

Statistical analyses and plotting for experiments related to the effects of secondary metabolites produced by *Xylaria necrophora* on soybean leaves

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Install packages needed.

First, create a vector of all the packages needed:

```
packages <- c("agricolae", "dplyr", "plyr", "ggplot2", "readr", "ggpubr", "car",  
             "rcompanion", "tidyverse", "ggsignif", "reshape", "rmdformats")
```

Install packages not yet installed

```
installed_packages <- packages %in% rownames(installed.packages())  
if (any(installed_packages == FALSE)) {  
  install.packages(packages[!installed_packages])  
}
```

Load all packages

```
invisible(lapply(packages, library, character.only = TRUE))
```

```
## Warning: package 'dplyr' was built under R version 4.0.5
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## intersect, setdiff, setequal, union
```

```

## -----

## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)

## -----

##
## Attaching package: 'plyr'

## The following objects are masked from 'package:dplyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize

## Warning: package 'readr' was built under R version 4.0.5

##
## Attaching package: 'ggpubr'

## The following object is masked from 'package:plyr':
##
##   mutate

## Loading required package: carData

## Warning: package 'carData' was built under R version 4.0.5

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##   recode

## -- Attaching packages ----- tidyverse 1.3.1 --

## v tibble  3.1.6      v stringr 1.4.0
## v tidyr   1.2.0      v forcats 0.5.1
## v purrr   0.3.4

## Warning: package 'tidyr' was built under R version 4.0.5

## -- Conflicts ----- tidyverse_conflicts() --
## x plyr::arrange() masks dplyr::arrange()
## x purrr::compact() masks plyr::compact()
## x plyr::count() masks dplyr::count()
## x plyr::failwith() masks dplyr::failwith()
## x dplyr::filter() masks stats::filter()

```

```
## x plyr::id()          masks dplyr::id()
## x dplyr::lag()        masks stats::lag()
## x ggpubr::mutate()    masks plyr::mutate(), dplyr::mutate()
## x car::recode()       masks dplyr::recode()
## x plyr::rename()      masks dplyr::rename()
## x purrr::some()       masks car::some()
## x plyr::summarise()   masks dplyr::summarise()
## x plyr::summarize()   masks dplyr::summarize()

##
## Attaching package: 'reshape'

## The following objects are masked from 'package:tidyr':
##
##     expand, smiths

## The following objects are masked from 'package:plyr':
##
##     rename, round_any

## The following object is masked from 'package:dplyr':
##
##     rename
```

Set the working directory to the directory where the output files will be saved.

In this example, we assume you have cloned/downloaded this repository to your “Documents” folder.

Change directory on mac/linux:

```
setwd("/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output")
```

Change directory on Windows (Windows 10 in this example):

```
setwd("C:/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output")
```

For this demonstration, we did not export the files in PDF to the output directory. If you wish to do so, do the following:

Step 1: Call the pdf command to start the plot

```
pdf(file = "/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output/
Figure1.pdf", # The directory you want to save the file in

width = 7, # The width of the plot in inches

height = 5) # The height of the plot in inches
```

Step 2: Add the code provided below for your desired plot.

Step 3: Run `dev.off()` to create the file!

```
dev.off()
```

For this example, we set the working directory to the following:

```
setwd("/Users/tedggarcia/Documents/Xylaria.Mycotoxins.2020/Manuscript/Submission/GitHubRepository/X.nec")
```

Loading digital chlorophyll content datasets (only one repetition of each experiment for illustration purposes). All datasets can be found in the folder named “raw_data”

ES2 = First experiment for 14 Days of exposure (DOE)

#ES4 = Repetition for 14 DOE

ES5 = First experiment for 7 DOE

#ES8 = Repetition for 7 DOE

#ES13A = Experiment testing potentially resistant cultivars (7DOE)

ES13B = Repetition of ES13A

ES14A = Experiment testing effects among plant species (7DOE)

#ES14B = Repetition of ES14A

```
ES2 <- read.csv("../raw_data/ES2.ChlorophyllContent.14DOE.Exp1.csv", header = T)
ES5 <- read.csv("../raw_data/ES5.ChlorophyllContent.7DOE.Exp1.csv", header = T)
ES13B <- read.csv("../raw_data/ES13B.ChlorophyllContent.7DOE.Exp2.Cultivars.csv",
                  header = T)
ES14A <- read.csv("../raw_data/ES14A.ChlorophyllContent.7DOE.Exp1.PlantSpecies.csv",
                  header = T)
```

Run Shapiro-Wilk Tests to check for normality

```
shapiro.test(ES2$chl)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  ES2$chl
## W = 0.74674, p-value < 2.2e-16
```

```
shapiro.test(ES5$chl)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: ES5$chl  
## W = 0.95514, p-value = 5.341e-10
```

```
shapiro.test(ES13B$chl)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: ES13B$chl  
## W = 0.95496, p-value = 2.7e-07
```

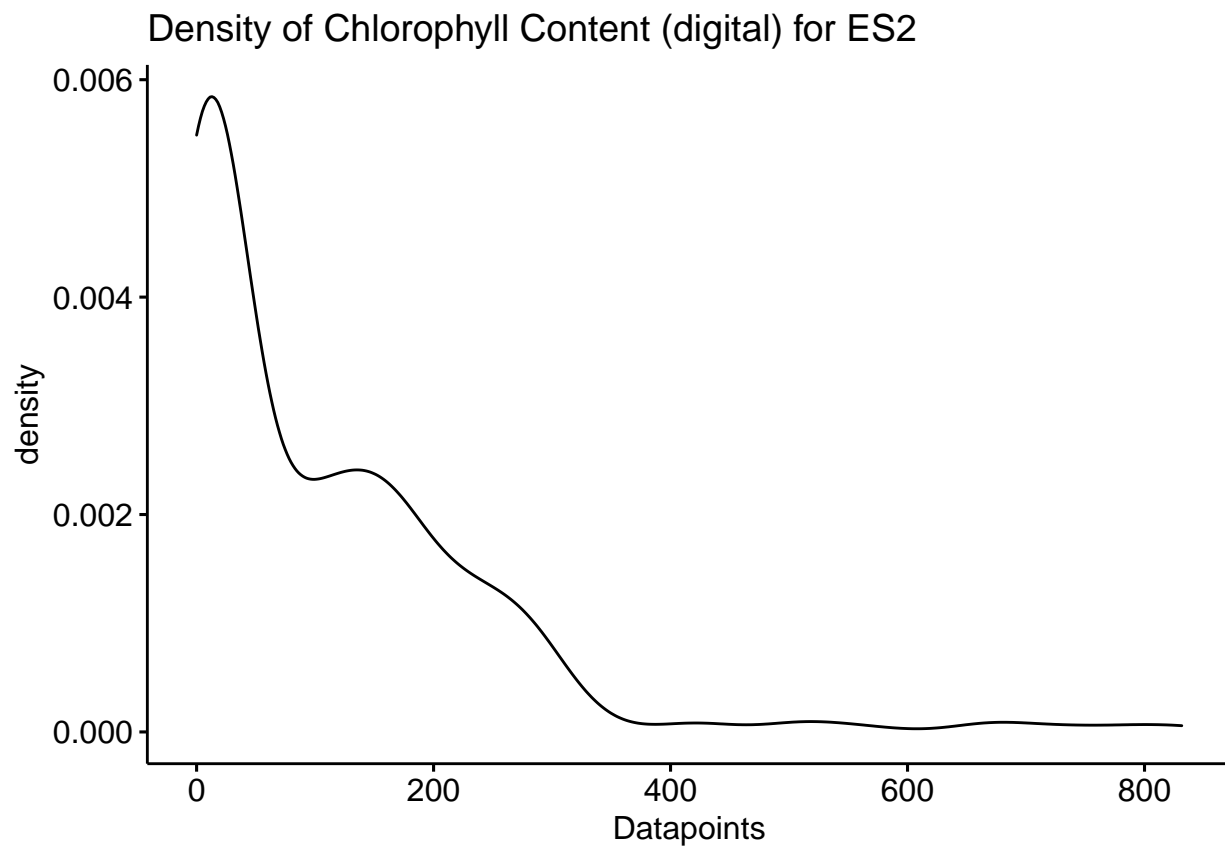
```
shapiro.test(ES14A$chl)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: ES14A$chl  
## W = 0.95203, p-value = 1.513e-06
```

Check the distribution of the data and assess if normalization is needed.

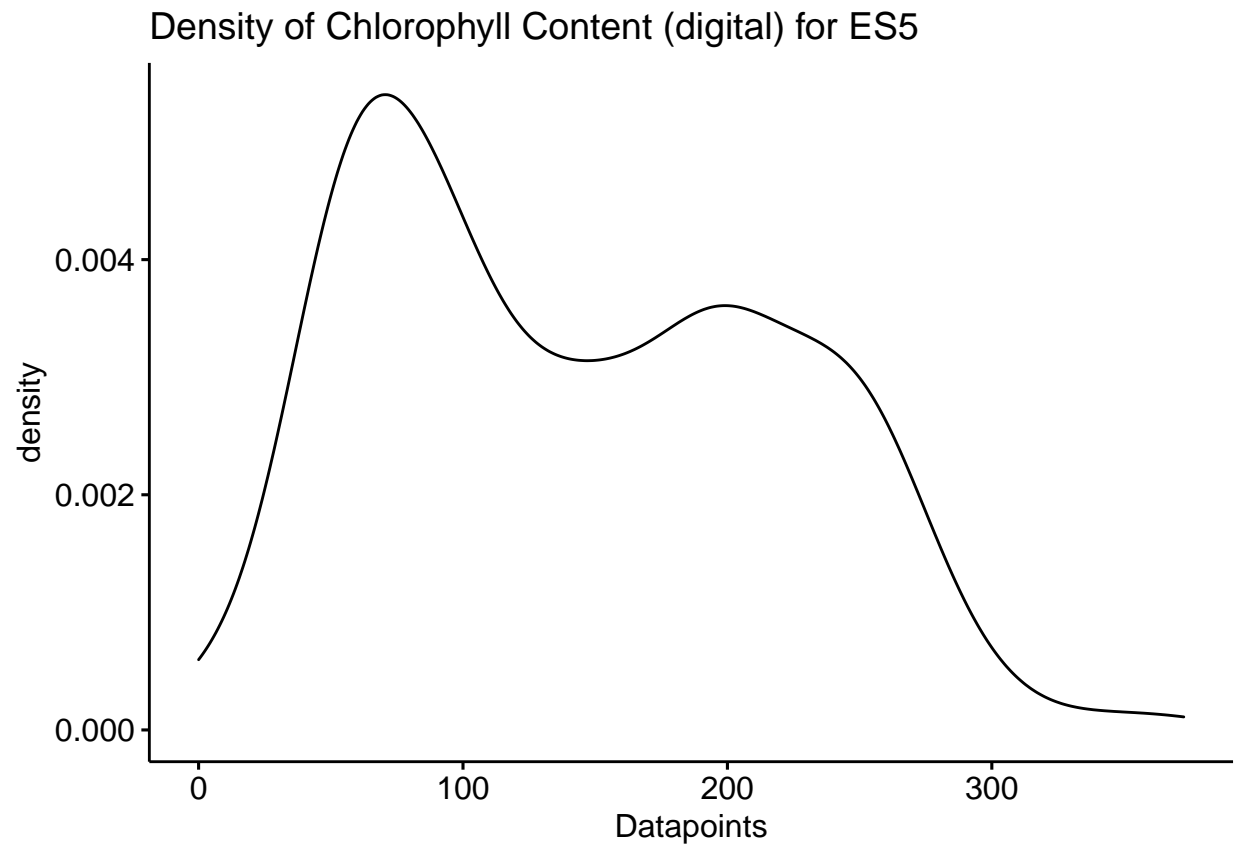
```
ggdensity(ES2$chl, main = "Density of Chlorophyll Content (digital) for ES2",  
           xlab = "Datapoints")
```

```
## Warning: Removed 60 rows containing non-finite values (stat_density).
```



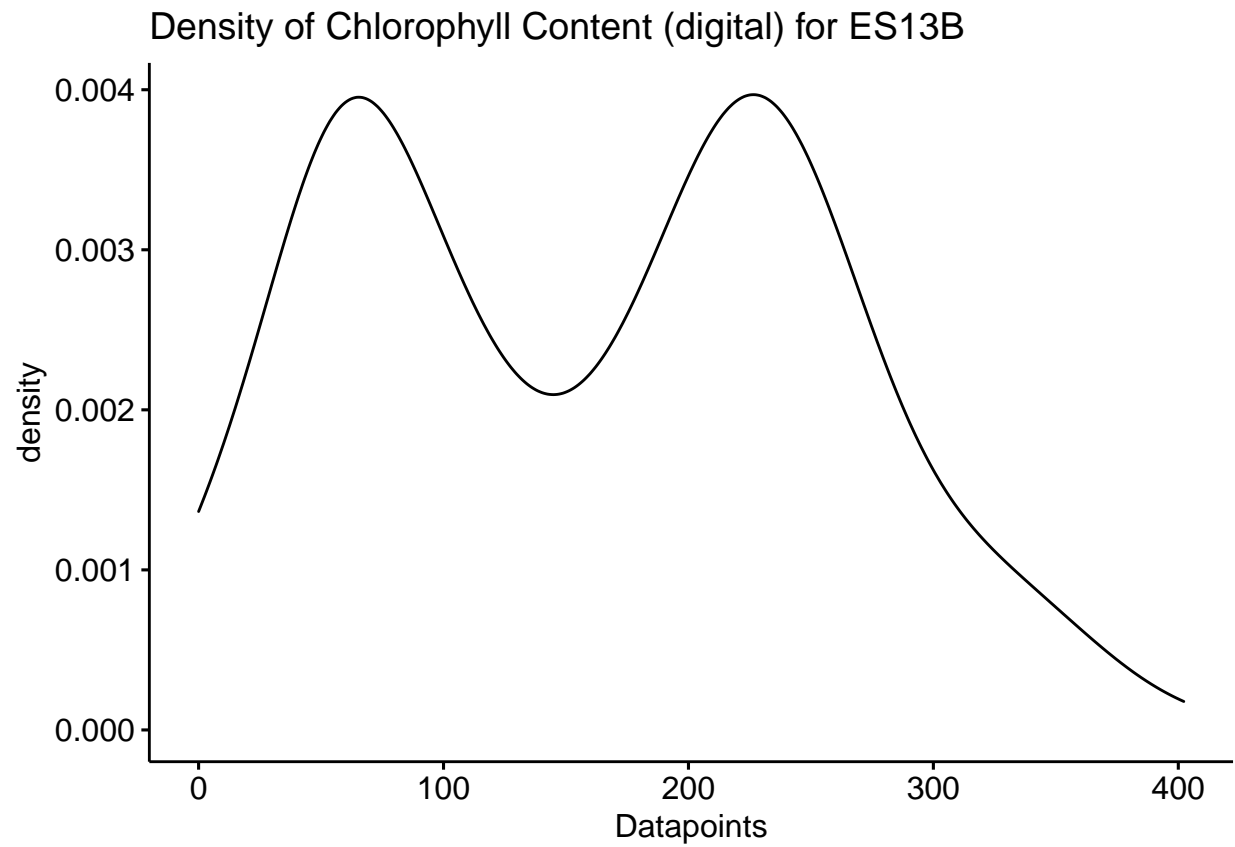
```
ggdensity(ES5$chl, main = "Density of Chlorophyll Content (digital) for ES5",  
          xlab = "Datapoints")
```

```
## Warning: Removed 12 rows containing non-finite values (stat_density).
```



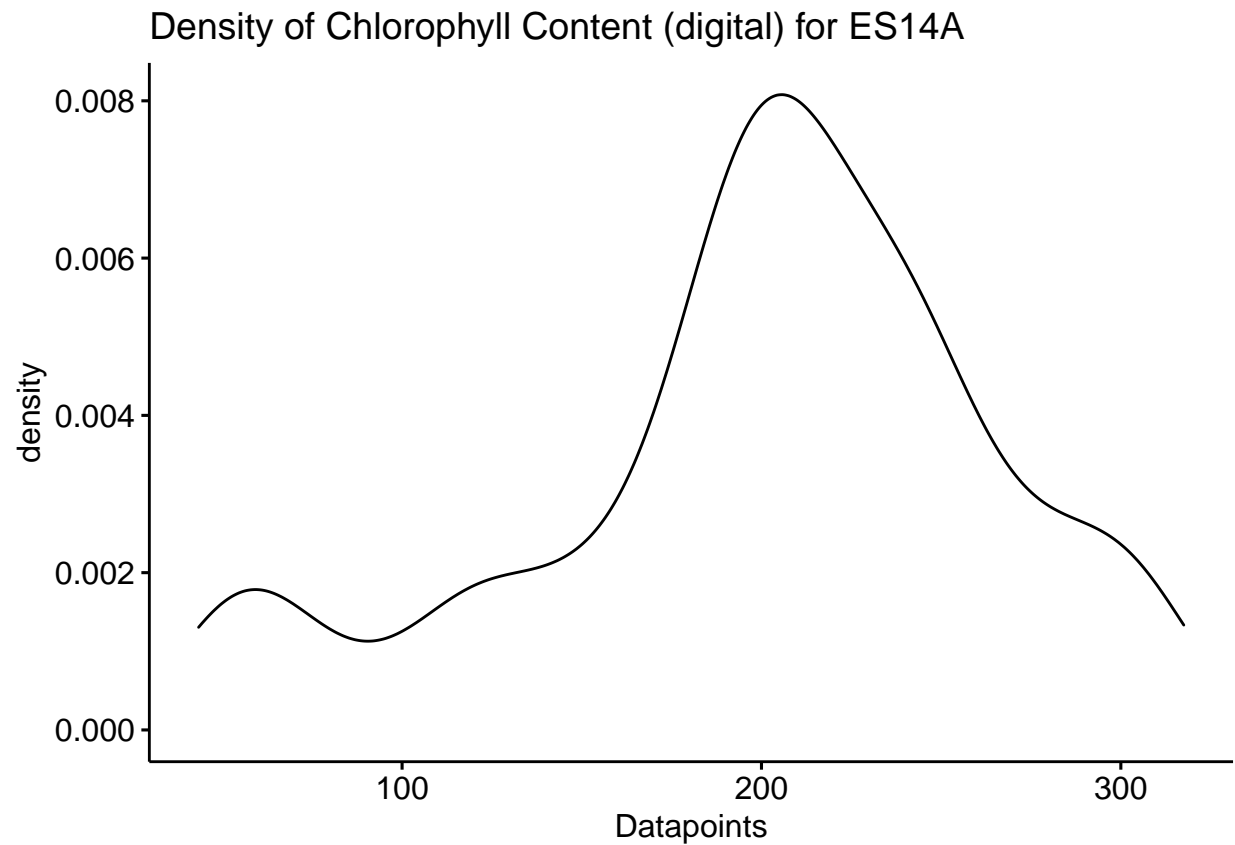
```
ggdensity(ES13B$chl, main = "Density of Chlorophyll Content (digital) for ES13B",  
          xlab = "Datapoints")
```

```
## Warning: Removed 6 rows containing non-finite values (stat_density).
```



```
ggdensity(ES14A$chl, main = "Density of Chlorophyll Content (digital) for ES14A",  
          xlab = "Datapoints")
```

```
## Warning: Removed 3 rows containing non-finite values (stat_density).
```

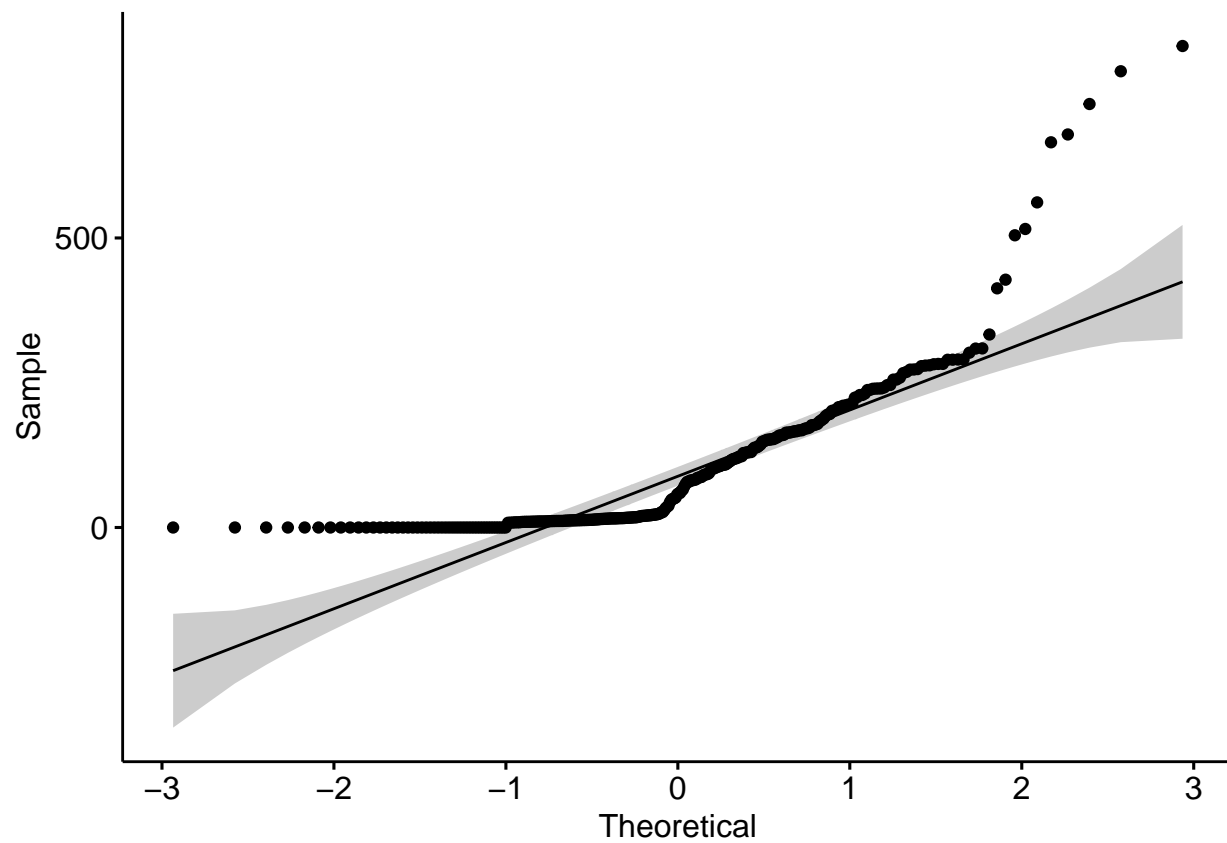



```
ggqqplot(ES2$chl)
```

```
## Warning: Removed 60 rows containing non-finite values (stat_qq).
```

```
## Warning: Removed 60 rows containing non-finite values (stat_qq_line).
```

```
## Removed 60 rows containing non-finite values (stat_qq_line).
```

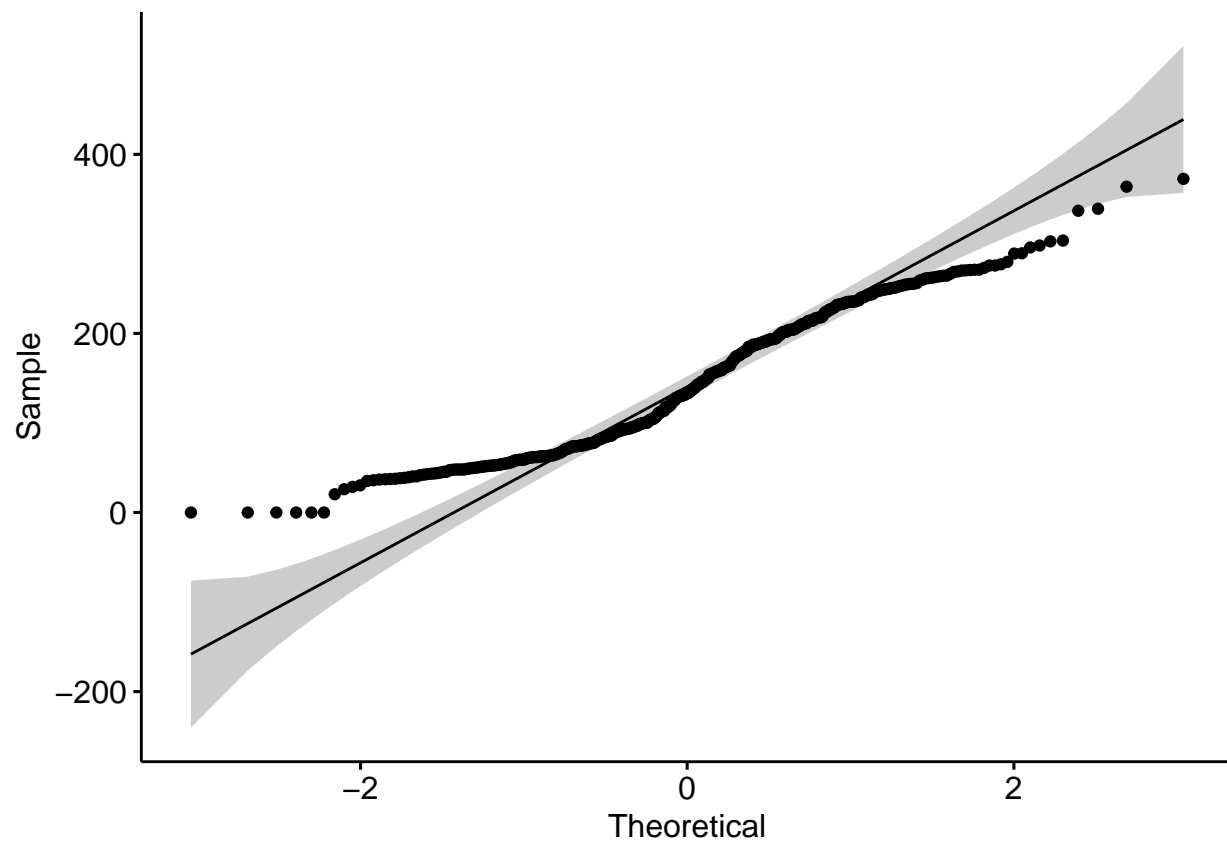


```
ggqqplot(ES5$ch1)
```

```
## Warning: Removed 12 rows containing non-finite values (stat_qq).
```

```
## Warning: Removed 12 rows containing non-finite values (stat_qq_line).
```

```
## Removed 12 rows containing non-finite values (stat_qq_line).
```

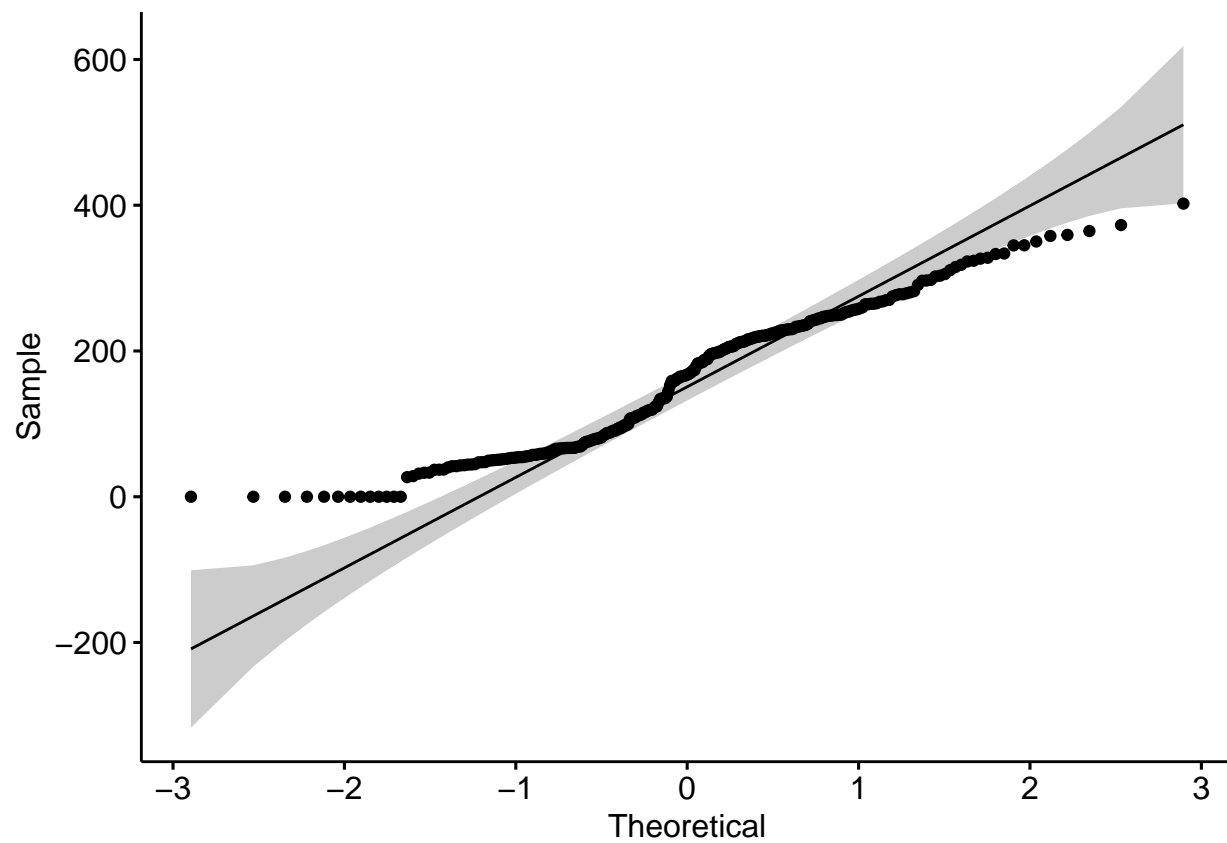


```
ggqqplot(ES13B$chl)
```

```
## Warning: Removed 6 rows containing non-finite values (stat_qq).
```

```
## Warning: Removed 6 rows containing non-finite values (stat_qq_line).
```

```
## Removed 6 rows containing non-finite values (stat_qq_line).
```

