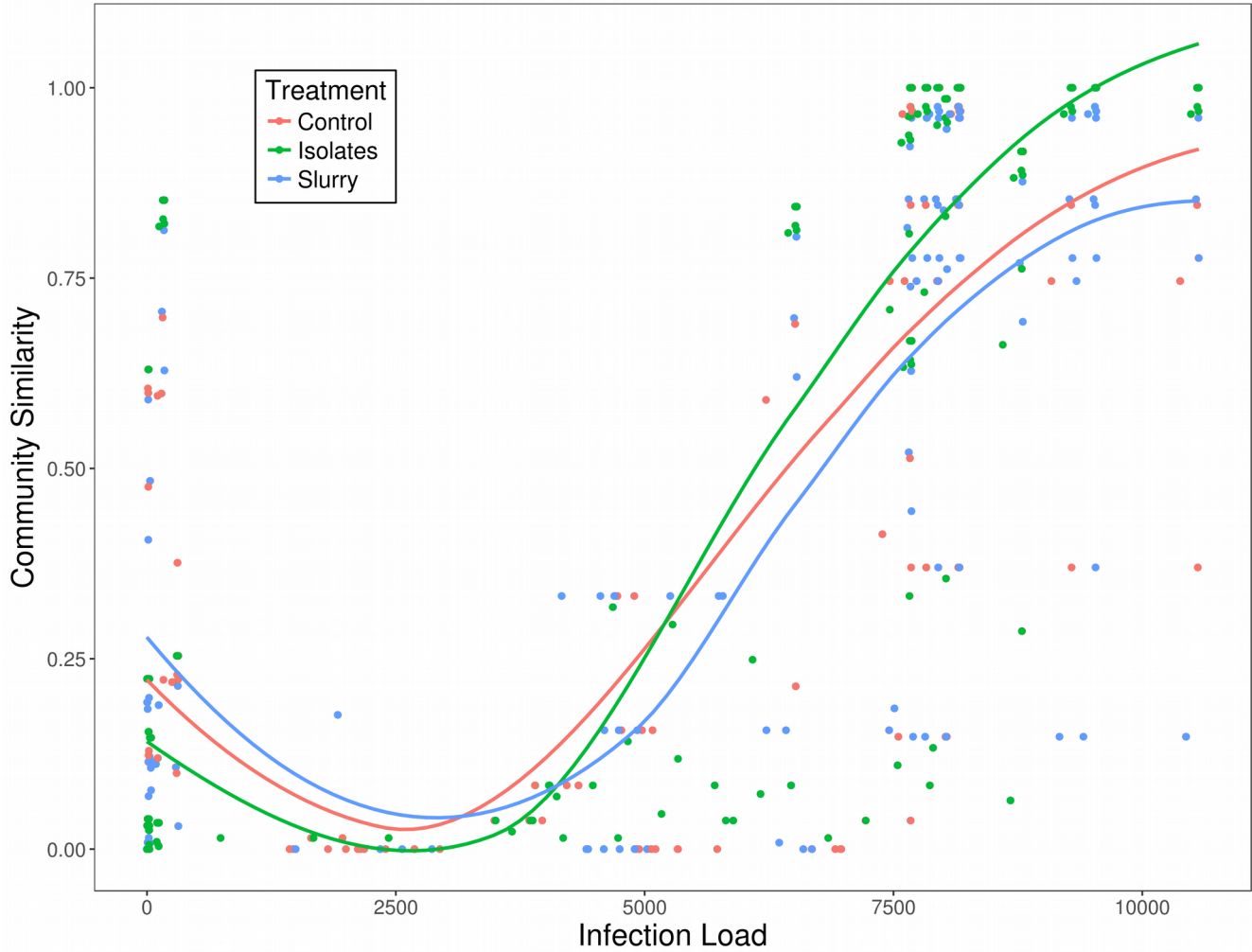


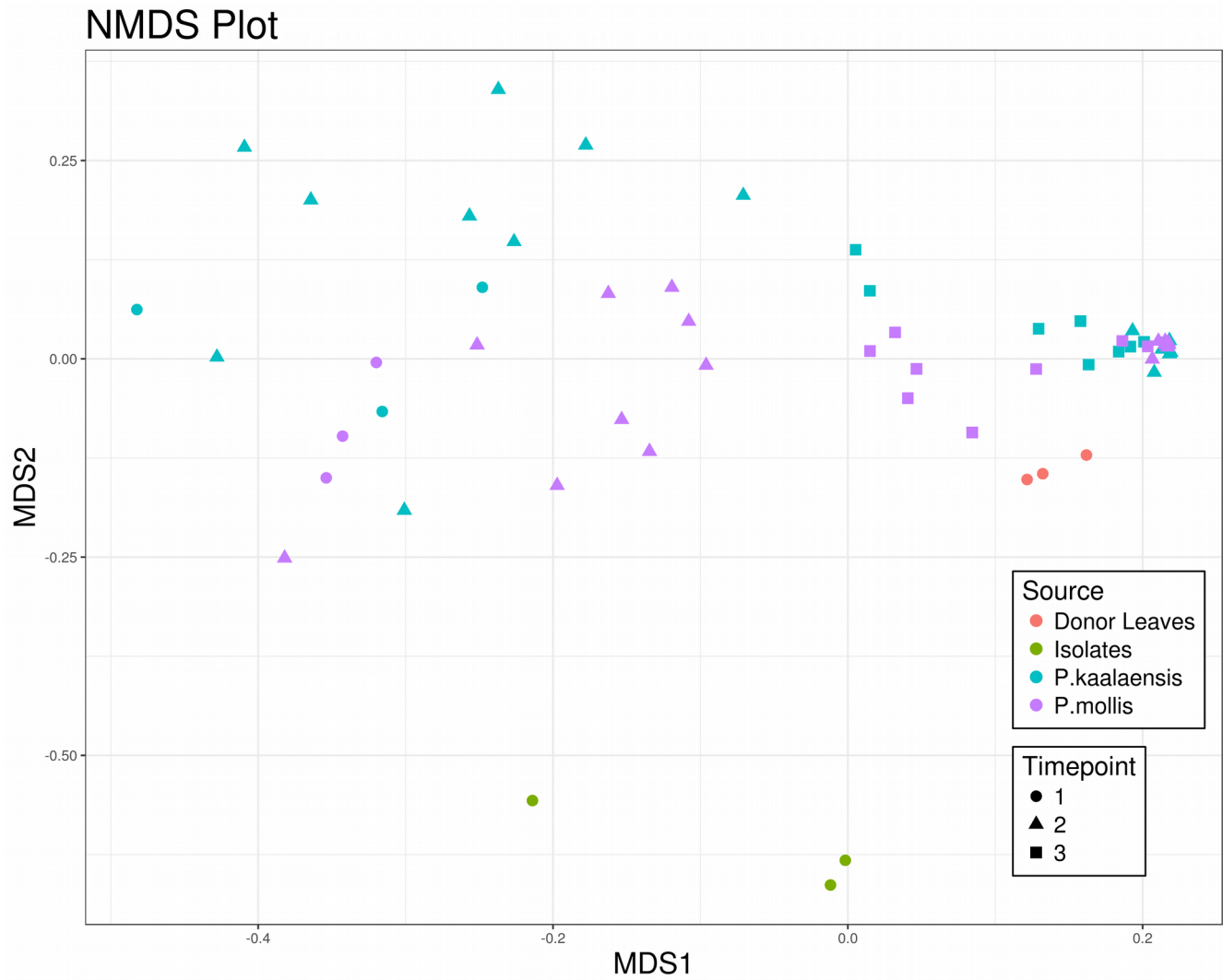
Supporting Information for:
Total foliar microbiome transplants confer disease resistance to a critically-endangered Hawaiian endemic

