

Statistical analyses and plotting for *Xylaria necrophora* secondary metabolites experiments

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Install packages needed.

We first create a vector of all the packages needed

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

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))
```

```
##  
## 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

##
## Attaching package: 'ggpubr'

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

## Loading required package: carData

##
## Attaching package: 'car'

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

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

## v tibble 3.1.4      v stringr 1.4.0
## v tidyr  1.1.3      v forcats 0.5.1
## v purrr  0.3.4

## -- 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 case, we assume you have cloned/downloaded this repository to your “Documents” folder.

Change directory on mac/linux:

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

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

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

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

Step 1: Call the pdf command to start the plot

```
pdf(file = "/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output/ Figure1.pdf", # T
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/X.necrophora.secondaryMetabolites/output/")
```

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

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

#ES4 = Repetition for 14 DOE

ES5 = First experiment for 7 DOE

#ES8 = Repetition for 7 DOE

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

ES13B = Repetition of ES13A

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

#ES14B = Repetition of ES14A

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

Run Shapiro-Wilk Tests to check for normality

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

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

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

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

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

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

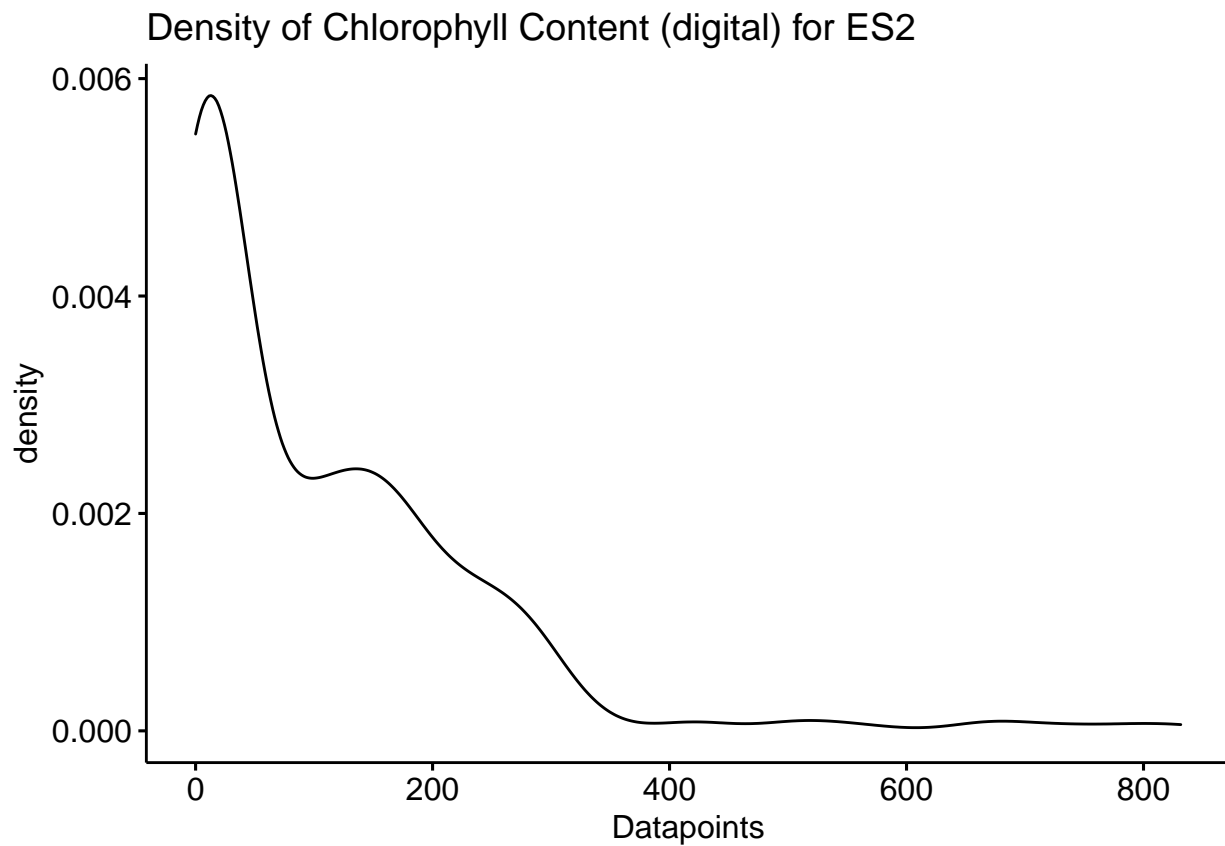
```
shapiro.test(ES14A$chl)
```

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

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

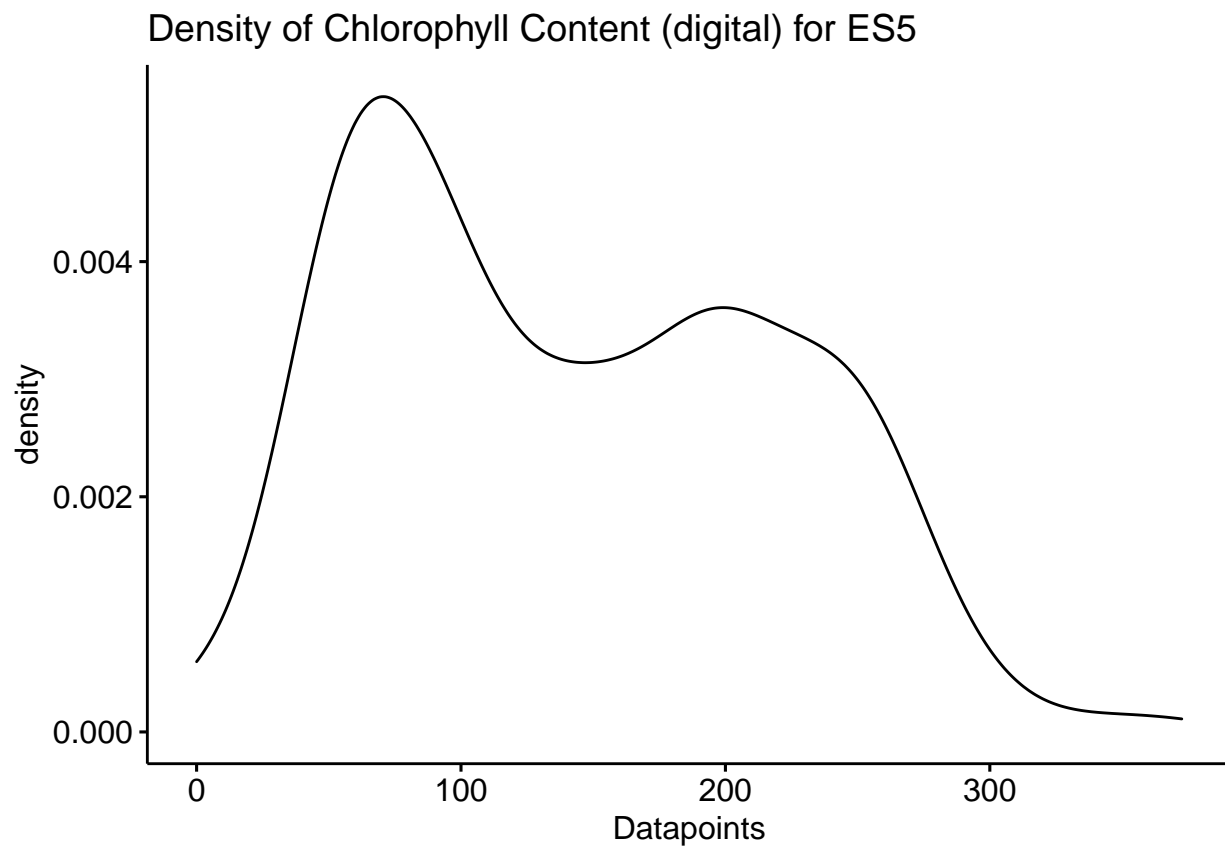
```
ggdensity(ES2$chl, main = "Density of Chlorophyll Content (digital) for ES2",  
          xlab = "Datapoints")
```

