

# Microbial Ecology Analysis Report

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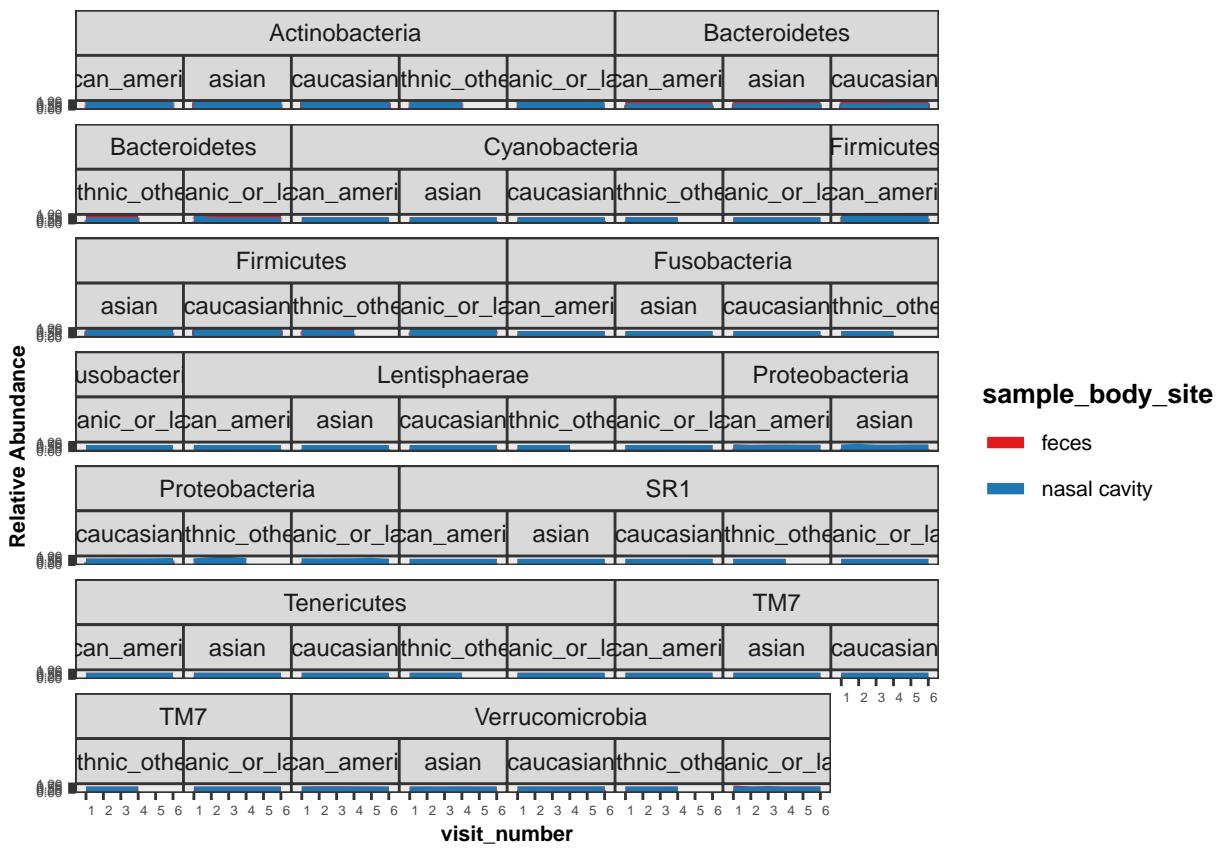
## 1. Alpha Diversity Analysis

### 1.1 Alpha Diversity Boxplots

```
alpha_boxplot_results <- generate_alpha_boxplot_long(data.obj = data.obj,
                                                       alpha.obj = alpha.obj,
                                                       alpha.name = alpha.name,
                                                       subject.var = subject.var,
                                                       time.var = time.var,
                                                       t0.level = t0.level,
                                                       ts.levels = ts.levels,
                                                       group.var = group.var,
                                                       strata.var = strata.var,
                                                       base.size = base.size,
                                                       theme.choice = theme.choice,
                                                       custom.theme = custom.theme,
                                                       palette = palette,
                                                       pdf = pdf,
                                                       file.ann = file.ann,
                                                       pdf.wid = pdf.wid,
                                                       pdf.hei = pdf.hei)
```

```
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
```

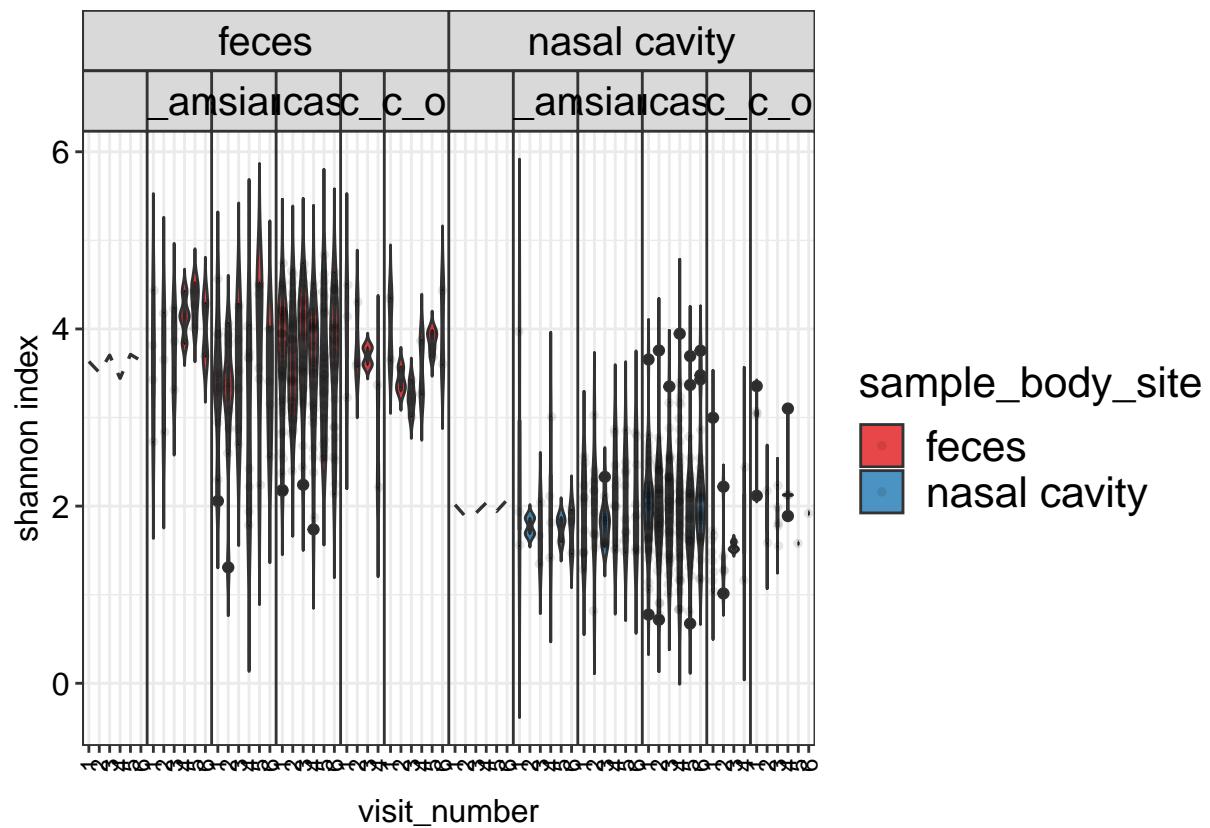
```
alpha_boxplot_results
```



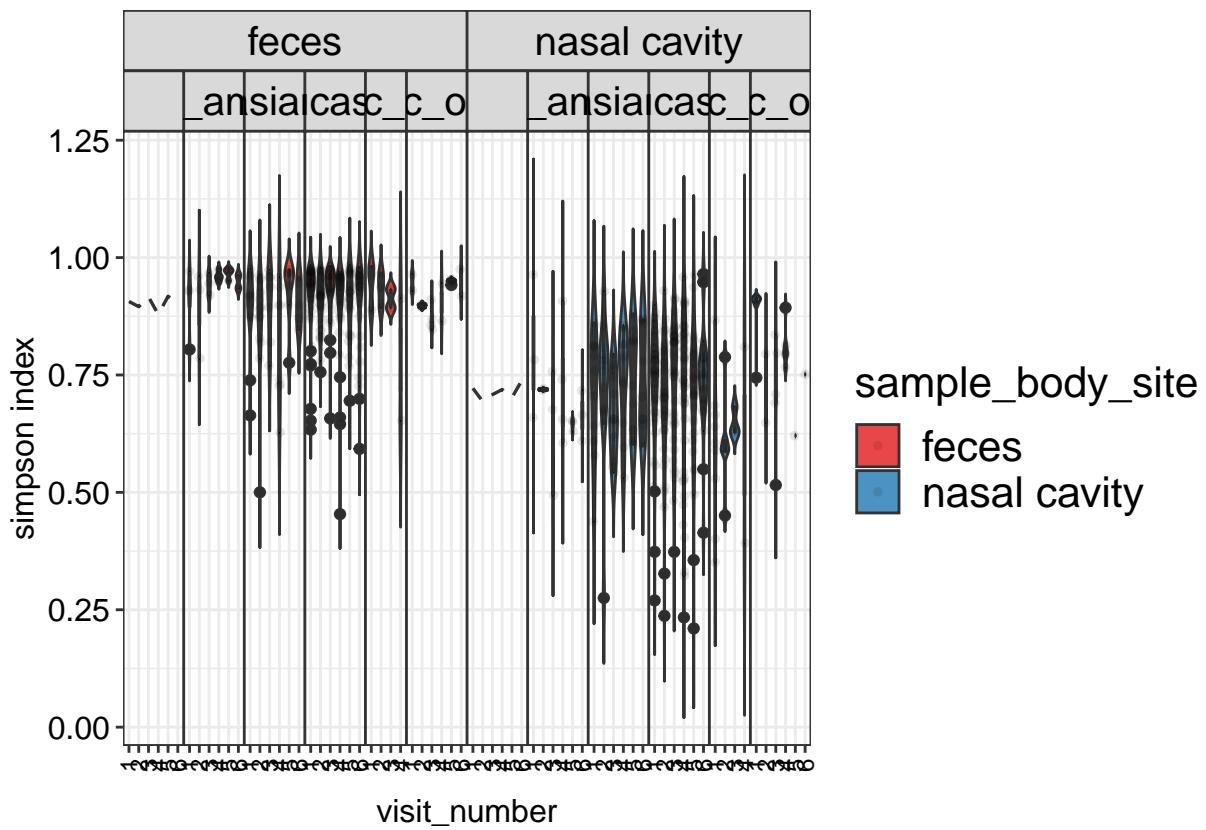
```

## [[1]]
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.

