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/donwloaded 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 demosntration, 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 exporuse (DOE)

#ES4 = Repetetion 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.
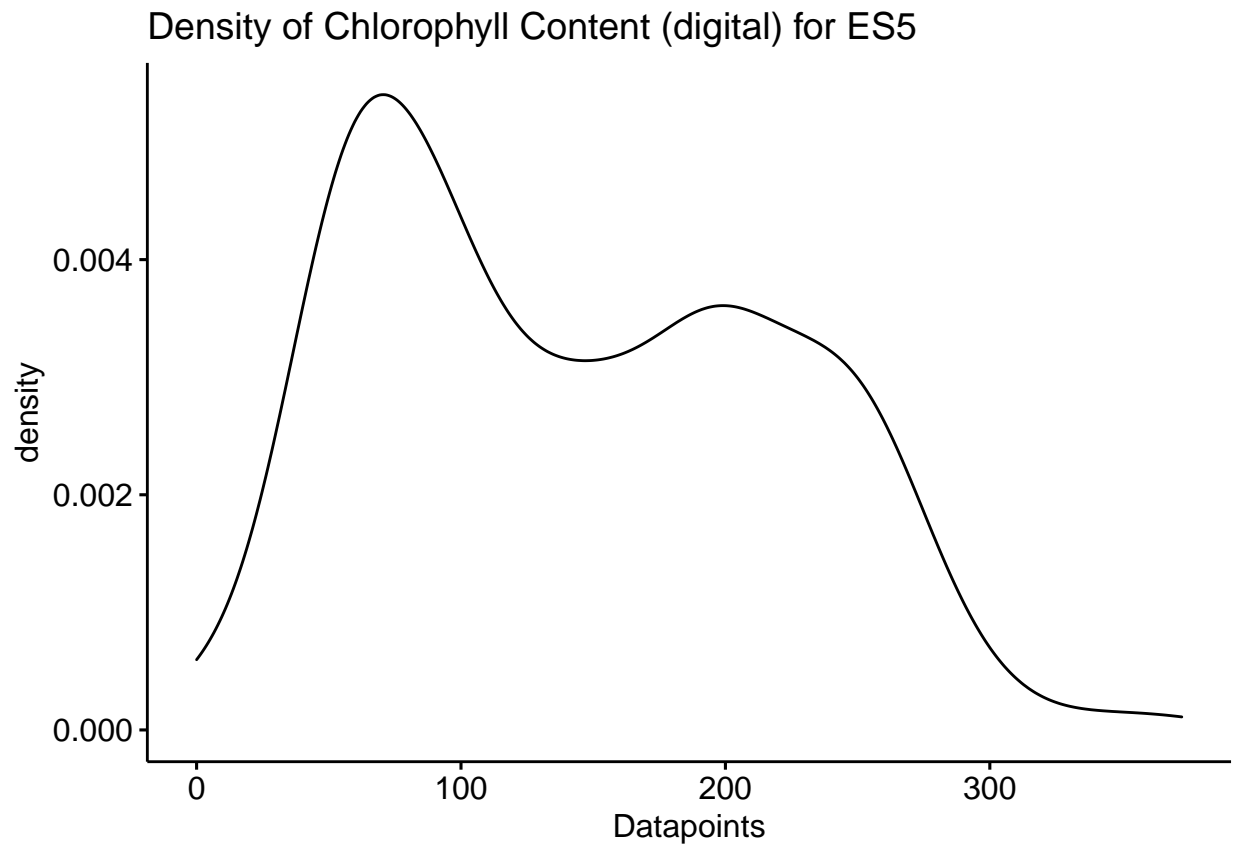
```
ggdensity(ES2$chl, main = "Density of Chlorophyll Content (digital) for ES2",
          xlab = "Datapoints")
```

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

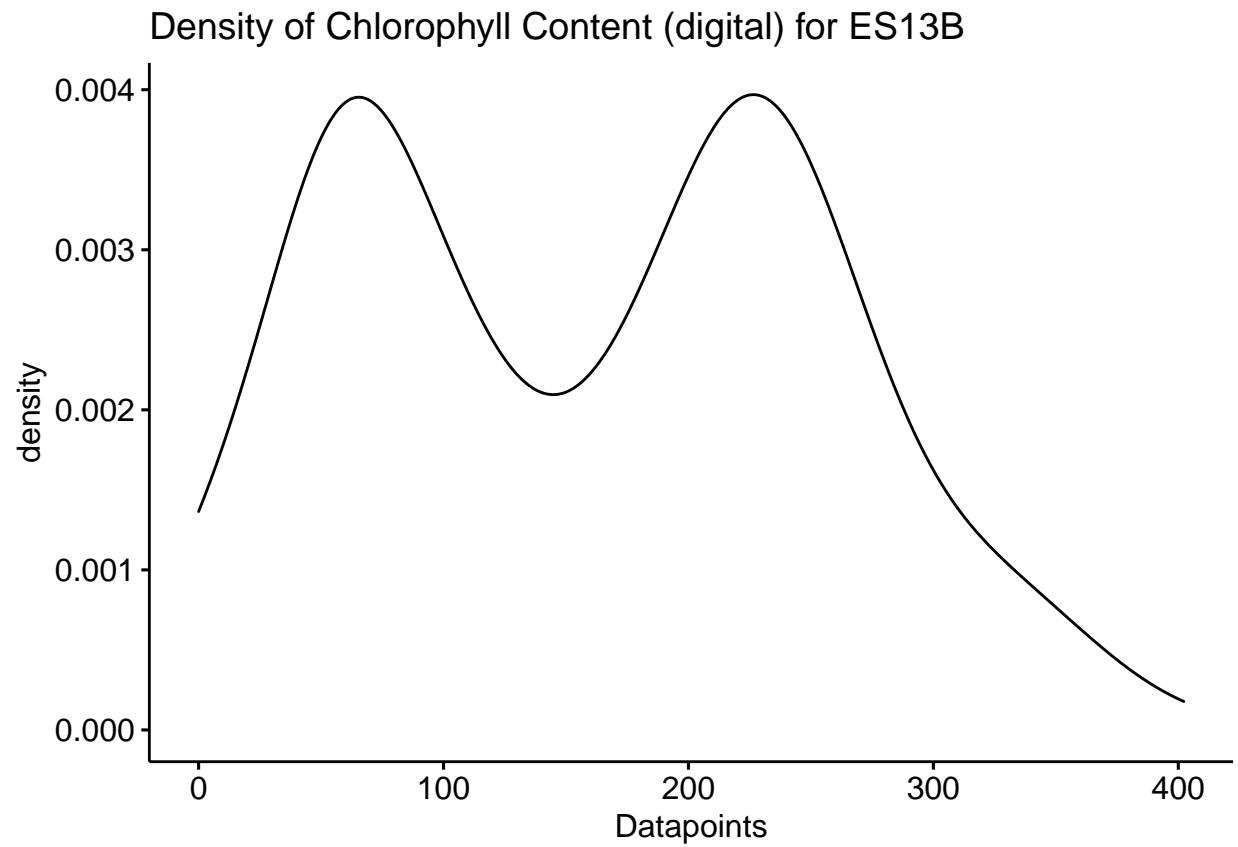## Density of Chlorophyll Content (digital) for ES2
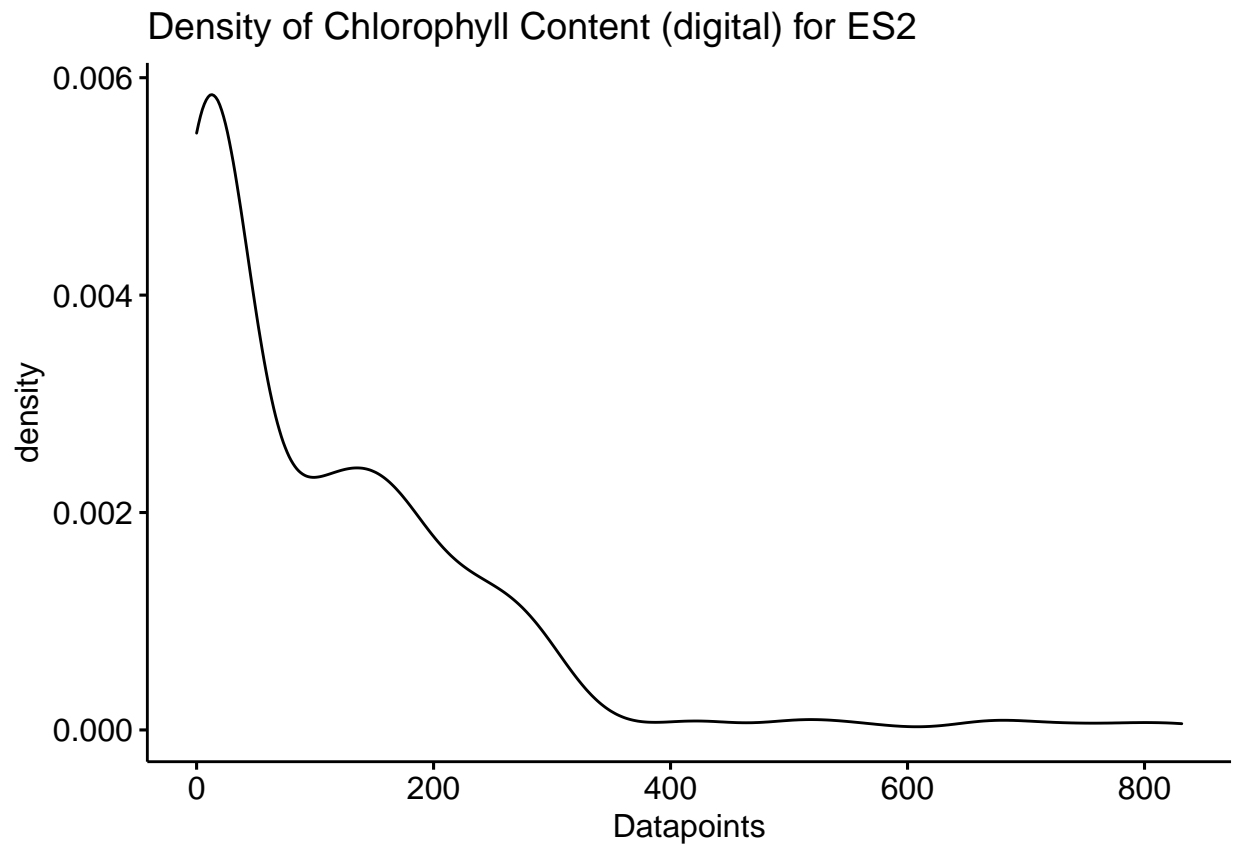

```
ggdensity(ES5$chl, main = "Density of Chlorophyll Content (digital) for ES5",
          xlab = "Datapoints")
```