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



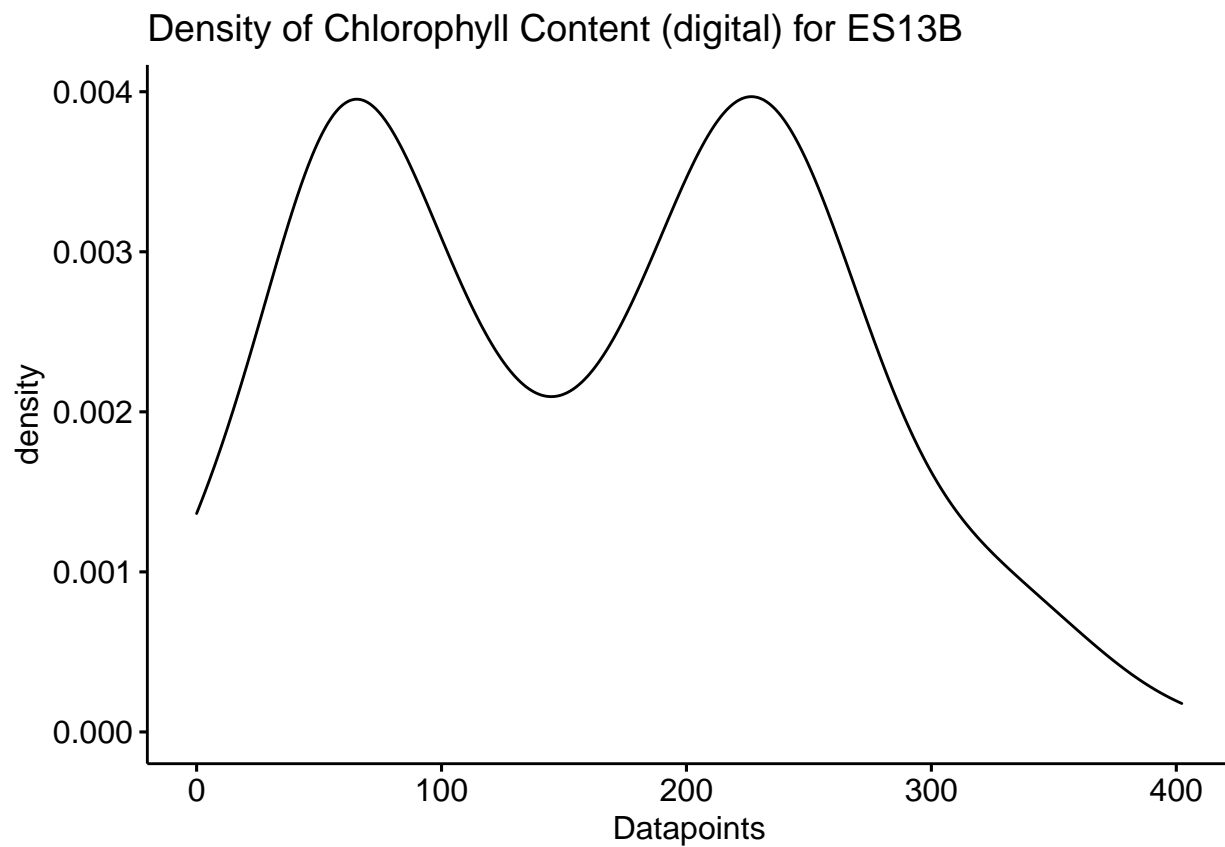
```
ggdensity(ES5$chl, main = "Density of Chlorophyll Content (digital) for ES5",  
          xlab = "Datapoints")
```

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



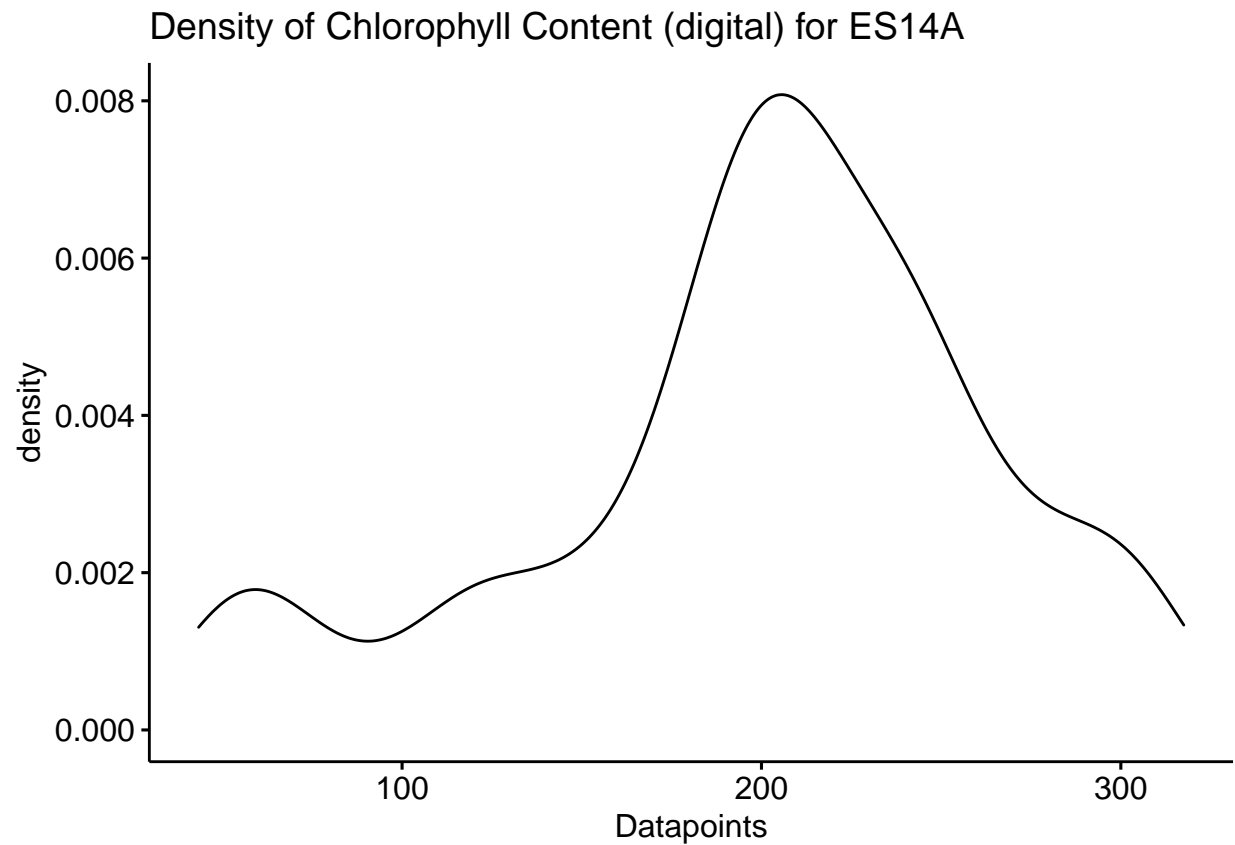
```
ggdensity(ES13B$chl, main = "Density of Chlorophyll Content (digital) for ES13B",  
          xlab = "Datapoints")
```