```



```
##
## [[2]]
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
```

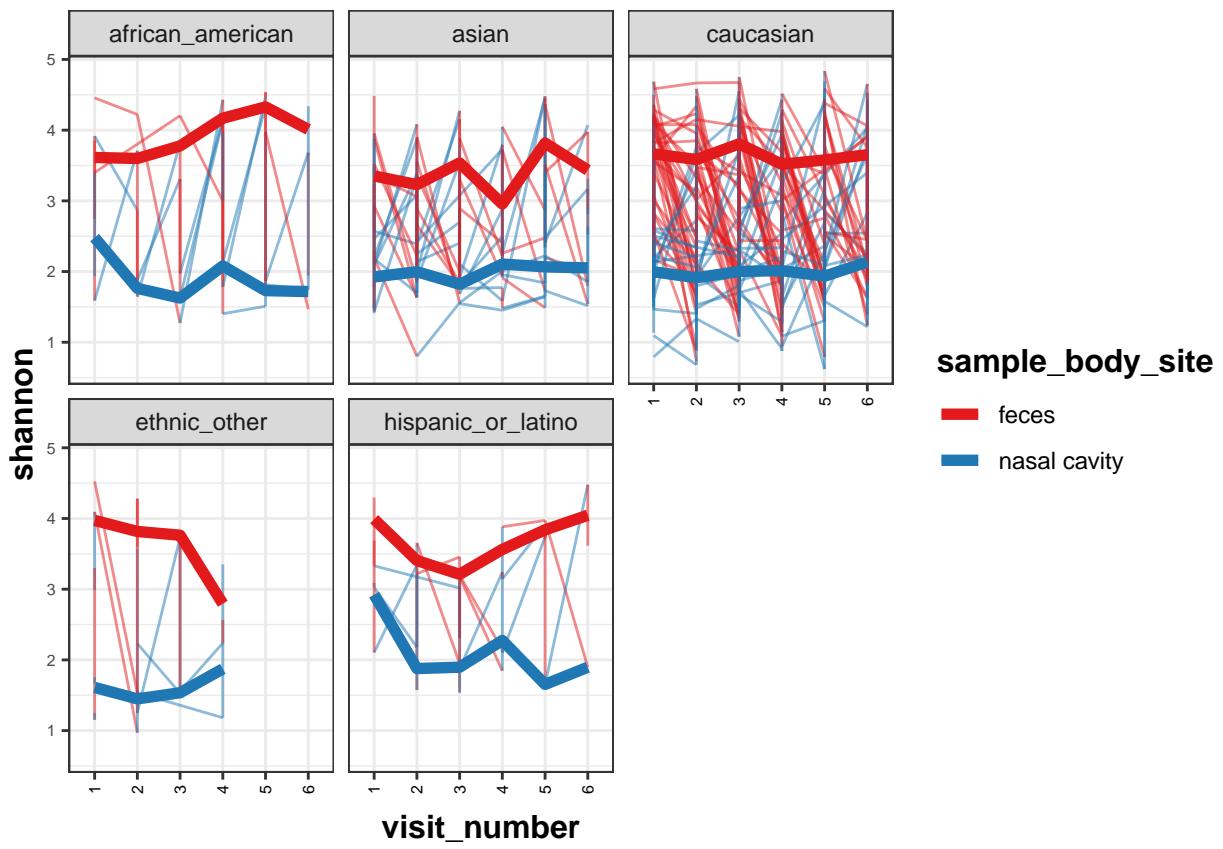


## 1.2 Alpha Diversity Spaghettiplots

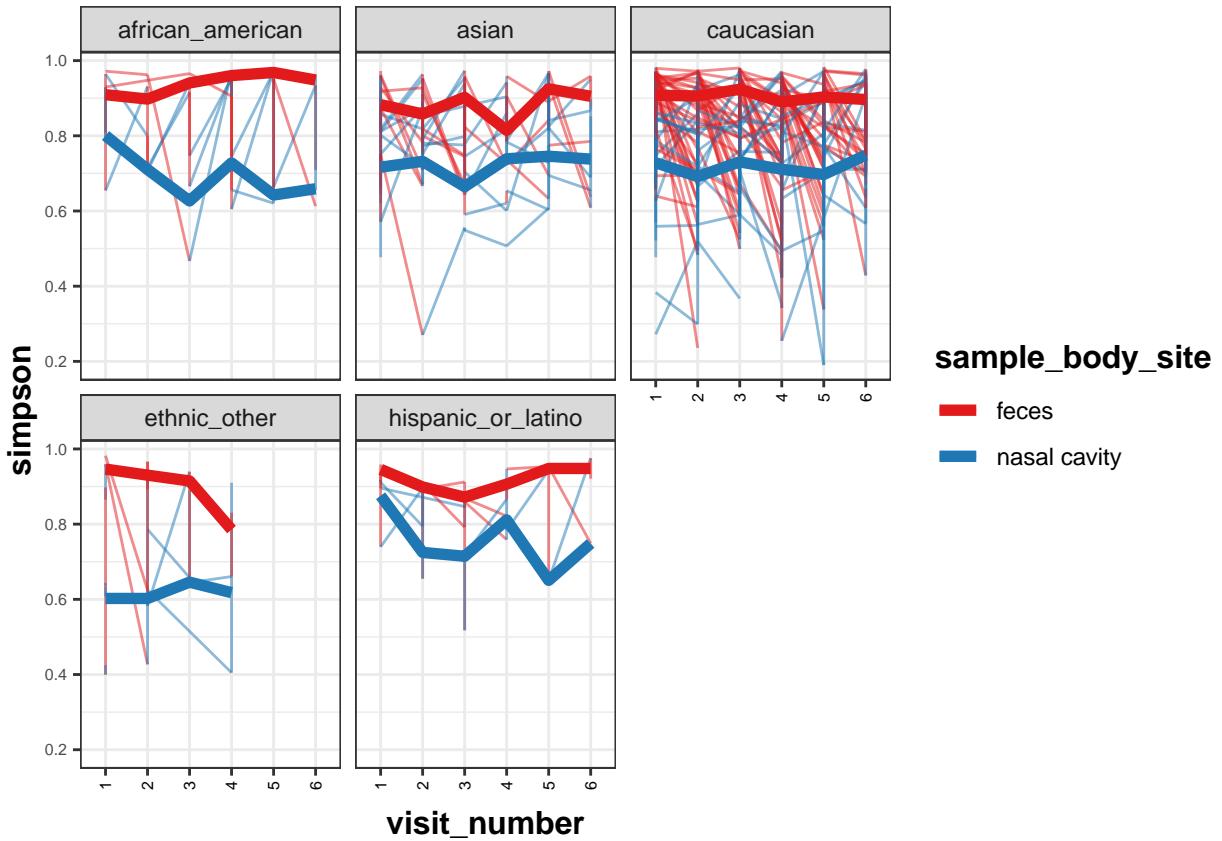
```
alpha_spaghettiplot_results <- generate_alpha_spaghettiplot_long(data.obj = data.obj,
alpha.obj = alpha.obj,
alpha.name = alpha.name,
subject.var = subject.var,
time.var = time.var,
t0.level = t0.level,
ts.levels = ts.levels,
group.var = group.var,
strata.var = strata.var,
base.size = base.size,
theme.choice = theme.choice,
custom.theme = custom.theme,
palette = palette,
pdf = pdf,
file.ann = file.ann,
pdf.wid = pdf.wid,
pdf.hei = pdf.hei)

alpha_spaghettiplot_results

## [[1]]
```



```
##  
## [[2]]
```



### 1.3 Alpha Diversity Test Results

```
alpha_test_results <- generate_alpha_test_long(data.obj = data.obj,
                                              alpha.obj = alpha.obj,
                                              time.var = time.var,
                                              t0.level = t0.level,
                                              ts.levels = ts.levels,
                                              alpha.name = alpha.name,
                                              subject.var = subject.var,
                                              group.var = group.var,
                                              adj.vars = adj.vars)
```

### shannon Index

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	3.818	0.1856	20.57	2.538e-31
visit_number 2	-0.1321	0.06998	-1.888	0.0595
visit_number 3	-0.05713	0.07223	-0.7909	0.4293
visit_number 4	-0.1032	0.07075	-1.459	0.1451
visit_number 5	-0.0538	0.07781	-0.6915	0.4895
visit_number 6	-0.04423	0.08006	-0.5525	0.5808
subject_raceasian	-0.3024	0.2051	-1.474	0.1455
subject_racecaucasian	-0.1558	0.1868	-0.834	0.4075
subject_raceethnic_other	-0.4633	0.2361	-1.962	0.05315
subject_racehispanic_or_latino	-0.004391	0.2684	-0.01636	0.987

Term	Estimate	Std.Error	Statistic	P.Value
sample_body_sitenasal cavity	-1.594	0.04374	-36.45	7.756e-152

### shannon Index Analysis

The variable (Intercept) has a statistically significant impact on the shannon diversity index with an estimate of 3.82.

The variable visit\_number 2 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.13.

The variable visit\_number 3 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.06.

The variable visit\_number 4 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.1.

The variable visit\_number 5 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.05.

The variable visit\_number 6 does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.04.

The variable subject\_raceasian does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.3.

The variable subject\_racecaucasian does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.16.

The variable subject\_raceethnic\_other does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is -0.46.

The variable subject\_racehispanic\_or\_latino does not appear to have a statistically significant effect on the shannon diversity index. The estimate of its effect is 0.

The variable sample\_body\_sitenasal cavity has a statistically significant impact on the shannon diversity index with an estimate of -1.59.

### simpson Index

Term	Estimate	Std.Error	Statistic	P.Value
(Intercept)	0.9299	0.0369	25.2	4.869e-34
visit_number 2	-0.02303	0.01301	-1.77	0.07718
visit_number 3	-0.01109	0.01343	-0.8255	0.4094
visit_number 4	-0.02248	0.01316	-1.709	0.08805
visit_number 5	-0.01553	0.01447	-1.074	0.2834
visit_number 6	-0.008564	0.01489	-0.5753	0.5653
subject_raceasian	-0.03187	0.04093	-0.7787	0.4395
subject_racecaucasian	-0.01636	0.0373	-0.4387	0.6626
subject_raceethnic_other	-0.09918	0.0467	-2.124	0.03714
subject_racehispanic_or_latino	0.0281	0.05374	0.5229	0.6033
sample_body_sitenasal cavity	-0.1824	0.008124	-22.45	2.433e-80

### simpson Index Analysis

The variable (Intercept) has a statistically significant impact on the simpson diversity index with an estimate of 0.93.

The variable visit\_number 2 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.02.

The variable visit\_number 3 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.01.

The variable visit\_number 4 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.02.

The variable visit\_number 5 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.02.

The variable visit\_number 6 does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.01.

The variable subject\_raceasian does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.03.

The variable subject\_racecaucasian does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is -0.02.

The variable subject\_raceethnic\_other has a statistically significant impact on the simpson diversity index with an estimate of -0.1.

The variable subject\_racehispanic\_or\_latino does not appear to have a statistically significant effect on the simpson diversity index. The estimate of its effect is 0.03.

The variable sample\_body\_sitenasal cavity has a statistically significant impact on the simpson diversity index with an estimate of -0.18.

