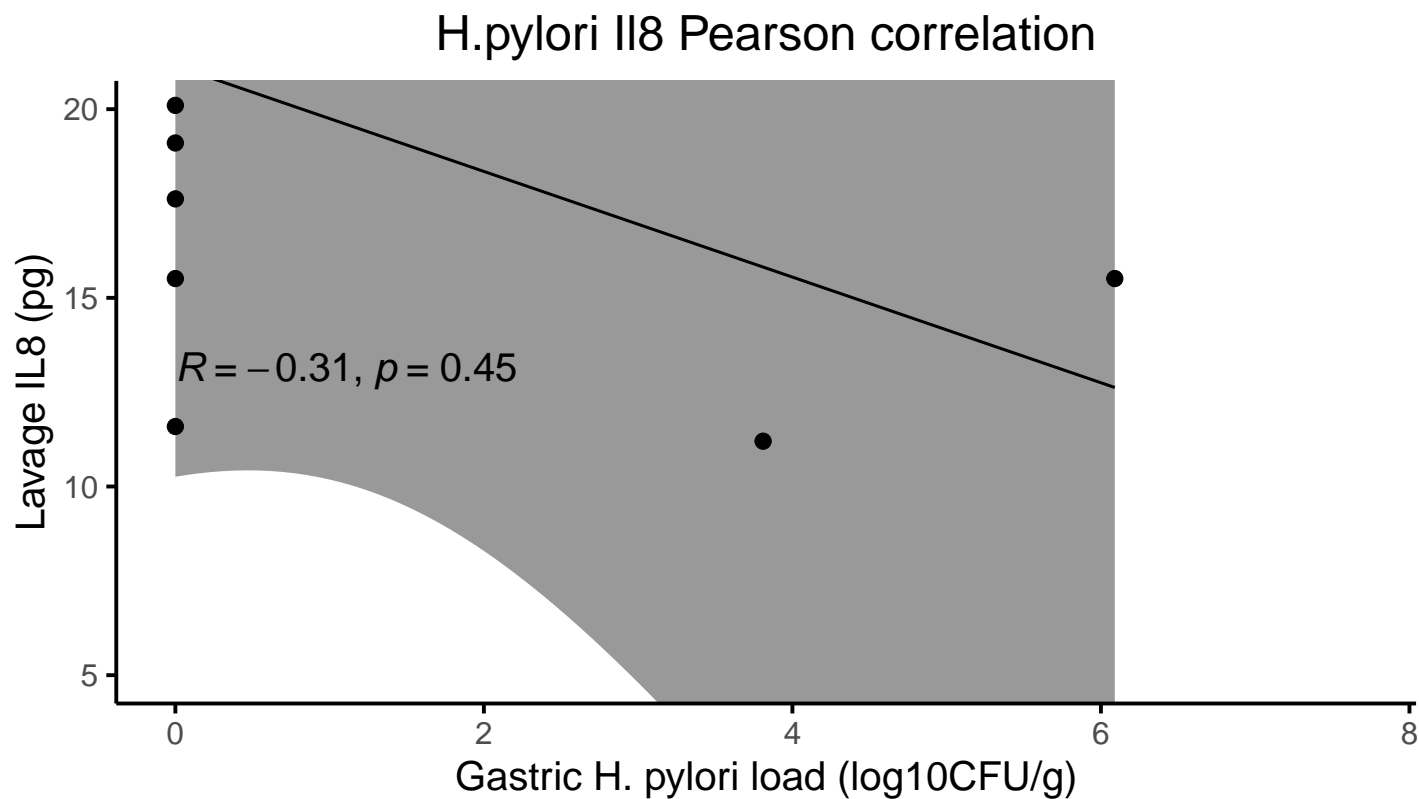


Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study

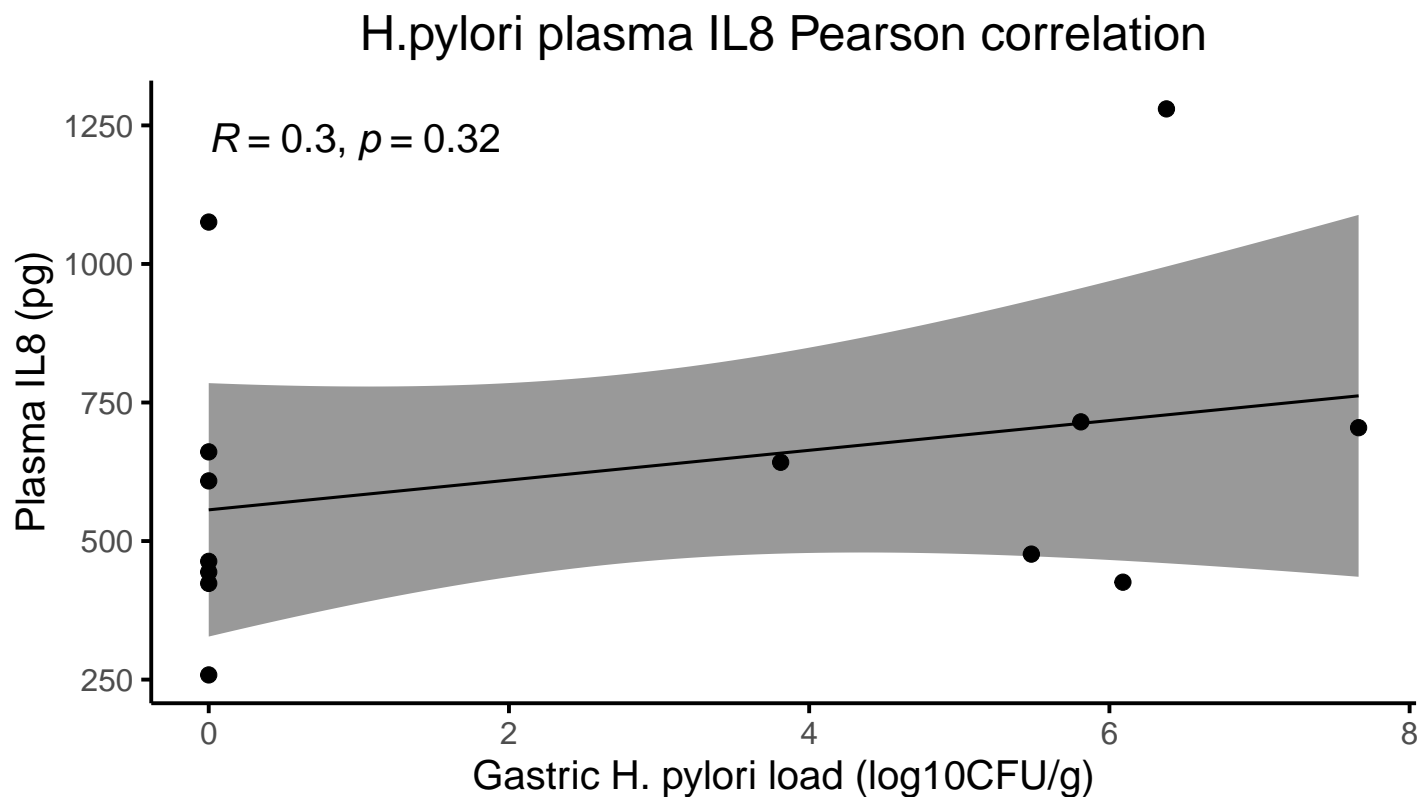
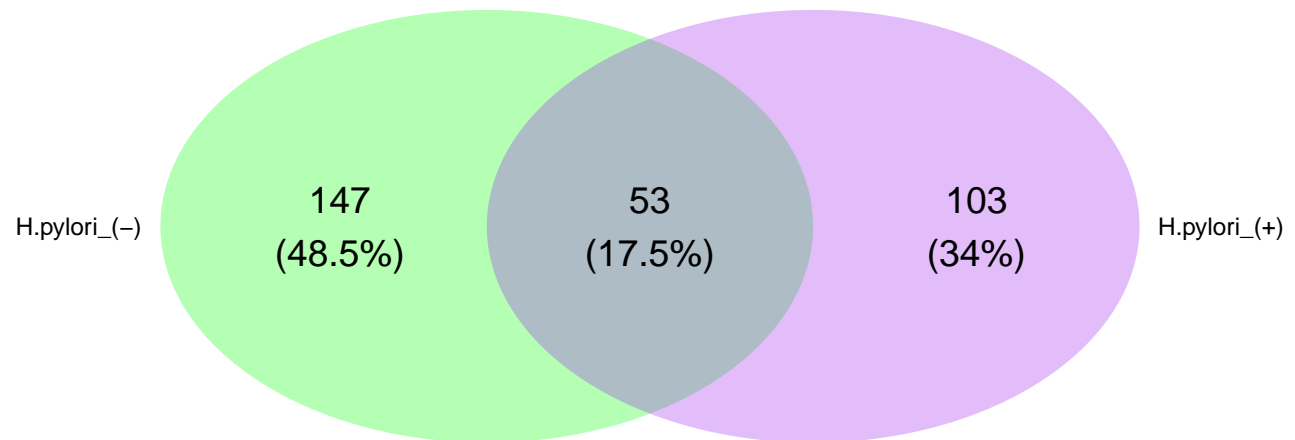


Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

Overlapping Taxa Between Sites and *H. pylori* Status

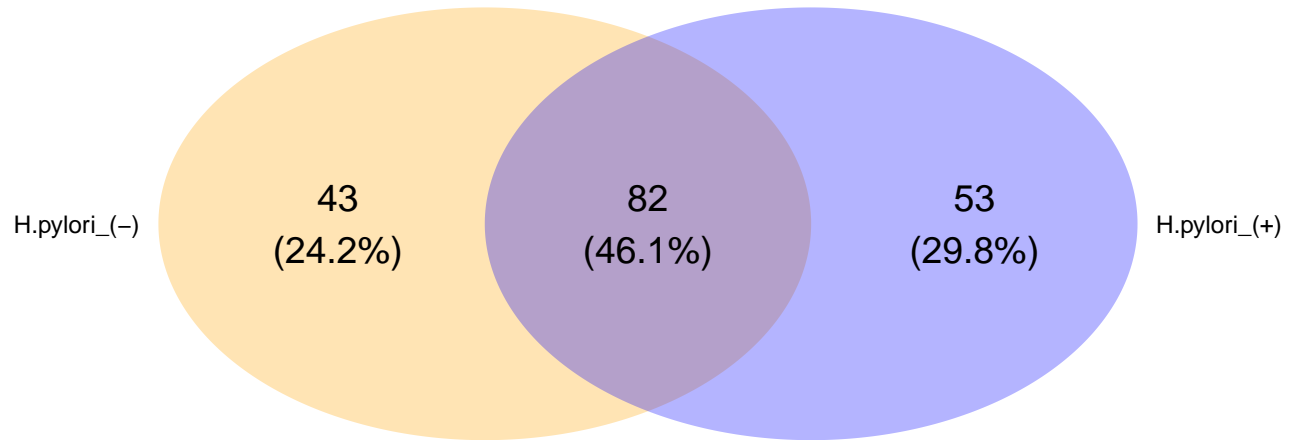
Lavage overlapping taxa

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



Buccal 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 swab

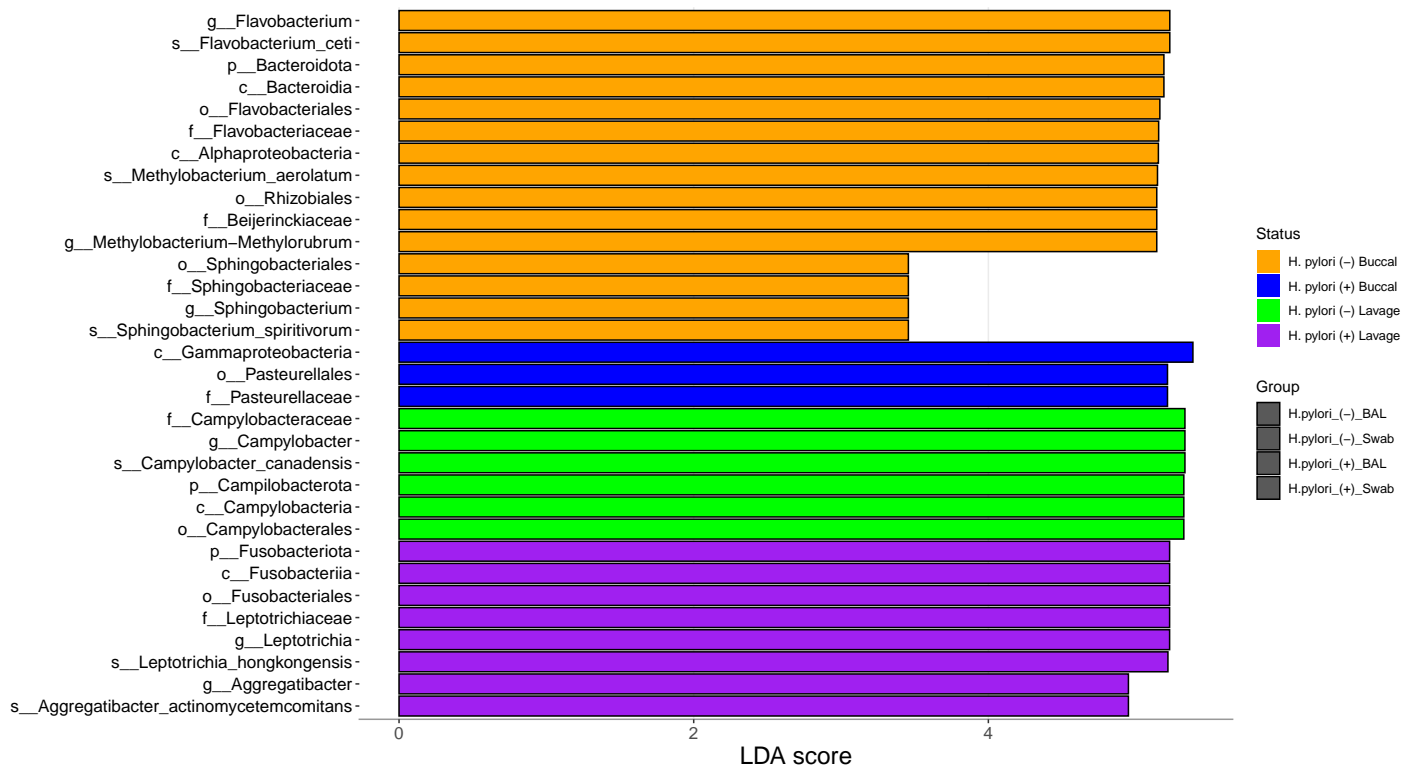
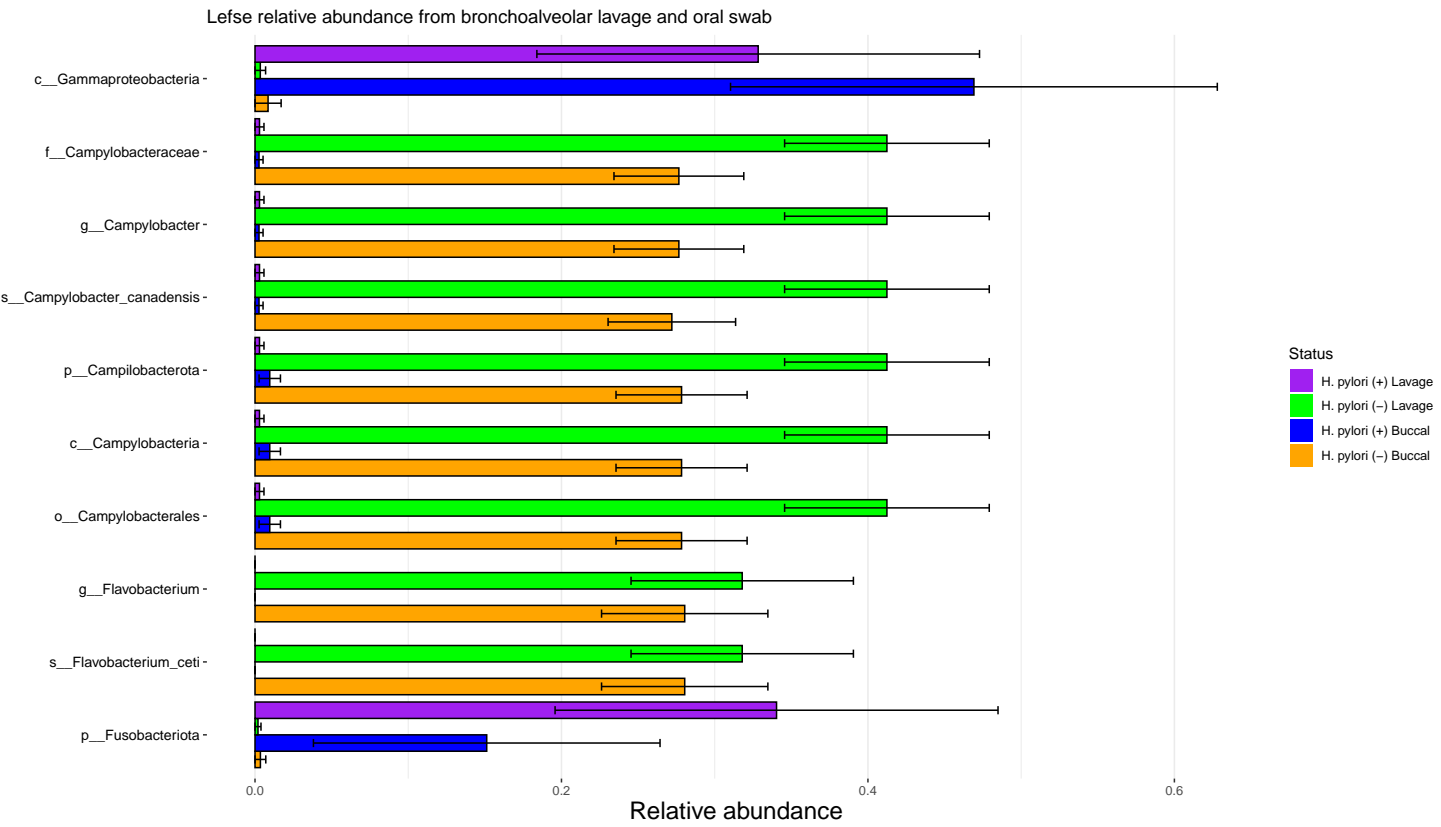