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



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

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

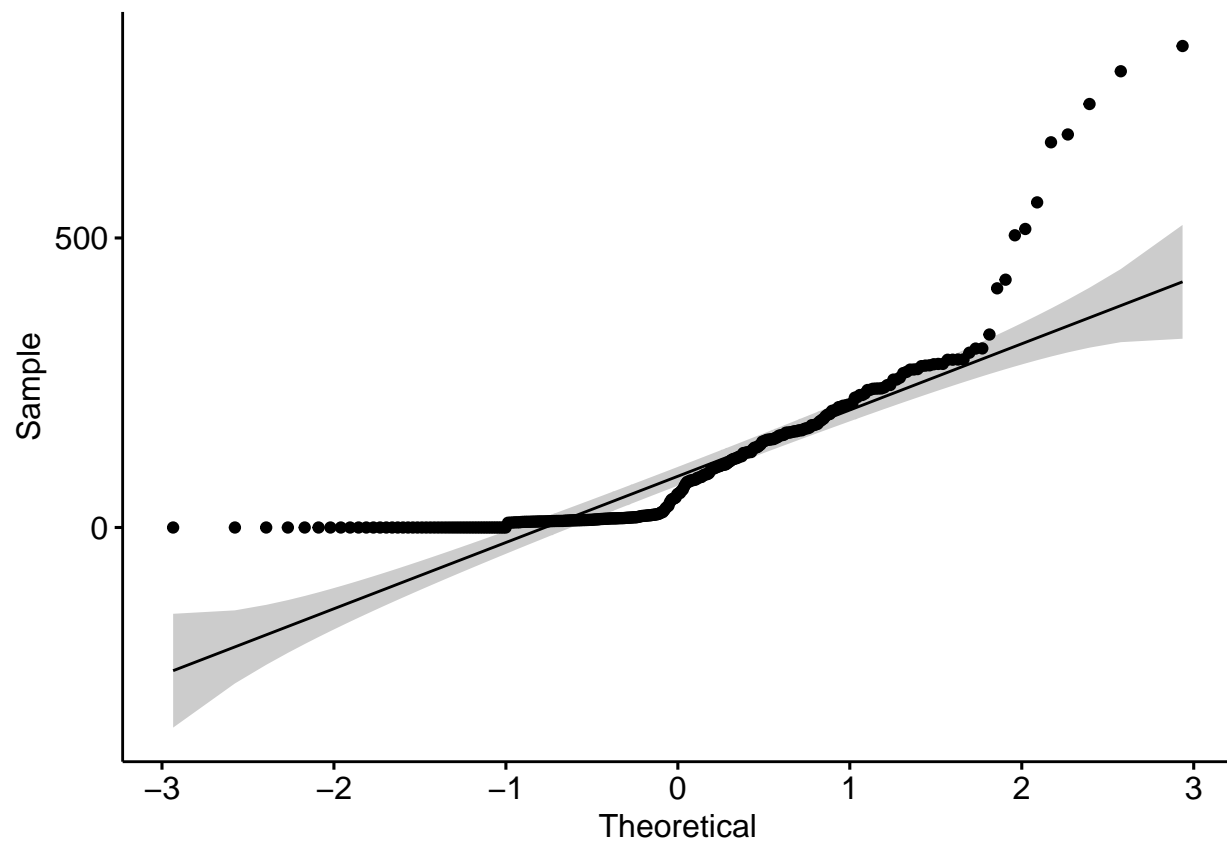


```
ggqqplot(ES2$chl)
```

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

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

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

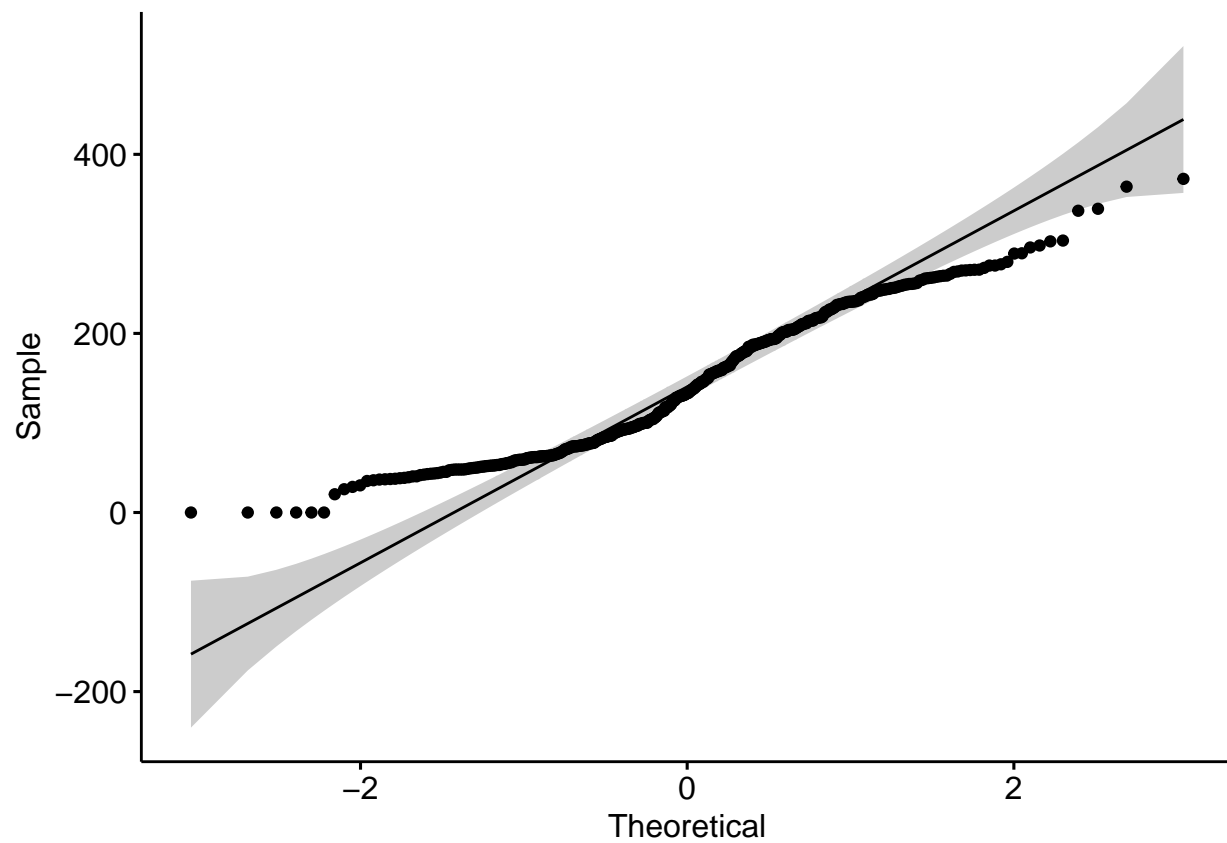



```
ggqqplot(ES5$ch1)
```

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

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