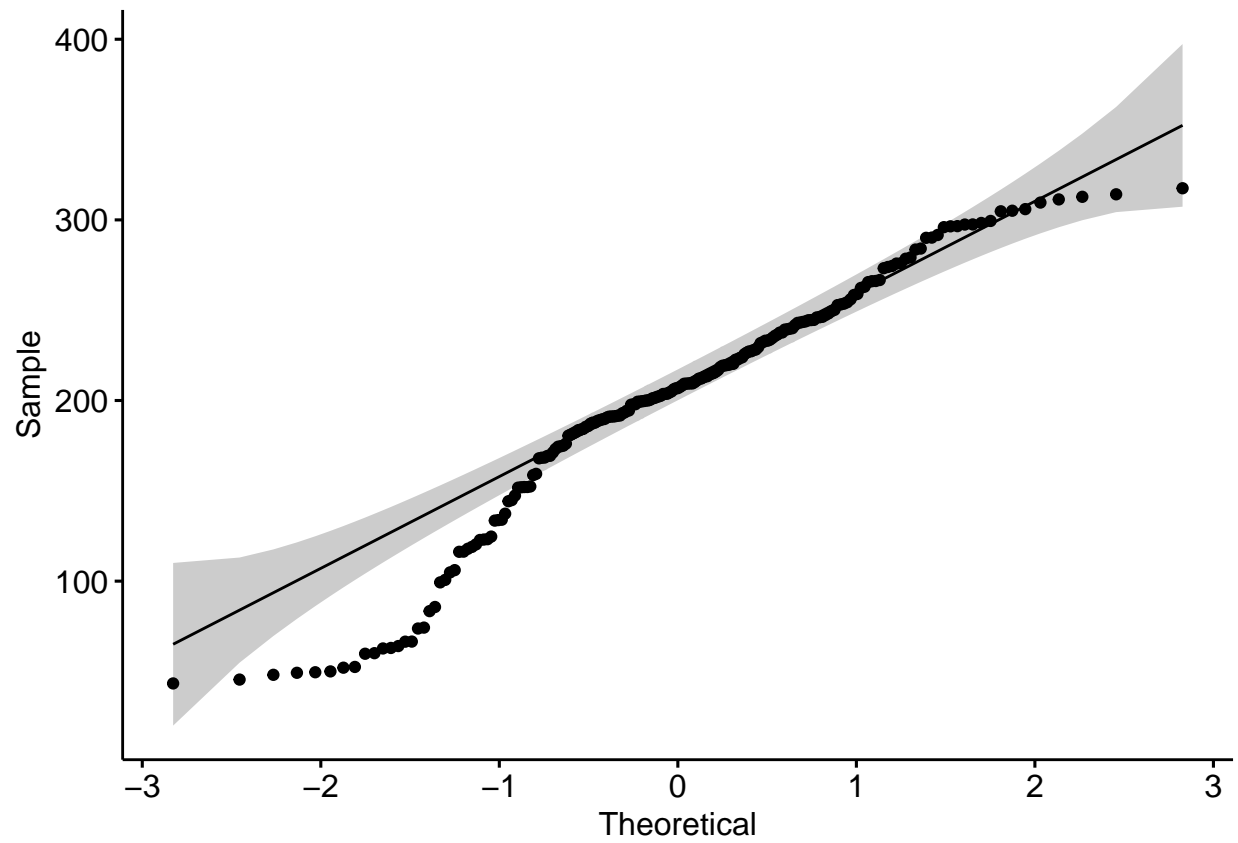


```
ggqqplot(ES14A$chl)
```

```
## Warning: Removed 3 rows containing non-finite values (stat_qq).
```

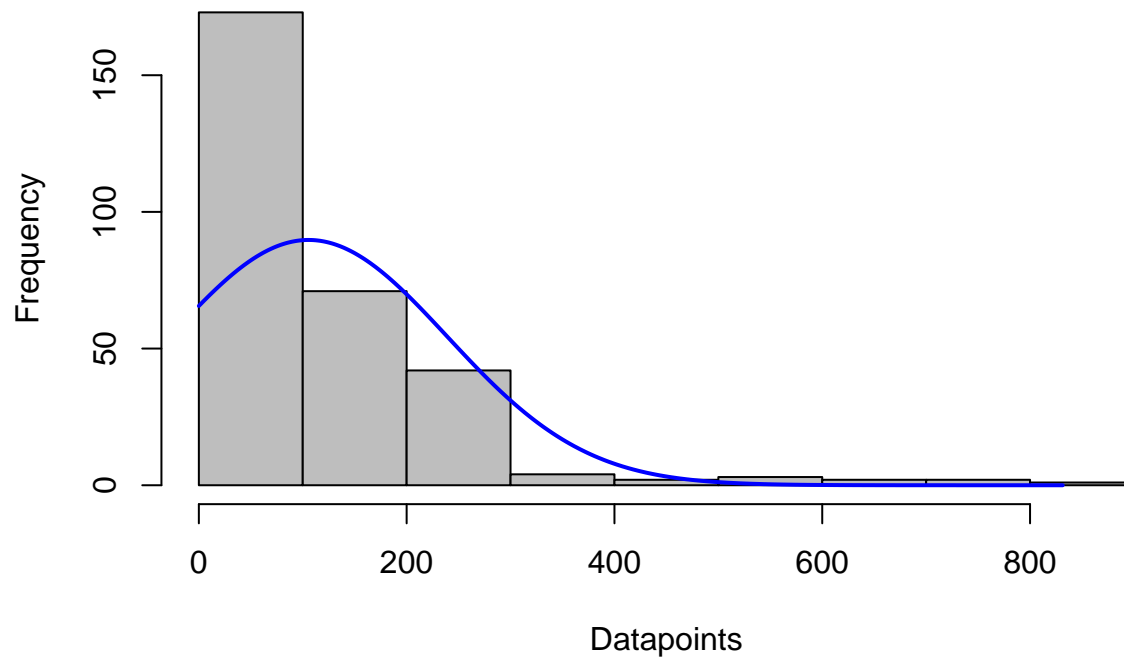
```
## Warning: Removed 3 rows containing non-finite values (stat_qq_line).
```

```
## Removed 3 rows containing non-finite values (stat_qq_line).
```



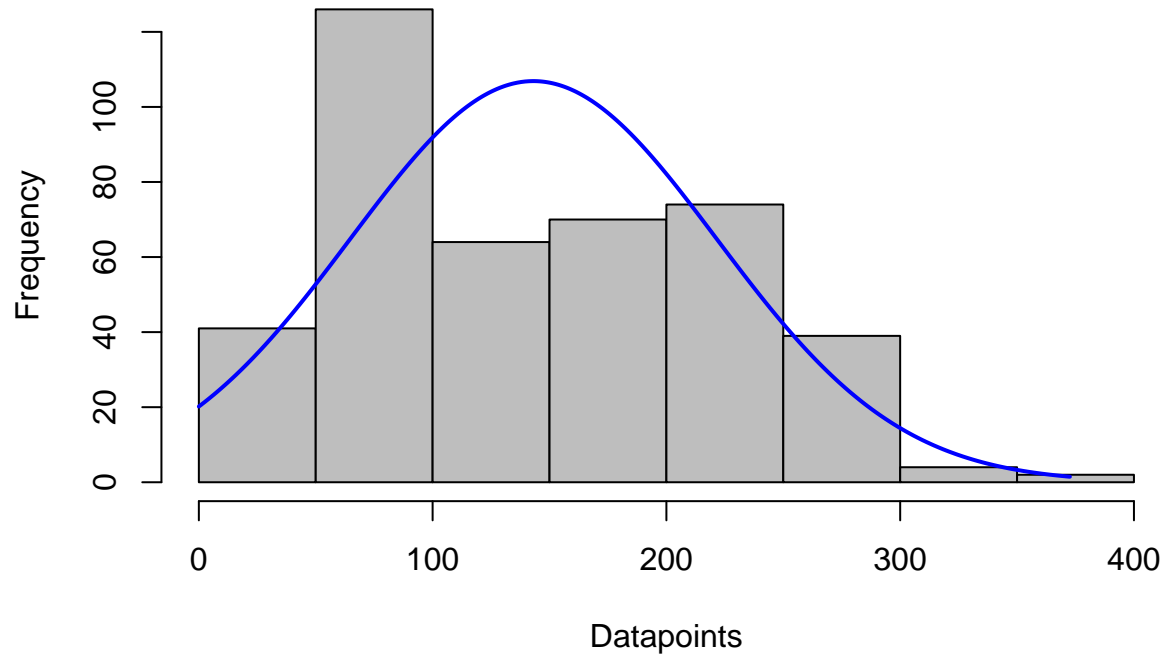
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES2



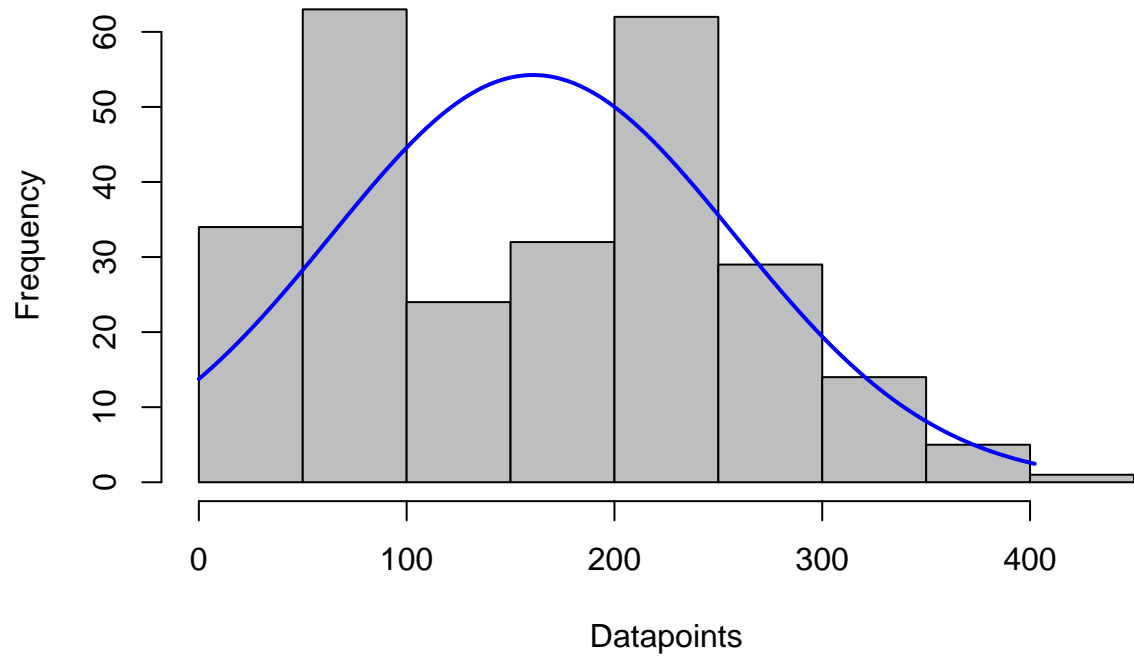
```
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES5



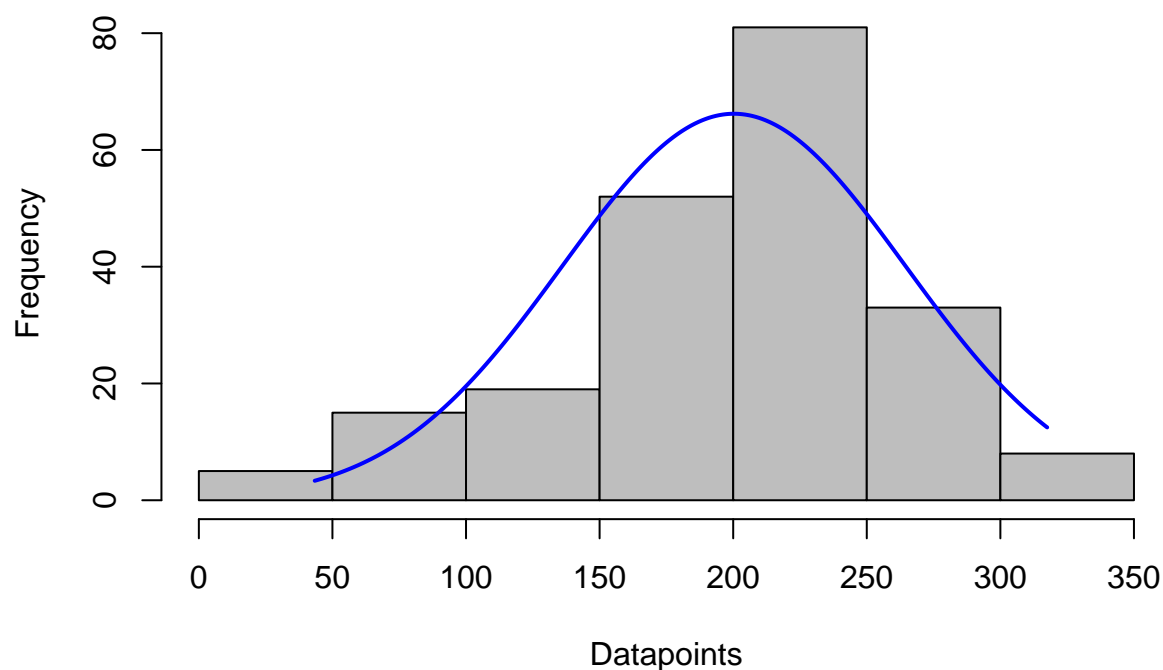
```
plotNormalHistogram(ES13B$chl, main = "Density of Chlorophyll Content (Digital) for E13B",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for E13B



```
plotNormalHistogram(ES14A$chl, main = "Density of Chlorophyll Content (Digital) for E14A",  
  xlab = "Datapoints")
```


Density of Chlorophyll Content (Digital) for E14A



Use the Tukey's tranformation method to normalize the distribution and append to datasets

```
ES2_ch1.tuk = transformTukey(ES2$ch1, plotit=FALSE)
```

```
##
##      lambda      W Shapiro.p.value
## 416  0.375 0.9449      3.664e-09
##
## if (lambda > 0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}
```

```
ES5_ch1.tuk = transformTukey(ES5$ch1, plotit=FALSE)
```

```
##
##      lambda      W Shapiro.p.value
## 427  0.65 0.9695      1.098e-07
##
## if (lambda > 0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}
```

```
ES13B_chl.tuk = transformTukey(ES13B$chl, plotit=FALSE)
```

```
##
##      lambda      W Shapiro.p.value
## 432  0.775 0.9604      1.226e-06
##
## if (lambda > 0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}
```

```
ES14A_chl.tuk = transformTukey(ES14A$chl, plotit=FALSE)
```

```
##
##      lambda      W Shapiro.p.value
## 470  1.725 0.979      0.00282
##
## if (lambda > 0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}
```

Append the transformed values to original datasets

```
ES2.mod <- cbind(ES2, ES2_chl.tuk)
ES5.mod <- cbind(ES5, ES5_chl.tuk)
ES13B.mod <- cbind(ES13B, ES13B_chl.tuk)
ES14A.mod <- cbind(ES14A, ES14A_chl.tuk)
```

Statistical analyses

Run ANOVA and Tukey's honest significance differences for raw chlorophyll content.

ES2 dataset (untransformed data)

As described above, this experiment was ran using cell-free culture filtrates (CFCFs) from three local strains of *Xylaria necrophora* (DMCC2126, DMCC2127, and DMCC2165) and one *Colletotrichum siamense* (DMCC2966) for 14 days (ES2)

```
##Extract all control (ES2), colletrichum, and X. necrophora
ES2.control <- subset(ES2.mod, Treatment== "control")
ES2.coll <- subset(ES2.mod, Treatment== "DMCC2966")
ES2.Xn <- subset(ES2.mod, Treatment== c("DMCC2126", "DMCC2127", "DMCC2165"))

ES2.control <- ES2.control %>%
  add_column(Species = "control")

ES2.coll <- ES2.coll %>%
  add_column(Species = "C.siamense")
```

```

ES2.Xn <- ES2.Xn %>%
  add_column(Species = "X.necrophora")

ES2.mod.v2 <- rbind(ES2.control, ES2.coll, ES2.Xn)

#Run ANOVA

ES2.mod.v2.lm <- lm (ES2.mod.v2$chl ~ ES2.mod.v2$Species +
                    ES2.mod.v2$Dilution +
                    ES2.mod.v2$Condition +
                    ES2.mod.v2$isoRep +
                    ES2.mod.v2$techRep +
                    ES2.mod.v2$sampleNumber)

ES2.mod.v2.lm

##
## Call:
## lm(formula = ES2.mod.v2$chl ~ ES2.mod.v2$Species + ES2.mod.v2$Dilution +
##     ES2.mod.v2$Condition + ES2.mod.v2$isoRep + ES2.mod.v2$techRep +
##     ES2.mod.v2$sampleNumber)
##
## Coefficients:
##              (Intercept)          ES2.mod.v2$Speciescontrol
##                   190.37                   42.37
## ES2.mod.v2$SpeciesX.necrophora    ES2.mod.v2$Dilution25fold
##                   -120.68                   -119.47
## ES2.mod.v2$ConditionStationary    ES2.mod.v2$isoRepisolateRep2
##                   -31.14                   32.50
##      ES2.mod.v2$techRepStem2      ES2.mod.v2$techRepStem3
##                   -27.84                   49.82
## ES2.mod.v2$sampleNumbersample2    ES2.mod.v2$sampleNumbersample3
##                   32.77                   39.91

summary(ES2.mod.v2.lm)

##
## Call:
## lm(formula = ES2.mod.v2$chl ~ ES2.mod.v2$Species + ES2.mod.v2$Dilution +
##     ES2.mod.v2$Condition + ES2.mod.v2$isoRep + ES2.mod.v2$techRep +
##     ES2.mod.v2$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -248.96  -74.34   -0.74   59.70  514.77
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      190.37     27.55   6.910 9.90e-11 ***
## ES2.mod.v2$Speciescontrol      42.37     22.05   1.921  0.0564 .
## ES2.mod.v2$SpeciesX.necrophora -120.68     22.05  -5.474 1.60e-07 ***
## ES2.mod.v2$Dilution25fold    -119.47     18.18  -6.571 6.17e-10 ***

```

```
## ES2.mod.v2$ConditionStationary    -31.14      18.18  -1.713   0.0885 .
## ES2.mod.v2$isoRepisolateRep2      32.50      18.14   1.791   0.0750 .
## ES2.mod.v2$techRepStem2           -27.84      23.51  -1.184   0.2379
## ES2.mod.v2$techRepStem3            49.82      21.13   2.358   0.0196 *
## ES2.mod.v2$sampleNumbersample2    32.77      22.00   1.490   0.1381
## ES2.mod.v2$sampleNumbersample3    39.91      22.02   1.812   0.0718 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 119.5 on 166 degrees of freedom
## (40 observations deleted due to missingness)
## Multiple R-squared:  0.4277, Adjusted R-squared:  0.3967
## F-statistic: 13.79 on 9 and 166 DF, p-value: < 2.2e-16
```

```
anova(ES2.mod.v2.lm)
```

```
## Analysis of Variance Table
##
## Response: ES2.mod.v2$chl
##
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ES2.mod.v2$Species      2  846902   423451 29.6422 9.824e-12 ***
## ES2.mod.v2$Dilution     1  624310   624310 43.7027 4.992e-10 ***
## ES2.mod.v2$Condition     1   30212    30212  2.1149 0.147764
## ES2.mod.v2$isoRep        1   37904    37904  2.6533 0.105230
## ES2.mod.v2$techRep       2  178878    89439  6.2609 0.002391 **
## ES2.mod.v2$sampleNumber  2   54292    27146  1.9003 0.152769
## Residuals              166 2371375    14285
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Extract all control (ES5: 7 DOE)
ES5.control <- subset(ES5.mod, Treatment== "control")
ES5.Xn <- subset(ES5.mod, Treatment== c("DMCC2126", "DMCC2127", "DMCC2165"))

ES5.control <- ES5.control %>%
  add_column(Species = "control")

ES5.Xn <- ES5.Xn %>%
  add_column(Species = "X.necrophora")

ES5.mod.v2 <- rbind(ES5.control, ES5.Xn)

#Run ANOVA by "species"

ES5.mod.v2.lm <- lm (ES5.mod.v2$chl ~ ES5.mod.v2$Species +
                    ES5.mod.v2$Dilution +
                    ES5.mod.v2$Condition +
                    ES5.mod.v2$isoRep +
                    ES5.mod.v2$techRep +
                    ES5.mod.v2$sampleNumber)

ES5.mod.v2.lm
```

```
##
```

```
## Call:
## lm(formula = ES5.mod.v2$chl ~ ES5.mod.v2$Species + ES5.mod.v2$Dilution +
##     ES5.mod.v2$Condition + ES5.mod.v2$isoRep + ES5.mod.v2$techRep +
##     ES5.mod.v2$sampleNumber)
##
## Coefficients:
##              (Intercept)  ES5.mod.v2$SpeciesX.necrophora
##                   204.46                      -66.84
##     ES5.mod.v2$Dilution25fold  ES5.mod.v2$ConditionStationary
##                   -47.47                      35.71
##     ES5.mod.v2$isoRepisolateRep2  ES5.mod.v2$isoRepisolateRep3
##                   -25.11                      -30.96
##     ES5.mod.v2$techRepstemRep2  ES5.mod.v2$techRepstemRep3
##                   -12.06                      11.26
##     ES5.mod.v2$sampleNumbersample2  ES5.mod.v2$sampleNumbersample3
##                   12.15                      28.88
```

```
summary(ES5.mod.v2.lm)
```

```
##
## Call:
## lm(formula = ES5.mod.v2$chl ~ ES5.mod.v2$Species + ES5.mod.v2$Dilution +
##     ES5.mod.v2$Condition + ES5.mod.v2$isoRep + ES5.mod.v2$techRep +
##     ES5.mod.v2$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -177.109  -40.050    0.166   40.290  160.338
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      204.459     13.966   14.640 < 2e-16 ***
## ES5.mod.v2$SpeciesX.necrophora -66.837      8.708  -7.675 7.37e-13 ***
## ES5.mod.v2$Dilution25fold    -47.471      8.708  -5.451 1.48e-07 ***
## ES5.mod.v2$ConditionStationary  35.714      8.708   4.101 6.00e-05 ***
## ES5.mod.v2$isoRepisolateRep2  -25.108     10.652  -2.357 0.01939 *
## ES5.mod.v2$isoRepisolateRep3  -30.963     10.606  -2.919 0.00391 **
## ES5.mod.v2$techRepstemRep2   -12.058     10.773  -1.119 0.26436
## ES5.mod.v2$techRepstemRep3    11.264     10.693   1.053 0.29345
## ES5.mod.v2$sampleNumbersample2  12.148     10.635   1.142 0.25472
## ES5.mod.v2$sampleNumbersample3  28.882     10.674   2.706 0.00741 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 62.68 on 198 degrees of freedom
## (8 observations deleted due to missingness)
## Multiple R-squared:  0.3975, Adjusted R-squared:  0.3701
## F-statistic: 14.51 on 9 and 198 DF, p-value: < 2.2e-16
```

```
anova(ES5.mod.v2.lm)
```

```
## Analysis of Variance Table
##
```

```
## Response: ES5.mod.v2$chl
##
##      Df Sum Sq Mean Sq F value    Pr(>F)
## ES5.mod.v2$Species      1 235287   235287 59.8872 5.029e-13 ***
## ES5.mod.v2$Dilution     1 125107   125107 31.8433 5.725e-08 ***
## ES5.mod.v2$Condition     1  65438    65438 16.6559 6.496e-05 ***
## ES5.mod.v2$isoRep        2  39008    19504  4.9643  0.007877 **
## ES5.mod.v2$techRep       2  19340     9670  2.4612  0.087937 .
## ES5.mod.v2$sampleNumber  2  29007    14504  3.6916  0.026664 *
## Residuals                198 777909     3929
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#####ES2 analysis (raw data)#####
ES2.chl.lm <- lm (ES2$chl ~ ES2$Treatment +
                  ES2$Dilution +
                  ES2$Condition +
                  ES2$isoRep +
                  ES2$techRep +
                  ES2$sampleNumber)
ES2.chl.lm
```

```
##
## Call:
## lm(formula = ES2$chl ~ ES2$Treatment + ES2$Dilution + ES2$Condition +
##     ES2$isoRep + ES2$techRep + ES2$sampleNumber)
##
## Coefficients:
##      (Intercept)      ES2$TreatmentDMCC2126      ES2$TreatmentDMCC2127
##           236.806           -140.175           -173.159
##      ES2$TreatmentDMCC2165      ES2$TreatmentDMCC2966      ES2$Dilution25fold
##          -169.865           -44.126           -102.848
##      ES2$ConditionStationary      ES2$isoRepisolateRep2      ES2$techRepStem2
##           -8.823           23.729           -24.695
##      ES2$techRepStem3      ES2$sampleNumbersample2      ES2$sampleNumbersample3
##           16.950           26.386           30.435
```

```
summary(ES2.chl.lm)
```

```
##
## Call:
## lm(formula = ES2$chl ~ ES2$Treatment + ES2$Dilution + ES2$Condition +
##     ES2$isoRep + ES2$techRep + ES2$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -231.24  -49.47    1.55   41.40   536.42
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    236.806    20.365  11.628 < 2e-16 ***
## ES2$TreatmentDMCC2126 -140.175    18.956  -7.395 1.70e-12 ***
## ES2$TreatmentDMCC2127 -173.159    19.204  -9.017 < 2e-16 ***
## ES2$TreatmentDMCC2165 -169.865    18.952  -8.963 < 2e-16 ***
```

```
## ES2$TreatmentDMCC2966    -44.126      18.481   -2.388    0.0176 *
## ES2$Dilution25fold      -102.848      11.998   -8.572  7.35e-16 ***
## ES2$ConditionStationary  -8.823       11.944   -0.739    0.4607
## ES2$IsoRepisolateRep2     23.729      11.964    1.983    0.0483 *
## ES2$techRepStem2         -24.695      15.316   -1.612    0.1080
## ES2$techRepStem3         16.950      14.020    1.209    0.2277
## ES2$sampleNumbersample2   26.386      14.436    1.828    0.0687 .
## ES2$sampleNumbersample3   30.435      14.489    2.101    0.0366 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 100.5 on 276 degrees of freedom
## (72 observations deleted due to missingness)
## Multiple R-squared:  0.4591, Adjusted R-squared:  0.4375
## F-statistic: 21.3 on 11 and 276 DF, p-value: < 2.2e-16
```

```
anova(ES2.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES2$chl
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES2$Treatment    4 1458908  364727 36.1018 < 2.2e-16 ***
## ES2$Dilution     1  732380  732380 72.4932 1.094e-15 ***
## ES2$Condition     1    3246    3246  0.3213  0.57128
## ES2$IsoRep        1   38119   38119  3.7732  0.05310 .
## ES2$techRep       2   80731   40366  3.9955  0.01947 *
## ES2$sampleNumber  2   53280   26640  2.6369  0.07338 .
## Residuals        276 2788355   10103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl by Treament
```

```
ES2.chl.treatment.HSD.test <- HSD.test(ES2.chl.lm, 'ES2$Treatment', group = T)
ES2.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##    10102.73 276 105.3393 95.41771
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##    Tukey ES2$Treatment    5          3.883285 0.05
##
## $means
##      ES2$chl      std  r Min      Max      Q25      Q50      Q75
## control 206.91423 217.07353 57    0 831.472  26.54900 138.046 272.67000
## DMCC2126  73.25279  74.61783 57    0 281.899  11.31300  29.554 129.60000
## DMCC2127  37.91085  49.89550 54    0 167.994   8.52575  15.327  49.05425
## DMCC2165  30.48823  45.19861 57    0 187.945   8.36200  14.000  20.43000
## DMCC2966 167.98710  89.73008 63    0 309.266 119.20850 177.714 233.30650
##
## $comparison
```

```
## NULL
##
## $groups
##      ES2$chl groups
## control 206.91423      a
## DMCC2966 167.98710      a
## DMCC2126 73.25279      b
## DMCC2127 37.91085      b
## DMCC2165 30.48823      b
##
## attr("class")
## [1] "group"

#Tukey's HSD for Variable chl by Dilution
ES2.chl.dilution.HSD.test <- HSD.test(ES2.chl.lm, 'ES2$Dilution', group = T)
ES2.chl.dilution.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
## 10102.73 276 105.3393 95.41771
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
## Tukey ES2$Dilution 2      2.784016 0.05
##
## $means
##      ES2$chl      std      r Min      Max      Q25      Q50      Q75
## 100fold 157.13270 159.97363 138 0 831.472 36.10000 129.1440 206.71875
## 25fold 57.68939 79.35162 150 0 309.266 9.85425 15.6685 99.75575
##
## $comparison
## NULL
##
## $groups
##      ES2$chl groups
## 100fold 157.13270      a
## 25fold 57.68939      b
##
## attr("class")
## [1] "group"
```

```
#Complete ANOVA for ES2 by treatment by dilution
ES2.comp.HSD.group <- HSD.test(ES2.chl.lm, c("ES2$Treatment", "ES2$Dilution"), group=TRUE, console=TRUE)
```

```
##
## Study: ES2.chl.lm ~ c("ES2$Treatment", "ES2$Dilution")
##
## HSD Test for ES2$chl
##
## Mean Square Error: 10102.73
##
## ES2$Treatment:ES2$Dilution, means
##
```



```

##          ES2.chl          std  r      Min      Max
## control:100fold  383.864000 223.675014 24 97.748 831.472
## control:25fold   78.223485  77.070835 33  0.000 268.776
## DMCC2126:100fold 127.480933  64.977439 30 10.433 281.899
## DMCC2126:25fold  12.999296  10.944223 27  0.000  51.676
## DMCC2127:100fold 58.980593  59.597226 27  0.000 167.994
## DMCC2127:25fold  16.841111  24.515869 27  0.000 112.319
## DMCC2165:100fold 58.801375  58.889805 24  0.000 187.945
## DMCC2165:25fold   9.896848   6.632284 33  0.000  19.414
## DMCC2966:100fold 171.013333  97.165275 33  0.000 301.867
## DMCC2966:25fold  164.658233  82.303611 30  0.000 309.266
##
## Alpha: 0.05 ; DF Error: 276
## Critical Value of Studentized Range: 4.511094
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##          ES2$chl groups
## control:100fold  383.864000      a
## DMCC2966:100fold 171.013333      b
## DMCC2966:25fold  164.658233      b
## DMCC2126:100fold 127.480933     bc
## control:25fold   78.223485     cd
## DMCC2127:100fold 58.980593     cd
## DMCC2165:100fold 58.801375     cd
## DMCC2127:25fold  16.841111      d
## DMCC2126:25fold  12.999296      d
## DMCC2165:25fold   9.896848      d