Table 2: Lefse taxa from bronchoalveolar lavage and oral swab

Taxa				Group	pvalue	LDA
k__Bacteria p__Proteobacteria c__Gammaproteobacteria	k__Bacteria p__Proteobacteria c__Gammaproteobacteria	k__Bacteria p__Proteobacteria c__Gammaproteobacteria	k__Bacteria p__Proteobacteria c__Gammaproteobacteria	H.pylori (-) Swab	0.001	5.388
k__Bacteria p__Campylobacteriales c__Campylobacteriaceae	k__Bacteria p__Campylobacteriales c__Campylobacteriaceae	k__Bacteria p__Campylobacteriales c__Campylobacteriaceae	k__Bacteria p__Campylobacteriales c__Campylobacteriaceae	H.pylori (+) BAL	0.000	5.334
k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter	H.pylori (+) BAL	0.000	5.334
k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	H.pylori (+) BAL	0.000	5.334
k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	k__Bacteria p__Campylobacteriales c__Campylobacteriales f__Campylobacter s__Campylobacter_canadensis	H.pylori (+) BAL	0.000	5.327

Lefse table

Relative abundance of differential taxa



Lefse and differential abundance for bronchoalveolar lavage

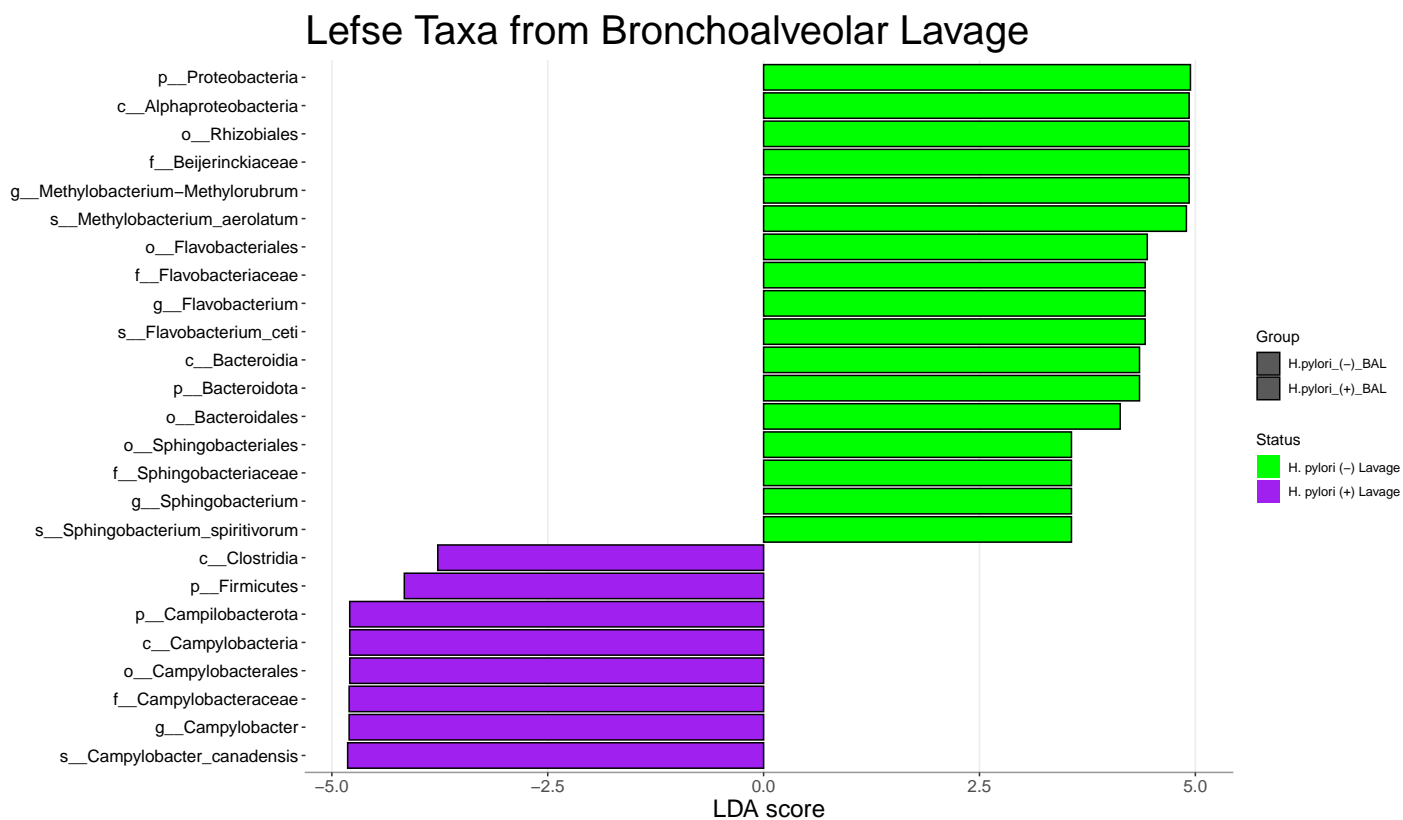
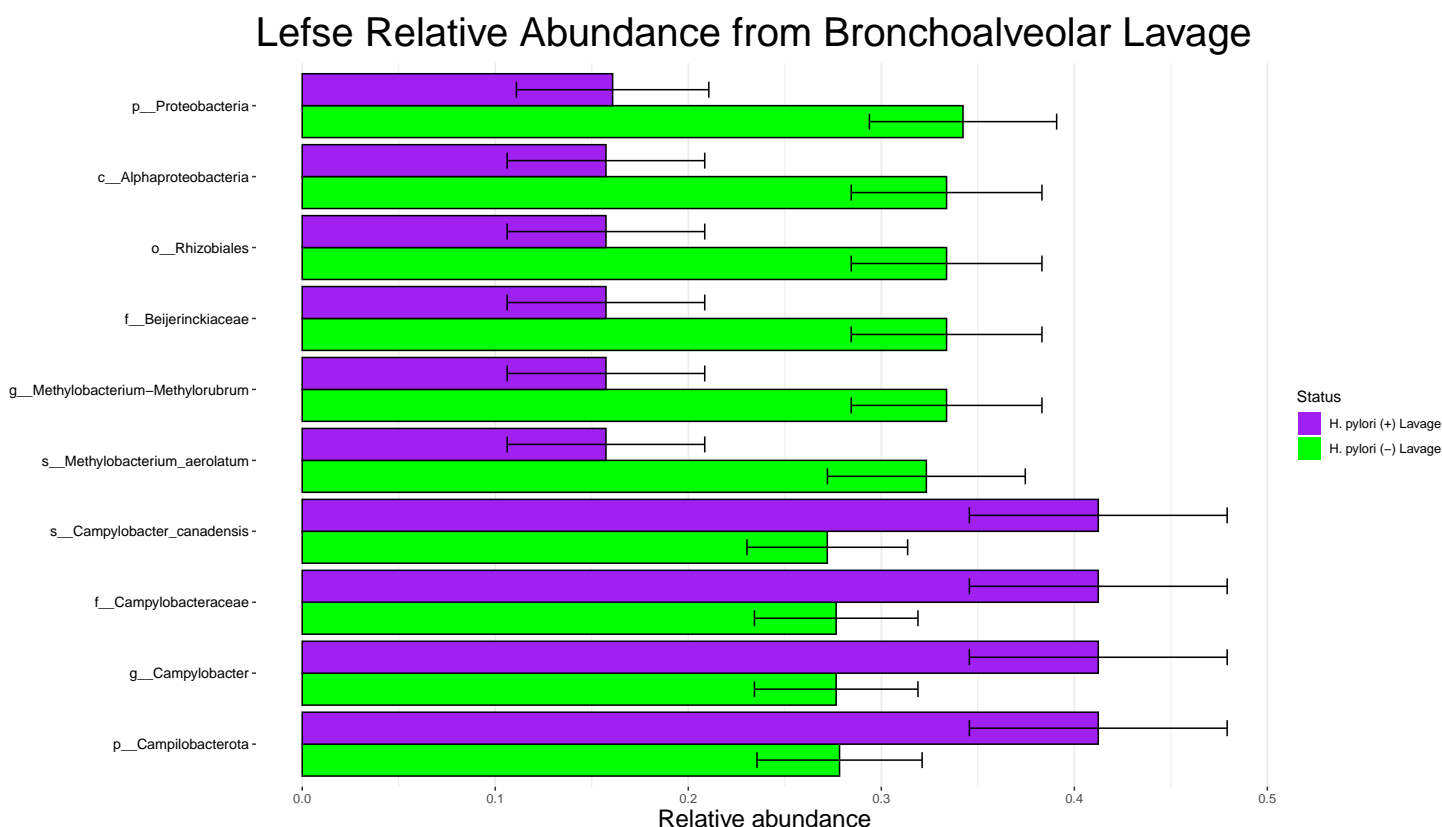


Table 3: Lefse Taxa from Bronchoalveolar Lavage[illegible]