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

Density of Chlorophyll Content (digital) for ES5


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

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

Density of Chlorophyll Content (digital) for ES13B


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

```
## Warning: Removed 3 rows containing non-finite values (stat_density).
```
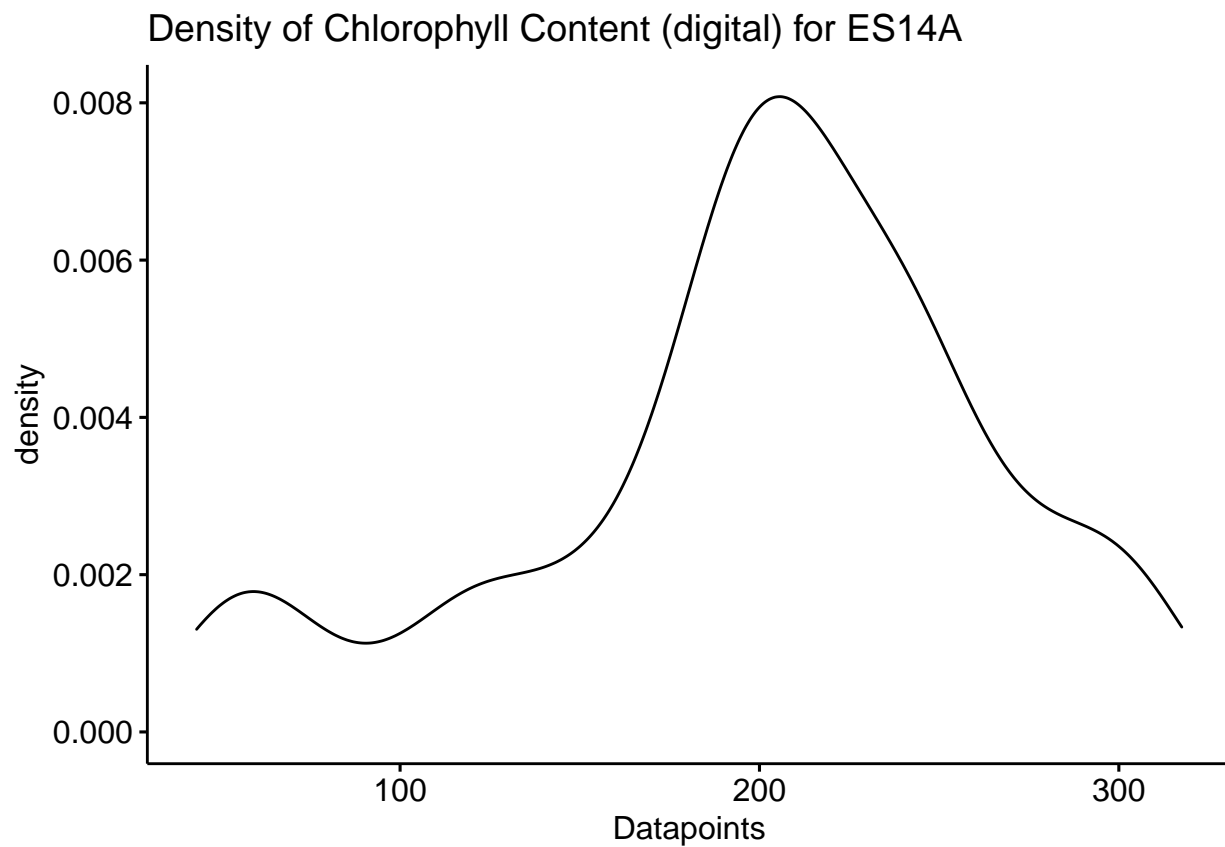
Density of Chlorophyll Content (digital) for ES14A


```
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$chl)
```

```
## 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).
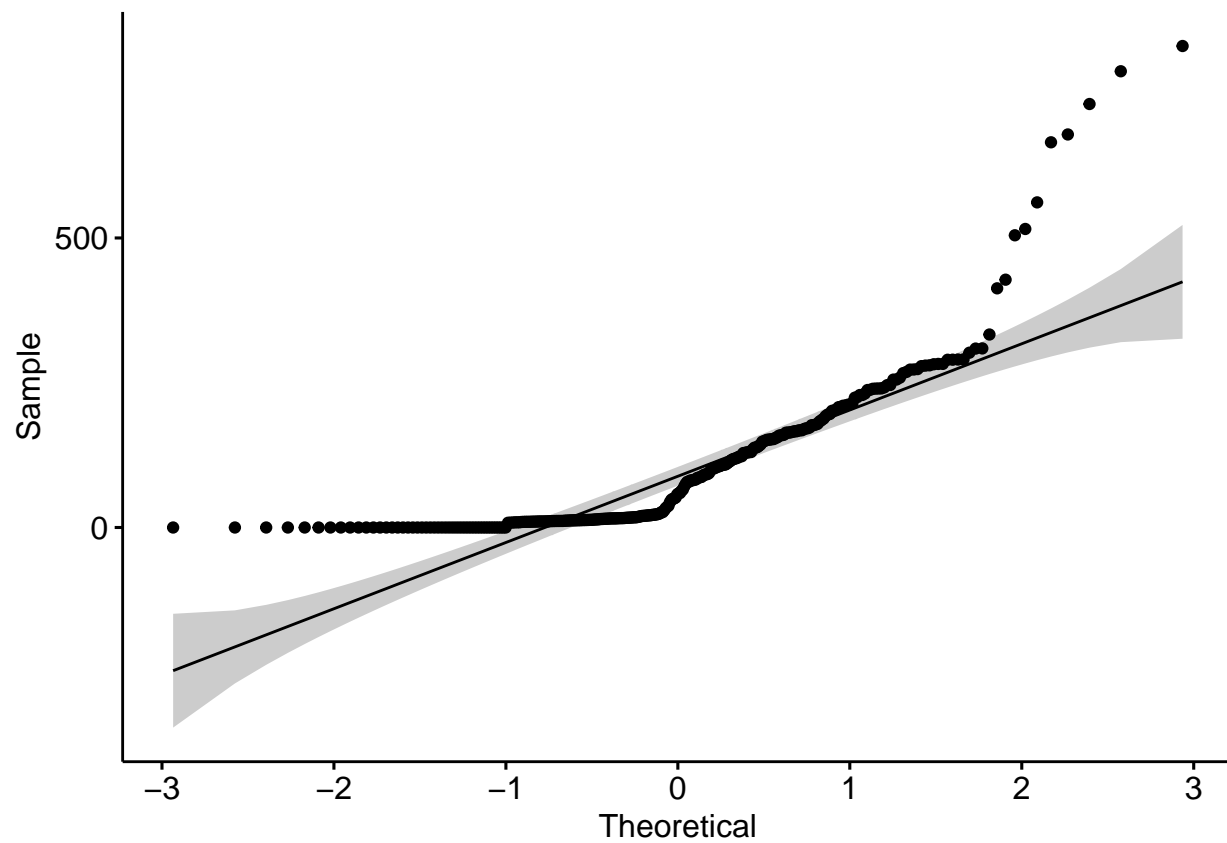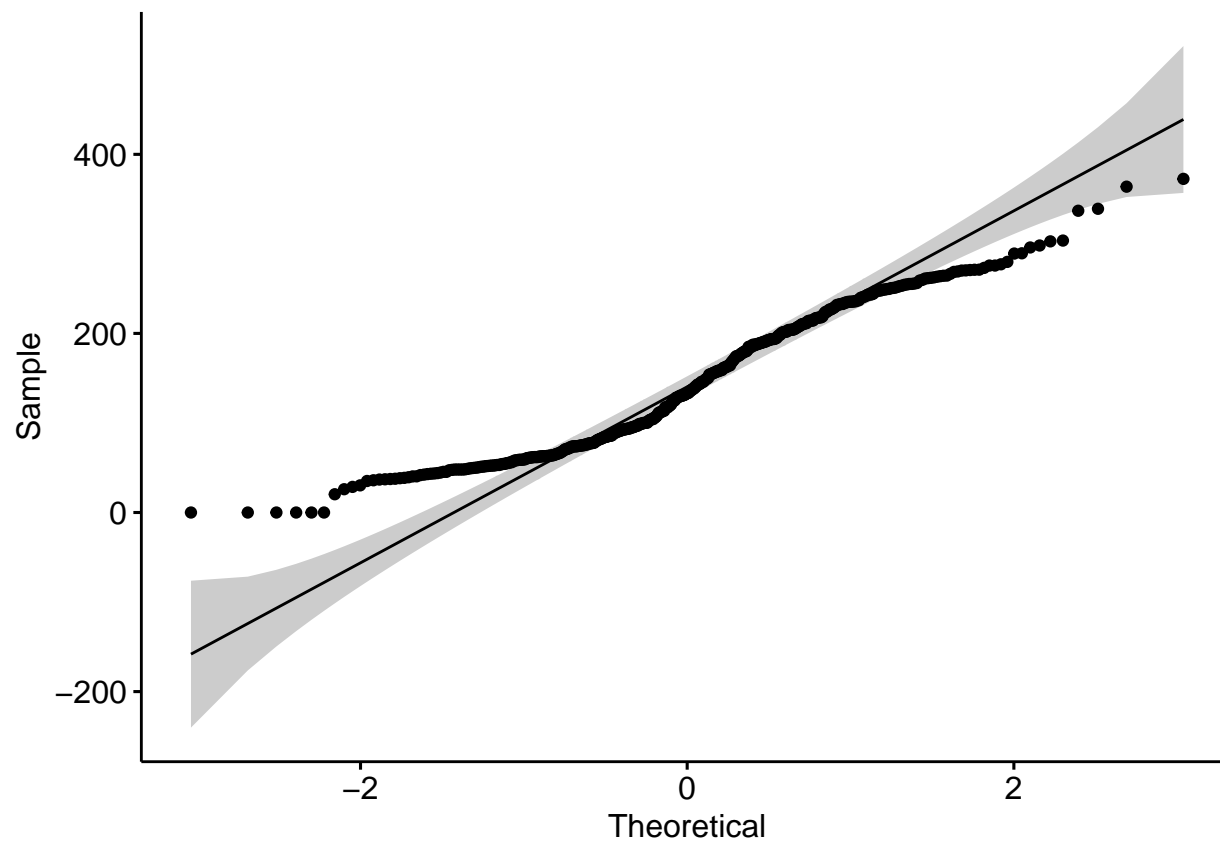## Removed 6 rows containing non-finite values (stat_qq_line).
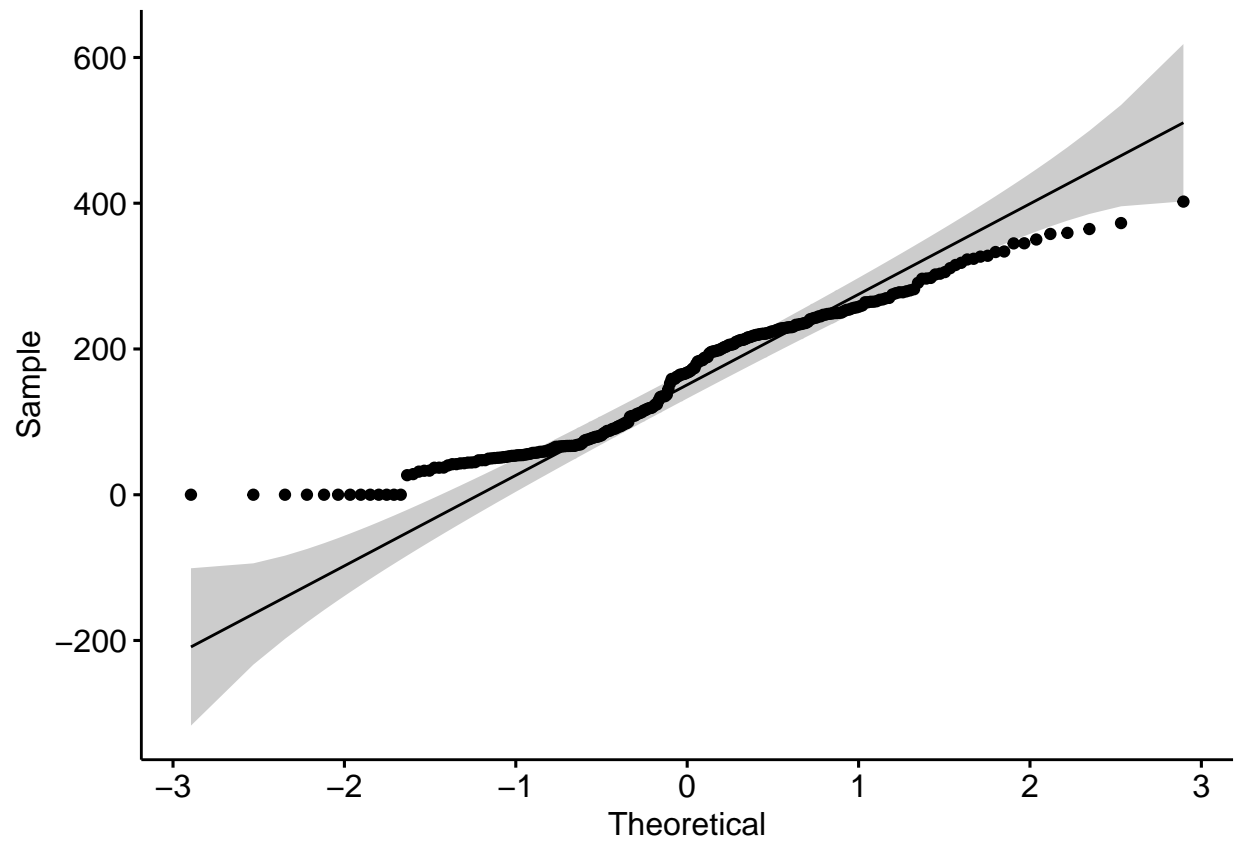
```
ggqqplot(ES14A$chl)
```

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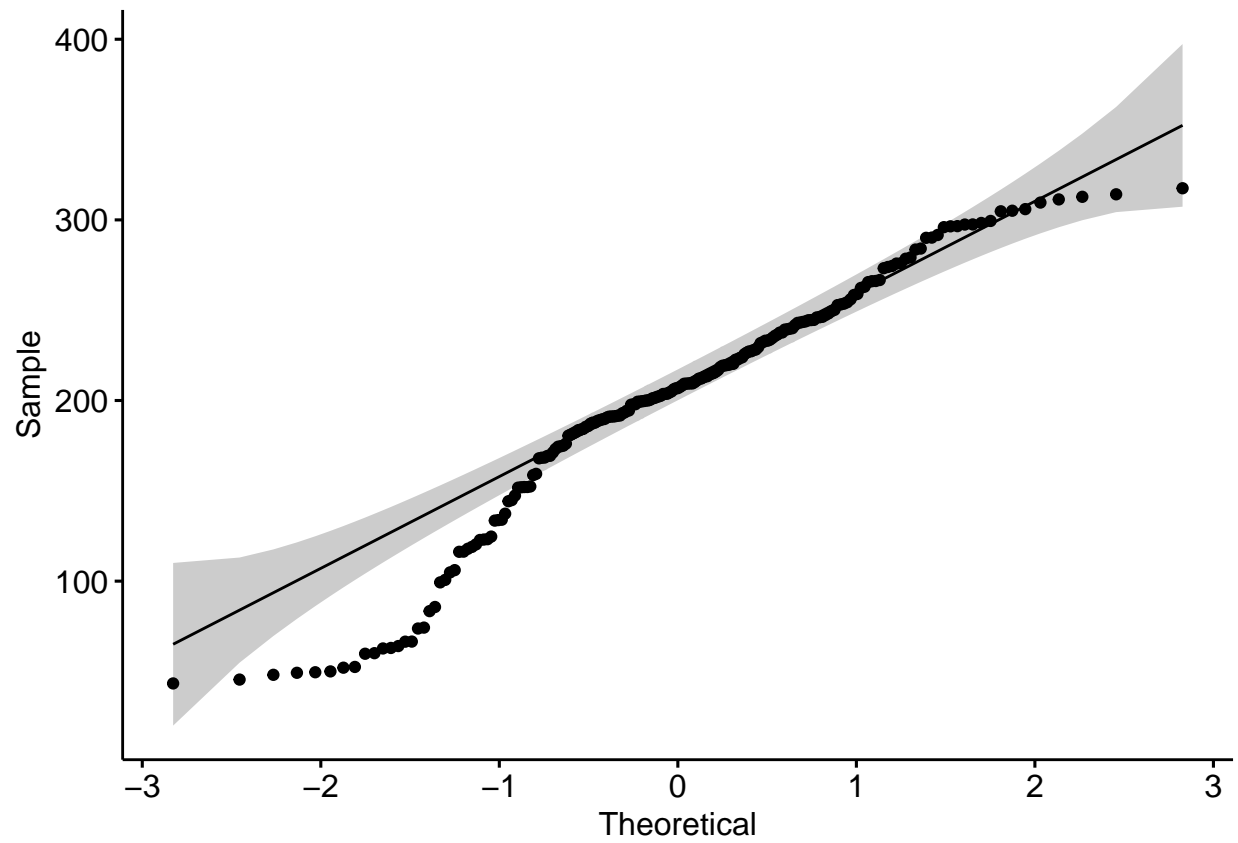
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2",
                    xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES2
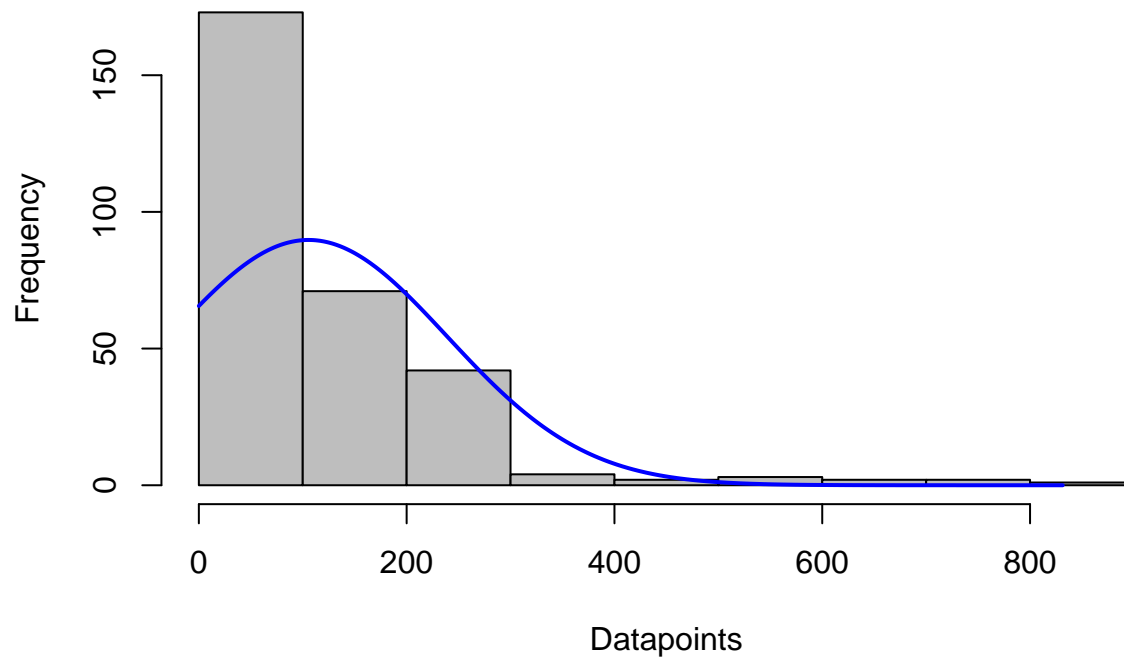

