230306_Reporte1Exploracion

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```r
library("phyloseq")
library("ggplot2")
library("vegan")
```

```
## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.6-4
```

```r
library("RColorBrewer")
library("stringi")
```

Cargado de datos originales

```r
setwd("/home/camila/GIT/Tesis_Maestria/Data/fresa_solena")
outpath = "/home/camila/GIT/Tesis_Maestria/Analisis_Comparativo/Fresa_Solena/Results_img"

fresa_kraken <- import_biom("fresa_kraken.biom")
colnames(fresa_kraken@tax_table@.Data) <- c("Kingdom", "Phylum", "Class", "Order", "Family", "Genus", "S
fresa_kraken@tax_table@.Data <- substr(fresa_kraken@tax_table@.Data,4,100)
colnames(fresa_kraken@otu_table@.Data) <- substr(colnames(fresa_kraken@otu_table@.Data),1,6)
metadata_fresa <- read.csv2("/home/camila/GIT/Tesis_Maestria/Data/fresa_solena/metadata.csv",header = 
fresa_kraken@sam_data <- sample_data(metadata_fresa)
fresa_kraken@sam_data$Sample<-row.names(fresa_kraken@sam_data)
colnames(fresa_kraken@sam_data)<-c('Treatment','Samples')
samples_to_remove <- c("MP2079","MP2080","MP2088","MP2109","MP2137")
fresa_kraken_fil <- prune_samples(!(sample_names(fresa_kraken) %in% samples_to_remove), fresa_kraken)
percentages_fil <- transform_sample_counts(fresa_kraken_fil, function(x) x*100 / sum(x) )
percentages_df <- psmelt(percentages_fil)
```

Subconjunto de "Eukaryota"

```r
merge_Eukaryota<-subset_taxa(fresa_kraken_fil,Kingdom=="Eukaryota")
```

1

Subconjunto de "Bacteria"

```
merge_Bacteria<-subset_taxa(fresa_kraken_fil,Kingdom=="Bacteria")
```

Funciones

Crea los subconjuntos de datos input phy phyliseq total tax rango al que queremos recortar output

```
glomToGraph<-function(phy,tax){
  ## creamos el subconjunto dependiendo del linaje taxonomico deseado
  glom <- tax_glom(phy, taxrank = tax)
  ## sacamos los porcentajes
  percentages <- transform_sample_counts(glom, function(x) x*100 / sum(x) )
  percentages_df <- psmelt(percentages)
  return(list(glom,percentages,percentages_df))
}
```

Graficar abundancias stackbar

input entra el percentages_df

```
Abundance_barras <- function(phy,tax,attribute,abundance_percentage){
  ##llamar funcion de datos
  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]] #phyloseq
  percentages <- Data[[2]] #phyloseq
  percentages_df <- Data[[3]] # dataframe
  ## Graficamos para cada subconjunto las barras de abundancia
  plot_barras <- ggplot(data=percentages_df, aes_string(x='Sample', y='Abundance', fill=tax ,color=attr
    scale_colour_manual(values=c('white','black')) +
    geom_bar(aes(), stat="identity", position="stack") +
    labs(title = "Abundance", x='Sample', y='Abundance', color = tax) +
    theme(legend.key.size = unit(0.2, "cm"),
          legend.key.width = unit(0.25,"cm"),
          legend.position = "bottom",
          legend.direction = "horizontal",
          legend.title=element_text(size=8, face = "bold"),
          legend.text=element_text(size=6),
          text = element_text(size=12),
          axis.text.x = element_text(angle=90, size=5, hjust=1, vjust=0.5))
  percentages_df$tax<-percentages_df[,ncol(percentages_df)]
  percentages_df$tax[percentages_df$Abundance < abundance_percentage] <- "abundance_percentage"
  percentages_df$tax <- as.factor(percentages_df$tax)
  plot_percentages <- ggplot(data=percentages_df, aes_string(x='Sample', y='Abundance', fill='tax' ,col
    scale_colour_manual(values=c('white','black')) +
    geom_bar(aes(), stat="identity", position="stack") +
    labs(title = "Abundance", x='Sample', y='Abundance', color = tax) +
    theme(legend.key.size = unit(0.3, "cm"),
          legend.key.width = unit(0.5,"cm"),
          legend.position = "bottom",
```

```
        legend.direction = "horizontal",
        legend.title=element_text(size=10, face = "bold"),
        legend.text=element_text(size=8),
        text = element_text(size=12),
        axis.text.x = element_text(angle=90, size=5, hjust=1, vjust=0.5))
  return(list(plot_barras,plot_percentages))
}
```

Graficar betadiversity

```
Beta_diversity <- function(phy,tax,attribute,distance){

  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]]
  #CREAR UN GLOM AL 10%
  percentages <- Data[[2]]
  percentages_df <- Data[[3]]
  ## Beta diversidad
  meta_ord <- ordinate(physeq = percentages, method = "NMDS", distance = distance)
  plot_beta <- plot_ordination(physeq = percentages, ordination = meta_ord, color = attribute) +
    geom_text(mapping = aes(label = colnames(phy@otu_table@.Data)), size = 3, vjust = 1.5)
  return(plot_beta)
}
```

Graficar alphadiversity

```
Alpha_diversity <- function(phy,tax,attribute){
  ## llamamos la funcion que crea los dataset
  Data <- glomToGraph(phy,tax)
  glom <- Data[[1]]

  percentages <- Data[[2]]
  percentages_df <- Data[[3]]
  ## Alfa diversidad
  plot_alpha <- plot_richness(physeq = glom, measures = c("Observed","Chao1","Shannon","simpson"),x = at
  return(plot_alpha)
}
```
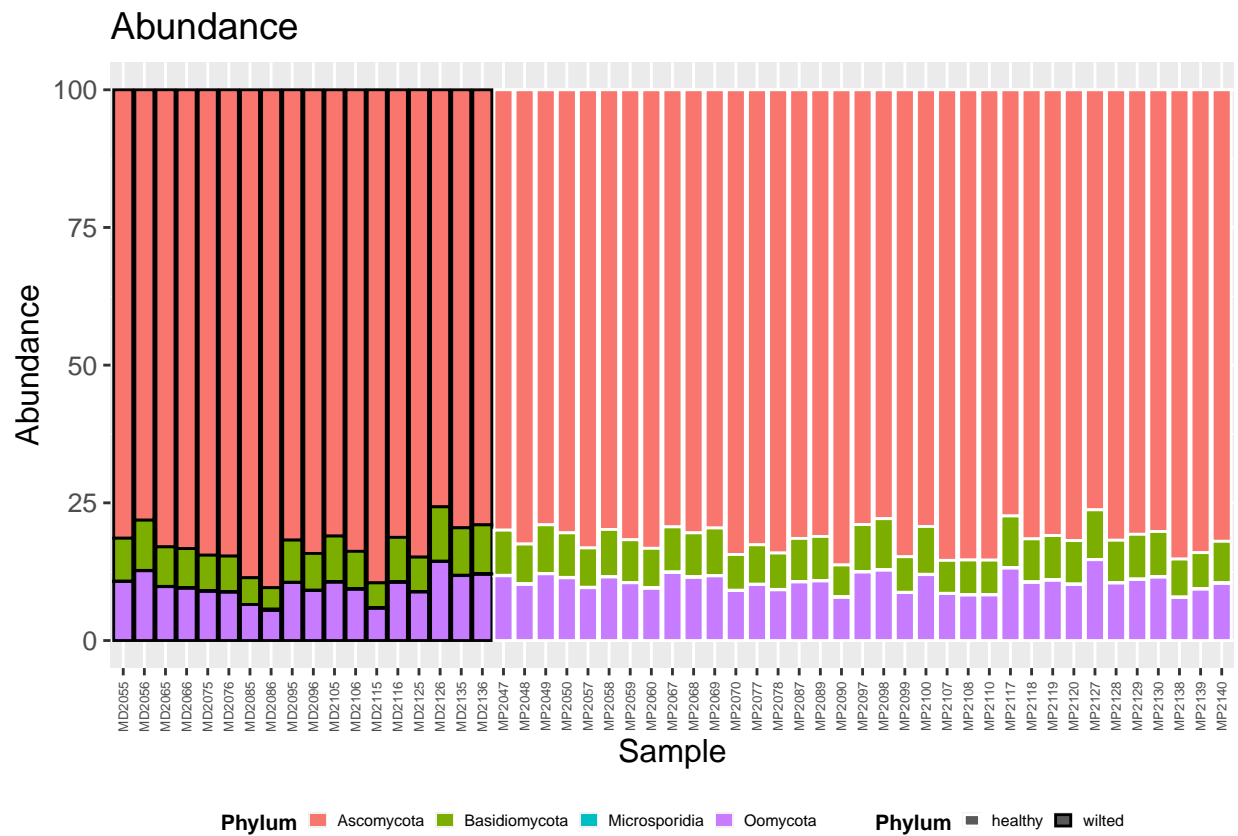
#————Eukarya by Phylum

```
Barras_Phylum <- Abundance_barras(merge_Eukaryota,'Phylum' , 'Treatment', 10.0)
```

```
## Warning: 'aes_string()' was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation ideoms with 'aes()'
```
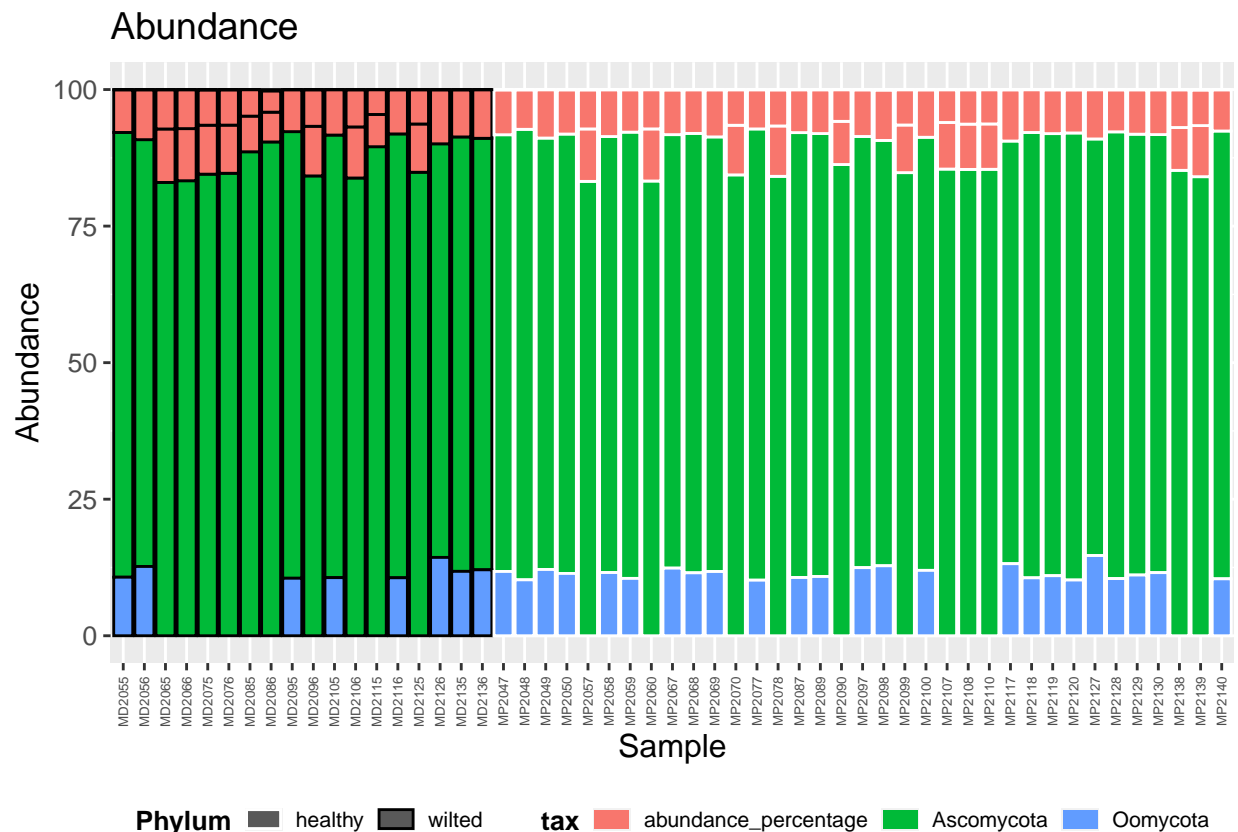
```
Barras_Phylum[1] # normal
```

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

Abundance

```
Barras_Phylum[2]
```

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

Abundance