Lefse table

Relative abundance of differential taxa



Lefse and differential abundance for oral swabs

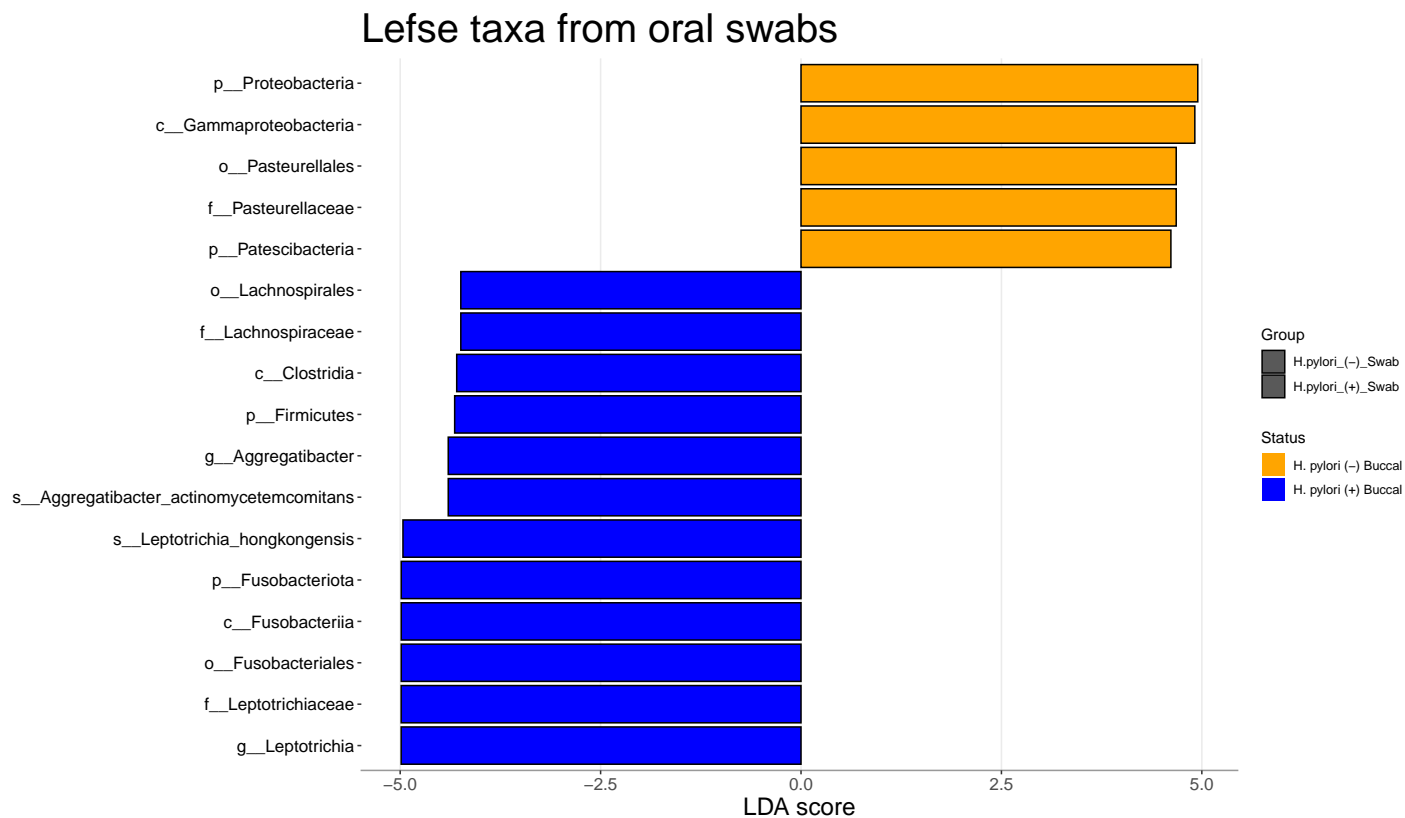
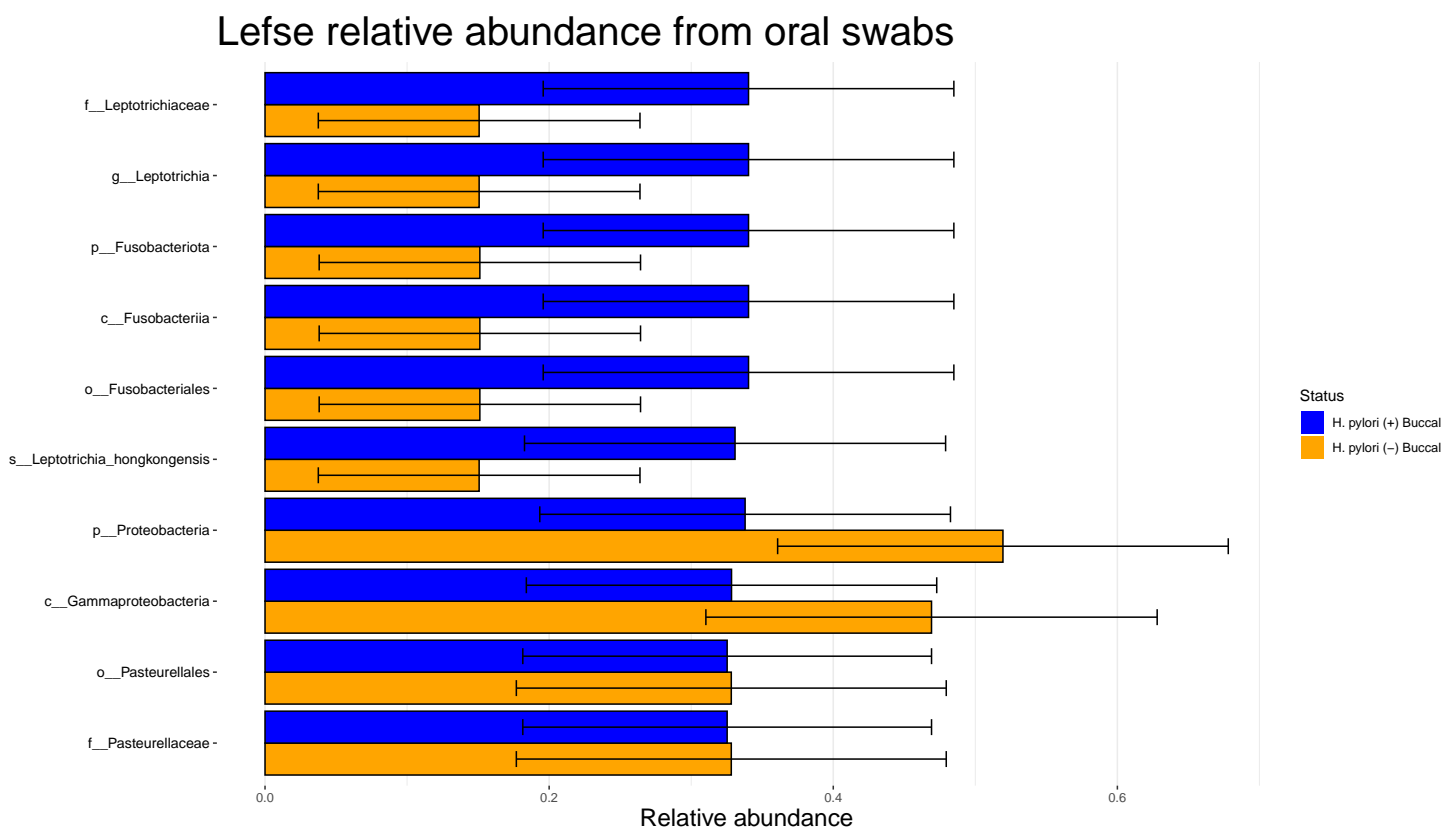


Table 4: Lefse Taxa from oral swabs[illegible]