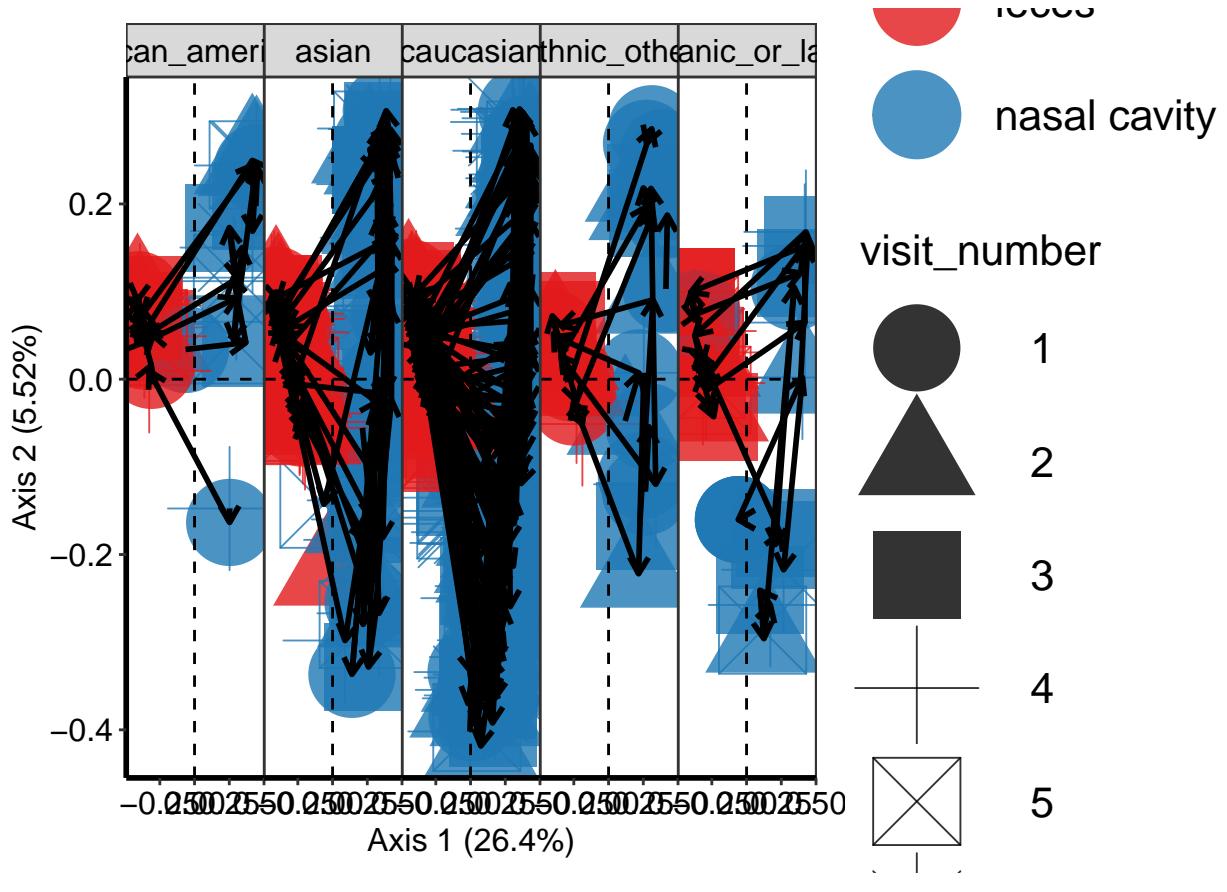
## 2. Beta Diversity Analysis

### 2.1 Beta Diversity Ordination

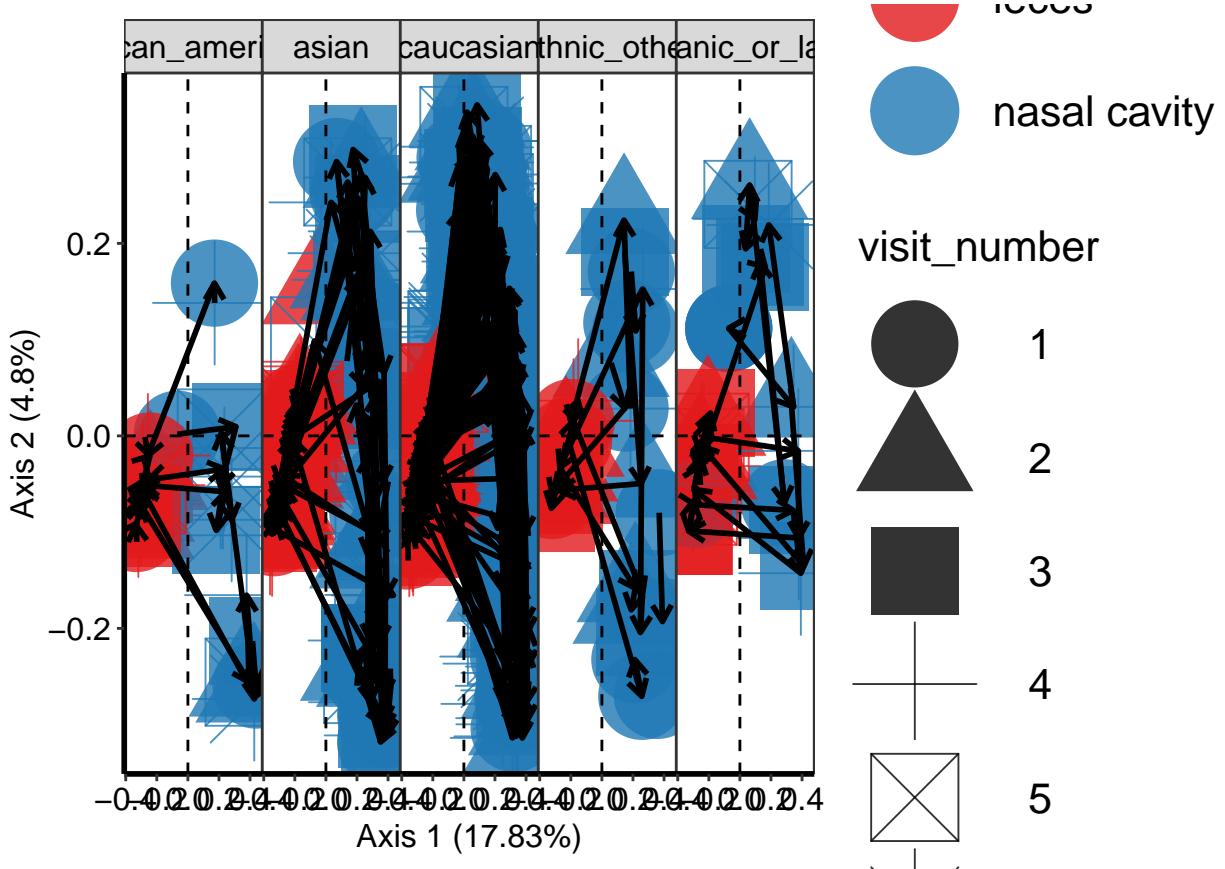
```
beta_ordination_results <- generate_beta_ordination_long(data.obj = data.obj,
                                                       dist.obj = dist.obj,
                                                       pc.obj = NULL,
                                                       subject.var = subject.var,
                                                       time.var = time.var,
                                                       t0.level = t0.level,
                                                       ts.levels = ts.levels,
                                                       group.var = group.var,
                                                       strata.var = strata.var,
                                                       dist.name = dist.name,
                                                       base.size = base.size,
                                                       theme.choice = theme.choice,
                                                       custom.theme = custom.theme,
                                                       palette = palette,
                                                       pdf = pdf,
                                                       file.ann = file.ann,
                                                       pdf.wid = pdf.wid,
                                                       pdf.hei = pdf.hei)

beta_ordination_results

## [[1]]
```



```
##  
## [[2]]
```



## 2.2 Beta Diversity PC Boxplot

```
pc_boxplot_longitudinal_results <- generate_beta_pc_boxplot_long(
  data.obj = data.obj,
  dist.obj = dist.obj,
  pc.obj = NULL,
  pc.ind = c(1, 2),
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t0.level,
  ts.levels = ts.levels,
  group.var = group.var,
  strata.var = strata.var,
  dist.name = dist.name,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)
```

```
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
```

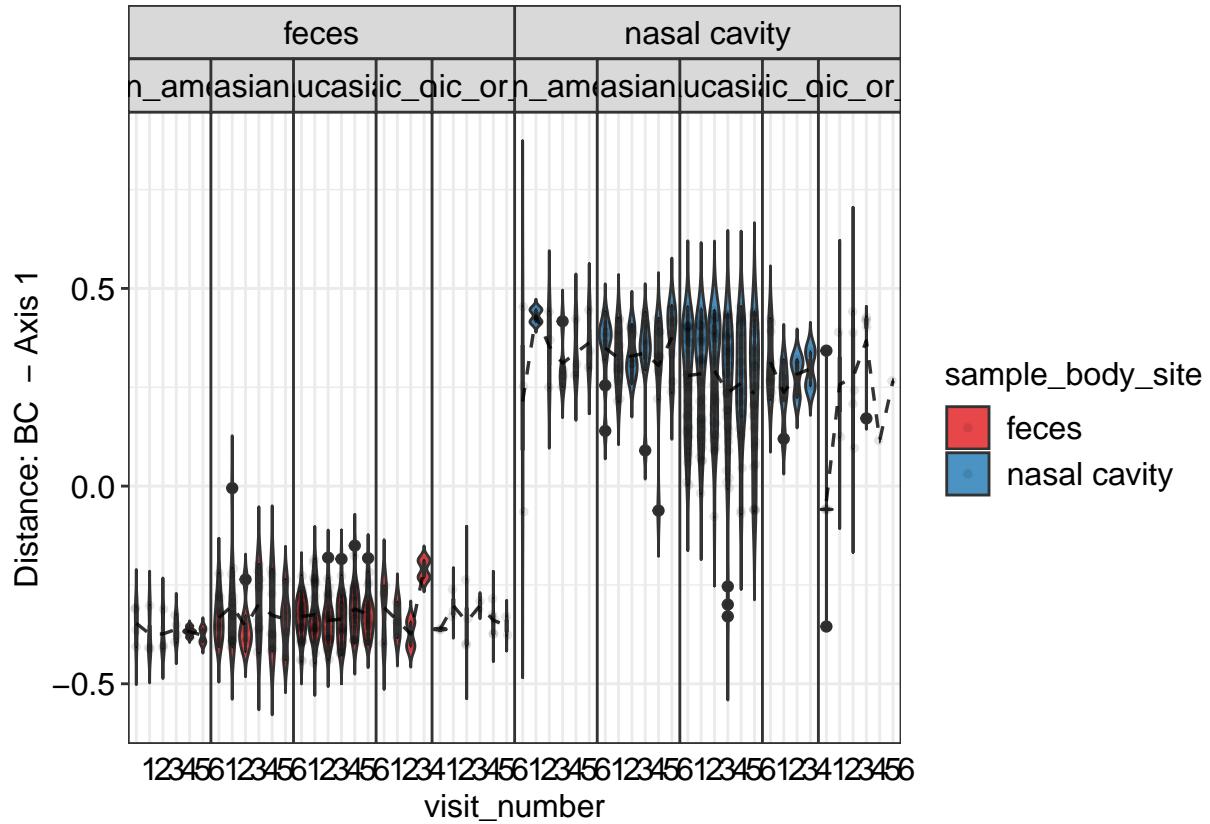
```

## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
pc_boxplot_longitudinal_results

## [[1]]
## [[1]][[1]]


## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.

```

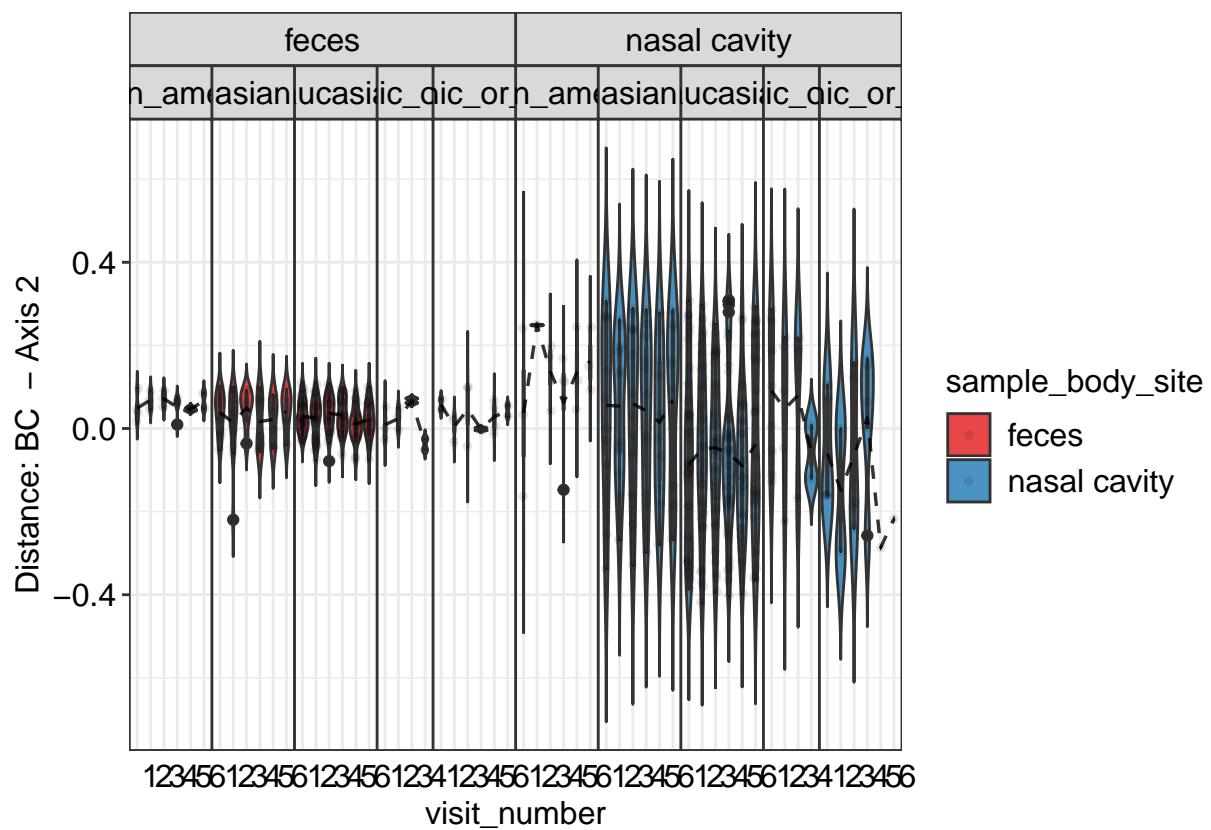


```

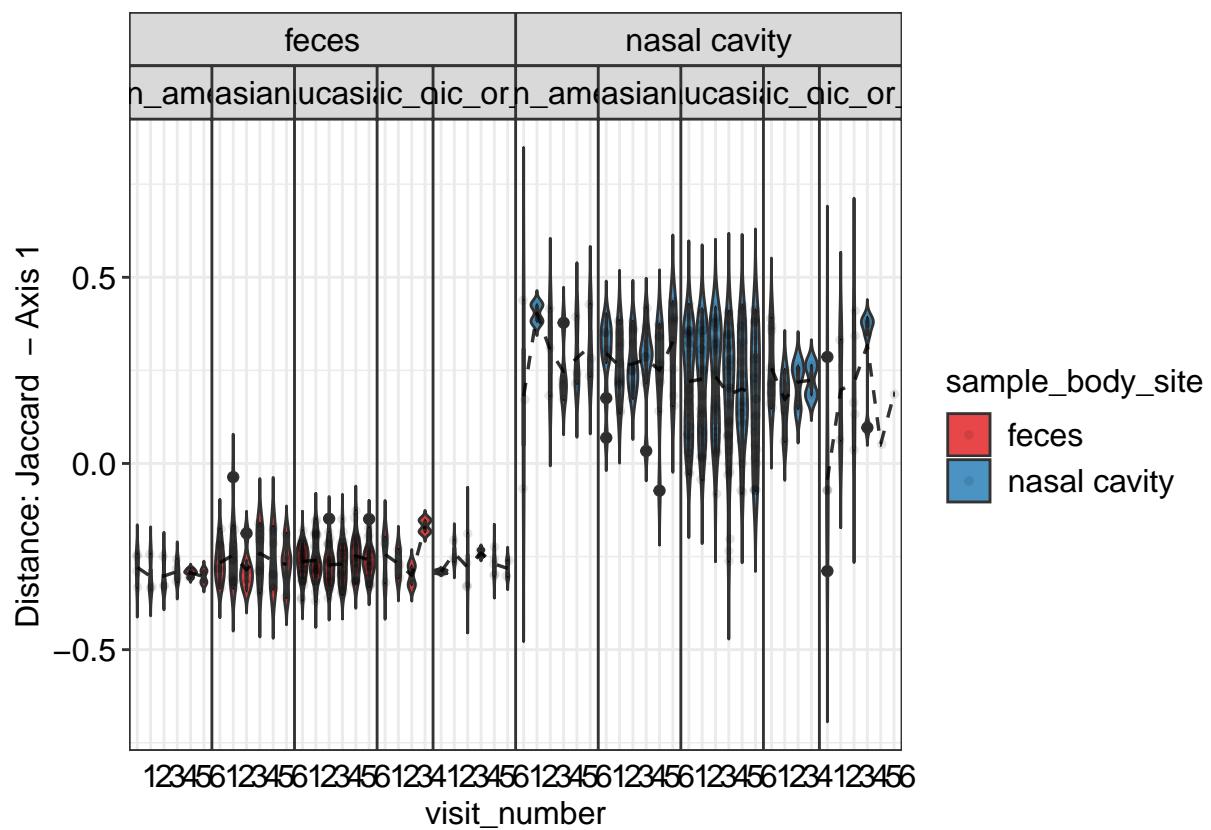
## 
## [[1]][[2]]


## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.

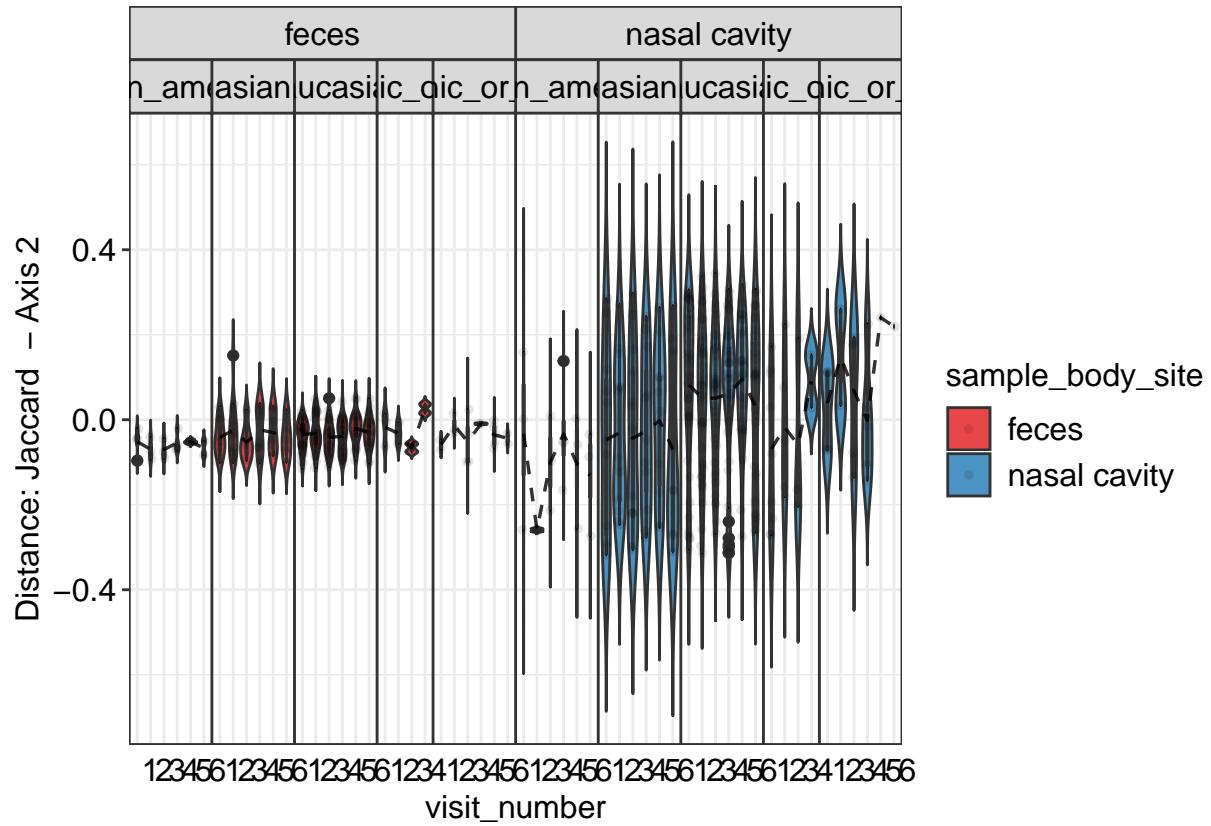
```



```
##
##
## [[2]]
## [[2]][[1]]
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
```



```
##
## [[2]][[2]]
## Warning: Groups with fewer than two data points have been dropped.
## Groups with fewer than two data points have been dropped.
```