```r
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5",
                    xlab = "Datapoints")
```

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
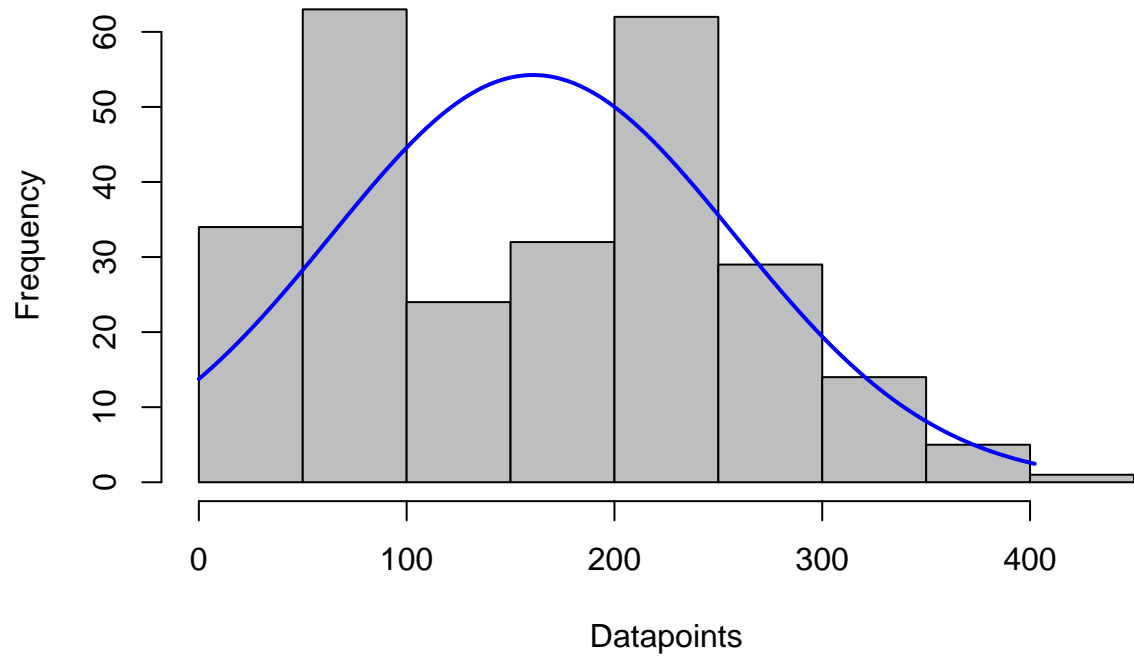

```
plotNormalHistogram(ES14A$chl, main = "Density of Chlorophyll Content (Digital) for E14A",
                    xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for E14A
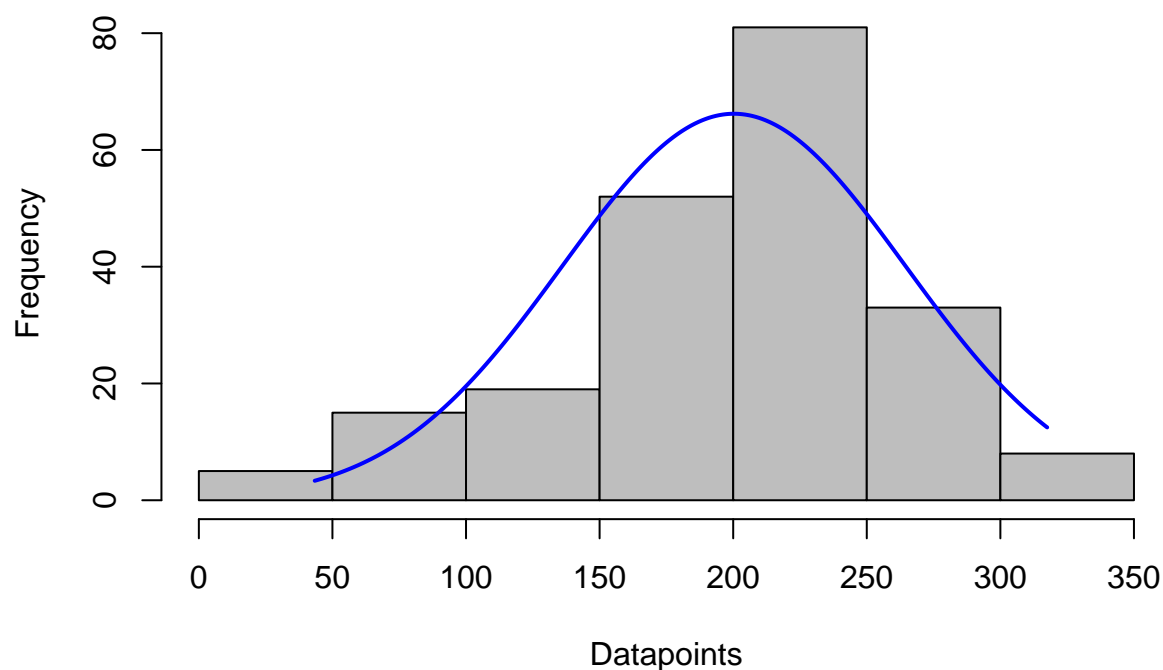
Use the Tukey's tranformation method to normalize the distribution and append to datasets

```
ES2_chl.tuk = transformTukey(ES2$chl, 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}
```
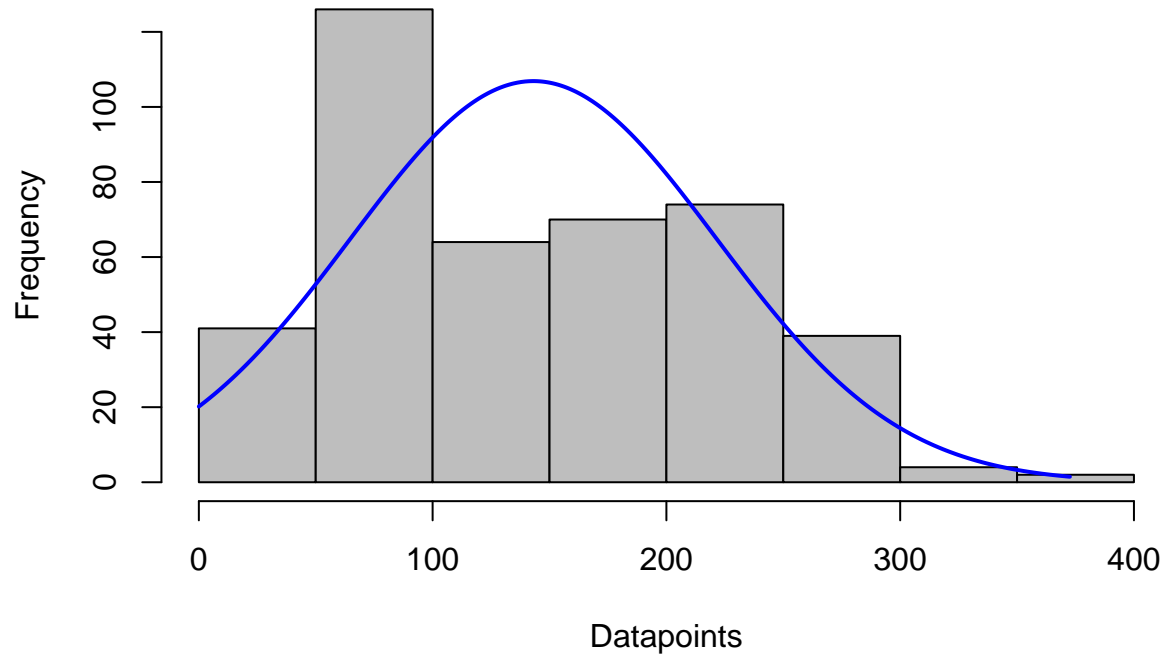
```
ES5_chl.tuk = transformTukey(ES5$chl, plotit=FALSE)
```

```
##
##      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 desribed 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
```

```r
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
```

```r
##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
```

```r
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
```

```r
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
```

```r
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$sampleNumber   2   53280   26640  2.6369    0.07338 .
## ES2$Residuals    276 2788355   10103
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#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
```

```r
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
```

```r
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_chl.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_chl.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.chl.lm, c("ES2.mod$Treatment",
                                                     "ES2.mod$Dilution"),
                                        group=TRUE,console=TRUE)
```

```
##
## Study: ES2.mod.chl.lm ~ c("ES2.mod$Treatment", "ES2.mod$Dilution")
##
## HSD Test for ES2.mod$ES2_chl.tuk
##
## Mean Square Error:  4.787063
##
## ES2.mod$Treatment:ES2.mod$Dilution,  means
##
##                  ES2.mod.ES2_chl.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_chl.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_chl.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_chl.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.chl.lm <- lm (ES5$chl ~ ES5$Treatment +
                            ES5$Dilution +
                            ES5$Condition +
                            ES5$isoRep +
                            ES5$techRep +
                            ES5$sampleNumber)
ES5.chl.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.chl.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 Treament
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 Treament
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_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
##                                  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_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
##
## 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.chl.lm <- lm (ES13B$chl ~ ES13B$Treatment +
                    ES13B$HostVariety +
                    ES13B$isoRepNumber +
                    ES13B$techRepNumber +
                    ES13B$SampleNumber)
ES13B.chl.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
```

```r
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$HostVarietyDG47X95     26.3892    16.0431   1.645   0.1012
## ES13B$HostVarietyOsage       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
```

```r
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
```