```
Beta_diversity(merge_Eukaryota , 'Phylum' , 'Treatment', 'bray')
```

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.01148681
## Run 1 stress 8.721705e-05
## ... New best solution
## ... Procrustes: rmse 0.03464635  max resid 0.0908184
## Run 2 stress 9.364796e-05
## ... Procrustes: rmse 6.118169e-05  max resid 0.0001669419
## ... Similar to previous best
## Run 3 stress 9.977146e-05
## ... Procrustes: rmse 9.808252e-05  max resid 0.0002475334
## ... Similar to previous best
## Run 4 stress 9.958837e-05
## ... Procrustes: rmse 6.144003e-05  max resid 0.0001913055
## ... Similar to previous best
## Run 5 stress 0.403632
## Run 6 stress 9.955129e-05
## ... Procrustes: rmse 0.0001058779  max resid 0.000248018
## ... Similar to previous best
## Run 7 stress 6.7419e-05
## ... New best solution
## ... Procrustes: rmse 4.841319e-05  max resid 0.0001301041
## ... Similar to previous best
```

```
## Run 8 stress 9.778231e-05
## ... Procrustes: rmse 0.0001011437  max resid 0.0002781668
## ... Similar to previous best
## Run 9 stress 9.847208e-05
## ... Procrustes: rmse 0.0002221607  max resid 0.00058567
## ... Similar to previous best
## Run 10 stress 7.057993e-05
## ... Procrustes: rmse 3.085713e-05  max resid 7.412321e-05
## ... Similar to previous best
## Run 11 stress 9.780103e-05
## ... Procrustes: rmse 0.0001009935  max resid 0.000264652
## ... Similar to previous best
## Run 12 stress 9.652241e-05
## ... Procrustes: rmse 8.824749e-05  max resid 0.0002392269
## ... Similar to previous best
## Run 13 stress 9.144417e-05
## ... Procrustes: rmse 8.458957e-05  max resid 0.000219765
## ... Similar to previous best
## Run 14 stress 9.942206e-05
## ... Procrustes: rmse 0.0001201951  max resid 0.000315776
## ... Similar to previous best
## Run 15 stress 9.427342e-05
## ... Procrustes: rmse 0.0001235418  max resid 0.0003150042
## ... Similar to previous best
## Run 16 stress 8.957695e-05
## ... Procrustes: rmse 0.0001086359  max resid 0.0002820845
## ... Similar to previous best
## Run 17 stress 6.748827e-05
## ... Procrustes: rmse 3.206075e-05  max resid 8.430626e-05
## ... Similar to previous best
## Run 18 stress 9.406671e-05
## ... Procrustes: rmse 8.437226e-05  max resid 0.0002109811
## ... Similar to previous best
## Run 19 stress 0.000103892
## ... Procrustes: rmse 0.000297204  max resid 0.0007786037
## ... Similar to previous best
## Run 20 stress 0.0008337584
## *** Best solution repeated 13 times


## Warning in metaMDS(veganifyOTU(physeq), distance, ...): stress is (nearly) zero:
## you may have insufficient data
```
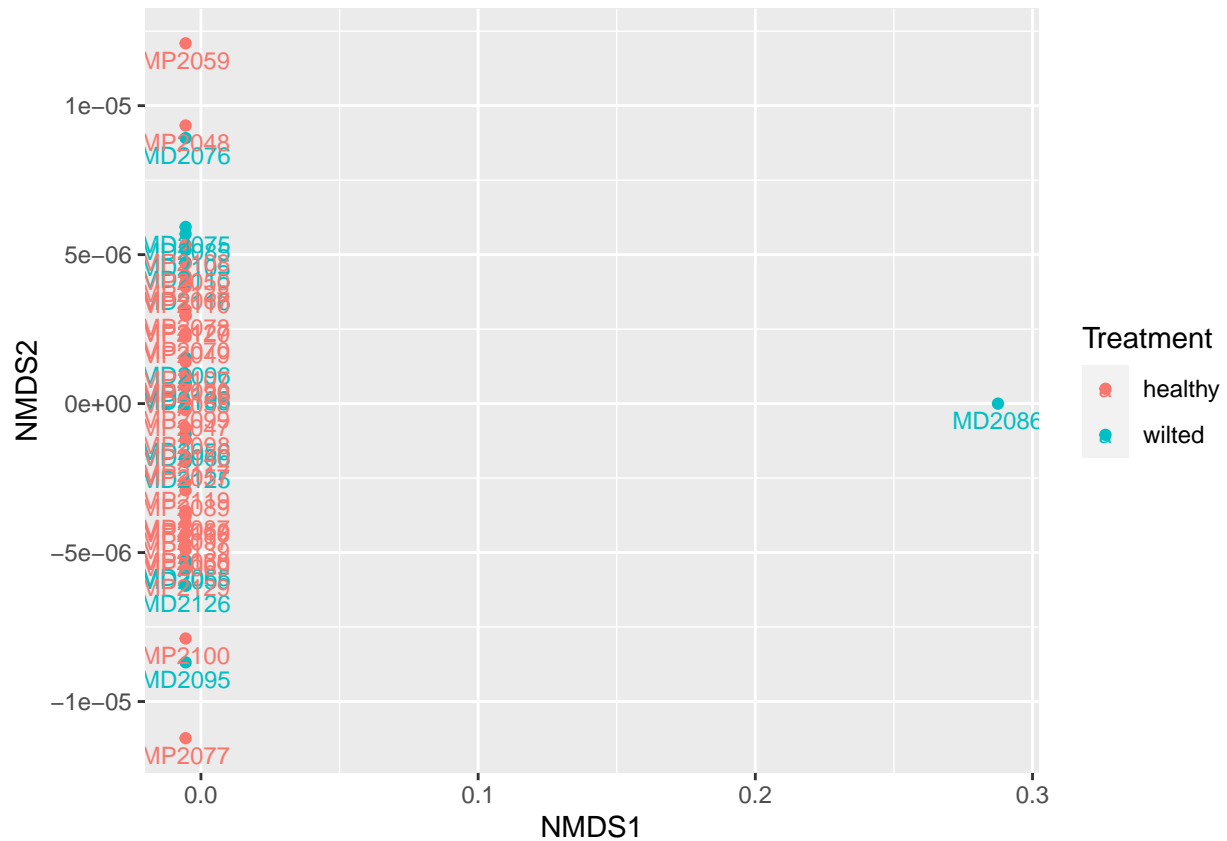
```
Alpha_diversity(merge_Eukaryota , 'Phylum' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
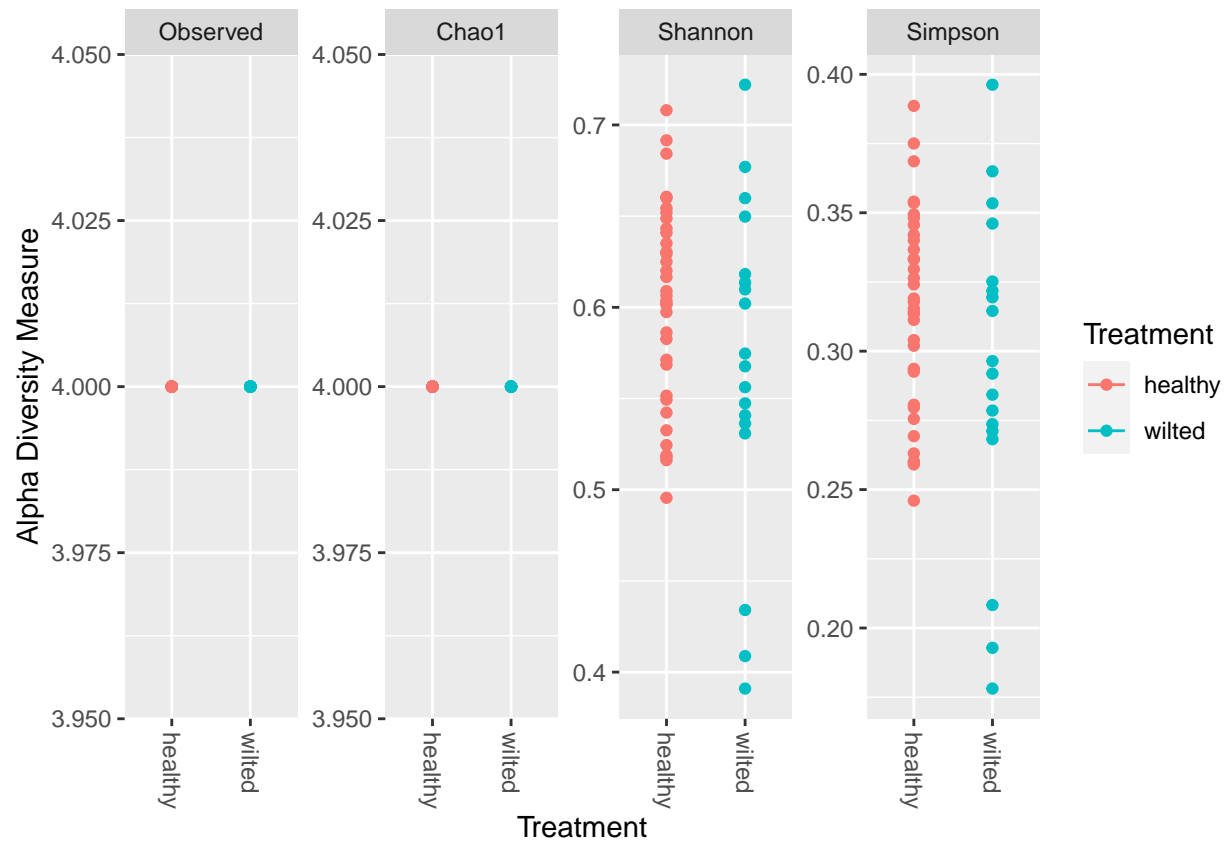
#———Eukarya by Family

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Family','Treatment',10.0)
Barras_Species[1]
```

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

Abundance

Family ▪ healthy ◼ wilted

Family
- Aspergillaceae
- Bionectriaceae
- Ceratobasidiaceae
- Chaetomiaceae
- Clavicipitaceae
- Cordycipitaceae
- Cryptococcaceae
- Debaryomycetaceae
- Didymosphaeriaceae
- Dipodascaceae
- Glomerellaceae
- Hypocreaceae
- Leptosphaeriaceae
- Malasseziaceae
- Marasmiaceae
- Mycosphaerellaceae
- Nectriaceae
- Ophiocordycipitaceae
- Peronosporaceae
- Phaffomycetaceae
- Phanerochaetaceae
- Pichiaceae
- Pyriculariaceae
- Pythiaceae
- Saccharomycetaceae
- Saccharomycodaceae
- Schizosaccharomycetaceae
- Sclerotiniaceae
- Sordar
- Sporoc
- Therm
- Trichod
- Trichon
- Unikar
- Ustilag

```
Barras_Species[2]
```

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

Abundance


```
Beta_diversity(merge_Eukaryota , 'Family' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1089081
## Run 1 stress 0.1089294
## ... Procrustes: rmse 0.00810509  max resid 0.05434305
## Run 2 stress 0.1089295
## ... Procrustes: rmse 0.008105083  max resid 0.05434649
## Run 3 stress 0.1089482
## ... Procrustes: rmse 0.008219776  max resid 0.05365826
## Run 4 stress 0.1089494
## ... Procrustes: rmse 0.008111652  max resid 0.05390688
## Run 5 stress 0.1089295
## ... Procrustes: rmse 0.008103132  max resid 0.0543525
## Run 6 stress 0.108929
## ... Procrustes: rmse 0.00815064  max resid 0.05419082
## Run 7 stress 0.1352083
## Run 8 stress 0.1088969
## ... New best solution
## ... Procrustes: rmse 0.002387824  max resid 0.009372516
## ... Similar to previous best
## Run 9 stress 0.1089084
## ... Procrustes: rmse 0.002391502  max resid 0.009369591
## ... Similar to previous best
## Run 10 stress 0.1298007
```

```
## Run 11 stress 0.1088879
## ... New best solution
## ... Procrustes: rmse 0.002004416  max resid 0.008998996
## ... Similar to previous best
## Run 12 stress 0.1088883
## ... Procrustes: rmse 0.001234226  max resid 0.006984763
## ... Similar to previous best
## Run 13 stress 0.1088966
## ... Procrustes: rmse 0.001743849  max resid 0.00903887
## ... Similar to previous best
## Run 14 stress 0.1089086
## ... Procrustes: rmse 0.002115096  max resid 0.009168435
## ... Similar to previous best
## Run 15 stress 0.1089098
## ... Procrustes: rmse 0.002113553  max resid 0.009206383
## ... Similar to previous best
## Run 16 stress 0.1089299
## ... Procrustes: rmse 0.008420913  max resid 0.05468767
## Run 17 stress 0.1091144
## ... Procrustes: rmse 0.008506053  max resid 0.04445378
## Run 18 stress 0.1088886
## ... Procrustes: rmse 0.001316898  max resid 0.007476201
## ... Similar to previous best
## Run 19 stress 0.108929
## ... Procrustes: rmse 0.008383055  max resid 0.05448714
## Run 20 stress 0.1088877
## ... New best solution
## ... Procrustes: rmse 0.000297331  max resid 0.001736161
## ... Similar to previous best
## *** Best solution repeated 1 times
```
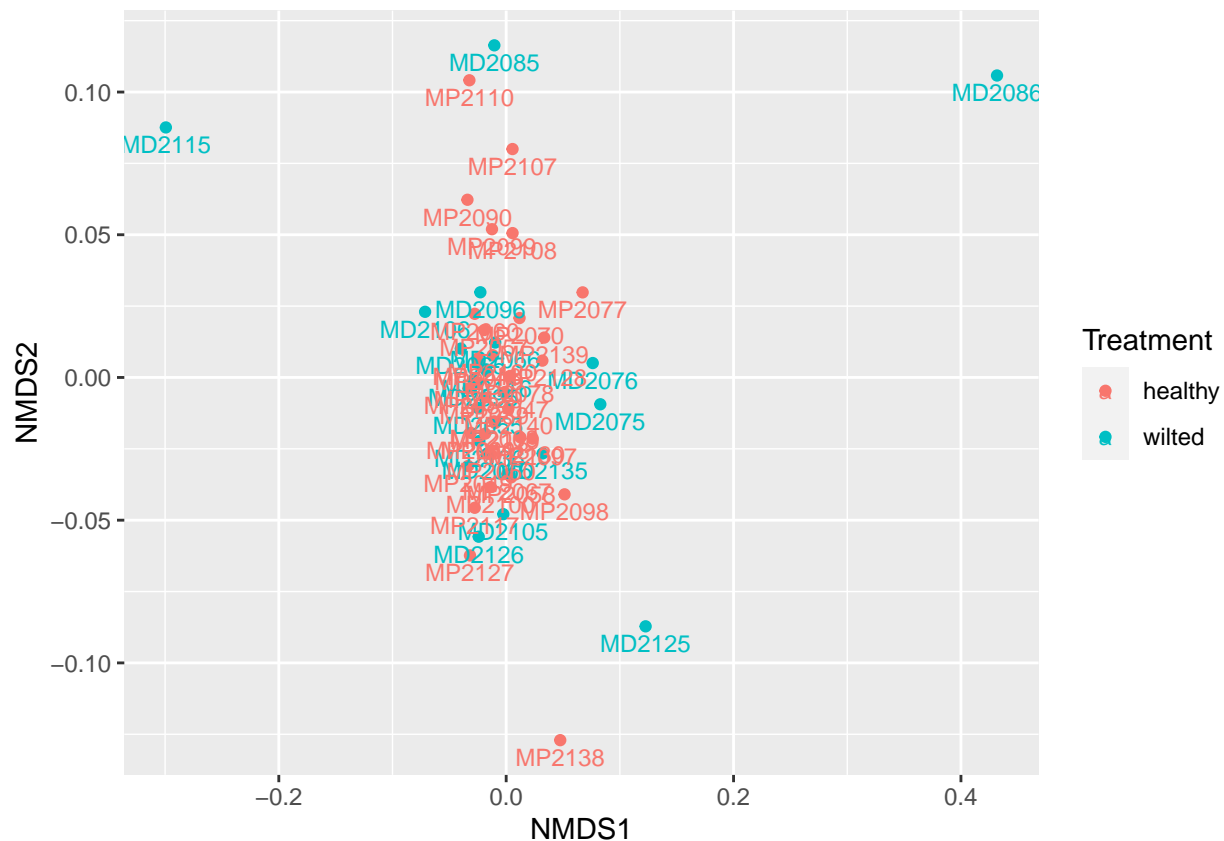
```
Alpha_diversity(merge_Eukaryota , 'Family' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
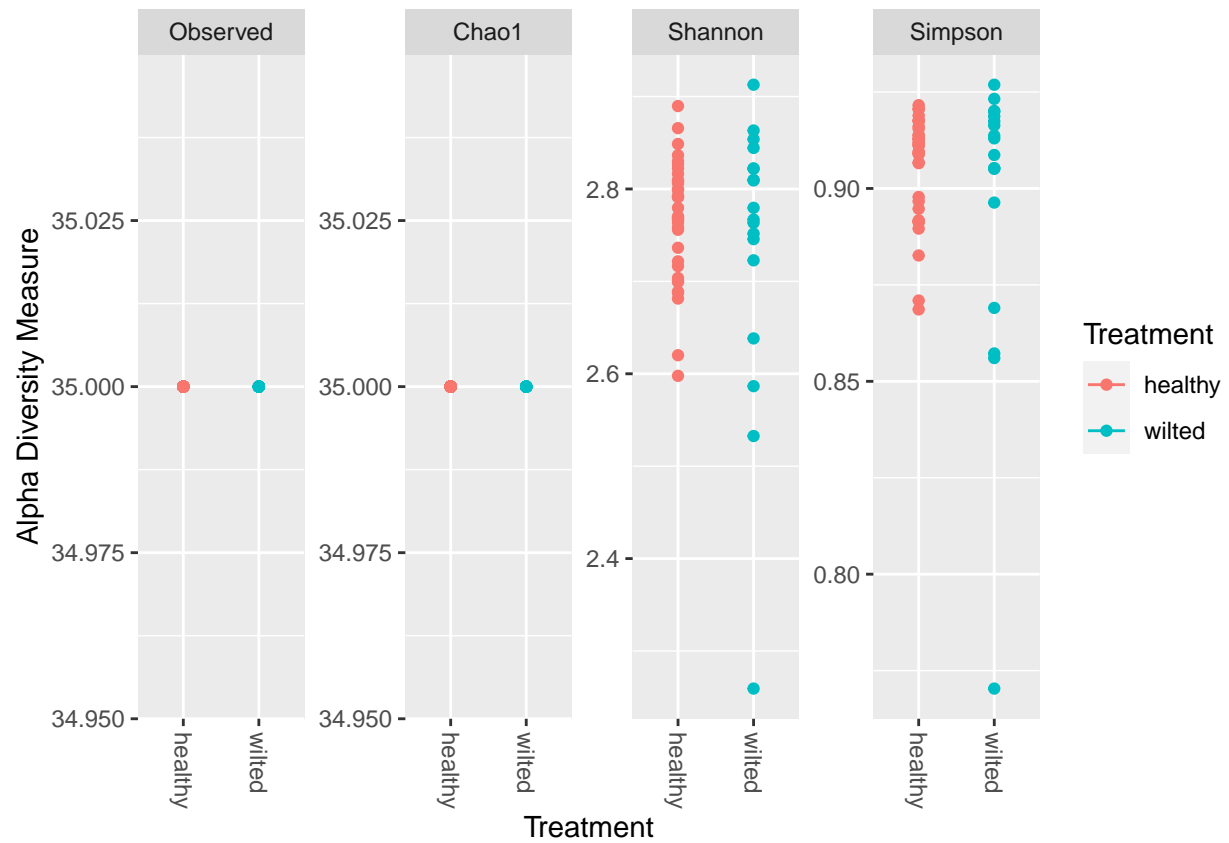
#———Eukarya by Genero

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Genus','Treatment',10.0)
Barras_Species[1]
```

