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

Odds ratios of variables based on H. pylori status

```
## List of 93
##  $ line                    :List of 6
##   ..$ colour      : chr "black"
##   ..$ size        : num 0.5
##   ..$ linetype    : num 1
##   ..$ lineend     : chr "butt"
##   ..$ arrow       : logi FALSE
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_line" "element"
##  $ rect                    :List of 5
##   ..$ fill        : chr "white"
##   ..$ colour      : chr "black"
##   ..$ size        : num 0.5
##   ..$ linetype    : num 1
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_rect" "element"
##  $ text                    :List of 11
##   ..$ family      : chr ""
##   ..$ face        : chr "plain"
##   ..$ colour      : chr "black"
##   ..$ size        : num 30
##   ..$ hjust       : num 0.5
##   ..$ vjust       : num 0.5
##   ..$ angle       : num 0
##   ..$ lineheight  : num 0.9
```

```
##    ..$ margin        : 'margin' num [1:4] 0points 0points 0points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug          : logi FALSE
##    ..$ inherit.blank: logi FALSE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ title                      : NULL
##  $ aspect.ratio               : NULL
##  $ axis.title                 : NULL
##  $ axis.title.x               :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : NULL
##    ..$ size       : NULL
##    ..$ hjust      : NULL
##    ..$ vjust      : num 1
##    ..$ angle      : NULL
##    ..$ lineheight : NULL
##    ..$ margin     : 'margin' num [1:4] 2.75points 0points 0points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug      : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.title.x.top           :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : NULL
##    ..$ size       : NULL
##    ..$ hjust      : NULL
##    ..$ vjust      : num 0
##    ..$ angle      : NULL
##    ..$ lineheight : NULL
##    ..$ margin     : 'margin' num [1:4] 0points 0points 2.75points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug      : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.title.x.bottom        : NULL
##  $ axis.title.y               :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : NULL
##    ..$ size       : NULL
##    ..$ hjust      : NULL
##    ..$ vjust      : num 1
##    ..$ angle      : num 90
##    ..$ lineheight : NULL
##    ..$ margin     : 'margin' num [1:4] 0points 2.75points 0points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug      : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.title.y.left          : NULL
##  $ axis.title.y.right         :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : NULL
##    ..$ size       : NULL
##    ..$ hjust      : NULL
##    ..$ vjust      : num 0
##    ..$ angle      : num -90
```

```
##    ..$ lineheight   : NULL
##    ..$ margin       : 'margin' num [1:4] 0points 0points 0points 2.75points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug        : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.text                : List of 11
##    ..$ family       : NULL
##    ..$ face         : NULL
##    ..$ colour       : chr "grey30"
##    ..$ size         : 'rel' num 0.8
##    ..$ hjust        : NULL
##    ..$ vjust        : NULL
##    ..$ angle        : NULL
##    ..$ lineheight   : NULL
##    ..$ margin       : NULL
##    ..$ debug        : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.text.x              : list()
##    ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  $ axis.text.x.top          :List of 11
##    ..$ family       : NULL
##    ..$ face         : NULL
##    ..$ colour       : NULL
##    ..$ size         : NULL
##    ..$ hjust        : NULL
##    ..$ vjust        : num 0
##    ..$ angle        : NULL
##    ..$ lineheight   : NULL
##    ..$ margin       : 'margin' num [1:4] 0points 0points 2.2points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug        : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.text.x.bottom       : NULL
##  $ axis.text.y              :List of 11
##    ..$ family       : NULL
##    ..$ face         : NULL
##    ..$ colour       : NULL
##    ..$ size         : num 25
##    ..$ hjust        : num 1
##    ..$ vjust        : NULL
##    ..$ angle        : NULL
##    ..$ lineheight   : NULL
##    ..$ margin       : 'margin' num [1:4] 0points 2.2points 0points 0points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug        : NULL
##    ..$ inherit.blank: logi FALSE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.text.y.left         : NULL
##  $ axis.text.y.right        :List of 11
##    ..$ family       : NULL
##    ..$ face         : NULL
##    ..$ colour       : NULL
##    ..$ size         : NULL
##    ..$ hjust        : num 0
##    ..$ vjust        : NULL
##    ..$ angle        : NULL
##    ..$ lineheight   : NULL
```

```
##    ..$ margin      : 'margin' num [1:4] 0points 0points 0points 2.2points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug       : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ axis.ticks              :List of 6
##    ..$ colour      : chr "grey20"
##    ..$ size        : NULL
##    ..$ linetype    : NULL
##    ..$ lineend     : NULL
##    ..$ arrow       : logi FALSE
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_line" "element"
##  $ axis.ticks.x            : NULL
##  $ axis.ticks.x.top        : NULL
##  $ axis.ticks.x.bottom     : NULL
##  $ axis.ticks.y            : NULL
##  $ axis.ticks.y.left       : NULL
##  $ axis.ticks.y.right      : NULL
##  $ axis.ticks.length       : 'simpleUnit' num 2.75points
##    ..- attr(*, "unit")= int 8
##  $ axis.ticks.length.x     : NULL
##  $ axis.ticks.length.x.top : NULL
##  $ axis.ticks.length.x.bottom: NULL
##  $ axis.ticks.length.y     : NULL
##  $ axis.ticks.length.y.left : NULL
##  $ axis.ticks.length.y.right : NULL
##  $ axis.line               :List of 6
##    ..$ colour      : chr "black"
##    ..$ size        : 'rel' num 1
##    ..$ linetype    : NULL
##    ..$ lineend     : NULL
##    ..$ arrow       : logi FALSE
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_line" "element"
##  $ axis.line.x             : NULL
##  $ axis.line.x.top         : NULL
##  $ axis.line.x.bottom      : NULL
##  $ axis.line.y             : NULL
##  $ axis.line.y.left        : NULL
##  $ axis.line.y.right       : NULL
##  $ legend.background       :List of 5
##    ..$ fill        : NULL
##    ..$ colour      : logi NA
##    ..$ size        : NULL
##    ..$ linetype    : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_rect" "element"
##  $ legend.margin           : 'margin' num [1:4] 5.5points 5.5points 5.5points 5.5points
##    ..- attr(*, "unit")= int 8
##  $ legend.spacing          : 'simpleUnit' num 11points
##    ..- attr(*, "unit")= int 8
##  $ legend.spacing.x        : NULL
##  $ legend.spacing.y        : NULL
##  $ legend.key              : list()
##    ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  $ legend.key.size         : 'simpleUnit' num 1.2lines
##    ..- attr(*, "unit")= int 3
##  $ legend.key.height       : NULL
##  $ legend.key.width        : NULL
```

```
##  $ legend.text               :List of 11
##   ..$ family     : NULL
##   ..$ face       : NULL
##   ..$ colour     : NULL
##   ..$ size       : 'rel' num 0.8
##   ..$ hjust      : NULL
##   ..$ vjust      : NULL
##   ..$ angle      : NULL
##   ..$ lineheight : NULL
##   ..$ margin     : NULL
##   ..$ debug      : NULL
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ legend.text.align         : NULL
##  $ legend.title              :List of 11
##   ..$ family     : NULL
##   ..$ face       : NULL
##   ..$ colour     : NULL
##   ..$ size       : NULL
##   ..$ hjust      : num 0
##   ..$ vjust      : NULL
##   ..$ angle      : NULL
##   ..$ lineheight : NULL
##   ..$ margin     : NULL
##   ..$ debug      : NULL
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_text" "element"
##  $ legend.title.align        : NULL
##  $ legend.position           : chr "right"
##  $ legend.direction          : NULL
##  $ legend.justification      : chr "center"
##  $ legend.box                : NULL
##  $ legend.box.just           : NULL
##  $ legend.box.margin         : 'margin' num [1:4] 0cm 0cm 0cm 0cm
##   ..- attr(*, "unit")= int 1
##  $ legend.box.background      : list()
##   ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  $ legend.box.spacing         : 'simpleUnit' num 11points
##   ..- attr(*, "unit")= int 8
##  $ panel.background          :List of 5
##   ..$ fill       : chr "white"
##   ..$ colour     : logi NA
##   ..$ size       : NULL
##   ..$ linetype   : NULL
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_rect" "element"
##  $ panel.border              : list()
##   ..- attr(*, "class")= chr [1:2] "element_blank" "element"
##  $ panel.spacing             : 'simpleUnit' num 5.5points
##   ..- attr(*, "unit")= int 8
##  $ panel.spacing.x           : NULL
##  $ panel.spacing.y           : NULL
##  $ panel.grid                :List of 6
##   ..$ colour     : chr "grey92"
##   ..$ size       : NULL
##   ..$ linetype   : NULL
##   ..$ lineend    : NULL
##   ..$ arrow      : logi FALSE
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_line" "element"
```

```
## $ panel.grid.major       : list()
##  ..- attr(*, "class")= chr [1:2] "element_blank" "element"
## $ panel.grid.minor       : list()
##  ..- attr(*, "class")= chr [1:2] "element_blank" "element"
## $ panel.grid.major.x     : NULL
## $ panel.grid.major.y     : NULL
## $ panel.grid.minor.x     : NULL
## $ panel.grid.minor.y     : NULL
## $ panel.ontop            : logi FALSE
## $ plot.background        :List of 5
##  ..$ fill       : NULL
##  ..$ colour     : chr "white"
##  ..$ size       : NULL
##  ..$ linetype   : NULL
##  ..$ inherit.blank: logi TRUE
##  ..- attr(*, "class")= chr [1:2] "element_rect" "element"
## $ plot.title             :List of 11
##  ..$ family     : NULL
##  ..$ face       : NULL
##  ..$ colour     : NULL
##  ..$ size       : 'rel' num 1.2
##  ..$ hjust      : num 0.5
##  ..$ vjust      : num 1
##  ..$ angle      : NULL
##  ..$ lineheight : NULL
##  ..$ margin     : 'margin' num [1:4] 0points 0points 5.5points 0points
##  .. ..- attr(*, "unit")= int 8
##  ..$ debug      : NULL
##  ..$ inherit.blank: logi FALSE
##  ..- attr(*, "class")= chr [1:2] "element_text" "element"
## $ plot.title.position    : chr "panel"
## $ plot.subtitle          :List of 11
##  ..$ family     : NULL
##  ..$ face       : NULL
##  ..$ colour     : NULL
##  ..$ size       : NULL
##  ..$ hjust      : num 0
##  ..$ vjust      : num 1
##  ..$ angle      : NULL
##  ..$ lineheight : NULL
##  ..$ margin     : 'margin' num [1:4] 0points 0points 5.5points 0points
##  .. ..- attr(*, "unit")= int 8
##  ..$ debug      : NULL
##  ..$ inherit.blank: logi TRUE
##  ..- attr(*, "class")= chr [1:2] "element_text" "element"
## $ plot.caption           :List of 11
##  ..$ family     : NULL
##  ..$ face       : NULL
##  ..$ colour     : NULL
##  ..$ size       : 'rel' num 0.8
##  ..$ hjust      : num 1
##  ..$ vjust      : num 1
##  ..$ angle      : NULL
##  ..$ lineheight : NULL
##  ..$ margin     : 'margin' num [1:4] 5.5points 0points 0points 0points
##  .. ..- attr(*, "unit")= int 8
##  ..$ debug      : NULL
##  ..$ inherit.blank: logi TRUE
##  ..- attr(*, "class")= chr [1:2] "element_text" "element"
## $ plot.caption.position  : chr "panel"
```

```
##   $ plot.tag                    :List of 11
##    ..$ family      : NULL
##    ..$ face        : NULL
##    ..$ colour      : NULL
##    ..$ size        : 'rel' num 1.2
##    ..$ hjust       : num 0.5
##    ..$ vjust       : num 0.5
##    ..$ angle       : NULL
##    ..$ lineheight  : NULL
##    ..$ margin      : NULL
##    ..$ debug       : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##   $ plot.tag.position        : chr "topleft"
##   $ plot.margin              : 'margin' num [1:4] 5.5points 5.5points 5.5points 5.5points
##    ..- attr(*, "unit")= int 8
##   $ strip.background         :List of 5
##    ..$ fill       : chr "white"
##    ..$ colour     : chr "black"
##    ..$ size       : 'rel' num 2
##    ..$ linetype   : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_rect" "element"
##   $ strip.background.x       : NULL
##   $ strip.background.y       : NULL
##   $ strip.placement          : chr "inside"
##   $ strip.text               :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : chr "grey10"
##    ..$ size       : 'rel' num 0.8
##    ..$ hjust      : NULL
##    ..$ vjust      : NULL
##    ..$ angle      : NULL
##    ..$ lineheight : NULL
##    ..$ margin     : 'margin' num [1:4] 4.4points 4.4points 4.4points 4.4points
##    .. ..- attr(*, "unit")= int 8
##    ..$ debug      : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##   $ strip.text.x             : NULL
##   $ strip.text.y             :List of 11
##    ..$ family     : NULL
##    ..$ face       : NULL
##    ..$ colour     : NULL
##    ..$ size       : NULL
##    ..$ hjust      : NULL
##    ..$ vjust      : NULL
##    ..$ angle      : num -90
##    ..$ lineheight : NULL
##    ..$ margin     : NULL
##    ..$ debug      : NULL
##    ..$ inherit.blank: logi TRUE
##    ..- attr(*, "class")= chr [1:2] "element_text" "element"
##   $ strip.switch.pad.grid    : 'simpleUnit' num 2.75points
##    ..- attr(*, "unit")= int 8
##   $ strip.switch.pad.wrap    : 'simpleUnit' num 2.75points
##    ..- attr(*, "unit")= int 8
##   $ strip.text.y.left        :List of 11
##    ..$ family     : NULL
```

```
##   ..$ face         : NULL
##   ..$ colour       : NULL
##   ..$ size         : NULL
##   ..$ hjust        : NULL
##   ..$ vjust        : NULL
##   ..$ angle        : num 90
##   ..$ lineheight   : NULL
##   ..$ margin       : NULL
##   ..$ debug        : NULL
##   ..$ inherit.blank: logi TRUE
##   ..- attr(*, "class")= chr [1:2] "element_text" "element"
## - attr(*, "class")= chr [1:2] "theme" "gg"
## - attr(*, "complete")= logi TRUE
## - attr(*, "validate")= logi TRUE
```

Odds ratios of variables based on H. pylori status
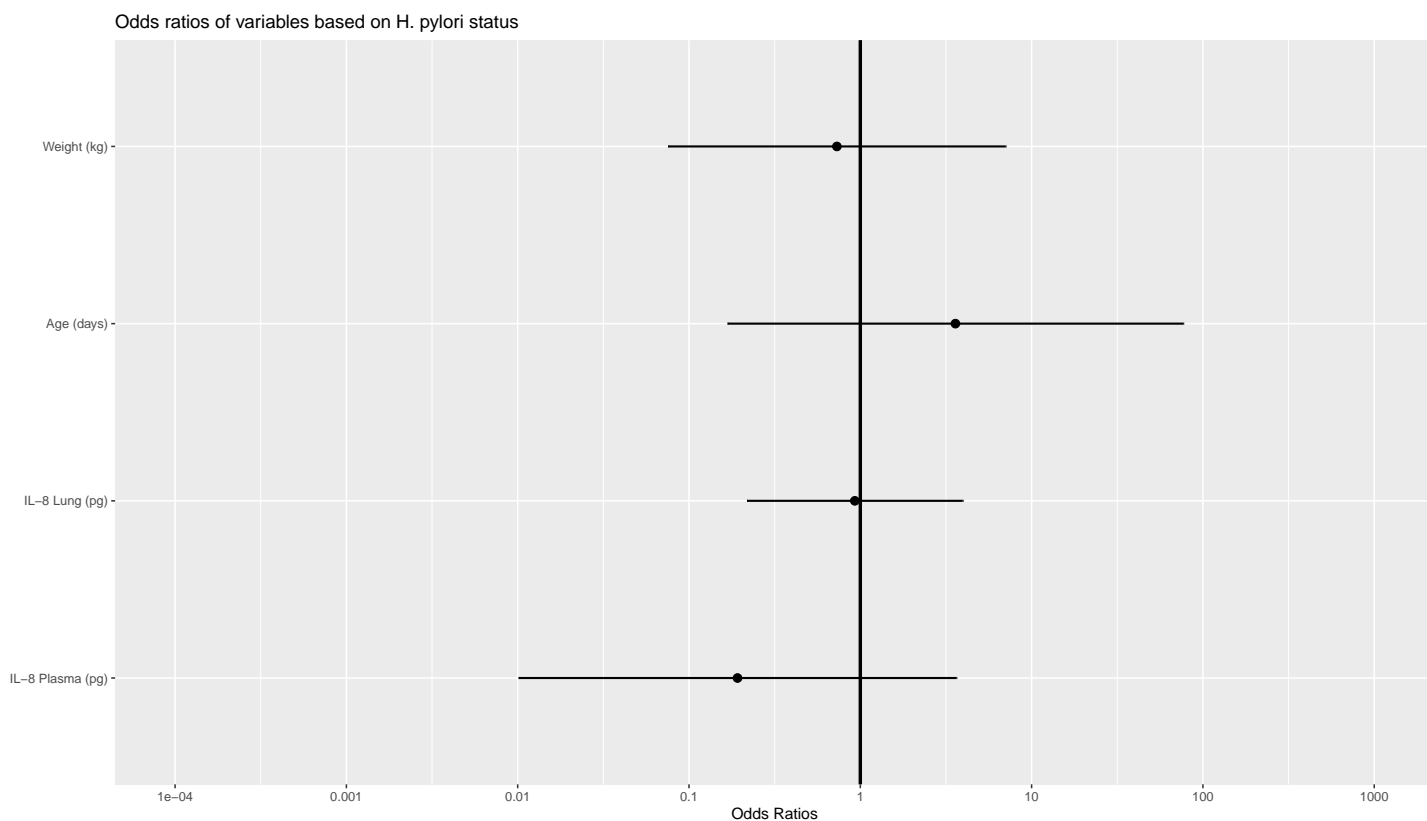
	OR	2.5 %	97.5 %	p
(Intercept)	0.018	0.000	110.146	0.410
ʻWeight (kg)ʻ	0.243	0.000	7254.525	0.786
ʻAge (days)ʻ	1.042	0.955	1.177	0.413
ʻIL-8 Lung (pg)ʻ	0.993	0.852	1.158	0.921
ʻIL-8 Plasma (pg)ʻ	0.996	0.985	1.001	0.271