P. kaala community similarity



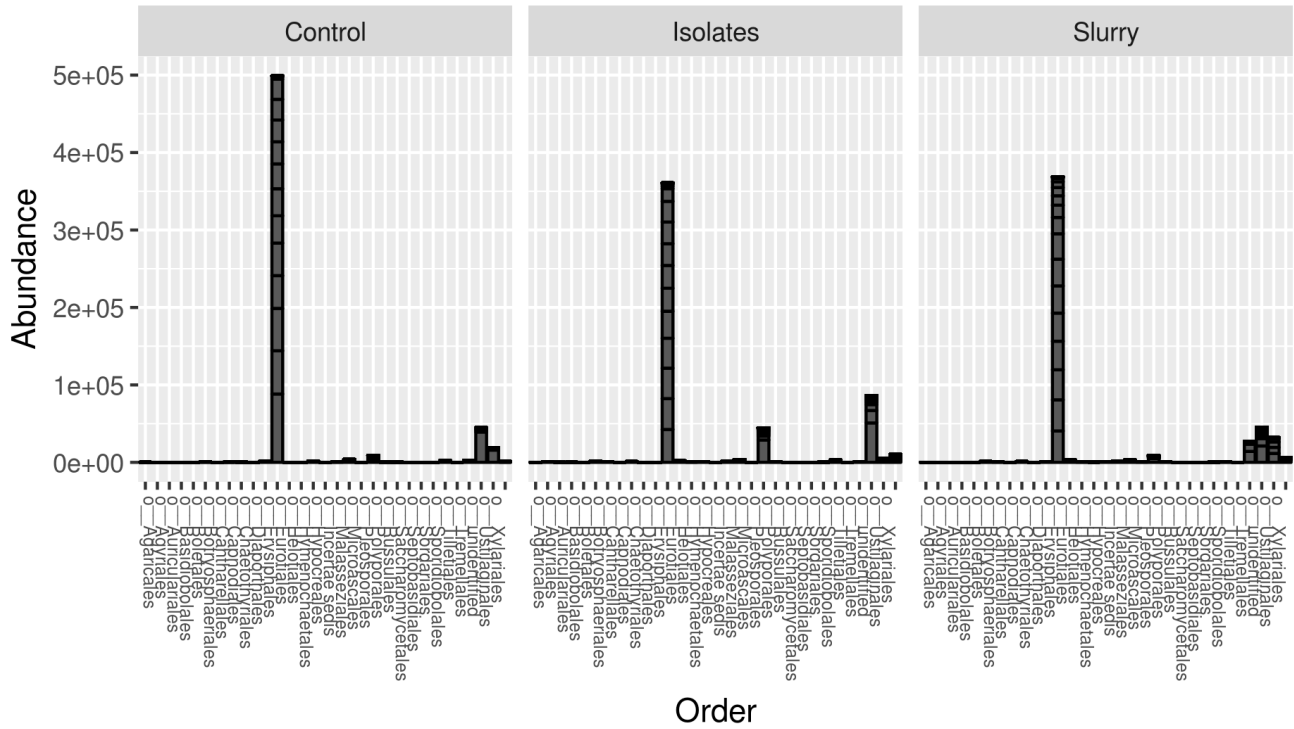