Lefse table

Relative abundance of differential taxa

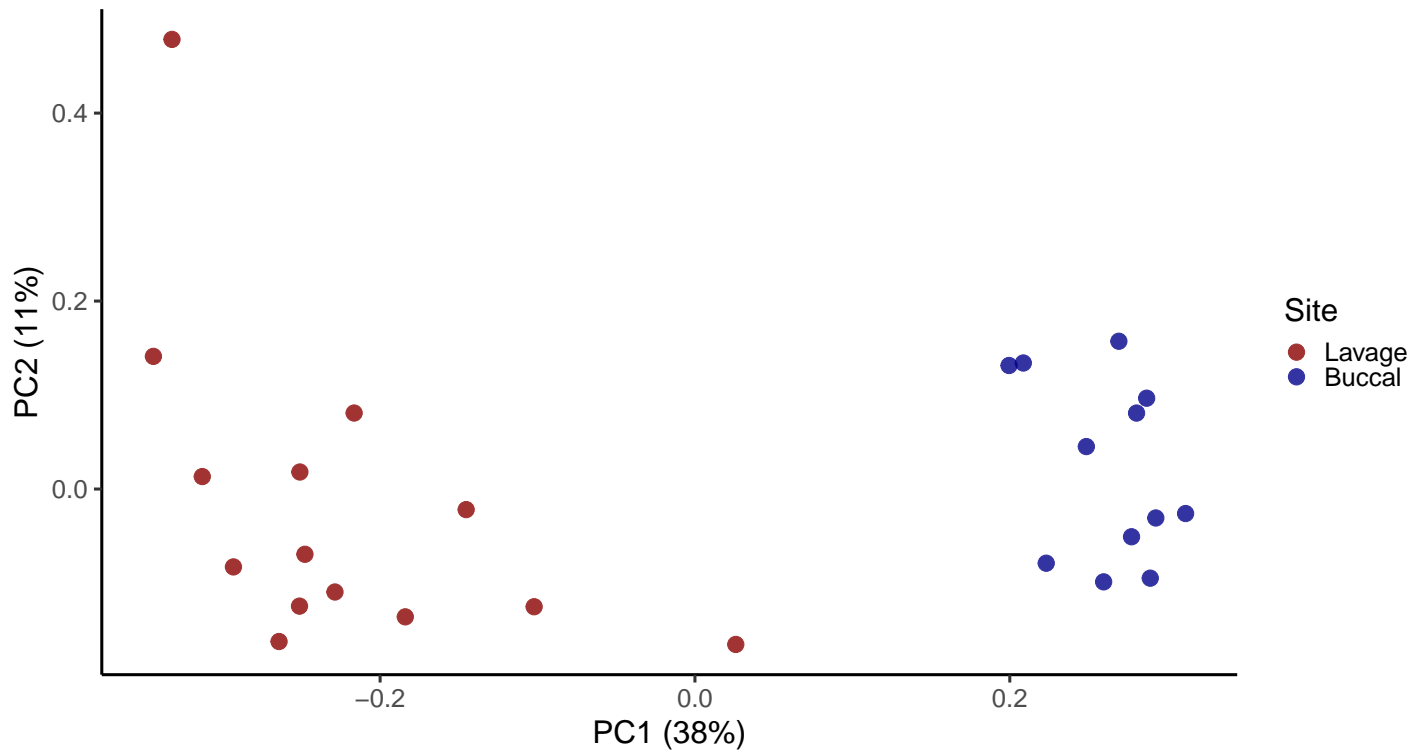


Beta diversity

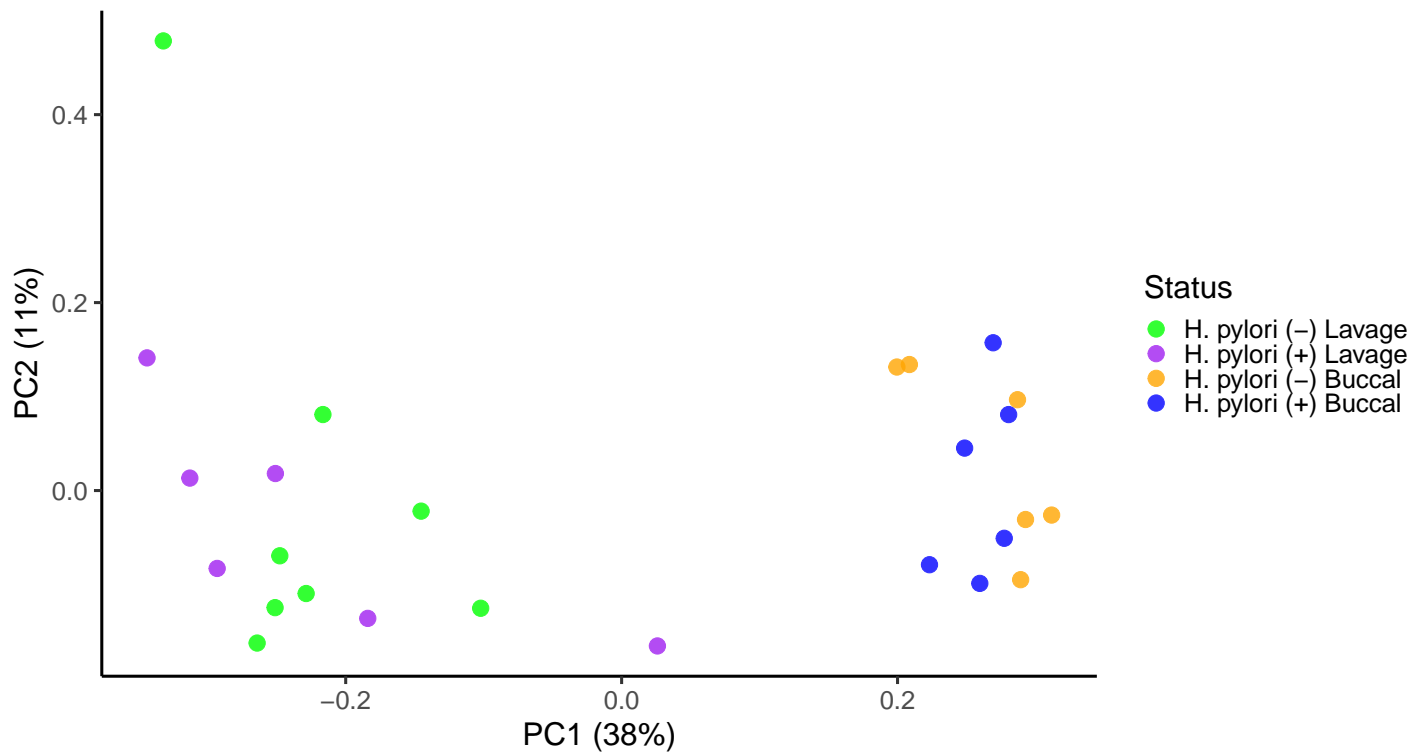
Unweighted unifrac PCoA plots

##	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

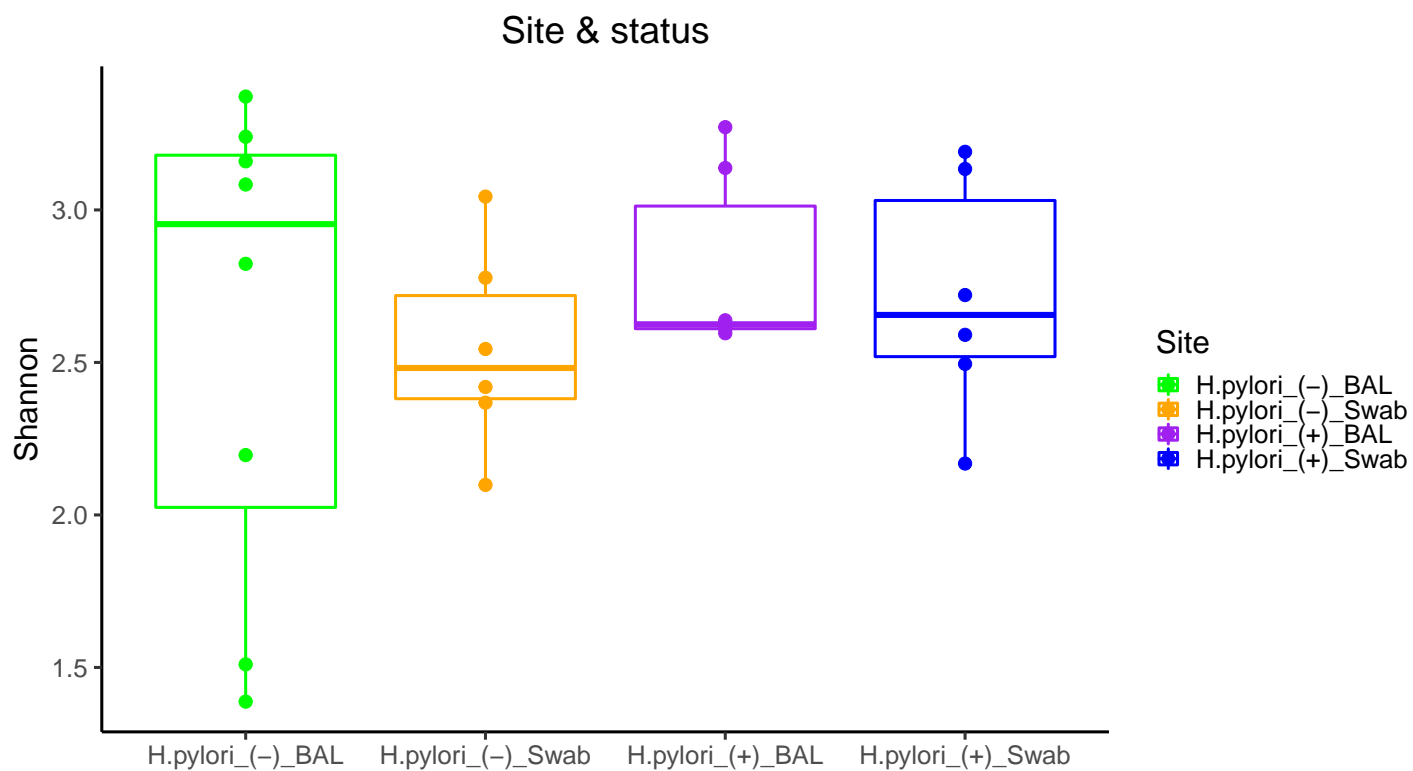


Status Unweighted unifrac PCoA

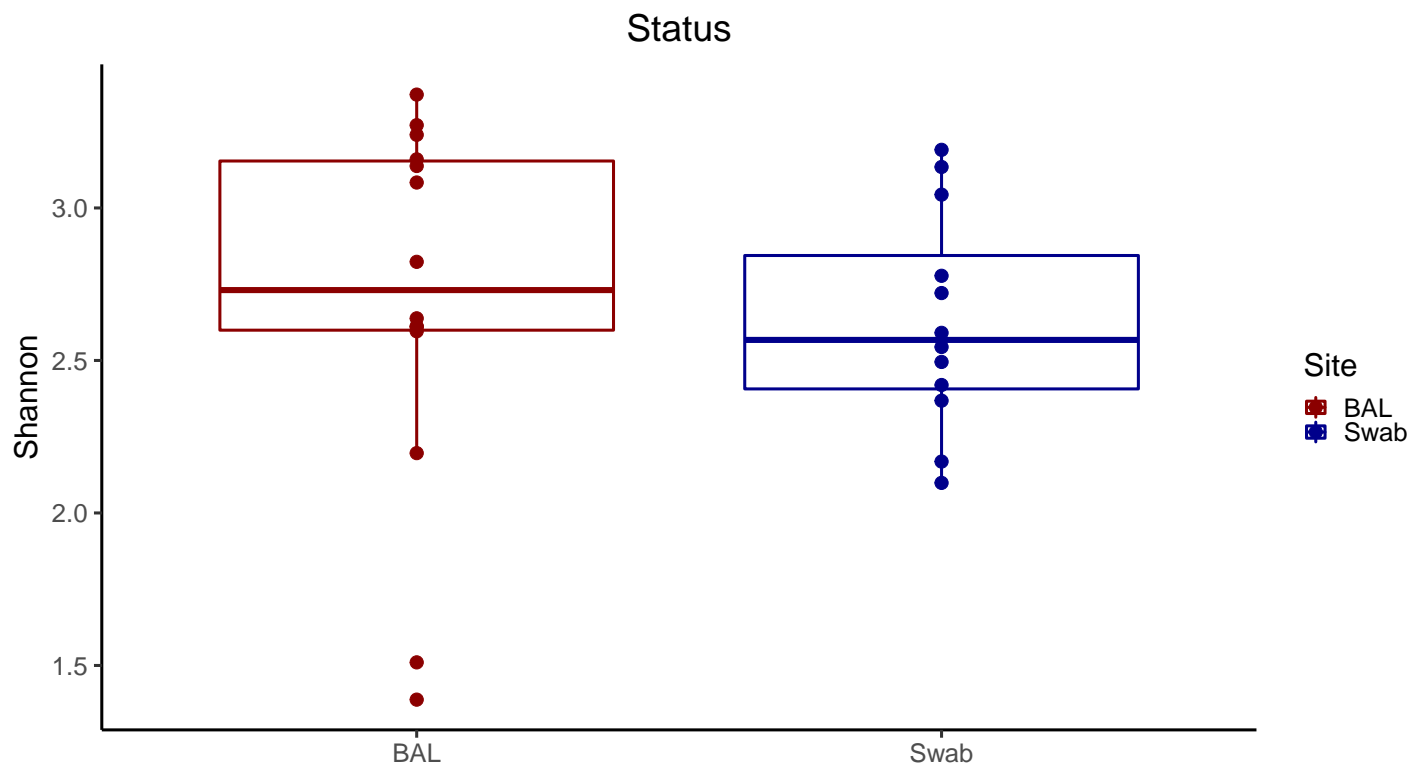


Alpha Diversity

Shannon index by site and H. pylori status



Shannon index by site only



Helicobacter positive respiratory samples

Helicobacter positive samples separated by site

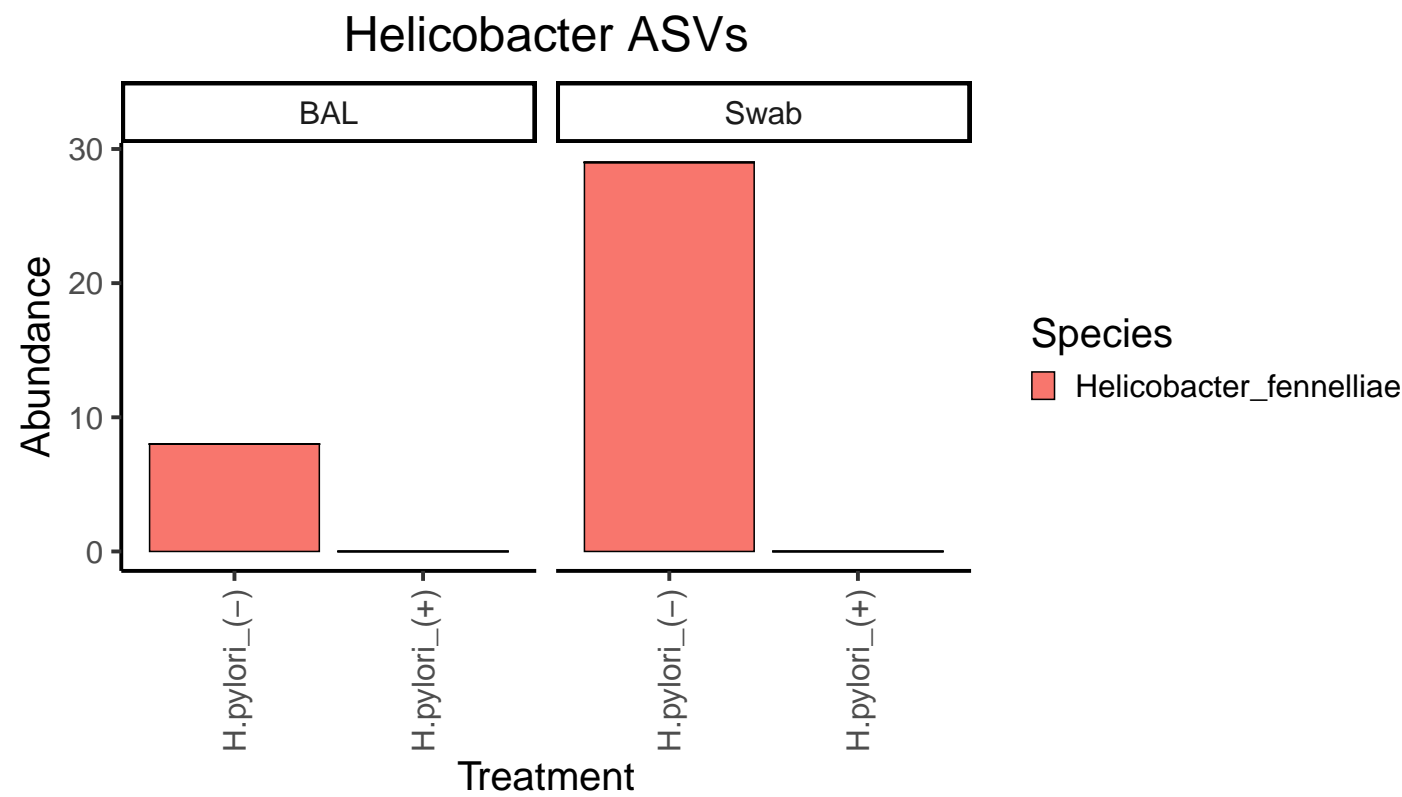
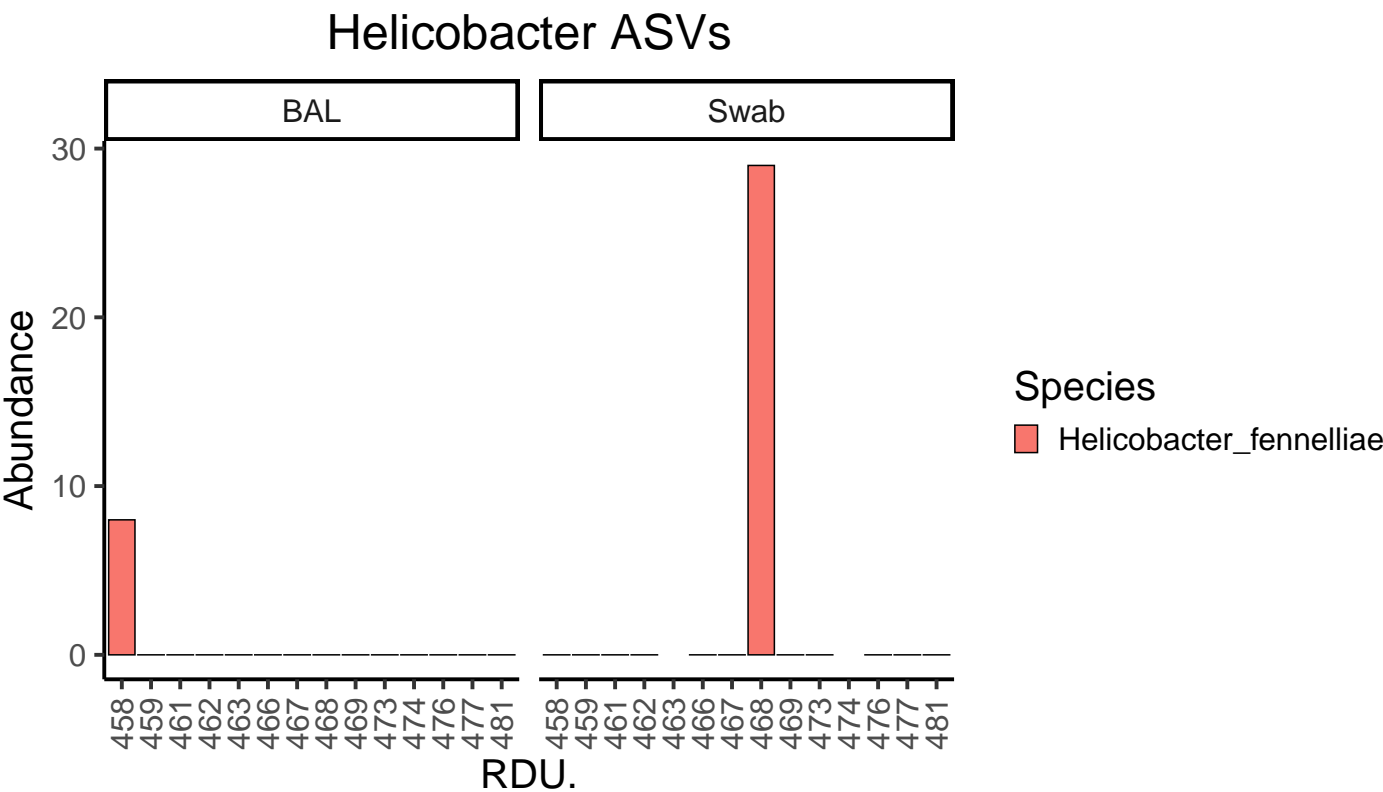


Table 5: All alpha diversity measurees

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	



Taxa barplots

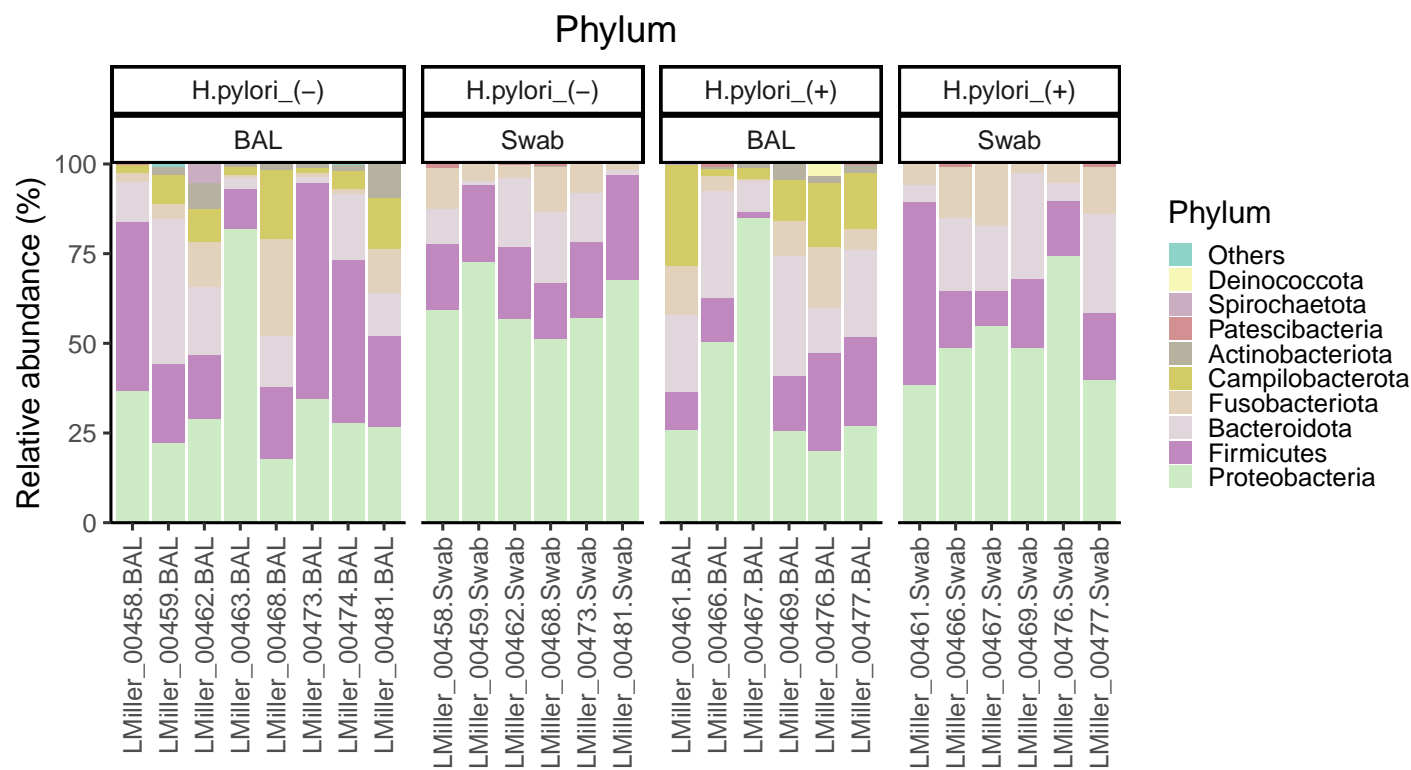


Figure 3: Microbiota Composition at Phylum level.