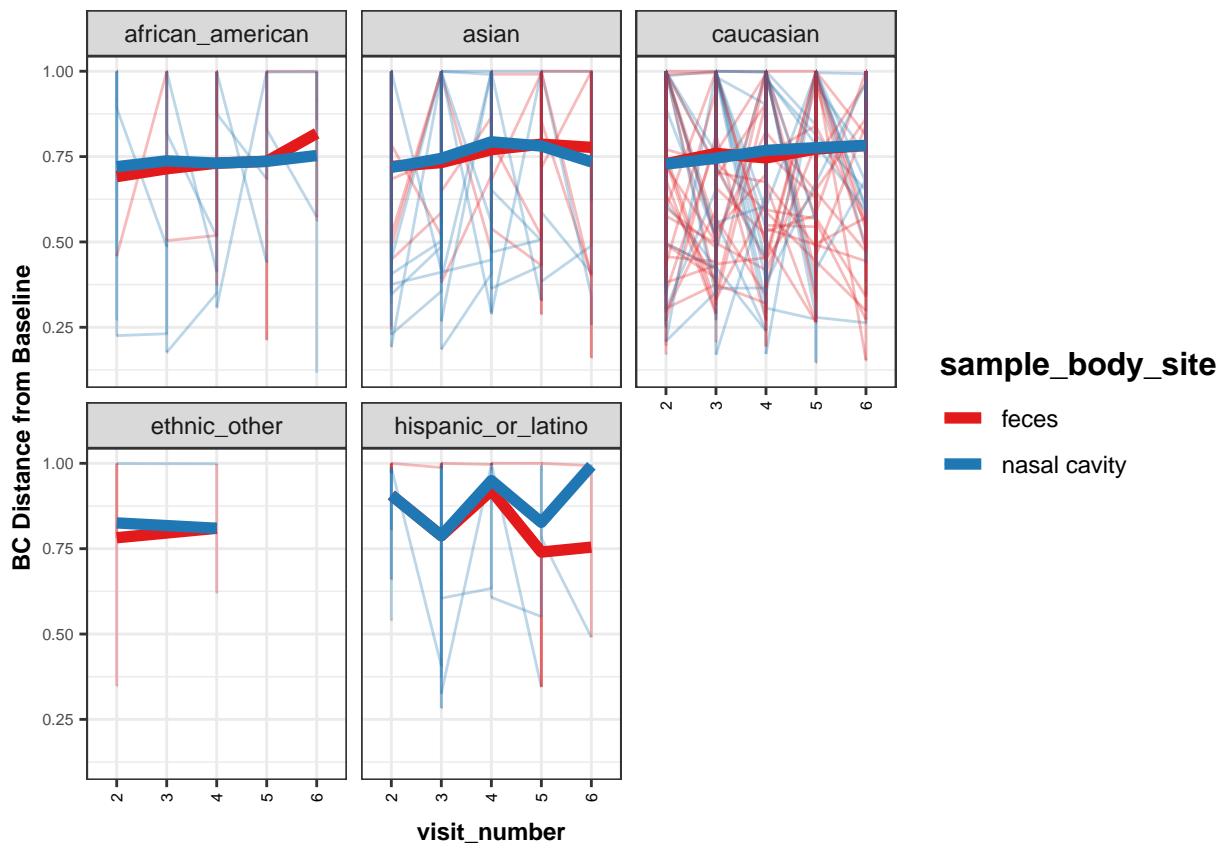


### 2.3 Beta Diversity Change Spaghetti Plot

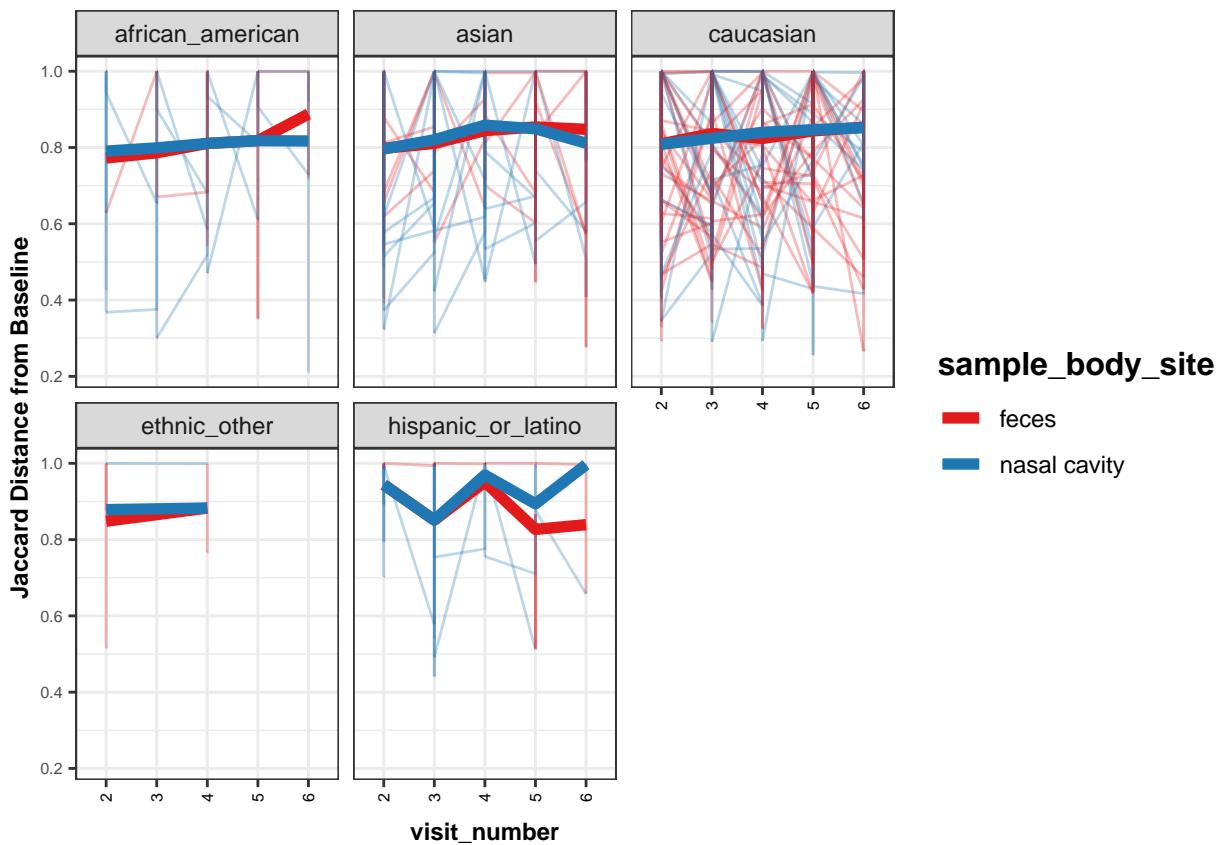
```

spaghettiplot_longitudinal_results <- generate_beta_change_spaghettiplot_long(
  data.obj = data.obj,
  dist.obj = dist.obj,
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t0.level,
  ts.levels = ts.levels,
  group.var = group.var,
  strata.var = strata.var,
  dist.name = dist.name,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)
spaghettiplot_longitudinal_results
## [[1]]

```



```
##  
## [[2]]
```



## 2.4 Beta Diversity Test Longitudinal

```
beta_test_longitudinal_results <- generate_beta_test_long(data.obj = data.obj,
                                                       dist.obj = dist.obj,
                                                       time.var = time.var,
                                                       t0.level = t0.level,
                                                       ts.levels = ts.levels,
                                                       subject.var = subject.var,
                                                       group.var = group.var,
                                                       adj.vars = adj.vars,
                                                       dist.name = dist.name)
```

## P-Tab Results

Term	D1.p.value	D2.p.value	omni.p.value
subject_race	0.001	0.001	0.001
sample_body_site	0.001	0.001	0.001
visit_number	0.879	0.833	0.857

### Beta Diversity PERMANOVA Analysis for Variable: subject\_race

The variable subject\_race has a statistically significant impact on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable subject\_race has a statistically significant impact on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

The variable subject\_race has a statistically significant impact on the beta diversity according to the omnibus PERMANOVA test.

#### Beta Diversity PERMANOVA Analysis for Variable: sample\_body\_site

The variable sample\_body\_site has a statistically significant impact on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable sample\_body\_site has a statistically significant impact on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

The variable sample\_body\_site has a statistically significant impact on the beta diversity according to the omnibus PERMANOVA test.

#### Beta Diversity PERMANOVA Analysis for Variable: visit\_number

The variable visit\_number does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable visit\_number does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

The variable visit\_number does not appear to have a statistically significant effect on the beta diversity according to the omnibus PERMANOVA test.

### AOV-Tab Results

Table 4: Table continues below

Variable	DF	Sum_Sq	Mean_Sq	F_Statistic	R_Squared	P_Value
subject_race	4	4.589	1.147	3.798	0.018	0.001
sample_body_site	1	59.42	59.418	196.722	0.232	0.001
visit_number	5	1.219	0.244	0.807	0.005	0.879
Residuals	631	190.6	0.302	NA	0.745	NA
Total	641	255.8	NA	NA	1	NA
subject_race	4	4.502	1.126	3.038	0.016	0.001
sample_body_site	1	38.65	38.653	104.308	0.139	0.001
visit_number	5	1.619	0.324	0.874	0.006	0.833
Residuals	631	233.8	0.371	NA	0.839	NA
Total	641	278.6	NA	NA	1	NA

Distance
BC
Jaccard

#### subject\_race Variable Analysis

The variable subject\_race has a statistically significant impact on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable subject\_race has a statistically significant impact on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

### **sample\_body\_site Variable Analysis**

The variable sample\_body\_site has a statistically significant impact on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable sample\_body\_site has a statistically significant impact on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

### **visit\_number Variable Analysis**

The variable visit\_number does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the BC distance matrix.

The variable visit\_number does not appear to have a statistically significant effect on the beta diversity according to the PERMANOVA test with the Jaccard distance matrix.