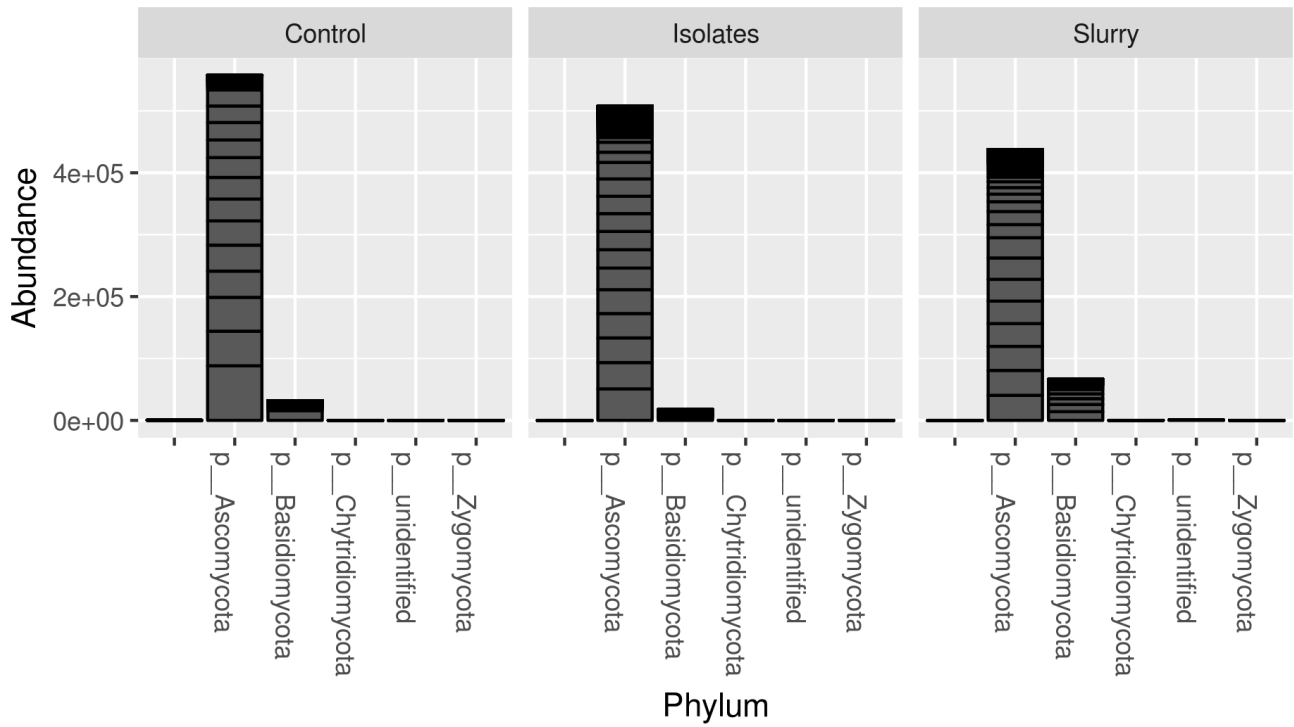
SI Figure 1) Community similarity vs. infection load