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

Abundance

Genus

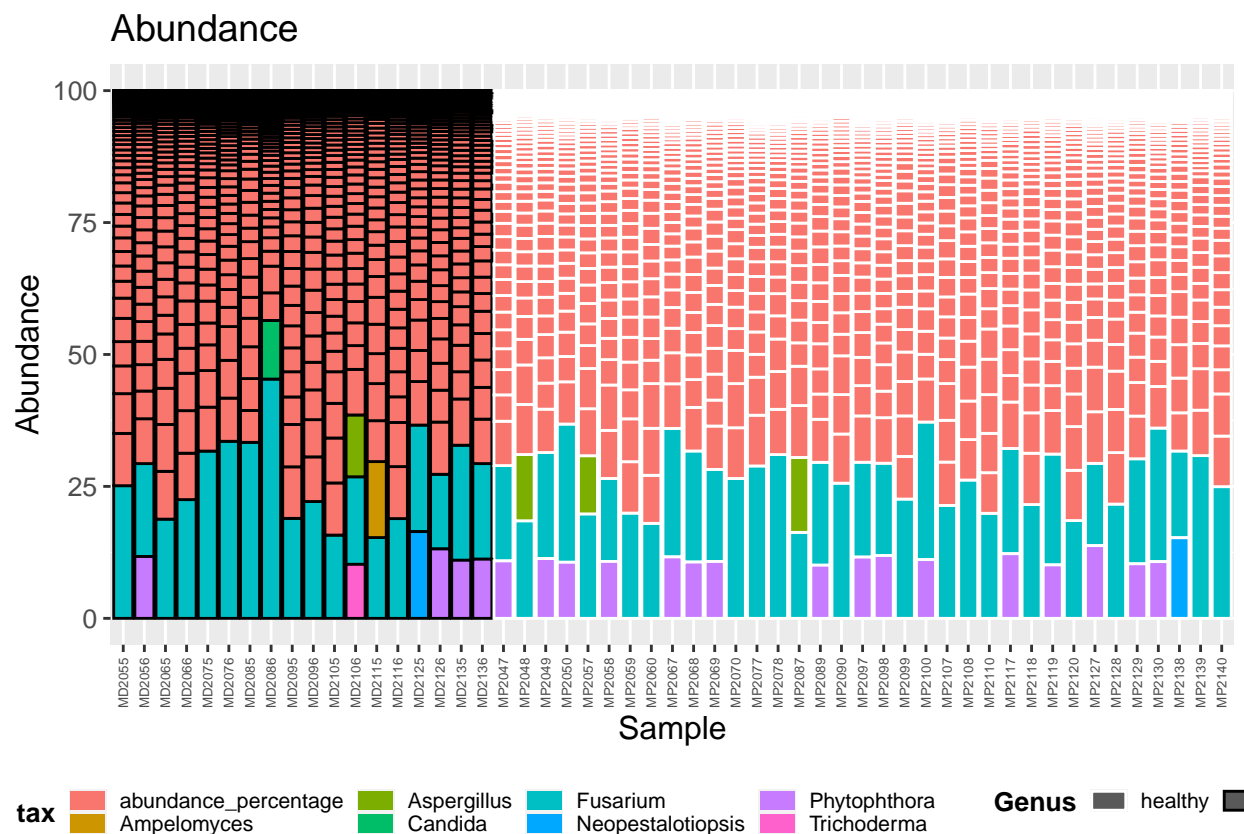|				
Ampelomyces	Drechmeria	Naumovozyma	Purpureocillium	Thermothelomyces
Aspergillus	Encephalitozoon	Neopestalotiopsis	Pyricularia	Thermothielavioides
Beauveria	Eremothecium	Neurospora	Pythium	Torulaspora
Botrytis	Fusarium	Ogataea	Rhizoctonia	Trichoderma
Brettanomyces	Kazachstania	Paecilomyces	Saccharomyces	Ustilaginoidea
Candida	Kluyveromyces	Paraphaeosphaeria	Saccharomycodes	Ustilago
Cercospora	Komagataella	Penicillium	Scheffersomyces	Yarrowia
Clonostachys	Lachancea	Phlebiopsis	Schizosaccharomyces	Zygosaccharomyces
Colletotrichum	Malassezia	Phytophthora	Sporisorium	Zygotorulaspora
Cordyceps	Marasmius	Pichia	Sugiyamaella	Zymoseptoria
Cryptococcus	Metarhizium	Pochonia	Talaromyces	
Debaryomyces	Nakaseomyces	Pseudozyma	Tetrapisispora	

Genus ■ healthy ■

```
Barras_Species[2]
```

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

Abundance

```
Beta_diversity(merge_Eukaryota , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.110709
## Run 1 stress 0.1107088
## ... New best solution
## ... Procrustes: rmse 0.0001430709  max resid 0.0008227195
## ... Similar to previous best
## Run 2 stress 0.1333688
## Run 3 stress 0.111982
## Run 4 stress 0.1108248
## ... Procrustes: rmse 0.006755681  max resid 0.03975663
## Run 5 stress 0.1107109
## ... Procrustes: rmse 0.001092784  max resid 0.006223585
## ... Similar to previous best
## Run 6 stress 0.1107098
## ... Procrustes: rmse 0.0003686945  max resid 0.002086262
## ... Similar to previous best
## Run 7 stress 0.1107323
## ... Procrustes: rmse 0.003431404  max resid 0.01929974
## Run 8 stress 0.1107095
## ... Procrustes: rmse 0.001012076  max resid 0.005794729
## ... Similar to previous best
## Run 9 stress 0.1128396
## Run 10 stress 0.1428407
```

```
## Run 11 stress 0.122383
## Run 12 stress 0.1117245
## Run 13 stress 0.1107095
## ... Procrustes: rmse 0.0002930055  max resid 0.001665347
## ... Similar to previous best
## Run 14 stress 0.110709
## ... Procrustes: rmse 0.0001317955  max resid 0.0007428215
## ... Similar to previous best
## Run 15 stress 0.1107092
## ... Procrustes: rmse 0.0008859866  max resid 0.005068244
## ... Similar to previous best
## Run 16 stress 0.1107093
## ... Procrustes: rmse 0.0009158685  max resid 0.005241076
## ... Similar to previous best
## Run 17 stress 0.1578415
## Run 18 stress 0.1107098
## ... Procrustes: rmse 0.001096519  max resid 0.006267109
## ... Similar to previous best
## Run 19 stress 0.1107098
## ... Procrustes: rmse 0.001074805  max resid 0.006153875
## ... Similar to previous best
## Run 20 stress 0.1305045
## *** Best solution repeated 10 times
```
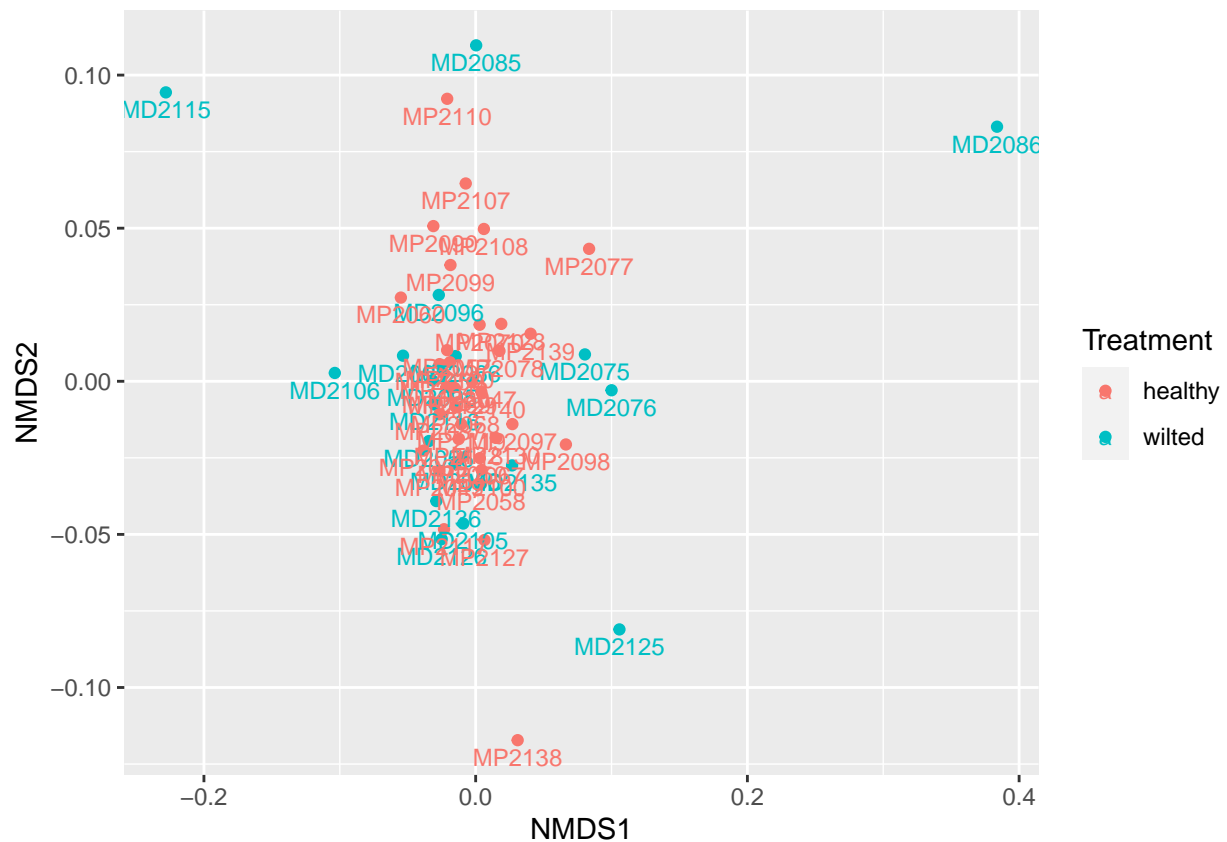
```
Alpha_diversity(merge_Eukaryota , 'Genus' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
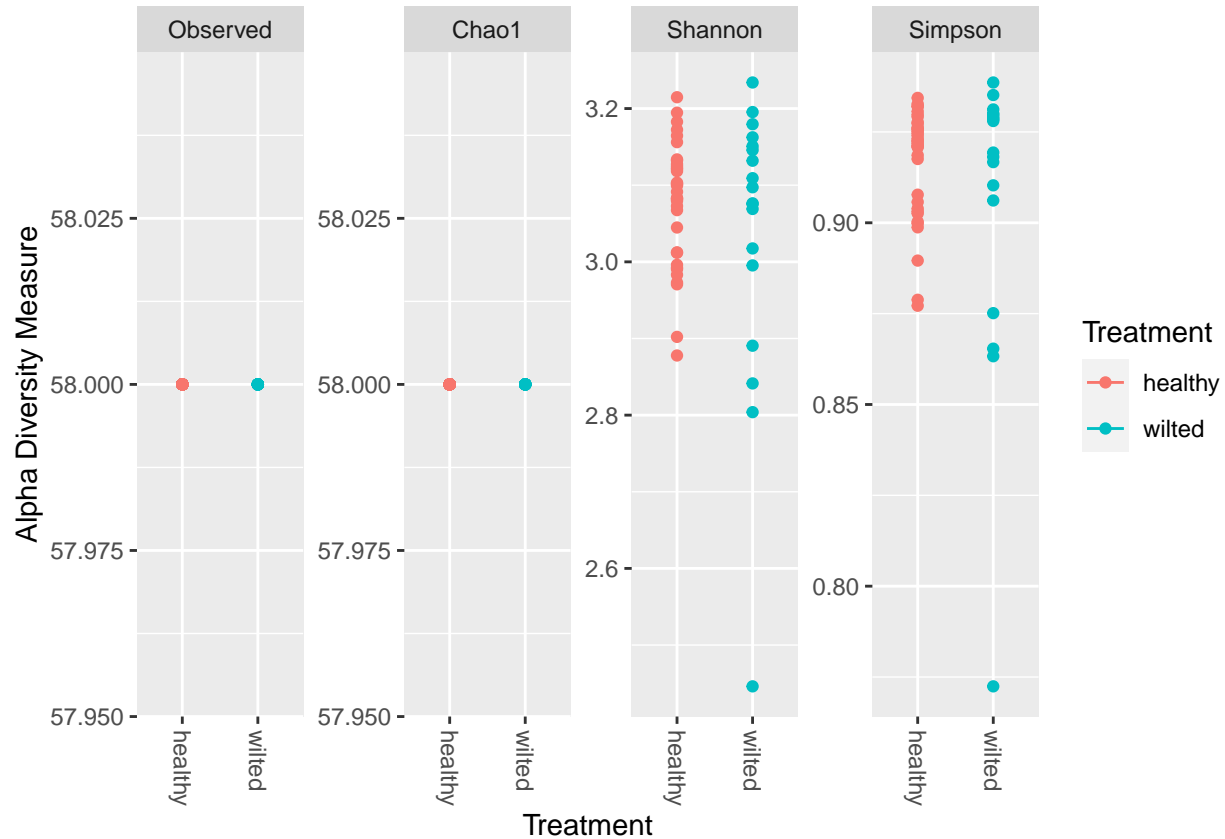

#———Eukarya by Species