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```
##
## $groups
##             ES13B$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"
```

```r
#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
##                        Q75
## Control:AG4632     234.2065
## Control:DG47E80    277.7645
## Control:DG47X95    275.6780
## Control:Osage      271.3380
## Control:P5414LLS   228.1255
## DMCC2165:AG4632    128.8945
## DMCC2165:DG47E80   201.5630
## DMCC2165:DG47X95   199.8590
## DMCC2165:Osage      81.3670
## DMCC2165:P5414LLS 102.5945
##
## $comparison
## NULL
##
## $groups
##                    ES13B$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
##
## 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
```

```r
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
```

```r
#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 specificy 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=TI
```

```
##
## 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
```

```
## $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
```

```r
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
```

```r
#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_chl.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_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
##                     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_chl.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
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', gr
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', 'ES
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

```r
# 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}
```

```r
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$ES2.root.tuk ~ ES2.root.noNAs.mod$Isolate +
                        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
```

```r
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
```

```r
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$Concent
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$I
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"

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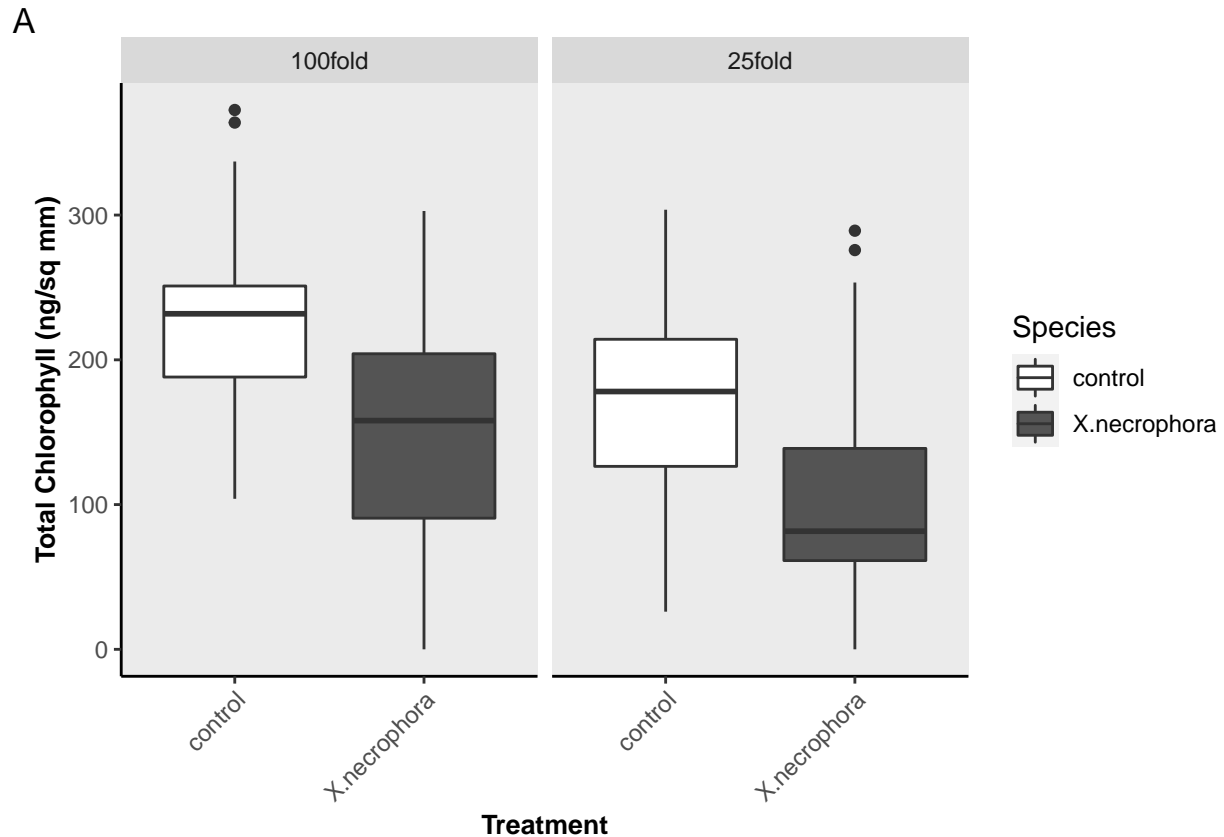
```
## Warning: Removed 8 rows containing non-finite values (stat_boxplot).
```

A


Individual plot for panel B

```r
##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).
```
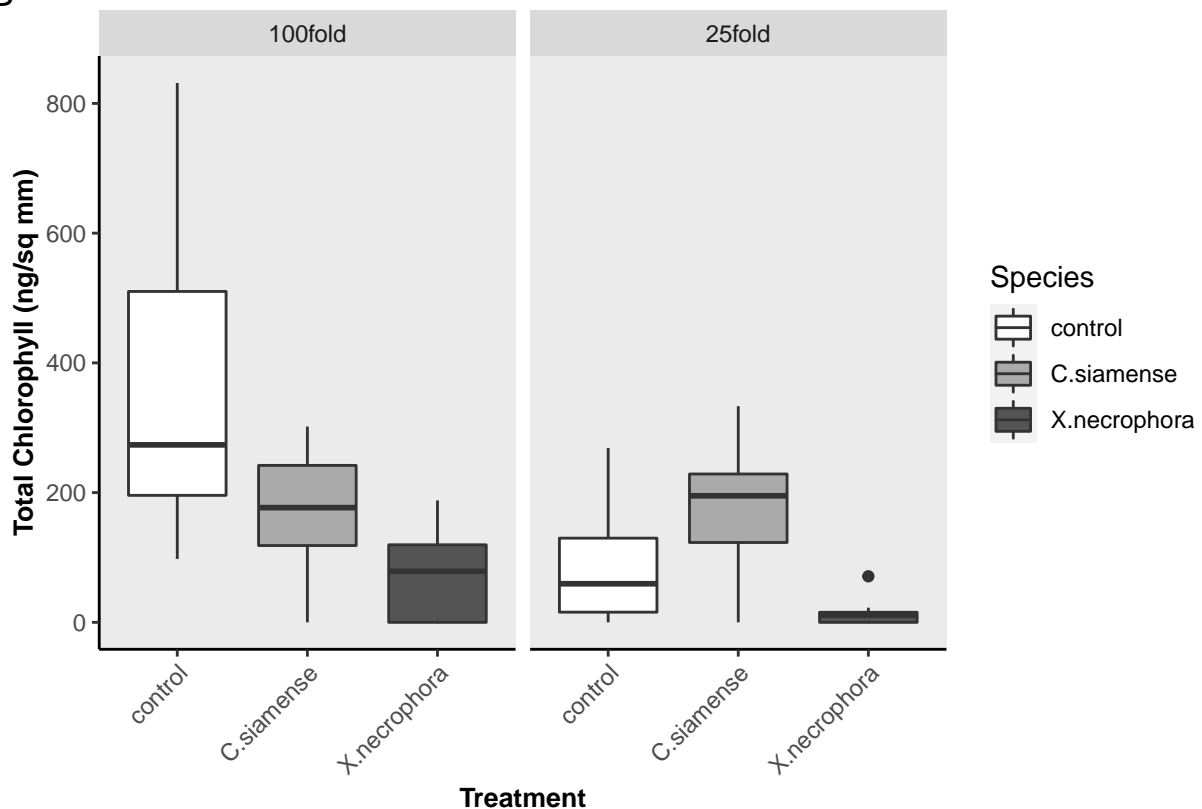

Individual panel C

```
#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).
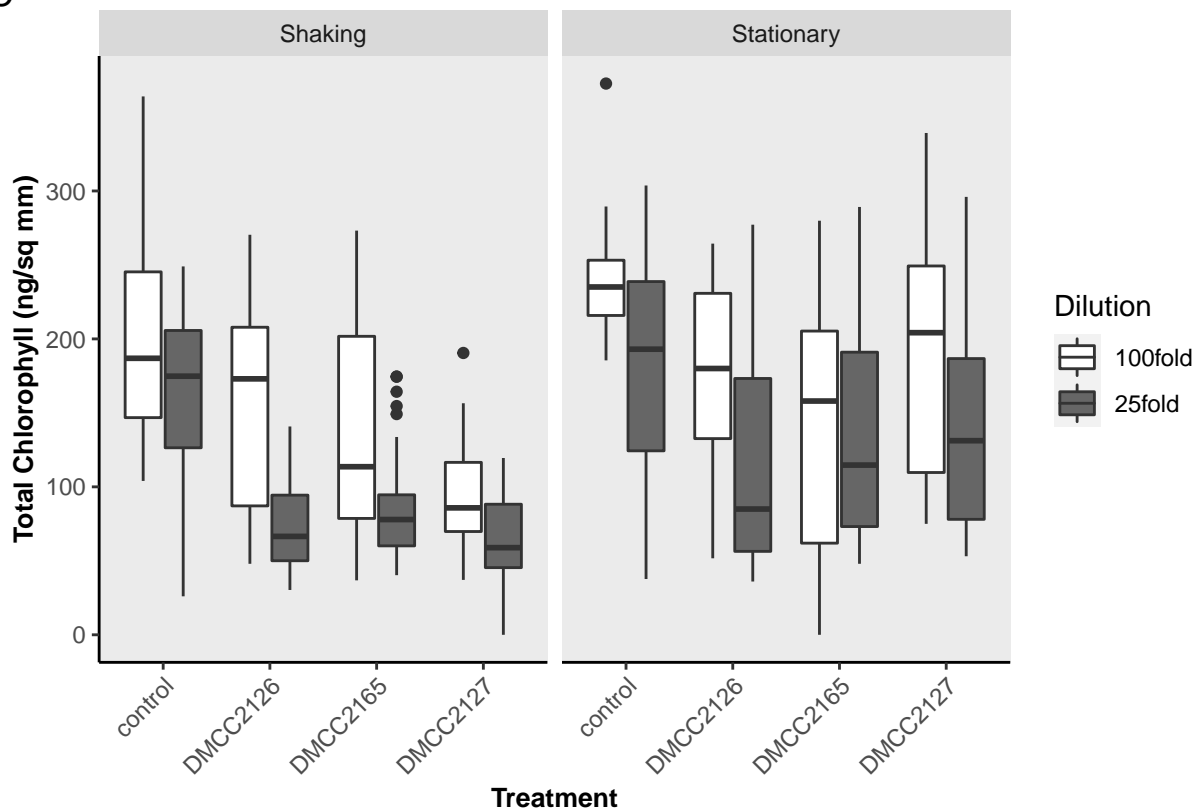
Individual panel D

```r
#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).
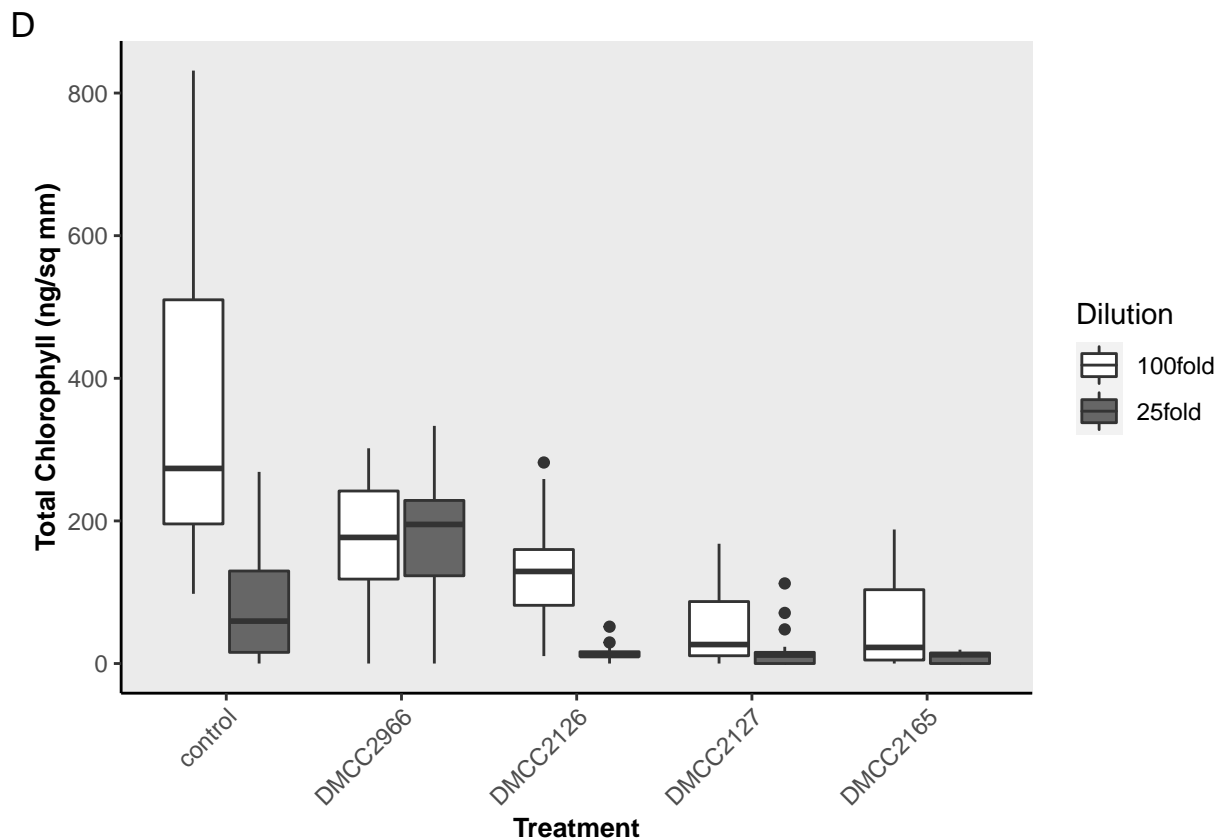
Plot composite figure 1