Bray-Curtis community similarity as a function of infection load similarity, showing that a major driver in community identity was *N. galeopsidis* infection rate. At very low and very high infection rates, endophytic communities were more similar. This reflects lower diversity in greenhouse-reared plants prior to treatment and the dominance of the pathogen, respectively. At intermediate infection rates, communities were more dissimilar, reflecting the establishment of inoculated communities prior to pathogen proliferation.



SI Figure 2) NMDS of donor and recipient communities

NMDS ordination of Bray-Curtis community similarity. Points are colored by treatment, with inoculum donors in red (*P. hirsuta* slurry) and green (fungal isolate slurry), and shapes represent sampling timepoints: Initial samples (circles), Mid-Growth samples (triangles), and Final samples (squares). Statistical analyses of Species and Timepoint are below.



SI Figure 3) Barcharts showing taxonomic profiles (at Phylum and Order levels) of endophytic communities grouped by treatment. Measurements are the sums across all sampling periods.

Code used to create figures:

```
# Code used to generate figures - R version 3.1.2 #  
# Associated data files are included in the .zip archive #
```

```
library(ggplot2)  
pd = position_dodge(3)
```

```
# Figure 1
```

```
disease_data = read.csv(file = "Plant_Disease_Progress.csv", stringsAsFactors = FALSE)  
disease_data$Date = as.Date(disease_data$Date)
```

```
Fig_1 = ggplot(disease_data, aes(x = Date, y = Percent.Infected, col = Group, width = 5)) +  
  geom_line(position=pd, size = 1.1) +  
  geom_errorbar(aes(ymin = (Percent.Infected - ci), ymax = (Percent.Infected + ci), width = c(disease_data$wd)),  
    position = pd, size = 1.1) +  
  labs(title = "Phyllostegia Disease Progression", x = "Date", y = "Disease Severity", col = "Treatment") +  
  theme_bw() + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), legend.background = element_rect(colour = "black")) +  
  scale_y_continuous(breaks = c(0,.25,.5,.75,1)) + coord_cartesian(ylim = c(-.1, 1.15)) +  
  facet_wrap(~ Facet, scales = "free_x") +  
  scale_color_manual(values = c("#CDCDCD", "#858585", "#4D4D4D")) +  
  theme(axis.text = element_text(size=16), axis.title = element_text(size = 18),  
    legend.text = element_text(size = 14), legend.title = element_text(size = 16),  
    plot.title = element_text(size = 20), strip.text.x = element_text(size = 12, face = 'bold'), legend.position = c(.615,.89))
```

```
# Figure 2
```

```
Slurry_Data <- read.csv(file = "Slurry_Taxa_data_Frame.csv")
```

```
Fig_2 = ggplot(Slurry_Data, mapping = aes(x = reorder(Species, 1/Rel_Abund), y = Rel_Abund, fill = Round)) +  
  geom_bar(stat = "identity") +  
  theme_bw() +  
  labs(x = "UNITE Taxonomy", y = "Relative abundance", title = "Composition of Slurry Treatments", fill = "Experimental\nRound") +  
  scale_fill_manual(values = gray.colors(3)) +  
  facet_wrap(~ Slurry_Source, scales = "free_x") +  
  theme(axis.text.x = element_text(angle=90, face = 'bold.italic', size = 12), axis.title = element_text(size = 18),  
    strip.text.x = element_text(size = 12, face = 'bold'), panel.grid.major = element_blank(),  
    panel.grid.minor = element_blank(), legend.background = element_rect(colour = "black"),  
    legend.text = element_text(size = 14), legend.title = element_text(size = 16),  
    plot.title = element_text(size = 20), legend.position = c(.9,.8))
```

```
# Figure 3
```

```
P.aphidis_v_Infection = read.csv(file = "P.aphidis_v_Infection.csv")
```

```
Fig_3 = ggplot(P.aphidis_v_Infection, mapping = aes(x = sqrt(P.aphidis_v_Infection$P.aphidis), y = P.aphidis_v_Infection$Infection_Load)) +  
  geom_point() +
```

```

stat_smooth(method = "loess", color = 'black') +
theme_bw() +
theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), legend.background = element_rect(colour = "black")) +
labs(x = expression(italic("Pseudozyma aphidis")~"abundance (sqrt)"), y = "Pathogen Infection Load") +
theme(axis.title = element_text(size = 14)) +
ggtitle(expression("Greater"~italic("P. aphidis")~"abundance results in lower disease severity")) +
theme(axis.title = element_text(size = 18), plot.title = element_text(size = 20), axis.text = element_text(size = 12))

```

Figure S1

```
PK.Infection.and.otus = read.csv(file = "Community_vs_Infection.csv")
```

```

Fig_S1 = ggplot(PK.Infection.and.otus, mapping = aes(x=jitter(PK.Infection.and.otus[,2]),
                                                    y = PK.Infection.and.otus[,1],
                                                    col = PK.Infection.and.otus[,3])) +
geom_point() +
geom_smooth(se = FALSE) +
theme_bw() +
labs(x = "Infection Load", y = "Community Similarity", colour = "Treatment") +
ggtitle(expression(italic("P. kaala")~"community similarity")) +
theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), legend.background = element_rect(colour = "Black"),
      axis.title = element_text(size = 18), axis.text = element_text(size = 12), plot.title = element_text(size = 20),
      legend.text = element_text(size = 14), legend.title = element_text(size = 16), legend.position = c(.2,.85))

```

Figure S2

```

NMDS = read.csv(file = "NMDS_Data.csv")
NMDS$Timepoint = factor(NMDS$Timepoint)

```

```

Fig_S2 = ggplot(NMDS, aes(x=MDS1, y=MDS2, col=Species, shape = Timepoint)) +
geom_point(size = 3) +
theme_bw() +
labs(title = "NMDS Plot", x= "MDS1", y= "MDS2") +
guides(col=guide_legend(title="Source")) +
theme(legend.text = element_text(size = 14), legend.title = element_text(size = 16),
      legend.background = element_rect(colour = "black"), title = element_text(size = 20, hjust = 0.5),
      axis.title = element_text(size = 18), legend.position = c(.9,.23))