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

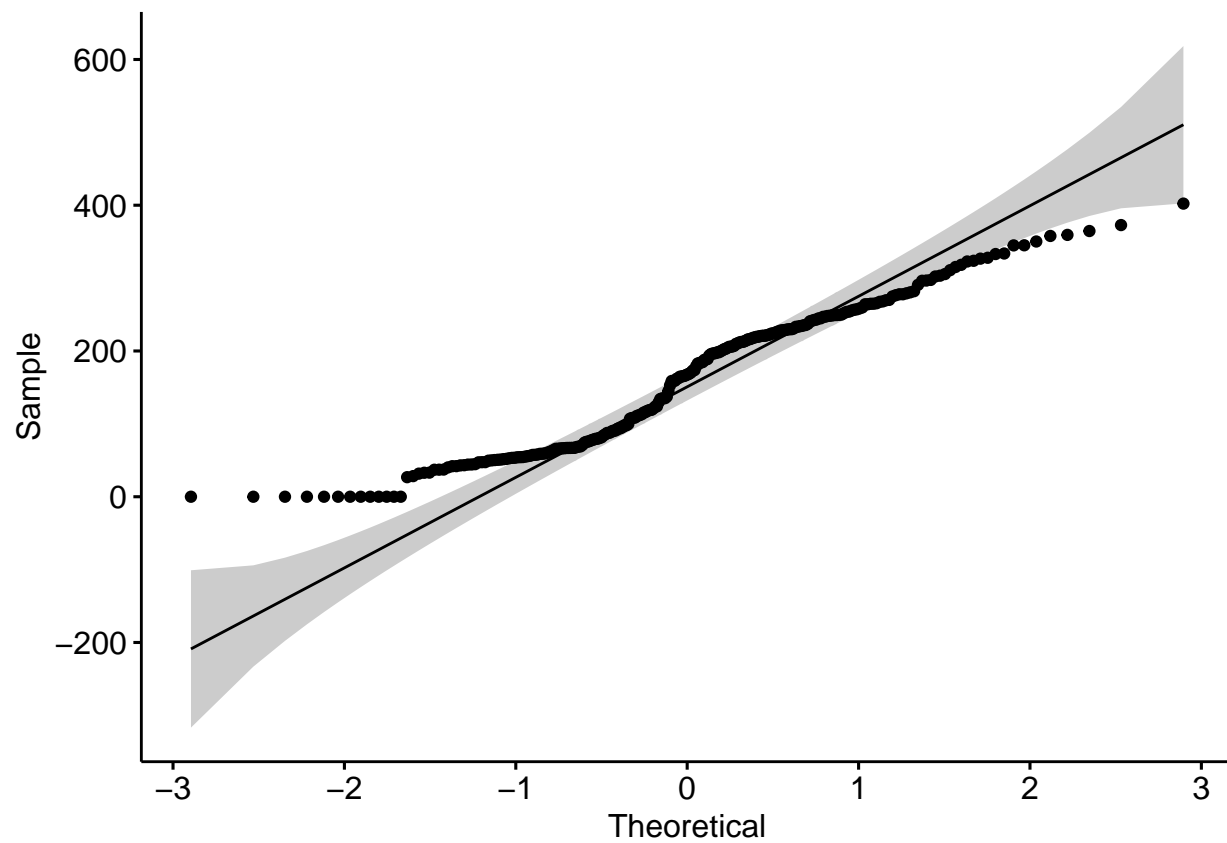


```
ggqqplot(ES13B$chl)
```

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

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

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

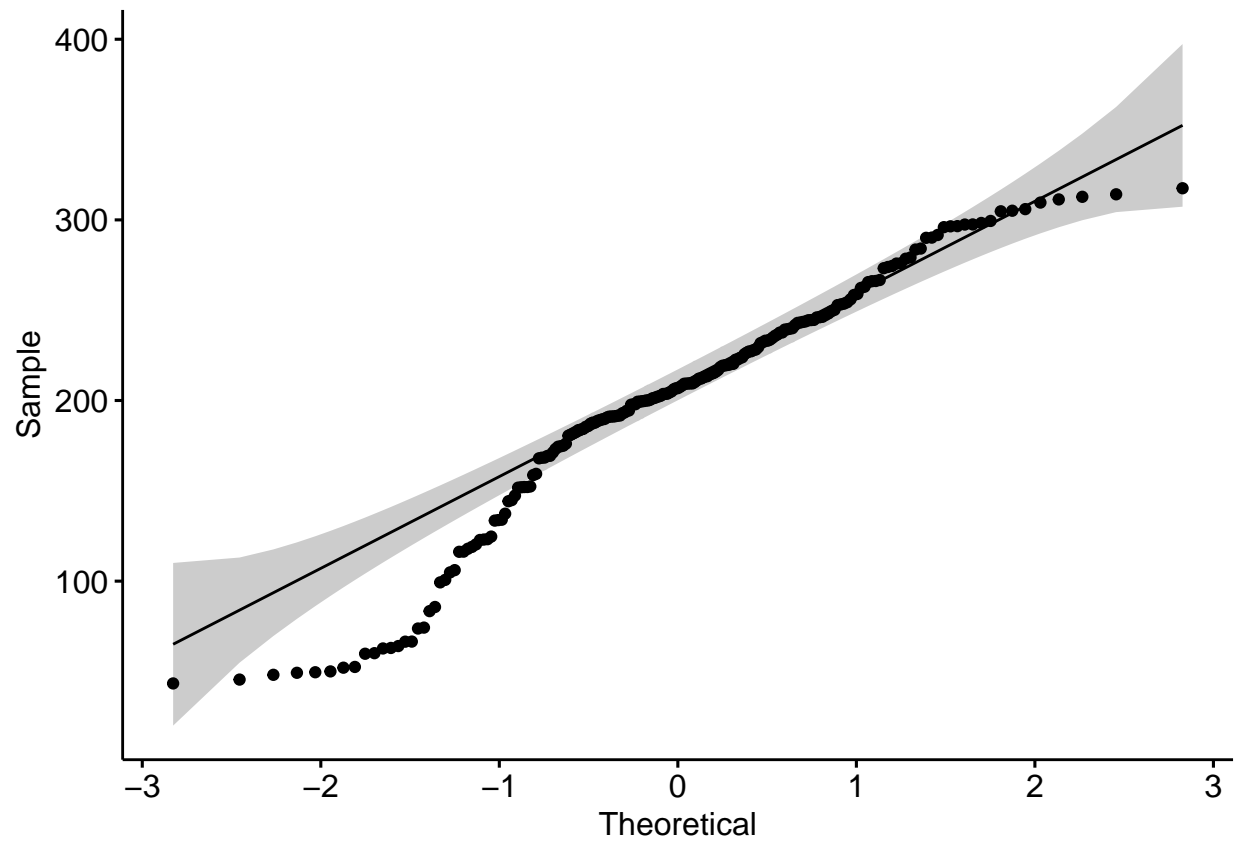


```
ggqqplot(ES14A$chl)
```

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

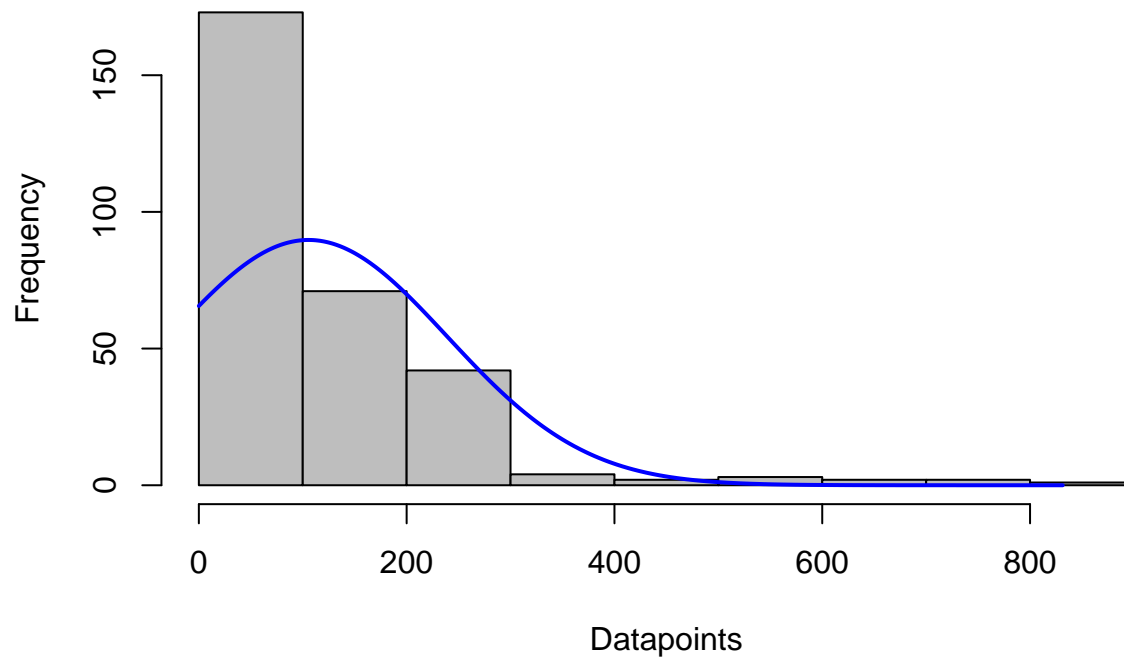
```
## Warning: Removed 3 rows containing non-finite values (stat_qq_line).
```