```

ES2.comp.HSD.group

```

## $statistics
##      MSError Df      Mean      CV
##    10102.73 276 105.3393 95.41771
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
##    Tukey ES2$Treatment:ES2$Dilution 10          4.511094 0.05
##
## $means
##          ES2$chl          std  r      Min      Max      Q25      Q50
## control:100fold  383.864000 223.675014 24 97.748 831.472 244.69000 280.5385
## control:25fold   78.223485  77.070835 33  0.000 268.776  15.68300  59.4900
## DMCC2126:100fold 127.480933  64.977439 30 10.433 281.899  81.64425 129.1440
## DMCC2126:25fold  12.999296  10.944223 27  0.000  51.676   9.86550  11.3130
## DMCC2127:100fold 58.980593  59.597226 27  0.000 167.994  12.11000  35.6240
## DMCC2127:25fold  16.841111  24.515869 27  0.000 112.319   0.00000  11.9040
## DMCC2165:100fold 58.801375  58.889805 24  0.000 187.945  14.21225  25.3885
## DMCC2165:25fold   9.896848   6.632284 33  0.000  19.414   0.00000  12.2830
## DMCC2966:100fold 171.013333  97.165275 33  0.000 301.867 118.40500 176.8540
## DMCC2966:25fold  164.658233  82.303611 30  0.000 309.266 120.78250 181.5795
##
##          Q75

```

```
## control:100fold 527.0058
## control:25fold 129.7670
## DMCC2126:100fold 159.8775
## DMCC2126:25fold 16.5335
## DMCC2127:100fold 90.5650
## DMCC2127:25fold 15.6860
## DMCC2165:100fold 105.9032
## DMCC2165:25fold 14.7740
## DMCC2966:100fold 241.9460
## DMCC2966:25fold 222.5877
##
## $comparison
## NULL
##
## $groups
##
##          ES2$chl groups
## control:100fold 383.864000      a
## DMCC2966:100fold 171.013333      b
## DMCC2966:25fold 164.658233      b
## DMCC2126:100fold 127.480933     bc
## control:25fold  78.223485      cd
## DMCC2127:100fold 58.980593      cd
## DMCC2165:100fold 58.801375      cd
## DMCC2127:25fold 16.841111      d
## DMCC2126:25fold 12.999296      d
## DMCC2165:25fold  9.896848      d
##
## attr("class")
## [1] "group"
```

Same analysis using the normalized dataset

```
#####ES2 analysis (normalized dataset)#####
ES2.mod.chl.lm <- lm (ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment +
                    ES2.mod$Dilution +
                    ES2.mod$Condition +
                    ES2.mod$isoRep +
                    ES2.mod$techRep +
                    ES2.mod$sampleNumber)
ES2.mod.chl.lm

##
## Call:
## lm(formula = ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution +
##    ES2.mod$Condition + ES2.mod$isoRep + ES2.mod$techRep + ES2.mod$sampleNumber)
##
## Coefficients:
##          (Intercept)      ES2.mod$TreatmentDMCC2126
##              7.52662                -2.19660
## ES2.mod$TreatmentDMCC2127  ES2.mod$TreatmentDMCC2165
##             -3.39025                -3.45003
## ES2.mod$TreatmentDMCC2966      ES2.mod$Dilution25fold
```

```
##           -0.21011           -2.34945
## ES2.mod$ConditionStationary ES2.mod$isoRepisolateRep2
##           -0.09975           0.73788
##           ES2.mod$techRepStem2           ES2.mod$techRepStem3
##           -0.70265           -0.27113
## ES2.mod$sampleNumbersample2 ES2.mod$sampleNumbersample3
##           -0.03389           -0.09430
```

```
summary(ES2.mod.chl.lm)
```

```
##
## Call:
## lm(formula = ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution +
##     ES2.mod$Condition + ES2.mod$isoRep + ES2.mod$techRep + ES2.mod$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.1829 -1.1889  0.4416  1.2936  4.5838
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      7.52662    0.44329   16.979 < 2e-16 ***
## ES2.mod$TreatmentDMCC2126 -2.19660    0.41262   -5.323 2.11e-07 ***
## ES2.mod$TreatmentDMCC2127 -3.39025    0.41803   -8.110 1.67e-14 ***
## ES2.mod$TreatmentDMCC2165 -3.45003    0.41254   -8.363 3.06e-15 ***
## ES2.mod$TreatmentDMCC2966 -0.21011    0.40229   -0.522  0.60190
## ES2.mod$Dilution25fold -2.34945    0.26117   -8.996 < 2e-16 ***
## ES2.mod$ConditionStationary -0.09975    0.26000   -0.384  0.70152
## ES2.mod$isoRepisolateRep2  0.73788    0.26043    2.833 0.00495 **
## ES2.mod$techRepStem2      -0.70265    0.33340   -2.108 0.03597 *
## ES2.mod$techRepStem3      -0.27113    0.30518   -0.888 0.37510
## ES2.mod$sampleNumbersample2 -0.03389    0.31425   -0.108 0.91420
## ES2.mod$sampleNumbersample3 -0.09430    0.31539   -0.299 0.76518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.188 on 276 degrees of freedom
## (72 observations deleted due to missingness)
## Multiple R-squared:  0.4559, Adjusted R-squared:  0.4342
## F-statistic: 21.02 on 11 and 276 DF, p-value: < 2.2e-16
```

```
anova(ES2.mod.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES2.mod$ES2_chl.tuk
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ES2.mod$Treatment      4  680.08   170.02  35.5165 < 2.2e-16 ***
## ES2.mod$Dilution       1  367.55   367.55  76.7802 < 2.2e-16 ***
## ES2.mod$Condition       1    0.63    0.63  0.1326  0.716072
## ES2.mod$isoRep          1   36.95   36.95  7.7190 0.005839 **
## ES2.mod$techRep         2   21.22   10.61  2.2166 0.110912
## ES2.mod$sampleNumber    2    0.44    0.22  0.0456 0.955457
```

```
## Residuals          276 1321.23    4.79
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl (tukey trans) by Treament
```

```
ES2.mod.chl.treatment.HSD.test <- HSD.test(ES2.mod.chl.lm, 'ES2.mod$Treatment', group = T)
ES2.mod.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  4.787063 276 4.479861 48.83937
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES2.mod$Treatment    5          3.883285 0.05
##
## $means
##      ES2.mod$ES2_chl.tuk      std  r Min      Max      Q25      Q50
## control          6.207956 3.276161 57   0 12.443509 3.419937 6.346130
## DMCC2126          4.140619 2.307227 57   0  8.294402 2.483657 3.560255
## DMCC2127          2.929858 2.131941 54   0  6.831014 2.232076 2.783162
## DMCC2165          2.663168 1.976045 57   0  7.124617 2.217514 2.690283
## DMCC2966          6.195529 2.505798 63   0  8.587655 6.006381 6.976629
##
##      Q75
## control  8.191511
## DMCC2126 6.197648
## DMCC2127 4.305207
## DMCC2165 3.099921
## DMCC2966 7.725989
##
## $comparison
## NULL
##
## $groups
##      ES2.mod$ES2_chl.tuk groups
## control          6.207956      a
## DMCC2966          6.195529      a
## DMCC2126          4.140619      b
## DMCC2127          2.929858      c
## DMCC2165          2.663168      c
##
## attr(,"class")
## [1] "group"
```

```
#Tukey's HSD for Variable chl (tukey trans) by Dilution
```

```
ES2.mod.chl.dilution.HSD.test <- HSD.test(ES2.mod.chl.lm, 'ES2.mod$Dilution', group = T)
ES2.mod.chl.dilution.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  4.787063 276 4.479861 48.83937
##
## $parameters
```

```

##      test          name.t ntr StudentizedRange alpha
##      Tukey ES2.mod$Dilution 2          2.784016 0.05
##
## $means
##      ES2.mod$ES2_ch1.tuk      std  r Min      Max      Q25      Q50
## 100fold          5.670079 2.877306 138  0 12.443509 3.837417 6.189452
## 25fold           3.384861 2.482893 150  0  8.587655 2.358352 2.806307
##
##      Q75
## 100fold 7.383524
## 25fold  5.616963
##
## $comparison
## NULL
##
## $groups
##      ES2.mod$ES2_ch1.tuk groups
## 100fold          5.670079      a
## 25fold           3.384861      b
##
## attr("class")
## [1] "group"

#Complete ANOVA for ES2.mod by treatment by dilution (tukey trans)
ES2.mod.comp.HSD.group <- HSD.test(ES2.mod.ch1.lm, c("ES2.mod$Treatment",
                                                    "ES2.mod$Dilution"),
                                   group=TRUE, console=TRUE)

##
## Study: ES2.mod.ch1.lm ~ c("ES2.mod$Treatment", "ES2.mod$Dilution")
##
## HSD Test for ES2.mod$ES2_ch1.tuk
##
## Mean Square Error:  4.787063
##
## ES2.mod$Treatment:ES2.mod$Dilution,  means
##
##      ES2.mod.ES2_ch1.tuk      std  r      Min      Max
## control:100fold          8.952842 2.033695 24 5.575585 12.443509
## control:25fold           4.211675 2.459674 33 0.000000  8.147445
## DMCC2126:100fold         5.904452 1.432971 30 2.409370  8.294402
## DMCC2126:25fold          2.180805 1.263683 27 0.000000  4.390190
## DMCC2127:100fold         3.720246 2.309541 27 0.000000  6.831014
## DMCC2127:25fold          2.139470 1.622868 27 0.000000  5.873811
## DMCC2165:100fold         3.677465 2.368645 24 0.000000  7.124617
## DMCC2165:25fold          1.925497 1.211620 33 0.000000  3.041187
## DMCC2966:100fold         6.114039 2.778697 33 0.000000  8.510026
## DMCC2966:25fold          6.285168 2.210961 30 0.000000  8.587655
##
## Alpha: 0.05 ; DF Error: 276
## Critical Value of Studentized Range: 4.511094
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.

```

```
##
##          ES2.mod$ES2_ch1.tuk groups
## control:100fold      8.952842      a
## DMCC2966:25fold      6.285168      b
## DMCC2966:100fold     6.114039      b
## DMCC2126:100fold     5.904452     bc
## control:25fold       4.211675     cd
## DMCC2127:100fold     3.720246     de
## DMCC2165:100fold     3.677465     de
## DMCC2126:25fold      2.180805      e
## DMCC2127:25fold      2.139470      e
## DMCC2165:25fold      1.925497      e
```

```
ES2.mod.comp.HSD.group
```

```
## $statistics
##      MSerror Df      Mean      CV
##    4.787063 276 4.479861 48.83937
##
## $parameters
##      test                                name.t ntr StudentizedRange alpha
##    Tukey ES2.mod$Treatment:ES2.mod$Dilution 10          4.511094 0.05
##
## $means
##          ES2.mod$ES2_ch1.tuk      std  r      Min      Max      Q25
## control:100fold      8.952842 2.033695 24 5.575585 12.443509 7.860042
## control:25fold      4.211675 2.459674 33 0.000000  8.147445 2.807281
## DMCC2126:100fold     5.904452 1.432971 30 2.409370  8.294402 5.211560
## DMCC2126:25fold     2.180805 1.263683 27 0.000000  4.390190 2.359361
## DMCC2127:100fold     3.720246 2.309541 27 0.000000  6.831014 2.547399
## DMCC2127:25fold     2.139470 1.622868 27 0.000000  5.873811 0.000000
## DMCC2165:100fold     3.677465 2.368645 24 0.000000  7.124617 2.700544
## DMCC2165:25fold     1.925497 1.211620 33 0.000000  3.041187 0.000000
## DMCC2966:100fold     6.114039 2.778697 33 0.000000  8.510026 5.991199
## DMCC2966:25fold     6.285168 2.210961 30 0.000000  8.587655 6.035946
##          Q50      Q75
## control:100fold  8.279323 10.486003
## control:25fold   4.628247  6.200641
## DMCC2126:100fold 6.189452  6.705312
## DMCC2126:25fold  2.483657  2.863395
## DMCC2127:100fold 3.818594  5.417472
## DMCC2127:25fold  2.531540  2.807481
## DMCC2165:100fold 3.362478  5.745663
## DMCC2165:25fold  2.561469  2.745123
## DMCC2966:100fold 6.963949  7.832392
## DMCC2966:25fold  7.032779  7.590879
##
## $comparison
## NULL
##
## $groups
##          ES2.mod$ES2_ch1.tuk groups
## control:100fold      8.952842      a
## DMCC2966:25fold      6.285168      b
```

```
## DMCC2966:100fold      6.114039      b
## DMCC2126:100fold      5.904452      bc
## control:25fold        4.211675      cd
## DMCC2127:100fold      3.720246      de
## DMCC2165:100fold      3.677465      de
## DMCC2126:25fold       2.180805      e
## DMCC2127:25fold       2.139470      e
## DMCC2165:25fold       1.925497      e
##
## attr(,"class")
## [1] "group"
```

Run analyses for ES5

This test was run for 7 DOE and photos were taken of the last day of exposure.

```
#####ES5 analysis#####
```

```
ES5.ch1.lm <- lm (ES5$chl ~ ES5$Treatment +
                  ES5$Dilution +
                  ES5$Condition +
                  ES5$isoRep +
                  ES5$techRep +
                  ES5$sampleNumber)
ES5.ch1.lm
```

```
##
## Call:
## lm(formula = ES5$chl ~ ES5$Treatment + ES5$Dilution + ES5$Condition +
##     ES5$isoRep + ES5$techRep + ES5$sampleNumber)
##
## Coefficients:
##             (Intercept)      ES5$TreatmentDMCC2126      ES5$TreatmentDMCC2127
##                192.365                -61.618                -70.990
##   ES5$TreatmentDMCC2165      ES5$Dilution25fold   ES5$ConditionStationary
##                -67.429                -46.539                 42.178
##   ES5$isoRepisolateRep2   ES5$isoRepisolateRep3      ES5$techRepstemRep2
##                -9.981                -22.792                -14.269
##   ES5$techRepstemRep3   ES5$sampleNumbersample2   ES5$sampleNumbersample3
##                19.985                 11.399                 25.312
```

```
summary(ES5.ch1.lm)
```

```
##
## Call:
## lm(formula = ES5$chl ~ ES5$Treatment + ES5$Dilution + ES5$Condition +
##     ES5$isoRep + ES5$techRep + ES5$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -182.445  -40.817   -5.474   42.676  187.396
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      192.365    10.836  17.753 < 2e-16 ***
## ES5$TreatmentDMCC2126  -61.618     8.801   -7.001 1.05e-11 ***
## ES5$TreatmentDMCC2127  -70.990     8.734   -8.128 5.27e-15 ***
## ES5$TreatmentDMCC2165  -67.429     8.798   -7.664 1.33e-13 ***
## ES5$Dilution25fold    -46.539     6.177   -7.534 3.19e-13 ***
## ES5$ConditionStationary  42.178     6.177    6.828 3.13e-11 ***
## ES5$IsoRepisolateRep2   -9.981     7.580   -1.317 0.188662
## ES5$IsoRepisolateRep3  -22.792     7.534   -3.025 0.002642 **
## ES5$techRepstemRep2    -14.269     7.620   -1.873 0.061849 .
## ES5$techRepstemRep3     19.985     7.536    2.652 0.008315 **
## ES5$sampleNumbersample2  11.399     7.557    1.509 0.132197
## ES5$sampleNumbersample3  25.312     7.557    3.350 0.000884 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 63.22 on 408 degrees of freedom
## (12 observations deleted due to missingness)
## Multiple R-squared:  0.3665, Adjusted R-squared:  0.3494
## F-statistic: 21.46 on 11 and 408 DF, p-value: < 2.2e-16
```

```
anova(ES5.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES5$chl
##               Df Sum Sq Mean Sq F value    Pr(>F)
## ES5$Treatment    3  351053   117018 29.2750 < 2.2e-16 ***
## ES5$Dilution     1  239796   239796 59.9912 7.615e-14 ***
## ES5$Condition     1  186231   186231 46.5904 3.179e-11 ***
## ES5$IsoRep        2   37850    18925  4.7345 0.009275 **
## ES5$techRep       2   83616    41808 10.4593 3.717e-05 ***
## ES5$sampleNumber  2   44997    22498  5.6285 0.003879 **
## Residuals        408 1630853    3997
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl by Treatment
```

```
ES5.chl.treatment.HSD.test <- HSD.test(ES5.chl.lm, 'ES5$Treatment', group = T)
ES5.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  3997.188 408 143.1371 44.16975
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##   Tukey ES5$Treatment    4          3.648176 0.05
##
## $means
##      ES5$chl      std      r Min      Max      Q25      Q50      Q75
## control 193.8353 69.20948 102 26.0 372.6 147.750 202.9 240.55
## DMCC2126 131.8714 73.80466 105 30.3 277.2  63.700 110.8 189.60
```



```
## DMCC2127 122.4120 75.41655 108 0.0 339.2 64.875 100.3 157.95
## DMCC2165 126.4705 73.67261 105 0.0 289.2 68.300 100.0 189.20
##
## $comparison
## NULL
##
## $groups
##      ES5$chl groups
## control 193.8353    a
## DMCC2126 131.8714    b
## DMCC2165 126.4705    b
## DMCC2127 122.4120    b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable chl by Dilution

```
ES5.chl.dilution.HSD.test <- HSD.test(ES5.chl.lm, 'ES5$Dilution', group = T)
ES5.chl.dilution.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV      MSD
## 3997.188 408 143.1371 44.16975 12.12889
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
## Tukey ES5$Dilution  2      2.780054 0.05
##
## $means
##      ES5$chl      std  r Min  Max  Q25  Q50  Q75
## 100fold 166.9881 77.60533 210  0 372.6 99.475 178.20 232.825
## 25fold 119.2862 71.77681 210  0 303.7 61.000 94.45 174.500
##
## $comparison
## NULL
##
## $groups
##      ES5$chl groups
## 100fold 166.9881    a
## 25fold 119.2862    b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable chl by Condition

```
ES5.chl.cond.HSD.test <- HSD.test(ES5.chl.lm, 'ES5$Condition', group = T)
ES5.chl.cond.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV      MSD
## 3997.188 408 143.1371 44.16975 12.12889
##
## $parameters
```

```

##      test          name.t ntr StudentizedRange alpha
##      Tukey ES5$Condition  2          2.780054  0.05
##
## $means
##           ES5$chl      std  r Min   Max   Q25   Q50   Q75
## Shaking    121.3619 70.21004 210   0 363.9 63.900 99.15 174.075
## Stationary 164.9124 80.22074 210   0 372.6 91.075 179.40 234.325
##
## $comparison
## NULL
##
## $groups
##           ES5$chl groups
## Stationary 164.9124      a
## Shaking    121.3619      b
##
## attr("class")
## [1] "group"

#Complete ANOVA for ES5 by treatment by condition, by dilution
ES5.comp.HSD.group <- HSD.test(ES5.chl.lm, c("ES5$Treatment", "ES5$Condition",
                                             "ES5$Dilution"), group=TRUE, console=TRUE)

##
## Study: ES5.chl.lm ~ c("ES5$Treatment", "ES5$Condition", "ES5$Dilution")
##
## HSD Test for ES5$chl
##
## Mean Square Error: 3997.188
##
## ES5$Treatment:ES5$Condition:ES5$Dilution, means
##
##           ES5.chl      std  r   Min   Max
## control:Shaking:100fold 200.02083 68.81458 24 104.0 363.9
## control:Shaking:25fold 158.22593 62.18883 27  26.0 249.0
## control:Stationary:100fold 238.50000 37.84527 27 185.5 372.6
## control:Stationary:25fold 177.46250 78.47053 24  37.7 303.7
## DMCC2126:Shaking:100fold 161.77500 70.00547 24  48.0 270.4
## DMCC2126:Shaking:25fold  75.53333 30.56325 27  30.3 140.8
## DMCC2126:Stationary:100fold 174.24815 63.63720 27  51.7 264.4
## DMCC2126:Stationary:25fold 119.25185 79.48387 27  36.0 277.2
## DMCC2127:Shaking:100fold  93.23333 39.13111 27  37.1 190.5
## DMCC2127:Shaking:25fold  61.84444 32.99067 27   0.0 119.5
## DMCC2127:Stationary:100fold 192.10370 77.79170 27  75.0 339.2
## DMCC2127:Stationary:25fold 142.46667 67.68053 27  53.1 296.0
## DMCC2165:Shaking:100fold 143.79630 71.66806 27  36.8 273.2
## DMCC2165:Shaking:25fold  89.69630 40.84195 27  40.3 174.5
## DMCC2165:Stationary:100fold 135.31852 85.93666 27   0.0 279.9
## DMCC2165:Stationary:25fold 138.39583 79.51052 24  48.0 289.2
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.87582
##
## Groups according to probability of means differences and alpha level( 0.05 )

```

```
##
## Treatments with the same letter are not significantly different.
##
##          ES5$chl groups
## control:Stationary:100fold 238.50000    a
## control:Shaking:100fold    200.02083   ab
## DMCC2127:Stationary:100fold 192.10370   abc
## control:Stationary:25fold  177.46250  abcd
## DMCC2126:Stationary:100fold 174.24815   bcd
## DMCC2126:Shaking:100fold   161.77500   bcd
## control:Shaking:25fold     158.22593   bcd
## DMCC2165:Shaking:100fold   143.79630  bcde
## DMCC2127:Stationary:25fold  142.46667  bcde
## DMCC2165:Stationary:25fold  138.39583  bcde
## DMCC2165:Stationary:100fold 135.31852   cde
## DMCC2126:Stationary:25fold  119.25185  def
## DMCC2127:Shaking:100fold   93.23333   ef
## DMCC2165:Shaking:25fold    89.69630   ef
## DMCC2126:Shaking:25fold    75.53333    f
## DMCC2127:Shaking:25fold    61.84444    f
```

```
ES5.comp.HSD.group
```

```
## $statistics
##      MSerror Df      Mean      CV
##   3997.188 408 143.1371 44.16975
##
## $parameters
##      test                                name.t ntr StudentizedRange alpha
##   Tukey ES5$Treatment:ES5$Condition:ES5$Dilution 16          4.87582 0.05
##
## $means
##                                ES5$chl      std r   Min   Max    Q25    Q50
## control:Shaking:100fold    200.02083 68.81458 24 104.0 363.9 146.800 186.90
## control:Shaking:25fold     158.22593 62.18883 27  26.0 249.0 126.400 174.80
## control:Stationary:100fold 238.50000 37.84527 27 185.5 372.6 215.850 235.10
## control:Stationary:25fold  177.46250 78.47053 24  37.7 303.7 124.350 193.05
## DMCC2126:Shaking:100fold   161.77500 70.00547 24  48.0 270.4  87.125 173.00
## DMCC2126:Shaking:25fold    75.53333 30.56325 27  30.3 140.8  50.050  66.50
## DMCC2126:Stationary:100fold 174.24815 63.63720 27  51.7 264.4 132.600 180.00
## DMCC2126:Stationary:25fold 119.25185 79.48387 27  36.0 277.2  56.400  85.00
## DMCC2127:Shaking:100fold   93.23333 39.13111 27  37.1 190.5  69.800  85.80
## DMCC2127:Shaking:25fold    61.84444 32.99067 27   0.0 119.5  45.400  58.90
## DMCC2127:Stationary:100fold 192.10370 77.79170 27  75.0 339.2 109.700 204.20
## DMCC2127:Stationary:25fold 142.46667 67.68053 27  53.1 296.0  78.050 131.20
## DMCC2165:Shaking:100fold   143.79630 71.66806 27  36.8 273.2  78.650 113.60
## DMCC2165:Shaking:25fold    89.69630 40.84195 27  40.3 174.5  60.100  77.90
## DMCC2165:Stationary:100fold 135.31852 85.93666 27   0.0 279.9  61.950 158.00
## DMCC2165:Stationary:25fold 138.39583 79.51052 24  48.0 289.2  73.150 114.70
##                                Q75
## control:Shaking:100fold    245.325
## control:Shaking:25fold     205.700
## control:Stationary:100fold 253.200
## control:Stationary:25fold  238.750
```

```
## DMCC2126:Shaking:100fold    207.875
## DMCC2126:Shaking:25fold      94.400
## DMCC2126:Stationary:100fold  230.800
## DMCC2126:Stationary:25fold   173.250
## DMCC2127:Shaking:100fold    116.550
## DMCC2127:Shaking:25fold      88.250
## DMCC2127:Stationary:100fold  249.300
## DMCC2127:Stationary:25fold   186.700
## DMCC2165:Shaking:100fold    201.750
## DMCC2165:Shaking:25fold      94.600
## DMCC2165:Stationary:100fold  205.300
## DMCC2165:Stationary:25fold   191.025
##
## $comparison
## NULL
##
## $groups
##
##          ES5$chl groups
## control:Stationary:100fold 238.50000    a
## control:Shaking:100fold    200.02083   ab
## DMCC2127:Stationary:100fold 192.10370   abc
## control:Stationary:25fold   177.46250  abcd
## DMCC2126:Stationary:100fold 174.24815   bcd
## DMCC2126:Shaking:100fold    161.77500   bcd
## control:Shaking:25fold      158.22593   bcd
## DMCC2165:Shaking:100fold    143.79630  bcde
## DMCC2127:Stationary:25fold   142.46667  bcde
## DMCC2165:Stationary:25fold   138.39583  bcde
## DMCC2165:Stationary:100fold 135.31852   cde
## DMCC2126:Stationary:25fold   119.25185  def
## DMCC2127:Shaking:100fold     93.23333   ef
## DMCC2165:Shaking:25fold      89.69630   ef
## DMCC2126:Shaking:25fold      75.53333    f
## DMCC2127:Shaking:25fold      61.84444    f
##
## attr(,"class")
## [1] "group"
```