```
Barras_Species <- Abundance_barras(merge_Eukaryota,'Species','Treatment',10.0)
Barras_Species[1]
```
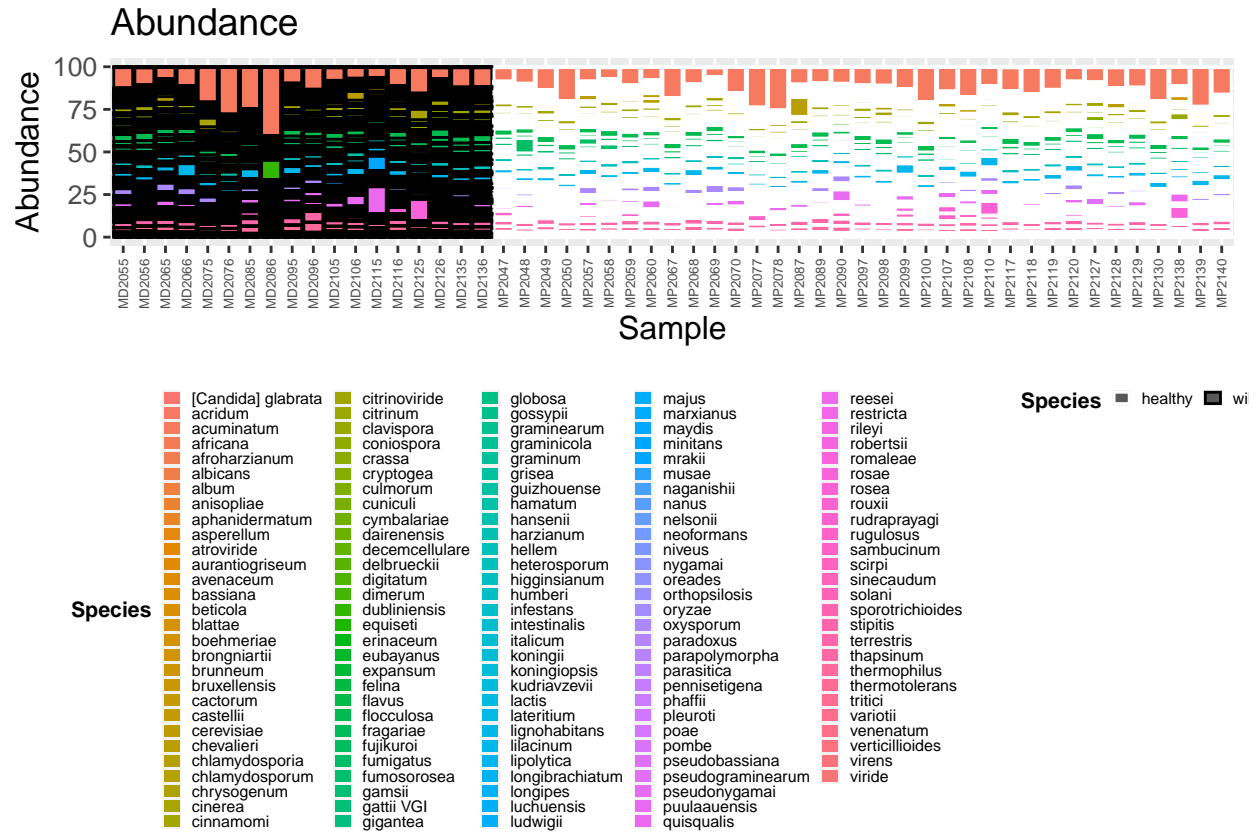
```
## [[1]]
```

```
Barras_Species[2]
```

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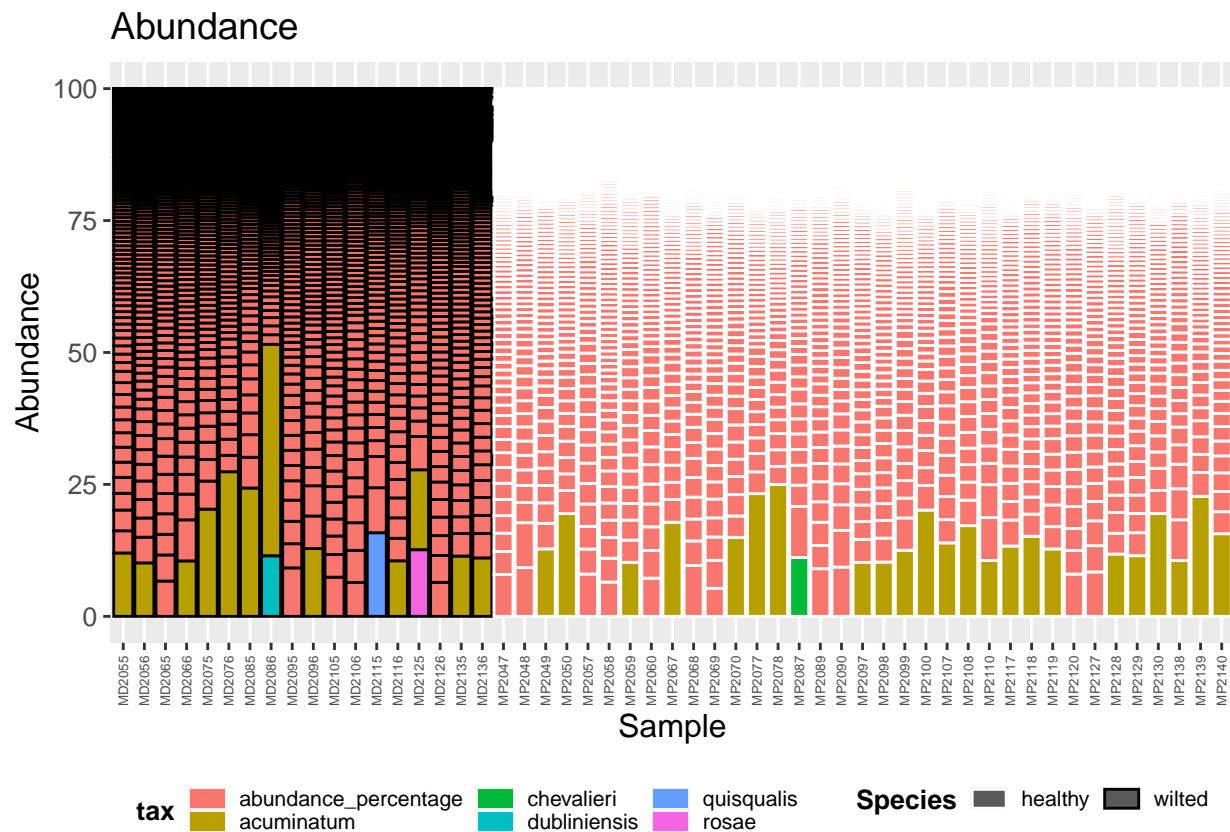
Abundance


```
Beta_diversity(merge_Eukaryota , 'Species' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1226512
## Run 1 stress 0.1272835
## Run 2 stress 0.1233307
## Run 3 stress 0.1272841
## Run 4 stress 0.1218542
## ... New best solution
## ... Procrustes: rmse 0.02022867  max resid 0.1286786
## Run 5 stress 0.1218541
## ... New best solution
## ... Procrustes: rmse 0.0004017162  max resid 0.002133187
## ... Similar to previous best
## Run 6 stress 0.1272837
## Run 7 stress 0.121854
## ... New best solution
## ... Procrustes: rmse 0.0003378467  max resid 0.002079134
## ... Similar to previous best
## Run 8 stress 0.1218544
## ... Procrustes: rmse 0.0002293358  max resid 0.001146213
## ... Similar to previous best
## Run 9 stress 0.1218547
## ... Procrustes: rmse 0.0006440675  max resid 0.003152215
## ... Similar to previous best
```

```
## Run 10 stress 0.1218542
## ... Procrustes: rmse 0.0001618773  max resid 0.000829501
## ... Similar to previous best
## Run 11 stress 0.1218542
## ... Procrustes: rmse 0.0001241795  max resid 0.0006225348
## ... Similar to previous best
## Run 12 stress 0.1272838
## Run 13 stress 0.1272837
## Run 14 stress 0.1218549
## ... Procrustes: rmse 0.0006863257  max resid 0.003361811
## ... Similar to previous best
## Run 15 stress 0.121855
## ... Procrustes: rmse 0.0007034878  max resid 0.003448169
## ... Similar to previous best
## Run 16 stress 0.1226506
## Run 17 stress 0.1218543
## ... Procrustes: rmse 0.00050226  max resid 0.002454841
## ... Similar to previous best
## Run 18 stress 0.1272833
## Run 19 stress 0.127829
## Run 20 stress 0.1522631
## *** Best solution repeated 8 times
```



```
Alpha_diversity(merge_Eukaryota , 'Species' , 'Treatment')
```

#————Bacteria by Phylum

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Phylum','Treatment',10.0)
Barras_Species[1]
```