### **Residuals Variable Analysis**

```
## Warning: NAs introduced by coercion
```

```
## Warning: NAs introduced by coercion
```

### **Total Variable Analysis**

```
## Warning: NAs introduced by coercion
```

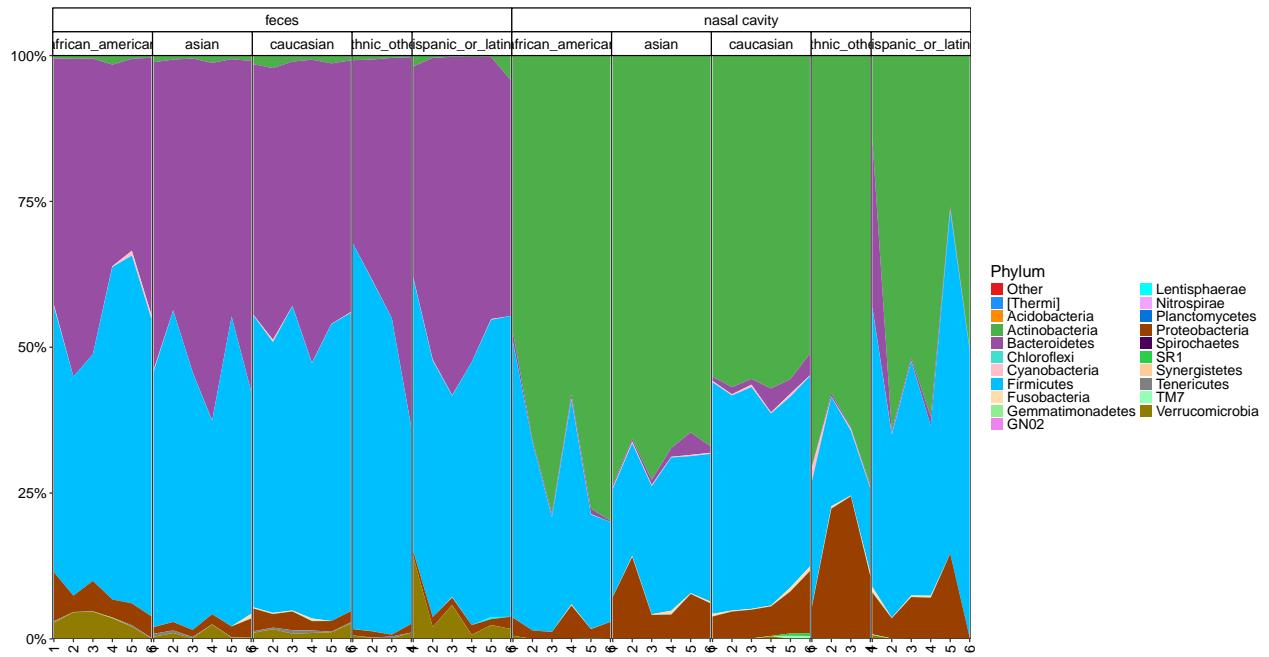
```
## Warning: NAs introduced by coercion
```

## **3. Taxonomic Feature Analysis**

### **3.1 Taxa Areaplot Longitudinal**

```
taxa_areaplot_long_results <- generate_taxa_areaplot_long(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t0.level,
  ts.levels = ts.levels,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  feature.number = 20,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)
taxa_areaplot_long_results
```

```
## [[1]]
```



### 3.2 Taxa Heatmap Longitudinal

```
taxa_heatmap_long_results <- generate_taxa_heatmap_long(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t0.level,
  ts.levels = ts.levels,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  features.plot = NULL,
  top.k.plot = NULL,
  top.k.func = NULL,
  prev.filter = prev.filter,
  abund.filter = abund.filter,
  base.size = base.size,
  palette = palette,
  cluster.cols = NULL,
  cluster.rows = NULL,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)
```

### 3.3 Taxa Change Heatmap Longitudinal

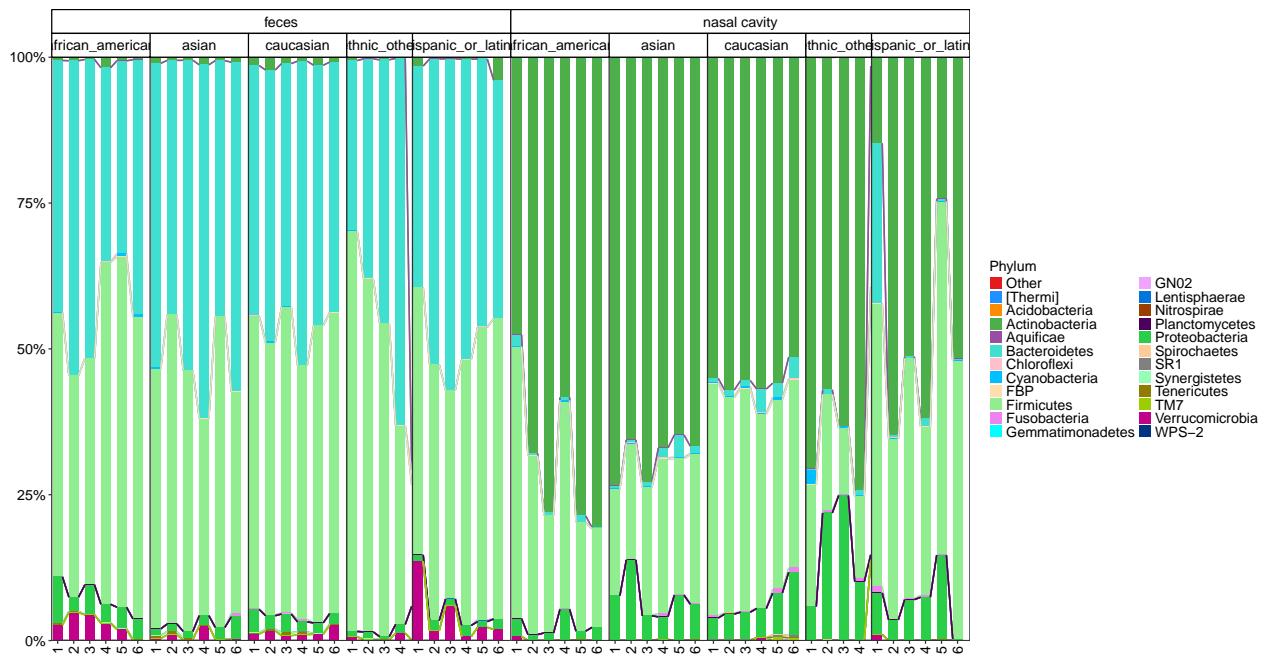
```
taxa_change_heatmap_long_results <- generate_taxa_change_heatmap_long(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  t0.level = t0.level,
  ts.levels = ts.levels,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  features.plot = NULL,
  top.k.plot = NULL,
  top.k.func = NULL,
  change.func = change.func,
  prev.filter = prev.filter,
  abund.filter = abund.filter,
  base.size = base.size,
  palette = palette,
  cluster.cols = NULL,
  cluster.rows = NULL,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)
```

### 3.4 Taxa Barplot Longitudinal

```
taxa_barplot_long_results <- generate_taxa_barplot_long(
  data.obj = data.obj,
  subject.var = subject.var,
  time.var = time.var,
  group.var = group.var,
  strata.var = strata.var,
  feature.level = feature.level,
  feature.dat.type = feature.dat.type,
  feature.number = 20,
  t0.level = t0.level,
  ts.levels = ts.levels,
  base.size = base.size,
  theme.choice = theme.choice,
  custom.theme = custom.theme,
  palette = palette,
  pdf = pdf,
  file.ann = file.ann,
  pdf.wid = pdf.wid,
  pdf.hei = pdf.hei
)

taxa_barplot_long_results

## [[1]]
```



### 3.5 Taxa Test

```
taxa_test_results <- generate_taxa_test_long(data.obj = data.obj,
                                              subject.var = subject.var,
                                              time.var = time.var,
                                              t0.level = t0.level,
                                              ts.levels = ts.levels,
                                              group.var = group.var,
                                              adj.vars = adj.vars,
                                              prev.filter = prev.filter,
                                              abund.filter = abund.filter,
                                              feature.level = feature.level,
                                              feature.dat.type = feature.dat.type,
                                              ...)
```

22 features are filtered! The filtered data has 642 samples and 11 features will be tested! Fit linear mixed effects models ... Completed.

## ## Taxa Test Results

- Phylum:

Table 6: Table continues below

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
Actinobacteria	feces	4323	-0.07264	0.5024
Actinobacteria	nasal cavity	4323	-0.07264	0.5024
Bacteroidetes	feces	387138	0.14	0.55
Bacteroidetes	nasal cavity	387138	0.14	0.55
Cyanobacteria	feces	506.5	0.0252	0.4485
Cyanobacteria	nasal cavity	506.5	0.0252	0.4485
Firmicutes	feces	583663	-0.4281	0.3398
Firmicutes	nasal cavity	583663	-0.4281	0.3398

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
Fusobacteria	feces	292	0.1475	0.4159
Fusobacteria	nasal cavity	292	0.1475	0.4159
Lentisphaerae	feces	310.5	-0.02412	0.2391
Lentisphaerae	nasal cavity	310.5	-0.02412	0.2391
Proteobacteria	feces	19438	-0.858	0.7191
Proteobacteria	nasal cavity	19438	-0.858	0.7191
SR1	feces	278.6	-0.001431	0.2001
SR1	nasal cavity	278.6	-0.001431	0.2001
Tenericutes	feces	738.4	-0.6752	0.3371
Tenericutes	nasal cavity	738.4	-0.6752	0.3371
TM7	feces	284.3	-0.08084	0.2034
TM7	nasal cavity	284.3	-0.08084	0.2034
Verrucomicrobia	feces	3028	-1.497	0.6005
Verrucomicrobia	nasal cavity	3028	-1.497	0.6005
Actinobacteria	feces	4323	-0.2224	0.4572
Actinobacteria	nasal cavity	4323	-0.2224	0.4572
Bacteroidetes	feces	387138	0.07386	0.5008
Bacteroidetes	nasal cavity	387138	0.07386	0.5008
Cyanobacteria	feces	506.5	0.04882	0.4084
Cyanobacteria	nasal cavity	506.5	0.04882	0.4084
Firmicutes	feces	583663	-0.05671	0.3095
Firmicutes	nasal cavity	583663	-0.05671	0.3095
Fusobacteria	feces	292	0.3634	0.3787
Fusobacteria	nasal cavity	292	0.3634	0.3787
Lentisphaerae	feces	310.5	0.02302	0.2179
Lentisphaerae	nasal cavity	310.5	0.02302	0.2179
Proteobacteria	feces	19438	-0.9529	0.6551
Proteobacteria	nasal cavity	19438	-0.9529	0.6551
SR1	feces	278.6	-0.01411	0.1824
SR1	nasal cavity	278.6	-0.01411	0.1824
Tenericutes	feces	738.4	-0.5079	0.307
Tenericutes	nasal cavity	738.4	-0.5079	0.307
TM7	feces	284.3	-0.006391	0.185
TM7	nasal cavity	284.3	-0.006391	0.185
Verrucomicrobia	feces	3028	-0.7117	0.5469
Verrucomicrobia	nasal cavity	3028	-0.7117	0.5469
Actinobacteria	feces	4323	-0.02822	0.6067
Actinobacteria	nasal cavity	4323	-0.02822	0.6067
Bacteroidetes	feces	387138	-0.1714	0.6468
Bacteroidetes	nasal cavity	387138	-0.1714	0.6468
Cyanobacteria	feces	506.5	-0.1136	0.5291
Cyanobacteria	nasal cavity	506.5	-0.1136	0.5291
Firmicutes	feces	583663	-0.505	0.3947
Firmicutes	nasal cavity	583663	-0.505	0.3947
Fusobacteria	feces	292	0.4992	0.4859
Fusobacteria	nasal cavity	292	0.4992	0.4859
Lentisphaerae	feces	310.5	0.1897	0.2736
Lentisphaerae	nasal cavity	310.5	0.1897	0.2736
Proteobacteria	feces	19438	-0.7367	0.829
Proteobacteria	nasal cavity	19438	-0.7367	0.829
SR1	feces	278.6	0.1027	0.2284
SR1	nasal cavity	278.6	0.1027	0.2284

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
Tenericutes	feces	738.4	-0.3798	0.3958
Tenericutes	nasal cavity	738.4	-0.3798	0.3958
TM7	feces	284.3	0.1841	0.2483
TM7	nasal cavity	284.3	0.1841	0.2483
Verrucomicrobia	feces	3028	-0.8558	0.6992
Verrucomicrobia	nasal cavity	3028	-0.8558	0.6992
Actinobacteria	feces	4323	-1.238	0.6465
Actinobacteria	nasal cavity	4323	-1.238	0.6465
Bacteroidetes	feces	387138	0.9129	0.7145
Bacteroidetes	nasal cavity	387138	0.9129	0.7145
Cyanobacteria	feces	506.5	-0.7109	0.5821
Cyanobacteria	nasal cavity	506.5	-0.7109	0.5821
Firmicutes	feces	583663	-0.09432	0.4433
Firmicutes	nasal cavity	583663	-0.09432	0.4433
Fusobacteria	feces	292	0.508	0.5415
Fusobacteria	nasal cavity	292	0.508	0.5415
Lentisphaerae	feces	310.5	0.2811	0.3136
Lentisphaerae	nasal cavity	310.5	0.2811	0.3136
Proteobacteria	feces	19438	-0.9872	0.9408
Proteobacteria	nasal cavity	19438	-0.9872	0.9408
SR1	feces	278.6	-0.2937	0.2627
SR1	nasal cavity	278.6	-0.2937	0.2627
Tenericutes	feces	738.4	-1.105	0.4382
Tenericutes	nasal cavity	738.4	-1.105	0.4382
TM7	feces	284.3	-0.185	0.2607
TM7	nasal cavity	284.3	-0.185	0.2607
Verrucomicrobia	feces	3028	0.2215	0.7829
Verrucomicrobia	nasal cavity	3028	0.2215	0.7829
Actinobacteria	feces	4323	6.641	0.1432
Actinobacteria	nasal cavity	4323	6.641	0.1432
Bacteroidetes	feces	387138	-7.571	0.1353
Bacteroidetes	nasal cavity	387138	-7.571	0.1353
Cyanobacteria	feces	506.5	0.5007	0.1124
Cyanobacteria	nasal cavity	506.5	0.5007	0.1124
Firmicutes	feces	583663	-1.31	0.07729
Firmicutes	nasal cavity	583663	-1.31	0.07729
Fusobacteria	feces	292	0.7785	0.09822
Fusobacteria	nasal cavity	292	0.7785	0.09822
Lentisphaerae	feces	310.5	-0.7262	0.04864
Lentisphaerae	nasal cavity	310.5	-0.7262	0.04864
Proteobacteria	feces	19438	0.4525	0.1547
Proteobacteria	nasal cavity	19438	0.4525	0.1547
SR1	feces	278.6	-0.432	0.03988
SR1	nasal cavity	278.6	-0.432	0.03988
Tenericutes	feces	738.4	-1.389	0.08212
Tenericutes	nasal cavity	738.4	-1.389	0.08212
TM7	feces	284.3	0.1464	0.06121
TM7	nasal cavity	284.3	0.1464	0.06121
Verrucomicrobia	feces	3028	-2.866	0.1386
Verrucomicrobia	nasal cavity	3028	-2.866	0.1386
Actinobacteria	feces	4323	0.06384	0.2284
Actinobacteria	nasal cavity	4323	0.06384	0.2284