Same analyses for ES5, using normalized data

```
#####ES5 analysis (normalized data) #####
ES5.mod.chl.lm <- lm (ES5.mod$ES5_chl.tuk ~ ES5.mod$Treatment +
                      ES5.mod$Dilution +
                      ES5.mod$Condition +
                      ES5.mod$IsoRep +
                      ES5.mod$techRep +
                      ES5.mod$sampleNumber)
ES5.mod.chl.lm

##
## Call:
## lm(formula = ES5.mod$ES5_chl.tuk ~ ES5.mod$Treatment + ES5.mod$Dilution +
```

```
##      ES5.mod$Condition + ES5.mod$isoRep + ES5.mod$techRep + ES5.mod$sampleNumber)
##
## Coefficients:
##              (Intercept)      ES5.mod$TreatmentDMCC2126
##                   30.278                   -7.067
##      ES5.mod$TreatmentDMCC2127      ES5.mod$TreatmentDMCC2165
##                   -8.357                   -7.928
##      ES5.mod$Dilution25fold      ES5.mod$ConditionStationary
##                   -5.443                   4.789
##      ES5.mod$isoRepisolateRep2      ES5.mod$isoRepisolateRep3
##                   -1.403                   -2.930
##      ES5.mod$techRepstemRep2      ES5.mod$techRepstemRep3
##                   -1.392                   2.517
##      ES5.mod$sampleNumbersample2      ES5.mod$sampleNumbersample3
##                   1.050                   2.548
```

```
summary(ES5.mod.chl.lm)
```

```
##
## Call:
## lm(formula = ES5.mod$ES5_chl.tuk ~ ES5.mod$Treatment + ES5.mod$Dilution +
##      ES5.mod$Condition + ES5.mod$isoRep + ES5.mod$techRep + ES5.mod$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -28.2842  -4.6883  -0.0798   5.3904  19.2000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    30.2777     1.3012  23.270 < 2e-16 ***
## ES5.mod$TreatmentDMCC2126    -7.0672     1.0568   -6.687 7.50e-11 ***
## ES5.mod$TreatmentDMCC2127    -8.3567     1.0488   -7.968 1.63e-14 ***
## ES5.mod$TreatmentDMCC2165    -7.9283     1.0565   -7.505 3.90e-13 ***
## ES5.mod$Dilution25fold     -5.4428     0.7417   -7.338 1.18e-12 ***
## ES5.mod$ConditionStationary    4.7890     0.7417    6.457 3.05e-10 ***
## ES5.mod$isoRepisolateRep2    -1.4026     0.9102   -1.541 0.12411
## ES5.mod$isoRepisolateRep3    -2.9300     0.9047   -3.239 0.00130 **
## ES5.mod$techRepstemRep2     -1.3920     0.9150   -1.521 0.12896
## ES5.mod$techRepstemRep3     2.5171     0.9049    2.782 0.00566 **
## ES5.mod$sampleNumbersample2    1.0500     0.9074    1.157 0.24789
## ES5.mod$sampleNumbersample3    2.5484     0.9074    2.808 0.00522 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.592 on 408 degrees of freedom
## (12 observations deleted due to missingness)
## Multiple R-squared:  0.3506, Adjusted R-squared:  0.3331
## F-statistic: 20.02 on 11 and 408 DF, p-value: < 2.2e-16
```

```
anova(ES5.mod.chl.lm)
```

```
## Analysis of Variance Table
##
```

```
## Response: ES5.mod$ES5_chl.tuk
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES5.mod$Treatment      3  4830.6   1610.2  27.9375 < 2.2e-16 ***
## ES5.mod$Dilution       1  3271.4   3271.4  56.7598 3.204e-13 ***
## ES5.mod$Condition      1  2403.9   2403.9  41.7082 3.018e-10 ***
## ES5.mod$isoRep         2    618.1    309.1   5.3623 0.005027 **
## ES5.mod$techRep        2   1110.4    555.2   9.6327 8.172e-05 ***
## ES5.mod$sampleNumber   2    459.3    229.6   3.9845 0.019330 *
## Residuals             408 23515.2     57.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl (tukey trans) by Treatment
ES5.mod.chl.treatment.HSD.test <- HSD.test(ES5.mod.chl.lm, 'ES5.mod$Treatment',
                                           group = T)
ES5.mod.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##      57.63529 408 24.21363 31.35338
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##      Tukey ES5.mod$Treatment      4      3.648176 0.05
##
## $means
##      ES5.mod$ES5_chl.tuk      std      r      Min      Max      Q25      Q50
## control      30.14562 7.609997 102 8.312519 46.91458 25.71521 31.60326
## DMCC2126      23.01374 8.709822 105 9.182009 38.70932 14.88301 21.32803
## DMCC2127      21.72436 9.135639 108 0.000000 44.13634 15.06086 19.99151
## DMCC2165      22.21139 9.151154 105 0.000000 39.79045 15.57304 19.95262
##
##      Q75
## control 35.30039
## DMCC2126 30.24091
## DMCC2127 26.85501
## DMCC2165 30.19943
##
## $comparison
## NULL
##
## $groups
##      ES5.mod$ES5_chl.tuk groups
## control      30.14562      a
## DMCC2126      23.01374      b
## DMCC2165      22.21139      b
## DMCC2127      21.72436      b
##
## attr(,"class")
## [1] "group"
```

```
#Tukey's HSD for Variable chl (tukey trans) by Dilution
ES5.mod.chl.dilution.HSD.test <- HSD.test(ES5.mod.chl.lm, 'ES5.mod$Dilution',
                                           group = T)
ES5.mod.chl.dilution.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV      MSD
##    57.63529 408 24.21363 31.35338 1.456424
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##    Tukey ES5.mod$Dilution 2      2.780054 0.05
##
## $means
##      ES5.mod$ES5_chl.tuk      std  r Min      Max      Q25      Q50
## 100fold      26.99820 9.029696 210  0 46.91458 19.88445 29.04621
## 25fold      21.42906 8.725273 210  0 41.07609 14.46985 19.22561
##
##      Q75
## 100fold 34.55964
## 25fold 28.65280
##
## $comparison
## NULL
##
## $groups
##      ES5.mod$ES5_chl.tuk groups
## 100fold      26.99820      a
## 25fold      21.42906      b
##
## attr("class")
## [1] "group"
```

```
#Tukey's HSD for Variable chl (tukey trans) by Condition
ES5.mod.chl.cond.HSD.test <- HSD.test(ES5.mod.chl.lm, 'ES5.mod$Condition', group = T)
ES5.mod.chl.cond.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV      MSD
##    57.63529 408 24.21363 31.35338 1.456424
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##    Tukey ES5.mod$Condition 2      2.780054 0.05
##
## $means
##      ES5.mod$ES5_chl.tuk      std  r Min      Max      Q25      Q50
## Shaking      21.73611 8.509070 210  0 46.19961 14.91331 19.84222
## Stationary      26.69114 9.407897 210  0 46.91458 18.77627 29.17320
##
##      Q75
## Shaking 28.60736
## Stationary 34.70420
##
## $comparison
## NULL
##
## $groups
##      ES5.mod$ES5_chl.tuk groups
## Stationary      26.69114      a
## Shaking      21.73611      b
```

```
##
## attr(,"class")
## [1] "group"

#Complete ANOVA for ES5.mod by treatment by condition, by dilution (tukey trans)
ES5.mod.comp.HSD.group <- HSD.test(ES5.mod.chl.lm, c("ES5.mod$Treatment",
                                                    "ES5.mod$Condition",
                                                    "ES5.mod$Dilution"),
                                   group=TRUE, console=TRUE)

##
## Study: ES5.mod.chl.lm ~ c("ES5.mod$Treatment", "ES5.mod$Condition", "ES5.mod$Dilution")
##
## HSD Test for ES5.mod$ES5_chl.tuk
##
## Mean Square Error: 57.63529
##
## ES5.mod$Treatment:ES5.mod$Condition:ES5.mod$Dilution, means
##
##
##          ES5.mod.ES5_chl.tuk      std  r      Min      Max
## control:Shaking:100fold      30.92160  6.877550  24  20.467824  46.19961
## control:Shaking:25fold      26.28822  7.584437  27   8.312519  36.10186
## control:Stationary:100fold    35.01510  3.511991  27  29.814226  46.91458
## control:Stationary:25fold    28.23105  8.847762  24  10.583319  41.07609
## DMCC2126:Shaking:100fold     26.63321  8.061394  24  12.382456  38.08942
## DMCC2126:Shaking:25fold     16.33068  4.334703  27   9.182009  24.92251
## DMCC2126:Stationary:100fold   28.13045  7.218510  27  12.994778  37.53790
## DMCC2126:Stationary:25fold   21.36280  9.304178  27  10.270619  38.70932
## DMCC2127:Shaking:100fold     18.70574  5.119409  27  10.473529  30.33414
## DMCC2127:Shaking:25fold     13.80400  6.101857  27   0.000000  22.40212
## DMCC2127:Stationary:100fold   29.90084  8.268740  27  16.549688  44.13634
## DMCC2127:Stationary:25fold   24.48688  7.726440  27  13.222435  40.39612
## DMCC2165:Shaking:100fold     24.56023  8.205647  27  10.418401  38.34533
## DMCC2165:Shaking:25fold     18.20998  5.258465  27  11.052188  28.65280
## DMCC2165:Stationary:100fold   22.51380 11.836979  27   0.000000  38.95398
## DMCC2165:Stationary:25fold   23.73032  9.225861  24  12.382456  39.79045
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.87582
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##          ES5.mod$ES5_chl.tuk groups
## control:Stationary:100fold      35.01510      a
## control:Shaking:100fold          30.92160     ab
## DMCC2127:Stationary:100fold      29.90084     ab
## control:Stationary:25fold        28.23105    abc
## DMCC2126:Stationary:100fold      28.13045    abc
## DMCC2126:Shaking:100fold         26.63321     bc
## control:Shaking:25fold           26.28822     bc
## DMCC2165:Shaking:100fold         24.56023    bcd
## DMCC2127:Stationary:25fold        24.48688    bcd
```


## DMCC2165:Stationary:25fold	23.73032	bcd
## DMCC2165:Stationary:100fold	22.51380	cde
## DMCC2126:Stationary:25fold	21.36280	cde
## DMCC2127:Shaking:100fold	18.70574	def
## DMCC2165:Shaking:25fold	18.20998	def
## DMCC2126:Shaking:25fold	16.33068	ef
## DMCC2127:Shaking:25fold	13.80400	f

ES5.mod.comp.HSD.group

```
## $statistics
##      MSerror Df      Mean      CV
##      57.63529 408 24.21363 31.35338
##
## $parameters
##      test                                     name.t ntr
##      Tukey ES5.mod$Treatment:ES5.mod$Condition:ES5.mod$Dilution 16
##      StudentizedRange alpha
##              4.87582 0.05
##
## $means
##                                     ES5.mod$ES5_ch1.tuk      std  r      Min      Max
## control:Shaking:100fold          30.92160  6.877550 24 20.467824 46.19961
## control:Shaking:25fold           26.28822  7.584437 27  8.312519 36.10186
## control:Stationary:100fold        35.01510  3.511991 27 29.814226 46.91458
## control:Stationary:25fold         28.23105  8.847762 24 10.583319 41.07609
## DMCC2126:Shaking:100fold          26.63321  8.061394 24 12.382456 38.08942
## DMCC2126:Shaking:25fold           16.33068  4.334703 27  9.182009 24.92251
## DMCC2126:Stationary:100fold        28.13045  7.218510 27 12.994778 37.53790
## DMCC2126:Stationary:25fold         21.36280  9.304178 27 10.270619 38.70932
## DMCC2127:Shaking:100fold          18.70574  5.119409 27 10.473529 30.33414
## DMCC2127:Shaking:25fold           13.80400  6.101857 27  0.000000 22.40212
## DMCC2127:Stationary:100fold        29.90084  8.268740 27 16.549688 44.13634
## DMCC2127:Stationary:25fold         24.48688  7.726440 27 13.222435 40.39612
## DMCC2165:Shaking:100fold          24.56023  8.205647 27 10.418401 38.34533
## DMCC2165:Shaking:25fold           18.20998  5.258465 27 11.052188 28.65280
## DMCC2165:Stationary:100fold        22.51380 11.836979 27  0.000000 38.95398
## DMCC2165:Stationary:25fold         23.73032  9.225861 24 12.382456 39.79045
##                                     Q25      Q50      Q75
## control:Shaking:100fold          25.60774 29.95578 35.75395
## control:Shaking:25fold           23.23414 28.68481 31.88435
## control:Stationary:100fold        32.89985 34.77877 36.49626
## control:Stationary:25fold         22.97996 30.57655 35.12646
## DMCC2126:Shaking:100fold          18.24222 28.49017 32.10254
## DMCC2126:Shaking:25fold           12.72170 15.30503 19.21892
## DMCC2126:Stationary:100fold        23.96670 29.23662 34.36364
## DMCC2126:Stationary:25fold         13.75020 17.95239 28.49754
## DMCC2127:Shaking:100fold          15.79238 18.06204 22.03937
## DMCC2127:Shaking:25fold           11.94225 14.14409 18.38373
## DMCC2127:Stationary:100fold        21.18901 31.73483 36.13001
## DMCC2127:Stationary:25fold         16.98374 23.80439 29.93923
## DMCC2165:Shaking:100fold          17.06819 21.67684 31.48681
## DMCC2165:Shaking:25fold           14.32943 16.96287 19.24541
## DMCC2165:Stationary:100fold        14.61527 26.86130 31.84574
```

```
## DMCC2165:Stationary:25fold 16.28243 21.81134 30.38458
##
## $comparison
## NULL
##
## $groups
##
## ES5.mod$ES5_ch1.tuk groups
## control:Stationary:100fold 35.01510 a
## control:Shaking:100fold 30.92160 ab
## DMCC2127:Stationary:100fold 29.90084 ab
## control:Stationary:25fold 28.23105 abc
## DMCC2126:Stationary:100fold 28.13045 abc
## DMCC2126:Shaking:100fold 26.63321 bc
## control:Shaking:25fold 26.28822 bc
## DMCC2165:Shaking:100fold 24.56023 bcd
## DMCC2127:Stationary:25fold 24.48688 bcd
## DMCC2165:Stationary:25fold 23.73032 bcd
## DMCC2165:Stationary:100fold 22.51380 cde
## DMCC2126:Stationary:25fold 21.36280 cde
## DMCC2127:Shaking:100fold 18.70574 def
## DMCC2165:Shaking:25fold 18.20998 def
## DMCC2126:Shaking:25fold 16.33068 ef
## DMCC2127:Shaking:25fold 13.80400 f
##
## attr("class")
## [1] "group"
```

Run analyses for ES13B

Testing variation among potentially resistant cultivars compared to known susceptible cultivars treated with CFCFs from *X. necrophora* (isolate DMCC 2165) to determine if resistance to direct application of SMs exist.

```
#Statistical analysis
#####ES13B###
ES13B.ch1.lm <- lm (ES13B$chl ~ ES13B$Treatment +
                    ES13B$HostVariety +
                    ES13B$isoRepNumber +
                    ES13B$techRepNumber +
                    ES13B$SampleNumber)
ES13B.ch1.lm

##
## Call:
## lm(formula = ES13B$chl ~ ES13B$Treatment + ES13B$HostVariety +
##     ES13B$isoRepNumber + ES13B$techRepNumber + ES13B$SampleNumber)
##
## Coefficients:
##             (Intercept)          ES13B$TreatmentDMCC2165
##             187.9400                -105.4678
##   ES13B$HostVarietyDG47E80   ES13B$HostVarietyDG47X95
##             27.8736                26.3892
##   ES13B$HostVarietyOsage    ES13B$HostVarietyP5414LLS
```

```
##              16.1981              -3.8273
## ES13B$isoRepNumberisoRep2 ES13B$isoRepNumberisoRep3
##              -7.3121              1.4292
## ES13B$techRepNumbertechRep2 ES13B$techRepNumbertechRep3
##              29.6658              8.0253
## ES13B$SampleNumbersample2 ES13B$SampleNumbersample3
##              0.7302              1.9473
```

```
summary(ES13B.chl.lm)
```

```
##
## Call:
## lm(formula = ES13B$chl ~ ES13B$Treatment + ES13B$HostVariety +
##     ES13B$isoRepNumber + ES13B$techRepNumber + ES13B$SampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -219.035  -47.751   -4.823   42.506  237.651
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      187.9400     17.1352  10.968 <2e-16 ***
## ES13B$TreatmentDMCC2165    -105.4678      9.9569  -10.592 <2e-16 ***
## ES13B$HostVarietyDG47E80     27.8736     15.5401   1.794  0.0741 .
## ES13B$HostVarietyDG47X95     26.3892     16.0431   1.645  0.1012
## ES13B$HostVarietyOusage     16.1981     15.5401   1.042  0.2983
## ES13B$HostVarietyP5414LLS    -3.8273     15.5401  -0.246  0.8057
## ES13B$isoRepNumberisoRep2    -7.3121     12.2504  -0.597  0.5511
## ES13B$isoRepNumberisoRep3     1.4292     12.1499   0.118  0.9065
## ES13B$techRepNumbertechRep2  29.6658     12.1499   2.442  0.0153 *
## ES13B$techRepNumbertechRep3   8.0253     12.1499   0.661  0.5095
## ES13B$SampleNumbersample2     0.7302     12.1733   0.060  0.9522
## ES13B$SampleNumbersample3     1.9473     12.1733   0.160  0.8730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 80.75 on 252 degrees of freedom
## (6 observations deleted due to missingness)
## Multiple R-squared:  0.337, Adjusted R-squared:  0.308
## F-statistic: 11.64 on 11 and 252 DF, p-value: < 2.2e-16
```

```
anova(ES13B.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES13B$chl
##              Df Sum Sq Mean Sq F value Pr(>F)
## ES13B$Treatment      1  745236   745236 114.2939 < 2e-16 ***
## ES13B$HostVariety     4   44757    11189   1.7160 0.14689
## ES13B$isoRepNumber    2    3558     1779   0.2728 0.76144
## ES13B$techRepNumber   2   41380    20690   3.1731 0.04355 *
## ES13B$SampleNumber    2     170        85   0.0131 0.98702
## Residuals           252 1643127    6520
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#Tukey's HSD for Variable chl by Treatment
ES13B.chl.treatment.HSD.test <- HSD.test(ES13B.chl.lm, 'ES13B$Treatment', group = T)
ES13B.chl.treatment.HSD.test

## $statistics
##      MSerror Df      Mean      CV
## 6520.345 252 160.8255 50.20887
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES13B$Treatment    2          2.785184 0.05
##
## $means
##      ES13B$chl      std  r Min      Max      Q25      Q50      Q75
## Control    212.7620 79.79142 135    0 402.241 166.577 220.922 257.822
## DMCC2165   106.4733 82.90892 129    0 350.226  51.563  71.243 161.827
##
## $comparison
## NULL
##
## $groups
##      ES13B$chl groups
## Control    212.7620      a
## DMCC2165   106.4733      b
##
## attr(,"class")
## [1] "group"

#Tukey's HSD for Variable chl by Soybean Cultivar
ES13B.chl.host_variety.HSD.test <- HSD.test(ES13B.chl.lm, 'ES13B$HostVariety', group = T)
ES13B.chl.host_variety.HSD.test

## $statistics
##      MSerror Df      Mean      CV
## 6520.345 252 160.8255 50.20887
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES13B$HostVariety    5          3.885737 0.05
##
## $means
##      ES13B$chl      std  r Min      Max      Q25      Q50      Q75
## AG4632    146.7014 89.25074 54    0 364.618 68.0405 134.5050 212.5315
## DG47E80   174.5750 94.89959 54    0 372.762 94.9610 203.4325 233.2080
## DG47X95   179.1090 97.67480 48    0 359.307 86.1180 192.7220 255.9690
## Osage     162.8995 111.37700 54    0 402.241 66.9080 155.3500 248.0178
## P5414LLS  142.8741 88.83067 54    0 318.243 59.8260 153.8800 221.6343
##
## $comparison
## NULL
```

```
##
## $groups
##      ES13B$chl groups
## DG47X95  179.1090      a
## DG47E80  174.5750      a
## Osage    162.8995      a
## AG4632   146.7014      a
## P5414LLS 142.8741      a
##
## attr(,"class")
## [1] "group"
```

```
#Complete ANOVA for ES13B
ES13B.comp.HSD.group <- HSD.test(ES13B.chl.lm, c("ES13B$Treatment", "ES13B$HostVariety"),
                                group=TRUE, console=TRUE)
```

```
##
## Study: ES13B.chl.lm ~ c("ES13B$Treatment", "ES13B$HostVariety")
##
## HSD Test for ES13B$chl
##
## Mean Square Error: 6520.345
##
## ES13B$Treatment:ES13B$HostVariety, means
##
##      ES13B.chl      std r      Min      Max
## Control:AG4632  190.99715  86.60398 27  0.000 364.618
## Control:DG47E80  228.60578  74.03698 27 99.638 372.762
## Control:DG47X95  217.34011  75.28029 27 62.560 359.307
## Control:Osage    236.66259  98.93830 27  0.000 402.241
## Control:P5414LLS 190.20437  49.79161 27 96.055 269.571
## DMCC2165:AG4632  102.40559  68.28138 27  0.000 279.119
## DMCC2165:DG47E80 120.54422  82.54428 27  0.000 268.043
## DMCC2165:DG47X95 129.95467 102.67650 21  0.000 350.226
## DMCC2165:Osage   89.13633  64.78778 27  0.000 305.544
## DMCC2165:P5414LLS 95.54374  94.62256 27  0.000 318.243
##
## Alpha: 0.05 ; DF Error: 252
## Critical Value of Studentized Range: 4.514628
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##      ES13B$chl groups
## Control:Osage    236.66259      a
## Control:DG47E80  228.60578      a
## Control:DG47X95  217.34011      a
## Control:AG4632   190.99715     ab
## Control:P5414LLS 190.20437     abc
## DMCC2165:DG47X95 129.95467     bcd
## DMCC2165:DG47E80 120.54422      cd
## DMCC2165:AG4632  102.40559      d
## DMCC2165:P5414LLS 95.54374      d
```

```
## DMCC2165:Osage      89.13633      d
```

```
ES13B.comp.HSD.group
```

```
## $statistics
```

```
##      MSerror Df      Mean      CV
```

```
##      6520.345 252 160.8255 50.20887
```

```
##
```

```
## $parameters
```

```
##      test                                name.t ntr StudentizedRange alpha
```

```
##      Tukey ES13B$Treatment:ES13B$HostVariety 10          4.514628 0.05
```

```
##
```

```
## $means
```

```
##      ES13B$chl      std r      Min      Max      Q25      Q50
```

```
## Control:AG4632      190.99715      86.60398 27      0.000      364.618      144.0055      209.592
```

```
## Control:DG47E80      228.60578      74.03698 27      99.638      372.762      206.6285      227.869
```

```
## Control:DG47X95      217.34011      75.28029 27      62.560      359.307      180.9375      220.770
```

```
## Control:Osage      236.66259      98.93830 27      0.000      402.241      220.1595      246.824
```

```
## Control:P5414LLS      190.20437      49.79161 27      96.055      269.571      163.7070      193.690
```

```
## DMCC2165:AG4632      102.40559      68.28138 27      0.000      279.119      55.0810      79.594
```

```
## DMCC2165:DG47E80      120.54422      82.54428 27      0.000      268.043      49.0770      93.402
```

```
## DMCC2165:DG47X95      129.95467      102.67650 21      0.000      350.226      47.3850      81.525
```

```
## DMCC2165:Osage      89.13633      64.78778 27      0.000      305.544      63.5255      67.114
```

```
## DMCC2165:P5414LLS      95.54374      94.62256 27      0.000      318.243      35.1075      57.848
```

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```

```
## attr(,"class")
```

```
## [1] "group"
```

Same analysis as above using the tukey normalized dataset

```
#Statistical analysis
####ES13B.mod###
ES13B.mod.chl.lm <- lm (ES13B.mod$ES13B_chl.tuk ~ ES13B.mod$Treatment +
                        ES13B.mod$HostVariety +
                        ES13B.mod$isoRepNumber +
                        ES13B.mod$techRepNumber +
                        ES13B.mod$SampleNumber)
ES13B.mod.chl.lm

##
## Call:
## lm(formula = ES13B.mod$ES13B_chl.tuk ~ ES13B.mod$Treatment +
##     ES13B.mod$HostVariety + ES13B.mod$isoRepNumber + ES13B.mod$techRepNumber +
##     ES13B.mod$SampleNumber)
##
## Coefficients:
##              (Intercept)          ES13B.mod$TreatmentDMCC2165
##                   56.4659                      -27.1569
##   ES13B.mod$HostVarietyDG47E80   ES13B.mod$HostVarietyDG47X95
##                   6.8552                      6.4268
##   ES13B.mod$HostVarietyOsage     ES13B.mod$HostVarietyP5414LLS
##                   3.2278                      -1.2888
##   ES13B.mod$isoRepNumberisoRep2   ES13B.mod$isoRepNumberisoRep3
##                   -1.8503                      0.1216
##   ES13B.mod$techRepNumbertechRep2 ES13B.mod$techRepNumbertechRep3
##                   7.5512                      2.1409
##   ES13B.mod$SampleNumbersample2   ES13B.mod$SampleNumbersample3
##                   0.6429                      0.7374
```

```
summary(ES13B.mod.chl.lm)
```

```
##
## Call:
## lm(formula = ES13B.mod$ES13B_chl.tuk ~ ES13B.mod$Treatment +
##     ES13B.mod$HostVariety + ES13B.mod$isoRepNumber + ES13B.mod$techRepNumber +
##     ES13B.mod$SampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -64.139 -11.806   0.251  11.105  58.266
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      56.4659     4.4320  12.740  <2e-16 ***
## ES13B.mod$TreatmentDMCC2165 -27.1569     2.5754 -10.545  <2e-16 ***
## ES13B.mod$HostVarietyDG47E80   6.8552     4.0195   1.705  0.0893 .
## ES13B.mod$HostVarietyDG47X95   6.4268     4.1496   1.549  0.1227
## ES13B.mod$HostVarietyOsage     3.2278     4.0195   0.803  0.4227
## ES13B.mod$HostVarietyP5414LLS -1.2888     4.0195  -0.321  0.7488
## ES13B.mod$isoRepNumberisoRep2 -1.8503     3.1686  -0.584  0.5598
```

```
## ES13B.mod$isoRepNumberisoRep3      0.1216      3.1426      0.039      0.9692
## ES13B.mod$techRepNumbertechRep2     7.5512      3.1426      2.403      0.0170 *
## ES13B.mod$techRepNumbertechRep3     2.1409      3.1426      0.681      0.4963
## ES13B.mod$SampleNumbersample2       0.6429      3.1486      0.204      0.8384
## ES13B.mod$SampleNumbersample3       0.7374      3.1486      0.234      0.8150
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 20.89 on 252 degrees of freedom
## (6 observations deleted due to missingness)
## Multiple R-squared:  0.3339, Adjusted R-squared:  0.3048
## F-statistic: 11.48 on 11 and 252 DF,  p-value: < 2.2e-16
```

```
anova(ES13B.mod.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES13B.mod$ES13B_chl.tuk
##              Df Sum Sq Mean Sq F value Pr(>F)
## ES13B.mod$Treatment      1  49427   49427 113.3105 < 2e-16 ***
## ES13B.mod$HostVariety     4   2794     698   1.6010 0.17455
## ES13B.mod$isoRepNumber     2    193     97   0.2216 0.80137
## ES13B.mod$techRepNumber    2   2663    1331   3.0519 0.04902 *
## ES13B.mod$SampleNumber     2     28     14   0.0325 0.96804
## Residuals                 252 109925     436
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl by Treatment
```

```
ES13B.mod.chl.treatment.HSD.test <- HSD.test(ES13B.mod.chl.lm, 'ES13B.mod$Treatment',
                                             group = T)
ES13B.mod.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  436.2119 252 49.24912 42.40824
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES13B.mod$Treatment      2      2.785184 0.05
##
## $means
##      ES13B.mod$ES13B_chl.tuk      std      r Min      Max      Q25      Q50
## Control      62.62462 19.91280 135      0 104.34627 52.69278 65.58208
## DMCC2165      35.25151 22.09171 129      0  93.72814 21.23548 27.28194
##      Q75
## Control      73.92184
## DMCC2165      51.52459
##
## $comparison
## NULL
##
## $groups
```



```
##          ES13B.mod$ES13B_chl.tuk groups
## Control          62.62462      a
## DMCC2165          35.25151      b
##
## attr("class")
## [1] "group"

#Tukey's HSD for Variable chl by Soybean Cultivar
ES13B.mod.chl.host_variety.HSD.test <- HSD.test(ES13B.mod.chl.lm,
                                                'ES13B.mod$HostVariety', group = T)
ES13B.mod.chl.host_variety.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  436.2119 252 49.24912 42.40824
##
## $parameters
##      test          name.t ntr StudentizedRange alpha
##  Tukey ES13B.mod$HostVariety  5      3.885737  0.05
##
## $means
##          ES13B.mod$ES13B_chl.tuk      std  r Min      Max      Q25      Q50
## AG4632          46.00199 23.04112 54  0 96.69957 26.32493 44.64489
## DG47E80          52.85715 24.31248 54  0 98.36929 34.08532 61.52054
## DG47X95          53.96776 24.74253 48  0 95.60617 31.59813 58.99393
## Osage          49.22977 28.48843 54  0 104.34627 25.98636 49.51131
## P5414LLS          44.71323 23.92033 54  0 87.02381 23.82148 49.53890
##
##          Q75
## AG4632  63.64317
## DG47E80  68.39115
## DG47X95  73.50975
## Osage    71.73382
## P5414LLS 65.74587
##
## $comparison
## NULL
##
## $groups
##          ES13B.mod$ES13B_chl.tuk groups
## DG47X95          53.96776      a
## DG47E80          52.85715      a
## Osage          49.22977      a
## AG4632          46.00199      a
## P5414LLS          44.71323      a
##
## attr("class")
## [1] "group"
```

```
#Complete ANOVA for ES13B.mod
ES13B.mod.comp.HSD.group <- HSD.test(ES13B.mod.chl.lm, c("ES13B.mod$Treatment",
                                                         "ES13B.mod$HostVariety"),
                                     group=TRUE,console=TRUE)
```

```
##
```

```

## Study: ES13B.mod.chl.lm ~ c("ES13B.mod$Treatment", "ES13B.mod$HostVariety")
##
## HSD Test for ES13B.mod$ES13B_chl.tuk
##
## Mean Square Error: 436.2119
##
## ES13B.mod$Treatment:ES13B.mod$HostVariety, means
##
##          ES13B.mod.ES13B_chl.tuk      std  r      Min      Max
## Control:AG4632          57.20904 22.03662 27  0.00000  96.69957
## Control:DG47E80          66.70288 17.20548 27 35.38176  98.36929
## Control:DG47X95          64.01404 17.93361 27 24.66777  95.60617
## Control:Osage            67.15363 26.52535 27  0.00000 104.34627
## Control:P5414LLS         58.04351 11.99680 27 34.39165  76.51943
## DMCC2165:AG4632          34.79495 18.32309 27  0.00000  78.61163
## DMCC2165:DG47E80          39.01143 22.59966 27  0.00000  76.18307
## DMCC2165:DG47X95          41.05111 26.62931 21  0.00000  93.72814
## DMCC2165:Osage            31.30592 16.83924 27  0.00000  84.32030
## DMCC2165:P5414LLS         31.38296 25.56143 27  0.00000  87.02381
##
## Alpha: 0.05 ; DF Error: 252
## Critical Value of Studentized Range: 4.514628
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##          ES13B.mod$ES13B_chl.tuk groups
## Control:Osage            67.15363      a
## Control:DG47E80          66.70288      a
## Control:DG47X95          64.01404      a
## Control:P5414LLS         58.04351     ab
## Control:AG4632          57.20904     ab
## DMCC2165:DG47X95          41.05111     bc
## DMCC2165:DG47E80          39.01143      c
## DMCC2165:AG4632          34.79495      c
## DMCC2165:P5414LLS         31.38296      c
## DMCC2165:Osage            31.30592      c