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

Abundance

Legend — Phylum:
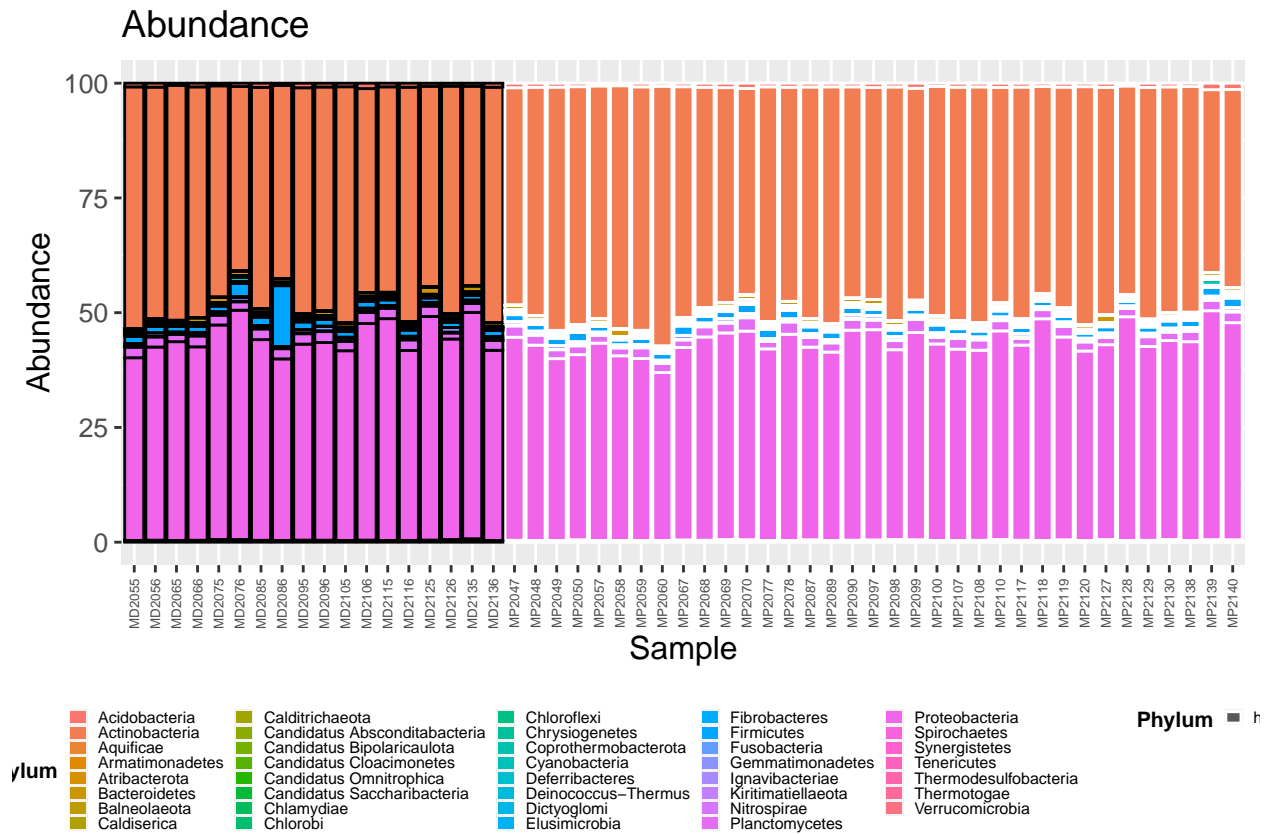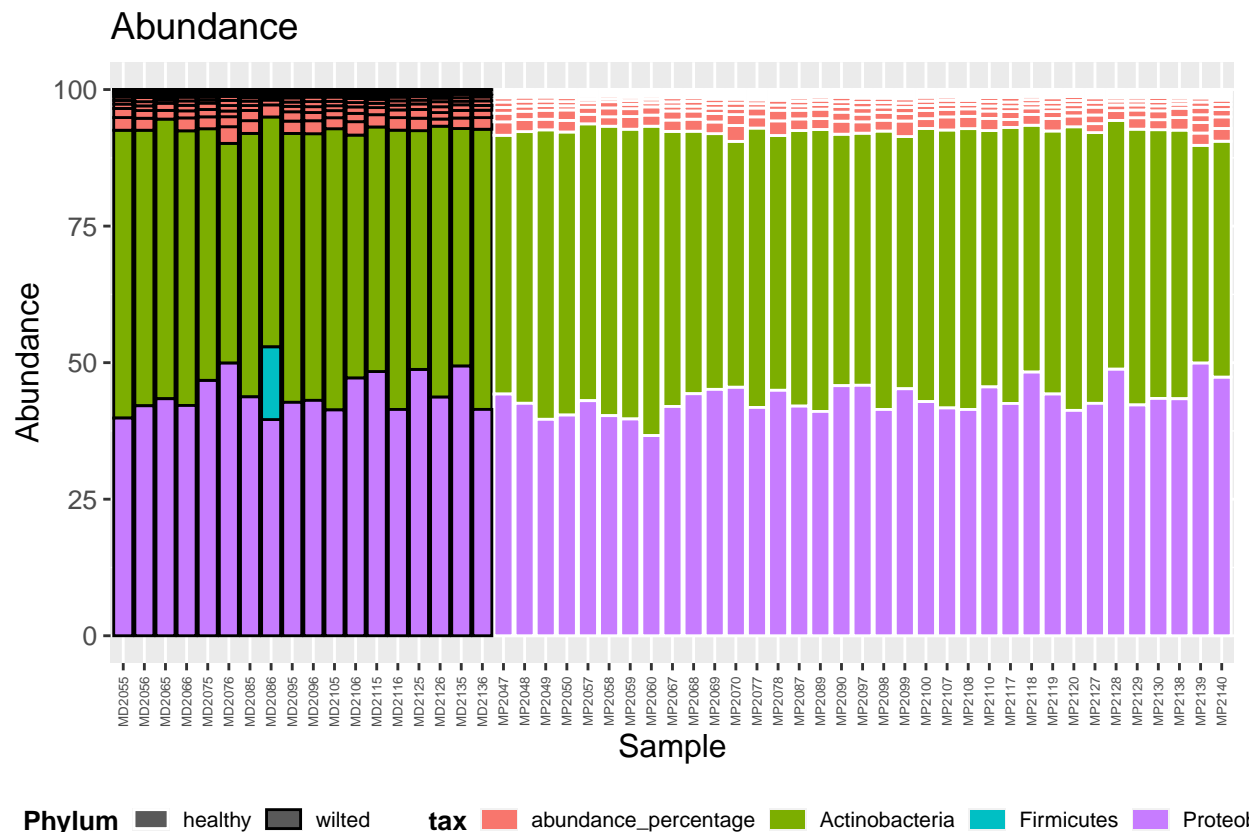
- Acidobacteria
- Actinobacteria
- Aquificae
- Armatimonadetes
- Atribacterota
- Bacteroidetes
- Balneolaeota
- Caldiserica
- Calditrichaeota
- Candidatus Absconditabacteria
- Candidatus Bipolaricaulota
- Candidatus Cloacimonetes
- Candidatus Omnitrophica
- Candidatus Saccharibacteria
- Chlamydiae
- Chlorobi
- Chloroflexi
- Chrysiogenetes
- Coprothermobacterota
- Cyanobacteria
- Deferribacteres
- Deinococcus–Thermus
- Dictyoglomi
- Elusimicrobia
- Fibrobacteres
- Firmicutes
- Fusobacteria
- Gemmatimonadetes
- Ignavibacteriae
- Kiritimatiellaeota
- Nitrospirae
- Planctomycetes
- Proteobacteria
- Spirochaetes
- Synergistetes
- Tenericutes
- Thermodesulfobacteria
- Thermotogae
- Verrucomicrobia

Phylum ▪ h

```
Barras_Species[2]
```

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

Abundance


```
Beta_diversity(merge_Bacteria , 'Phylum' , 'Treatment', 'bray')
```

```
## Square root transformation
## Wisconsin double standardization
## Run 0 stress 0.1520004
## Run 1 stress 0.16819
## Run 2 stress 0.1623133
## Run 3 stress 0.1541161
## Run 4 stress 0.1691792
## Run 5 stress 0.1709726
## Run 6 stress 0.1602944
## Run 7 stress 0.178741
## Run 8 stress 0.158135
## Run 9 stress 0.1552653
## Run 10 stress 0.1667695
## Run 11 stress 0.1520014
## ... Procrustes: rmse 0.001914816  max resid 0.01092158
## Run 12 stress 0.1736601
## Run 13 stress 0.1623133
## Run 14 stress 0.167969
## Run 15 stress 0.1619354
## Run 16 stress 0.1613696
## Run 17 stress 0.1601869
## Run 18 stress 0.1703255
## Run 19 stress 0.1520007
```

```
## ... Procrustes: rmse 0.0001885214   max resid 0.001050437
## ... Similar to previous best
## Run 20 stress 0.1616636
## *** Best solution repeated 1 times
```
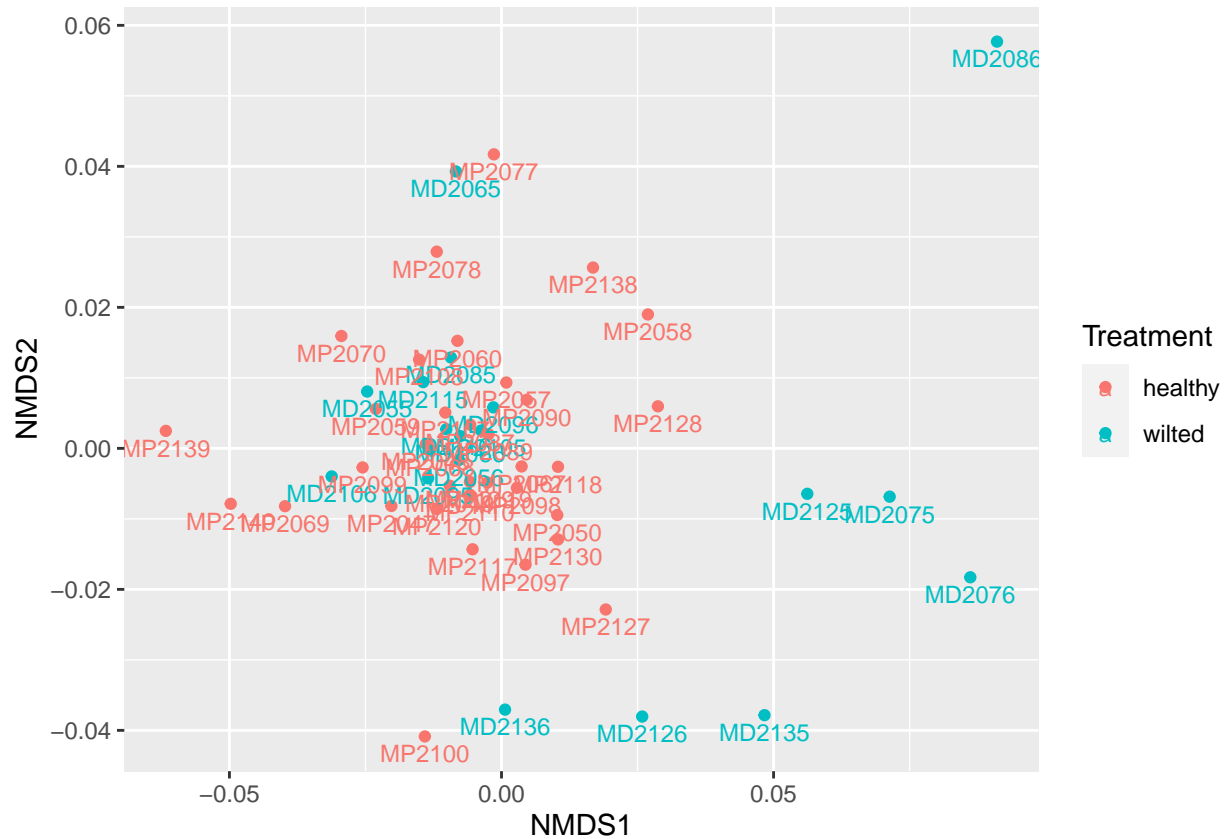


```
Alpha_diversity(merge_Bacteria , 'Phylum' , 'Treatment')
```

```
## Warning in estimate_richness(physeq, split = TRUE, measures = measures): The data you have provided
## any singletons. This is highly suspicious. Results of richness
## estimates (for example) are probably unreliable, or wrong, if you have already
## trimmed low-abundance taxa from the data.
##
## We recommended that you find the un-trimmed data and retry.
```
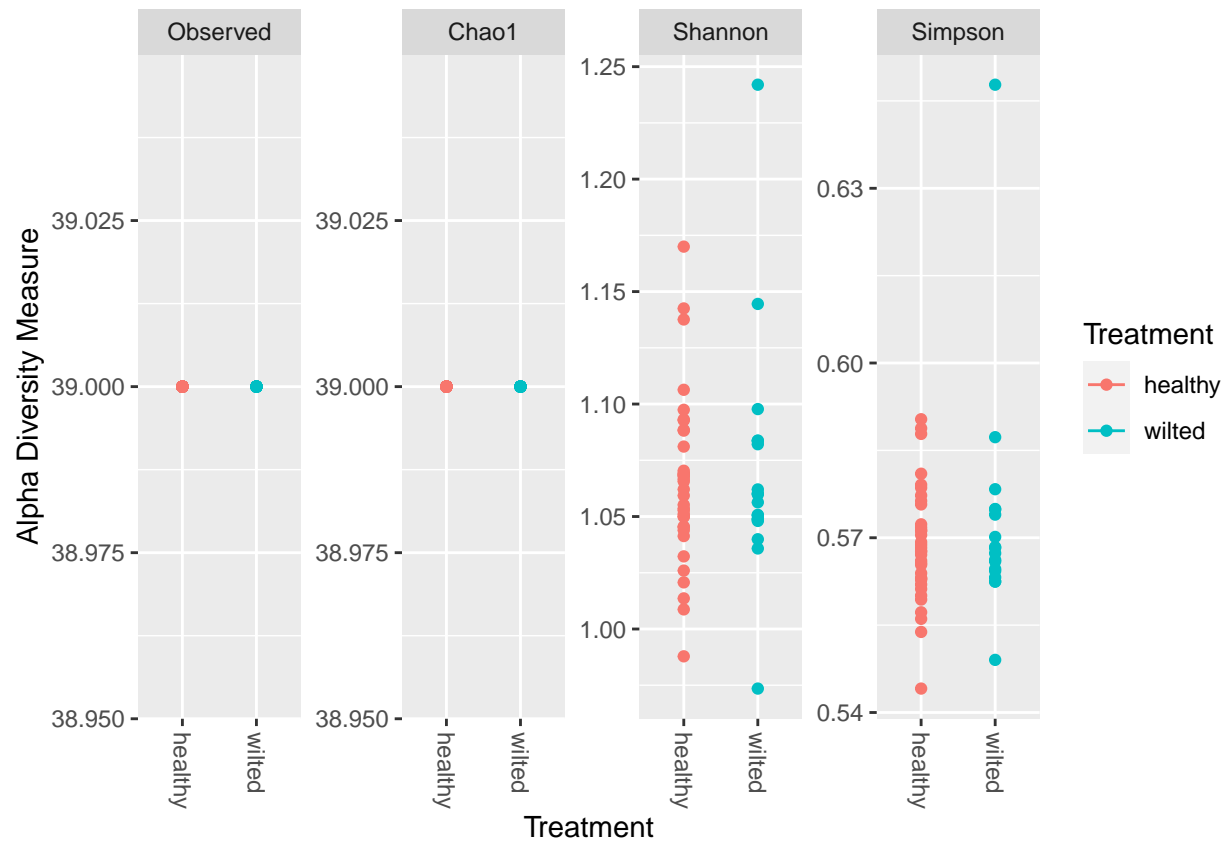
#———Bacteria by Familia