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
Bacteroidetes	feces	387138	-0.07094	0.2161
Bacteroidetes	nasal cavity	387138	-0.07094	0.2161
Cyanobacteria	feces	506.5	-0.1774	0.1794
Cyanobacteria	nasal cavity	506.5	-0.1774	0.1794
Firmicutes	feces	583663	-0.08395	0.1235
Firmicutes	nasal cavity	583663	-0.08395	0.1235
Fusobacteria	feces	292	-0.003337	0.1569
Fusobacteria	nasal cavity	292	-0.003337	0.1569
Lentisphaerae	feces	310.5	0.1193	0.07786
Lentisphaerae	nasal cavity	310.5	0.1193	0.07786
Proteobacteria	feces	19438	-0.2727	0.2475
Proteobacteria	nasal cavity	19438	-0.2727	0.2475
SR1	feces	278.6	0.09891	0.06386
SR1	nasal cavity	278.6	0.09891	0.06386
Tenericutes	feces	738.4	0.04662	0.1312
Tenericutes	nasal cavity	738.4	0.04662	0.1312
TM7	feces	284.3	-0.006519	0.09751
TM7	nasal cavity	284.3	-0.006519	0.09751
Verrucomicrobia	feces	3028	-0.03456	0.2216
Verrucomicrobia	nasal cavity	3028	-0.03456	0.2216
Actinobacteria	feces	4323	0.07432	0.2351
Actinobacteria	nasal cavity	4323	0.07432	0.2351
Bacteroidetes	feces	387138	-0.1052	0.2228
Bacteroidetes	nasal cavity	387138	-0.1052	0.2228
Cyanobacteria	feces	506.5	0.09283	0.1849
Cyanobacteria	nasal cavity	506.5	0.09283	0.1849
Firmicutes	feces	583663	-0.1397	0.1274
Firmicutes	nasal cavity	583663	-0.1397	0.1274
Fusobacteria	feces	292	-0.3047	0.1618
Fusobacteria	nasal cavity	292	-0.3047	0.1618
Lentisphaerae	feces	310.5	0.03174	0.08039
Lentisphaerae	nasal cavity	310.5	0.03174	0.08039
Proteobacteria	feces	19438	-0.2222	0.2554
Proteobacteria	nasal cavity	19438	-0.2222	0.2554
SR1	feces	278.6	-0.02083	0.06594
SR1	nasal cavity	278.6	-0.02083	0.06594
Tenericutes	feces	738.4	0.1928	0.1352
Tenericutes	nasal cavity	738.4	0.1928	0.1352
TM7	feces	284.3	-0.02487	0.1003
TM7	nasal cavity	284.3	-0.02487	0.1003
Verrucomicrobia	feces	3028	-0.4282	0.2285
Verrucomicrobia	nasal cavity	3028	-0.4282	0.2285
Actinobacteria	feces	4323	-0.2002	0.2303
Actinobacteria	nasal cavity	4323	-0.2002	0.2303
Bacteroidetes	feces	387138	0.3314	0.2183
Bacteroidetes	nasal cavity	387138	0.3314	0.2183
Cyanobacteria	feces	506.5	-0.2034	0.1812
Cyanobacteria	nasal cavity	506.5	-0.2034	0.1812
Firmicutes	feces	583663	-0.2235	0.1248
Firmicutes	nasal cavity	583663	-0.2235	0.1248
Fusobacteria	feces	292	-0.1159	0.1585
Fusobacteria	nasal cavity	292	-0.1159	0.1585

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
Lentisphaerae	feces	310.5	0.04907	0.07874
Lentisphaerae	nasal cavity	310.5	0.04907	0.07874
Proteobacteria	feces	19438	-0.3298	0.2502
Proteobacteria	nasal cavity	19438	-0.3298	0.2502
SR1	feces	278.6	0.04984	0.06458
SR1	nasal cavity	278.6	0.04984	0.06458
Tenericutes	feces	738.4	0.02433	0.1325
Tenericutes	nasal cavity	738.4	0.02433	0.1325
TM7	feces	284.3	0.02549	0.09831
TM7	nasal cavity	284.3	0.02549	0.09831
Verrucomicrobia	feces	3028	-0.007621	0.2239
Verrucomicrobia	nasal cavity	3028	-0.007621	0.2239
Actinobacteria	feces	4323	-0.01716	0.2532
Actinobacteria	nasal cavity	4323	-0.01716	0.2532
Bacteroidetes	feces	387138	-0.2512	0.24
Bacteroidetes	nasal cavity	387138	-0.2512	0.24
Cyanobacteria	feces	506.5	-0.01519	0.1992
Cyanobacteria	nasal cavity	506.5	-0.01519	0.1992
Firmicutes	feces	583663	-0.2243	0.1373
Firmicutes	nasal cavity	583663	-0.2243	0.1373
Fusobacteria	feces	292	-0.3655	0.1744
Fusobacteria	nasal cavity	292	-0.3655	0.1744
Lentisphaerae	feces	310.5	0.0507	0.0866
Lentisphaerae	nasal cavity	310.5	0.0507	0.0866
Proteobacteria	feces	19438	-0.2233	0.2752
Proteobacteria	nasal cavity	19438	-0.2233	0.2752
SR1	feces	278.6	-0.001024	0.07102
SR1	nasal cavity	278.6	-0.001024	0.07102
Tenericutes	feces	738.4	-0.002139	0.1457
Tenericutes	nasal cavity	738.4	-0.002139	0.1457
TM7	feces	284.3	0.05526	0.108
TM7	nasal cavity	284.3	0.05526	0.108
Verrucomicrobia	feces	3028	-0.04653	0.2462
Verrucomicrobia	nasal cavity	3028	-0.04653	0.2462
Actinobacteria	feces	4323	0.003862	0.2603
Actinobacteria	nasal cavity	4323	0.003862	0.2603
Bacteroidetes	feces	387138	-0.03628	0.2469
Bacteroidetes	nasal cavity	387138	-0.03628	0.2469
Cyanobacteria	feces	506.5	-0.2094	0.2049
Cyanobacteria	nasal cavity	506.5	-0.2094	0.2049
Firmicutes	feces	583663	-0.1648	0.1413
Firmicutes	nasal cavity	583663	-0.1648	0.1413
Fusobacteria	feces	292	-0.1358	0.1794
Fusobacteria	nasal cavity	292	-0.1358	0.1794
Lentisphaerae	feces	310.5	0.03593	0.0891
Lentisphaerae	nasal cavity	310.5	0.03593	0.0891
Proteobacteria	feces	19438	0.04086	0.2831
Proteobacteria	nasal cavity	19438	0.04086	0.2831
SR1	feces	278.6	0.02322	0.07308
SR1	nasal cavity	278.6	0.02322	0.07308
Tenericutes	feces	738.4	-0.05476	0.1498
Tenericutes	nasal cavity	738.4	-0.05476	0.1498

Variable	Group	Base.Mean	Log2.Fold.Change	LFC.SE
TM7	feces	284.3	0.1265	0.1111
TM7	nasal cavity	284.3	0.1265	0.1111
Verrucomicrobia	feces	3028	-0.09639	0.2533
Verrucomicrobia	nasal cavity	3028	-0.09639	0.2533

Table 7: Table continues below

Stat	P.Value	Adjusted.P.Value	Mean.Abandance	Mean.Prevalence
-0.1446	0.8855	0.9943	0.01119	1
-0.1446	0.8855	0.9943	0.5832	1
0.2545	0.8	0.9943	0.4568	1
0.2545	0.8	0.9943	0.02118	1
0.05618	0.9554	0.9943	0.001024	1
0.05618	0.9554	0.9943	0.002002	1
-1.26	0.2123	0.6525	0.4812	1
-1.26	0.2123	0.6525	0.319	1
0.3547	0.724	0.9943	0.0006737	1
0.3547	0.724	0.9943	0.002223	1
-0.1009	0.9199	0.9943	0.0003472	1
-0.1009	0.9199	0.9943	0.0002596	1
-1.193	0.2373	0.6525	0.02387	1
-1.193	0.2373	0.6525	0.0565	1
-0.007153	0.9943	0.9943	0.00025	1
-0.007153	0.9943	0.9943	0.0002685	1
-2.003	0.04905	0.2698	0.001271	1
-2.003	0.04905	0.2698	0.0002592	1
-0.3975	0.6923	0.9943	0.0002669	1
-0.3975	0.6923	0.9943	0.0006711	1
-2.493	0.01502	0.1652	0.01156	1
-2.493	0.01502	0.1652	0.0008063	1
-0.4866	0.6281	0.9725	0.01119	1
-0.4866	0.6281	0.9725	0.5832	1
0.1475	0.8832	0.9725	0.4568	1
0.1475	0.8832	0.9725	0.02118	1
0.1195	0.9052	0.9725	0.001024	1
0.1195	0.9052	0.9725	0.002002	1
-0.1832	0.8552	0.9725	0.4812	1
-0.1832	0.8552	0.9725	0.319	1
0.9596	0.3411	0.9381	0.0006737	1
0.9596	0.3411	0.9381	0.002223	1
0.1056	0.9162	0.9725	0.0003472	1
0.1056	0.9162	0.9725	0.0002596	1
-1.454	0.1508	0.7241	0.02387	1
-1.454	0.1508	0.7241	0.0565	1
-0.07738	0.9386	0.9725	0.00025	1
-0.07738	0.9386	0.9725	0.0002685	1
-1.655	0.1025	0.7241	0.001271	1
-1.655	0.1025	0.7241	0.0002592	1
-0.03454	0.9725	0.9725	0.0002669	1
-0.03454	0.9725	0.9725	0.0006711	1
-1.301	0.1975	0.7241	0.01156	1

Stat	P.Value	Adjusted.P.Value	Mean.Abandance	Mean.Prevalence
-1.301	0.1975	0.7241	0.0008063	1
-0.04651	0.963	0.963	0.01119	1
-0.04651	0.963	0.963	0.5832	1
-0.265	0.7916	0.9135	0.4568	1
-0.265	0.7916	0.9135	0.02118	1
-0.2147	0.8305	0.9135	0.001024	1
-0.2147	0.8305	0.9135	0.002002	1
-1.279	0.2043	0.7699	0.4812	1
-1.279	0.2043	0.7699	0.319	1
1.027	0.3072	0.7699	0.0006737	1
1.027	0.3072	0.7699	0.002223	1
0.6933	0.4899	0.7699	0.0003472	1
0.6933	0.4899	0.7699	0.0002596	1
-0.8887	0.3767	0.7699	0.02387	1
-0.8887	0.3767	0.7699	0.0565	1
0.4494	0.6543	0.8997	0.00025	1
0.4494	0.6543	0.8997	0.0002685	1
-0.9595	0.3397	0.7699	0.001271	1
-0.9595	0.3397	0.7699	0.0002592	1
0.7415	0.4601	0.7699	0.0002669	1
0.7415	0.4601	0.7699	0.0006711	1
-1.224	0.224	0.7699	0.01156	1
-1.224	0.224	0.7699	0.0008063	1
-1.915	0.06014	0.3308	0.01119	1
-1.915	0.06014	0.3308	0.5832	1
1.278	0.2068	0.5136	0.4568	1
1.278	0.2068	0.5136	0.02118	1
-1.221	0.2267	0.5136	0.001024	1
-1.221	0.2267	0.5136	0.002002	1
-0.2128	0.8323	0.8323	0.4812	1
-0.2128	0.8323	0.8323	0.319	1
0.9381	0.3524	0.5136	0.0006737	1
0.9381	0.3524	0.5136	0.002223	1
0.8962	0.3735	0.5136	0.0003472	1
0.8962	0.3735	0.5136	0.0002596	1
-1.049	0.2985	0.5136	0.02387	1
-1.049	0.2985	0.5136	0.0565	1
-1.118	0.2681	0.5136	0.00025	1
-1.118	0.2681	0.5136	0.0002685	1
-2.522	0.01421	0.1563	0.001271	1
-2.522	0.01421	0.1563	0.0002592	1
-0.7095	0.4809	0.5877	0.0002669	1
-0.7095	0.4809	0.5877	0.0006711	1
0.2829	0.7782	0.8323	0.01156	1
0.2829	0.7782	0.8323	0.0008063	1
46.36	8.995e-200	4.947e-199	0.01119	1
46.36	8.995e-200	4.947e-199	0.5832	1
-55.95	1.266e-236	1.393e-235	0.4568	1
-55.95	1.266e-236	1.393e-235	0.02118	1
4.456	1.002e-05	1.224e-05	0.001024	1
4.456	1.002e-05	1.224e-05	0.002002	1
-16.95	1.146e-52	2.906e-52	0.4812	1

