1. Full community:

**Before treatment:**

Weighted Unifrac:

adonis2(dist\_wb ~ Site \* Treatment, data= sd\_adonis, strata = sd\_adonis$Site, permutations = 1000)

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_wb ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 0.41936 0.45516 6.0217 0.2248

Treatment 2 0.03052 0.03313 1.0957 0.3576

Site:Treatment 10 0.22076 0.23960 1.5850 0.1908

Residual 18 0.25071 0.27211

Total 35 0.92135 1.00000

Unweighted Unifrac:

> adonis2(dist\_uwb ~ Site \* Treatment, data= sd\_adonis, strata = sd\_adonis$Site, permutations = 1000)

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_uwb ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 1.6070 0.21675 1.7565 0.05395 .

Treatment 2 0.4292 0.05789 1.1728 0.13686

Site:Treatment 10 2.0843 0.28113 1.1391 0.06793 .

Residual 18 3.2936 0.44423

Total 35 7.4142 1.00000

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**After treatment:**

Weighted Unifrac:

> adonis2(dist\_wb ~ Site \* Treatment, data= sd\_adonis, strata = sd\_adonis$Site, permutations = 1000)

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_wb ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 0.35498 0.45494 5.5119 0.2228

Treatment 2 0.01927 0.02469 0.7478 0.5834

Site:Treatment 10 0.17418 0.22323 1.3523 0.1718

Residual 18 0.23185 0.29714

Total 35 0.78028 1.00000

unweighted Unifrac:

> adonis2(dist\_uwb ~ Site \* Treatment, data= sd\_adonis, strata = sd\_adonis$Site, permutations = 1000)

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_uwb ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 1.8283 0.29557 2.6075 0.16184

Treatment 2 0.3601 0.05821 1.2839 0.03297 \*

Site:Treatment 10 1.4731 0.23815 1.0505 0.27672

Residual 18 2.5242 0.40806

Total 35 6.1857 1.00000

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**After treatment pairwise adonis**

pairwise.adonis2(dist\_uwb ~Treatment, strata = "Site", data = sd\_adonis, nperm = 1000)

$parent\_call

[1] "dist\_uwb ~ Treatment , strata = Site , permutations 1000"

$CF\_vs\_CON

Df SumOfSqs R2 F Pr(>F)

Treatment 1 0.1789 0.0436 1.0029 0.1508

Residual 22 3.9251 0.9564

Total 23 4.1041 1.0000

**$CF\_vs\_ORG**

**Df SumOfSqs R2 F Pr(>F)**

**Treatment 1 0.2037 0.05132 1.1901 0.02997 \***

**Residual 22 3.7654 0.94868**

**Total 23 3.9691 1.00000**

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

$CON\_vs\_ORG

Df SumOfSqs R2 F Pr(>F)

Treatment 1 0.1575 0.03825 0.8749 0.1618

Residual 22 3.9607 0.96175

Total 23 4.1182 1.00000

1. Acetobacteria

"OTU\_122"

Kruskal-Wallis rank sum test

data: unlist(aceto\_df[i]) by aceto\_df$Treatment

Kruskal-Wallis chi-squared = 10.637, df = 2, p-value = 0.004899

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: aceto\_df$OTU\_122 and aceto\_df$Treatment

CF CON

CON 0.3165 -

ORG 0.0033 0.0329

P value adjustment method: holm

"OTU\_282"

Kruskal-Wallis rank sum test

data: unlist(aceto\_df[i]) by aceto\_df$Treatment

Kruskal-Wallis chi-squared = 6.1258, df = 2, p-value = 0.04675

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: aceto\_df$OTU\_282 and aceto\_df$Treatment

CF CON

CON 0.332 -

ORG 0.049 0.332

P value adjustment method: holm

1. Lactobacillus

Kruskal-Wallis rank sum test

data: unlist(lacto\_df[i]) by lacto\_df$Treatment

Kruskal-Wallis chi-squared = 5.8292, df = 2, p-value = 0.05423

[1] "OTU\_568"

No pairwise diffs.

1. Core (@genus) post treatment

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_core\_w\_genus ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 1.52946 0.50078 5.8185 0.2917

Treatment 2 0.04970 0.01627 0.4726 0.7552

Site:Treatment 9 0.63385 0.20754 1.3396 0.2388

Residual 16 0.84116 0.27541

Total 32 3.05417 1.00000

> #unweighted unifrac

> adonis2(dist\_core\_uw\_genus ~ Site \* Treatment, data= sd\_adonis, strata = sd\_adonis$Site, permutations = 1000)

Permutation test for adonis under reduced model

Terms added sequentially (first to last)

Blocks: strata

Permutation: free

Number of permutations: 1000

adonis2(formula = dist\_core\_uw\_genus ~ Site \* Treatment, data = sd\_adonis, permutations = 1000, strata = sd\_adonis$Site)

Df SumOfSqs R2 F Pr(>F)

Site 5 0.146016 0.48308 6.3818 0.1439

Treatment 2 0.012268 0.04059 1.3404 0.3117

Site:Treatment 9 0.070759 0.23410 1.7181 0.1439

Residual 16 0.073217 0.24223

Total 32 0.302259 1.00000