```

ES13B.mod.comp.HSD.group

```

## $statistics
##      MSerror Df      Mean      CV
##    436.2119 252 49.24912 42.40824
##
## $parameters
##      test                                name.t ntr StudentizedRange alpha
##    Tukey ES13B.mod$Treatment:ES13B.mod$HostVariety 10          4.514628 0.05
##
## $means
##          ES13B.mod$ES13B_chl.tuk      std  r      Min      Max
## Control:AG4632          57.20904 22.03662 27  0.00000  96.69957
## Control:DG47E80          66.70288 17.20548 27 35.38176  98.36929
## Control:DG47X95          64.01404 17.93361 27 24.66777  95.60617

```

```

## Control:Osage                67.15363 26.52535 27 0.00000 104.34627
## Control:P5414LLS            58.04351 11.99680 27 34.39165 76.51943
## DMCC2165:AG4632             34.79495 18.32309 27 0.00000 78.61163
## DMCC2165:DG47E80            39.01143 22.59966 27 0.00000 76.18307
## DMCC2165:DG47X95            41.05111 26.62931 21 0.00000 93.72814
## DMCC2165:Osage              31.30592 16.83924 27 0.00000 84.32030
## DMCC2165:P5414LLS           31.38296 25.56143 27 0.00000 87.02381
##                               Q25      Q50      Q75
## Control:AG4632      47.05388 62.96010 68.61805
## Control:DG47E80     62.26497 67.17475 78.30087
## Control:DG47X95     56.17982 65.54711 77.85944
## Control:Osage       65.40652 71.46612 76.90405
## Control:P5414LLS    51.98765 59.22541 67.22892
## DMCC2165:AG4632     22.34657 29.72913 43.18888
## DMCC2165:DG47E80    20.43572 33.65317 61.08024
## DMCC2165:DG47X95    19.88940 30.28659 60.68214
## DMCC2165:Osage      24.95960 26.04835 30.23822
## DMCC2165:P5414LLS   15.75931 23.21526 36.18682
##
## $comparison
## NULL
##
## $groups
##           ES13B.mod$ES13B_chl.tuk groups
## Control:Osage                67.15363      a
## Control:DG47E80              66.70288      a
## Control:DG47X95              64.01404      a
## Control:P5414LLS             58.04351     ab
## Control:AG4632               57.20904     ab
## DMCC2165:DG47X95             41.05111     bc
## DMCC2165:DG47E80             39.01143      c
## DMCC2165:AG4632              34.79495      c
## DMCC2165:P5414LLS            31.38296      c
## DMCC2165:Osage               31.30592      c
##
## attr("class")
## [1] "group"

```

Run analyses for ES14A

This dataset contains chlorophyll content measured among plant species treated with CFCFs from *X. necrophora* (isolate DMCC 2165) to estimate the specificity of SMs.

```

#####ES14A###
ES14A.chl.lm <- lm (ES14A$chl ~ ES14A$Treatment +
                    ES14A$Host + ES14A$isoRepNumber +
                    ES14A$techRepNumber +
                    ES14A$LeafSampleNumber)
ES14A.chl.lm

```

```

##
## Call:
## lm(formula = ES14A$chl ~ ES14A$Treatment + ES14A$Host + ES14A$isoRepNumber +

```

```
##      ES14A$techRepNumber + ES14A$LeafSampleNumber)
##
## Coefficients:
##              (Intercept)          ES14A$TreatmentDMCC2165
##                204.803                -39.317
##      ES14A$HostPeanut          ES14A$HostSoybean
##                71.821                -20.797
##      ES14A$HostTomato      ES14A$isoRepNumberisoRep2
##                20.597                8.076
##      ES14A$isoRepNumberisoRep3  ES14A$techRepNumbertechRep2
##                10.061                -3.623
##      ES14A$techRepNumbertechRep3 ES14A$LeafSampleNumbersample2
##                -2.447                -2.221
##      ES14A$LeafSampleNumbersample3
##                -17.082

summary(ES14A.chl.lm)

##
## Call:
## lm(formula = ES14A$chl ~ ES14A$Treatment + ES14A$Host + ES14A$isoRepNumber +
##      ES14A$techRepNumber + ES14A$LeafSampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -152.26  -25.67    3.28   28.37  140.22
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      204.803    11.492  17.821 < 2e-16 ***
## ES14A$TreatmentDMCC2165 -39.317     6.956  -5.652 5.34e-08 ***
## ES14A$HostPeanut      71.821     9.760   7.359 4.58e-12 ***
## ES14A$HostSoybean    -20.797     9.760  -2.131  0.0343 *
## ES14A$HostTomato     20.597     9.914   2.078  0.0390 *
## ES14A$isoRepNumberisoRep2  8.076     8.552   0.944  0.3461
## ES14A$isoRepNumberisoRep3 10.061     8.452   1.190  0.2353
## ES14A$techRepNumbertechRep2 -3.623     8.552  -0.424  0.6723
## ES14A$techRepNumbertechRep3 -2.447     8.552  -0.286  0.7751
## ES14A$LeafSampleNumbersample2 -2.221     8.512  -0.261  0.7944
## ES14A$LeafSampleNumbersample3 -17.082     8.512  -2.007  0.0461 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 50.71 on 202 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.4051, Adjusted R-squared:  0.3756
## F-statistic: 13.75 on 10 and 202 DF, p-value: < 2.2e-16
```

```
anova(ES14A.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES14A$chl
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES14A$Treatment      1  81494    81494 31.6869 6.003e-08 ***
## ES14A$Host            3 255475    85158 33.1116 < 2.2e-16 ***
## ES14A$IsoRepNumber    2   4050     2025  0.7874  0.4564
## ES14A$techRepNumber   2    478      239  0.0930  0.9112
## ES14A$LeafSampleNumber 2  12250     6125  2.3815  0.0950 .
## Residuals            202 519515     2572
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tukey's HSD for Variable chl by Treatment

```
ES14A.chl.treatment.HSD.test <- HSD.test(ES14A.chl.lm, 'ES14A$Treatment', group = T)
ES14A.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
## 2571.854 202 200.2661 25.32304
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES14A$Treatment      2      2.788514 0.05
##
## $means
##      ES14A$chl      std      r      Min      Max      Q25      Q50      Q75
## Control    220.1037 48.30845 105 74.284 312.775 199.7190 220.323 244.5180
## DMCC2165   180.9794 71.63395 108 43.371 317.520 136.5077 190.138 227.8515
##
## $comparison
## NULL
##
## $groups
##      ES14A$chl groups
## Control    220.1037      a
## DMCC2165   180.9794      b
##
## attr(,"class")
## [1] "group"
```

#Tukey's HSD for Variable chl by Plant Species

```
ES14A.chl.host.HSD.test <- HSD.test(ES14A.chl.lm, 'ES14A$Host', group = T)
ES14A.chl.host.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
## 2571.854 202 200.2661 25.32304
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##  Tukey ES14A$Host      4      3.663584 0.05
##
## $means
##      ES14A$chl      std      r      Min      Max      Q25      Q50      Q75
## Cotton    182.7328 41.22083 54  99.321 258.986 151.8048 189.3455 208.6360
```

```
## Peanut    254.5536 39.15515 54 104.832 317.520 232.0955 254.8250 282.4742
## Soybean   161.9354 88.07831 54  43.371 312.775  66.5095 174.5450 226.9425
## Tomato    201.9352 26.66869 51 117.923 244.624 187.7870 203.6790 219.5155
##
## $comparison
## NULL
##
## $groups
##      ES14A$chl groups
## Peanut    254.5536      a
## Tomato    201.9352      b
## Cotton    182.7328     bc
## Soybean   161.9354      c
##
## attr("class")
## [1] "group"
```

#Complete ANOVA for ES14A

```
ES14A.comp.HSD.group <- HSD.test(ES14A.chl.lm, c("ES14A$Treatment", "ES14A$Host"), group=TRUE, console=TRUE)
```

```
##
## Study: ES14A.chl.lm ~ c("ES14A$Treatment", "ES14A$Host")
##
## HSD Test for ES14A$chl
##
## Mean Square Error: 2571.854
##
## ES14A$Treatment:ES14A$Host, means
##
##      ES14A.chl      std r      Min      Max
## Control:Cotton  194.11622 42.12477 27 106.098 254.411
## Control:Peanut  243.47885 43.34219 27 104.832 305.065
## Control:Soybean 226.62589 63.78820 27  74.284 312.775
## Control:Tomato  215.70517 17.85696 24 183.593 244.624
## DMCC2165:Cotton 171.34937 37.68338 27  99.321 258.986
## DMCC2165:Peanut 265.62833 31.49505 27 200.016 317.520
## DMCC2165:Soybean 97.24481 55.25735 27  43.371 210.220
## DMCC2165:Tomato 189.69526 27.47809 27 117.923 236.489
##
## Alpha: 0.05 ; DF Error: 202
## Critical Value of Studentized Range: 4.331714
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##      ES14A$chl groups
## DMCC2165:Peanut 265.62833      a
## Control:Peanut  243.47885     ab
## Control:Soybean 226.62589    abc
## Control:Tomato  215.70517     bc
## Control:Cotton  194.11622     cd
## DMCC2165:Tomato 189.69526     cd
## DMCC2165:Cotton 171.34937      d
```

```
## DMCC2165:Soybean 97.24481 e
```

```
ES14A.comp.HSD.group
```

```
## $statistics
##      MSError Df      Mean      CV
##    2571.854 202 200.2661 25.32304
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
##    Tukey ES14A$Treatment:ES14A$Host      8      4.331714 0.05
##
## $means
##              ES14A$chl      std r      Min      Max      Q25      Q50
## Control:Cotton    194.11622 42.12477 27 106.098 254.411 172.7065 201.2180
## Control:Peanut    243.47885 43.34219 27 104.832 305.065 220.0160 244.4330
## Control:Soybean   226.62589 63.78820 27  74.284 312.775 205.7205 227.9410
## Control:Tomato    215.70517 17.85696 24 183.593 244.624 203.4402 214.3875
## DMCC2165:Cotton   171.34937 37.68338 27  99.321 258.986 146.1180 180.5490
## DMCC2165:Peanut   265.62833 31.49505 27 200.016 317.520 247.1435 262.9750
## DMCC2165:Soybean  97.24481 55.25735 27  43.371 210.220  52.2970  66.4980
## DMCC2165:Tomato   189.69526 27.47809 27 117.923 236.489 178.0980 191.1460
##
##              Q75
## Control:Cotton    229.7960
## Control:Peanut    274.2060
## Control:Soybean   274.5295
## Control:Tomato    227.4280
## DMCC2165:Cotton   198.6270
## DMCC2165:Peanut   290.1215
## DMCC2165:Soybean  143.0605
## DMCC2165:Tomato   206.2940
##
## $comparison
## NULL
##
## $groups
##              ES14A$chl groups
## DMCC2165:Peanut 265.62833      a
## Control:Peanut  243.47885     ab
## Control:Soybean 226.62589    abc
## Control:Tomato  215.70517     bc
## Control:Cotton  194.11622     cd
## DMCC2165:Tomato 189.69526     cd
## DMCC2165:Cotton 171.34937      d
## DMCC2165:Soybean 97.24481      e
##
## attr(,"class")
## [1] "group"
```

Same analysis as above using Tukey's normalized data.

```
#####ES14A.mod.mod###
ES14A.mod.chl.lm <- lm (ES14A.mod$ES14A_chl.tuk ~ ES14A.mod$Treatment +
                        ES14A.mod$Host +
                        ES14A.mod$isoRepNumber +
                        ES14A.mod$techRepNumber +
                        ES14A.mod$LeafSampleNumber)
ES14A.mod.chl.lm
```

```
##
## Call:
## lm(formula = ES14A.mod$ES14A_chl.tuk ~ ES14A.mod$Treatment +
##     ES14A.mod$Host + ES14A.mod$isoRepNumber + ES14A.mod$techRepNumber +
##     ES14A.mod$LeafSampleNumber)
##
## Coefficients:
##              (Intercept)          ES14A.mod$TreatmentDMCC2165
##                   9573.32                   -2709.06
##          ES14A.mod$HostPeanut          ES14A.mod$HostSoybean
##                   6109.14                   -562.35
##          ES14A.mod$HostTomato      ES14A.mod$isoRepNumberisoRep2
##                   1457.89                   752.80
##      ES14A.mod$isoRepNumberisoRep3      ES14A.mod$techRepNumbertechRep2
##                   707.59                   -175.15
##      ES14A.mod$techRepNumbertechRep3      ES14A.mod$LeafSampleNumbersample2
##                   -380.75                   -57.52
##      ES14A.mod$LeafSampleNumbersample3
##                   -831.24
```

```
summary(ES14A.mod.chl.lm)
```

```
##
## Call:
## lm(formula = ES14A.mod$ES14A_chl.tuk ~ ES14A.mod$Treatment +
##     ES14A.mod$Host + ES14A.mod$isoRepNumber + ES14A.mod$techRepNumber +
##     ES14A.mod$LeafSampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11413  -2124     40    2186  11598
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9573.32    861.86  11.108 < 2e-16 ***
## ES14A.mod$TreatmentDMCC2165 -2709.06    521.66  -5.193 5.03e-07 ***
## ES14A.mod$HostPeanut      6109.14    731.96   8.346 1.10e-14 ***
## ES14A.mod$HostSoybean    -562.35    731.96  -0.768  0.4432
## ES14A.mod$HostTomato     1457.89    743.48   1.961  0.0513 .
## ES14A.mod$isoRepNumberisoRep2    752.80    641.39   1.174  0.2419
## ES14A.mod$isoRepNumberisoRep3    707.59    633.89   1.116  0.2656
## ES14A.mod$techRepNumbertechRep2 -175.15    641.39  -0.273  0.7851
## ES14A.mod$techRepNumbertechRep3 -380.75    641.39  -0.594  0.5534
## ES14A.mod$LeafSampleNumbersample2  -57.52    638.34  -0.090  0.9283
```



```
## ES14A.mod$LeafSampleNumbersample3 -831.24      638.34 -1.302    0.1943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3803 on 202 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.3985, Adjusted R-squared:  0.3687
## F-statistic: 13.38 on 10 and 202 DF,  p-value: < 2.2e-16
```

```
anova(ES14A.mod.chl.lm)
```

```
## Analysis of Variance Table
##
## Response: ES14A.mod$ES14A_chl.tuk
##              Df      Sum Sq   Mean Sq F value    Pr(>F)
## ES14A.mod$Treatment      1 389423237 389423237 26.9209 5.141e-07 ***
## ES14A.mod$Host           3 1485413072 495137691 34.2289 < 2.2e-16 ***
## ES14A.mod$isoRepNumber    2  25123911 12561955  0.8684  0.4212
## ES14A.mod$techRepNumber   2   5115841  2557921  0.1768  0.8381
## ES14A.mod$LeafSampleNumber 2  30598645 15299322  1.0576  0.3492
## Residuals                202 2922025050 14465471
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable chl by Treatment
```

```
ES14A.mod.chl.treatment.HSD.test <- HSD.test(ES14A.mod.chl.lm, 'ES14A.mod$Treatment', group = T)
ES14A.mod.chl.treatment.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
## 14465471 202 9953.906 38.20962
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
## Tukey ES14A.mod$Treatment      2      2.788514 0.05
##
## $means
##      ES14A.mod$ES14A_chl.tuk      std      r      Min      Max      Q25
## Control      11325.224 3958.923 105 1687.6965 20150.01 9294.444
## DMCC2165      8620.679 5150.335 108 667.0663 20680.22 4821.441
##      Q50      Q75
## Control 11009.769 13177.60
## DMCC2165 8538.763 11666.87
##
## $comparison
## NULL
##
## $groups
##      ES14A.mod$ES14A_chl.tuk groups
## Control      11325.224      a
## DMCC2165      8620.679      b
##
## attr(,"class")
## [1] "group"
```

#Tukey's HSD for Variable chl by Plant Species

```
ES14A.mod.chl.host.HSD.test <- HSD.test(ES14A.mod.chl.lm, 'ES14A.mod$Host', group = T)
ES14A.mod.chl.host.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  14465471 202 9953.906 38.20962
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##   Tukey ES14A.mod$Host   4      3.663584  0.05
##
## $means
##      ES14A.mod$ES14A_chl.tuk      std r      Min      Max      Q25
## Cotton      8224.039 3055.399 54 2785.4532 14551.29  5790.517
## Peanut      14333.182 3553.092 54 3057.3977 20680.22 12044.169
## Soybean      7661.688 6130.187 54  667.0663 20150.01  1394.679
## Tomato      9575.703 2068.306 51 3745.4797 13187.45  8357.435
##
##      Q50      Q75
## Cotton  8477.450 10021.99
## Peanut 14150.559 16902.50
## Soybean 7366.996 11586.99
## Tomato  9614.624 10940.26
##
## $comparison
## NULL
##
## $groups
##      ES14A.mod$ES14A_chl.tuk groups
## Peanut      14333.182      a
## Tomato      9575.703      b
## Cotton      8224.039      b
## Soybean      7661.688      b
##
## attr(,"class")
## [1] "group"
```

#Complete ANOVA for ES14A.mod

```
ES14A.mod.comp.HSD.group <- HSD.test(ES14A.mod.chl.lm, c("ES14A.mod$Treatment",
                                                         "ES14A.mod$Host"),
                                     group=TRUE,console=TRUE)
```

```
##
## Study: ES14A.mod.chl.lm ~ c("ES14A.mod$Treatment", "ES14A.mod$Host")
##
## HSD Test for ES14A.mod$ES14A_chl.tuk
##
## Mean Square Error:  14465471
##
## ES14A.mod$Treatment:ES14A.mod$Host,  means
##
##      ES14A.mod.ES14A_chl.tuk      std r      Min      Max
## Control:Cotton      9103.740 3172.165 27 3121.3676 14110.73
```

```

## Control:Peanut          13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean         12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato          10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton         7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut         15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean        3195.045 3010.793 27 667.0663 10153.43
## DMCC2165:Tomato         8613.327 2039.245 27 3745.4797 12440.10
##
## Alpha: 0.05 ; DF Error: 202
## Critical Value of Studentized Range: 4.331714
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##          ES14A.mod$ES14A_ch1.tuk groups
## DMCC2165:Peanut          15330.007      a
## Control:Peanut           13336.356     ab
## Control:Soybean          12128.331     bc
## Control:Tomato           10658.376    bcd
## Control:Cotton           9103.740     cde
## DMCC2165:Tomato          8613.327      de
## DMCC2165:Cotton          7344.338       e
## DMCC2165:Soybean         3195.045       f

```

ES14A.mod.comp.HSD.group

```

## $statistics
##      MSError Df      Mean      CV
##  14465471 202 9953.906 38.20962
##
## $parameters
##      test                      name.t ntr StudentizedRange alpha
##   Tukey ES14A.mod$Treatment:ES14A.mod$Host      8      4.331714 0.05
##
## $means
##          ES14A.mod$ES14A_ch1.tuk      std r      Min      Max
## Control:Cotton          9103.740 3172.165 27 3121.3676 14110.73
## Control:Peanut          13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean          12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato          10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton          7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut          15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean         3195.045 3010.793 27 667.0663 10153.43
## DMCC2165:Tomato          8613.327 2039.245 27 3745.4797 12440.10
##
##          Q25      Q50      Q75
## Control:Cotton    7235.4241 9415.107 11840.543
## Control:Peanut    10983.3242 13169.695 16057.689
## Control:Soybean    9787.4152 11674.646 16090.596
## Control:Tomato     9595.2157 10503.255 11629.391
## DMCC2165:Cotton    5421.6757 7809.559 9207.086
## DMCC2165:Peanut   13422.7747 14940.064 17699.067
## DMCC2165:Soybean    921.2485 1394.263 5240.336
## DMCC2165:Tomato    7629.0246 8616.978 9828.773

```

```
##
## $comparison
## NULL
##
## $groups
##          ES14A.mod$ES14A_ch1.tuk groups
## DMCC2165:Peanut          15330.007    a
## Control:Peanut          13336.356    ab
## Control:Soybean         12128.331    bc
## Control:Tomato          10658.376   bcd
## Control:Cotton           9103.740   cde
## DMCC2165:Tomato          8613.327    de
## DMCC2165:Cotton          7344.338    e
## DMCC2165:Soybean         3195.045    f
##
## attr("class")
## [1] "group"
```

Statistical analyses for root lenght

Loading dataset (root growth)

```
ES2.root <- read.csv("../raw_data/ES2.rootMeasurements.csv", header = T)

#Clean dataset for plotting and analyses
ES2.root.noNAs <- na.omit(ES2.root)
```

Initial statistical analysis (raw data)

```
#ES2 longest root statistical analysis
ES2.root.noNAs.lm <- lm (ES2.root.noNAs$Length ~ ES2.root.noNAs$Isolate + ES2.root.noNAs$Condition + ES2.root.noNAs$Concentration)
ES2.root.noNAs.lm

##
## Call:
## lm(formula = ES2.root.noNAs$Length ~ ES2.root.noNAs$Isolate +
##     ES2.root.noNAs$Condition + ES2.root.noNAs$Concentration,
##     na.action = na.exclude)
##
## Coefficients:
##              (Intercept)          ES2.root.noNAs$IsolateDMCC2126
##                   38.608                      -10.916
##     ES2.root.noNAs$IsolateDMCC2127      ES2.root.noNAs$IsolateDMCC2165
##                   -8.786                      -12.099
##     ES2.root.noNAs$IsolateDMCC2966  ES2.root.noNAs$ConditionStationary
##                   13.649                      -6.885
## ES2.root.noNAs$Concentration25fold
##                   -25.132
```

```
summary(ES2.root.noNAs.lm)
```

```
##
## Call:
## lm(formula = ES2.root.noNAs$Length ~ ES2.root.noNAs$Isolate +
##     ES2.root.noNAs$Condition + ES2.root.noNAs$Concentration,
##     na.action = na.exclude)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -30.264  -8.173   1.284   7.818  22.674
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   38.608     3.659   10.550 3.33e-15 ***
## ES2.root.noNAs$IsolateDMCC2126  -10.916     5.457   -2.000  0.05008 .
## ES2.root.noNAs$IsolateDMCC2127   -8.786     5.223   -1.682  0.09781 .
## ES2.root.noNAs$IsolateDMCC2165  -12.099     4.986   -2.427  0.01832 *
## ES2.root.noNAs$IsolateDMCC2966   13.649     4.199    3.250  0.00191 **
## ES2.root.noNAs$ConditionStationary -6.885     3.178   -2.167  0.03431 *
## ES2.root.noNAs$Concentration25fold -25.132     3.492   -7.197 1.26e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.49 on 59 degrees of freedom
## Multiple R-squared:  0.5919, Adjusted R-squared:  0.5504
## F-statistic: 14.26 on 6 and 59 DF,  p-value: 5.795e-10
```

```
anova(ES2.root.noNAs.lm)
```

```
## Analysis of Variance Table
##
## Response: ES2.root.noNAs$Length
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES2.root.noNAs$Isolate      4 4955.4  1238.8   7.9369 3.450e-05 ***
## ES2.root.noNAs$Condition     1  317.6    317.6   2.0349   0.159
## ES2.root.noNAs$Concentration  1 8084.1  8084.1  51.7926 1.256e-09 ***
## Residuals                   59 9209.1    156.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Tukey's HSD for Variable Condition
```

```
ES2.root.noNAs.condition.HSD.test <- HSD.test(ES2.root.noNAs.lm,
                                              'ES2.root.noNAs$Condition', group = T)
ES2.root.noNAs.condition.HSD.test
```

```
## $statistics
##  MSerror Df      Mean      CV
##  156.086 59 26.46406 47.20907
##
## $parameters
```

```
##      test                      name.t ntr StudentizedRange alpha
##      Tukey ES2.root.noNAs$Condition  2          2.829835  0.05
##
## $means
##      ES2.root.noNAs$Length      std r   Min    Max    Q25    Q50    Q75
## Shaking                      27.54116 19.14552 37 0.759 67.578 14.983 24.544 36.420
## Stationary                    25.08983 18.19797 29 0.982 68.045 13.602 17.404 38.714
##
## $comparison
## NULL
##
## $groups
##      ES2.root.noNAs$Length groups
## Shaking                      27.54116      a
## Stationary                    25.08983      a
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable Concentration

```
ES2.root.noNAs.Concentration.HSD.test <- HSD.test(ES2.root.noNAs.lm, 'ES2.root.noNAs$Concentration', group = T)
ES2.root.noNAs.Concentration.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##      156.086 59 26.46406 47.20907
##
## $parameters
##      test                      name.t ntr StudentizedRange alpha
##      Tukey ES2.root.noNAs$Concentration  2          2.829835  0.05
##
## $means
##      ES2.root.noNAs$Length      std r   Min    Max    Q25    Q50    Q75
## 100fold                      33.41979 18.02719 43 2.261 68.045 16.7635 31.069 47.0615
## 25fold                      13.45987 11.57407 23 0.759 38.442  1.8595 14.252 19.0160
##
## $comparison
## NULL
##
## $groups
##      ES2.root.noNAs$Length groups
## 100fold                      33.41979      a
## 25fold                      13.45987      b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable Isolate

```
ES2.root.noNAs.isolate.HSD.test <- HSD.test(ES2.root.noNAs.lm, 'ES2.root.noNAs$Isolate', group = T)
ES2.root.noNAs.isolate.HSD.test
```

```
## $statistics
```

```
## MSerror Df Mean CV
## 156.086 59 26.46406 47.20907
##
## $parameters
## test name.t ntr StudentizedRange alpha
## Tukey ES2.root.noNAs$Isolate 5 3.97949 0.05
##
## $means
## ES2.root.noNAs$Length std r Min Max Q25 Q50 Q75
## Control 25.46106 14.42338 16 0.759 53.277 15.1875 21.304 32.42575
## DMCC2126 23.86656 15.08114 9 2.261 43.013 13.8810 28.594 35.49300
## DMCC2127 13.56456 13.67932 9 1.131 36.420 1.7050 15.283 15.82100
## DMCC2165 18.80955 13.95768 11 0.885 46.821 10.3030 15.075 27.10500
## DMCC2966 37.87933 21.47743 21 0.982 68.045 24.5440 33.212 58.57400
##
## $comparison
## NULL
##
## $groups
## ES2.root.noNAs$Length groups
## DMCC2966 37.87933 a
## Control 25.46106 b
## DMCC2126 23.86656 b
## DMCC2165 18.80955 b
## DMCC2127 13.56456 b
##
## attr("class")
## [1] "group"
```

```
#Tukey's HSD for Treatment and concentration
```

```
ES2.root.noNAs.leafsec.treat.dil.HSD.test <- HSD.test(ES2.root.noNAs.lm, c('ES2.root.noNAs$Isolate', 'ES2.root.noNAs$Concentration'), 'ES2.root.noNAs$Length', 'ES2.root.noNAs$leafsec.treat.dil.HSD.test')
```

```
## $statistics
## MSerror Df Mean CV
## 156.086 59 26.46406 47.20907
##
## $parameters
## test name.t ntr
## Tukey ES2.root.noNAs$Isolate:ES2.root.noNAs$Concentration 9
## StudentizedRange alpha
## 4.55324 0.05
##
## $means
## ES2.root.noNAs$Length std r Min Max Q25
## Control:100fold 34.51244 12.257238 9 19.375 53.277 26.42600
## Control:25fold 13.82357 6.234620 7 0.759 20.628 13.92700
## DMCC2126:100fold 23.86656 15.081139 9 2.261 43.013 13.88100
## DMCC2127:100fold 25.15625 11.174660 4 15.283 36.420 15.68650
## DMCC2127:25fold 4.29120 6.223480 5 1.131 15.405 1.20100
## DMCC2165:100fold 22.60056 12.426130 9 7.425 46.821 14.98300
## DMCC2165:25fold 1.75000 1.223295 2 0.885 2.615 1.31750
## DMCC2966:100fold 50.63417 17.328417 12 15.108 68.045 43.24375
## DMCC2966:25fold 20.87289 13.073765 9 0.982 38.442 13.88400
```

```
##           Q50      Q75
## Control:100fold 30.2620 41.43500
## Control:25fold 14.8050 16.35950
## DMCC2126:100fold 28.5940 35.49300
## DMCC2127:100fold 24.4610 33.93075
## DMCC2127:25fold 1.7050 2.01400
## DMCC2165:100fold 17.7060 30.29700
## DMCC2165:25fold 1.7500 2.18250
## DMCC2966:100fold 55.6675 64.10850
## DMCC2966:25fold 24.5440 29.70700
##
## $comparison
## NULL
##
## $groups
##           ES2.root.noNAs$Length groups
## DMCC2966:100fold          50.63417      a
## Control:100fold          34.51244     ab
## DMCC2127:100fold          25.15625     bc
## DMCC2126:100fold          23.86656     bc
## DMCC2165:100fold          22.60056     bc
## DMCC2966:25fold          20.87289     bc
## Control:25fold           13.82357      c
## DMCC2127:25fold           4.29120      c
## DMCC2165:25fold           1.75000      c
##
## attr("class")
## [1] "group"
```

Comparison after normalization of data

```
# Used the same Tukey's normalization methods used above
ES2.root.tuk = transformTukey(ES2.root.noNAs$Length, plotit=FALSE)
```

```
##
##      lambda      W Shapiro.p.value
## 427    0.65 0.964          0.0525
##
## if (lambda > 0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}
```

```
ES2.root.noNAs.mod = cbind(ES2.root.noNAs, ES2.root.tuk)
```

```
#ES2 longest root statistical analysis after normalization
ES2.root.noNAs.mod.lm <- lm (ES2.root.noNAs.mod$ES2.root.tuk ~ ES2.root.noNAs.mod$Isolete +
                           ES2.root.noNAs.mod$Condition +
                           ES2.root.noNAs.mod$Concentration, na.action=na.exclude)
ES2.root.noNAs.mod.lm
```