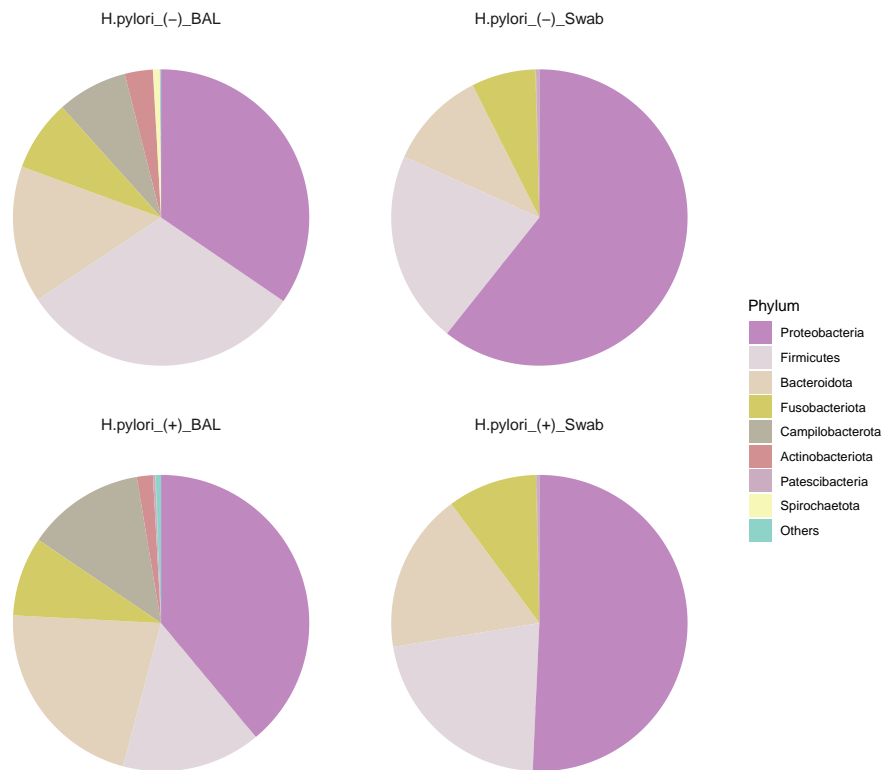


Figure 4: Microbiota Composition at Phylum level.

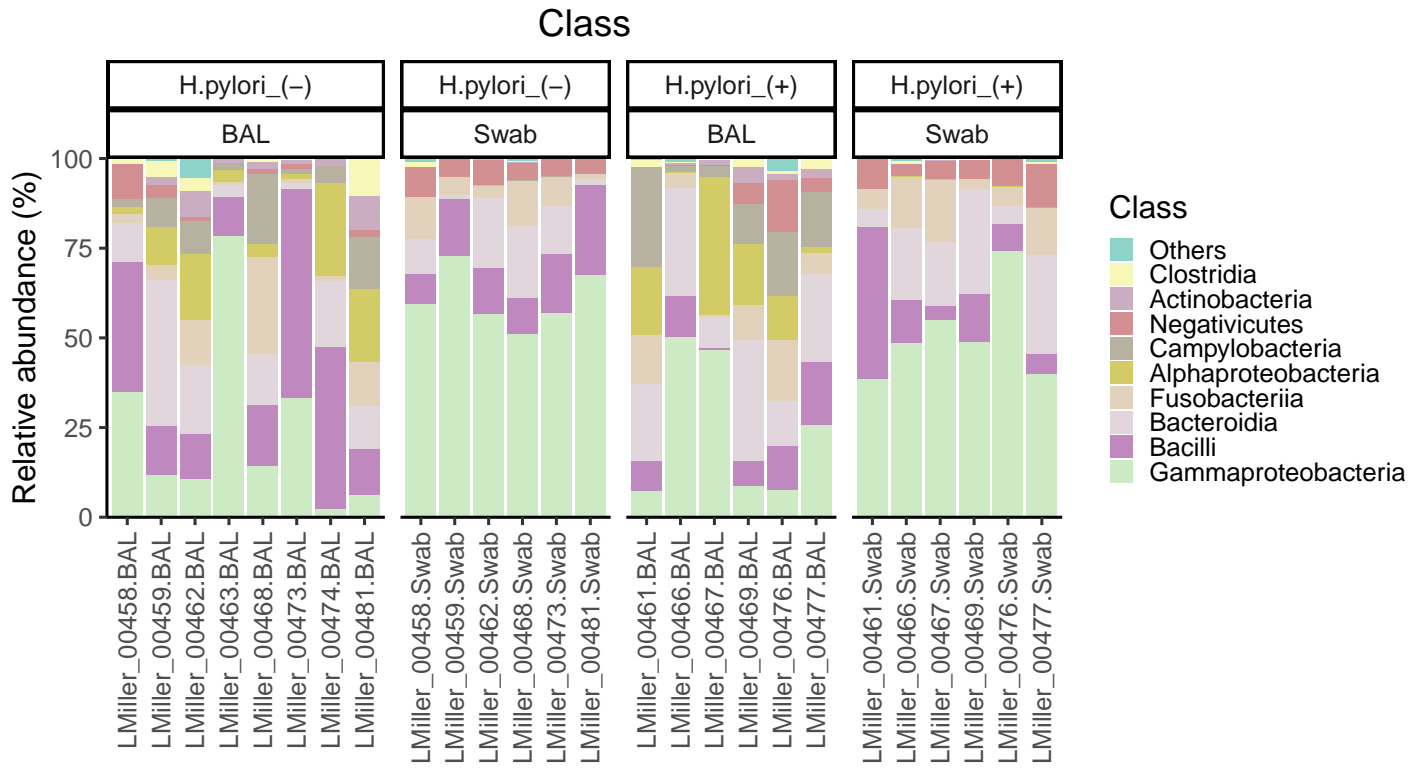


Figure 5: Microbiota Composition at Class level.

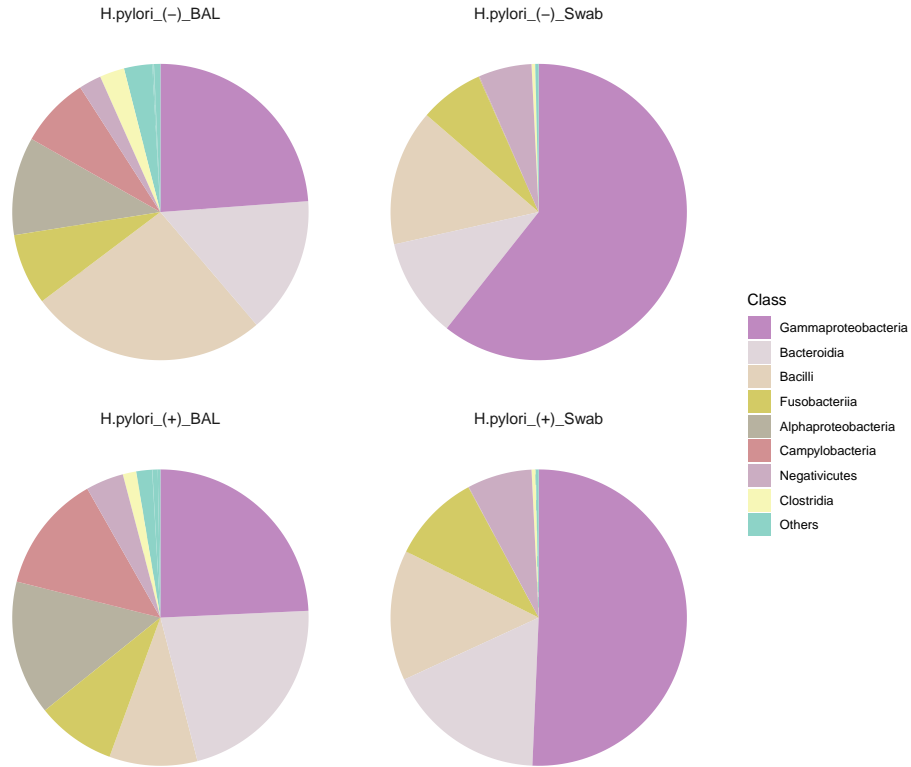


Figure 6: Microbiota Composition at Class level.

Table 6: 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%

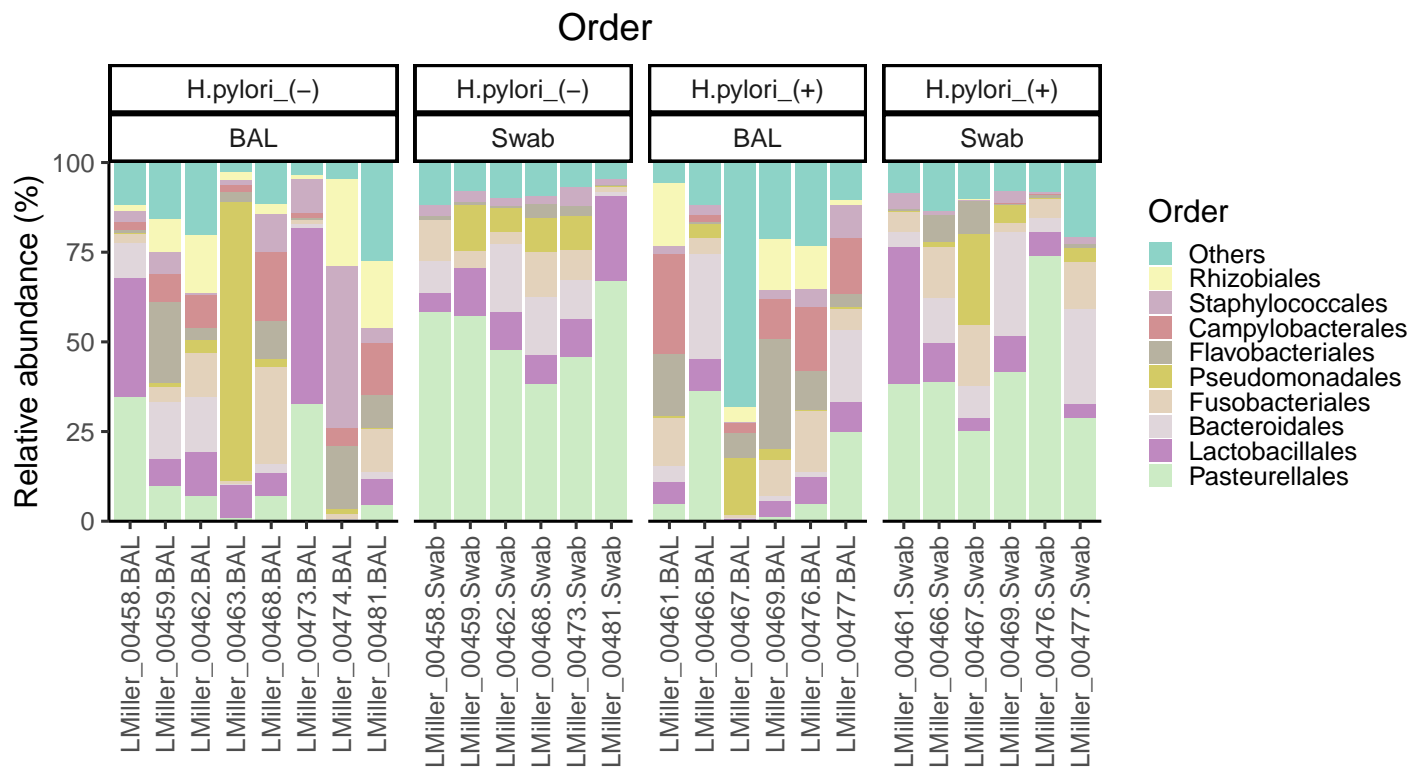


Figure 7: Microbiota Composition at Order level.

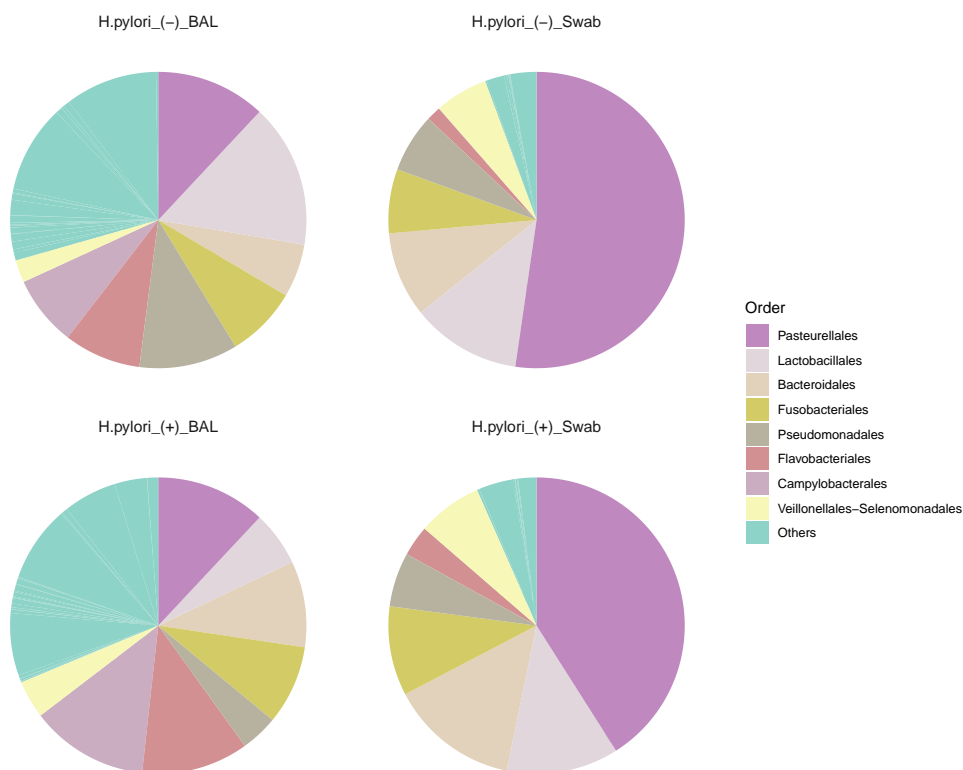


Figure 8: Microbiota Composition at Order level.