```r
###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.v2, 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).
```
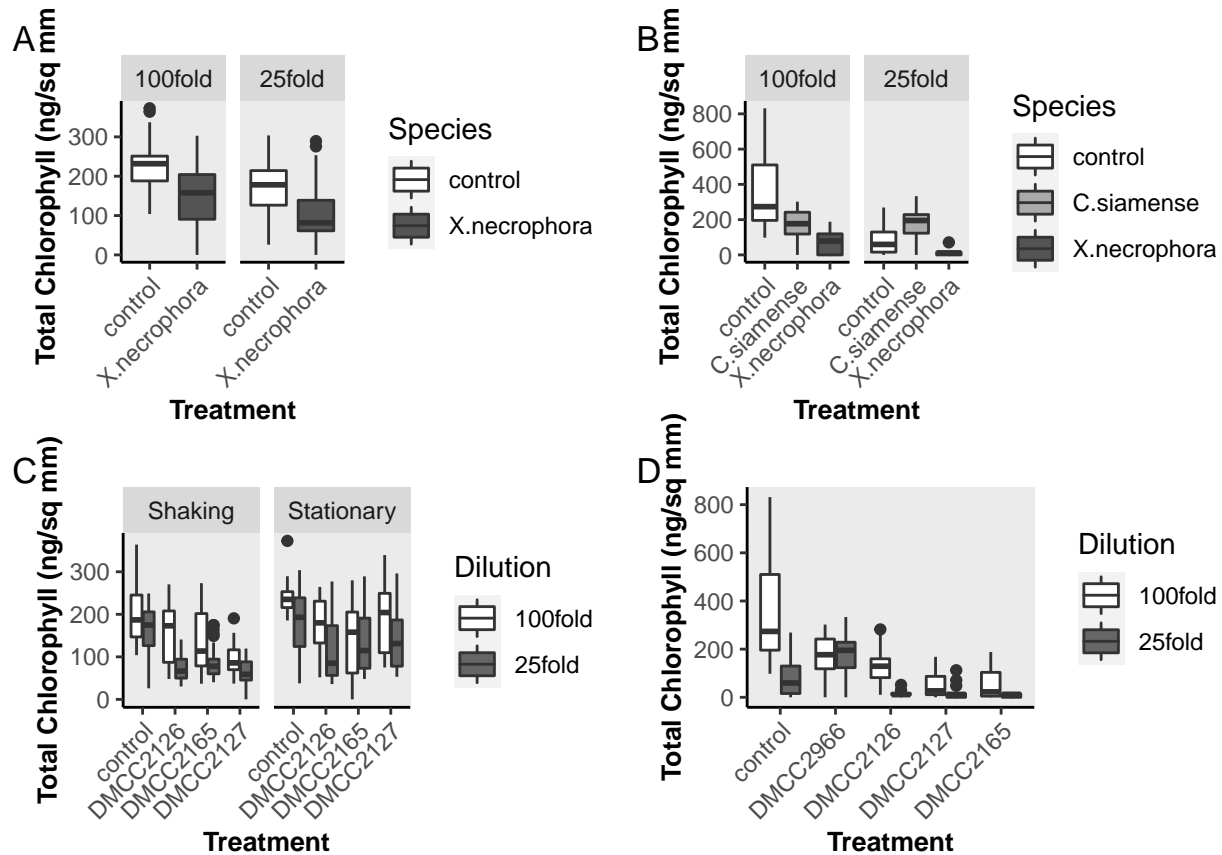

## Plotting root length panel (Figure 2)

```r
#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
```
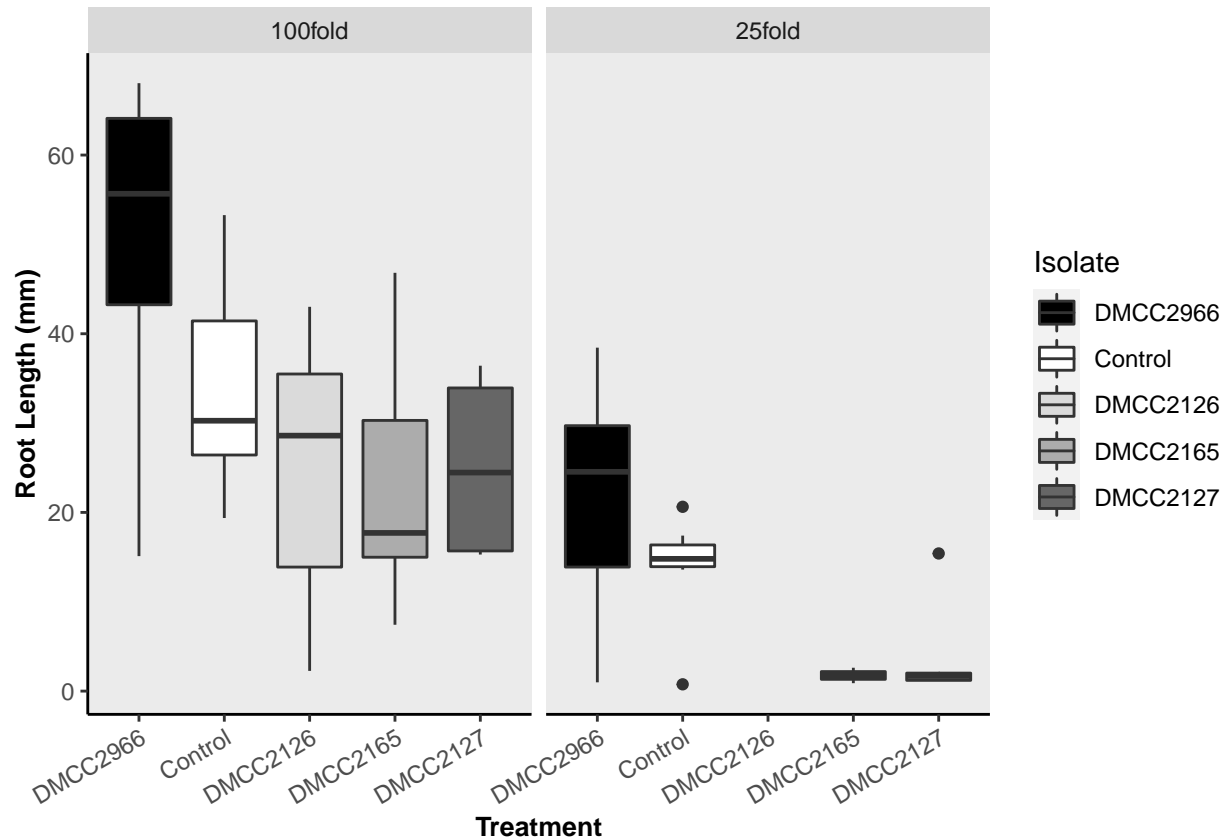


```
#dev.off()
```

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).
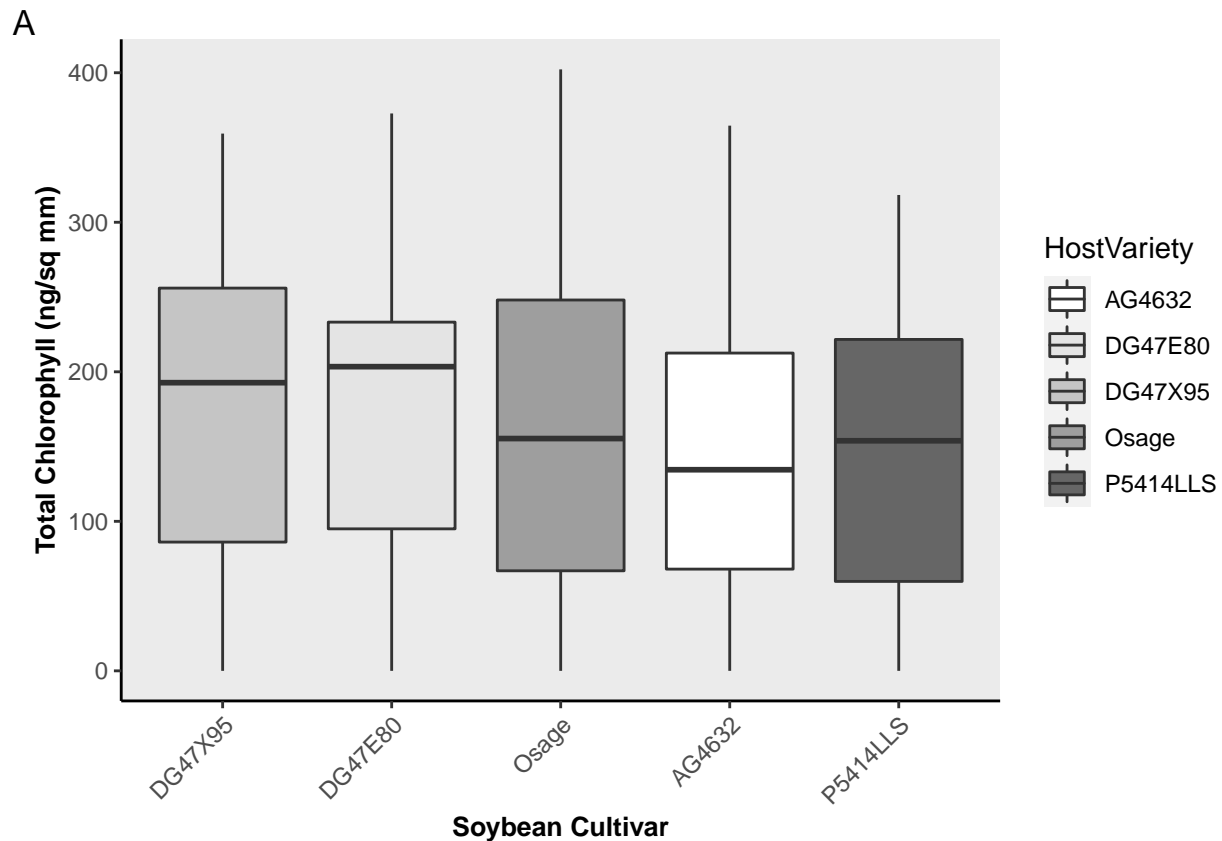
Individual panel B