```
##
```



```
## Call:
## lm(formula = ES2.root.noNAs.mod$ES2.root.tuk ~ ES2.root.noNAs.mod$Isolate +
##      ES2.root.noNAs.mod$Condition + ES2.root.noNAs.mod$Concentration,
##      na.action = na.exclude)
##
## Coefficients:
##              (Intercept)      ES2.root.noNAs.mod$IsolateDMCC2126
##                   10.769                      -2.553
##      ES2.root.noNAs.mod$IsolateDMCC2127      ES2.root.noNAs.mod$IsolateDMCC2165
##                   -2.390                      -2.826
##      ES2.root.noNAs.mod$IsolateDMCC2966      ES2.root.noNAs.mod$ConditionStationary
##                   2.501                      -1.414
##      ES2.root.noNAs.mod$Concentration25fold
##                   -5.617
```

```
summary(ES2.root.noNAs.mod.lm)
```

```
##
## Call:
## lm(formula = ES2.root.noNAs.mod$ES2.root.tuk ~ ES2.root.noNAs.mod$Isolate +
##      ES2.root.noNAs.mod$Condition + ES2.root.noNAs.mod$Concentration,
##      na.action = na.exclude)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.015 -1.626  0.381  1.994  4.728
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.7694     0.7898  13.635 < 2e-16 ***
## ES2.root.noNAs.mod$IsolateDMCC2126      -2.5526     1.1779   -2.167  0.0343 *
## ES2.root.noNAs.mod$IsolateDMCC2127      -2.3895     1.1273   -2.120  0.0382 *
## ES2.root.noNAs.mod$IsolateDMCC2165      -2.8263     1.0762   -2.626  0.0110 *
## ES2.root.noNAs.mod$IsolateDMCC2966       2.5010     0.9064    2.759  0.0077 **
## ES2.root.noNAs.mod$ConditionStationary    -1.4140     0.6859   -2.062  0.0437 *
## ES2.root.noNAs.mod$Concentration25fold    -5.6168     0.7537   -7.452 4.64e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.697 on 59 degrees of freedom
## Multiple R-squared:  0.5978, Adjusted R-squared:  0.5569
## F-statistic: 14.61 on 6 and 59 DF,  p-value: 3.856e-10
```

```
anova(ES2.root.noNAs.mod.lm)
```

```
## Analysis of Variance Table
##
## Response: ES2.root.noNAs.mod$ES2.root.tuk
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES2.root.noNAs.mod$Isolate      4 221.55    55.39  7.6175 5.116e-05 ***
## ES2.root.noNAs.mod$Condition      1  12.18    12.18  1.6751  0.2006
## ES2.root.noNAs.mod$Concentration  1 403.79   403.79 55.5332 4.637e-10 ***
## Residuals                    59 429.00     7.27
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tukey's HSD for Variable Condition

```
ES2.root.noNAs.mod.condition.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, 'ES2.root.noNAs.mod$Condition'
ES2.root.noNAs.mod.condition.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  7.271182 59 7.841521 34.38763
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
##  Tukey ES2.root.noNAs.mod$Condition  2          2.829835  0.05
##
## $means
##      ES2.root.noNAs.mod$ES2.root.tuk      std r      Min      Max
## Shaking              8.046515 4.162235 37 0.8359054 15.46584
## Stationary              7.579976 3.961030 29 0.9882628 15.53522
##      Q25      Q50      Q75
## Shaking  5.809506 8.006901 10.34835
## Stationary 5.455591 6.403566 10.76748
##
## $comparison
## NULL
##
## $groups
##      ES2.root.noNAs.mod$ES2.root.tuk groups
## Shaking              8.046515      a
## Stationary              7.579976      a
##
## attr(,"class")
## [1] "group"
```

#Tukey's HSD for Variable Concentration

```
ES2.root.noNAs.mod.Concentration.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, 'ES2.root.noNAs.mod$Concen
ES2.root.noNAs.mod.Concentration.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##  7.271182 59 7.841521 34.38763
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
##  Tukey ES2.root.noNAs.mod$Concentration  2          2.829835  0.05
##
## $means
##      ES2.root.noNAs.mod$ES2.root.tuk      std r      Min      Max      Q25
## 100fold              9.428687 3.551457 43 1.6993990 15.53522 6.247133
## 25fold              4.874211 3.204748 23 0.8359054 10.71825 1.495429
##      Q50      Q75
```

```
## 100fold 9.332817 12.224510
## 25fold 5.623663 6.777533
##
## $comparison
## NULL
##
## $groups
## ES2.root.noNAs.mod$ES2.root.tuk groups
## 100fold 9.428687 a
## 25fold 4.874211 b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable Isolate

```
ES2.root.noNAs.mod.isolate.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, 'ES2.root.noNAs.mod$Isolate', gr
ES2.root.noNAs.mod.isolate.HSD.test
```

```
## $statistics
## MSerror Df Mean CV
## 7.271182 59 7.841521 34.38763
##
## $parameters
## test name.t ntr StudentizedRange alpha
## Tukey ES2.root.noNAs.mod$Isolate 5 3.97949 0.05
##
## $means
## ES2.root.noNAs.mod$ES2.root.tuk std r Min Max
## Control 7.870193 3.154754 16 0.8359054 13.25107
## DMCC2126 7.431287 3.579335 9 1.6993990 11.53028
## DMCC2127 4.788109 3.676082 9 1.0833049 10.34835
## DMCC2165 6.279095 3.393188 11 0.9236621 12.18390
## DMCC2966 10.122508 4.300847 21 0.9882628 15.53522
## Q25 Q50 Q75
## Control 5.860782 7.302137 9.581929
## DMCC2126 5.528069 8.842574 10.176367
## DMCC2127 1.414558 5.884853 6.018691
## DMCC2165 4.513060 5.832668 8.526954
## DMCC2966 8.006901 9.746345 14.093153
##
## $comparison
## NULL
##
## $groups
## ES2.root.noNAs.mod$ES2.root.tuk groups
## DMCC2966 10.122508 a
## Control 7.870193 ab
## DMCC2126 7.431287 ab
## DMCC2165 6.279095 b
## DMCC2127 4.788109 b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Treatment and concentration

```
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, c('ES2.root.noNAs.mod$'
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test
```

```
## $statistics
##      MSerror Df      Mean      CV
##      7.271182 59 7.841521 34.38763
##
## $parameters
##      test                                     name.t ntr
##      Tukey ES2.root.noNAs.mod$Isolate:ES2.root.noNAs.mod$Concentration    9
##      StudentizedRange alpha
##              4.55324  0.05
##
## $means
##              ES2.root.noNAs.mod$ES2.root.tuk      std  r      Min
## Control:100fold              9.866162 2.2929937  9 6.8660524
## Control:25fold              5.303948 2.0522425  7 0.8359054
## DMCC2126:100fold            7.431287 3.5793348  9 1.6993990
## DMCC2127:100fold            7.994262 2.3727767  4 5.8848527
## DMCC2127:25fold            2.223187 2.0740415  5 1.0833049
## DMCC2165:100fold            7.364275 2.6551730  9 3.6808888
## DMCC2165:25fold            1.395787 0.6676861  2 0.9236621
## DMCC2966:100fold           12.625081 3.0906845 12 5.8409641
## DMCC2966:25fold            6.785744 3.3449518  9 0.9882628
##
##              Max      Q25      Q50      Q75
## Control:100fold 13.251067 8.400796 9.174522 11.253530
## Control:25fold  7.151500 5.539627 5.764551  6.148213
## DMCC2126:100fold 11.530279 5.528069 8.842574 10.176367
## DMCC2127:100fold 10.348346 5.985232 7.871925  9.880956
## DMCC2127:25fold  5.915345 1.126427 1.414558  1.576299
## DMCC2165:100fold 12.183903 5.809506 6.475574  9.181418
## DMCC2165:25fold  1.867913 1.159725 1.395787  1.631850
## DMCC2966:100fold 15.535225 11.532042 13.630329 14.944422
## DMCC2966:25fold 10.718250 5.528846 8.006901  9.064800
##
## $comparison
## NULL
##
## $groups
##              ES2.root.noNAs.mod$ES2.root.tuk groups
## DMCC2966:100fold            12.625081      a
## Control:100fold            9.866162      ab
## DMCC2127:100fold            7.994262     abc
## DMCC2126:100fold            7.431287      bc
## DMCC2165:100fold            7.364275      bc
## DMCC2966:25fold            6.785744      bc
## Control:25fold            5.303948       c
## DMCC2127:25fold            2.223187       c
## DMCC2165:25fold            1.395787       c
##
## attr(,"class")
## [1] "group"
```

Plotting individual plots and composite figures

Individual plots for figure 1

Extract the information needed for panel “A”

```
##Extract all control (ES5: 7 DOE)
ES5.control <- subset(ES5.mod, Treatment== "control")
ES5.Xn <- subset(ES5.mod, Treatment== c("DMCC2126", "DMCC2127", "DMCC2165"))

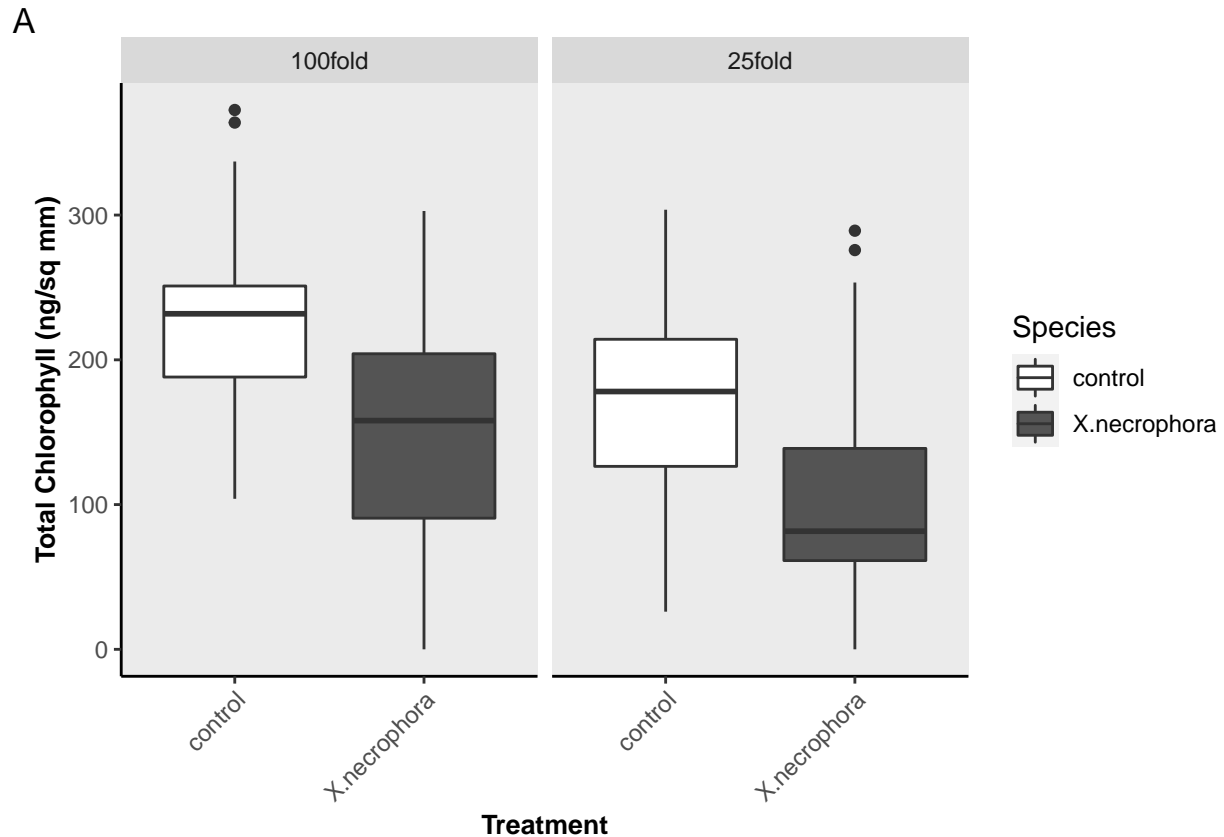
ES5.control <- ES5.control %>%
  add_column(Species = "control")

ES5.Xn <- ES5.Xn %>%
  add_column(Species = "X.necrophora")

ES5.mod.v2 <- rbind(ES5.control, ES5.Xn)

ES5.mod.ggplot <- ggplot(ES5.mod.v2, aes(x = reorder(Species, -chl, na.rm = TRUE),
                                              y = chl, fill = Species)) +
  geom_boxplot() + #geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  #scale_fill_grey(start = 1, end = 0.4) + labs(tag = "A") +
  scale_fill_manual(values = c("#FFFFFF", "#545454"))+ labs(tag = "A") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +
  facet_wrap(~ Dilution)
ES5.mod.ggplot
```

```
## Warning: Removed 8 rows containing non-finite values (stat_boxplot).
```



Individual plot for panel B

```
##Extract all control (ES2), colletrichum, and X. necrophora
ES2.control <- subset(ES2.mod, Treatment== "control")
ES2.coll <- subset(ES2.mod, Treatment== "DMCC2966")
ES2.Xn <- subset(ES2.mod, Treatment== c("DMCC2126", "DMCC2127", "DMCC2165"))

ES2.control <- ES2.control %>%
  add_column(Species = "control")

ES2.coll <- ES2.coll %>%
  add_column(Species = "C.siamense")

ES2.Xn <- ES2.Xn %>%
  add_column(Species = "X.necrophora")

ES2.mod.v2 <- rbind(ES2.control, ES2.coll, ES2.Xn)

#plot for figure by species by dilution factor

#Reorganizing for plotting

ES2.mod.v2$Species <- factor(ES2.mod.v2$Species,
  levels = c("control", "C.siamense", "X.necrophora"))
```

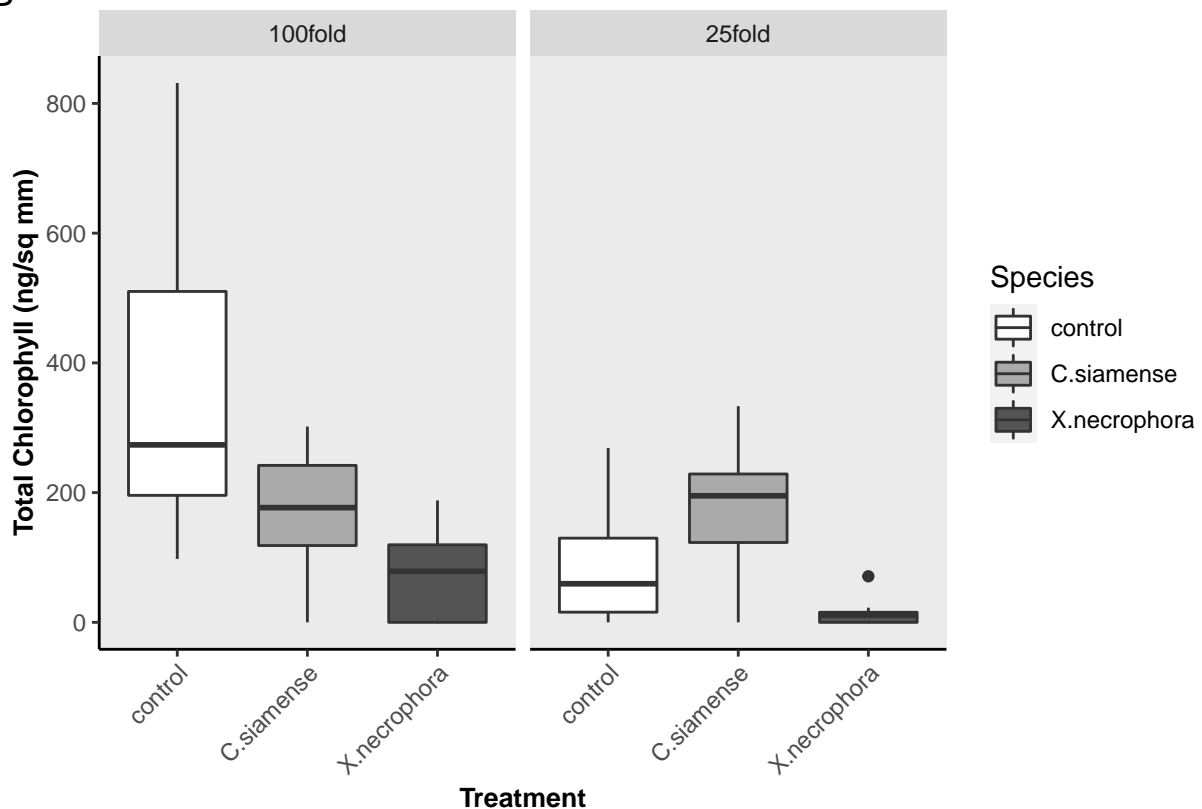
```

#Plot with ggplot
ES2.mod.v2.ggplot <- ggplot(ES2.mod.v2, aes(x = reorder(Species, -chl, na.rm = TRUE),
                                                    y = chl, fill = Species)) + geom_boxplot() + #geom_point(ae
# scale_fill_grey("control" = 1, "C.siamense" =0.7, "X.necrophora"= 0.4)
scale_fill_manual(values = c("#FFFFFF", "#AAAAAA", "#545454"))+ labs(tag = "B") +
xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
      axis.title.x = element_text(size=10, face = "bold"),
      axis.title.y = element_text(size = 10, face = "bold"),
      axis.text.x = element_text(angle = 45, hjust = 1)) +
theme(panel.border = element_blank(),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      axis.line = element_line(colour = "black")) +
facet_wrap(~ Dilution)
ES2.mod.v2.ggplot

```

```
## Warning: Removed 32 rows containing non-finite values (stat_boxplot).
```

B

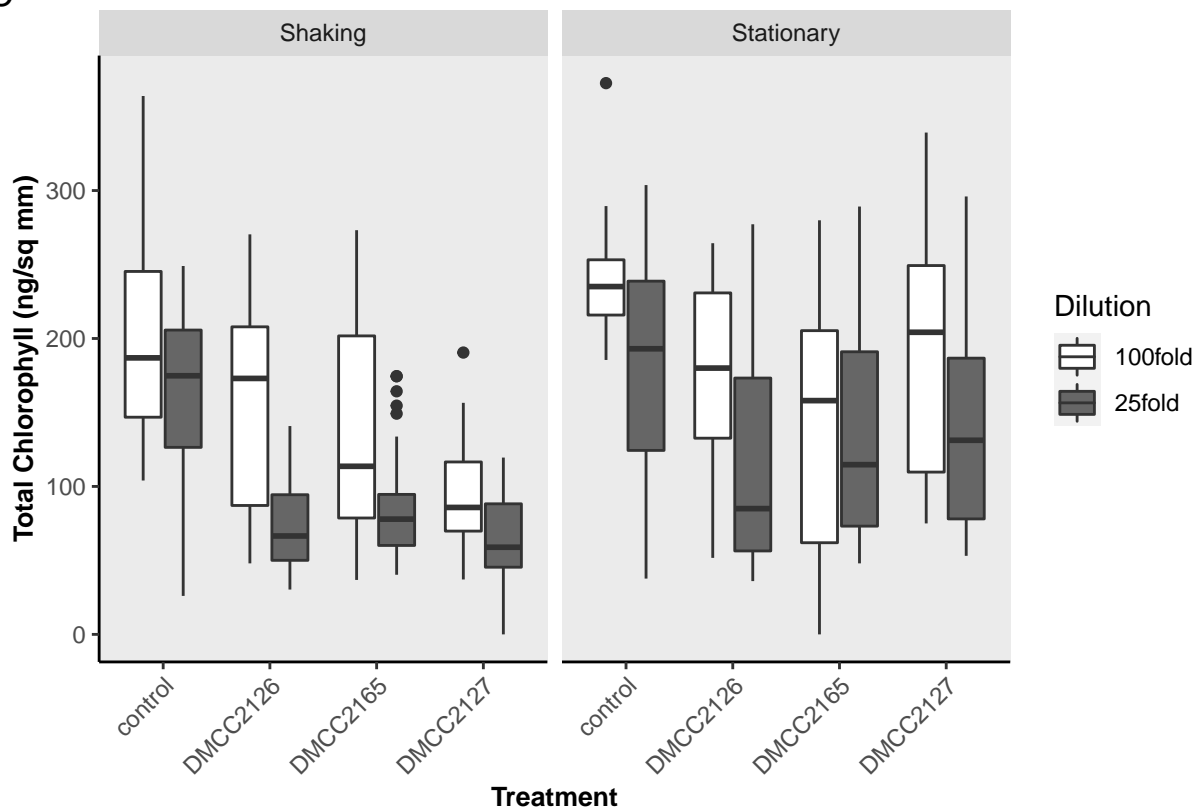


Individual panel C

```
#ES5 by treatment by dilution, no title
ES5.mod.ggplot.v2 <- ggplot(ES5.mod, aes(x = reorder(Treatment, -chl, na.rm = TRUE),
                                                    y = chl, fill = Dilution)) +
  geom_boxplot() + #geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "C") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black")) +
  facet_wrap(~ Condition)
ES5.mod.ggplot.v2
```

```
## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```

C



```
#Reorder for visualization purposes
ES5.mod.new <- ES5.mod
ES5.mod.new$Condition <- factor(ES5.mod.new$Condition, # Reordering group factor levels
                                levels = c("Stationary", "Shaking"))
```



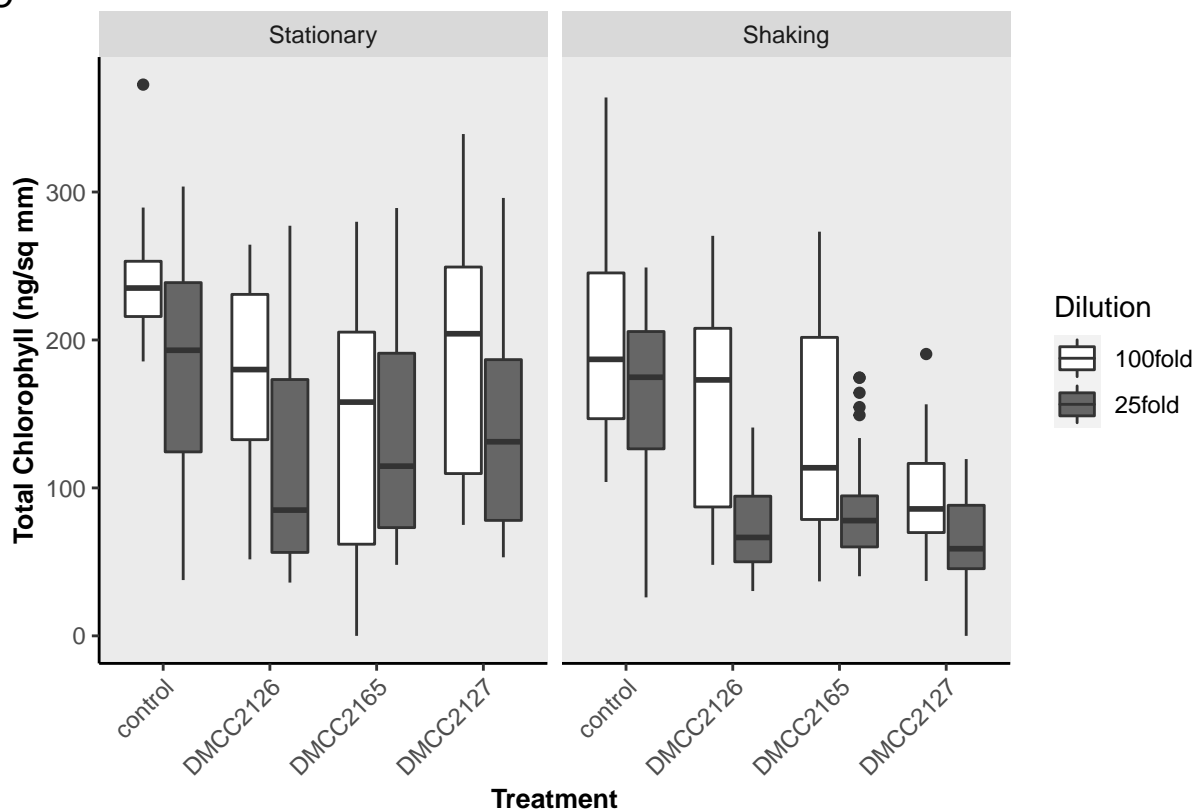
```

#Plot reordered factors
ES5.mod.ggplot.v3 <- ggplot(ES5.mod.new, aes(x = reorder(Treatment, -chl, na.rm = TRUE),
                                                    y = chl, fill = Dilution)) +
  geom_boxplot() + #geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "C") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black")) +
  facet_wrap(~ Condition)
ES5.mod.ggplot.v3

```

```
## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```

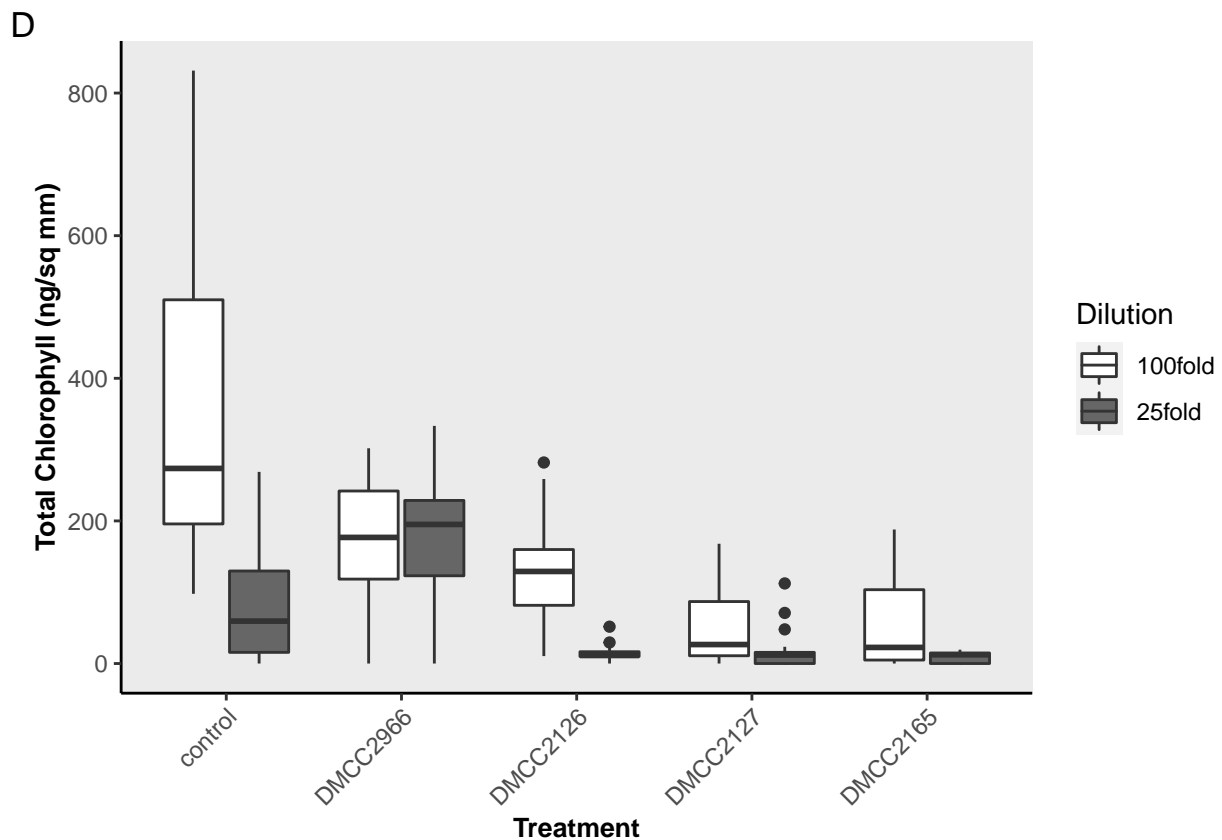
C



Individual panel D

```
#ES2 by treatment by dilution, by growth conditions no title
ES2.mod.ggplot.v2 <- ggplot(ES2.mod, aes(x = reorder(Treatment, -chl, na.rm = TRUE),
                                                  y = chl, fill = Dilution)) +
  geom_boxplot() + #geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "D") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"))
ES2.mod.ggplot.v2
```

```
## Warning: Removed 60 rows containing non-finite values (stat_boxplot).
```