Table 7: 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%

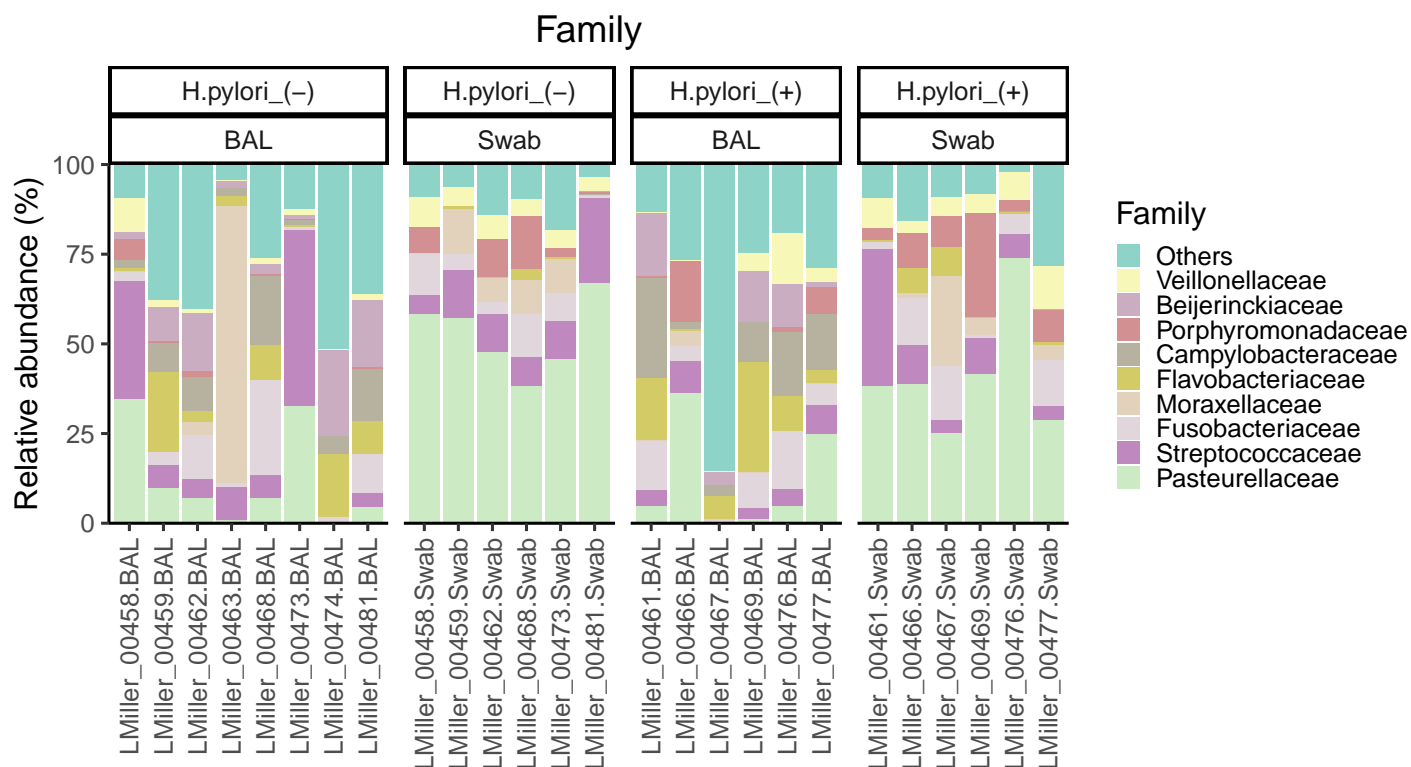


Figure 9: Microbiota Composition at Family level.

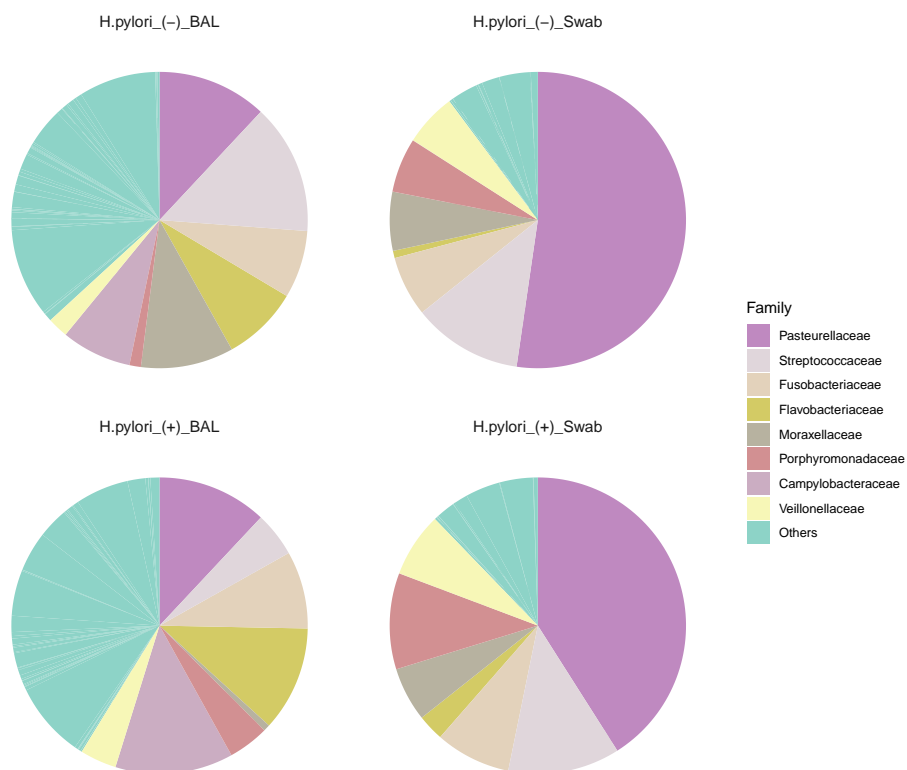


Figure 10: Microbiota Composition at Family level.

Table 8: 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%

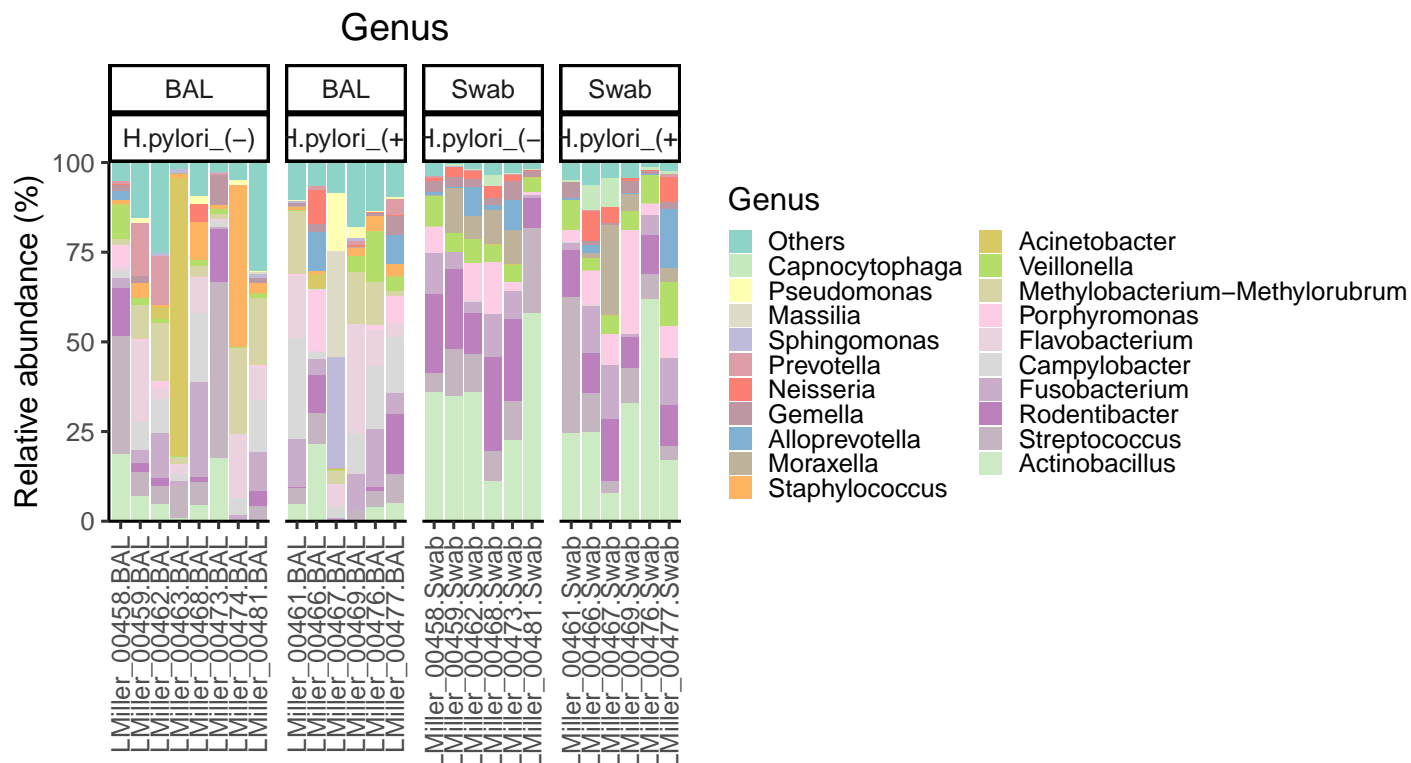


Figure 11: Microbiota Composition at Genus level.

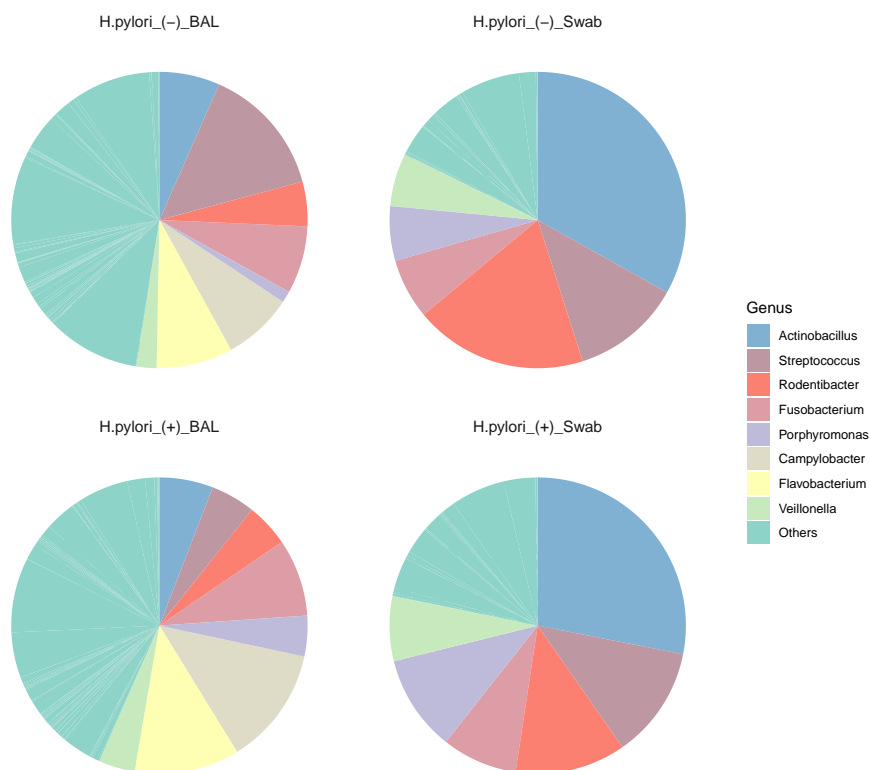


Figure 12: Microbiota Composition at Genus level.

Table 9: 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%

Genera correlation with IL8 concentration (Serum and BAL)

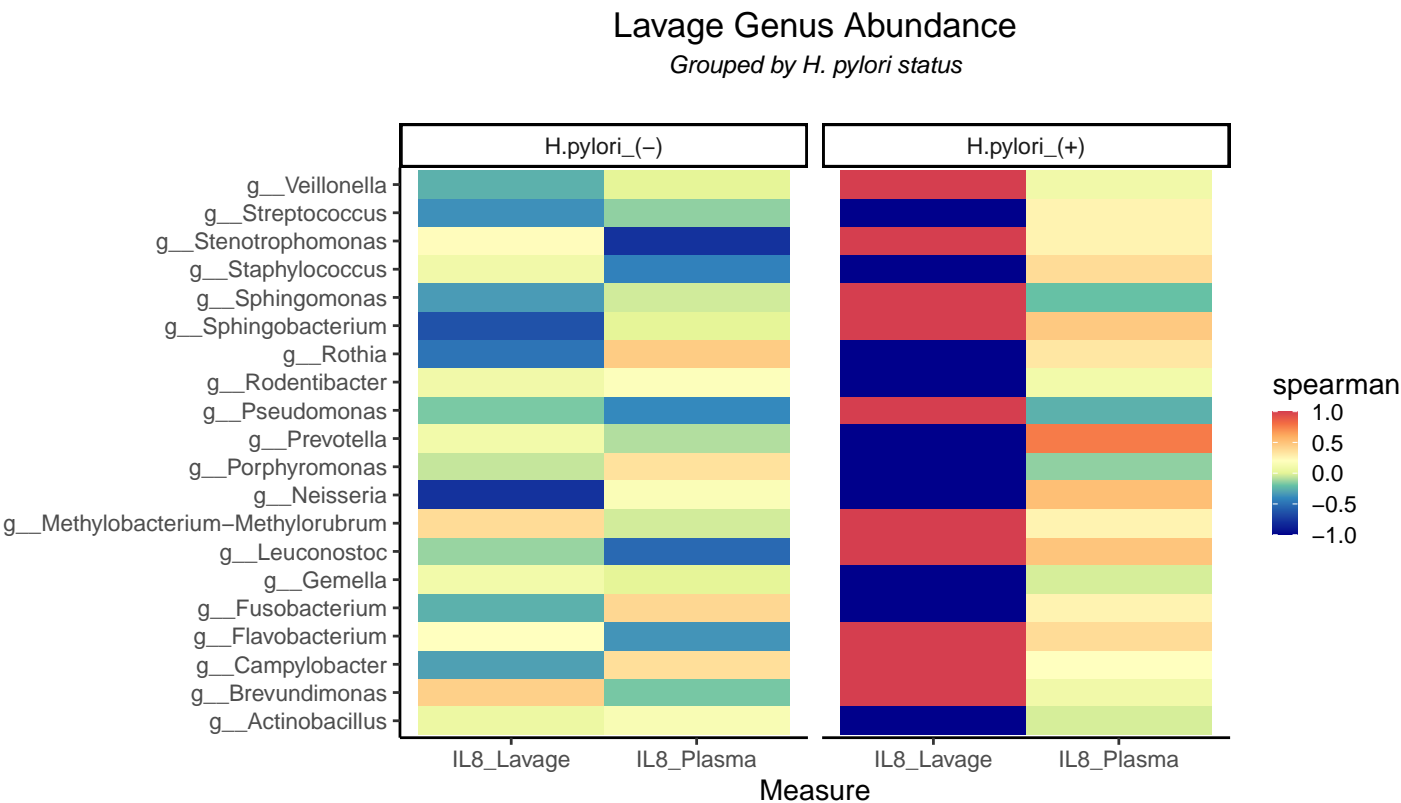


Figure 13: IL8 and lavage genus abundance Spearman correlations separated by H. pylori status