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



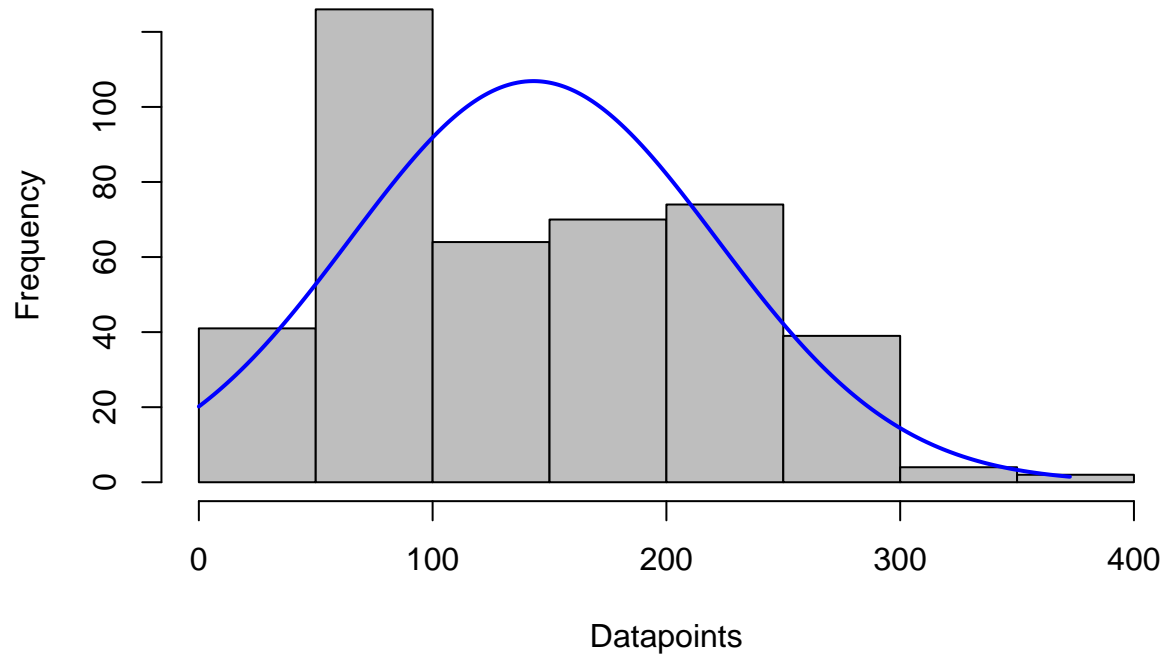
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES2



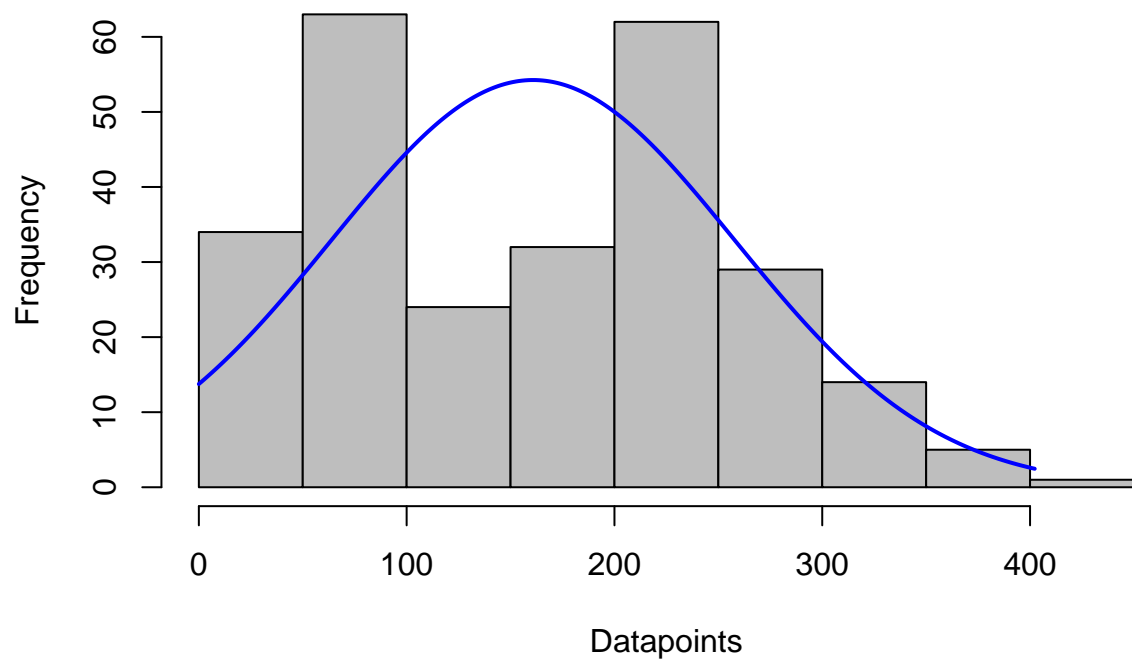
```
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES5



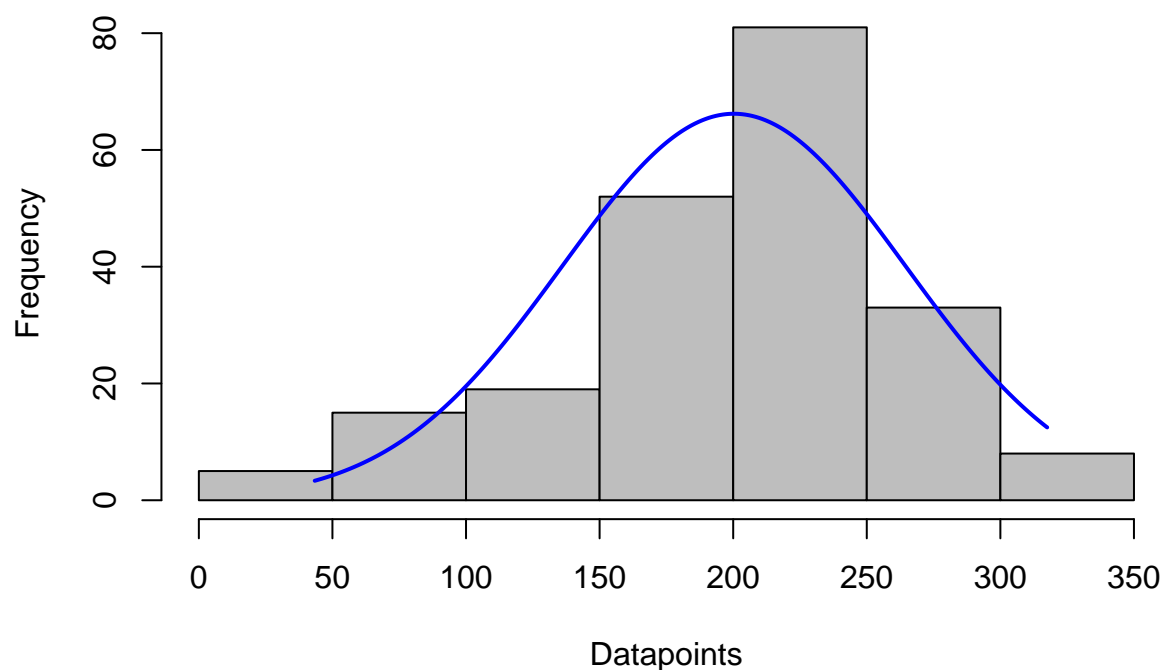
```
plotNormalHistogram(ES13B$chl, main = "Density of Chlorophyll Content (Digital) for E13B",  
  xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for E13B



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

Density of Chlorophyll Content (Digital) for E14A



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

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

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

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

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



```
ES13B_ch1.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_ch1.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_ch1.tuk)
ES5.mod <- cbind(ES5, ES5_ch1.tuk)
ES13B.mod <- cbind(ES13B, ES13B_ch1.tuk)
ES14A.mod <- cbind(ES14A, ES14A_ch1.tuk)
```

Statistical analyses

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

ES2 dataset (untransformed data)

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

```
#####ES2 analysis (raw data)#####
ES2.ch1.anova <- lm (ES2$chl ~ ES2$Treatment +
                    ES2$Dilution +
                    ES2$Condition +
                    ES2$isoRep +
                    ES2$techRep +
                    ES2$sampleNumber)
ES2.ch1.anova
```

```
##
## 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.anova)
```

```
##
## Call:
## lm(formula = ES2$chl ~ ES2$Treatment + ES2$Dilution + ES2$Condition +
##     ES2$isoRep + ES2$techRep + ES2$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -231.24  -49.47    1.55   41.40  536.42
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    236.806    20.365   11.628 < 2e-16 ***
## ES2$TreatmentDMCC2126 -140.175    18.956   -7.395 1.70e-12 ***
## ES2$TreatmentDMCC2127 -173.159    19.204   -9.017 < 2e-16 ***
## ES2$TreatmentDMCC2165 -169.865    18.952   -8.963 < 2e-16 ***
## ES2$TreatmentDMCC2966  -44.126    18.481   -2.388  0.0176 *
## ES2$Dilution25fold  -102.848    11.998   -8.572 7.35e-16 ***
## ES2$ConditionStationary  -8.823    11.944   -0.739  0.4607
## ES2$isoRepisolateRep2    23.729    11.964    1.983  0.0483 *
## ES2$techRepStem2       -24.695    15.316   -1.612  0.1080
## ES2$techRepStem3        16.950    14.020    1.209  0.2277
## ES2$sampleNumbersample2  26.386    14.436    1.828  0.0687 .
## ES2$sampleNumbersample3  30.435    14.489    2.101  0.0366 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 100.5 on 276 degrees of freedom
## (72 observations deleted due to missingness)
## Multiple R-squared:  0.4591, Adjusted R-squared:  0.4375
## F-statistic: 21.3 on 11 and 276 DF, p-value: < 2.2e-16
```