Plot composite figure 1

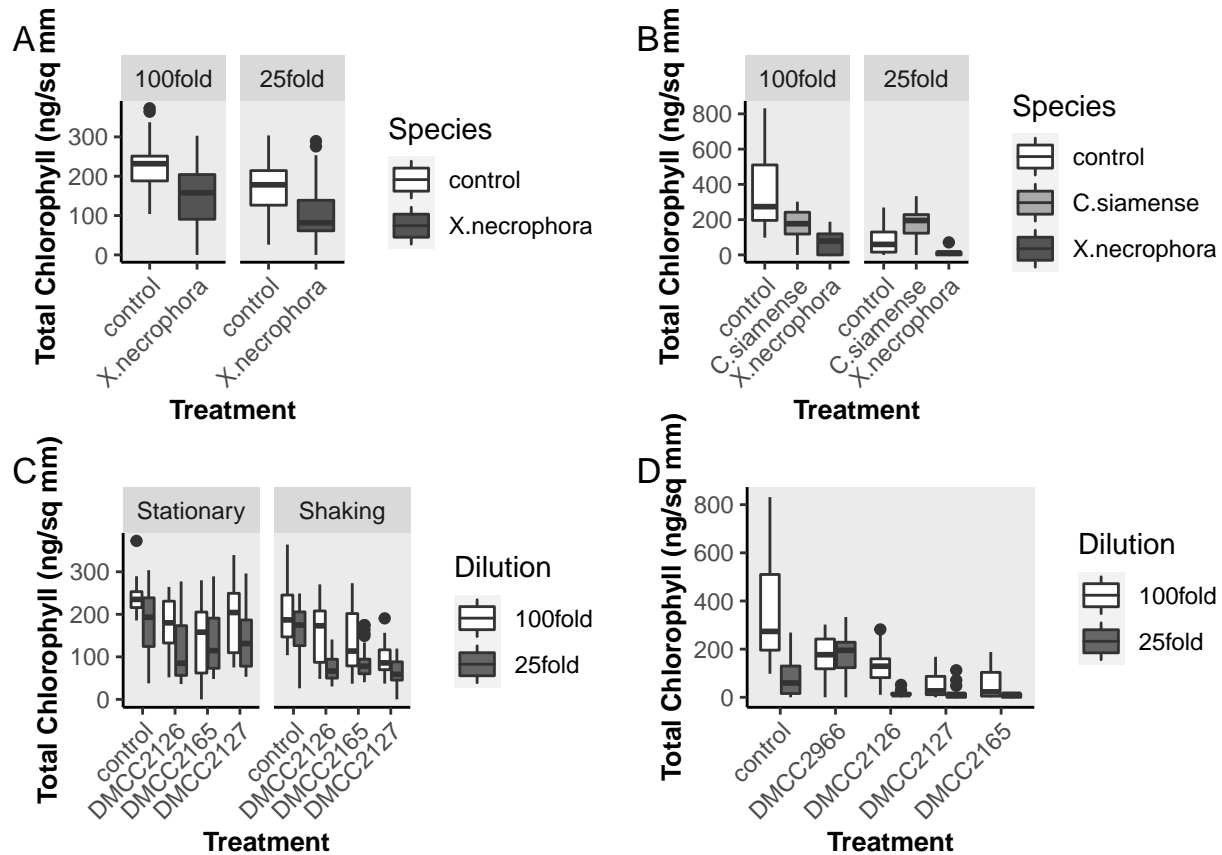
```
###Grid for composite figure 1 (updated 05/11/2022). Using ES2 and ES5 only.
gridExtra::grid.arrange(ES5.mod.ggplot, ES2.mod.v2.ggplot, ES5.mod.ggplot.v3, ES2.mod.ggplot.v2, ncol=2)
```

```
## Warning: Removed 8 rows containing non-finite values (stat_boxplot).

## Warning: Removed 32 rows containing non-finite values (stat_boxplot).

## Warning: Removed 12 rows containing non-finite values (stat_boxplot).

## Warning: Removed 60 rows containing non-finite values (stat_boxplot).
```



Plotting root length panel (Figure 2)

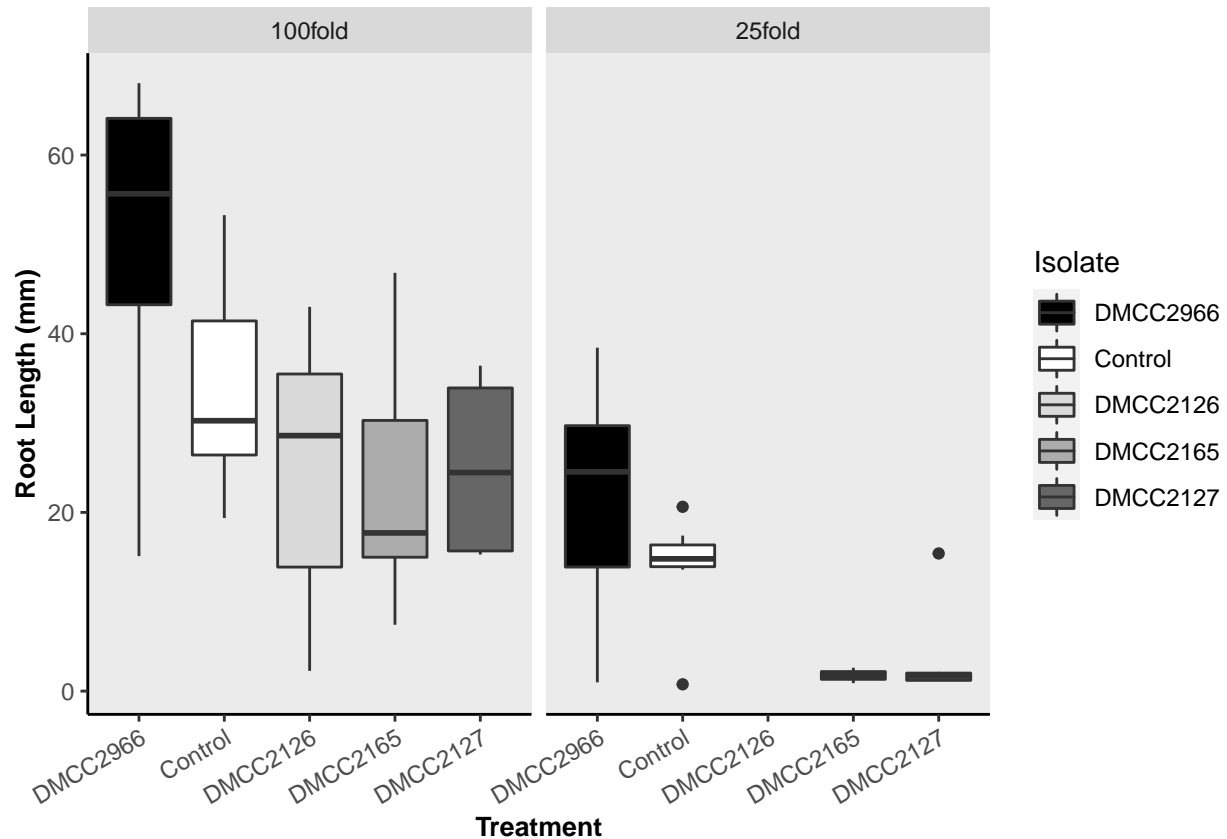
```
#Plate for Figure 2 FINAL (USE THIS ONE, because no differences between Shaking and stat were observed)
ES2.root.noNAs.mod$Isolate <- with(ES2.root.noNAs.mod, reorder(Isolate, -Length))
ES2.root.noNAs.mod.ggplot.plate <- ggplot(ES2.root.noNAs.mod, aes(x = Isolate,
  y = Length,
  fill = Isolate)) +

  geom_boxplot() +
  #scale_fill_grey(start = 1, end = 0.4) +
  #scale_fill_manual(values = c("Control"="green", "DMCC2966"="green", "DMCC2126"="gold", "DMCC2165"="g
  #ggtitle("Root Length at 14 Days After Exposure") +
  scale_fill_manual(values = c("#000000", "#FFFFFF", "#DADADA", "#ACACAC", "#666666")) + #labs(tag
  xlab("Treatment") + ylab("Root Length (mm)") +
  theme(plot.title = element_text(size = 14, hjust = 0.5, face = "bold"),
```

```

axis.title.x = element_text(size=10, face = "bold"),
axis.title.y = element_text(size = 10, face = "bold"),
axis.text.x = element_text(angle = 30, hjust = 1)) +
theme(panel.border = element_blank(),
panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
axis.line = element_line(colour = "black")) +
facet_wrap(~ Concentration)
ES2.root.noNAs.mod.ggplot.plate

```



```
#dev.off()
```

Plotting individual plots and composite figure 4

Individual panels A, B, C, and D.

```

###Plot HostVariety only w/ outliers
ES13B.ByHosCult <- ggplot(ES13B.mod, aes(x = reorder(HostVariety, -chl, na.rm = TRUE),
y = chl, fill=HostVariety)) +
  geom_boxplot() +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "A") +
  xlab("Soybean Cultivar") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),

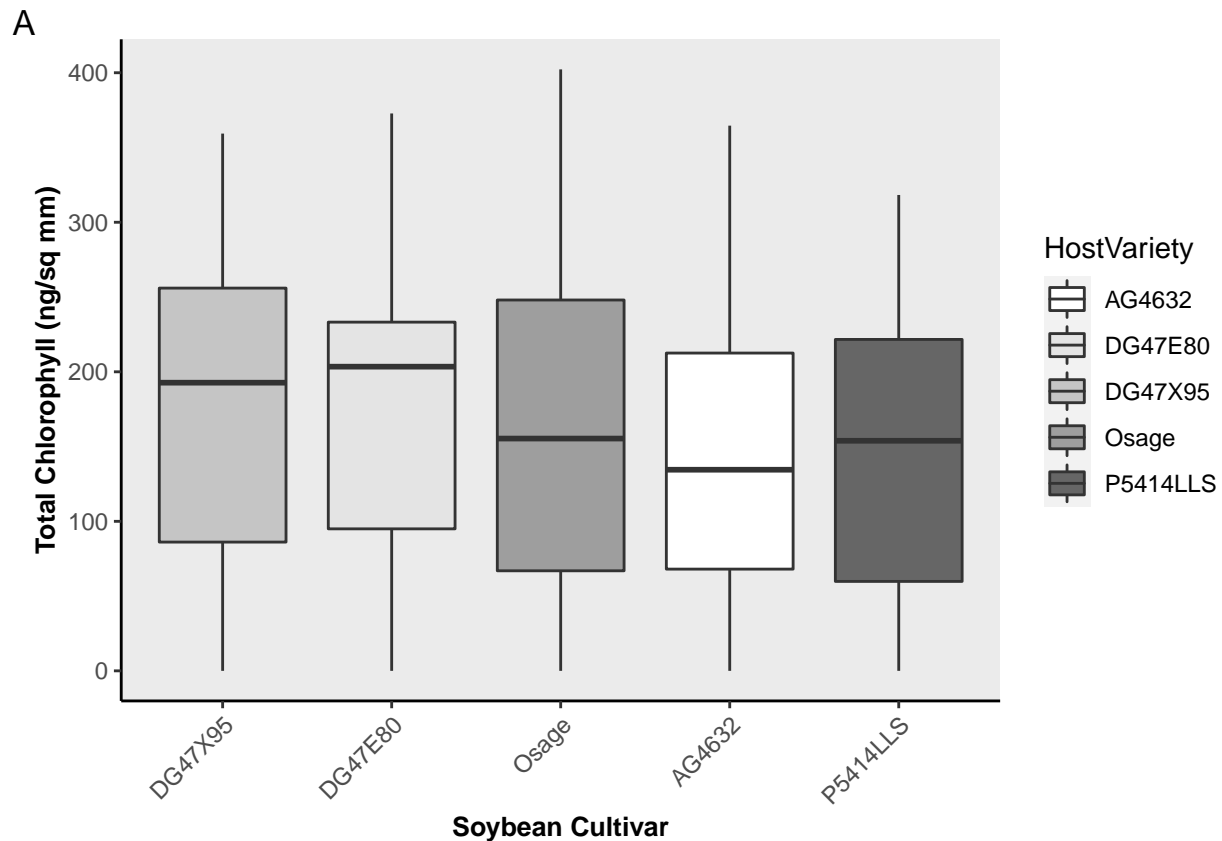
```

```

axis.title.x = element_text(size=10, face = "bold"),
axis.title.y = element_text(size = 10, face = "bold"),
axis.text.x = element_text(angle = 45, hjust = 1)) +
theme(panel.border = element_blank(),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      axis.line = element_line(colour = "black"))
ES13B.ByHosCult

```

Warning: Removed 6 rows containing non-finite values (stat_boxplot).



Individual panel B

```

####Plot by variety by treatment w/ outliers
ES13B.ggplot.ByCultByTreat <- ggplot(ES13B.mod, aes(x = reorder(HostVariety, -chl,
                                                             na.rm = TRUE),
                                                             y = chl, fill=Treatment)) +
  geom_boxplot() + #+ geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "B") +
  xlab("Soybean Cultivar") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),

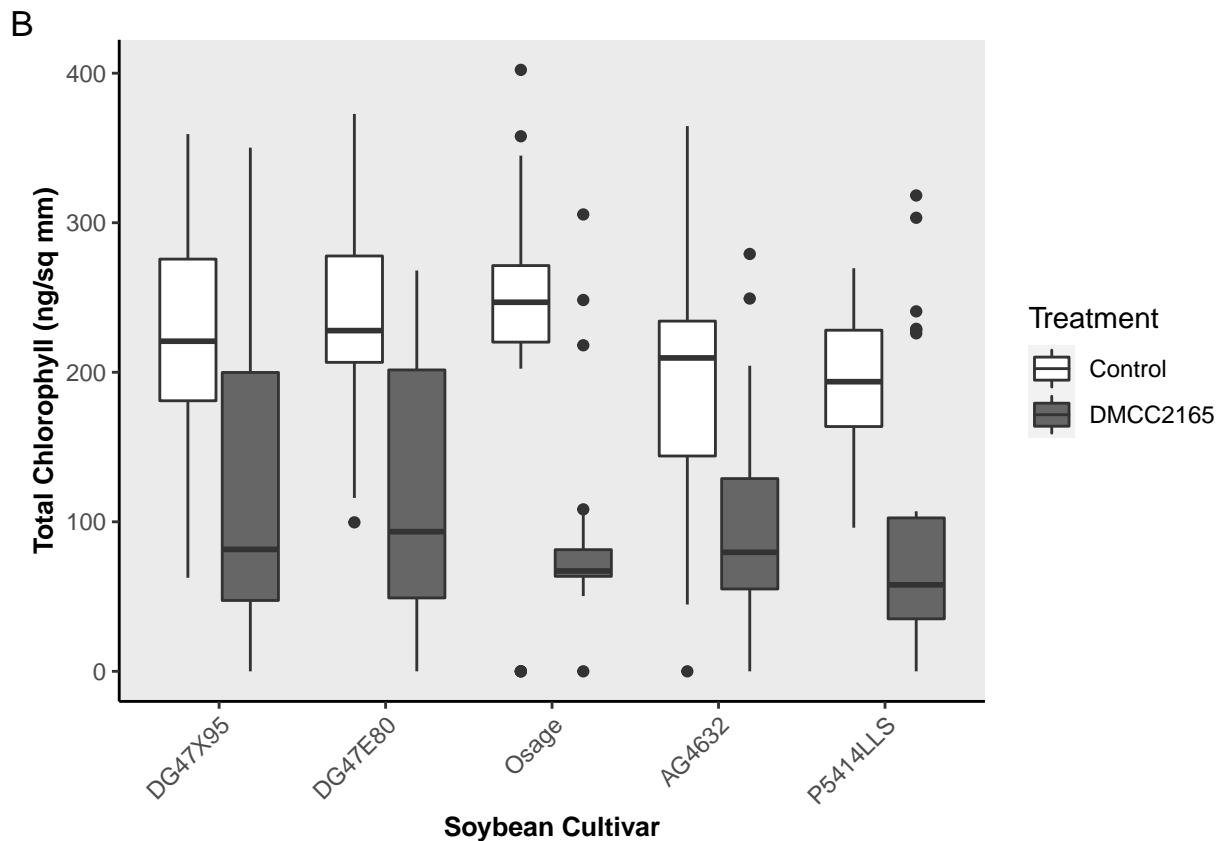
```

```

axis.title.y =element_text(size = 10, face = "bold"),
axis.text.x = element_text(angle = 45, hjust = 1)) +
theme(panel.border = element_blank(),
panel.grid.major = element_blank(),
panel.grid.minor = element_blank(),
axis.line = element_line(colour = "black"))
ES13B.ggplot.ByCultByTreat

```

Warning: Removed 6 rows containing non-finite values (stat_boxplot).



Panel C

```

###Plot By Host only w/ outliers for grid
ES14A.ggplot.ByHost <- ggplot(ES14A.mod, aes(x = reorder(Host, -chl, na.rm = TRUE),
y = chl, fill=Host)) +
  geom_boxplot() + #+ geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "C") +
  xlab("Plant Species") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
axis.title.x = element_text(size=10, face = "bold"),
axis.title.y = element_text(size = 10, face = "bold"),
axis.text.x = element_text(angle = 45, hjust = 1)) +

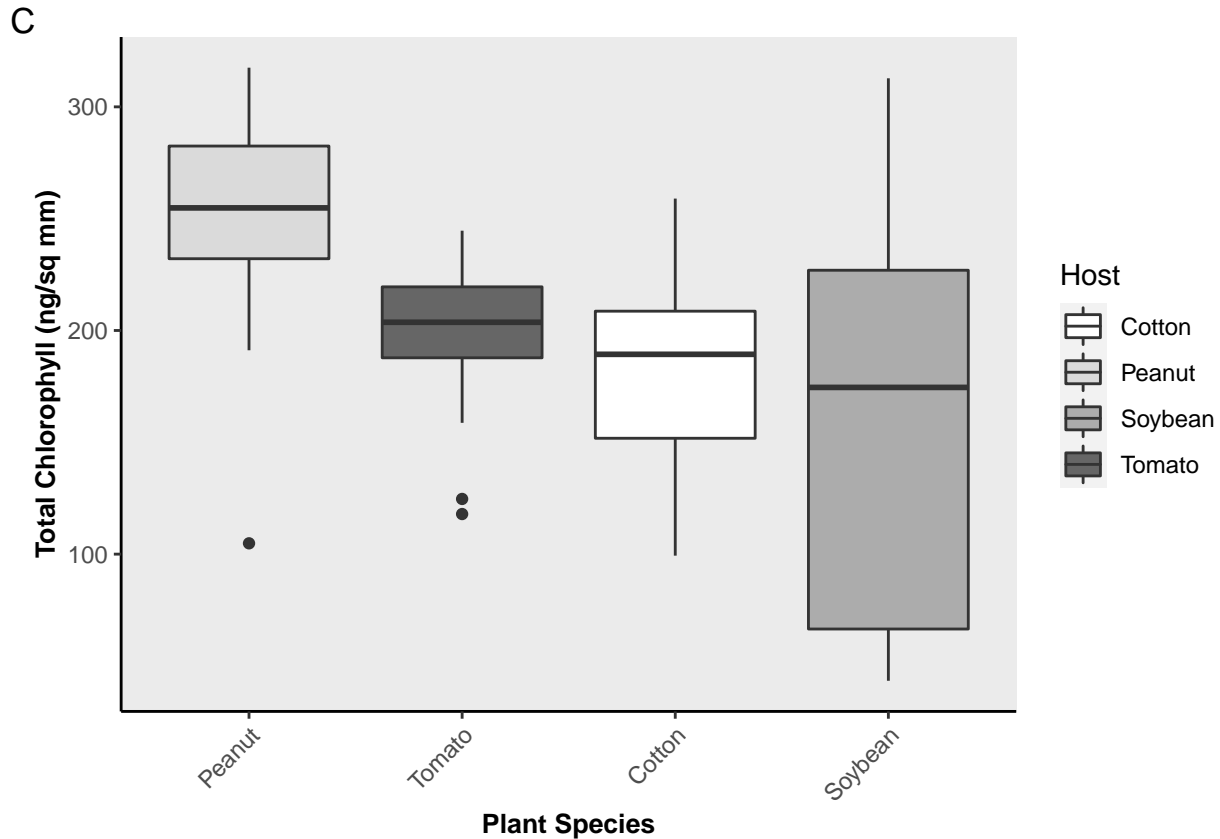
```

```

theme(panel.border = element_blank(),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      axis.line = element_line(colour = "black"))
ES14A.ggplot.ByHost

```

Warning: Removed 3 rows containing non-finite values (stat_boxplot).



Panel D

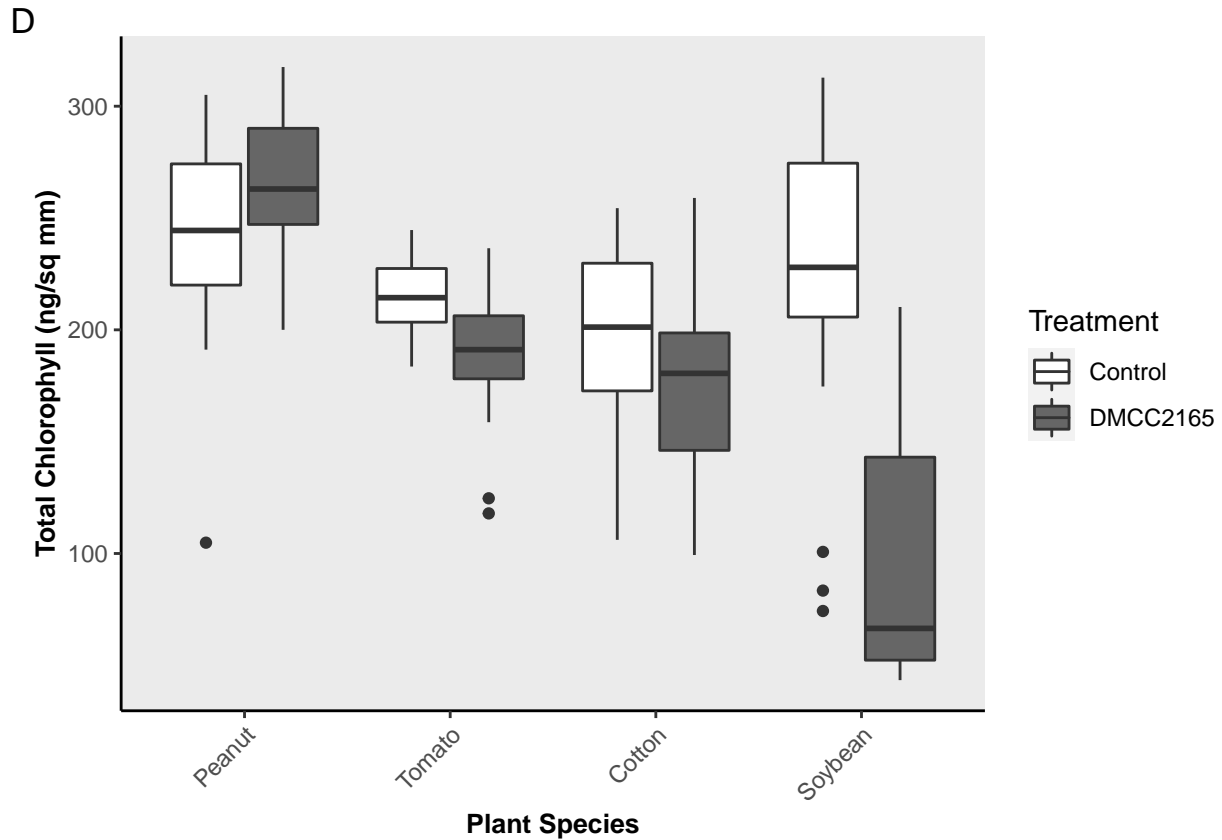
```

###Plot by host by treatment w/ outliers
ES14A.ggplot.ByHostByTreat <- ggplot(ES14A.mod, aes(x = reorder(Host, -chl, na.rm = TRUE),
                                                    y = chl, fill=Treatment)) +
  geom_boxplot() + #+ geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "D") +
  xlab("Plant Species") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(), panel.grid.minor = element_blank(),

```

```
axis.line = element_line(colour = "black"))
ES14A.ggplot.ByHostByTreat
```

```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```

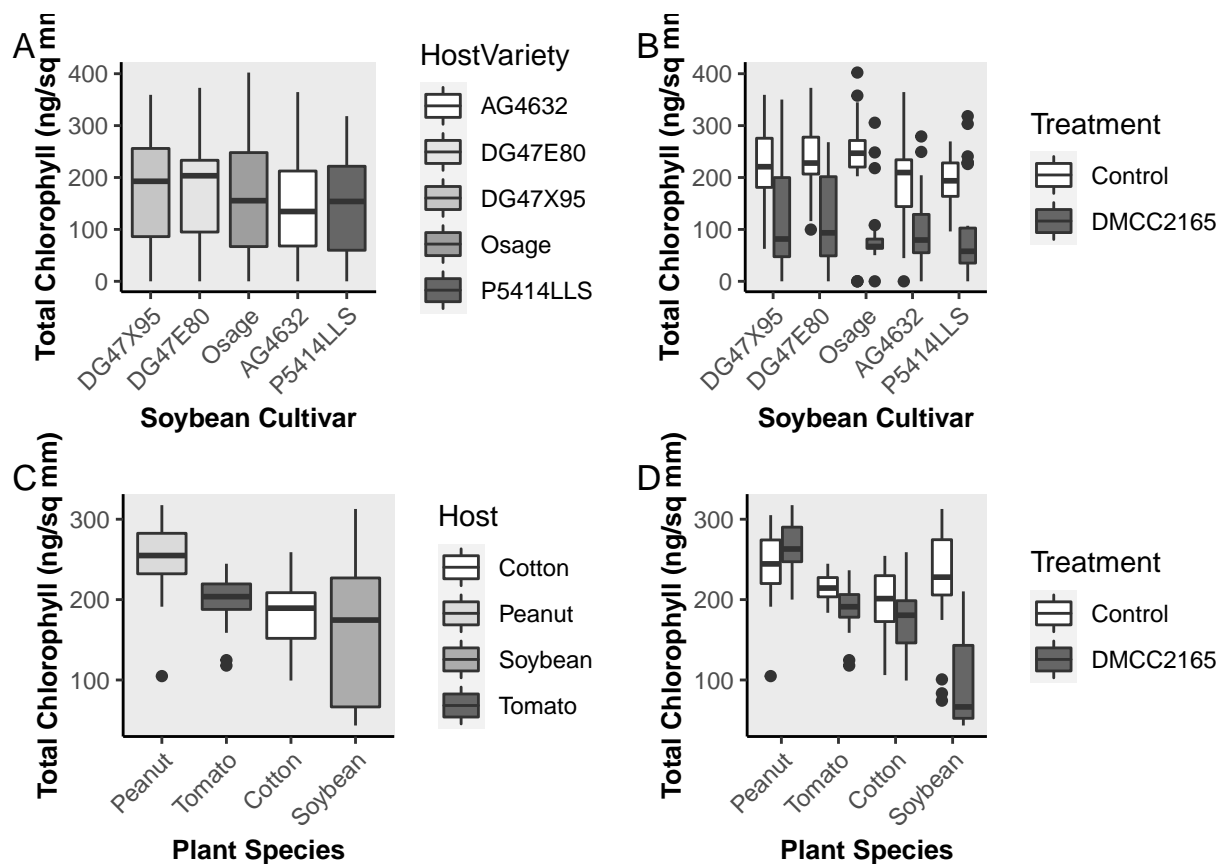


Composite figure 4

```
###Grid for composite figure 4 (05/14/2022). Using ES13B and ES14 only.
gridExtra::grid.arrange(ES13B.ByHosCult,
  ES13B.ggplot.ByCultByTreat ,
  ES14A.ggplot.ByHost,
  ES14A.ggplot.ByHostByTreat, ncol=2)
```

```
## Warning: Removed 6 rows containing non-finite values (stat_boxplot).
## Removed 6 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
## Removed 3 rows containing non-finite values (stat_boxplot).
```

Supplementary Materials/Figures

Plotting Supplementary Figure 1

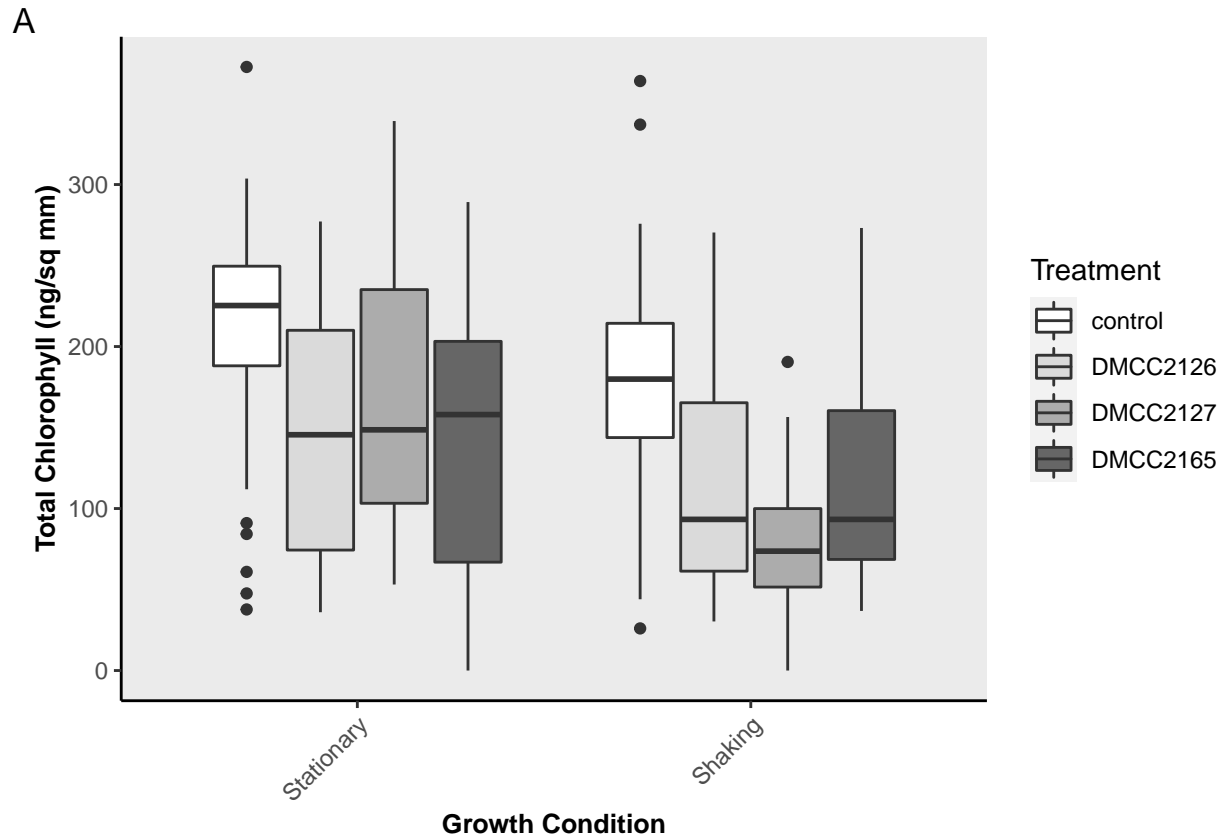
This composite figure contains the comparisons between fermentation conditions (shaking vs stationary) and dilutions (25 vs 100-fold) per strains.