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Family','Treatment',10.0)
Barras_Species[1]
```

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

Family

|			
Actinomycetaceae	Chthonomonadaceae	Halobacteriovoraceae	Nocardiaceae
Actinopolymorphaceae	Clostridiaceae	Halobacteroidaceae	Nocardioidaceae
Actinopolysporaceae	Clostridiales Family XVI. Incertae Sedis	Halomonadaceae	Nocardiopsaceae
Aerococcaceae	Clostridiales Family XVII. Incertae Sedis	Halothiobacillaceae	Nostocaceae
Aeromonadaceae	Cohaesibacteraceae	Hapalosiphonaceae	Oceanospirillaceae
Akkermansiaceae	Coleofasciculaceae	Helicobacteraceae	Oculatellaceae
Alcaligenaceae	Colwelliaceae	Heliobacteriaceae	Odoribacteraceae
Alcanivoracaceae	Comamonadaceae	Holosporaceae	Oleiphilaceae
Alicyclobacillaceae	Conexibacteraceae	Hydrogenimonaceae	Opitutaceae
Alteromonadaceae	Coprothermobacteraceae	Hydrogenophilaceae	Orbaceae
Amoebophilaceae	Coriobacteriaceae	Hydrogenothermaceae	Ornithinimicrobiaceae
Amorphaceae	Corynebacteriaceae	Hyellaceae	Oscillatoriaceae
Anaerohalosphaeraceae	Coxiellaceae	Hymenobacteraceae	Oscillospiraceae
Anaerolineaceae	Crocinitomicaceae	Hyphomicrobiaceae	Oxalobacteraceae
Anaeromyxobacteraceae	Cyclobacteriaceae	Hyphomonadaceae	Paenibacillaceae
Anaplasmataceae	Cytophagaceae	Iamiaceae	Paludibacteraceae
Aphanizomenonaceae	Deferribacteraceae	Ichthyobacteriaceae	Parachlamydiaceae
Aphanothecaceae	Dehalococcoidaceae	Idiomarinaceae	Parvibaculaceae
Aquificaceae	Deinococcaceae	Ignavibacteriaceae	Parvularculaceae
Archangiaceae	Demequinaceae	Ilumatobacteraceae	Pasteurellaceae
Arcobacteraceae	Dermabacteraceae	Immundisolibacteraceae	Pectobacteriaceae
Ardenticatenaceae	Dermacoccaceae	Intrasporangiaceae	Pelagibacteraceae
Atopobiaceae	Dermatophilaceae	Isosphaeraceae	Peptococcaceae
Atribacteraceae	Dermocarpellaceae	Jatrophihabitantaceae	Peptoniphilaceae
Aurantimonadaceae	Desulfallaceae	Jiangellaceae	Peptostreptococcaceae
Azonexaceae	Desulfarculaceae	Jonesiaceae	Petrotogaceae
Azospirillaceae	Desulfitobacteriaceae	Kaistiaceae	Phototrophicaceae
Bacillaceae	Desulfobacteraceae	Kangiellaceae	Phreatobacteraceae
Bacteriovoracaceae	Desulfobulbaceae	Kineosporiaceae	Phycisphaeraceae
Bacteroidaceae	Desulfocapsaceae	Kiritimatiellaceae	Phyllobacteriaceae
Baekduiaceae	Desulfohalobiaceae	Kofleriaceae	Pirellulaceae
Barnesiellaceae	Desulfomicrobiaceae	Koleobacteraceae	Piscirickettsiaceae
Bartonellaceae	Desulfosudaceae	Kordiimonadaceae	Planctomycetaceae
Bdellovibrionaceae	Desulfotomaculaceae	Kosmotogaceae	Planococcaceae
Beijerinckiaceae	Desulfovibrionaceae	Kribbellaceae	Pleomorphomonadaceae
Bernardetiaceae	Desulfurellaceae	Ktedonosporobacteraceae	Polyangiaceae
Beutenbergiaceae	Desulfurobacteriaceae	Kytococcaceae	Porphyromonadaceae
Bifidobacteriaceae	Desulfuromonadaceae	Labilitrichaceae	Prevotellaceae
Blastochloridaceae	Devosiaceae	Lachnospiraceae	Prochlorococcaceae
Blattabacteriaceae	Dictyoglomaceae	Lacipirellulaceae	Prochlorotrichaceae
Bogoriellaceae	Dietziaceae	Lactobacillaceae	Prolixibacteraceae
Borreliaceae	Dissulfurispiraceae	Lawsonellaceae	Promicromonosporaceae
Boseaceae	Dysgonomonadaceae	Legionellaceae	Propionibacteriaceae
Brachyspiraceae	Ectothiorhodospiraceae	Leptolyngbyaceae	Proteinivoraceae
Bradymonadaceae	Eggerthellaceae	Leptospiraceae	Pseudanabaenaceae
Bradyrhizobiaceae	Egibacteraceae	Leptotrichiaceae	Pseudoalteromonadaceae
Breoghaniaceae	Egicoccaceae	Lichenihabitantaceae	Pseudomonadaceae
Brevibacteriaceae	Elioraeaceae	Limnochordaceae	Pseudonocardiaceae
Brucellaceae	Elusimicrobiaceae	Listeriaceae	Psychromonadaceae
Bruguierivoracaceae	Emcibacteraceae	Litoricolaceae	Puniceicoccaceae
Bryobacteraceae	Endomicrobiaceae	Magnetococcaceae	Rhabdochlamydiaceae
Budviciaceae	Endozoicomonadaceae	Mangrovivirgaceae	Rhizobiaceae
Burkholderiaceae	Enterobacteriaceae	Maricaulaceae	Rhodanobacteraceae
Caedimonadaceae	Enterococcaceae	Marinifilaceae	Rhodobacteraceae
Caldilineaceae	Entomoplasmataceae	Marinilabiliaceae	Rhodocyclaceae
Caldisericaceae	Erwiniaceae	Marinobacteraceae	Rhodospirillaceae
Calditrichaceae	Erysipelotrichaceae	Mariprofundaceae	Rhodothermaceae
Calotrichaceae	Erythrobacteraceae	Marivirgaceae	Rickettsiaceae
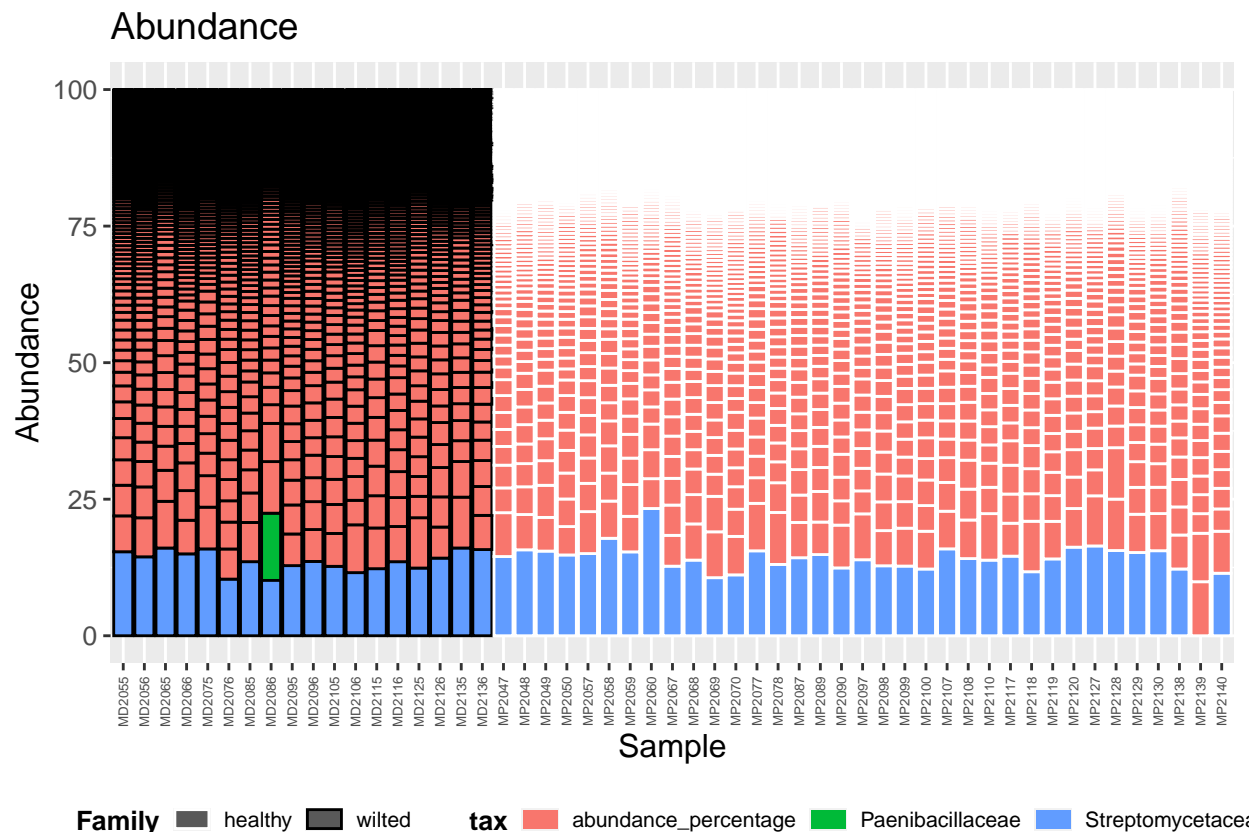
```
Barras_Species[2]
```

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

Abundance

```
Beta_diversity(merge_Bacteria , 'Family' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1412073
## Run 1 stress 0.1370739
## ... New best solution
## ... Procrustes: rmse 0.06910163  max resid 0.3765617
## Run 2 stress 0.140102
## Run 3 stress 0.1519217
## Run 4 stress 0.1390461
## Run 5 stress 0.1546341
## Run 6 stress 0.1657309
## Run 7 stress 0.1559361
## Run 8 stress 0.1371727
## ... Procrustes: rmse 0.00977985  max resid 0.055084
## Run 9 stress 0.1369864
## ... New best solution
## ... Procrustes: rmse 0.004817045  max resid 0.03094354
## Run 10 stress 0.15754
## Run 11 stress 0.1396581
## Run 12 stress 0.1405619
## Run 13 stress 0.1400274
## Run 14 stress 0.140563
## Run 15 stress 0.140516
## Run 16 stress 0.1474197
```

```
## Run 17 stress 0.1441745
## Run 18 stress 0.1412071
## Run 19 stress 0.1369869
## ... Procrustes: rmse 0.000200629  max resid 0.0006816655
## ... Similar to previous best
## Run 20 stress 0.1396639
## *** Best solution repeated 1 times
```
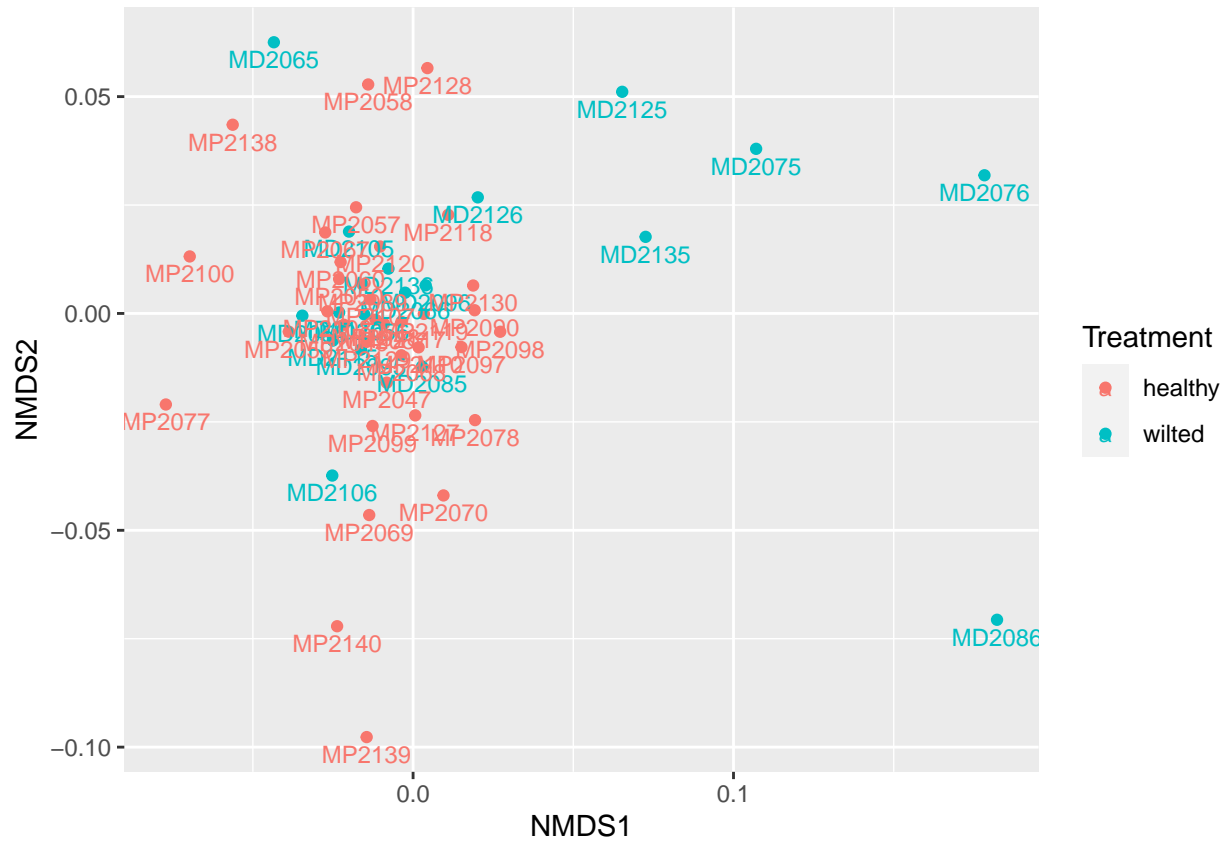