```

Clustal alignment of OTUs assigned to *N. galeopsidis* and voucher sequence from Hawaii found on *P. kaalaensis* (GenBank Accession: AB498948.1)

CLUSTAL O(1.2.3) multiple sequence alignment

AB498948.1_Neoerysiphe_galeopsidis	CAGAGCGTGAGGCTCTGCCGGCTTCCCGCCGCGCAGAGTCGACCTCCACCCGTGTT	60
New.ReferenceOTU120	CATAGCTTGAGGCTCTGCCGGCTTCCCGCTCTCTCAGAGTCGACCTCCACCCGTGTT	60
New.CleanUp.ReferenceOTU1041_singleton	GGGAGCGTGAGGGGGGGGGGGCTTCCCGCCGCGCAGAGTCGACCTCCACCCGTGTT	60
New.CleanUp.ReferenceOTU136_singleton	CATATCTTGAGGCTCTGCCGGCTTCCCGCCGCGCAGAGTCGACCTCCACCCGTGTT	60
New.CleanUp.ReferenceOTU154_singleton	GGGAGCGTGAGGCTGTGCCGGCTTCCCGCCGCGCAGAGGGGGGGCTCCACCCGTGTT	60
New.CleanUp.ReferenceOTU320_singleton	CATAGCGTGAGGCTCTGCCGGCTTCCCGCCGCTCTCAGAGTCGACCTCCACCCGTGTT	60
	* * * * *	
AB498948.1_Neoerysiphe_galeopsidis	AACCTATATCATGTTGCTTTGGCGGATCGAGCCCTCGGCCA-CGGCTTTTGTGGAGCG	119
New.ReferenceOTU120	AACCTTTATCATGTTGCTTTGGCGGATCGAGCCCTCGGCCACCGGCTTTTGTGGAGCG	120
New.CleanUp.ReferenceOTU1041_singleton	AACCTTTATCATGTTGCTTTGGCGGATCGAGCCCTCGGCCACCGGCTTTTGTGGAGCG	120
New.CleanUp.ReferenceOTU136_singleton	AACCTTTATCATGTTGATTTGGCGGATCGAGCCCTCGGCCACCGGCTTTTGTGGAGCG	120
New.CleanUp.ReferenceOTU154_singleton	AACCTTTATCATGTTGCTTTGGCGGATCGAGCCCTCGGCCACCGGCTTTTGTGGAGCG	120
New.CleanUp.ReferenceOTU320_singleton	AACCTTTATCATGTTGATTTGGCGGATCGAGCCCTCGGCCACCGGCTTTTGTGGAGCG	120

AB498948.1_Neoerysiphe_galeopsidis	TGTCGGCCAAAGACTCAACCTAACTCGTGTAACATGCAGTCTAAGGAAAGATTTGAAT	179
New.ReferenceOTU120	TGTCGGCCAAAGACTCAACCTAACTCGTGTAACATGCAGTCTAAGGAAAGATTTGAAT	180
New.CleanUp.ReferenceOTU_singleton	TGTCGGCCAAAGACTCAACCTAACTCGTGTAACATGCAGTCTAAGGAAAGATTTGAAT	180
New.CleanUp.ReferenceOTU136_singleton	TGTCGGCCAAAGACTCAAAATAACTCGTGTAACATGAAGTCTAAGGAAAGATTTGAAT	180
New.CleanUp.ReferenceOTU154_singleton	TGTCGGCCAAAGACTCAACCTAACTCGTGTAACATGCAGTCTAAGGAAAGATTTGAAT	180
New.CleanUp.ReferenceOTU320_singleton	TGTCGGCCAAAGACTCAACATAACTAGTGTAATAATGCAGTCTAAGGAAAGATTTGAAT	180

AB498948.1_Neoerysiphe_galeopsidis	CATTA	184
New.ReferenceOTU120	AATTA	185
New.CleanUp.ReferenceOTU1041_singleton	CATTA	185
New.CleanUp.ReferenceOTU136_singleton	AATTA	185
New.CleanUp.ReferenceOTU154_singleton	CATTA	185
New.CleanUp.ReferenceOTU320_singleton	CATTA	185