H.pylori Il8 Pearson correlation
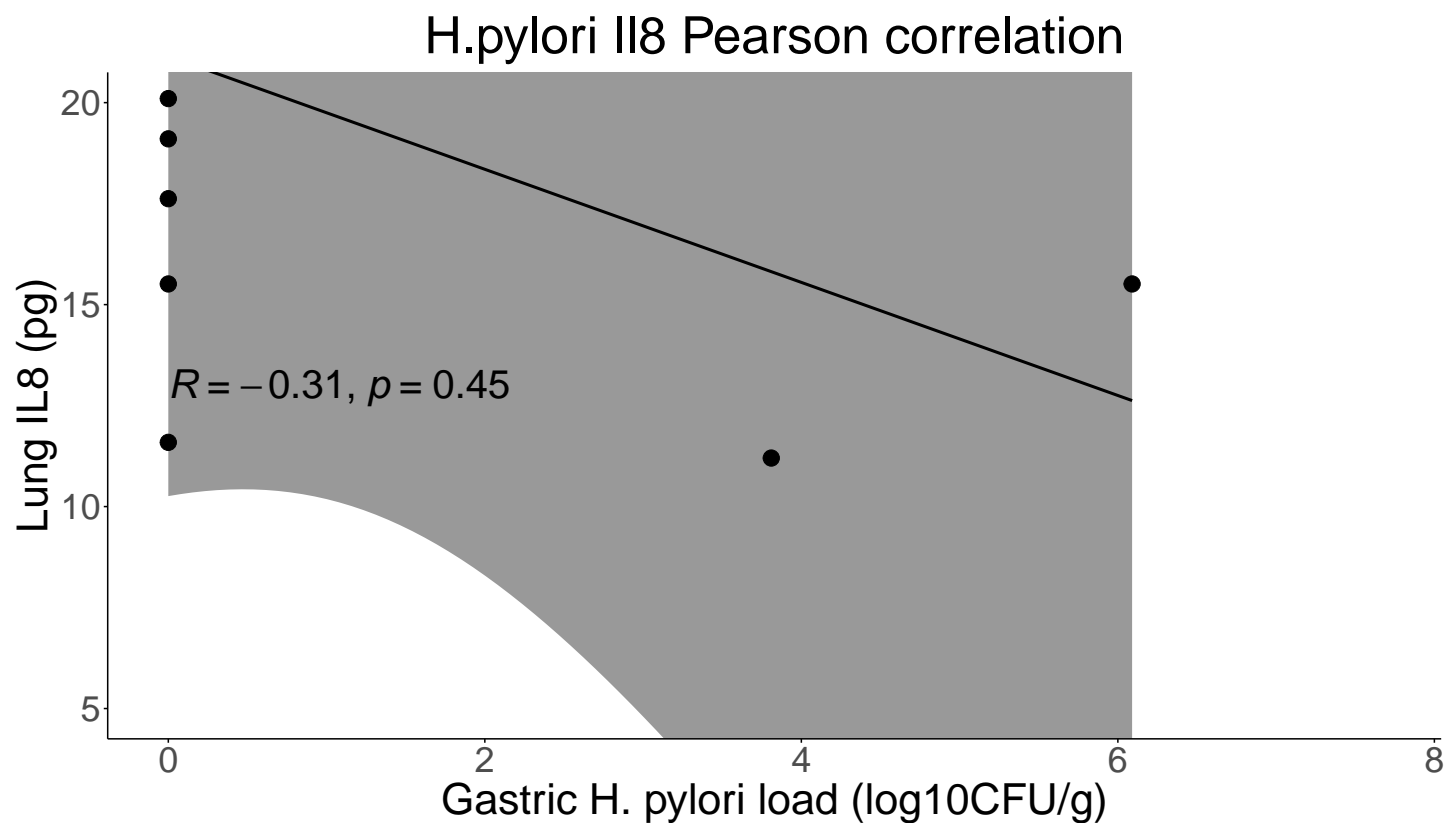
Figure 1: This plot only includes animals that had material sequenced and not all 25 animals from the study

H.pylori plasma IL8 Pearson correlation
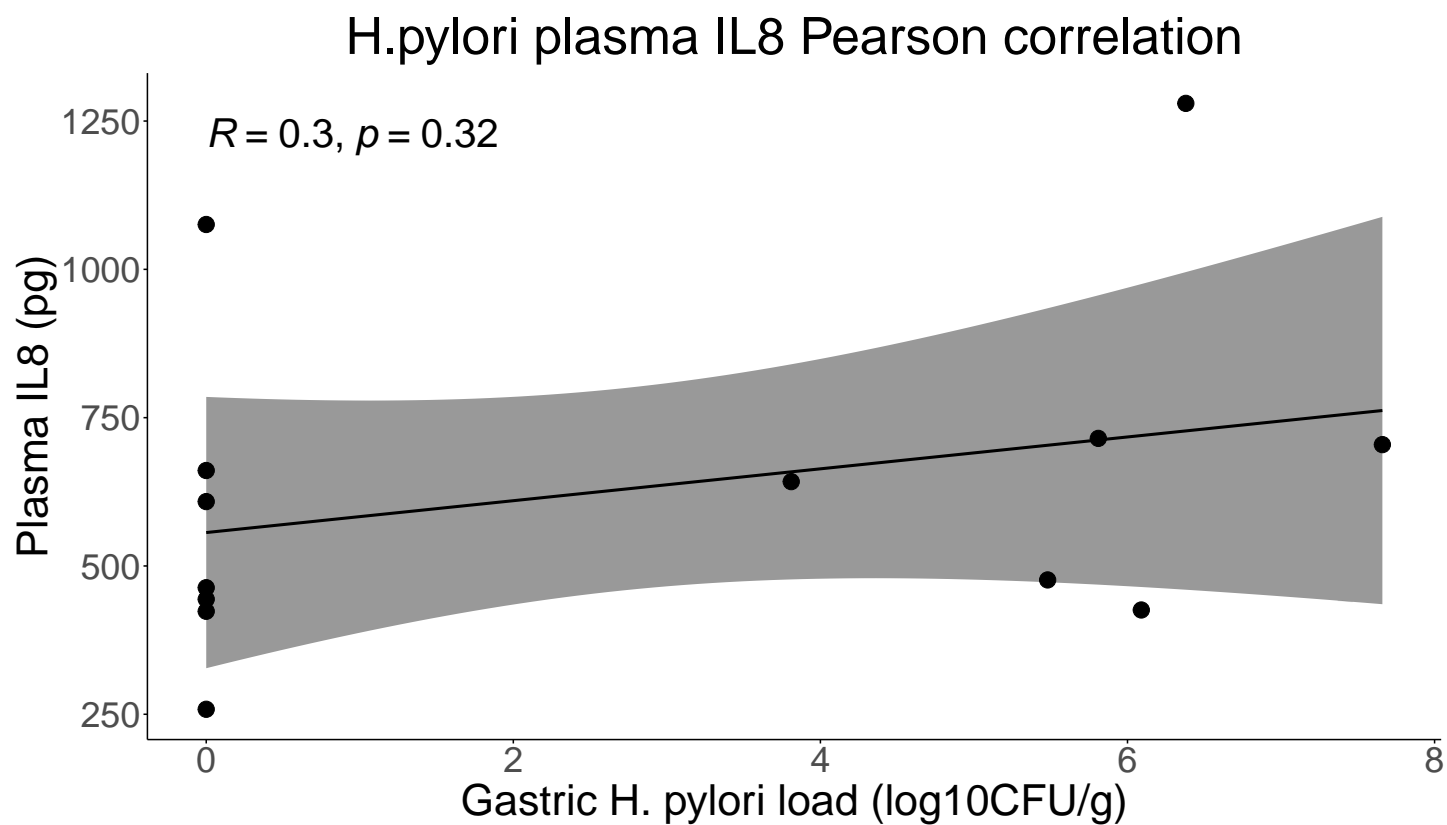
Figure 2: This plot only includes animals that had material sequenced and not all 25 animals from the study

Lavage overlapping taxa

Overlapping taxa between H. pylori (+) and (−) in lavage Lung
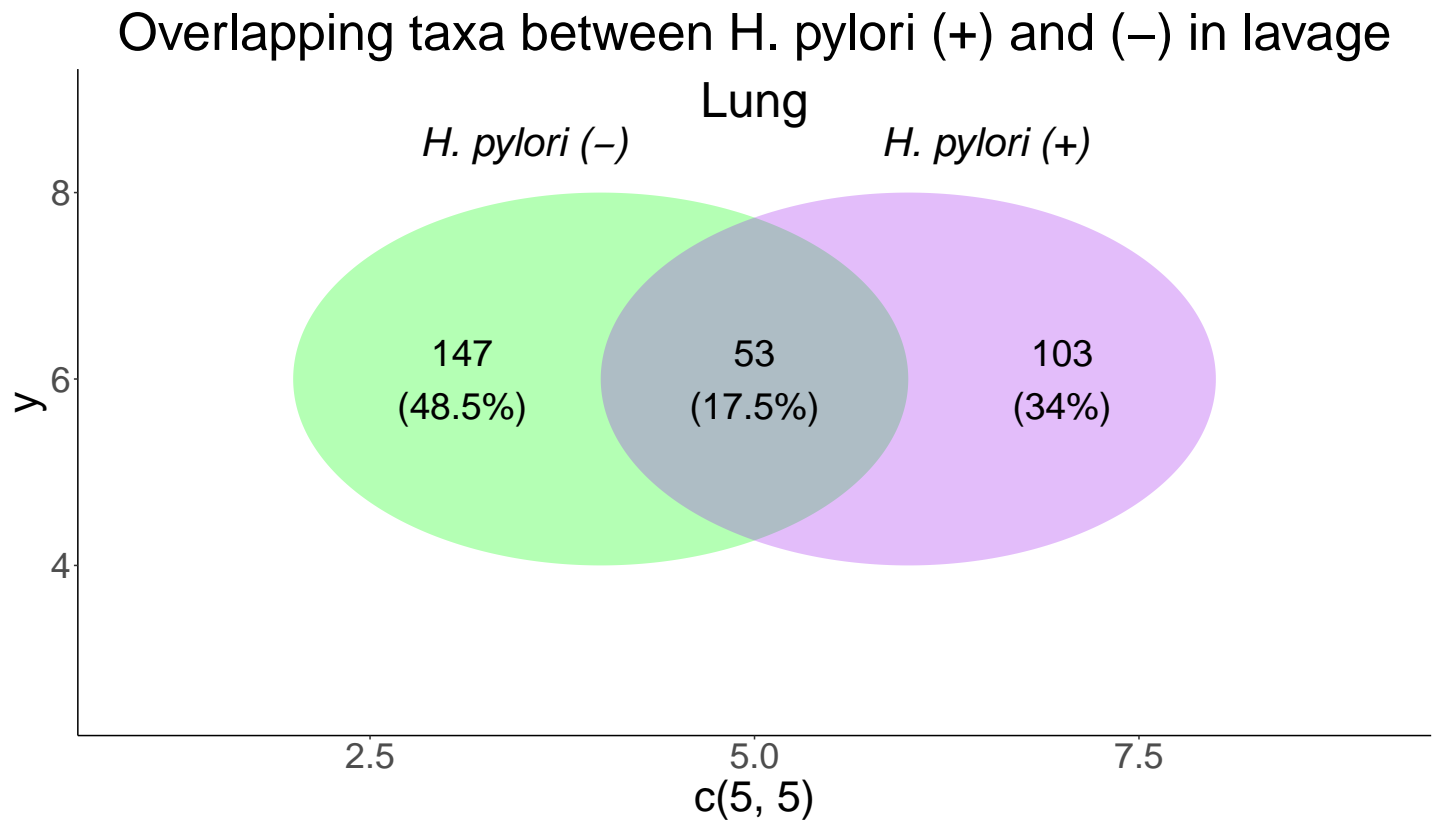
Overlapping taxa between H. pylori (+) and (−) in buccal cavity
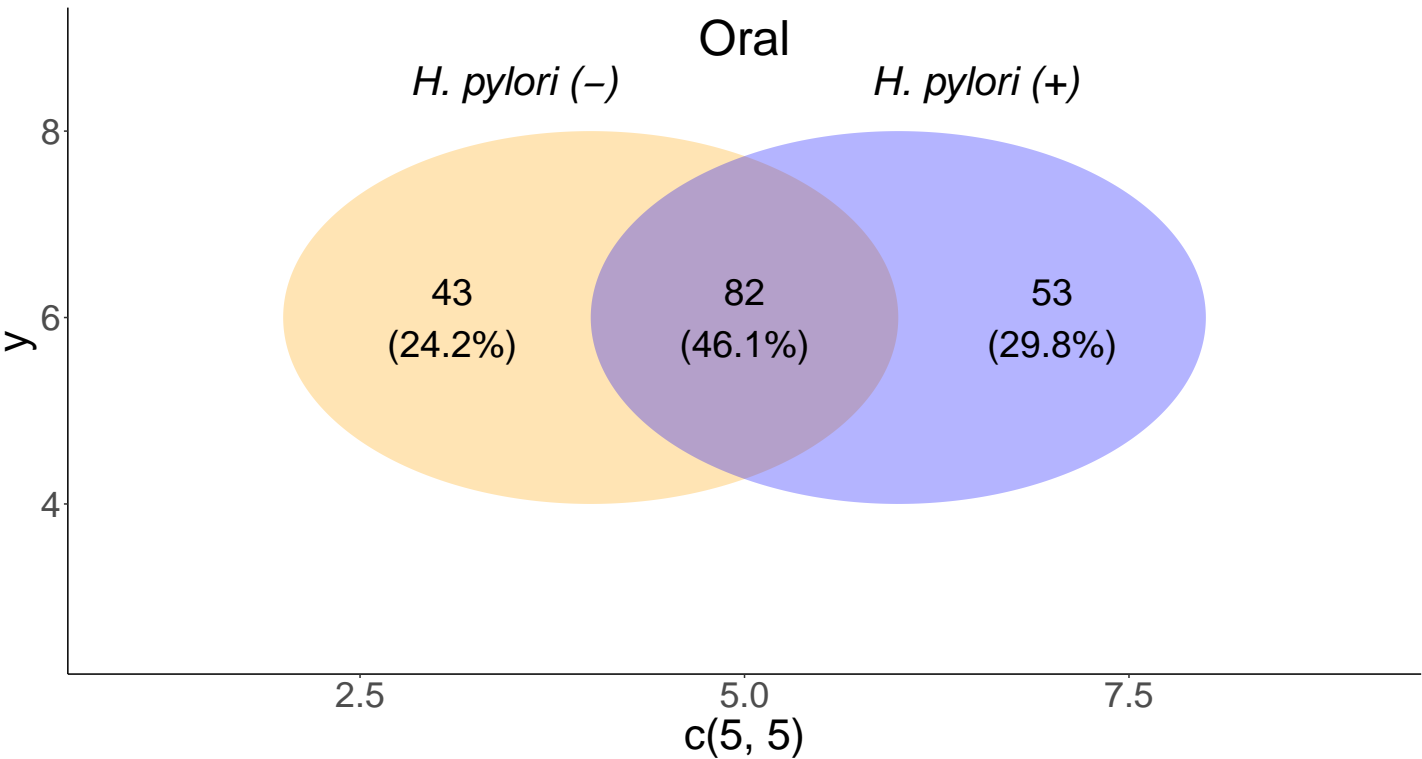
Oral