```
#Panel A

#ES5 by conditions (side by side)
ES5.mod.ggplot.v3 <- ggplot(ES5.mod, aes(x = reorder(Condition, -chl, na.rm = TRUE),
                                              y = chl, fill=Treatment)) +

  geom_boxplot() +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "A") +
  xlab("Growth Condition") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"))
ES5.mod.ggplot.v3
```

```
## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```

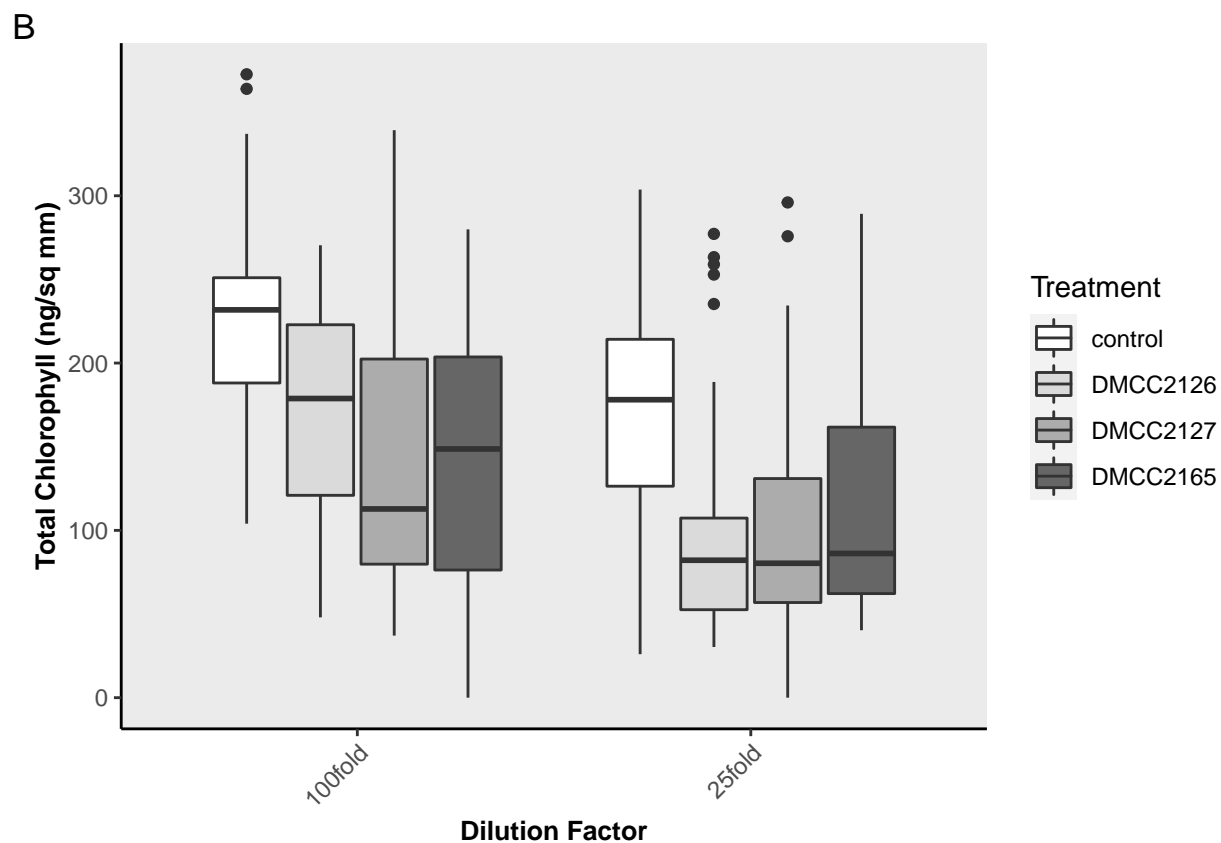


#Panel B

#ES5 by dilutions (side by side)

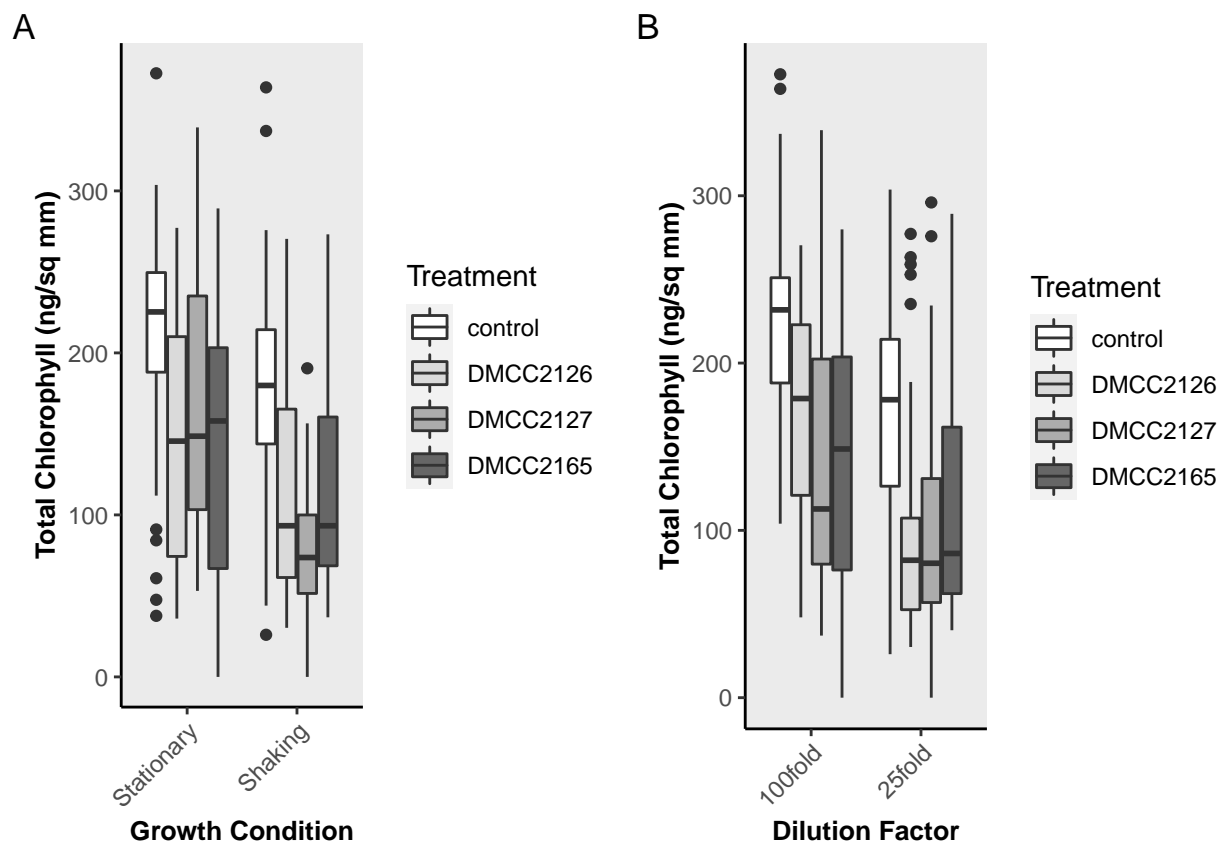
```
ES5.mod.ggplot.v4 <- ggplot(ES5.mod, aes(x = reorder(Dilution, -chl, na.rm = TRUE),
                                                  y = chl, fill=Treatment)) +
  geom_boxplot() +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "B") +
  xlab("Dilution Factor") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"))
ES5.mod.ggplot.v4
```

```
## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
```



```
###Grid for supplementary figure 1 (updated 05/14/2022). Using ES2 and ES5 only.
gridExtra::grid.arrange(ES5.mod.ggplot.v3,
  ES5.mod.ggplot.v4,
  ncol=2)
```

```
## Warning: Removed 12 rows containing non-finite values (stat_boxplot).
## Removed 12 rows containing non-finite values (stat_boxplot).
```



Plotting Supplementary Figure 2

This composite figure contained validation chlorophyll content (chemical vs digital extractions) on panel A, fungal biomass based on Whatmat No 1 filter weight on panel B, measurements of pH from initial potato dextrose broth and filtered stock cell-free culture filtrates (CFCFs) on panel C, and the pearson correlation between final pH and digital chlorophyll content on panel D.

Loading datasets for composite figure

```
#Load datasets
ES10.chem <- read.csv("../raw_data/ES10.chem.chl.csv", header = T)
#Chlorophyll content obtained chemically for a dataset with all biomass and pH measurements

ES10.digital <- read.csv("../raw_data/ES10.digital.chl.csv", header = T)
#Chlorophyll content obtained digitally for a dataset with all biomass and pH measurements

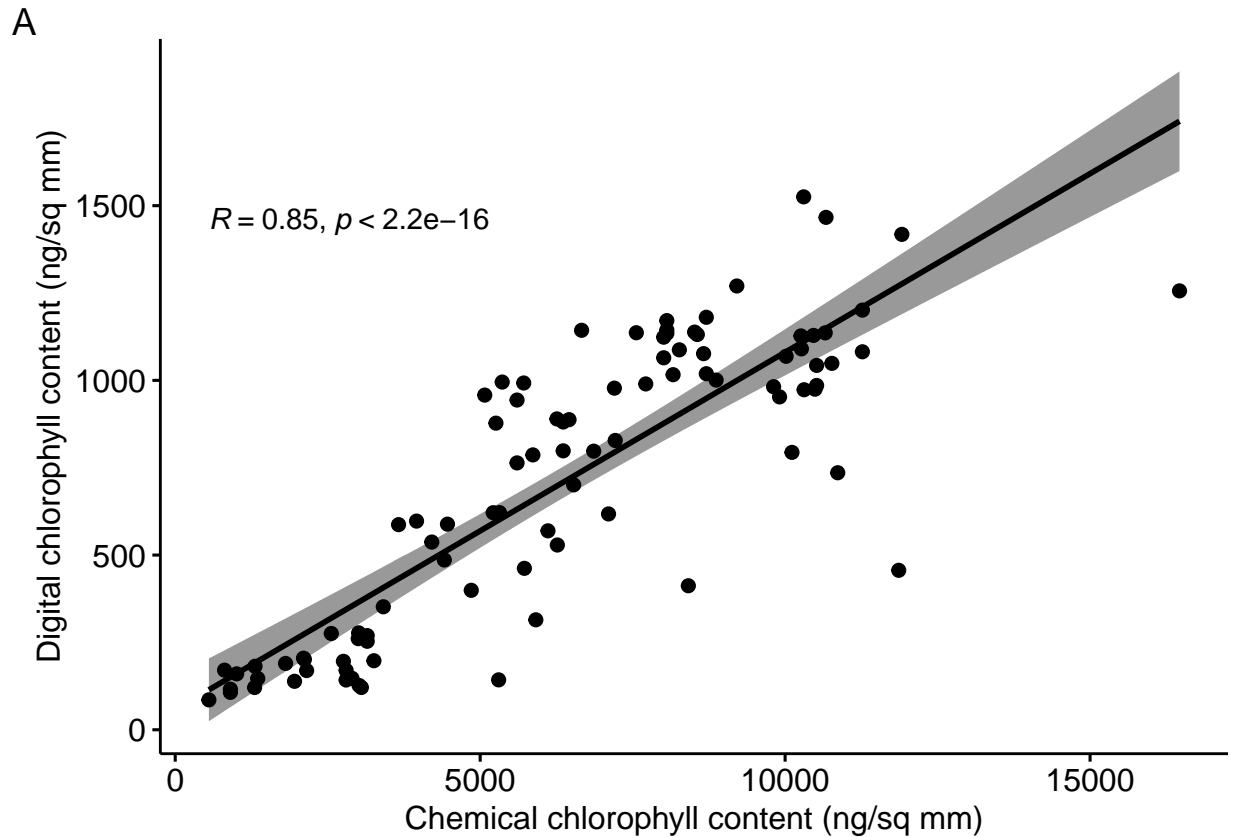
BiomassAndpH.metadata <- read.csv("../raw_data/FilteringTreatments.metadata.csv",
                                     header = T)
```

Summarizing and aggregating datasets

```
#Obtaining sums for ES10 because digital measurements=3 per experimental unit,  
#but chemical measurements=1 per experimental unit.  
  
ES10.digital.sum <- aggregate(ES10.digital$chl,list(ES10.digital$ExpCode),sum)  
  
names(ES10.digital.sum)[names(ES10.digital.sum) == "x"] <- "dig.chl"  
  
#Merging ES10 chem and ES10 digital  
ES10.chem.dig = merge(ES10.chem, ES10.digital.sum, by.x='ExpCode', by.y='Group.1')  
  
#Pearson correlations for ES10  
cor(ES10.chem.dig$chl, ES10.chem.dig$dig.chl, method="pearson")  
  
## [1] 0.8450695
```

Plotting Supplementary Figure 2 panel A

```
ES10.chem.dig.ggplot <- ggscatter(ES10.chem.dig, x = "chl", y = "dig.chl",  
                                add = "reg.line", conf.int = TRUE,  
                                cor.coef = TRUE,  
                                cor.method = "pearson",  
                                xlab = "Chemical chlorophyll content (ng/sq mm)",  
                                ylab = "Digital chlorophyll content (ng/sq mm)") +  
  labs(tag = "A")  
  
ES10.chem.dig.ggplot  
  
## 'geom_smooth()' using formula 'y ~ x'
```

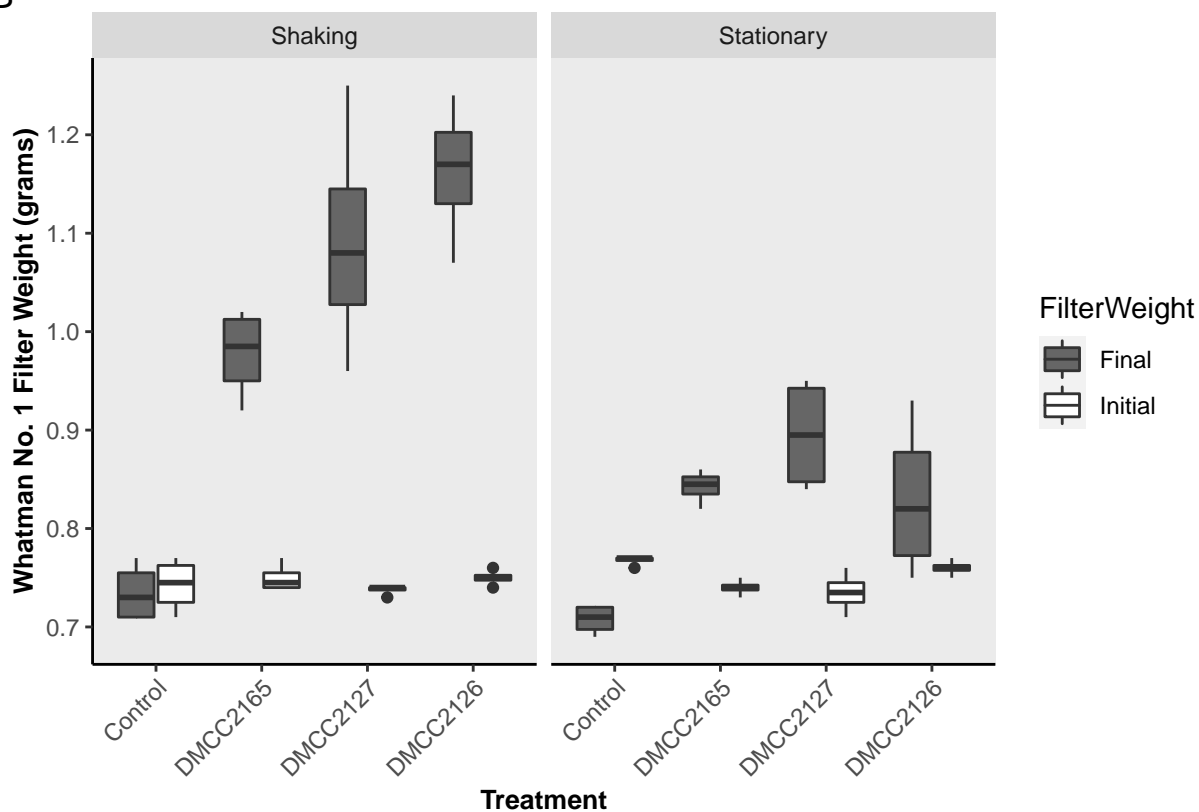


Plotting Biomass by Treatment by Condition

(Supplementary Figure 2, Panel B)

```
# Supplementary figure 2 panel B
## ES5 by dilutions (side by side)
BiomassAndpH.metadata.ggplot.B <- ggplot(BiomassAndpH.metadata,
                                           aes(x = reorder(Isolate, +Weight_grams),
                                               y = Weight_grams, fill=FilterWeight)) +
  geom_boxplot() + #geom_point(aes(colour = factor(LeafSampleNumber)))# + geom_jitter()
  scale_fill_grey(start = 0.4, end = 1) + labs(tag = "B") +
  xlab("Treatment") + ylab("Whatman No. 1 Filter Weight (grams)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size = 10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black")) +
  facet_wrap(~ Condition)
BiomassAndpH.metadata.ggplot.B
```

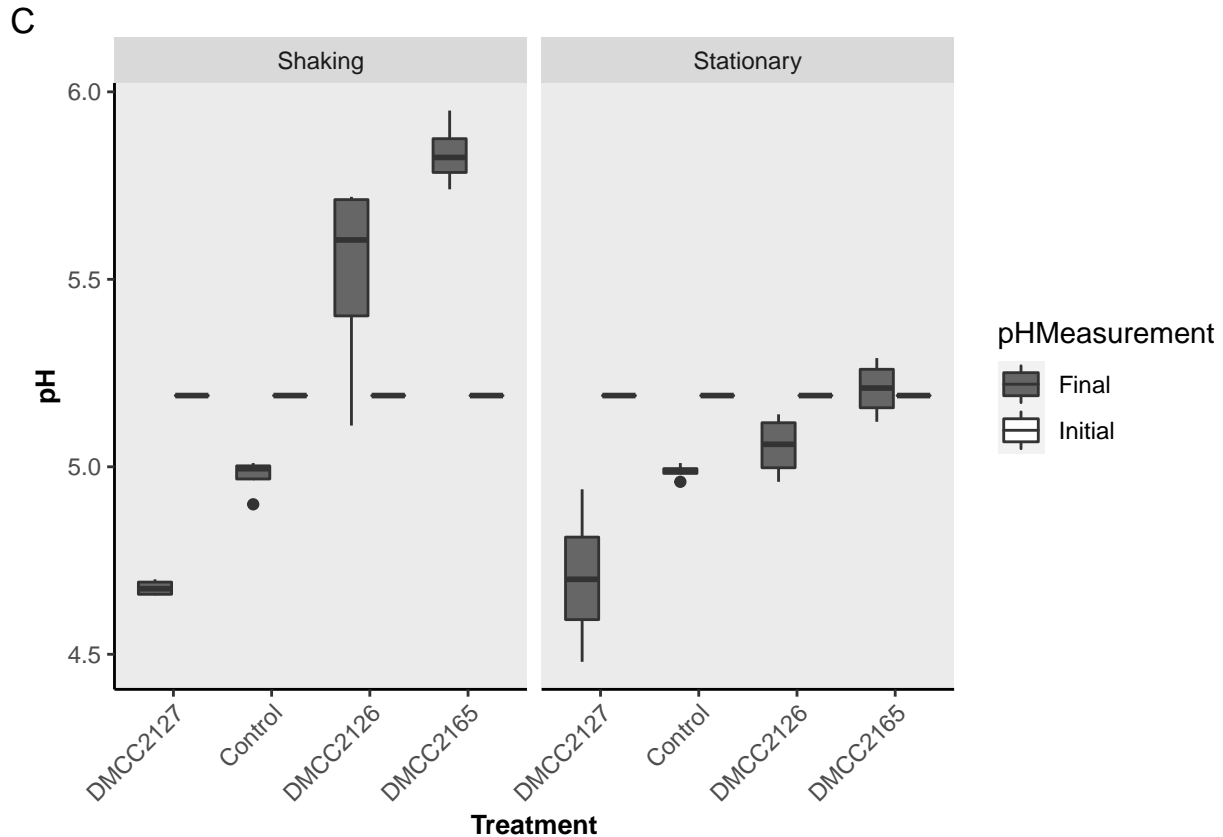
B



Supplementary figure 2 panel C

```
#ES5 by dilutions (side by side)
BiomassAndpH.metadata.pH.ggplot.C <- ggplot(BiomassAndpH.metadata,
      aes(x = reorder(Isolate, +pH),
          y = pH, fill=pHMeasurement)) +

  geom_boxplot() +
  scale_fill_grey(start =0.4, end = 1) + labs(tag = "C") +
  xlab("Treatment") + ylab("pH") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black")) +
  facet_wrap(~ Condition)
BiomassAndpH.metadata.pH.ggplot.C
```



Supplementary figure 2 panel D

```
ES8.chem <- read.csv("../raw_data/ES8_chem.chl.csv", header = T)
ES8.digital <- read.csv("../raw_data/ES8.digital.chl.csv", header = T)

ES8.digital.sum <- aggregate(ES8.digital$chl, list(ES8.digital$ExpCode), sum)
names(ES8.digital.sum)[names(ES8.digital.sum) == "x"] <- "dig.chl"

ES8.chem.dig = merge(ES8.chem, ES8.digital.sum, by.x='ExpCode', by.y='Group.1')

FinalpHvsChl.reg <- ggscatter(ES8.chem.dig, x = "dig.chl", y = "FinalpH",
                             add = "reg.line", conf.int = TRUE,
                             cor.coef = TRUE, cor.method = "pearson",
                             xlab = "Digital chlorophyll content (ng/sq mm)",
                             ylab = "Final pH") + labs(tag = "D")

FinalpHvsChl.reg

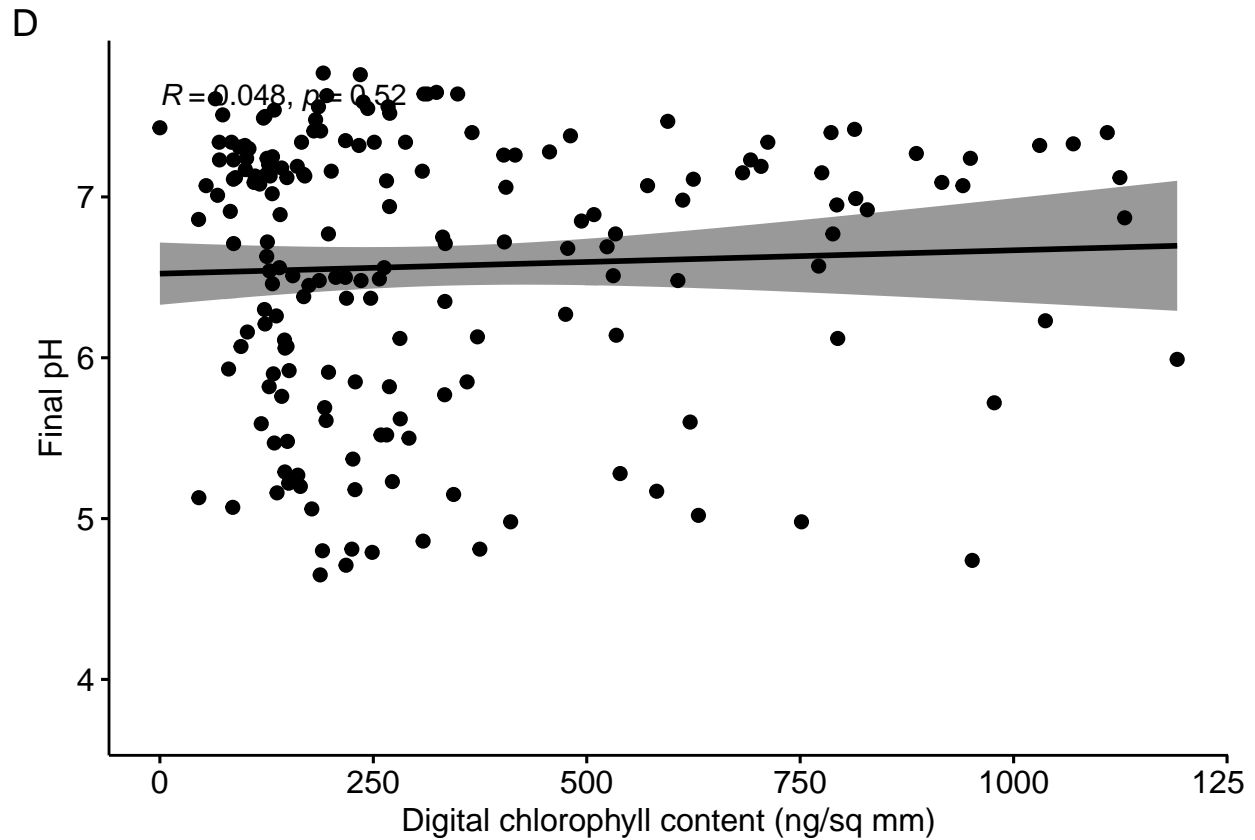
## 'geom_smooth()' using formula 'y ~ x'

## Warning: Removed 11 rows containing non-finite values (stat_smooth).

## Warning: Removed 11 rows containing non-finite values (stat_cor).
```



```
## Warning: Removed 11 rows containing missing values (geom_point).
```



Supplementary Figure 2 composite. Updated on 08/02/2021

```
gridExtra::grid.arrange(ES10.chem.dig.ggplot, BiomassAndpH.metadata.ggplot.B, BiomassAndpH.metadata.pH.)
```

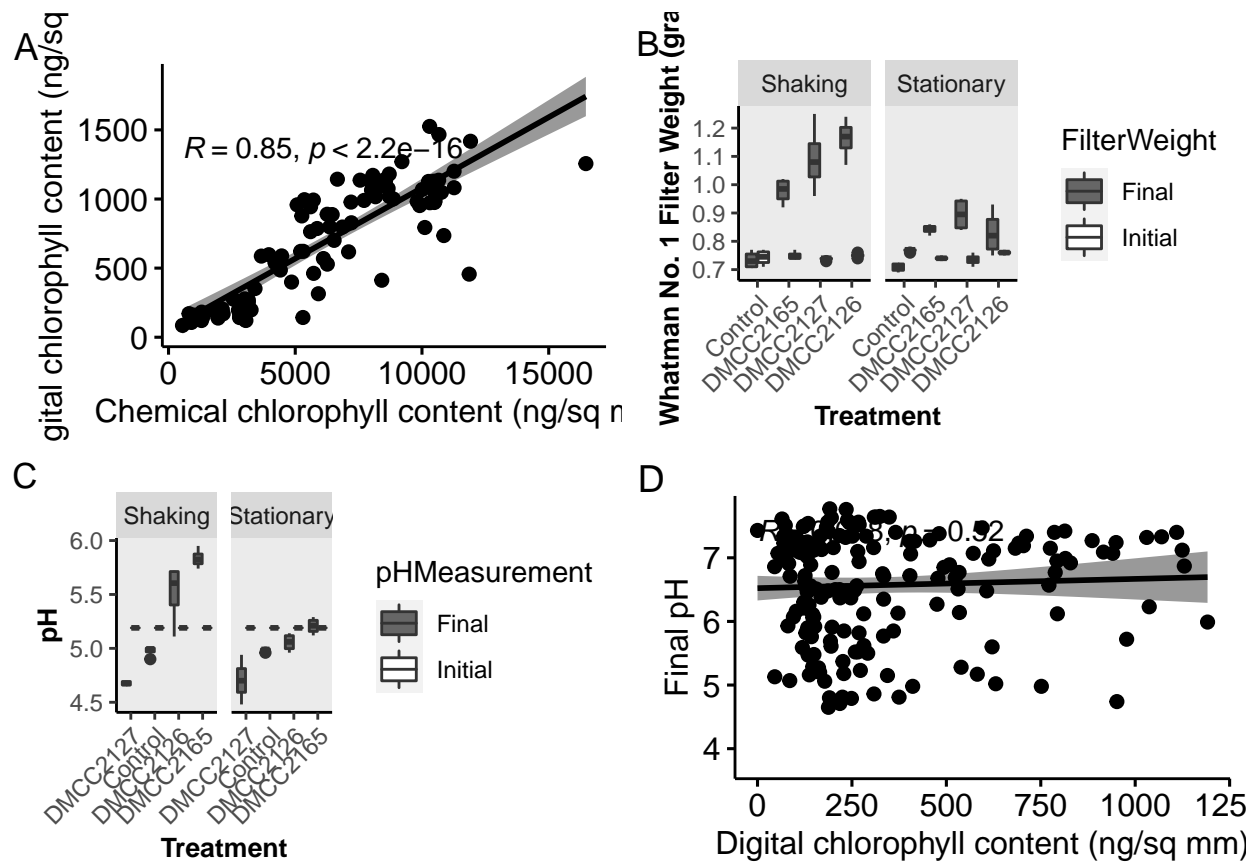
```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## 'geom_smooth()' using formula 'y ~ x'
```

```
## Warning: Removed 11 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 11 rows containing non-finite values (stat_cor).
```

```
## Warning: Removed 11 rows containing missing values (geom_point).
```



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