```
###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).
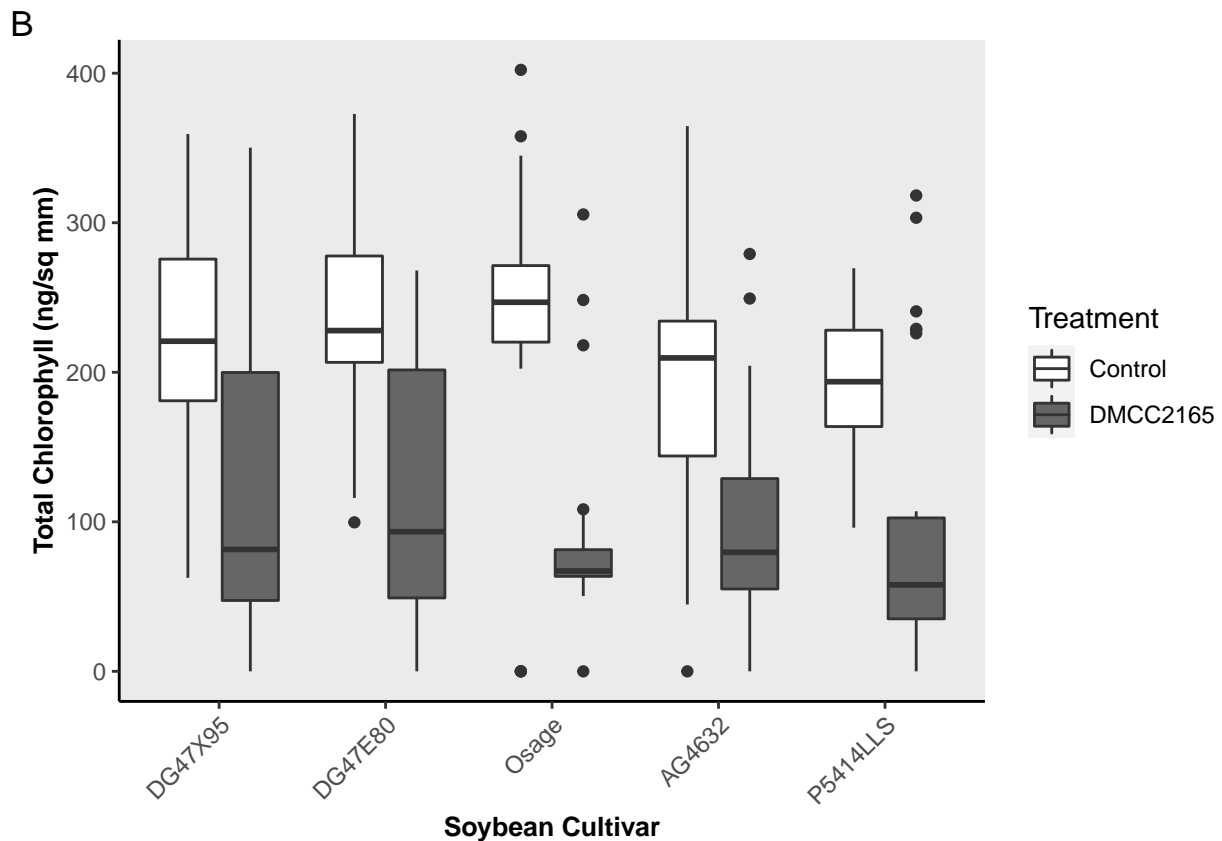
Panel C

```
###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).
```
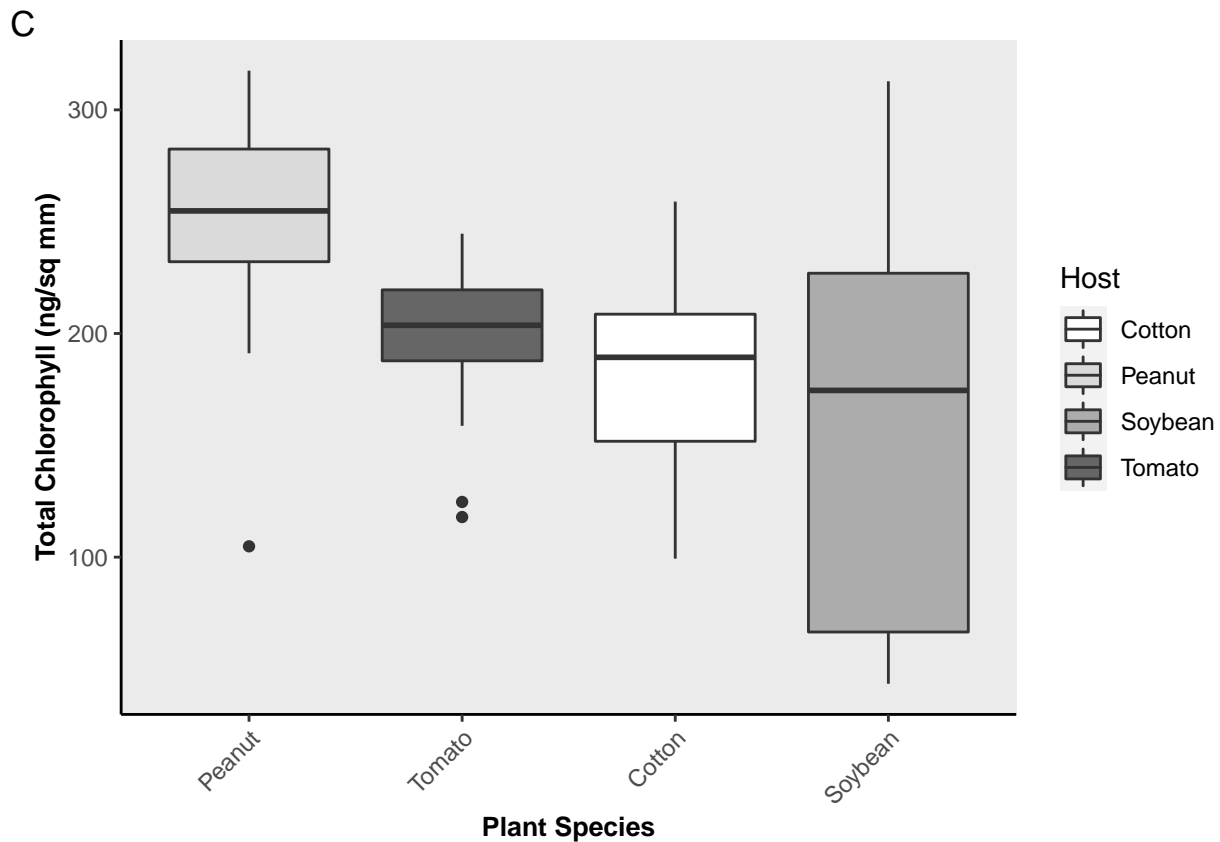

Panel D

```
###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).
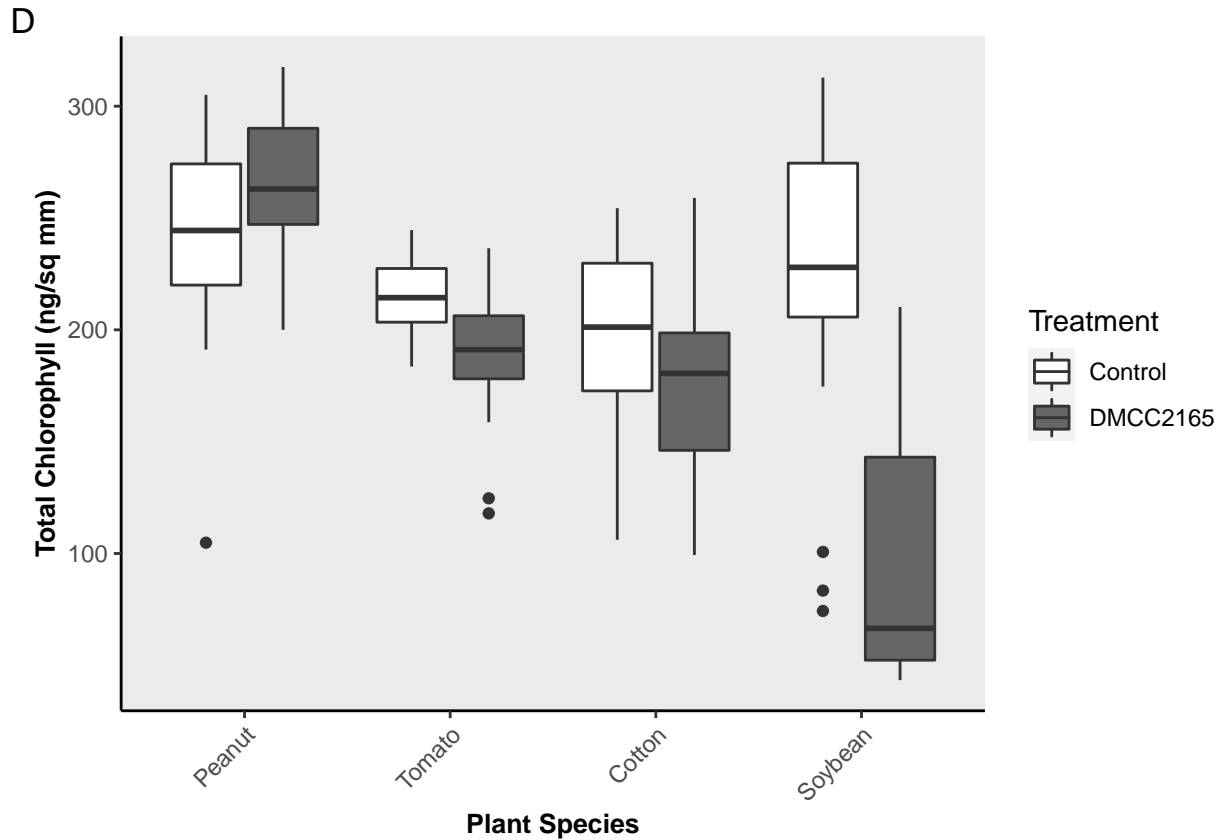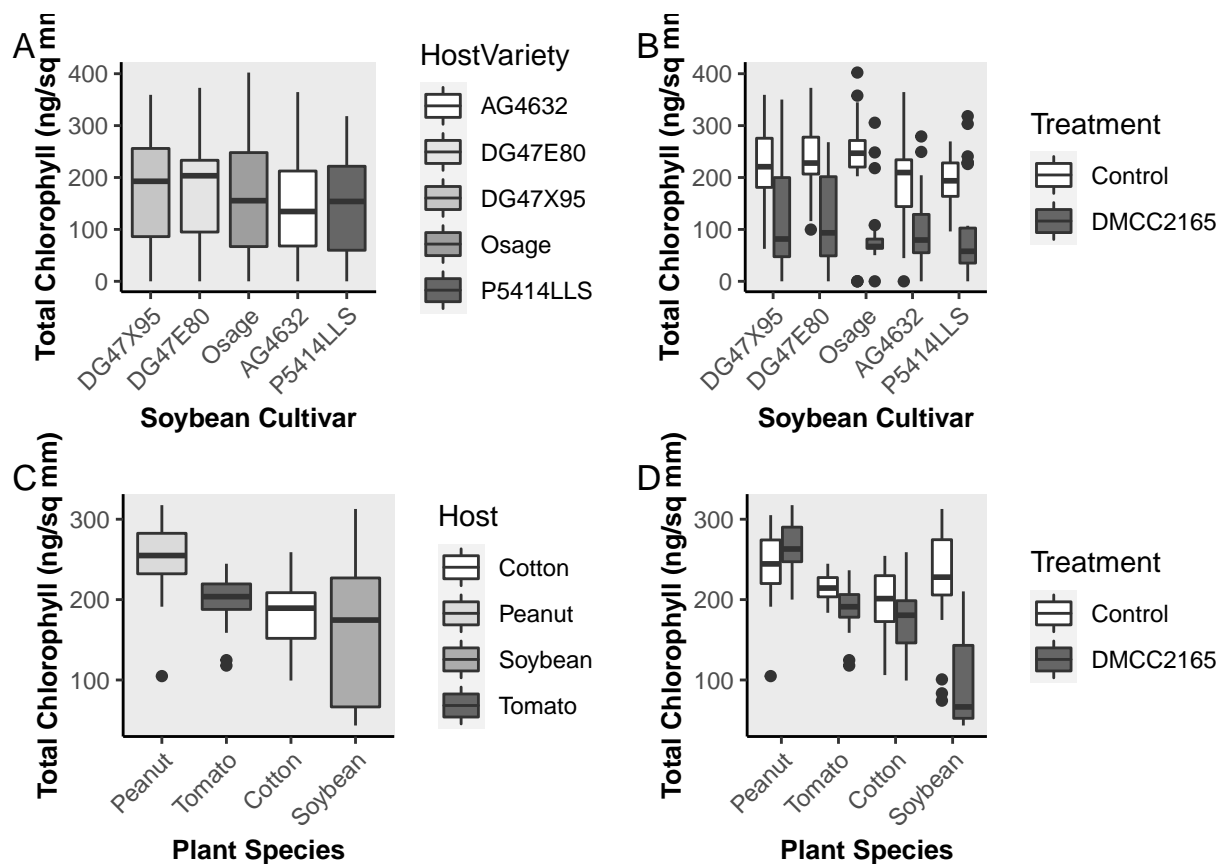

Composite figure 4