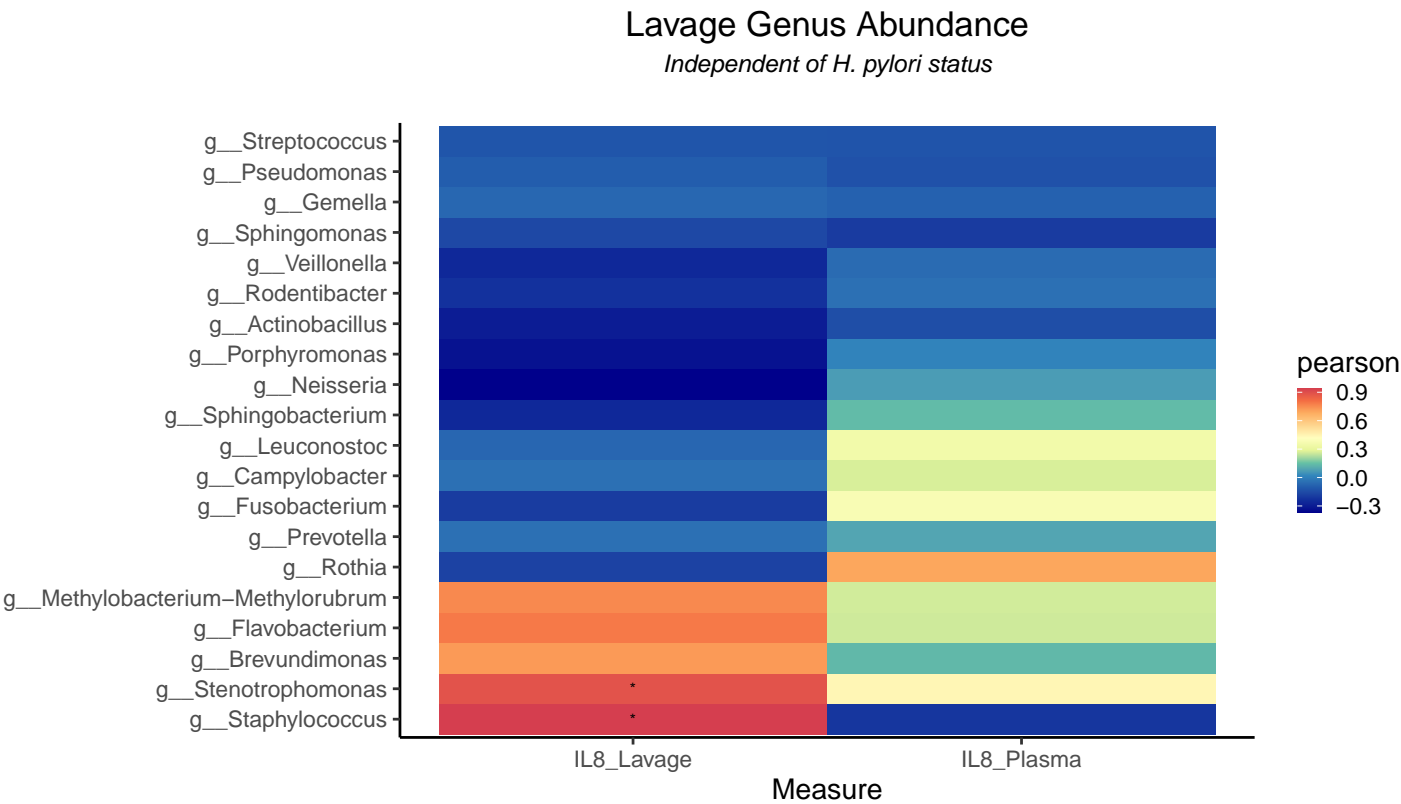


Figure 14: IL8 and lavage genus abundance Spearman correlations independent of H. pylori status

Table 10: 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%

Table 11: Independent of *H. pylori* status

Type	Taxa	Env	Correlation	Pvalue	AdjPvalue	Significance
V1	BAL k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Xanthomonadales f__Xanthomonadaceae g__Stenotrophomonas	IL8_Lavage	0.88	0.00	0.04	*
V2	BAL k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pseudomonadales f__Pseudomonadaceae g__Pseudomonas	IL8_Lavage	-0.10	0.82	0.92	
V3	BAL k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Caulobacteriales f__Caulobacteraceae g__Brevundimonas	IL8_Lavage	0.72	0.05	0.18	
V4	BAL k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Streptococcaceae g__Streptococcus	IL8_Lavage	-0.12	0.77	0.92	
V5	BAL k__Bacteria p__Firmicutes c__Bacilli o__Lactobacillales f__Leuconostocaceae g__Leuconostoc	IL8_Lavage	-0.07	0.87	0.92	
V6	BAL k__Bacteria p__Fusobacteriota c__Fusobacteriia o__Fusobacteriales f__Fusobacteriaceae g__Fusobacterium	IL8_Lavage	-0.20	0.64	0.92	
V7	BAL k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae g__Rodentibacter	IL8_Lavage	-0.22	0.59	0.92	*
V8	BAL k__Bacteria p__Campilobacterota c__Campylobacteria o__Campylobacteriales f__Campylobacteraceae g__Campylobacter	IL8_Lavage	-0.04	0.92	0.92	
V9	BAL k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Staphylococcaceae g__Staphylococcus	IL8_Lavage	0.93	0.00	0.01	
V10	BAL k__Bacteria p__Firmicutes c__Negativicutes o__Veillonellales f__Veillonellaceae g__Veillonella	IL8_Lavage	-0.25	0.54	0.92	
V11	BAL k__Bacteria p__Bacteroidota c__Bacteroidia o__Flavobacteriales f__Flavobacteriaceae g__Flavobacterium	IL8_Lavage	0.78	0.02	0.15	
V12	BAL k__Bacteria p__Actinobacteriota c__Actinobacteria o__Micrococcales f__Micrococcaceae g__Rothia	IL8_Lavage	-0.18	0.68	0.92	
V13	BAL k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Rhizobiales f__Beijerinckiaceae g__Methylobacterium-Methylobacter	IL8_Lavage	0.75	0.03	0.16	
V14	BAL k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Porphyromonadaceae g__Porphyromonas	IL8_Lavage	-0.33	0.43	0.92	
V15	BAL k__Bacteria p__Bacteroidota c__Bacteroidia o__Sphingobacteriales f__Sphingobacteriaceae g__Sphingobacterium	IL8_Lavage	-0.25	0.54	0.92	
V16	BAL k__Bacteria p__Proteobacteria c__Alphaproteobacteria o__Sphingomonadales f__Sphingomonadaceae g__Sphingomonas	IL8_Lavage	-0.16	0.71	0.92	
V17	BAL k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Pasteurellales f__Pasteurellaceae g__Actinobacillus	IL8_Lavage	-0.29	0.48	0.92	
V18	BAL k__Bacteria p__Bacteroidota c__Bacteroidia o__Bacteroidales f__Prevotellaceae g__Prevotella	IL8_Lavage	-0.04	0.92	0.92	
V19	BAL k__Bacteria p__Firmicutes c__Bacilli o__Staphylococcales f__Gemellaceae g__Gemella	IL8_Lavage	-0.07	0.87	0.92	
V20	BAL k__Bacteria p__Proteobacteria c__Gammaproteobacteria o__Burkholderiales f__Neisseriaceae g__Neisseria	IL8_Lavage	-0.37	0.37	0.92	

Lavage Alpha Diversity
*Independent of *H. pylori* status*

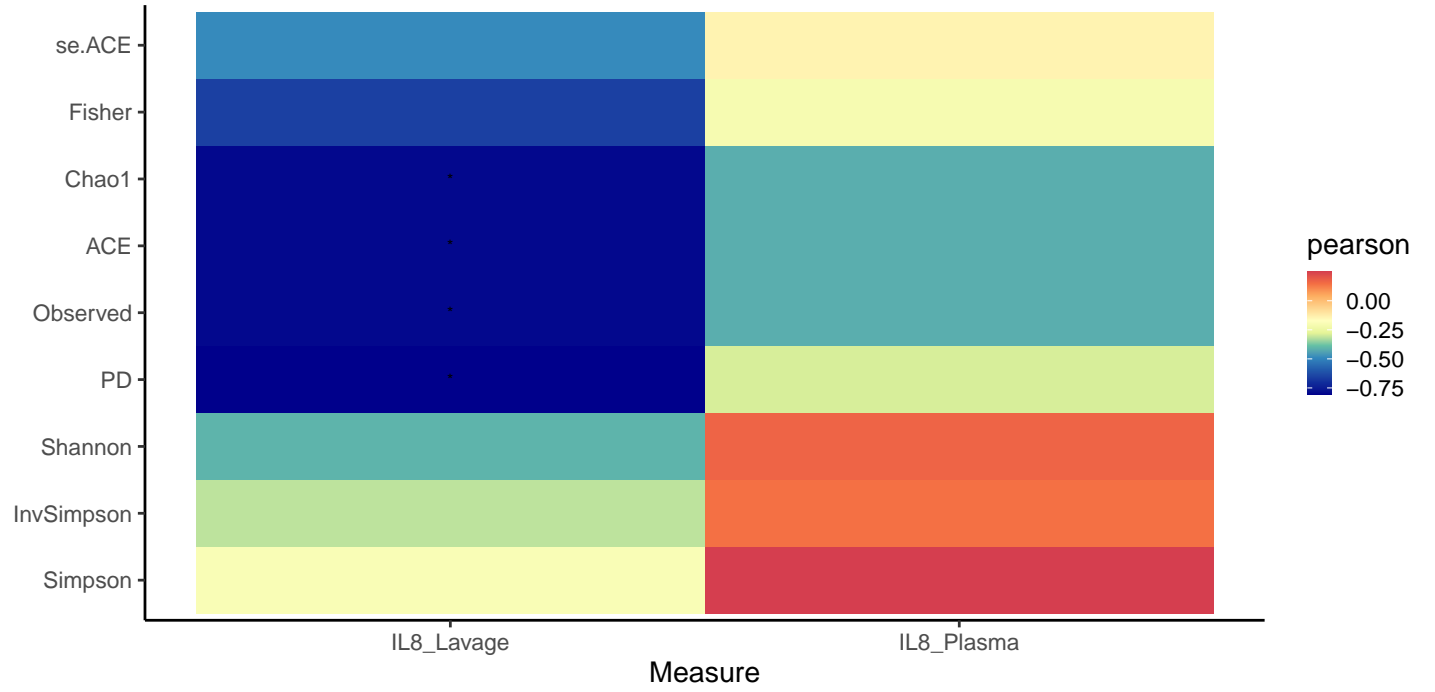
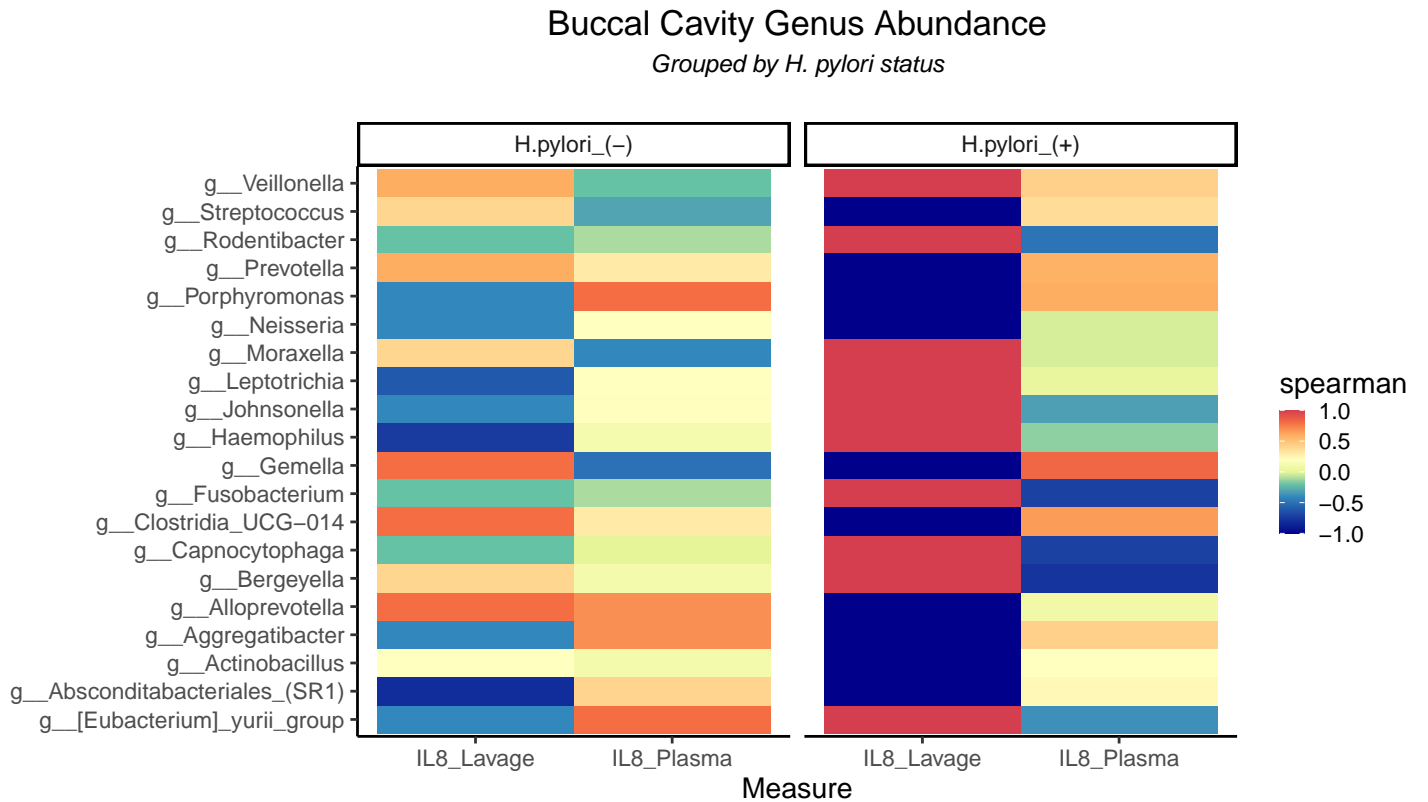


Figure 15: IL8 and lavage alpha diversity Spearman correlations independent of *H. pylori* status.