Lefse analysis and differential abundance for both sites

Lefse taxa from bronchoalveolar lavage and oral s
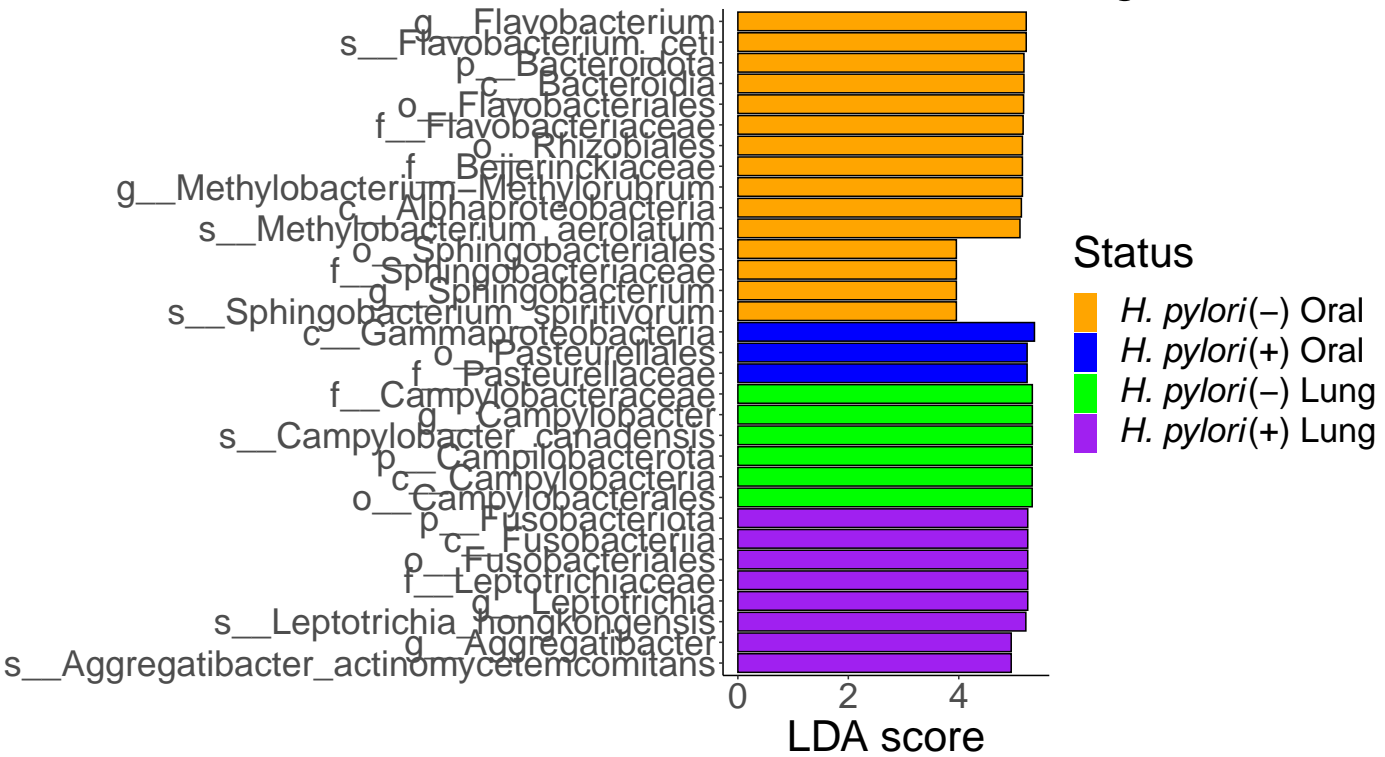
Relative abundance of differential taxa

efse relative abundance from bronchoalveolar lavage and oral sv

Status
- *H. pylori*(+) Lung
- *H. pylori*(−) Lung
- *H. pylori*(+) Oral
- *H. pylori*(−) Oral

Relative abundance
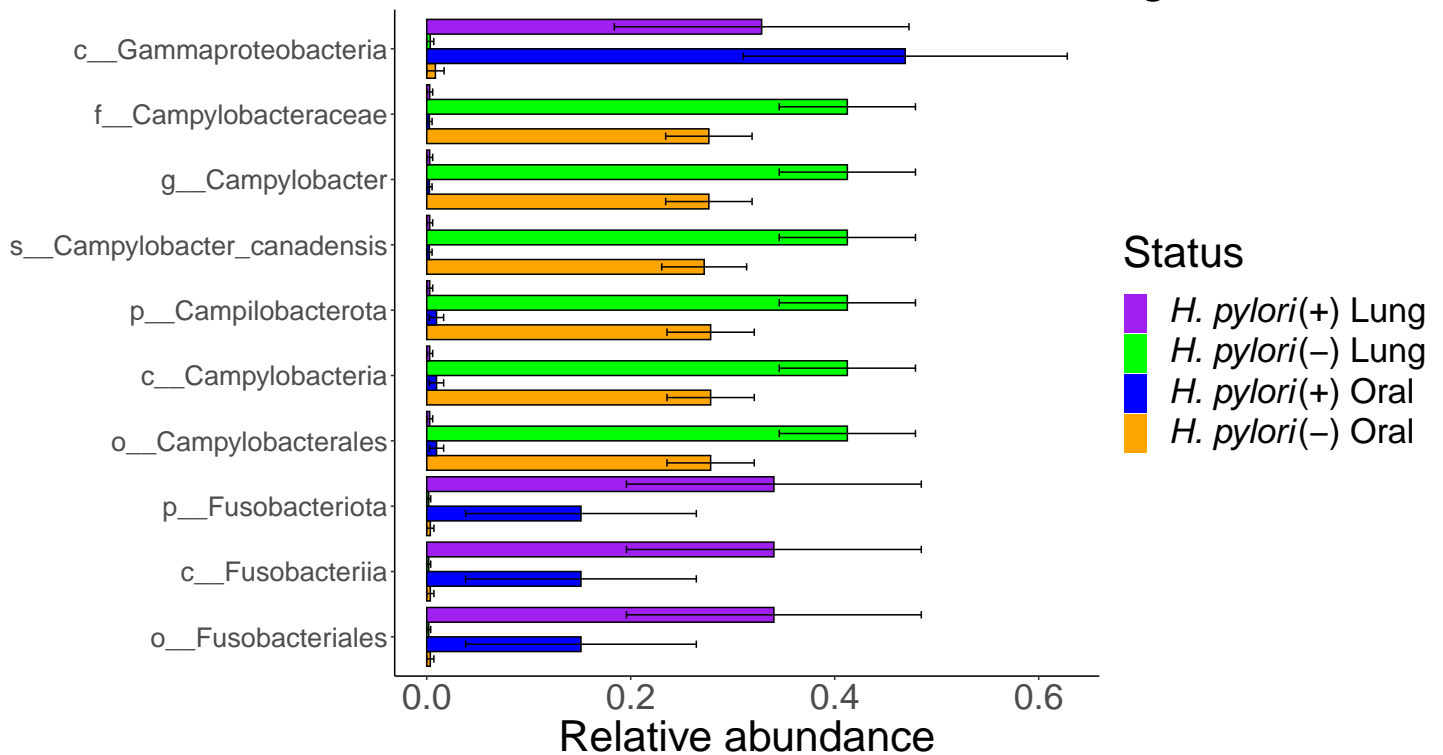
Lefse and differential abundance for bronchoalveolar lavage

Lefse Taxa from Bronchoalveolar Lavage

Status
- *H. pylori*(−) Lung
- *H. pylori*(+) Lung

LDA score

Relative abundance of differential taxa
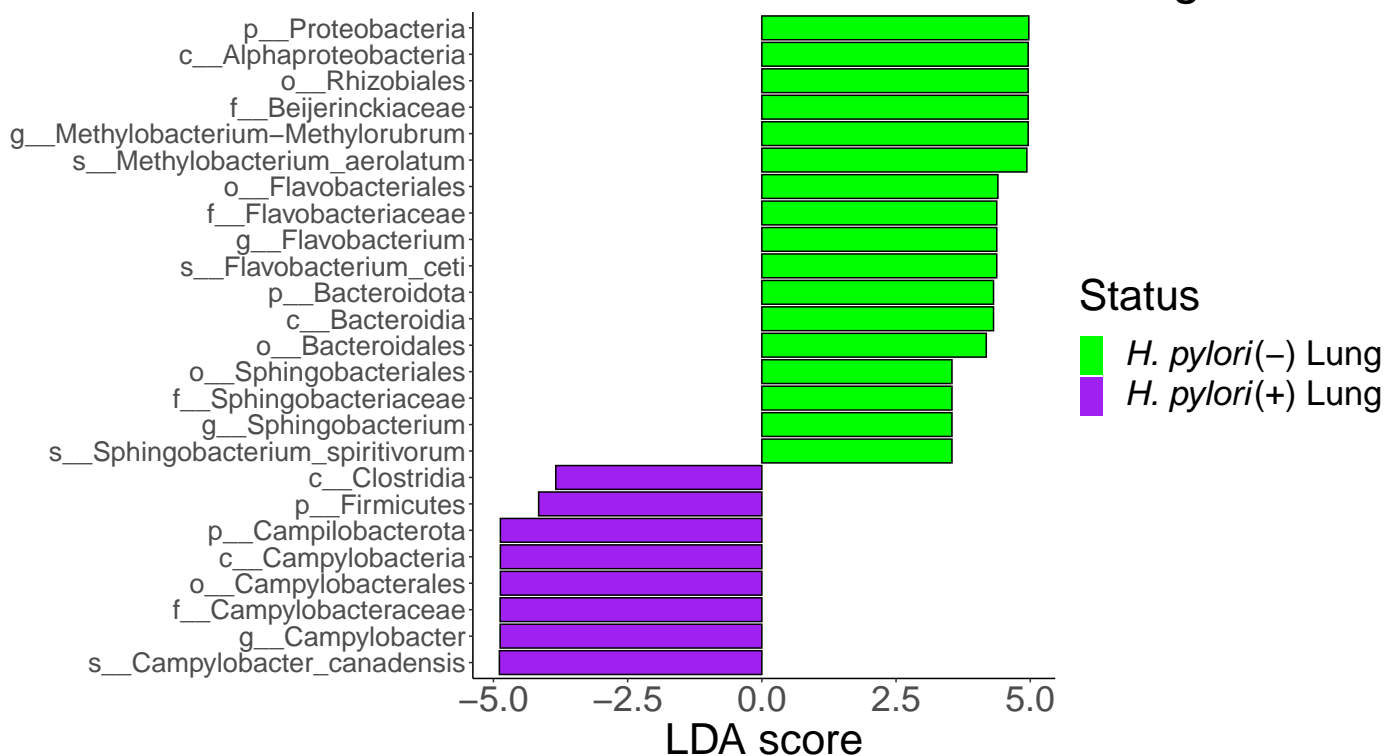
Lefse Relative Abundance from Bronchoalveolar Lavage
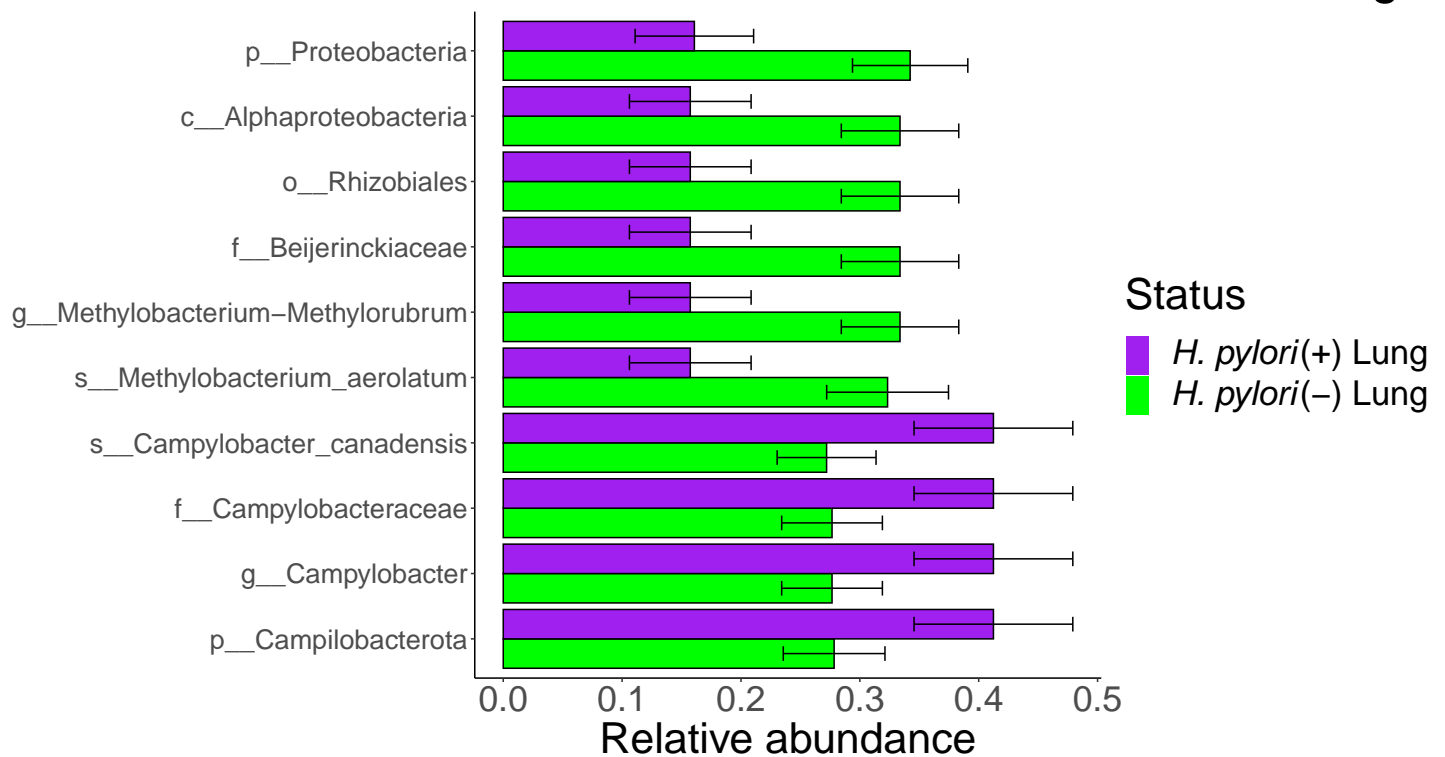
Lefse and differential abundance for oral swabs

Lefse taxa from oral swabs
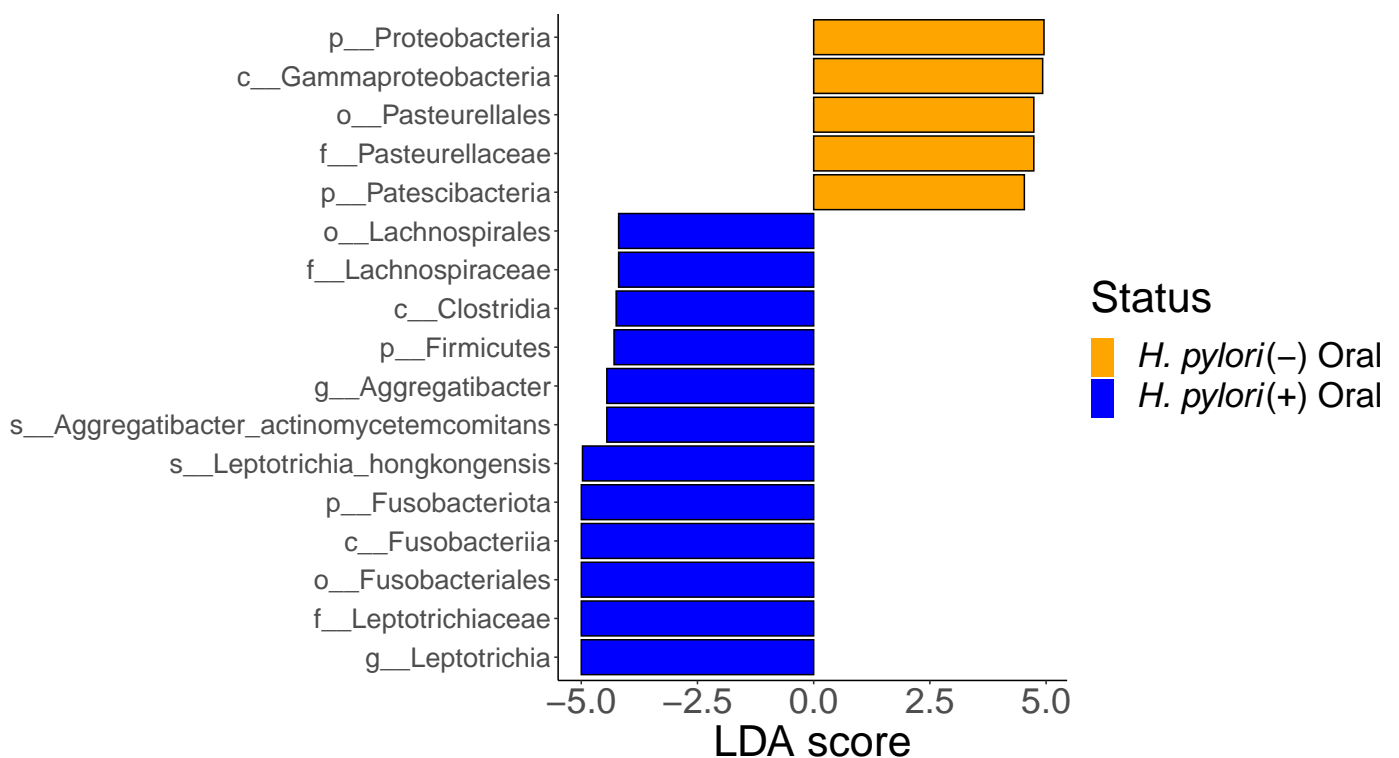
Relative abundance of differential taxa