```
Alpha_diversity(merge_Bacteria , 'Family' , 'Treatment')
```
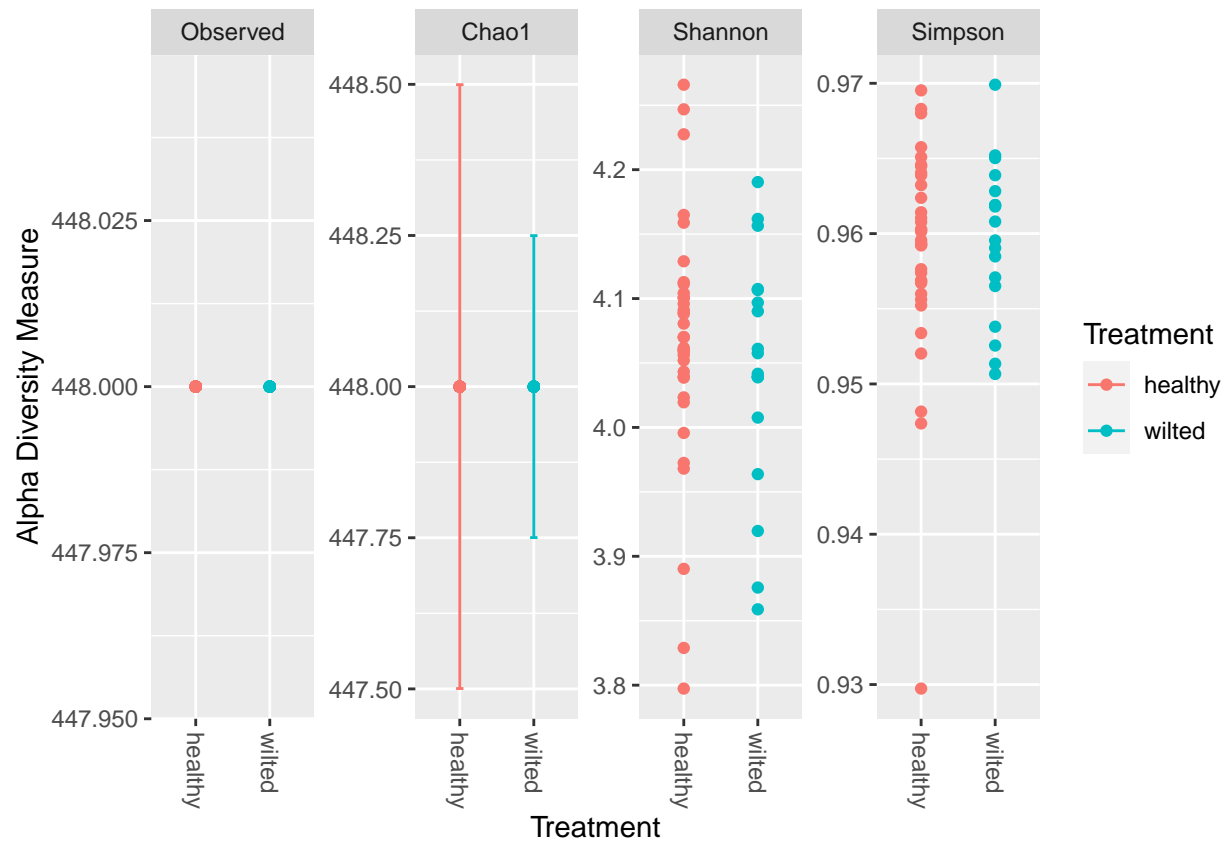
#———Bacteria by Genero

```
Barras_Species <- Abundance_barras(merge_Bacteria,'Genus','Treatment',10.0)
Barras_Species[1]
```

[[1]]

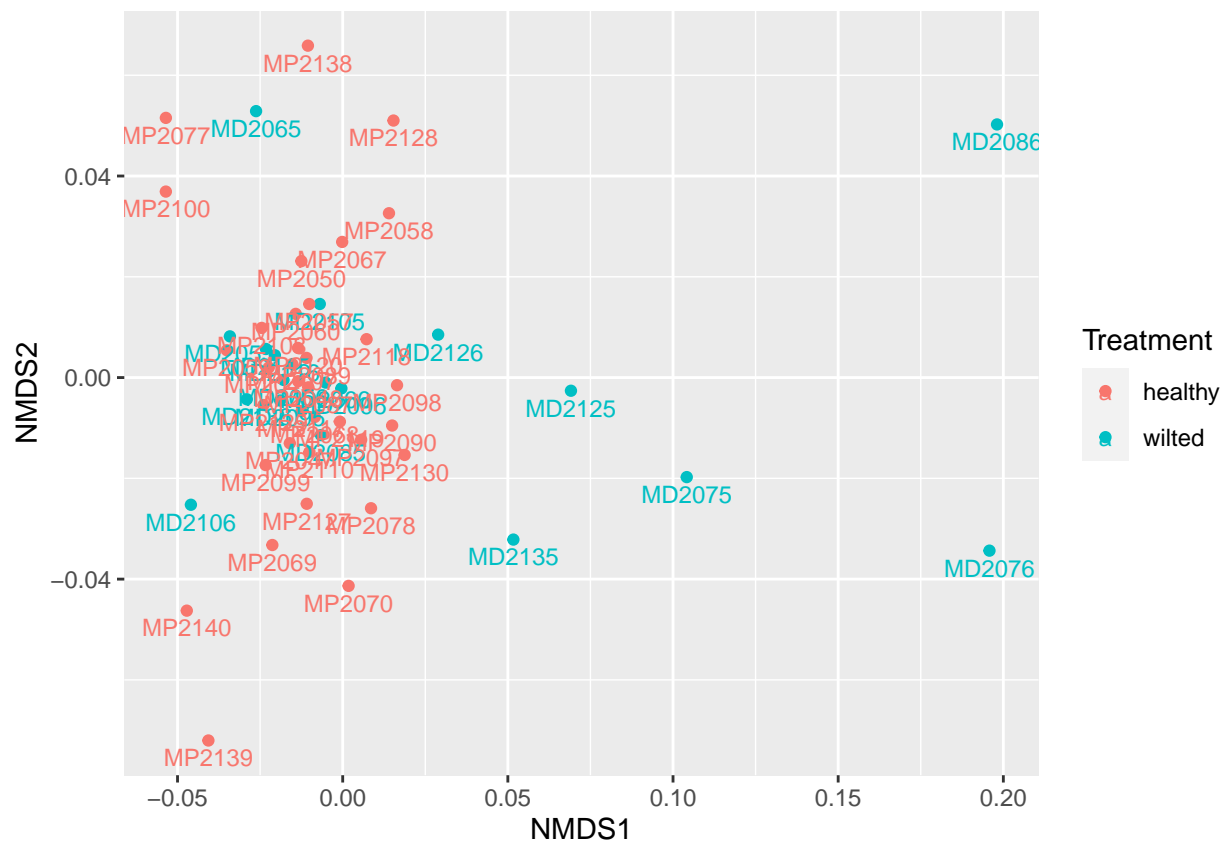|				
lex	Desulfarculus	Labrenzia	Paremcibacter	Subtercola
flexum	Desulfatibacillum	Labrys	Paroceanicella	Succinivibrio
habitans	Desulfitobacterium	Laceyella	Parolsenella	Suicoccus
luna	Desulfobacca	Lachnoanaerobaculum	Parvibaculum	Sulfidibacter
marina	Desulfobacter	Lachnoclostridium	Parvimonas	Sulfitobacter
ncola	Desulfobacula	Lachnospira	Parvularcula	Sulfuricaulis
rhabdus	Desulfobulbus	Lacibacter	Pasteurella	Sulfuricella
rufa	Desulfocapsa	Lacimicrobium	Paucibacter	Sulfuricurvum
salimonas	Desulfococcus	Lacinutrix	Paucilactobacillus	Sulfuriferula
salinus	Desulfocurvibacter	Lacipirellula	Pauljensenia	Sulfuriflexus
sediminimonas	Desulfofarcimen	Lacrimispora	Pectinatus	Sulfurifustis
sphaera	Desulfoglaeba	Lacticaseibacillus	Pectobacterium	Sulfurihydrogenibium
talea	Desulfohalobium	Lactiplantibacillus	Pediococcus	Sulfurimicrobium
iibacter	Desulfoluna	Lactobacillus	Pedobacter	Sulfurimonas
hidicoccus	Desulfolutivibrio	Lactococcus	Pedococcus	Sulfuriroseicoccus
hnia	Desulfomarina	Lacunisphaera	Pelagerythrobacter	Sulfuritalea
nobacterium	Desulfomicrobium	Lancefieldella	Pelagibacterium	Sulfuritortus
angium	Desulfomonile	Lapidilactobacillus	Pelagovum	Sulfurivermis
bacter	Desulfonema	Laribacter	Pelistega	Sulfurospirillum
cibacterium	Desulforamulus	Larkinella	Pelobacter	Sulfurovum
ibacter	Desulforapulum	Latilactobacillus	Pelodictyon	Sutcliffiella
imonas	Desulfosarcina	Lautropia	Pelolinea	Sutterella
natoleum	Desulfoscipio	Lawsonella	Pelosinus	Suttonella
nicicoccus	Desulfosediminicola	Lawsonia	Pengzhenrongella	Swingsia
nophonus	Desulfosporosinus	Leadbetterella	Peptacetobacter	Symbiobacterium
robacter	Desulfosudis	Leclercia	Peptoclostridium	Symmachiella
a	Desulfotalea	Lederbergia	Peptoniphilus	Synechococcus
ccacaulis	Desulfotomaculum	Leeuwenhoekiella	Peribacillus	Synechocystis
lassotoga	Desulfovibrio	Legionella	Periweissella	Syntrophobacter
ntibacter	Desulfurispirillum	Leifsonia	Permianibacter	Syntrophobotulus
obium	Desulfurivibrio	Leisingera	Persephonella	Syntrophomonas
acter	Desulfurobacterium	Lelliottia	Persicimonas	Syntrophotalea
ntiacibacter	Desulfuromonas	Leminorella	Peteryoungia	Syntrophothermus
ntimicrobium	Devosia	Lentibacillus	Petrimonas	Syntrophus
ntimonas	Devriesea	Lentilactobacillus	Petrocella	Tabrizicola
ticoccus	Dialister	Lentilitoribacter	Petrotoga	Tamlana
imonas	Diaminobutyricimonas	Lentzea	Phaeobacter	Tannerella
liella	Diaphorobacter	Leptodesmis	Phascolarctobacterium	Tardibacter
idibacter	Dichelobacter	Leptolyngbya	Phenylobacterium	Tardiphaga
wickia	Dickeya	Leptospira	Phnomibacter	Tateyamaria
acterium	Dictyoglomus	Leptospirillum	Phocaeicola	Tatlockia
rcus	Dietzia	Leptothermofonsia	Phoenicibacter	Tatumella
hizobium	Dinoroseobacter	Leptothrix	Photobacterium	Tautonia
spira	Dissulfurimicrobium	Leptotrichia	Photorhabdus	Taylorella
spirillum	Dissulfurispira	Leucobacter	Phototrophicus	Telmatocola
obacter	Dokdonella	Leuconostoc	Phreatobacter	Tenacibaculum
llus	Dokdonia	Levilactobacillus	Phycicoccus	Tenuifilum
erioplanes	Dolichospermum	Liberibacter	Phycisphaera	Tepidanaerobacter
eriovorax	Dolosigranulum	Lichenicola	Phyllobacterium	Tepidibacter
eroides	Dongshaea	Lichenihabitans	Phytobacter	Tepidiforma
duia	Dorea	Ligilactobacillus	Phytohabitans	Tepidimonas
esiella	Draconibacterium	Lignipirellula	Pigmentiphaga	Tepiditoga
onella	Duganella	Limihaloglobus	Pikeienuella	Terasakiella
ia	Duncaniella	Limnobacter	Pimelobacter	Teredinibacter
lea	Dyadobacter	Limnobaculum	Pirellula	Terribacillus
lovibrio	Dyella	Limnochorda	Pirellulimonas	Terricaulis
giatoa	Dysgonomonas	Limnoglobus	Piscirickettsia	Terriglobus
rinckia	Dysosmobacter	Limnohabitans	Pistricoccus	Terrihabitans

Barras_Species[2]

[[1]]
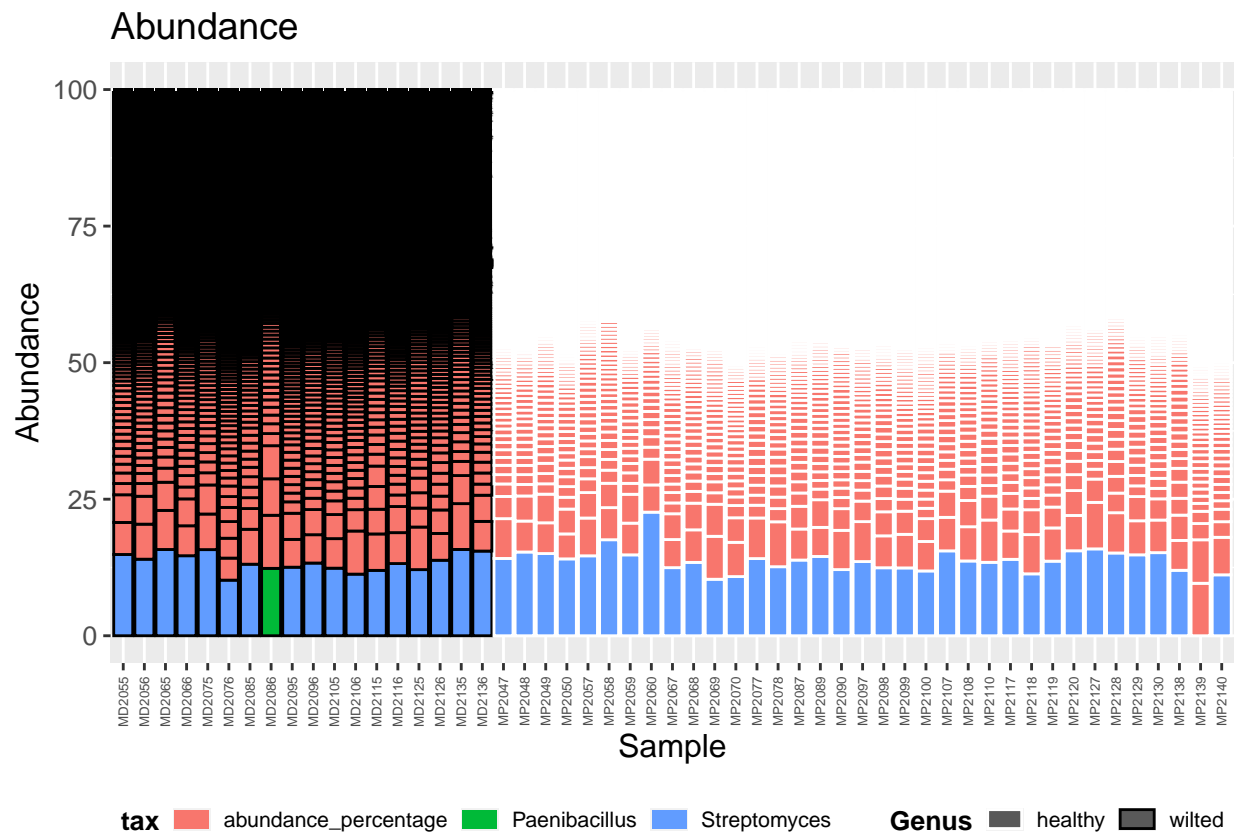
Abundance