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

```
## Analysis of Variance Table
##
## Response: ES2$chl
```

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

#Tukey's HSD for Variable chl by Treatment

```
ES2.chl.treatment.HSD.test <- HSD.test(ES2.chl.anova, '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.anova, '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.anova, c("ES2$Treatment", "ES2$Dilution"), group=TRUE, console=TRUE)

##
## Study: ES2.chl.anova ~ 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.anova <- 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.anova
```

```
##
## Call:
## lm(formula = ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution +
##     ES2.mod$Condition + ES2.mod$isoRep + ES2.mod$techRep + ES2.mod$sampleNumber)
##
## Coefficients:
##              (Intercept)    ES2.mod$TreatmentDMCC2126
##                   7.52662                   -2.19660
##   ES2.mod$TreatmentDMCC2127    ES2.mod$TreatmentDMCC2165
##                   -3.39025                   -3.45003
##   ES2.mod$TreatmentDMCC2966    ES2.mod$Dilution25fold
##                   -0.21011                   -2.34945
##   ES2.mod$ConditionStationary    ES2.mod$isoRepisolateRep2
##                   -0.09975                    0.73788
##         ES2.mod$techRepStem2    ES2.mod$techRepStem3
##                   -0.70265                   -0.27113
##   ES2.mod$sampleNumbersample2    ES2.mod$sampleNumbersample3
##                   -0.03389                   -0.09430
```

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

```
##
## Call:
## lm(formula = ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution +
##     ES2.mod$Condition + ES2.mod$isoRep + ES2.mod$techRep + ES2.mod$sampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.1829 -1.1889  0.4416  1.2936  4.5838
##
## Coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          7.52662    0.44329 16.979 < 2e-16 ***
## ES2.mod$TreatmentDMCC2126 -2.19660    0.41262 -5.323 2.11e-07 ***
## ES2.mod$TreatmentDMCC2127 -3.39025    0.41803 -8.110 1.67e-14 ***
## ES2.mod$TreatmentDMCC2165 -3.45003    0.41254 -8.363 3.06e-15 ***
## ES2.mod$TreatmentDMCC2966 -0.21011    0.40229 -0.522 0.60190
## ES2.mod$Dilution25fold -2.34945    0.26117 -8.996 < 2e-16 ***
## ES2.mod$ConditionStationary -0.09975    0.26000 -0.384 0.70152
## ES2.mod$isoRepisolateRep2  0.73788    0.26043  2.833 0.00495 **
## ES2.mod$techRepStem2      -0.70265    0.33340 -2.108 0.03597 *
## ES2.mod$techRepStem3      -0.27113    0.30518 -0.888 0.37510
## ES2.mod$sampleNumbersample2 -0.03389    0.31425 -0.108 0.91420
## ES2.mod$sampleNumbersample3 -0.09430    0.31539 -0.299 0.76518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.188 on 276 degrees of freedom
## (72 observations deleted due to missingness)
## Multiple R-squared:  0.4559, Adjusted R-squared:  0.4342
## F-statistic: 21.02 on 11 and 276 DF, p-value: < 2.2e-16
```

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

```
## 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.anova, '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.anova, '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.anova, c("ES2.mod$Treatment",
"ES2.mod$Dilution"),
group=TRUE,console=TRUE)
```

```
##
## Study: ES2.mod.chl.anova ~ 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_ch1.tuk      std  r      Min      Max      Q25
## control:100fold      8.952842 2.033695 24 5.575585 12.443509 7.860042
## control:25fold      4.211675 2.459674 33 0.000000  8.147445 2.807281
## DMCC2126:100fold      5.904452 1.432971 30 2.409370  8.294402 5.211560
## DMCC2126:25fold      2.180805 1.263683 27 0.000000  4.390190 2.359361
## DMCC2127:100fold      3.720246 2.309541 27 0.000000  6.831014 2.547399
## DMCC2127:25fold      2.139470 1.622868 27 0.000000  5.873811 0.000000
## DMCC2165:100fold      3.677465 2.368645 24 0.000000  7.124617 2.700544
## DMCC2165:25fold      1.925497 1.211620 33 0.000000  3.041187 0.000000
## DMCC2966:100fold      6.114039 2.778697 33 0.000000  8.510026 5.991199
## DMCC2966:25fold      6.285168 2.210961 30 0.000000  8.587655 6.035946
##
##      Q50      Q75
## control:100fold 8.279323 10.486003
## control:25fold 4.628247 6.200641
## DMCC2126:100fold 6.189452 6.705312
## DMCC2126:25fold 2.483657 2.863395
## DMCC2127:100fold 3.818594 5.417472
## DMCC2127:25fold 2.531540 2.807481
## DMCC2165:100fold 3.362478 5.745663
## DMCC2165:25fold 2.561469 2.745123
## DMCC2966:100fold 6.963949 7.832392
## DMCC2966:25fold 7.032779 7.590879
##
## $comparison
## NULL
##
## $groups
##      ES2.mod$ES2_ch1.tuk groups
## control:100fold      8.952842      a
## DMCC2966:25fold      6.285168      b
## DMCC2966:100fold      6.114039      b
## DMCC2126:100fold      5.904452      bc
## control:25fold      4.211675      cd
## DMCC2127:100fold      3.720246      de
## DMCC2165:100fold      3.677465      de
## DMCC2126:25fold      2.180805      e
## DMCC2127:25fold      2.139470      e
## DMCC2165:25fold      1.925497      e
##
## attr(,"class")
## [1] "group"
```

Run analyses for ES5

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

```
#####ES5 analysis#####
ES5.ch1.anova <- lm (ES5$chl ~ ES5$Treatment +
                    ES5$Dilution +
```

```

                                ES5$Condition +
                                ES5$isoRep +
                                ES5$techRep +
                                ES5$sampleNumber)
ES5.ch1.anova

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

```

```
summary(ES5.ch1.anova)
```

```

##
## 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.anova)
```

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

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

```
ES5.chl.treatment.HSD.test <- HSD.test(ES5.chl.anova, '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.anova, '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.anova, '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.anova, c("ES5$Treatment", "ES5$Condition",
"ES5$Dilution"), group=TRUE, console=TRUE)
```

```
##
## Study: ES5.chl.anova ~ 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.anova <- 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.anova
```

```
##
## 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.anova)
```

```
##
## 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.anova)
```

```
## 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.anova, '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.anova, '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.anova, '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.anova, c("ES5.mod$Treatment",
      "ES5.mod$Condition",
      "ES5.mod$Dilution"),
      group=TRUE,console=TRUE)
```

```
##
## Study: ES5.mod.chl.anova ~ 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_ch1.tuk groups
## control:Stationary:100fold      35.01510      a
## control:Shaking:100fold         30.92160     ab
## DMCC2127:Stationary:100fold     29.90084     ab
## control:Stationary:25fold       28.23105    abc
## DMCC2126:Stationary:100fold     28.13045    abc
## DMCC2126:Shaking:100fold        26.63321     bc
## control:Shaking:25fold          26.28822     bc
## DMCC2165:Shaking:100fold        24.56023    bcd
## DMCC2127:Stationary:25fold      24.48688    bcd
## DMCC2165:Stationary:25fold      23.73032    bcd
## DMCC2165:Stationary:100fold     22.51380    cde
## DMCC2126:Stationary:25fold      21.36280    cde
## DMCC2127:Shaking:100fold       18.70574    def
## DMCC2165:Shaking:25fold         18.20998    def
## DMCC2126:Shaking:25fold         16.33068     ef
## DMCC2127:Shaking:25fold         13.80400      f