Lefse relative abundance from oral swabs
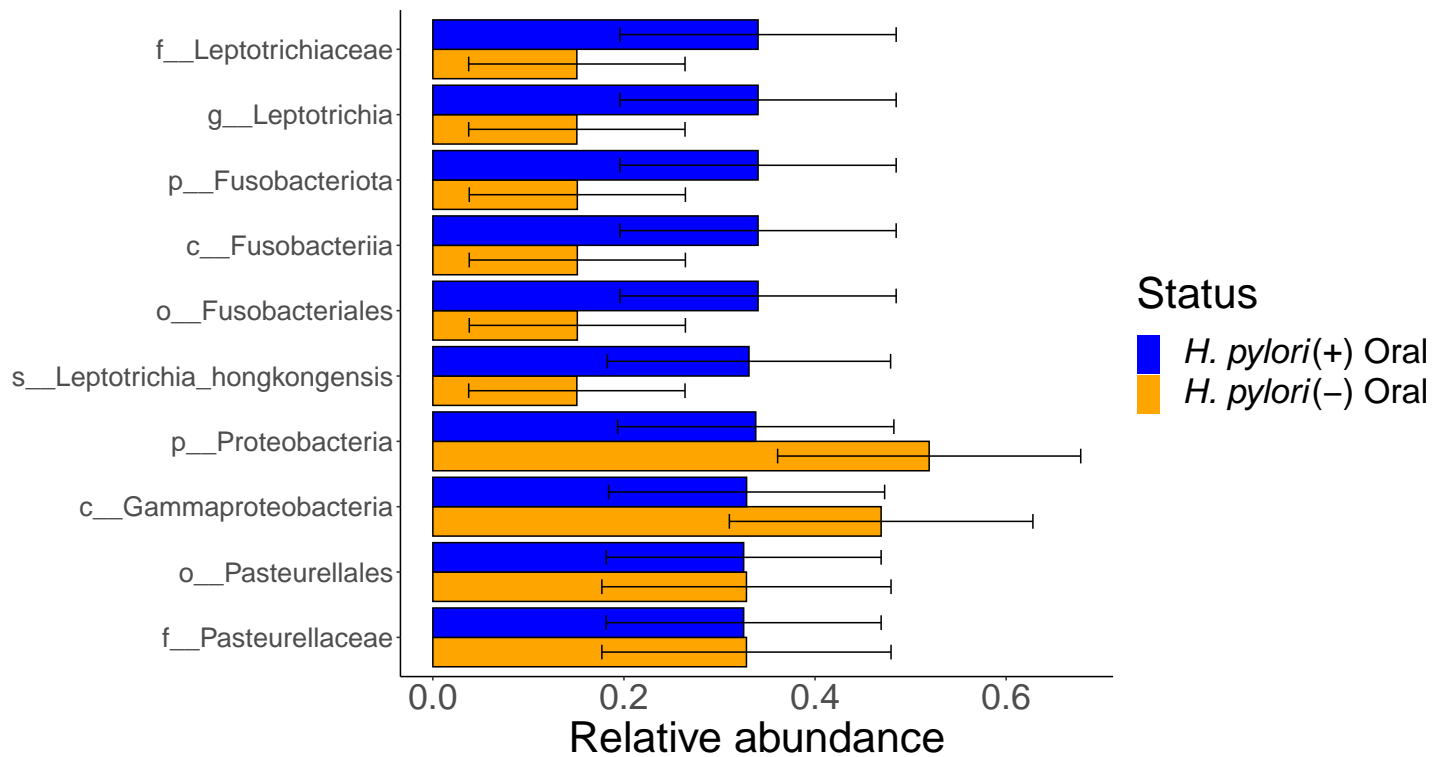
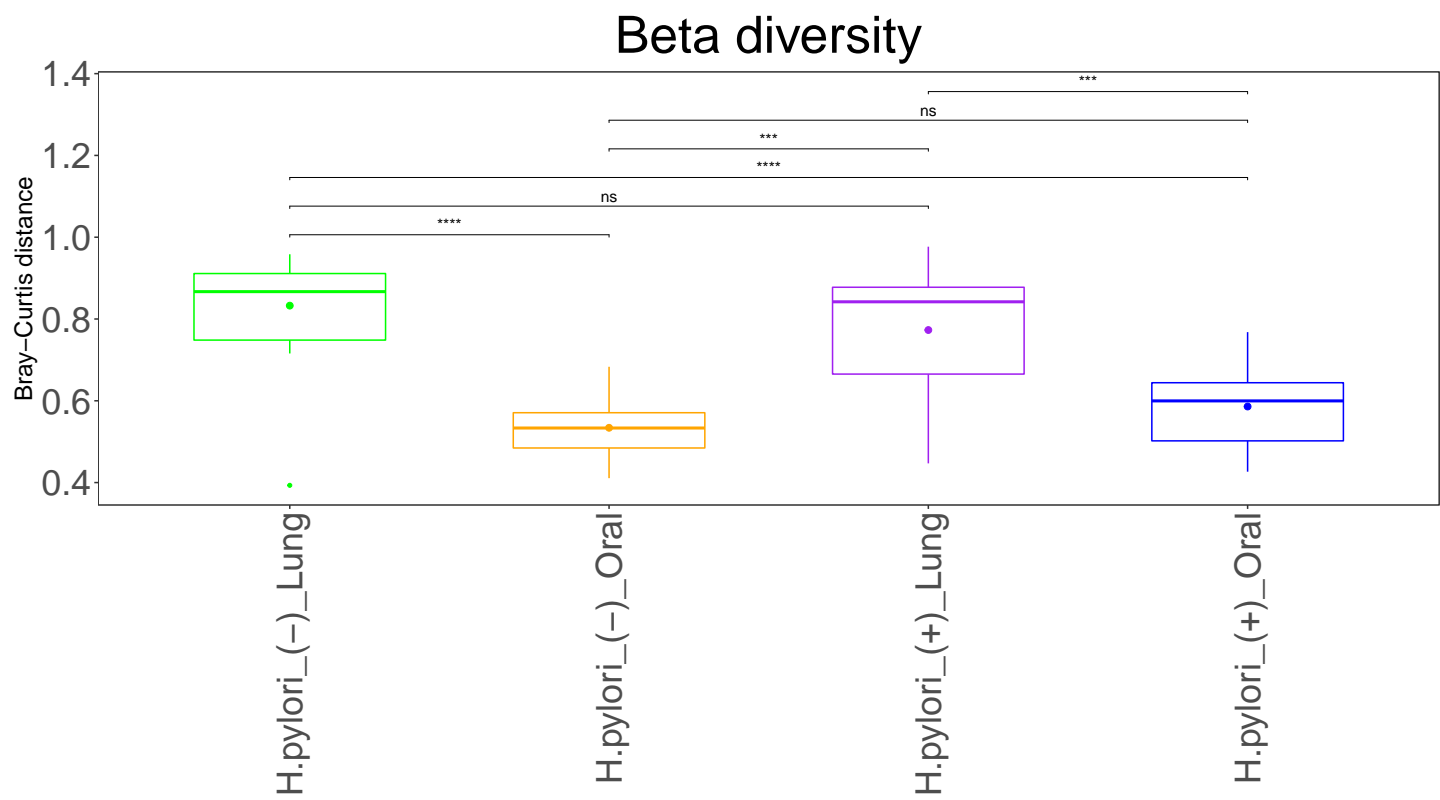**Beta diversity**