```
Beta_diversity(merge_Bacteria , 'Genus' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1467945
## Run 1 stress 0.1467191
## ... New best solution
## ... Procrustes: rmse 0.006994208  max resid 0.0318946
## Run 2 stress 0.1519322
## Run 3 stress 0.1438318
## ... New best solution
## ... Procrustes: rmse 0.06799394  max resid 0.2978133
## Run 4 stress 0.153021
## Run 5 stress 0.1509042
## Run 6 stress 0.1493099
## Run 7 stress 0.1496769
## Run 8 stress 0.1511171
## Run 9 stress 0.1439572
## ... Procrustes: rmse 0.05561392  max resid 0.3037726
## Run 10 stress 0.1490814
## Run 11 stress 0.1432832
## ... New best solution
## ... Procrustes: rmse 0.04881375  max resid 0.2908548
## Run 12 stress 0.151198
## Run 13 stress 0.1432835
## ... Procrustes: rmse 0.0002963102  max resid 0.00120805
```

```
## ... Similar to previous best
## Run 14 stress 0.1505586
## Run 15 stress 0.1441257
## Run 16 stress 0.1452
## Run 17 stress 0.1556212
## Run 18 stress 0.1458782
## Run 19 stress 0.1432847
## ... Procrustes: rmse 0.0006905785  max resid 0.002935408
## ... Similar to previous best
## Run 20 stress 0.1433194
## ... Procrustes: rmse 0.002855445  max resid 0.01756279
## *** Best solution repeated 2 times
```
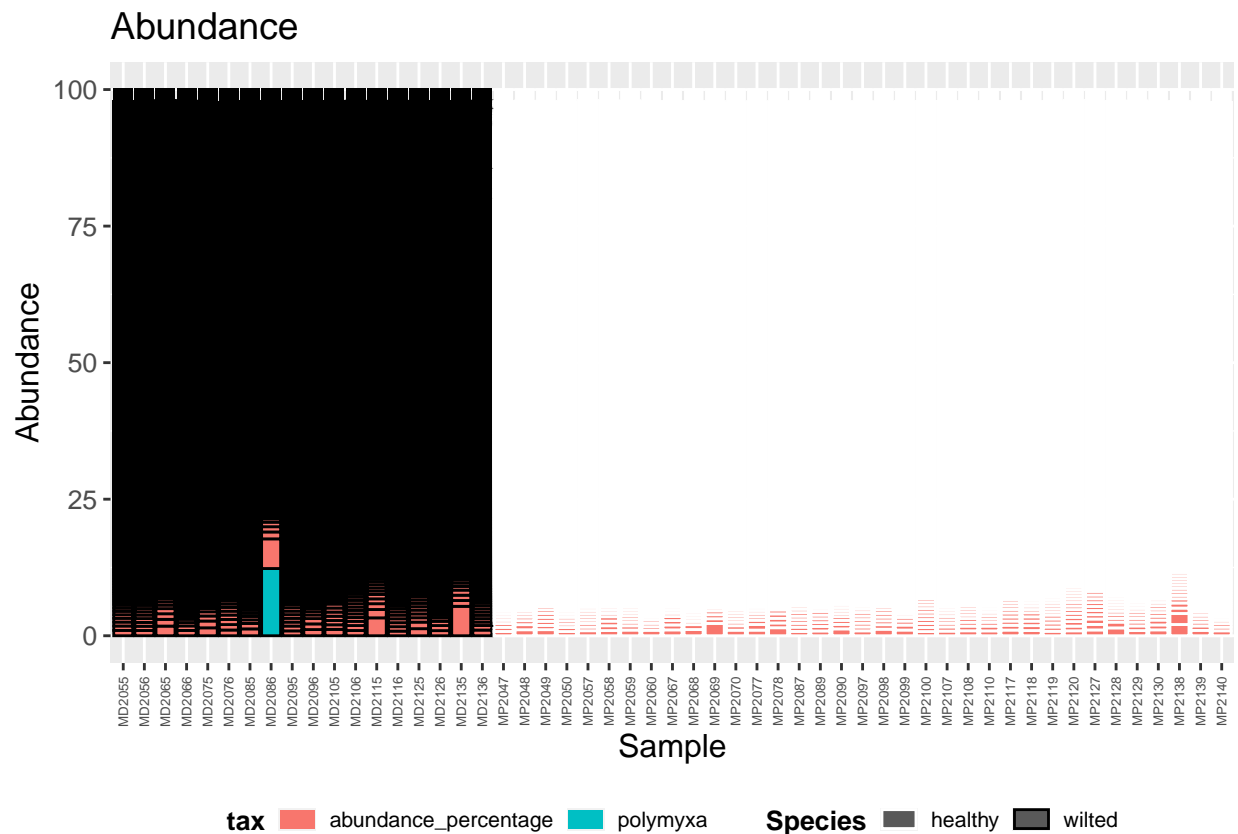


```
Alpha_diversity(merge_Bacteria , 'Genus' , 'Treatment')
```

#———Bacteria by Species

```r
Barras_Species <- Abundance_barras(merge_Bacteria,'Species','Treatment',10.0)
Barras_Species[1]
```

[[1]]

lactamica
lactarius
lactatifermentans
lactatiformans
lactis
lactucae
lacunae
lacus
lacuslunae
lacustris
laguerreae
laidlawii
laixinhei
lalkuanensis
laminatus
lanienae
lanii
lansingensis
lanthieri
lapagei
lapidicaptus
lapsinanis
lari
lariciata
larrymoorei
larvae
lata
latens
laterosporus
laumondii
lautus
lavamentivorans
lavendulae
leachii
leadbetteri
leeuwenhoekii
leguminosarum
lehensis
lekithochrous
lemovicicum
lemurum
lenghuensis
lenta
lentiflavum
lentis
lentocellum
lentus
leopoldii
leprae
lepromatosis
leptomitoformis
lettingae
liangguodongii
liangshanensis
liaowanqingii
libanensis
licheniformis

sp. 'Soap Lake #7'
sp. (Blaberus giganteus)
sp. (Blatta orientalis)
sp. (Blattella germanica)
sp. (Cryptocercus kyebangensis)
sp. (Cryptocercus punctulatus) str. Cpu
sp. (ex Adelges kitamiensis)
sp. (ex Biomphalaria glabrata)
sp. (Mastotermes darwiniensis)
sp. (Nauphoeta cinerea)
sp. (Periplaneta americana)
sp. 001
sp. 007
sp. 008
sp. 02C 26
sp. 09C 129
sp. 09RB8471
sp. 09RB8910
sp. 1_2014MBL_MicDiv
sp. 1_2015MBL_MicDiv
sp. 1-1C
sp. 1.5R
sp. 1(2017)
sp. 103DPR2
sp. 1063
sp. 107-1
sp. 1070
sp. 10FS3-1
sp. 10M-3C3
sp. 10RB9215
sp. 11-1-2
sp. 11-B-312
sp. 113-1-2
sp. 113-3-3
sp. 113-3-9
sp. 1137
sp. 113P3
sp. 114
sp. 11515TR
sp. 116-D4
sp. 119287
sp. 11B
sp. 11kri321
sp. 12200R-103
sp. 13-15
sp. 131
sp. 131-2-1
sp. 131-2-5
sp. 131-3-5
sp. 13159349
sp. 135
sp. 140616W15
sp. 14171R-50
sp. 14181154
sp. 143-21
sp. 144S4
sp. 15-184

sp. KSB-15
sp. KSM-R2A25
sp. KSM-R2A30
sp. KT 15
sp. KT25b
sp. KTR9
sp. KUDC0405
sp. KUDC0406
sp. KUDC1026
sp. KUDC1714
sp. KUIN-1
sp. Kuro-4
sp. KW1
sp. KX20019
sp. KY-GH-1
sp. KY-YJ-3
sp. KY3
sp. KY5
sp. KY70
sp. KY75
sp. L-07
sp. L-2-11
sp. L-8-10
sp. L-8-3
sp. L-A4
sp. L12M9
sp. L1A13
sp. L1A34
sp. L1A9
sp. L1I39
sp. L1SW
sp. L2A1
sp. L2A11
sp. L3-i22
sp. L3-i23
sp. L3A3
sp. L3A6
sp. L3A8
sp. L5
sp. L51/94
sp. L5B5
sp. L6-1
sp. L9-4
sp. LA-2-3-30-S1-D2
sp. LA112445
sp. LA31
sp. LAB-08
sp. LADL05-105
sp. LAS2
sp. LB1
sp. LBG001
sp. LBUM 1475
sp. LBUM 1480
sp. LBUM 1482
sp. LBUM920
sp. LC2018020214
sp. LC6

sp. X
sp. X
sp. X
sp. X
sp. X
sp. X
sp. X
sp. X
sp. X
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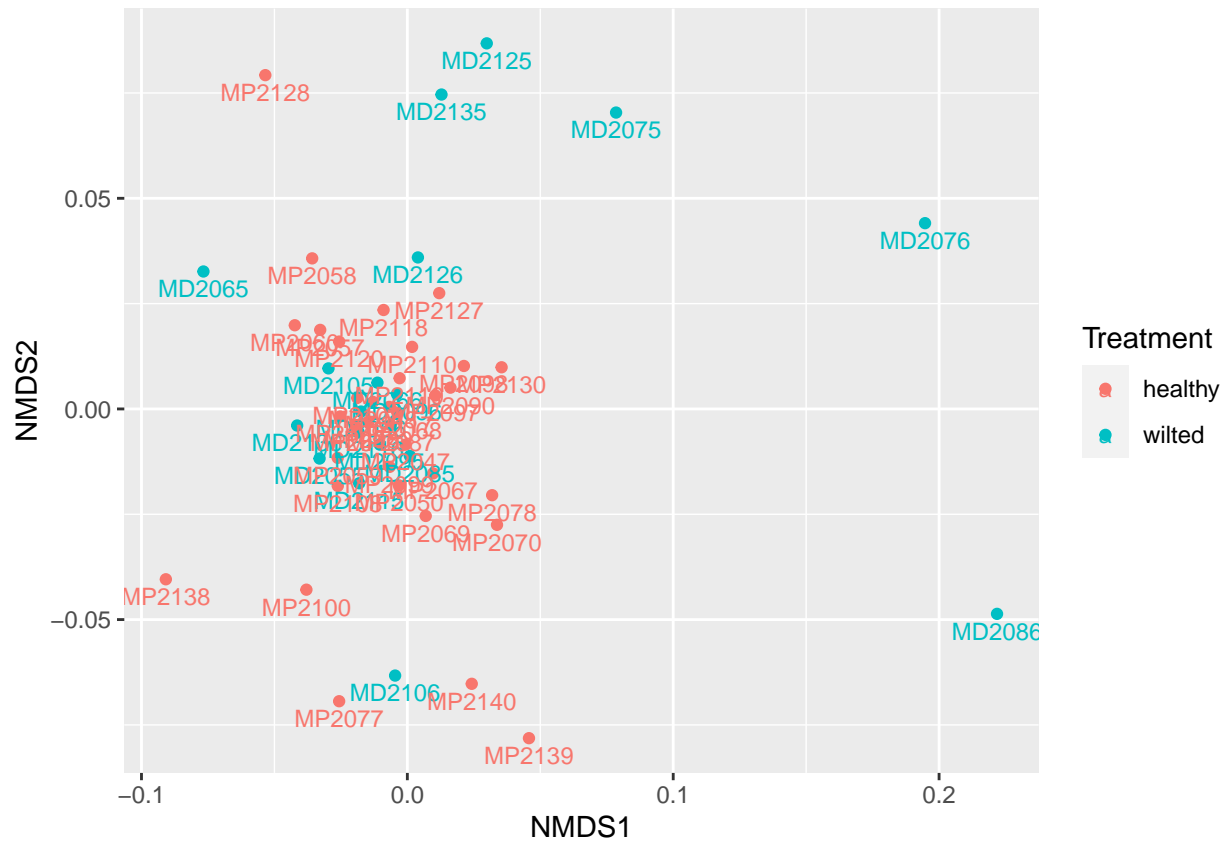sp. Y
sp. Y

Barras_Species[2]

[[1]]

```
Beta_diversity(merge_Bacteria , 'Species' , 'Treatment', 'bray')
```

```
## Wisconsin double standardization
## Run 0 stress 0.1597841
## Run 1 stress 0.1576521
## ... New best solution
## ... Procrustes: rmse 0.04834007  max resid 0.2875313
## Run 2 stress 0.183516
## Run 3 stress 0.164273
## Run 4 stress 0.1706613
## Run 5 stress 0.1577447
## ... Procrustes: rmse 0.03589464  max resid 0.1614319
## Run 6 stress 0.1766066
## Run 7 stress 0.1571296
## ... New best solution
## ... Procrustes: rmse 0.02695248  max resid 0.1420126
## Run 8 stress 0.171069
## Run 9 stress 0.1590799
## Run 10 stress 0.1745134
## Run 11 stress 0.1809985
## Run 12 stress 0.161869
## Run 13 stress 0.16364
## Run 14 stress 0.1602454
## Run 15 stress 0.1670562
## Run 16 stress 0.160579
```

```
## Run 17 stress 0.1590695
## Run 18 stress 0.1582786
## Run 19 stress 0.1705433
## Run 20 stress 0.1780395
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      2: no. of iterations >= maxit
##     18: stress ratio > sratmax
```



```
Alpha_diversity(merge_Bacteria , 'Species' , 'Treatment')
```