```

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

```

## $statistics
##   MSerror Df      Mean      CV
##   57.63529 408 24.21363 31.35338
##
## $parameters
##   test                                     name.t ntr
##   Tukey ES5.mod$Treatment:ES5.mod$Condition:ES5.mod$Dilution 16
##   StudentizedRange alpha
##         4.87582 0.05
##

```

```

## $means
##
## ES5.mod$ES5_ch1.tuk      std  r      Min      Max
## control:Shaking:100fold    30.92160  6.877550  24  20.467824  46.19961
## control:Shaking:25fold     26.28822  7.584437  27   8.312519  36.10186
## control:Stationary:100fold  35.01510  3.511991  27  29.814226  46.91458
## control:Stationary:25fold  28.23105  8.847762  24  10.583319  41.07609
## DMCC2126:Shaking:100fold   26.63321  8.061394  24  12.382456  38.08942
## DMCC2126:Shaking:25fold    16.33068  4.334703  27   9.182009  24.92251
## DMCC2126:Stationary:100fold 28.13045  7.218510  27  12.994778  37.53790
## DMCC2126:Stationary:25fold  21.36280  9.304178  27  10.270619  38.70932
## DMCC2127:Shaking:100fold   18.70574  5.119409  27  10.473529  30.33414
## DMCC2127:Shaking:25fold    13.80400  6.101857  27   0.000000  22.40212
## DMCC2127:Stationary:100fold 29.90084  8.268740  27  16.549688  44.13634
## DMCC2127:Stationary:25fold  24.48688  7.726440  27  13.222435  40.39612
## DMCC2165:Shaking:100fold   24.56023  8.205647  27  10.418401  38.34533
## DMCC2165:Shaking:25fold    18.20998  5.258465  27  11.052188  28.65280
## DMCC2165:Stationary:100fold 22.51380 11.836979  27   0.000000  38.95398
## DMCC2165:Stationary:25fold  23.73032  9.225861  24  12.382456  39.79045
##
##          Q25      Q50      Q75
## control:Shaking:100fold   25.60774 29.95578 35.75395
## control:Shaking:25fold    23.23414 28.68481 31.88435
## control:Stationary:100fold 32.89985 34.77877 36.49626
## control:Stationary:25fold  22.97996 30.57655 35.12646
## DMCC2126:Shaking:100fold   18.24222 28.49017 32.10254
## DMCC2126:Shaking:25fold    12.72170 15.30503 19.21892
## DMCC2126:Stationary:100fold 23.96670 29.23662 34.36364
## DMCC2126:Stationary:25fold  13.75020 17.95239 28.49754
## DMCC2127:Shaking:100fold   15.79238 18.06204 22.03937
## DMCC2127:Shaking:25fold    11.94225 14.14409 18.38373
## DMCC2127:Stationary:100fold 21.18901 31.73483 36.13001
## DMCC2127:Stationary:25fold  16.98374 23.80439 29.93923
## DMCC2165:Shaking:100fold   17.06819 21.67684 31.48681
## DMCC2165:Shaking:25fold    14.32943 16.96287 19.24541
## DMCC2165:Stationary:100fold 14.61527 26.86130 31.84574
## DMCC2165:Stationary:25fold  16.28243 21.81134 30.38458
##
## $comparison
## NULL
##
## $groups
##
## ES5.mod$ES5_ch1.tuk groups
## control:Stationary:100fold    35.01510      a
## control:Shaking:100fold        30.92160     ab
## DMCC2127:Stationary:100fold    29.90084     ab
## control:Stationary:25fold      28.23105    abc
## DMCC2126:Stationary:100fold    28.13045    abc
## DMCC2126:Shaking:100fold       26.63321     bc
## control:Shaking:25fold         26.28822     bc
## DMCC2165:Shaking:100fold       24.56023    bcd
## DMCC2127:Stationary:25fold     24.48688    bcd
## DMCC2165:Stationary:25fold     23.73032    bcd
## DMCC2165:Stationary:100fold    22.51380    cde
## DMCC2126:Stationary:25fold     21.36280    cde
## DMCC2127:Shaking:100fold       18.70574    def

```

```
## DMCC2165:Shaking:25fold      18.20998    def
## DMCC2126:Shaking:25fold      16.33068    ef
## DMCC2127:Shaking:25fold      13.80400    f
##
## attr("class")
## [1] "group"
```

Run analyses for ES13B

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

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

##
## Call:
## lm(formula = ES13B$chl ~ ES13B$Treatment + ES13B$HostVariety +
##     ES13B$isoRepNumber + ES13B$techRepNumber + ES13B$SampleNumber)
##
## Coefficients:
##             (Intercept)      ES13B$TreatmentDMCC2165
##                187.9400                -105.4678
##   ES13B$HostVarietyDG47E80  ES13B$HostVarietyDG47X95
##                27.8736                26.3892
##   ES13B$HostVarietyOsage    ES13B$HostVarietyP5414LLS
##                16.1981                -3.8273
##   ES13B$isoRepNumberisoRep2  ES13B$isoRepNumberisoRep3
##                -7.3121                 1.4292
## ES13B$techRepNumbertechRep2  ES13B$techRepNumbertechRep3
##                29.6658                 8.0253
##   ES13B$SampleNumbersample2  ES13B$SampleNumbersample3
##                 0.7302                 1.9473

summary(ES13B.chl.anova)

##
## 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
```

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

```
## 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.anova, '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.anova, 'ES13B$HostVariety', group = T)
ES13B.chl.host_variety.HSD.test
```

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

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

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

##
## 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.anova)
```

```
##
## Call:
## lm(formula = ES13B.mod$ES13B_chl.tuk ~ ES13B.mod$Treatment +
##      ES13B.mod$HostVariety + ES13B.mod$isoRepNumber + ES13B.mod$techRepNumber +
##      ES13B.mod$SampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -64.139 -11.806   0.251  11.105  58.266
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      56.4659     4.4320  12.740  <2e-16 ***
## ES13B.mod$TreatmentDMCC2165    -27.1569     2.5754  -10.545  <2e-16 ***
## ES13B.mod$HostVarietyDG47E80     6.8552     4.0195   1.705  0.0893 .
## ES13B.mod$HostVarietyDG47X95     6.4268     4.1496   1.549  0.1227
## ES13B.mod$HostVarietyOsage       3.2278     4.0195   0.803  0.4227
## ES13B.mod$HostVarietyP5414LLS    -1.2888     4.0195  -0.321  0.7488
## ES13B.mod$isoRepNumberisoRep2    -1.8503     3.1686  -0.584  0.5598
## ES13B.mod$isoRepNumberisoRep3     0.1216     3.1426   0.039  0.9692
## ES13B.mod$techRepNumbertechRep2   7.5512     3.1426   2.403  0.0170 *
## ES13B.mod$techRepNumbertechRep3   2.1409     3.1426   0.681  0.4963
## ES13B.mod$SampleNumbersample2     0.6429     3.1486   0.204  0.8384
## ES13B.mod$SampleNumbersample3     0.7374     3.1486   0.234  0.8150
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 20.89 on 252 degrees of freedom
## (6 observations deleted due to missingness)
## Multiple R-squared:  0.3339, Adjusted R-squared:  0.3048
## F-statistic: 11.48 on 11 and 252 DF, p-value: < 2.2e-16
```