Unweighted 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
```
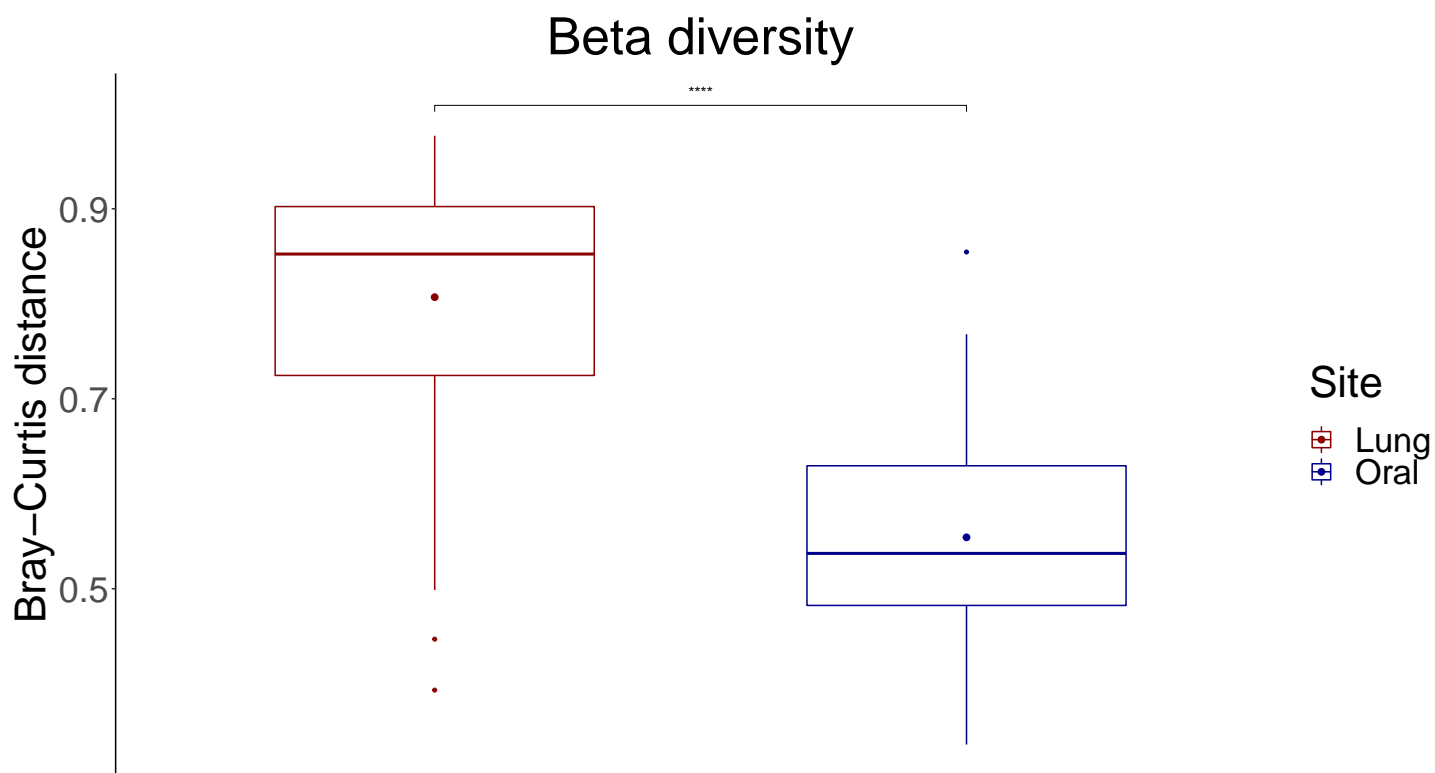
Unweighted unifrac PCoA
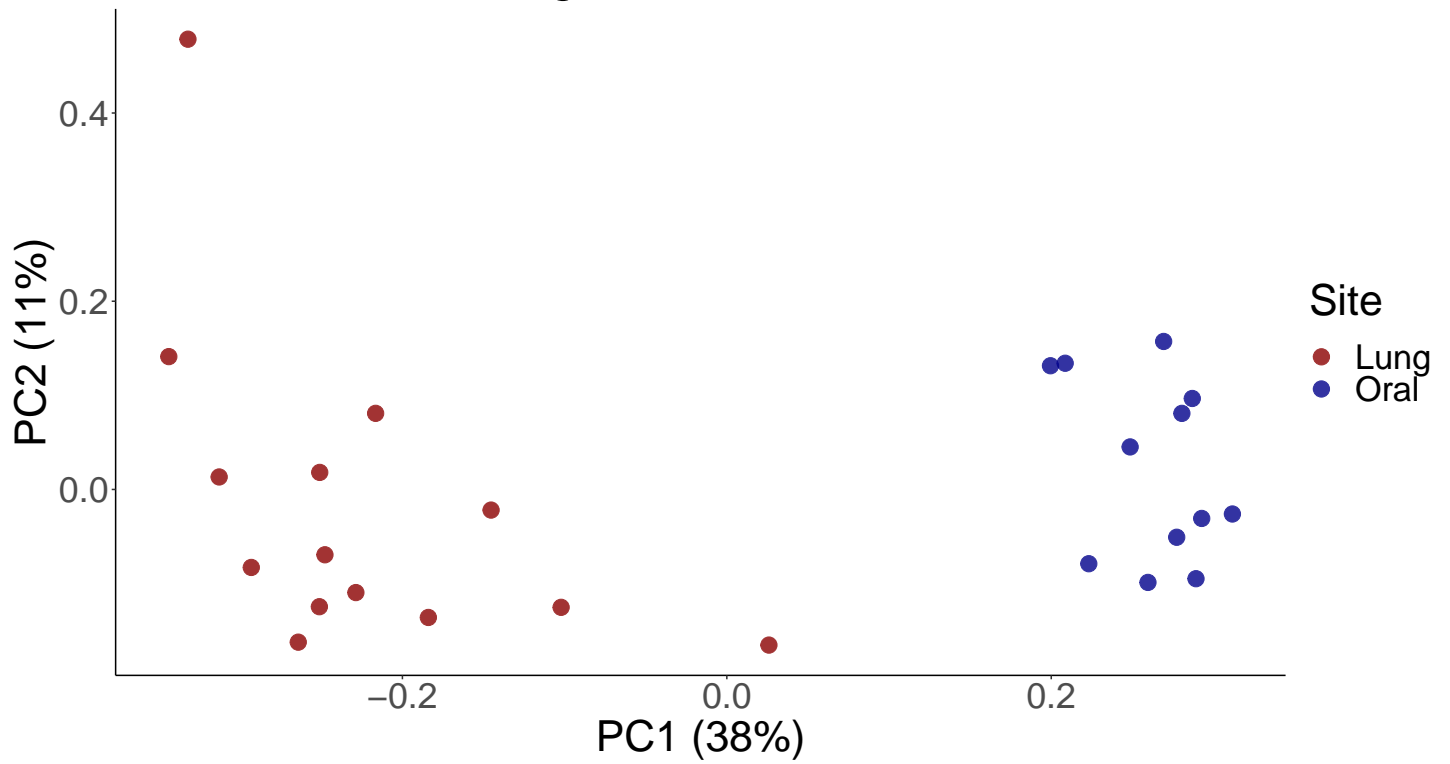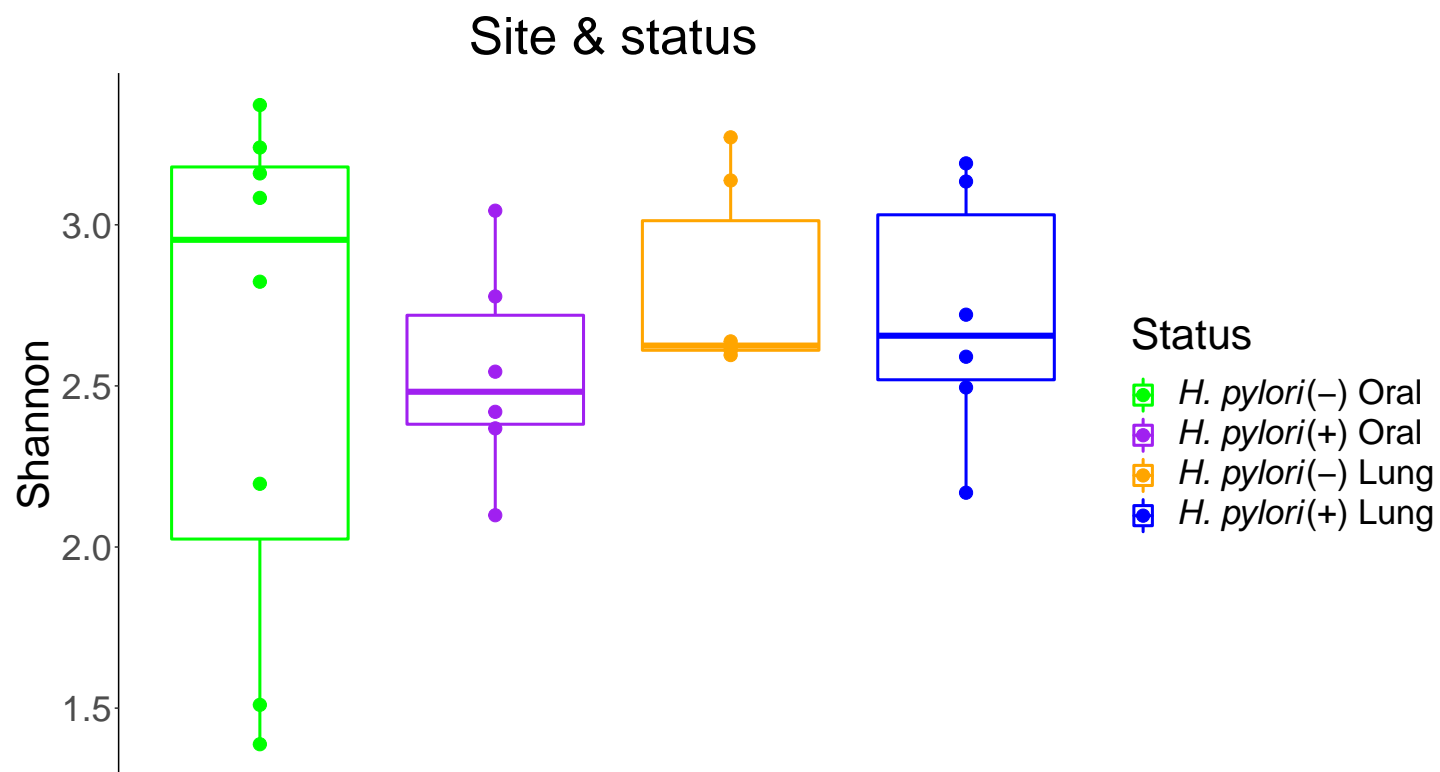
Status Unweighted unifrac PCoA
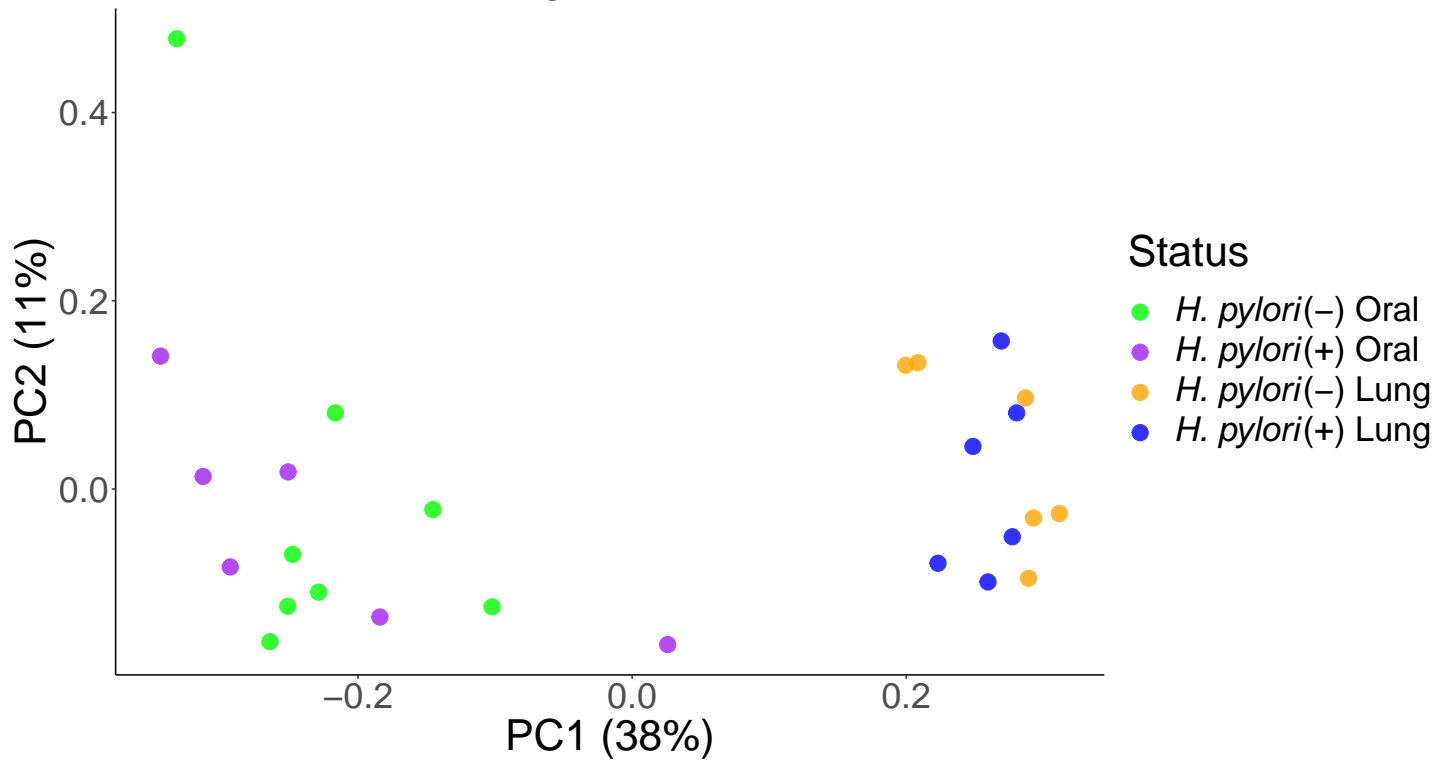
Bray-Curtis

Shannon index by site and H. pylori status
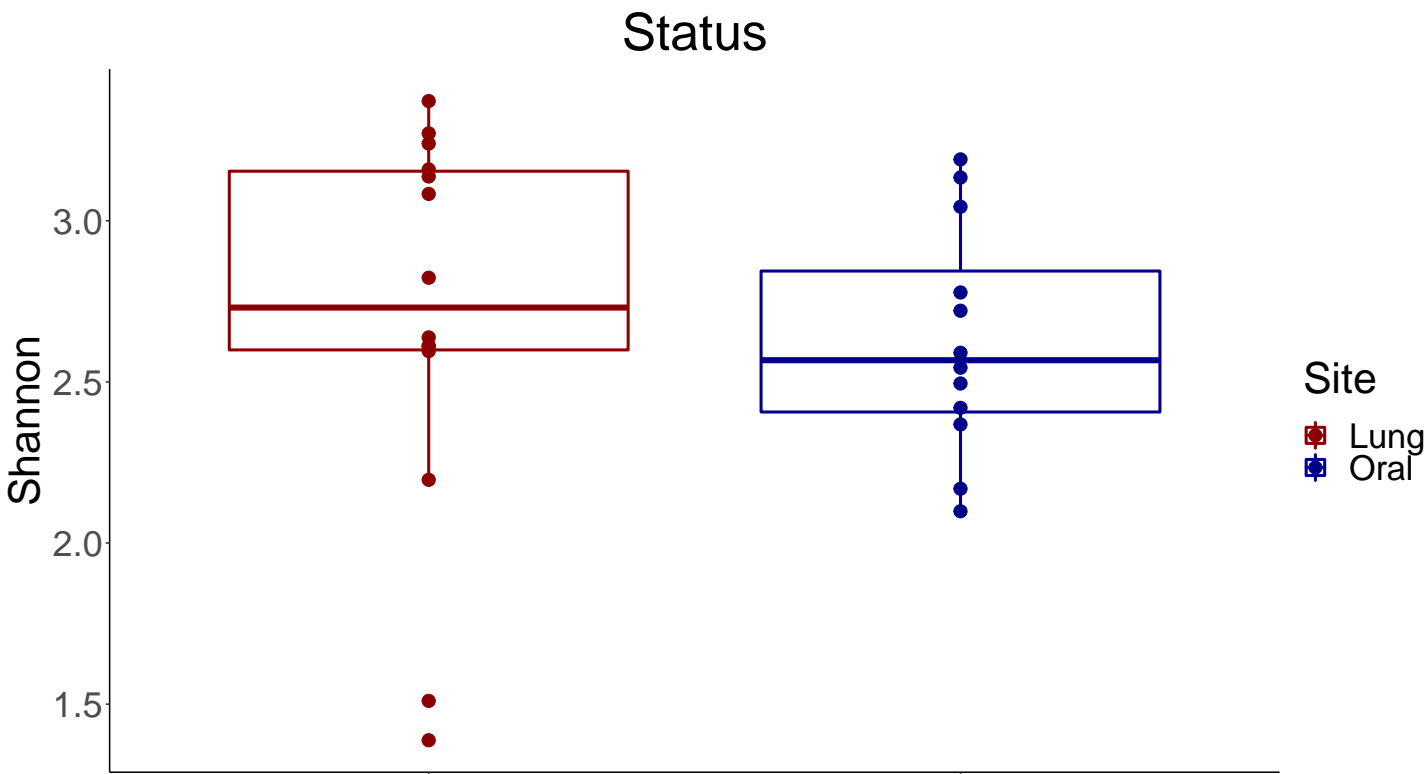
Table 2: All alpha diversity measurees

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

Helicobacter positive respiratory samples

Helicobacter positive samples separated by site

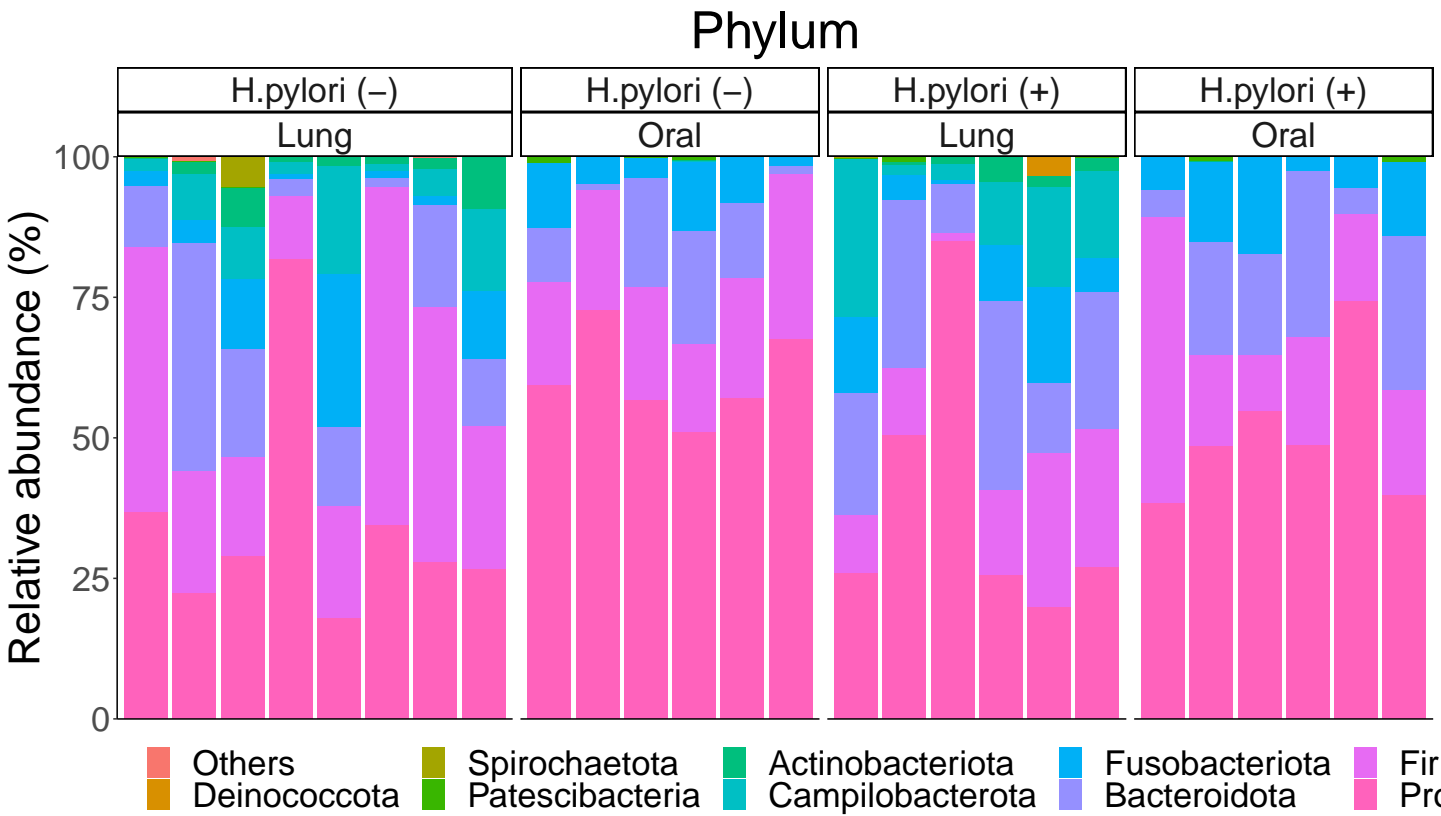# Helicobacter ASVs
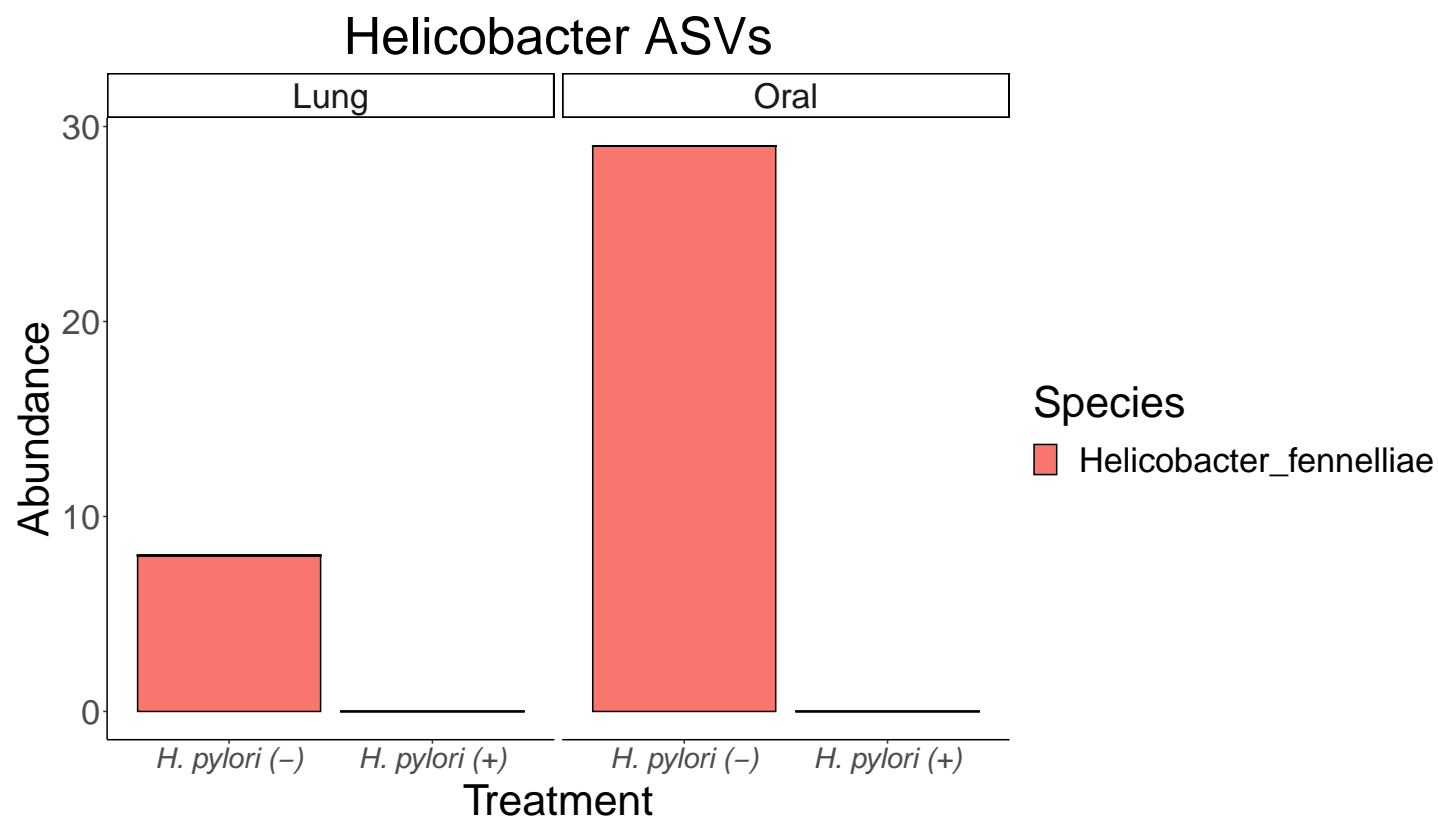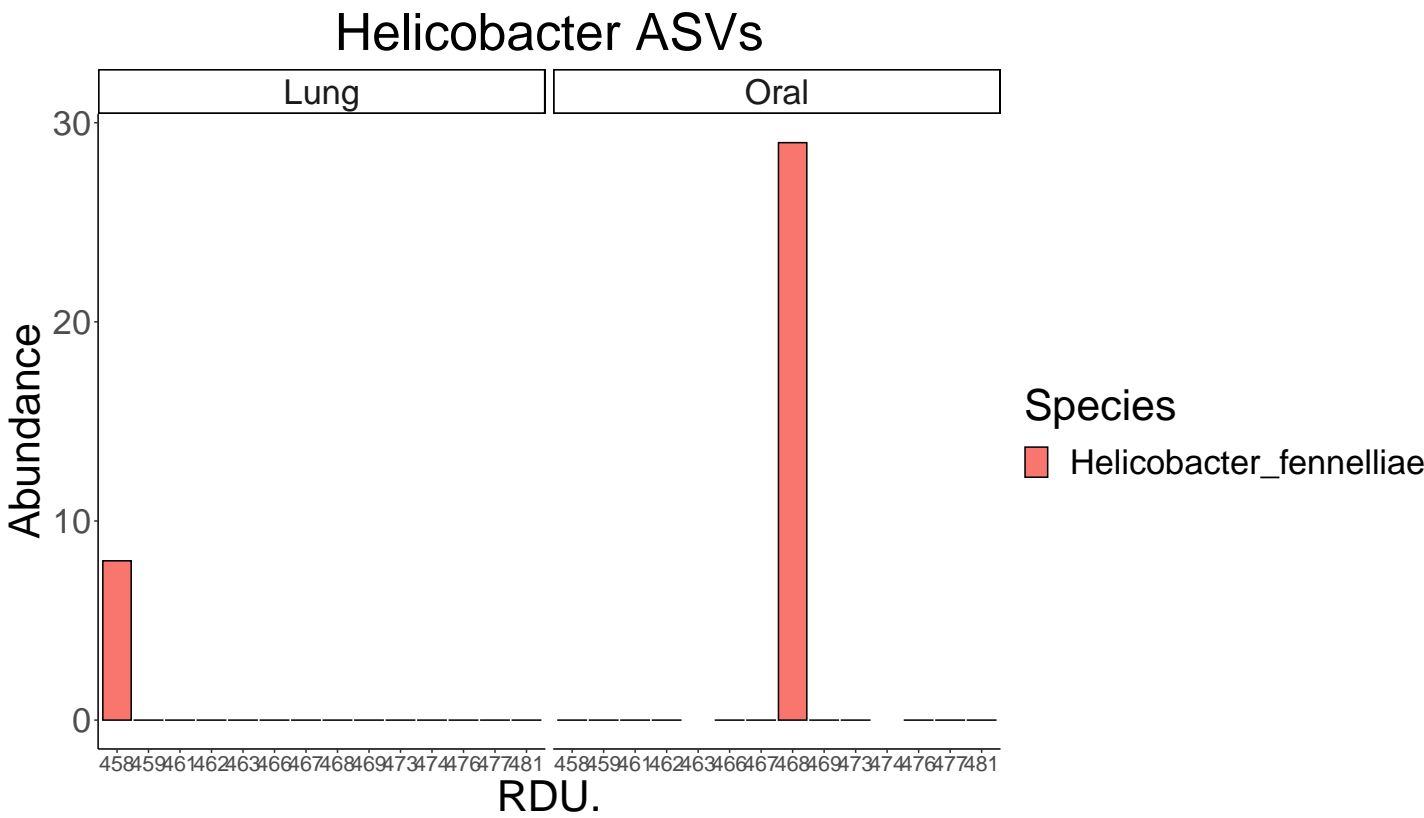
Taxa barplots

Figure 3: Microbiota Composition at Phylum level.

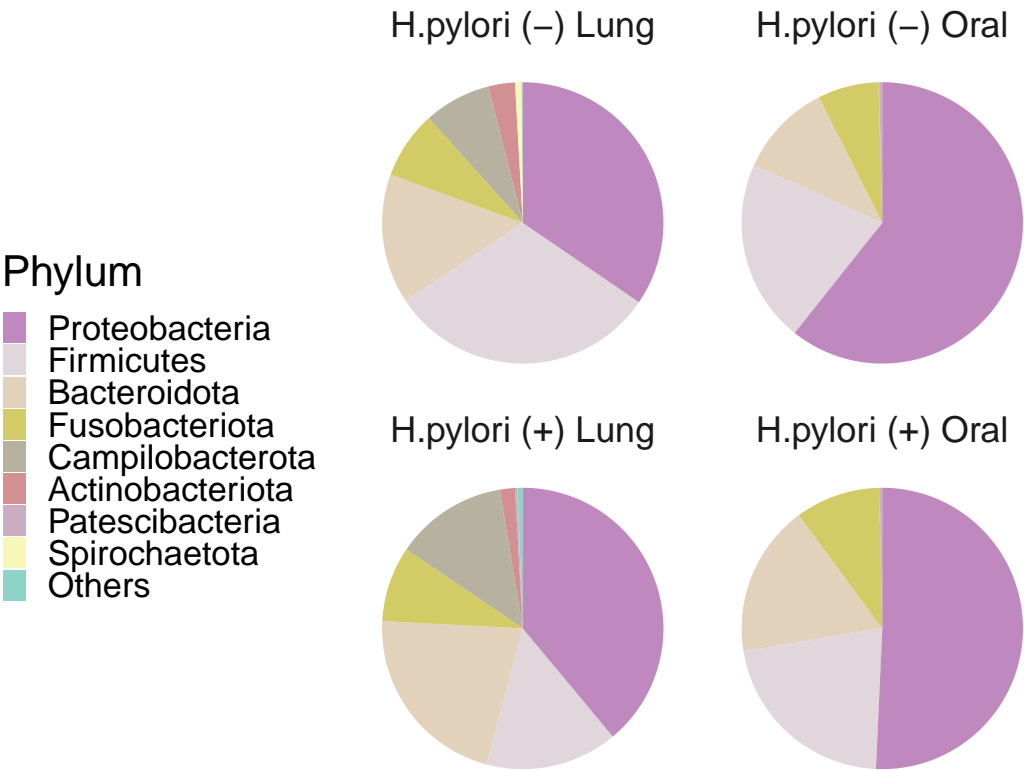**Figure 4:** Microbiota Composition at Phylum level.

Table 3: Phylum Average Relative Abundance

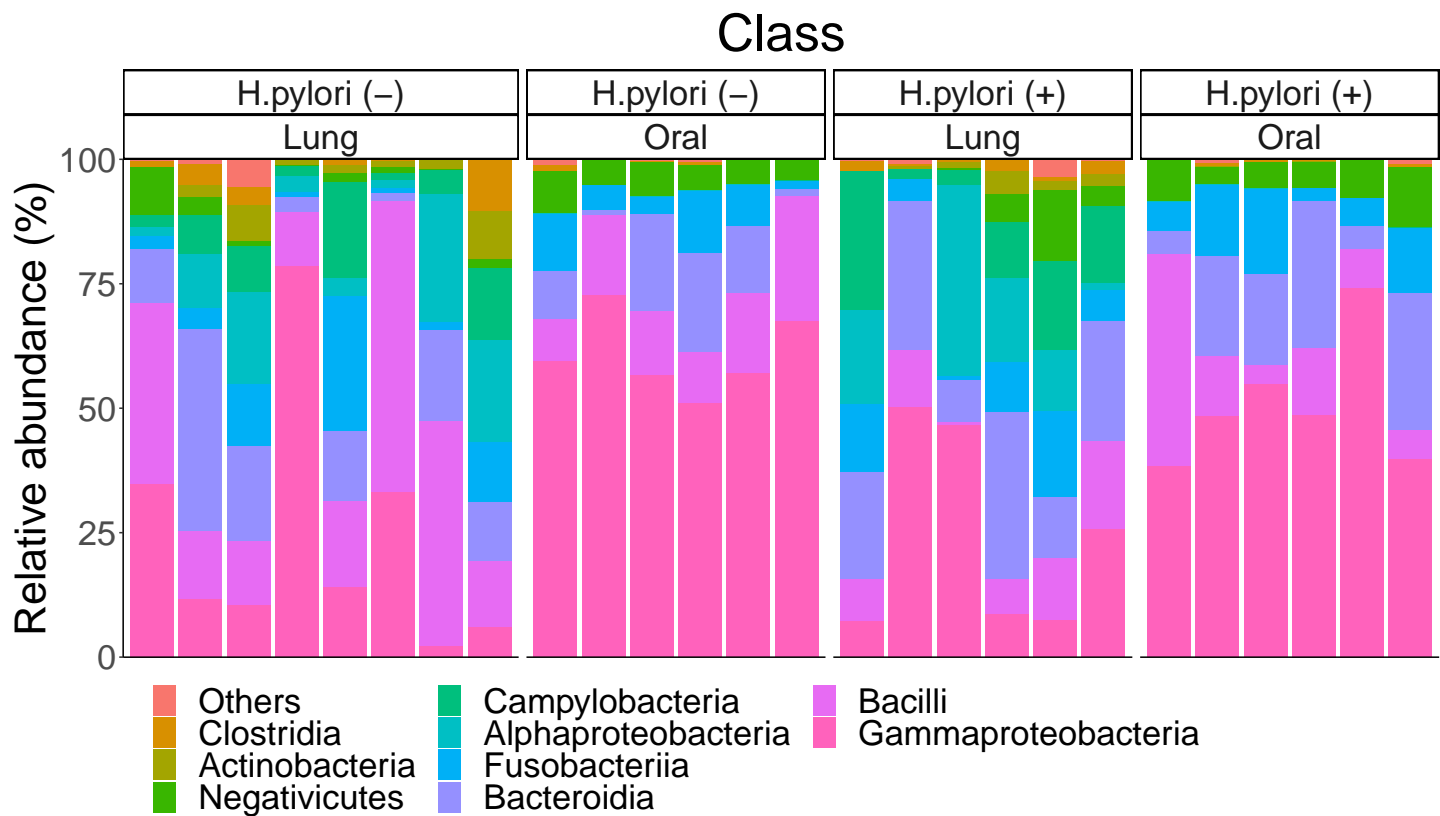| Taxonomy	Sample	Average Percent Abundance
Acidobacteriota	H.pylori (+) Lung	0.1%
Actinobacteriota	H.pylori (-) Lung	3.1%
Actinobacteriota	H.pylori (+) Lung	1.8%
Actinobacteriota	H.pylori (+) Oral	0.1%
Actinobacteriota	H.pylori (-) Oral	0%
Bacteroidota	H.pylori (+) Lung	21.7%
Bacteroidota	H.pylori (+)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

Figure 5: Microbiota Composition at Class level.

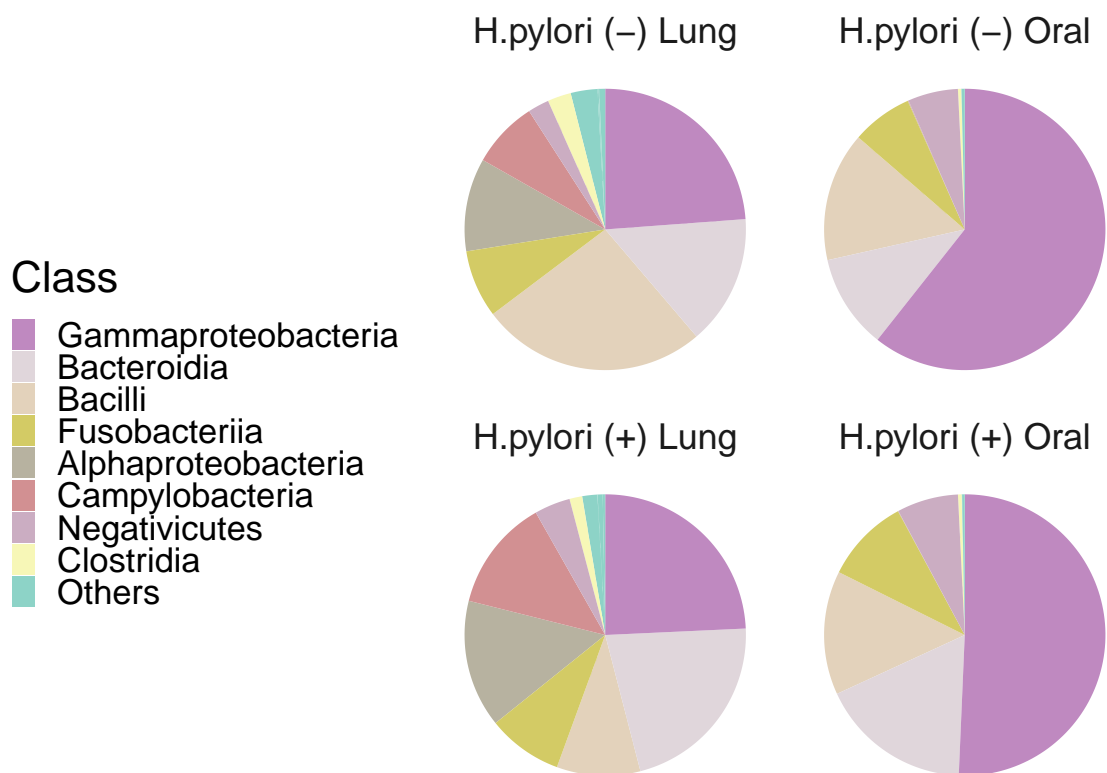**Figure 6:** Microbiota Composition at Class level.

Table 4: Class Average Relative Abundance

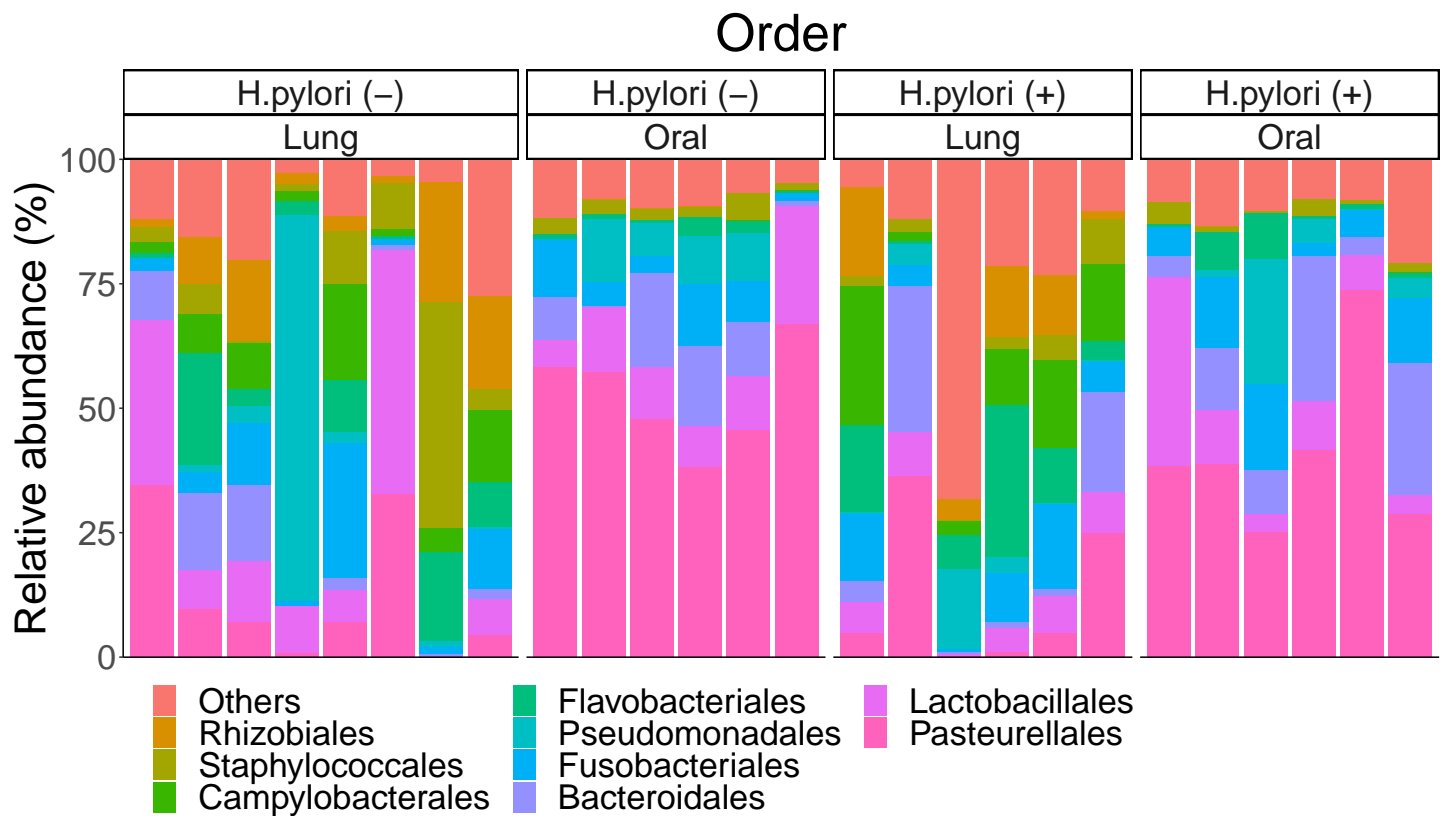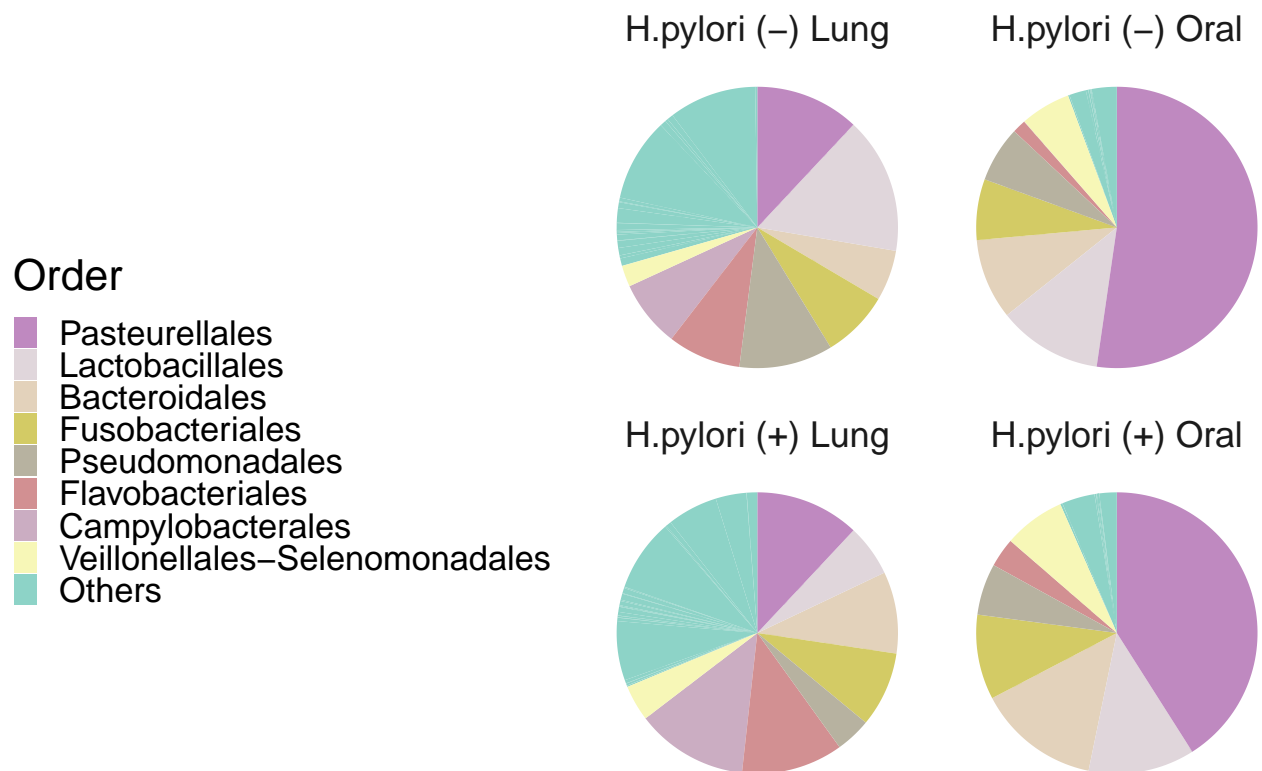| Taxonomy	Sample	Average Percent Abundance
Actinobacteria	H.pylori (-) Lung	3.1%
Actinobacteria	H.pylori (+) Lung	1.7%
Alphaproteobacteria	H.pylori (+) Lung	14.7%
Alphaproteobacteria	H.pylori (-) Lung	10.7%
Bacilli	H.pylori (-) Lung	26%
Bacilli	H.pylori (-) Oral	14.9%
Bacilli	H.pylori (+) Oral	14.2%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

Figure 7: Microbiota Composition at Order level.