Table 12: Independent of *H. pylori* status

	Type	Taxa	Env	Correlation	Pvalue	AdjPvalue	Significance
V1	All	Observed	IL8_Lavage	-0.79	0.02	0.04	*
V2	All	Chao1	IL8_Lavage	-0.79	0.02	0.04	*
V4	All	ACE	IL8_Lavage	-0.79	0.02	0.04	*
V5	All	se.ACE	IL8_Lavage	-0.49	0.22	0.33	
V6	All	Shannon	IL8_Lavage	-0.41	0.31	0.40	
V7	All	Simpson	IL8_Lavage	-0.20	0.64	0.64	
V8	All	InvSimpson	IL8_Lavage	-0.32	0.44	0.50	
V9	All	Fisher	IL8_Lavage	-0.66	0.08	0.14	
V11	All	PD	IL8_Lavage	-0.81	0.02	0.04	*
V12	All	Observed	IL8_Plasma	-0.42	0.15	0.46	
V13	All	Chao1	IL8_Plasma	-0.42	0.15	0.46	
V15	All	ACE	IL8_Plasma	-0.42	0.15	0.46	
V16	All	se.ACE	IL8_Plasma	-0.14	0.65	0.65	
V17	All	Shannon	IL8_Plasma	0.17	0.59	0.65	
V18	All	Simpson	IL8_Plasma	0.25	0.41	0.65	
V19	All	InvSimpson	IL8_Plasma	0.14	0.65	0.65	
V20	All	Fisher	IL8_Plasma	-0.21	0.49	0.65	
V22	All	PD	IL8_Plasma	-0.29	0.33	0.65	
NA	NA	NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA	NA	NA

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

Buccal Cavity Genus Abundance

Independent of H. pylori status

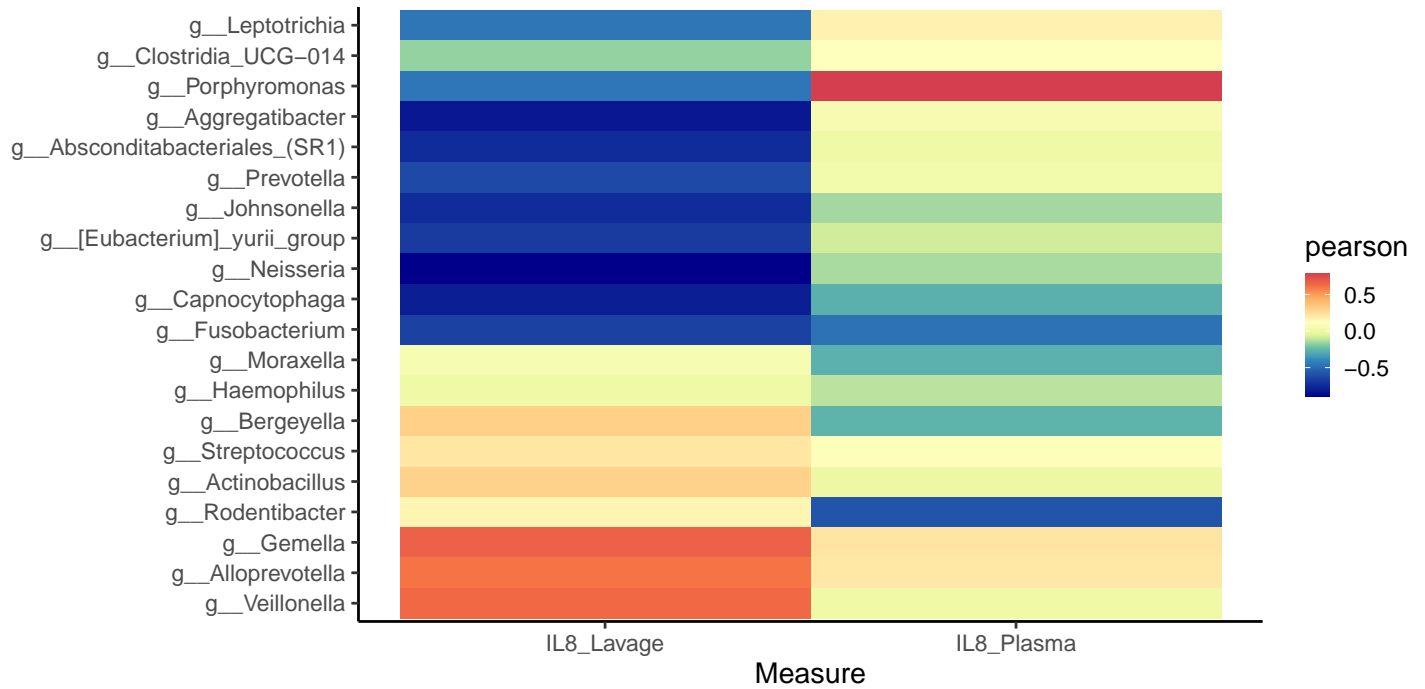


Figure 17: IL8 and Buccal genus abundance Spearman correlations independent of *H. pylori* status

Table 13: Independent of *H. pylori* status

Type	Taxa	Env	Correlation	Pvalue	AdjPvalue	Significance
V1	Swab k_Bacteria p_Fusobacteriota c_Fusobacteriia o_Fusobacteriales f_Leptotrichiaceae g_Leptotrichia	IL8_Lavage	-0.45	0.37	0.57	
V2	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Rodentibacter	IL8_Lavage	0.16	0.76	0.85	
V3	Swab k_Bacteria p_Firmicutes c_Bacilli o_Staphylococcales f_Gemellaceae g_Gemella	IL8_Lavage	0.67	0.15	0.36	
V4	Swab k_Bacteria p_Firmicutes c_Clostridia o_Peptostreptococcales-Tissierellales f_Peptostreptococcaceae g_[Eubacterium]_yurii_group	IL8_Lavage	-0.67	0.14	0.36	
V5	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pseudomonadales f_Moraxellaceae g_Moraxella	IL8_Lavage	0.07	0.90	0.95	
V6	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Burkholderiales f_Neisseriaceae g_Neisseria	IL8_Lavage	-0.89	0.02	0.34	
V7	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Actinobacillus	IL8_Lavage	0.30	0.56	0.74	
V8	Swab k_Bacteria p_Bacteroidota c_Bacteroidales f_Porphyromonadaceae g_Porphyromonas	IL8_Lavage	-0.45	0.37	0.57	
V9	Swab k_Bacteria p_Fusobacteriota c_Fusobacteriia o_Fusobacteriales f_Fusobacteriaceae g_Fusobacterium	IL8_Lavage	-0.65	0.16	0.36	
V10	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Aggregatibacter	IL8_Lavage	-0.82	0.04	0.36	
V11	Swab k_Bacteria p_Firmicutes c_Clostridia o_Lachnospirales f_Lachnospiraceae g_Johnsonella	IL8_Lavage	-0.73	0.10	0.36	
V12	Swab k_Bacteria p_Firmicutes c_Negativicutes o_Veillonellales-Selenomonadales f_Veillonellaceae g_Veillonella	IL8_Lavage	0.64	0.17	0.36	
V13	Swab k_Bacteria p_Firmicutes c_Bacilli o_Lactobacillales f_Streptococcaceae g_Streptococcus	IL8_Lavage	0.22	0.68	0.85	
V14	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Flavobacteriales f_Flavobacteriaceae g_Capnocytophaga	IL8_Lavage	-0.79	0.06	0.36	
V15	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Bacteroidales f_Prevotellaceae g_Alloprevotella	IL8_Lavage	0.61	0.20	0.36	
V16	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Bacteroidales f_Prevotellaceae g_Prevotella	IL8_Lavage	-0.62	0.19	0.36	
V17	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Flavobacteriales f_Weeksellaceae g_Bergeyella	IL8_Lavage	0.31	0.55	0.74	
V18	Swab k_Bacteria p_Firmicutes c_Clostridia o_Clostridia_UCG-014 f_Clostridia_UCG-014 g_Clostridia_UCG-014	IL8_Lavage	-0.17	0.75	0.85	
V19	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Haemophilus	IL8_Lavage	0.01	0.99	0.99	
V20	Swab k_Bacteria p_Patescibacteria c_Gracilibacteria o_Absconditabacteriales_(SR1) f_Absconditabacteriales_(SR1) g_Absconditabacteriales_(SR1)	IL8_Lavage	-0.73	0.10	0.36	
V21	Swab k_Bacteria p_Fusobacteriota c_Fusobacteriia o_Fusobacteriales f_Leptotrichiaceae g_Leptotrichia	IL8_Plasma	0.17	0.61	0.99	
V22	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Rodentibacter	IL8_Plasma	-0.57	0.06	0.64	
V23	Swab k_Bacteria p_Firmicutes c_Bacilli o_Staphylococcales f_Gemellaceae g_Gemella	IL8_Plasma	0.23	0.50	0.99	
V24	Swab k_Bacteria p_Firmicutes c_Clostridia o_Peptostreptococcales-Tissierellales f_Peptostreptococcaceae g_[Eubacterium]_yurii_group	IL8_Plasma	-0.08	0.81	0.99	
V25	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pseudomonadales f_Moraxellaceae g_Moraxella	IL8_Plasma	-0.27	0.42	0.99	
V26	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Burkholderiales f_Neisseriaceae g_Neisseria	IL8_Plasma	-0.14	0.69	0.99	
V27	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Actinobacillus	IL8_Plasma	0.00	0.99	0.99	
V28	Swab k_Bacteria p_Bacteroidota c_Bacteroidales f_Porphyromonadaceae g_Porphyromonas	IL8_Plasma	0.79	0.00	0.07	
V29	Swab k_Bacteria p_Fusobacteriota c_Fusobacteriia o_Fusobacteriales f_Fusobacteriaceae g_Fusobacterium	IL8_Plasma	-0.47	0.15	0.98	
V30	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Aggregatibacter	IL8_Plasma	0.06	0.87	0.99	
V31	Swab k_Bacteria p_Firmicutes c_Clostridia o_Lachnospirales f_Lachnospiraceae g_Johnsonella	IL8_Plasma	-0.14	0.67	0.99	
V32	Swab k_Bacteria p_Firmicutes c_Negativicutes o_Veillonellales-Selenomonadales f_Veillonellaceae g_Veillonella	IL8_Plasma	0.01	0.98	0.99	
V33	Swab k_Bacteria p_Firmicutes c_Bacilli o_Lactobacillales f_Streptococcaceae g_Streptococcus	IL8_Plasma	0.10	0.77	0.99	
V34	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Flavobacteriales f_Flavobacteriaceae g_Capnocytophaga	IL8_Plasma	-0.27	0.42	0.99	
V35	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Bacteroidales f_Prevotellaceae g_Alloprevotella	IL8_Plasma	0.21	0.53	0.99	
V36	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Bacteroidales f_Prevotellaceae g_Prevotella	IL8_Plasma	0.03	0.93	0.99	
V37	Swab k_Bacteria p_Bacteroidota c_Bacteroidia o_Flavobacteriales f_Weeksellaceae g_Bergeyella	IL8_Plasma	-0.26	0.44	0.99	
V38	Swab k_Bacteria p_Firmicutes c_Clostridia o_Clostridia_UCG-014 f_Clostridia_UCG-014 g_Clostridia_UCG-014	IL8_Plasma	0.11	0.75	0.99	
V39	Swab k_Bacteria p_Proteobacteria c_Gammaproteobacteria o_Pasteurellales f_Pasteurellaceae g_Haemophilus	IL8_Plasma	-0.11	0.74	0.99	
V40	Swab k_Bacteria p_Patescibacteria c_Gracilibacteria o_Absconditabacteriales_(SR1) f_Absconditabacteriales_(SR1) g_Absconditabacteriales_(SR1)	IL8_Plasma	0.01	0.97	0.99	

Buccal Cavity Alpha Diversity

Independent of *H. pylori* status

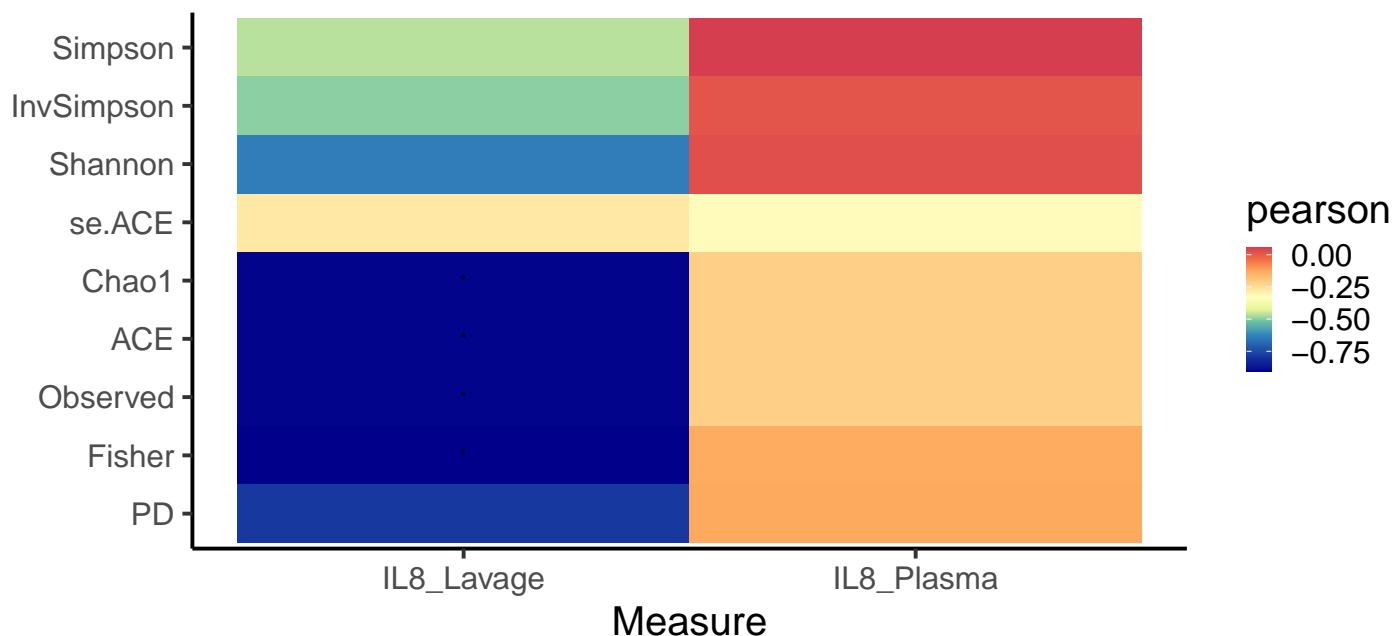


Figure 18: IL8 and Buccal alpha diversity Spearman correlations independent of *H. pylori* status

Table 14: Independent of *H. pylori* status

	Type	Taxa	Env	Correlation	Pvalue	AdjPvalue	Significance
V1	All	Observed	IL8_Lavage	-0.89	0.02	0.04	*
V2	All	Chao1	IL8_Lavage	-0.89	0.02	0.04	*
V4	All	ACE	IL8_Lavage	-0.89	0.02	0.04	*
V5	All	se.ACE	IL8_Lavage	-0.28	0.60	0.60	
V6	All	Shannon	IL8_Lavage	-0.64	0.17	0.26	
V7	All	Simpson	IL8_Lavage	-0.46	0.36	0.40	
V8	All	InvSimpson	IL8_Lavage	-0.50	0.32	0.40	
V9	All	Fisher	IL8_Lavage	-0.90	0.01	0.04	*
V11	All	PD	IL8_Lavage	-0.78	0.07	0.12	
V12	All	Observed	IL8_Plasma	-0.22	0.52	0.97	
V13	All	Chao1	IL8_Plasma	-0.22	0.52	0.97	
V15	All	ACE	IL8_Plasma	-0.22	0.52	0.97	
V16	All	se.ACE	IL8_Plasma	-0.32	0.34	0.97	
V17	All	Shannon	IL8_Plasma	0.02	0.95	0.97	
V18	All	Simpson	IL8_Plasma	0.05	0.88	0.97	
V19	All	InvSimpson	IL8_Plasma	0.01	0.97	0.97	
V20	All	Fisher	IL8_Plasma	-0.13	0.69	0.97	
V22	All	PD	IL8_Plasma	-0.13	0.70	0.97	
NA	NA	NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA	NA	NA

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
```

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## [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

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## [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		