Stat	P.Value	Adjusted.P.Value	Mean.Abandance	Mean.Prevalence
-16.95	1.146e-52	2.906e-52	0.319	1
7.926	1.162e-14	1.598e-14	0.0006737	1
7.926	1.162e-14	1.598e-14	0.002223	1
-14.93	6.75e-43	1.238e-42	0.0003472	1
-14.93	6.75e-43	1.238e-42	0.0002596	1
2.924	0.003589	0.003948	0.02387	1
2.924	0.003589	0.003948	0.0565	1
-10.83	5.081e-25	7.985e-25	0.00025	1
-10.83	5.081e-25	7.985e-25	0.0002685	1
-16.91	1.321e-52	2.906e-52	0.001271	1
-16.91	1.321e-52	2.906e-52	0.0002592	1
2.392	0.01705	0.01705	0.0002669	1
2.392	0.01705	0.01705	0.0006711	1
-20.67	9.548e-72	3.501e-71	0.01156	1
-20.67	9.548e-72	3.501e-71	0.0008063	1
0.2795	0.7799	0.983	0.01119	1
0.2795	0.7799	0.983	0.5832	1
-0.3283	0.7428	0.983	0.4568	1
-0.3283	0.7428	0.983	0.02118	1
-0.9889	0.3231	0.8885	0.001024	1
-0.9889	0.3231	0.8885	0.002002	1
-0.6795	0.4971	0.983	0.4812	1
-0.6795	0.4971	0.983	0.319	1
-0.02126	0.983	0.983	0.0006737	1
-0.02126	0.983	0.983	0.002223	1
1.533	0.1259	0.6925	0.0003472	1
1.533	0.1259	0.6925	0.0002596	1
-1.102	0.2711	0.8885	0.02387	1
-1.102	0.2711	0.8885	0.0565	1
1.549	0.1219	0.6925	0.00025	1
1.549	0.1219	0.6925	0.0002685	1
0.3554	0.7224	0.983	0.001271	1
0.3554	0.7224	0.983	0.0002592	1
-0.06685	0.9467	0.983	0.0002669	1
-0.06685	0.9467	0.983	0.0006711	1
-0.156	0.8761	0.983	0.01156	1
-0.156	0.8761	0.983	0.0008063	1
0.3162	0.752	0.8043	0.01119	1
0.3162	0.752	0.8043	0.5832	1
-0.4723	0.6369	0.8043	0.4568	1
-0.4723	0.6369	0.8043	0.02118	1
0.502	0.6159	0.8043	0.001024	1
0.502	0.6159	0.8043	0.002002	1
-1.096	0.2736	0.7524	0.4812	1
-1.096	0.2736	0.7524	0.319	1
-1.883	0.06022	0.338	0.0006737	1
-1.883	0.06022	0.338	0.002223	1
0.3949	0.6931	0.8043	0.0003472	1
0.3949	0.6931	0.8043	0.0002596	1
-0.87	0.3847	0.8043	0.02387	1
-0.87	0.3847	0.8043	0.0565	1
-0.3158	0.7522	0.8043	0.00025	1

Stat	P.Value	Adjusted.P.Value	Mean.Abandance	Mean.Prevalence
-0.3158	0.7522	0.8043	0.0002685	1
1.426	0.1543	0.5659	0.001271	1
1.426	0.1543	0.5659	0.0002592	1
-0.2479	0.8043	0.8043	0.0002669	1
-0.2479	0.8043	0.8043	0.0006711	1
-1.874	0.06145	0.338	0.01156	1
-1.874	0.06145	0.338	0.0008063	1
-0.8692	0.3851	0.731	0.01119	1
-0.8692	0.3851	0.731	0.5832	1
1.518	0.1294	0.6894	0.4568	1
1.518	0.1294	0.6894	0.02118	1
-1.123	0.2621	0.7207	0.001024	1
-1.123	0.2621	0.7207	0.002002	1
-1.79	0.07394	0.6894	0.4812	1
-1.79	0.07394	0.6894	0.319	1
-0.7308	0.4652	0.731	0.0006737	1
-0.7308	0.4652	0.731	0.002223	1
0.6232	0.5334	0.7334	0.0003472	1
0.6232	0.5334	0.7334	0.0002596	1
-1.318	0.188	0.6894	0.02387	1
-1.318	0.188	0.6894	0.0565	1
0.7718	0.4406	0.731	0.00025	1
0.7718	0.4406	0.731	0.0002685	1
0.1837	0.8543	0.9398	0.001271	1
0.1837	0.8543	0.9398	0.0002592	1
0.2592	0.7955	0.9398	0.0002669	1
0.2592	0.7955	0.9398	0.0006711	1
-0.03404	0.9729	0.9729	0.01156	1
-0.03404	0.9729	0.9729	0.0008063	1
-0.06777	0.946	0.9885	0.01119	1
-0.06777	0.946	0.9885	0.5832	1
-1.046	0.2958	0.9885	0.4568	1
-1.046	0.2958	0.9885	0.02118	1
-0.07625	0.9392	0.9885	0.001024	1
-0.07625	0.9392	0.9885	0.002002	1
-1.633	0.1029	0.566	0.4812	1
-1.633	0.1029	0.566	0.319	1
-2.096	0.03649	0.4014	0.0006737	1
-2.096	0.03649	0.4014	0.002223	1
0.5855	0.5585	0.9885	0.0003472	1
0.5855	0.5585	0.9885	0.0002596	1
-0.8116	0.4174	0.9885	0.02387	1
-0.8116	0.4174	0.9885	0.0565	1
-0.01442	0.9885	0.9885	0.00025	1
-0.01442	0.9885	0.9885	0.0002685	1
-0.01468	0.9883	0.9885	0.001271	1
-0.01468	0.9883	0.9885	0.0002592	1
0.5114	0.6092	0.9885	0.0002669	1
0.5114	0.6092	0.9885	0.0006711	1
-0.189	0.8502	0.9885	0.01156	1
-0.189	0.8502	0.9885	0.0008063	1
0.01483	0.9882	0.9882	0.01119	1

Stat	P.Value	Adjusted.P.Value	Mean.Abandance	Mean.Prevalence
0.01483	0.9882	0.9882	0.5832	1
-0.1469	0.8832	0.9738	0.4568	1
-0.1469	0.8832	0.9738	0.02118	1
-1.022	0.3074	0.9738	0.001024	1
-1.022	0.3074	0.9738	0.002002	1
-1.166	0.2439	0.9738	0.4812	1
-1.166	0.2439	0.9738	0.319	1
-0.757	0.4493	0.9738	0.0006737	1
-0.757	0.4493	0.9738	0.002223	1
0.4032	0.6869	0.9738	0.0003472	1
0.4032	0.6869	0.9738	0.0002596	1
0.1443	0.8853	0.9738	0.02387	1
0.1443	0.8853	0.9738	0.0565	1
0.3178	0.7508	0.9738	0.00025	1
0.3178	0.7508	0.9738	0.0002685	1
-0.3654	0.7149	0.9738	0.001271	1
-0.3654	0.7149	0.9738	0.0002592	1
1.139	0.2551	0.9738	0.0002669	1
1.139	0.2551	0.9738	0.0006711	1
-0.3806	0.7037	0.9738	0.01156	1
-0.3806	0.7037	0.9738	0.0008063	1