```
###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.
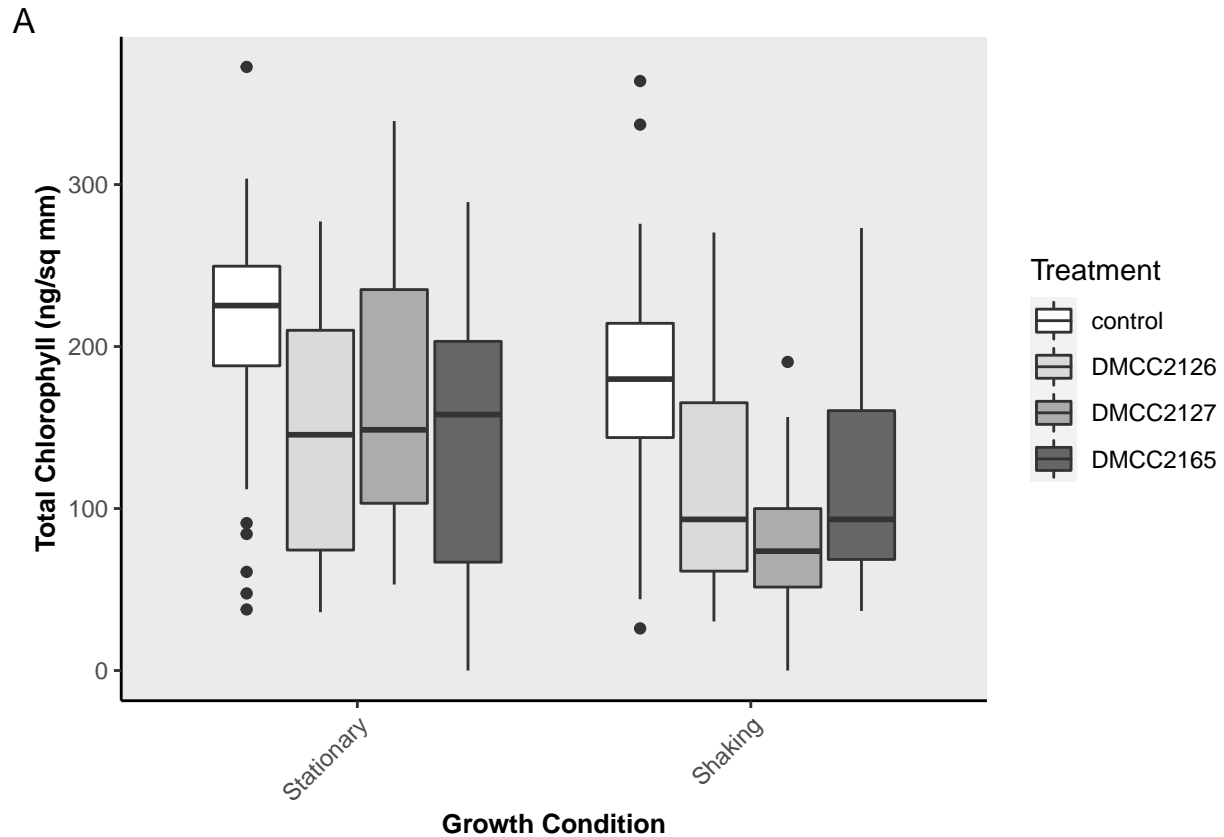
```r
#Panel A

#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).

A


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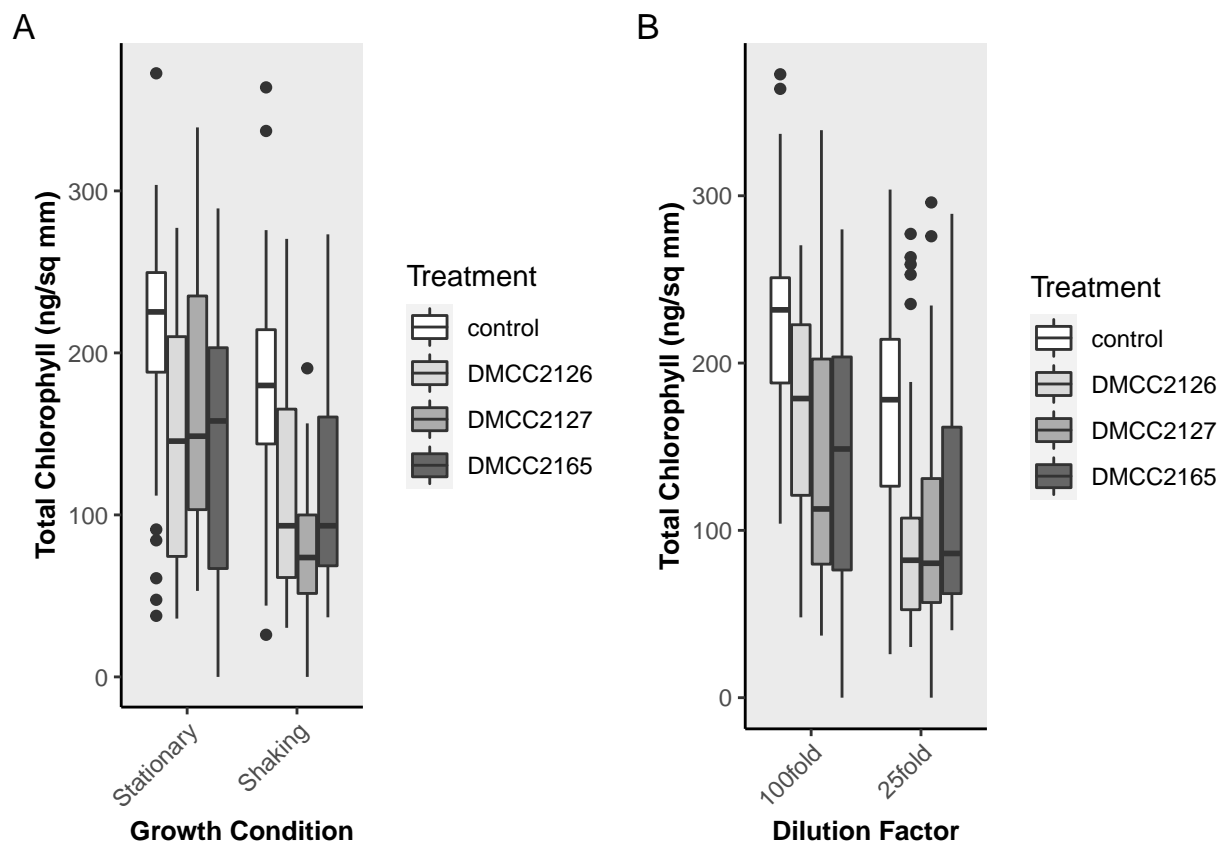
Warning: Removed 12 rows containing non-finite values (stat_boxplot).

B
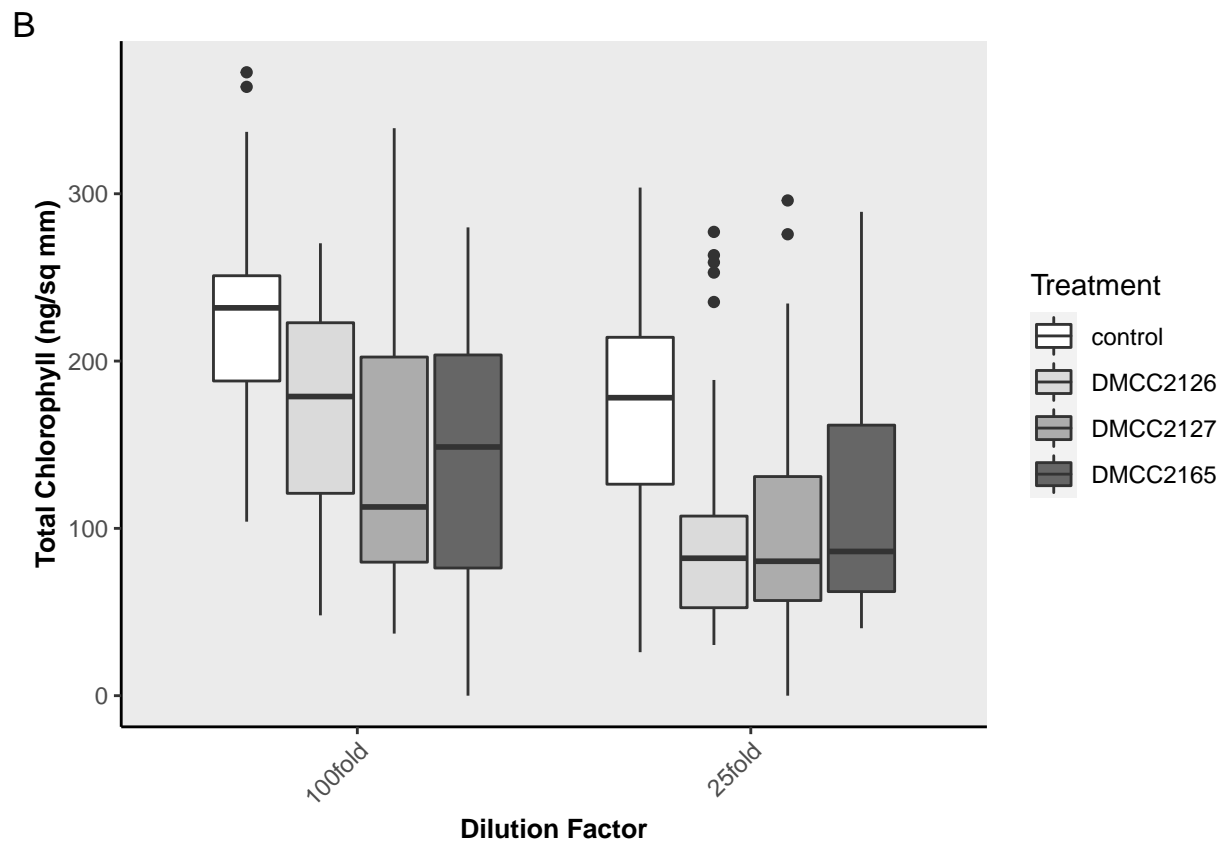

```
###Grid for supplementary figure 1 (updated 05/14/2022). Using ES2 and ES5 only.
gridExtra::grid.arrange(ES5.mod.ggplot.v3,
                        ES5.mod.ggplot.v4,
                        ncol=2)
```

```
## 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)
```

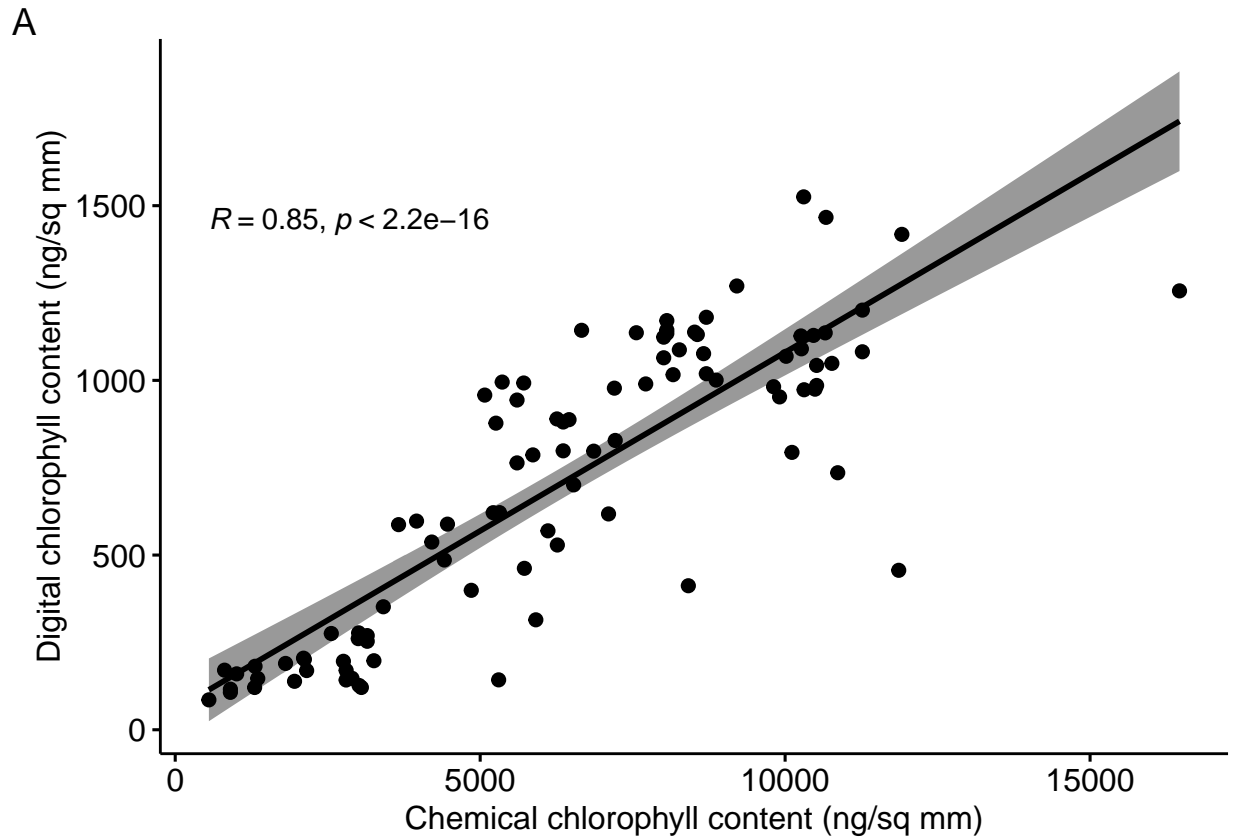**Summarizing and aggregating datasets**