Figure 8: Microbiota Composition at Order level.

Table 5: Order Average Relative Abundance

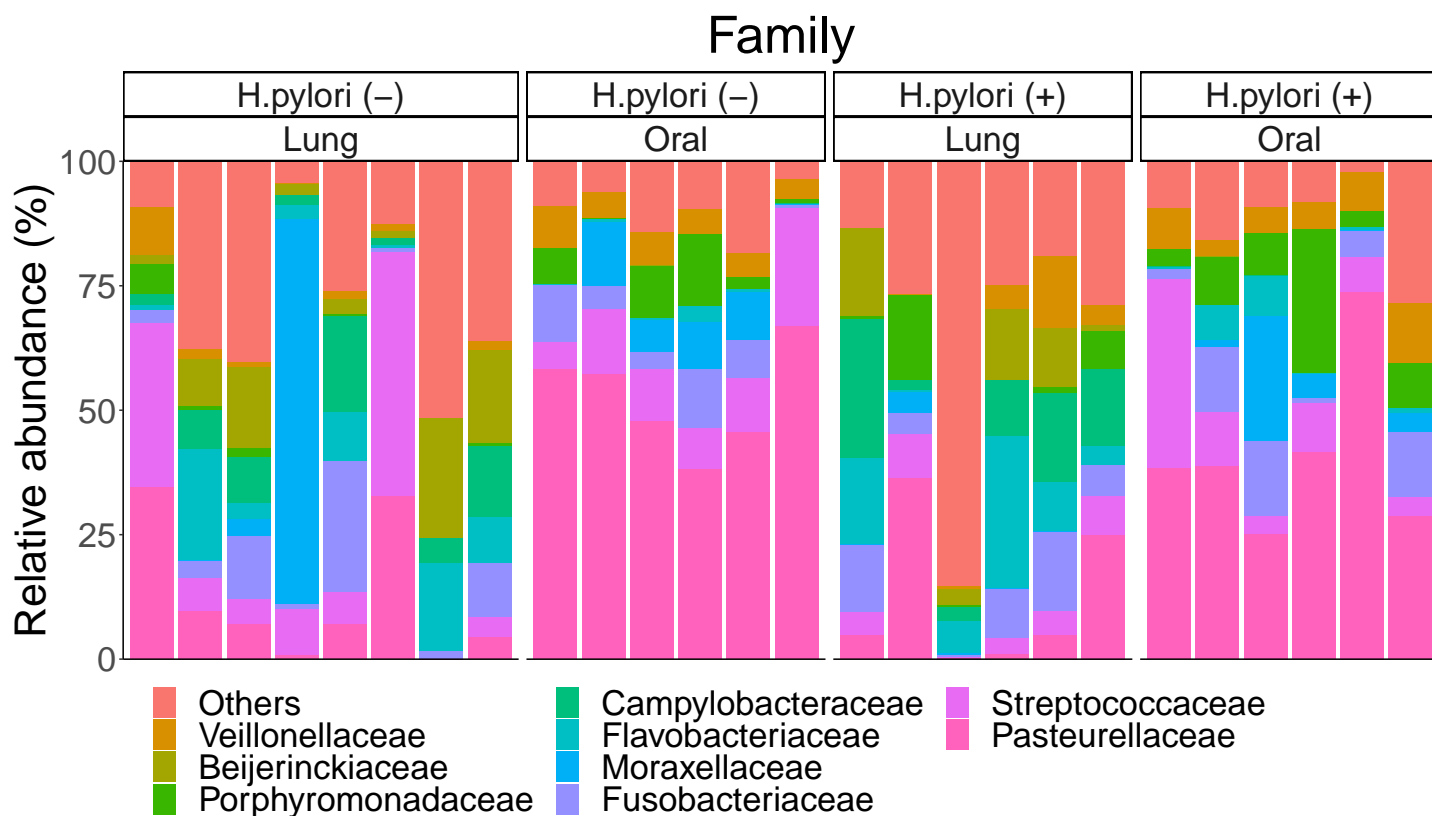| Taxonomy	Sample	Average Percent Abundance
Bacteroidales	H.pylori (+) Oral	14.1%
Bacteroidales	H.pylori (+) Lung	9.4%
Bacteroidales	H.pylori (-) Oral	9.3%
Bacteroidales	H.pylori (-) Lung	5.8%
Burkholderiales	H.pylori (+) Lung	6.8%
Campylobacterales	H.pylori (+) Lung	12.9%
Campylobacterales	H.pylori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

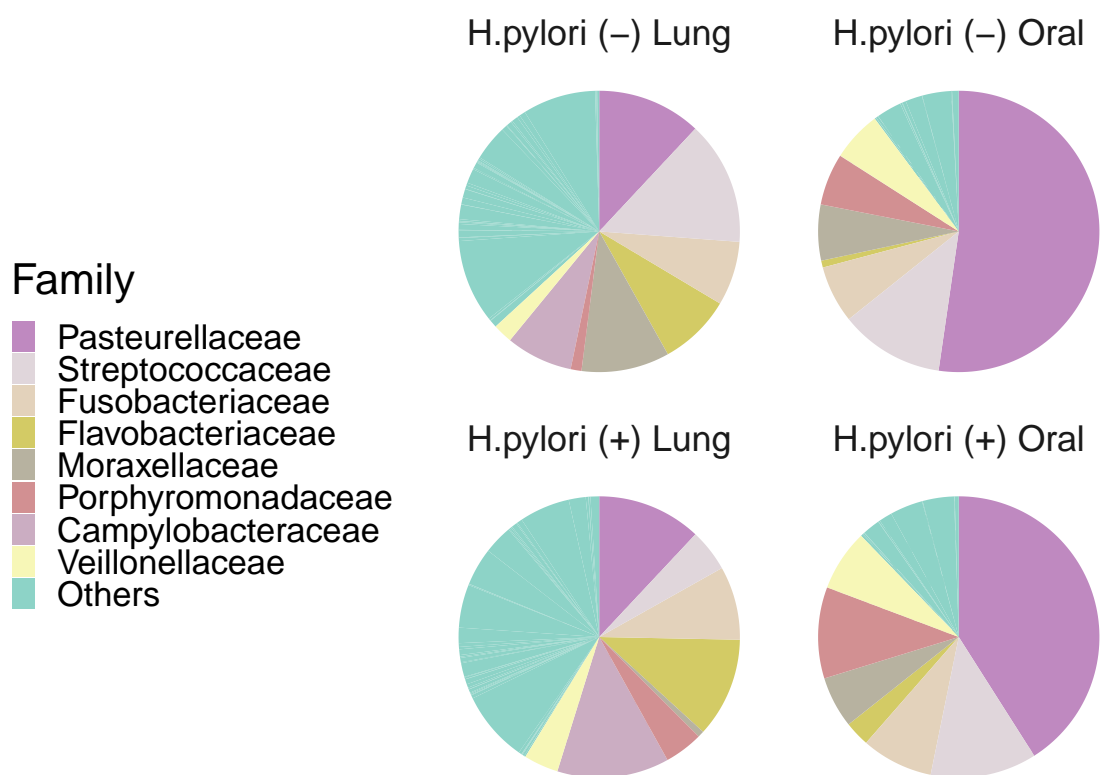**Figure 9:** Microbiota Composition at Family level.

Figure 10: Microbiota Composition at Family level.

Table 6: Family Average Relative Abundance

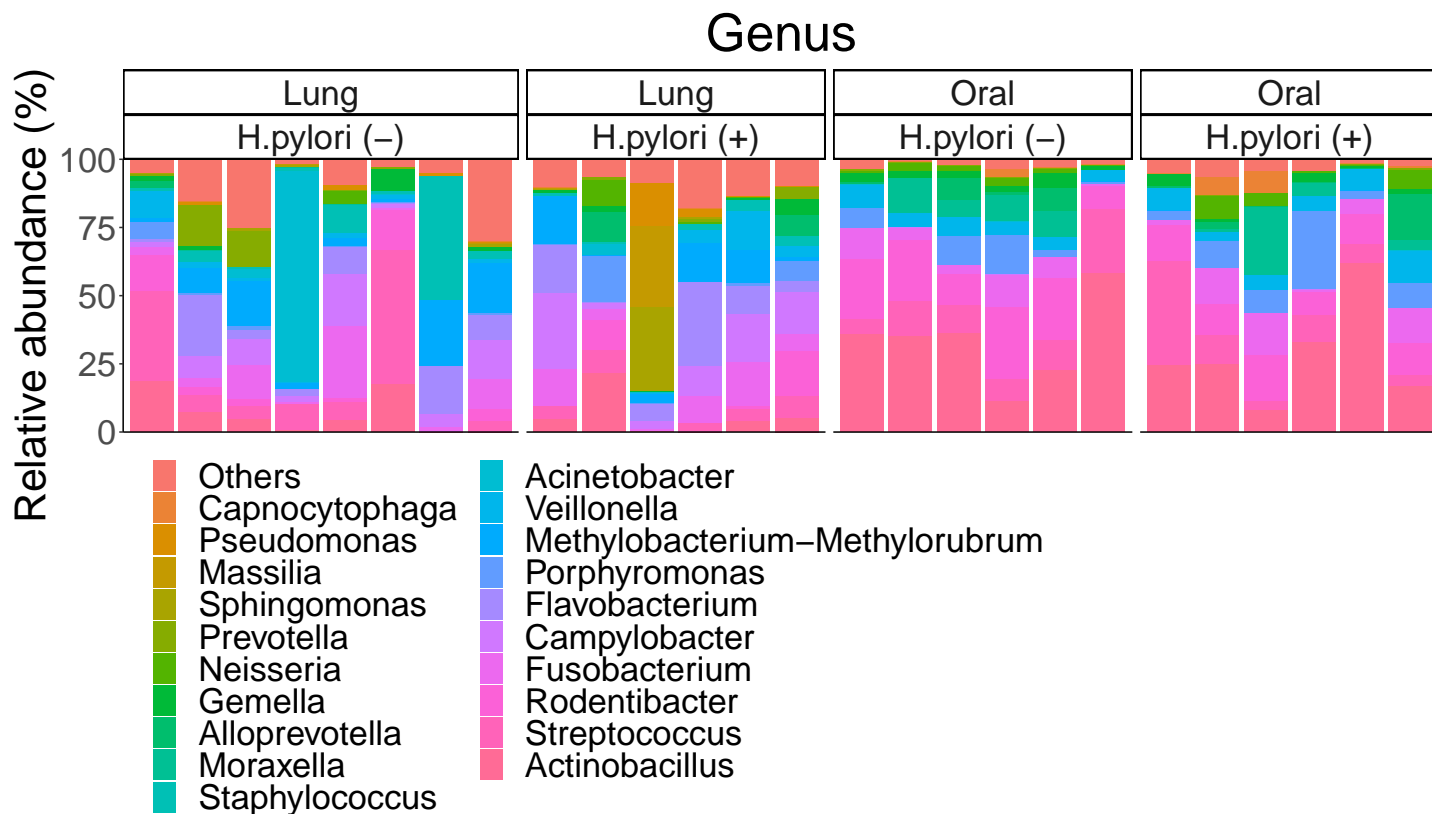| Taxonomy	Sample	Average Percent Abundance
Beijerinckiaceae	H.pylori (-) Lung	9.5%
Beijerinckiaceae	H.pylori (+) Lung	8.1%
Campylobacteraceae	H.pylori (+) Lung	12.9%
Campylobacteraceae	H.pylori (-) Lung	7.7%
Flavobacteriaceae	H.pylori (+) Lung	11.5%
Flavobacteriaceae	H.pylori (-) Lung	8.3%
Fusobacteriaceae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

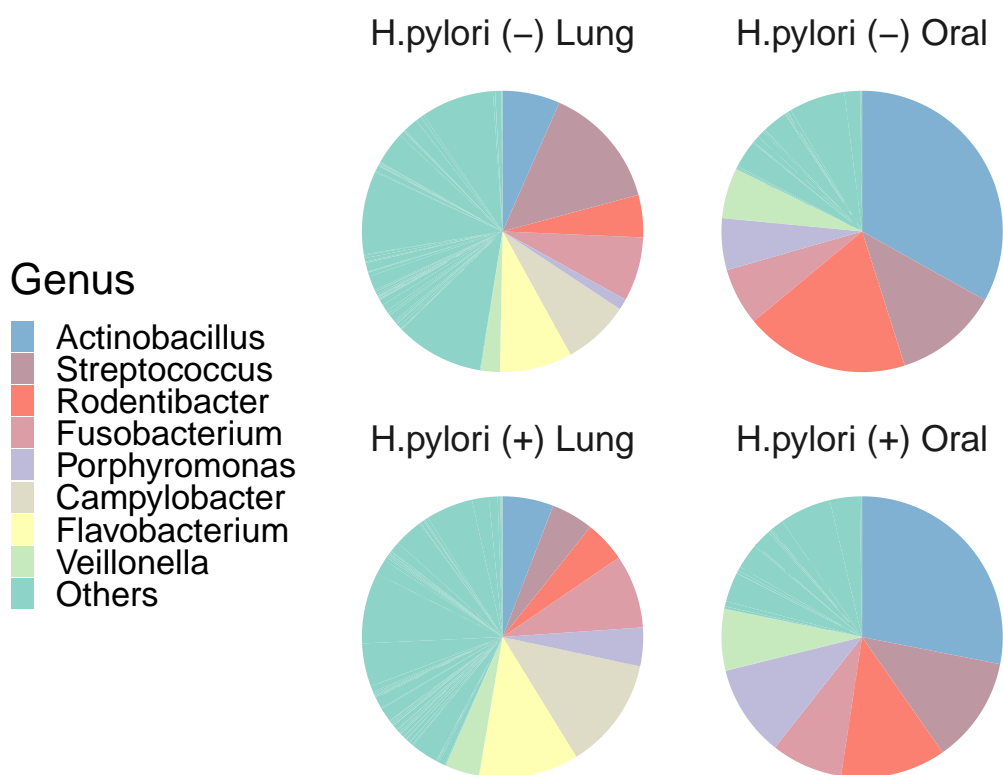**Figure 11:** Microbiota Composition at Genus level.

Figure 12: Microbiota Composition at Genus level.

Table 7: Genus Average Relative Abundance

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

Genera correlation with Il8 concentration (Serum and BAL)

Lavage Genus Abundance
Grouped by H. pylori status

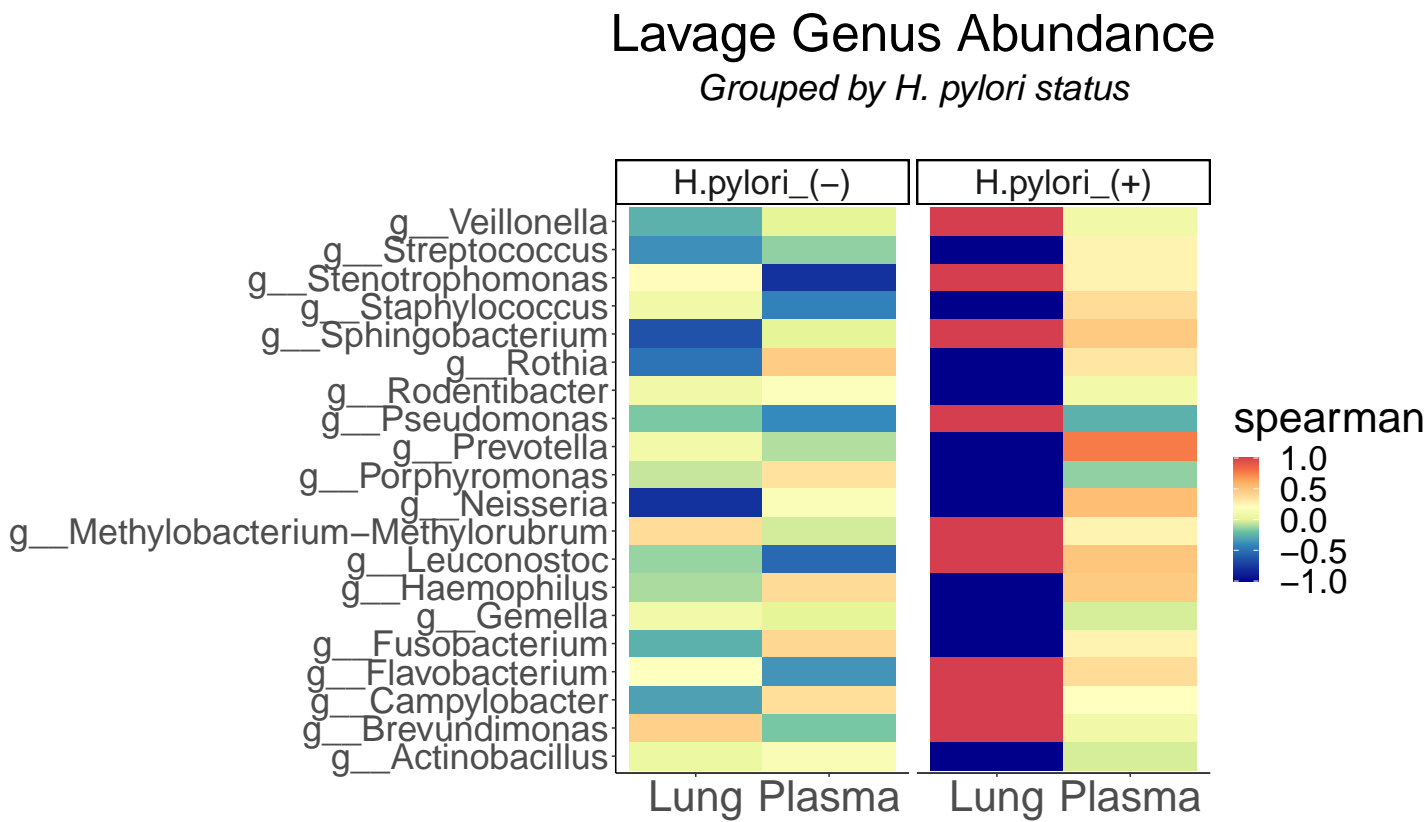**Figure 13:** IL8 and lavage genus abundance Spearman correlations separated by H. pylori status

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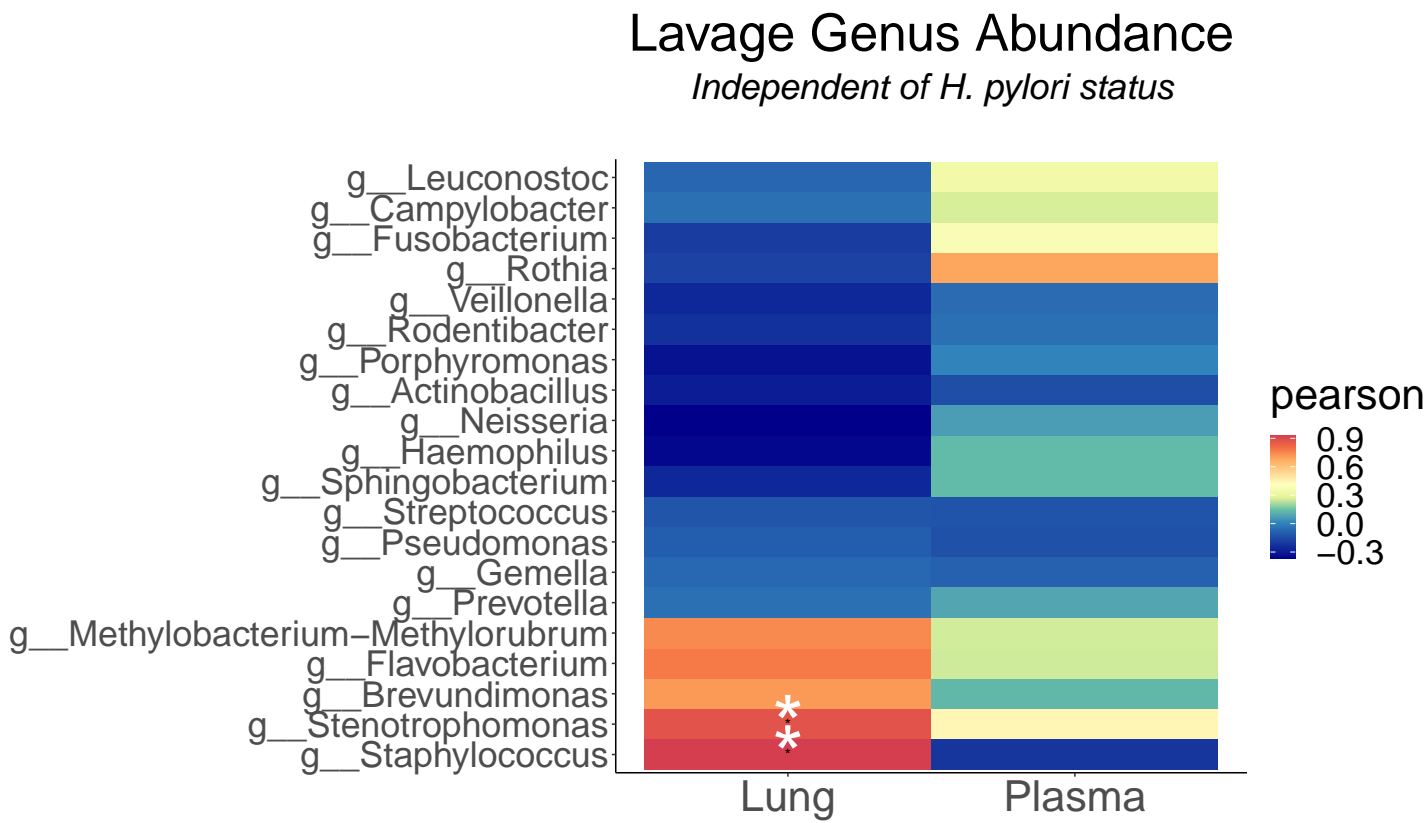
Figure 14: IL8 and lavage genus abundance Spearman correlations independent of H. pylori status

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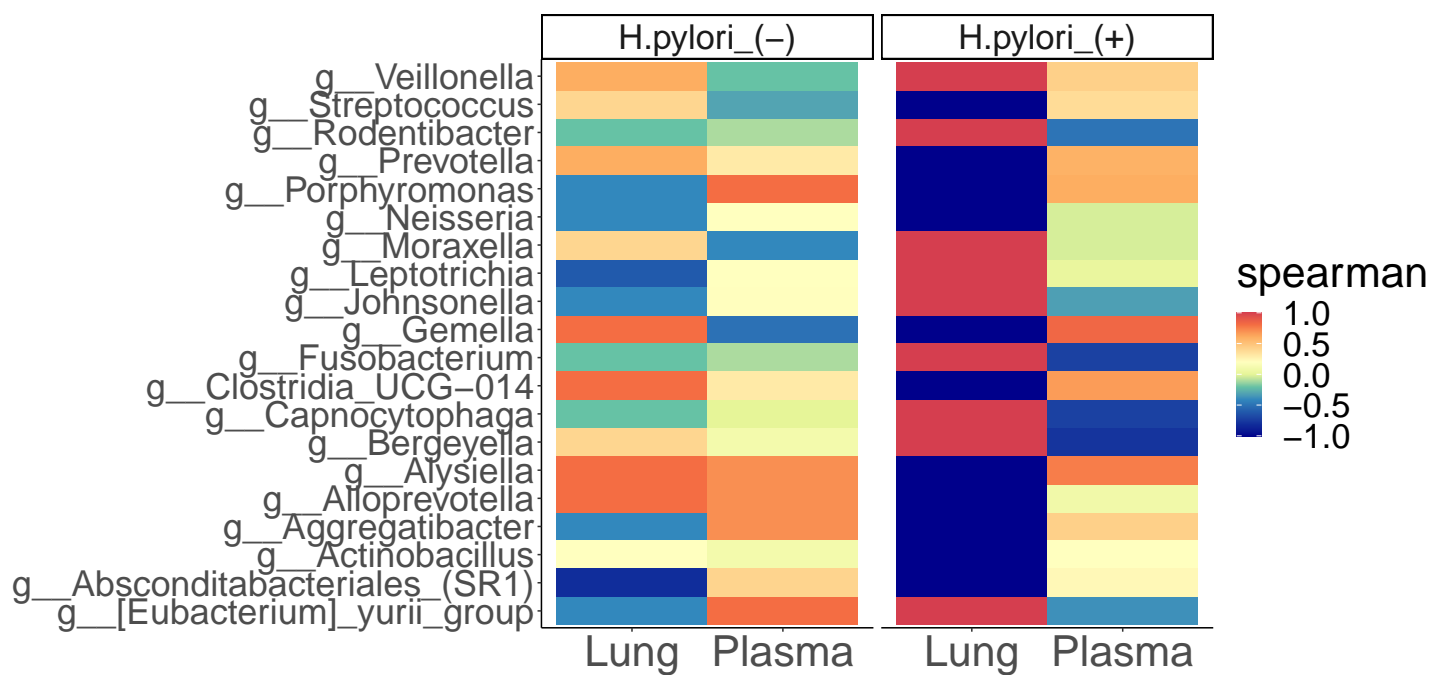
Figure 16: IL8 and Buccal genus abundance Spearman correlations separated by H. pylori status