Output.Element
subject_raceasian
subject_racecaucasian

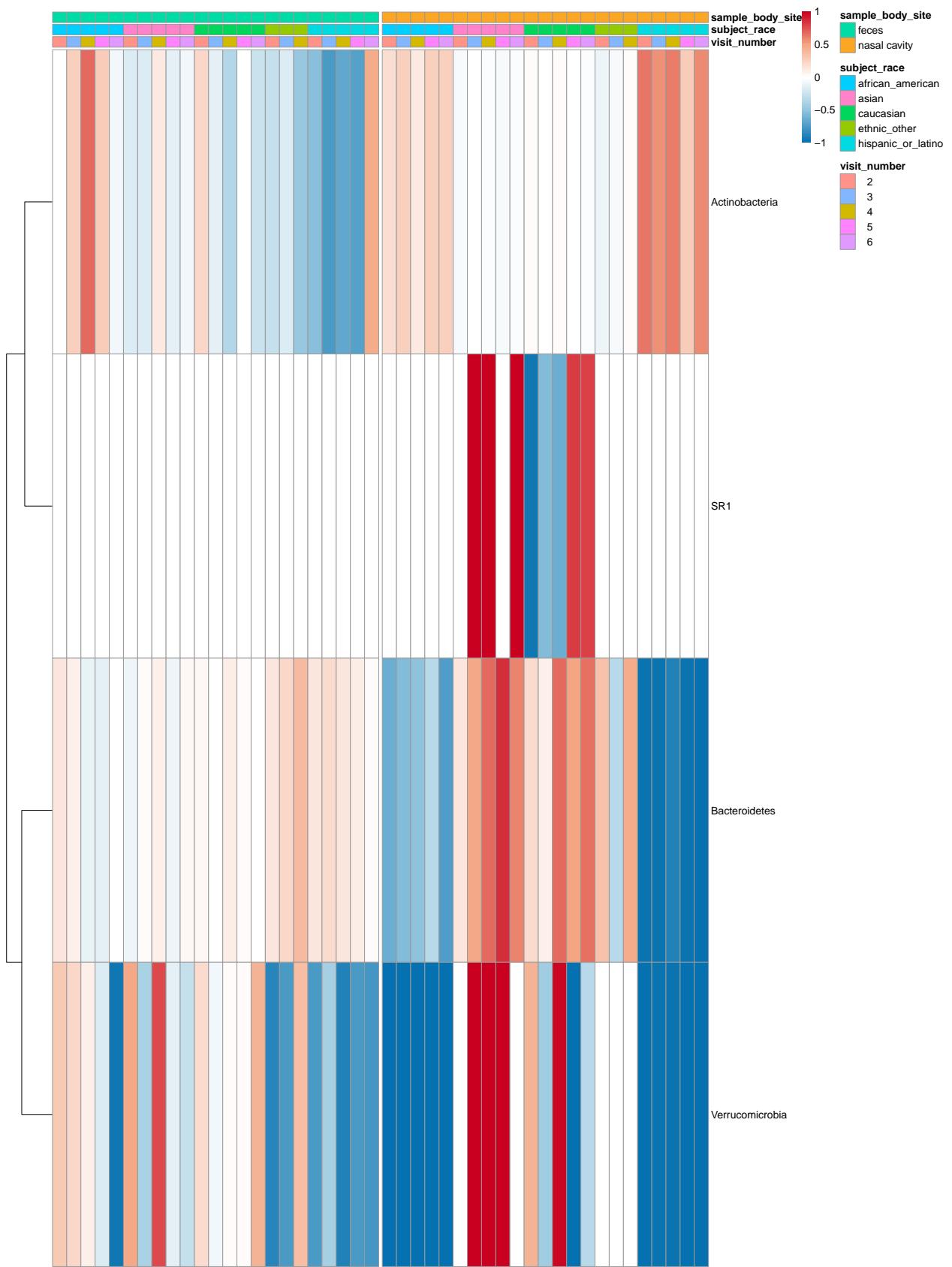






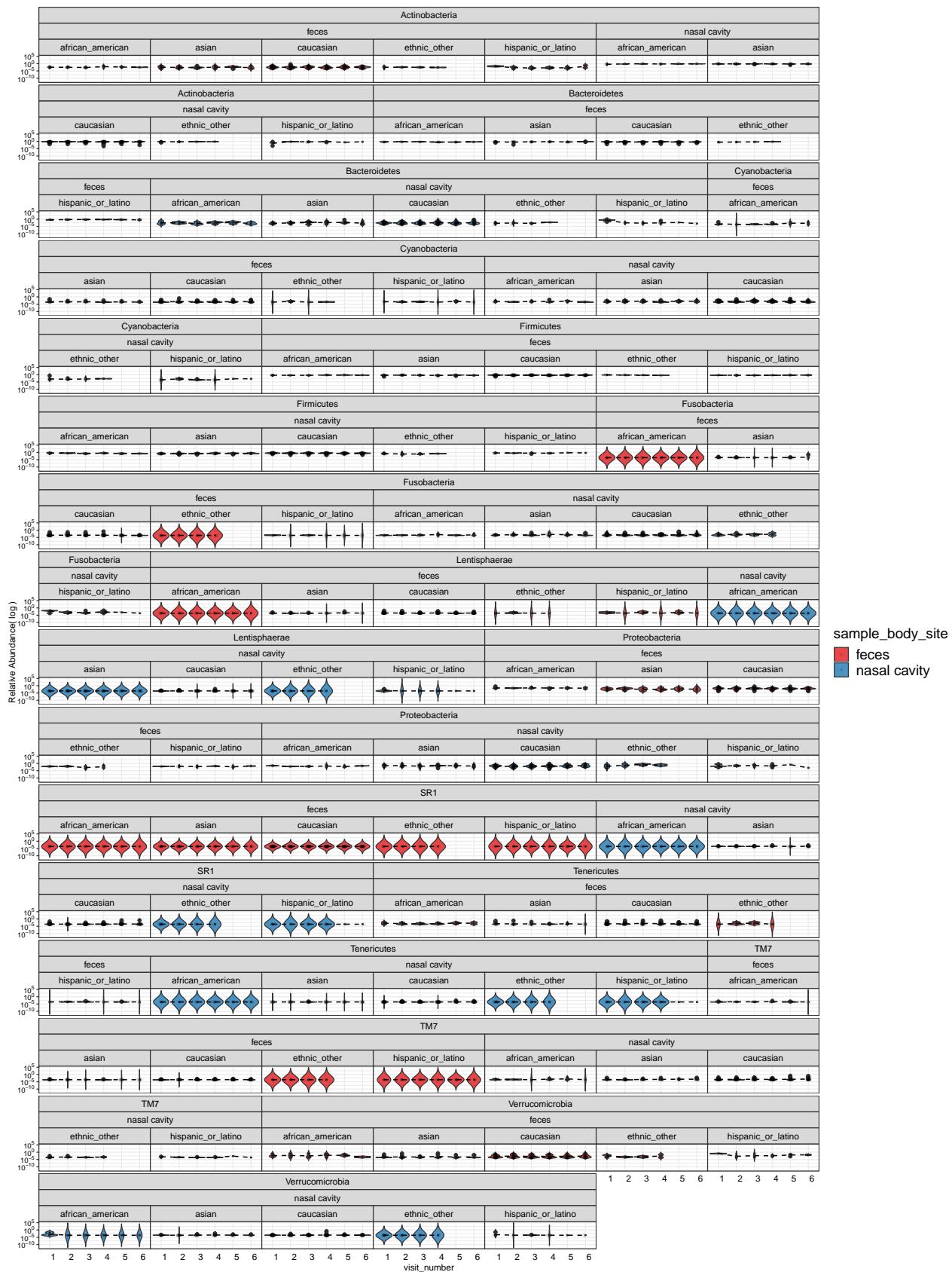
### 3.6 Taxa Boxplot for Significant Taxa

```
feature.dat.type = feature.dat.type,
features.plot = significant_taxa,
Transform = Transform,
top.k.plot = top.k.plot,
top.k.func = top.k.func,
prev.filter = prev.filter,
abund.filter = abund.filter,
base.size = 10,
theme.choice = theme.choice,
custom.theme = custom.theme,
palette = palette,
pdf = pdf,
file.ann = file.ann,
pdf.wid = pdf.wid,
pdf.hei = pdf.hei)
```



```
## [[1]]
```





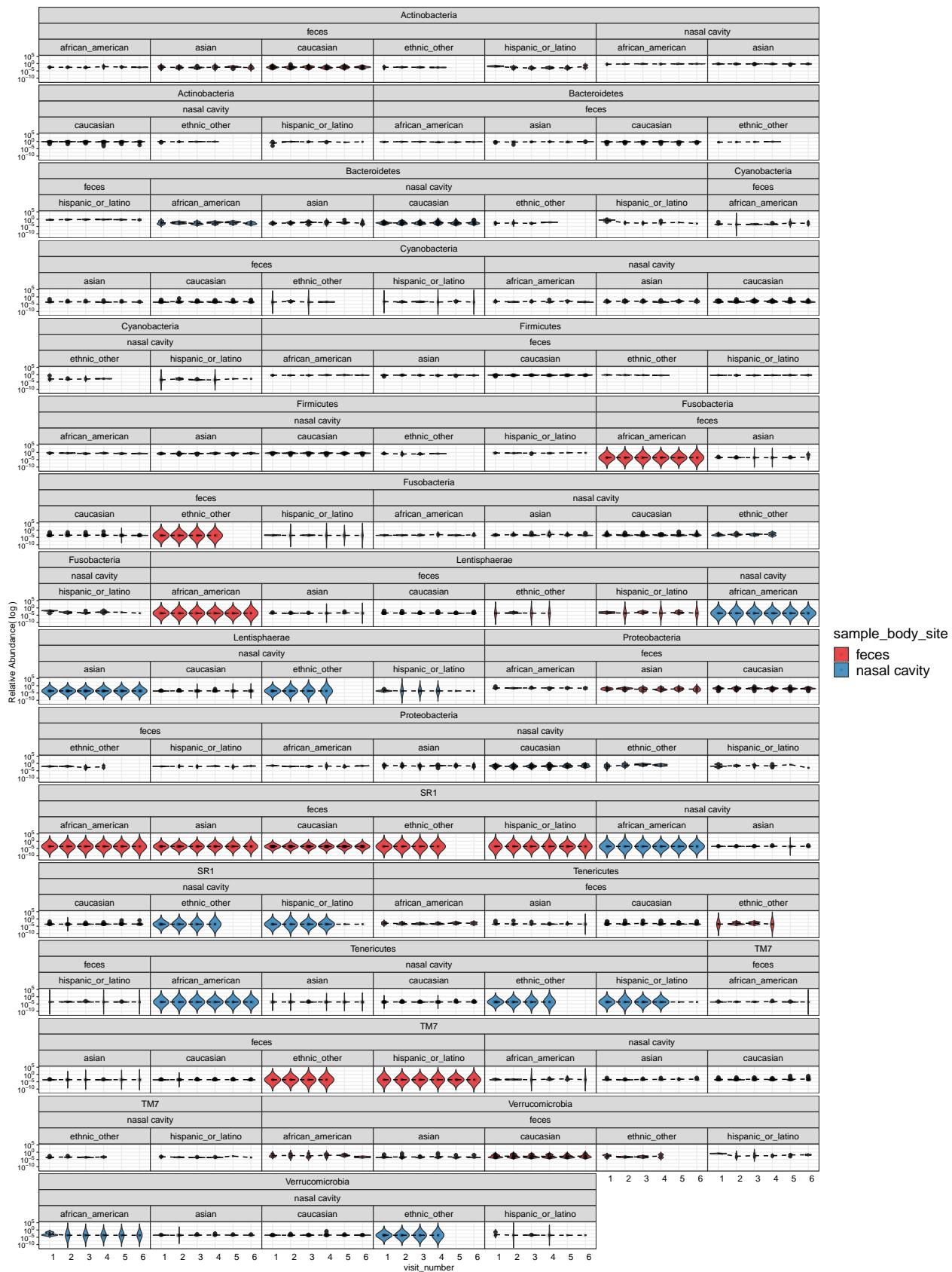


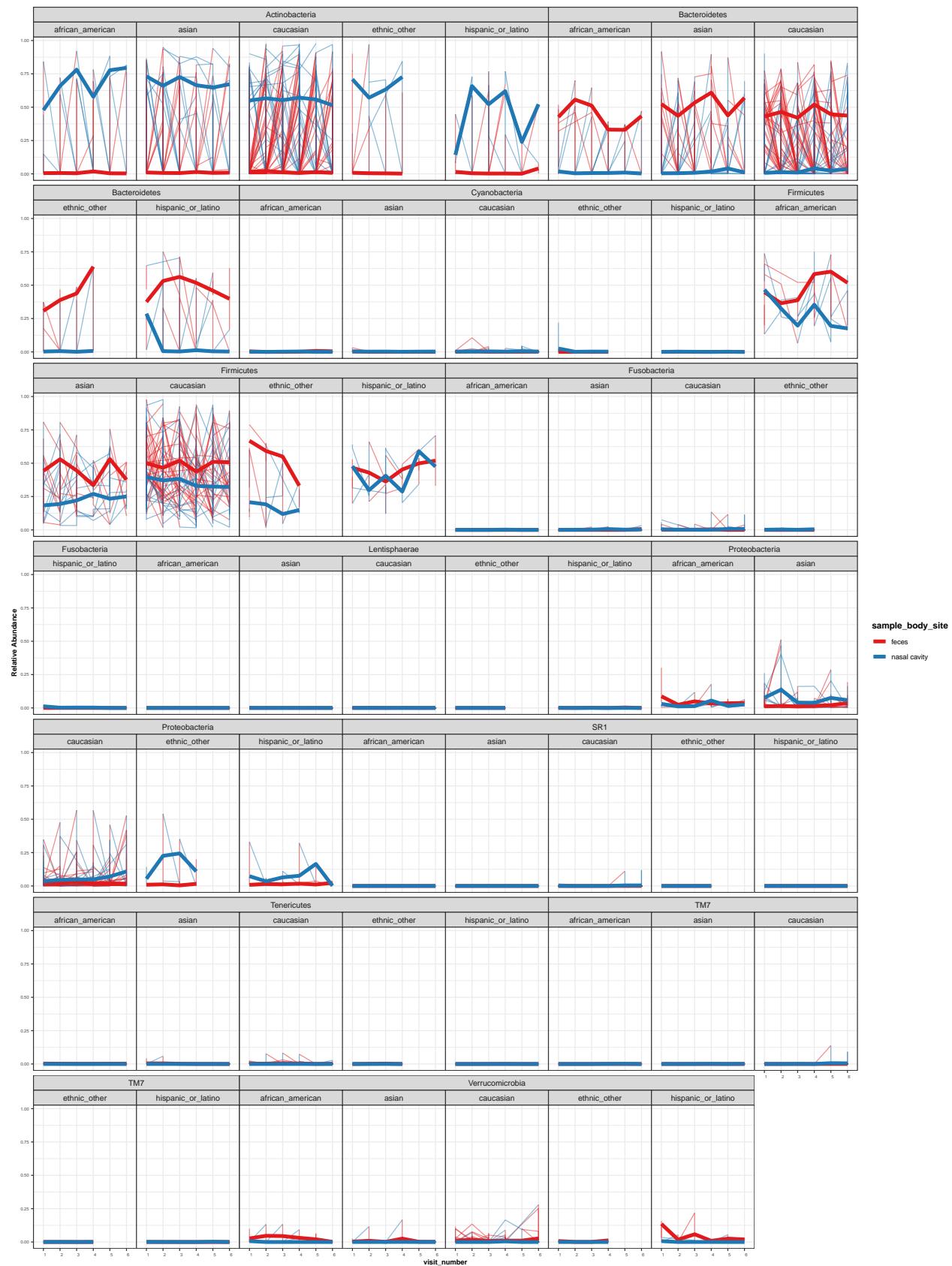
The boxplot results for individual taxa or features can be found in the current working directory. The relevant file is named: taxa\_indiv\_boxplot\_long\_subject\_subject\_id\_time\_visit\_number\_feature\_level\_Phylum\_transform\_log\_prev\_filter\_1e-04\_abund\_filter\_1e-04\_group\_sample\_body\_site\_strata\_subject\_race\_Phylum.pdf. Please refer to this file for more detailed visualizations.

### 3.7 Taxa Spaghettiplot for Significant Taxa

```
taxa_spaghettiplot_results <- generate_taxa_spaghettiplot_long(data.obj = data.obj,
                                                               subject.var = subject.var,
                                                               time.var = time.var,
                                                               group.var = group.var,
                                                               strata.var = strata.var,
                                                               t0.level = t0.level,
                                                               ts.levels = ts.levels,
                                                               feature.level = feature.level,
                                                               feature.dat.type = feature.dat.type,
                                                               features.plot = significant_taxa,
                                                               top.k.plot = top.k.plot,
                                                               top.k.func = top.k.func,
                                                               prev.filter = prev.filter,
                                                               abund.filter = abund.filter,
                                                               base.size = 10,
                                                               theme.choice = theme.choice,
                                                               custom.theme = custom.theme,
                                                               palette = palette,
                                                               pdf = pdf,
                                                               file.ann = file.ann,
                                                               pdf.wid = pdf.wid,
                                                               pdf.hei = pdf.hei)

taxa_spaghettiplot_results
```





```
taxa_indiv_spaghettiplot_results <- generate_taxa_indiv_spaghettiplot_long(data.obj = data.obj,
                                                               subject.var = subject.var,
                                                               time.var = time.var,
                                                               t0.level = t0.level,
                                                               ts.levels = ts.levels,
                                                               group.var = group.var,
                                                               strata.var = strata.var,
                                                               change.base = change.base,
                                                               change.func = change.func,
                                                               feature.level = feature.level,
                                                               features.plot = significant_taxa,
                                                               feature.dat.type = feature.dat.type,
                                                               top.k.plot = top.k.plot,
                                                               top.k.func = top.k.func,
                                                               prev.filter = prev.filter,
                                                               abund.filter = abund.filter,
                                                               base.size = 10,
                                                               theme.choice = theme.choice,
                                                               custom.theme = custom.theme,
                                                               palette = palette,
                                                               pdf = TRUE,
                                                               file.ann = file.ann,
                                                               pdf.wid = pdf.wid,
                                                               pdf.hei = pdf.hei)
```

The spaghettiplot results for individual taxa or features can be found in the current working directory. The relevant file is named: taxa\_indiv\_spaghettiplot\_long\_subject\_subject\_id\_time\_visit\_number\_group\_sample\_body\_site\_strata\_subject\_race\_feature\_level\_Phylum\_prev\_filter\_1e-04\_abund\_filter\_1e-04\_base\_size\_12\_theme\_choice\_bw\_pdf\_wid\_11\_pdf\_hei\_8.5.pdf. Please refer to this file for more detailed visualizations.