```
#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'
```

A

$R = 0.85$, $p < 2.2e{-}16$

Digital chlorophyll content (ng/sq mm) (y-axis: 0, 500, 1000, 1500)

Chemical chlorophyll content (ng/sq mm) (x-axis: 0, 5000, 10000, 15000)

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
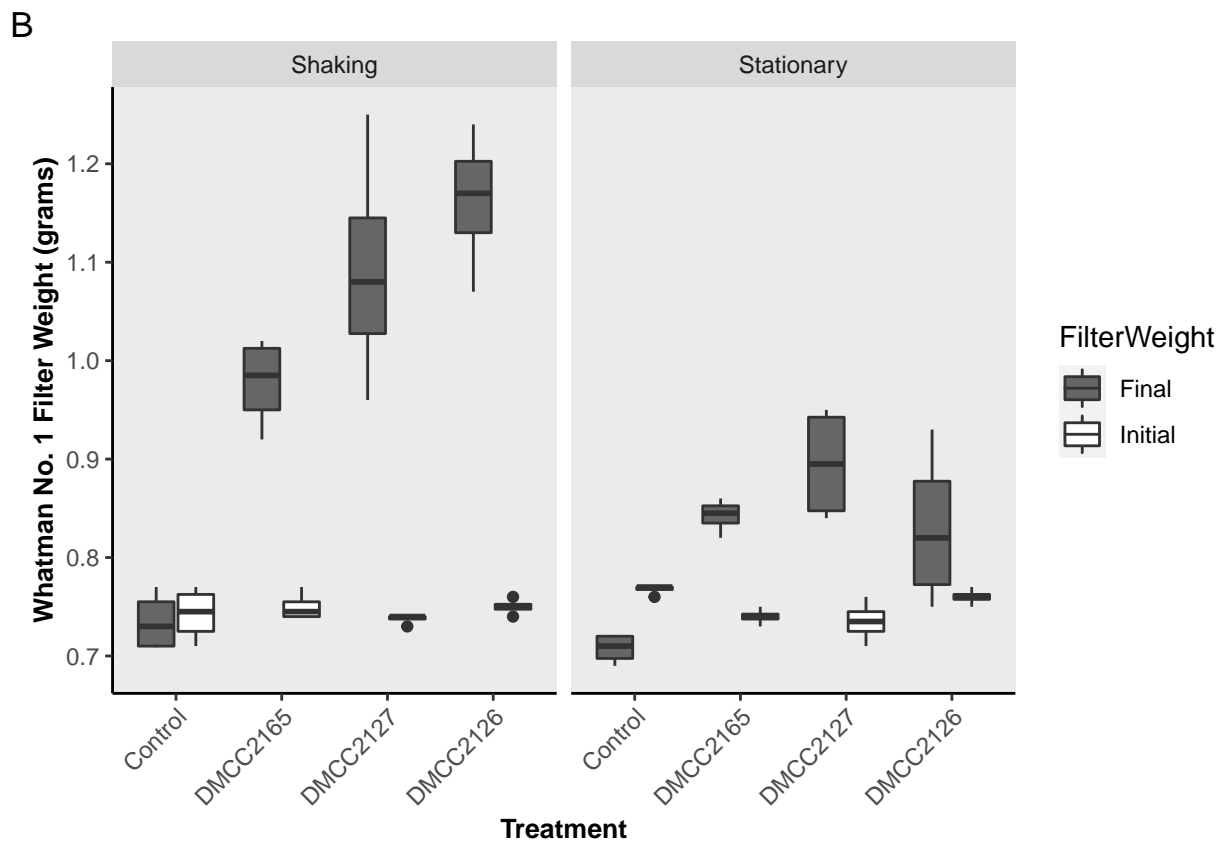
Supplementary figure 2 panel C

```r
#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
```

C
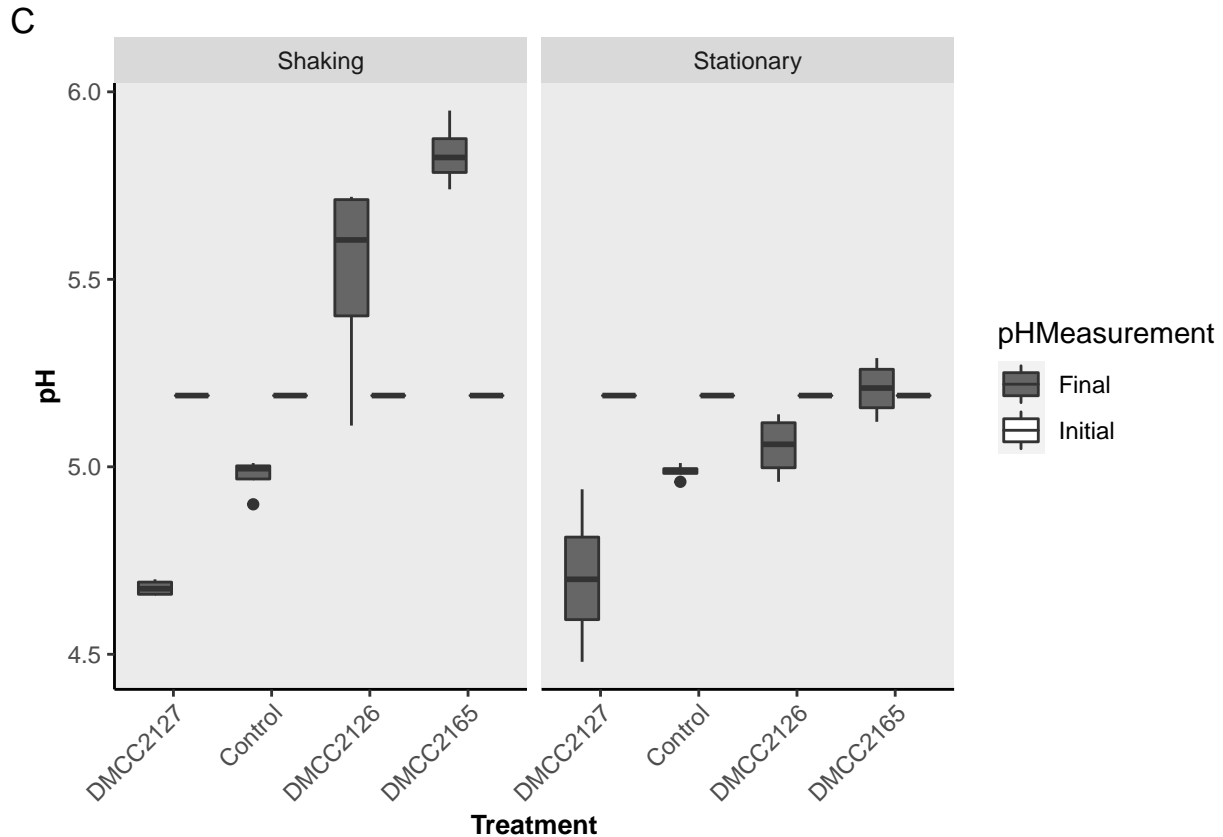
Supplementary figure 2 panel D

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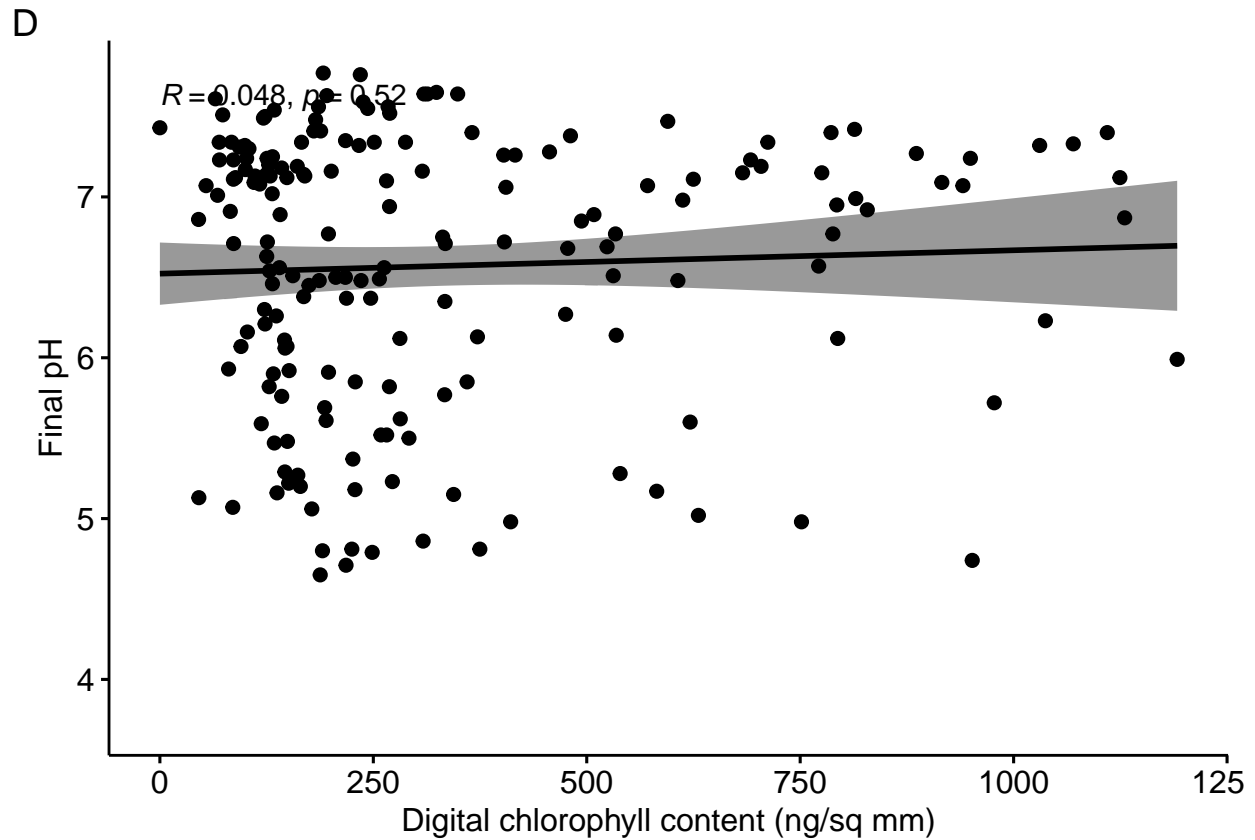
```
## 'geom_smooth()' using formula 'y ~ x'

## 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).
```

D

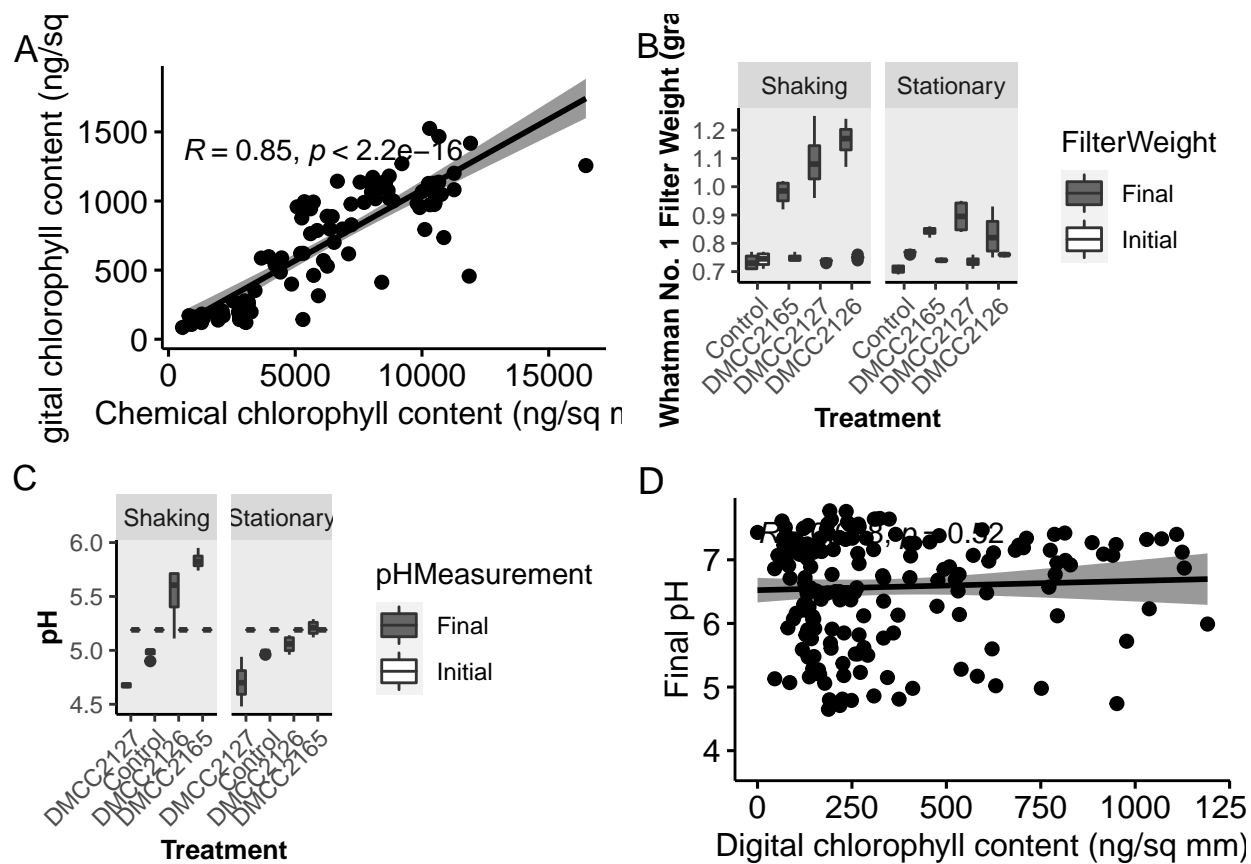**Supplementary Figure 2 composite. Updated on 08/02/2021**

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

```
## '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).
```

A — Scatterplot of Digital chlorophyll content (ng/sq mm) versus Chemical chlorophyll content (ng/sq mm). $R = 0.85$, $p < 2.2e{-}16$

B — Boxplots of Whatman No. 1 Filter Weight (grams) by Treatment (Control, DMCC2165, DMCC2127, DMCC2126) for Shaking and Stationary, showing Final and Initial FilterWeight.

C — Boxplots of pH by Treatment (DMCC2127, Control, DMCC2126, DMCC2165) for Shaking and Stationary, showing Final and Initial pHMeasurement.

D — Scatterplot of Final pH versus Digital chlorophyll content (ng/sq mm).

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