Permanova results for community distance matrix:

PLANT SPECIES

adonis(otus_dist ~ Species)

Permutation: free

Number of permutations: 999

Terms added sequentially (first to last)

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Species	3	1.4645	0.48818	1.7158	0.07901	0.063
Residuals	60	17.0712	0.28452		0.92099	
Total	63	18.5358			1.00000	

TIMEPOINT

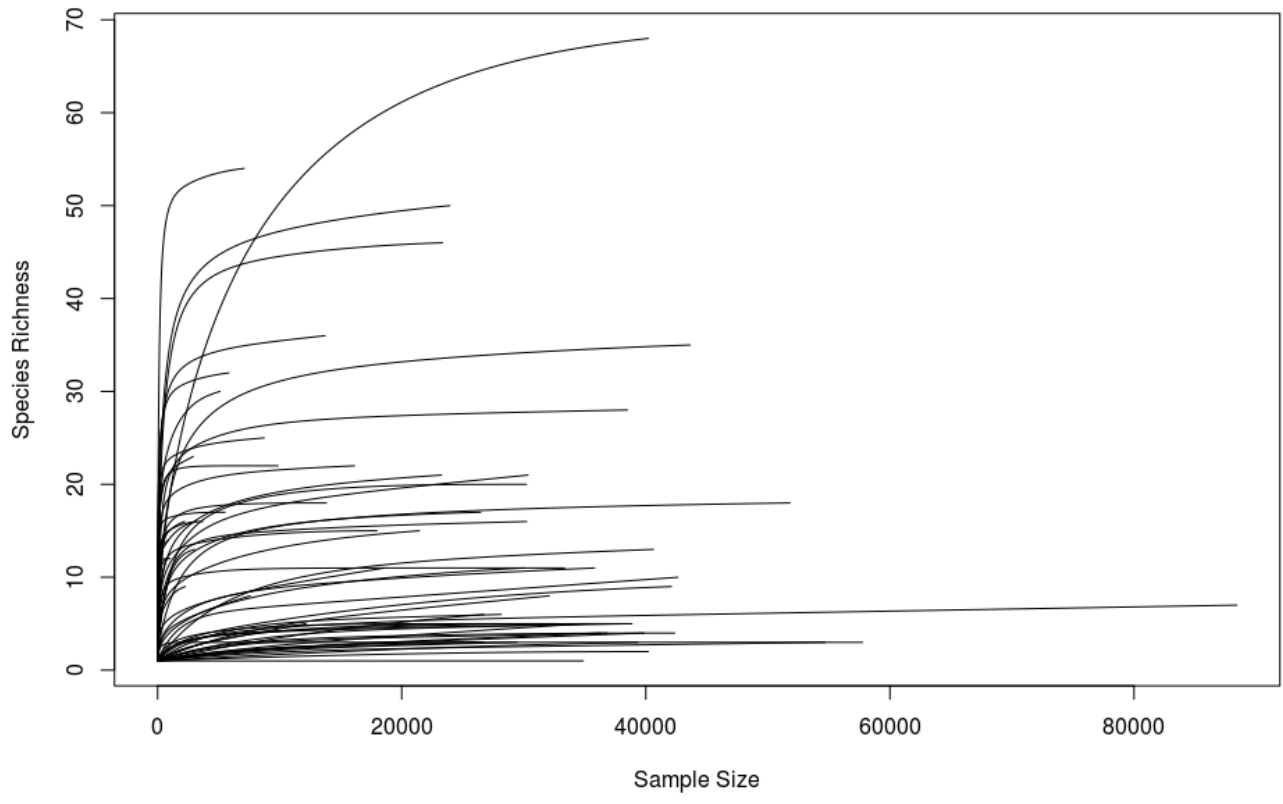
adonis(otus_dist ~ Timepoint)

Permutation: free

Number of permutations: 999

Terms added sequentially (first to last)

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Timepoint	1	2.2945	2.29446	8.7589	0.12379	0.001
Residuals	62	16.2413	0.26196		0.87621	
Total	63	18.5358			1.00000	



SI Figure 4) *Rarefaction curves of all samples*