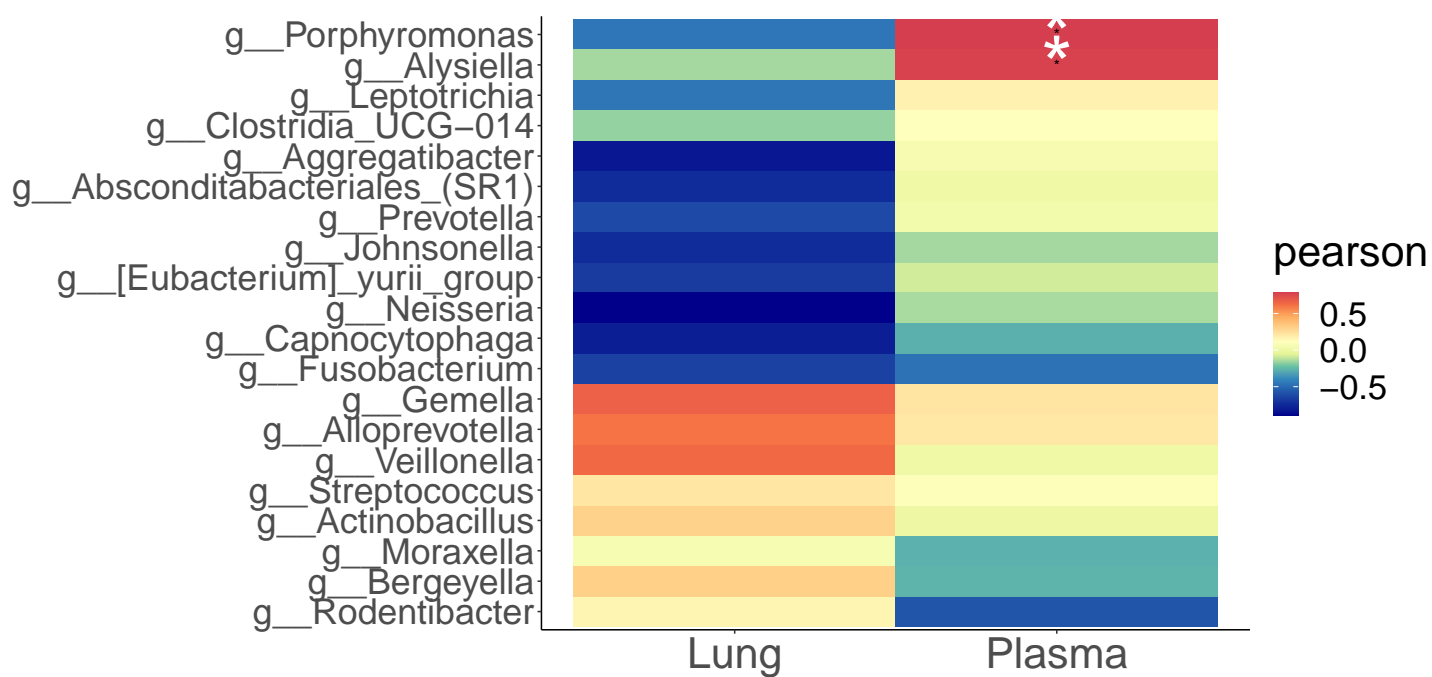
Figure 17: IL8 and Buccal genus abundance Spearman correlations independent of H. pylori status
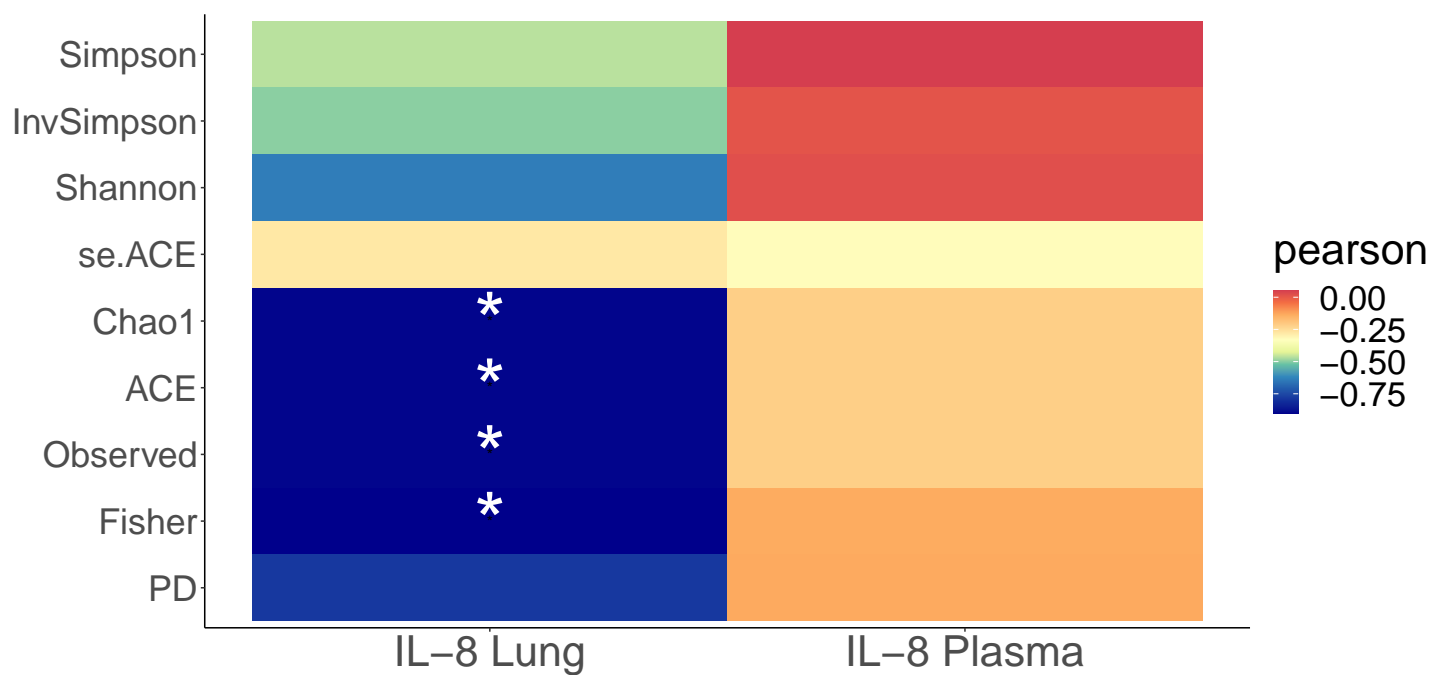
Figure 18: IL8 and Buccal alpha diversity Spearman correlations independent of H. pylori status

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
## [13] purrr_0.3.4            readr_2.1.2
## [15] tidyr_1.2.0            tibble_3.1.7
## [17] tidyverse_1.3.1        qiime2R_0.99.6
## [19] DESeq2_1.34.0          SummarizedExperiment_1.24.0
## [21] Biobase_2.54.0         MatrixGenerics_1.6.0
## [23] matrixStats_0.62.0     GenomicRanges_1.46.1
## [25] GenomeInfoDb_1.30.0    IRanges_2.28.0
## [27] S4Vectors_0.32.3       BiocGenerics_0.40.0
## [29] microbiome_1.16.0      ggplot2_3.3.6
## [31] phyloseq_1.38.0        readxl_1.4.0
## [33] sjPlot_2.8.10
##
## loaded via a namespace (and not attached):
##   [1] estimability_1.3     bit64_4.0.5          knitr_1.39
##   [4] DelayedArray_0.20.0  data.table_1.14.2    rpart_4.1.16
##   [7] KEGGREST_1.34.0      RCurl_1.98-1.7       generics_0.1.2
##  [10] timeSeries_3062.100  RSQLite_2.2.8        VGAM_1.1-8
##  [13] bit_4.0.4            tzdb_0.3.0           webshot_0.5.3
##  [16] xml2_1.3.3           lubridate_1.8.0     httpuv_1.6.5
##  [19] assertthat_0.2.1     xfun_0.31            fBasics_3042.89.1
##  [22] hms_1.1.1            evaluate_0.15        promises_1.2.0.1
##  [25] fansi_1.0.3          dbplyr_2.2.0         igraph_1.3.1
##  [28] DBI_1.1.2            geneplotter_1.72.0   htmlwidgets_1.6.2
##  [31] ellipsis_0.3.2       backports_1.4.1      insight_0.17.1
##  [34] permute_0.9-7        picante_1.8.2        annotate_1.72.0
##  [37] vctrs_0.4.1          sjlabelled_1.2.0     abind_1.4-5
##  [40] cachem_1.0.6         withr_2.5.0          checkmate_2.2.0
##  [43] emmeans_1.7.4-1      vegan_2.6-2          svglite_2.1.0
##  [46] cluster_2.1.3        ape_5.6-2            lazyeval_0.2.2
##  [49] crayon_1.5.1         genefilter_1.76.0    pkgconfig_2.0.3
##  [52] zCompositions_1.4.0-1 labeling_0.4.2      nlme_3.1-157
##  [55] nnet_7.3-17          rlang_1.0.2          spatial_7.3-15
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##  [61] randomForest_4.7-1.1     cellranger_1.1.0          datawizard_0.4.1
##  [64] Matrix_1.4-1             carData_3.0-5             Rhdf5lib_1.16.0
##  [67] boot_1.3-28              reprex_2.0.1              base64enc_0.1-3
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##  [73] parameters_0.18.1        bitops_1.0-7              rhdf5filters_1.6.0
##  [76] Biostrings_2.62.0        blob_1.2.3                GUniFrac_1.6
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##  [82] scales_1.2.0             memoise_2.0.1             plyr_1.8.7
##  [85] zlibbioc_1.40.0          compiler_4.1.3            tinytex_0.39
##  [88] clue_0.3-60              lme4_1.1-29               cli_3.6.1
##  [91] ade4_1.7-19              XVector_0.34.0            htmlTable_2.4.1
##  [94] Formula_1.2-5            MASS_7.3-57               mgcv_1.8-40
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## [115] digest_0.6.29            shiny_1.7.1               Rcpp_1.0.8.3
## [118] car_3.0-13               broom_0.8.0               performance_0.9.0
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## [130] modeest_2.4.0            truncnorm_1.0-9           splines_4.1.3
## [133] yulab.utils_0.0.4        rmutil_1.1.9              statmod_1.4.36
## [136] multtest_2.50.0          systemfonts_1.0.4         xtable_1.8-4
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## [157] survival_3.3-1           biomformat_1.22.0         munsell_0.5.0
## [160] rhdf5_2.38.0             GenomeInfoDbData_1.2.7   iterators_1.0.14
## [163] labelled_2.9.1           sjmisc_2.8.9              haven_2.5.0
## [166] reshape2_1.4.4           gtable_0.3.0              bayestestR_0.12.1
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