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

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

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

#Tukey's HSD for Variable chl by Treatment

```
ES13B.mod.chl.treatment.HSD.test <- HSD.test(ES13B.mod.chl.anova, '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.anova,
                                                '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_ch1.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_ch1.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.ch1.anova, c("ES13B.mod$Treatment",
                                                             "ES13B.mod$HostVariety"),
                                     group=TRUE,console=TRUE)

##
## Study: ES13B.mod.ch1.anova ~ c("ES13B.mod$Treatment", "ES13B.mod$HostVariety")
##
## HSD Test for ES13B.mod$ES13B_ch1.tuk
##
## Mean Square Error:  436.2119
##
## ES13B.mod$Treatment:ES13B.mod$HostVariety,  means
##
##      ES13B.mod.ES13B_ch1.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_ch1.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_ch1.tuk      std  r      Min      Max
## Control:AG4632          57.20904 22.03662 27  0.00000  96.69957
## Control:DG47E80          66.70288 17.20548 27 35.38176  98.36929
## Control:DG47X95          64.01404 17.93361 27 24.66777  95.60617
## Control:Osage           67.15363 26.52535 27  0.00000 104.34627
## Control:P5414LLS        58.04351 11.99680 27 34.39165  76.51943
## DMCC2165:AG4632         34.79495 18.32309 27  0.00000  78.61163
## DMCC2165:DG47E80        39.01143 22.59966 27  0.00000  76.18307
## DMCC2165:DG47X95        41.05111 26.62931 21  0.00000  93.72814
## DMCC2165:Osage          31.30592 16.83924 27  0.00000  84.32030
## DMCC2165:P5414LLS      31.38296 25.56143 27  0.00000  87.02381
##
##               Q25      Q50      Q75
## Control:AG4632    47.05388 62.96010 68.61805
## Control:DG47E80    62.26497 67.17475 78.30087
## Control:DG47X95    56.17982 65.54711 77.85944
## Control:Osage      65.40652 71.46612 76.90405
## Control:P5414LLS   51.98765 59.22541 67.22892
## DMCC2165:AG4632    22.34657 29.72913 43.18888
## DMCC2165:DG47E80    20.43572 33.65317 61.08024
## DMCC2165:DG47X95    19.88940 30.28659 60.68214
## DMCC2165:Osage     24.95960 26.04835 30.23822

```

```
## DMCC2165:P5414LLS 15.75931 23.21526 36.18682
##
## $comparison
## NULL
##
## $groups
##          ES13B.mod$ES13B_chl.tuk groups
## Control:Osage          67.15363      a
## Control:DG47E80        66.70288      a
## Control:DG47X95        64.01404      a
## Control:P5414LLS       58.04351     ab
## Control:AG4632         57.20904     ab
## DMCC2165:DG47X95       41.05111     bc
## DMCC2165:DG47E80       39.01143      c
## DMCC2165:AG4632        34.79495      c
## DMCC2165:P5414LLS     31.38296      c
## DMCC2165:Osage         31.30592      c
##
## attr("class")
## [1] "group"
```

Run analyses for ES14A

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

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

```
##
## 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.anova)
```

```
##
## 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.anova)
```

```
## 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.anova, '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.anova, '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.anova, c("ES14A$Treatment", "ES14A$Host"), group=TRUE, consol
```

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

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

```
## $statistics
##      MSerror Df      Mean      CV
##    2571.854 202 200.2661 25.32304
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
##    Tukey ES14A$Treatment:ES14A$Host  8          4.331714 0.05
##
## $means
##          ES14A$chl      std r      Min      Max      Q25      Q50
## Control:Cotton  194.11622 42.12477 27 106.098 254.411 172.7065 201.2180
## Control:Peanut  243.47885 43.34219 27 104.832 305.065 220.0160 244.4330
```

```
## Control:Soybean 226.62589 63.78820 27 74.284 312.775 205.7205 227.9410
## Control:Tomato 215.70517 17.85696 24 183.593 244.624 203.4402 214.3875
## DMCC2165:Cotton 171.34937 37.68338 27 99.321 258.986 146.1180 180.5490
## DMCC2165:Peanut 265.62833 31.49505 27 200.016 317.520 247.1435 262.9750
## DMCC2165:Soybean 97.24481 55.25735 27 43.371 210.220 52.2970 66.4980
## DMCC2165:Tomato 189.69526 27.47809 27 117.923 236.489 178.0980 191.1460
## Q75
## Control:Cotton 229.7960
## Control:Peanut 274.2060
## Control:Soybean 274.5295
## Control:Tomato 227.4280
## DMCC2165:Cotton 198.6270
## DMCC2165:Peanut 290.1215
## DMCC2165:Soybean 143.0605
## DMCC2165:Tomato 206.2940
##
## $comparison
## NULL
##
## $groups
## ES14A$chl groups
## DMCC2165:Peanut 265.62833 a
## Control:Peanut 243.47885 ab
## Control:Soybean 226.62589 abc
## Control:Tomato 215.70517 bc
## Control:Cotton 194.11622 cd
## DMCC2165:Tomato 189.69526 cd
## DMCC2165:Cotton 171.34937 d
## DMCC2165:Soybean 97.24481 e
##
## attr("class")
## [1] "group"
```

Same analysis as above using Tukey's normalized data.

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

##
## 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.anova)
```

```
##
## Call:
## lm(formula = ES14A.mod$ES14A_chl.tuk ~ ES14A.mod$Treatment +
##     ES14A.mod$Host + ES14A.mod$isoRepNumber + ES14A.mod$techRepNumber +
##     ES14A.mod$LeafSampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11413  -2124      40    2186   11598
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9573.32      861.86  11.108 < 2e-16 ***
## ES14A.mod$TreatmentDMCC2165 -2709.06      521.66  -5.193 5.03e-07 ***
## ES14A.mod$HostPeanut      6109.14      731.96   8.346 1.10e-14 ***
## ES14A.mod$HostSoybean     -562.35      731.96  -0.768  0.4432
## ES14A.mod$HostTomato     1457.89      743.48   1.961  0.0513 .
## ES14A.mod$isoRepNumberisoRep2    752.80      641.39   1.174  0.2419
## ES14A.mod$isoRepNumberisoRep3    707.59      633.89   1.116  0.2656
## ES14A.mod$techRepNumbertechRep2 -175.15      641.39  -0.273  0.7851
## ES14A.mod$techRepNumbertechRep3 -380.75      641.39  -0.594  0.5534
## ES14A.mod$LeafSampleNumbersample2  -57.52      638.34  -0.090  0.9283
## ES14A.mod$LeafSampleNumbersample3 -831.24      638.34  -1.302  0.1943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3803 on 202 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.3985, Adjusted R-squared:  0.3687
## F-statistic: 13.38 on 10 and 202 DF, p-value: < 2.2e-16
```

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

```
## Analysis of Variance Table
##
## Response: ES14A.mod$ES14A_chl.tuk
##              Df      Sum Sq   Mean Sq F value    Pr(>F)
## ES14A.mod$Treatment      1 389423237 389423237 26.9209 5.141e-07 ***
## ES14A.mod$Host           3 1485413072 495137691 34.2289 < 2.2e-16 ***
## ES14A.mod$isoRepNumber    2  25123911 12561955  0.8684  0.4212
```

```
## ES14A.mod$techRepNumber      2      5115841      2557921      0.1768      0.8381
## ES14A.mod$LeafSampleNumber   2      30598645      15299322      1.0576      0.3492
## Residuals                    202      2922025050      14465471
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tukey's HSD for Variable chl by Treatment

```
ES14A.mod.chl.treatment.HSD.test <- HSD.test(ES14A.mod.chl.anova, '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.anova, '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_ch1.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.ch1.anova, c("ES14A.mod$Treatment",
                                                             "ES14A.mod$Host"),
                                     group=TRUE,console=TRUE)
```

```
##
## Study: ES14A.mod.ch1.anova ~ c("ES14A.mod$Treatment", "ES14A.mod$Host")
##
## HSD Test for ES14A.mod$ES14A_ch1.tuk
##
## Mean Square Error:  14465471
##
## ES14A.mod$Treatment:ES14A.mod$Host,  means
##
##      ES14A.mod.ES14A_ch1.tuk      std  r      Min      Max
## Control:Cotton          9103.740 3172.165 27 3121.3676 14110.73
## Control:Peanut         13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean        12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato         10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton         7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut        15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean        3195.045 3010.793 27  667.0663 10153.43
## DMCC2165:Tomato         8613.327 2039.245 27 3745.4797 12440.10
##
## Alpha: 0.05 ; DF Error: 202
## Critical Value of Studentized Range: 4.331714
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##      ES14A.mod$ES14A_ch1.tuk groups
## DMCC2165:Peanut          15330.007      a
```

## Control:Peanut	13336.356	ab
## Control:Soybean	12128.331	bc
## Control:Tomato	10658.376	bcd
## Control:Cotton	9103.740	cde
## DMCC2165:Tomato	8613.327	de
## DMCC2165:Cotton	7344.338	e
## DMCC2165:Soybean	3195.045	f

ES14A.mod.comp.HSD.group

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

Plotting individual plots and composite figures

Individual plots for figure 1

Extract the information needed for panel “A”

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

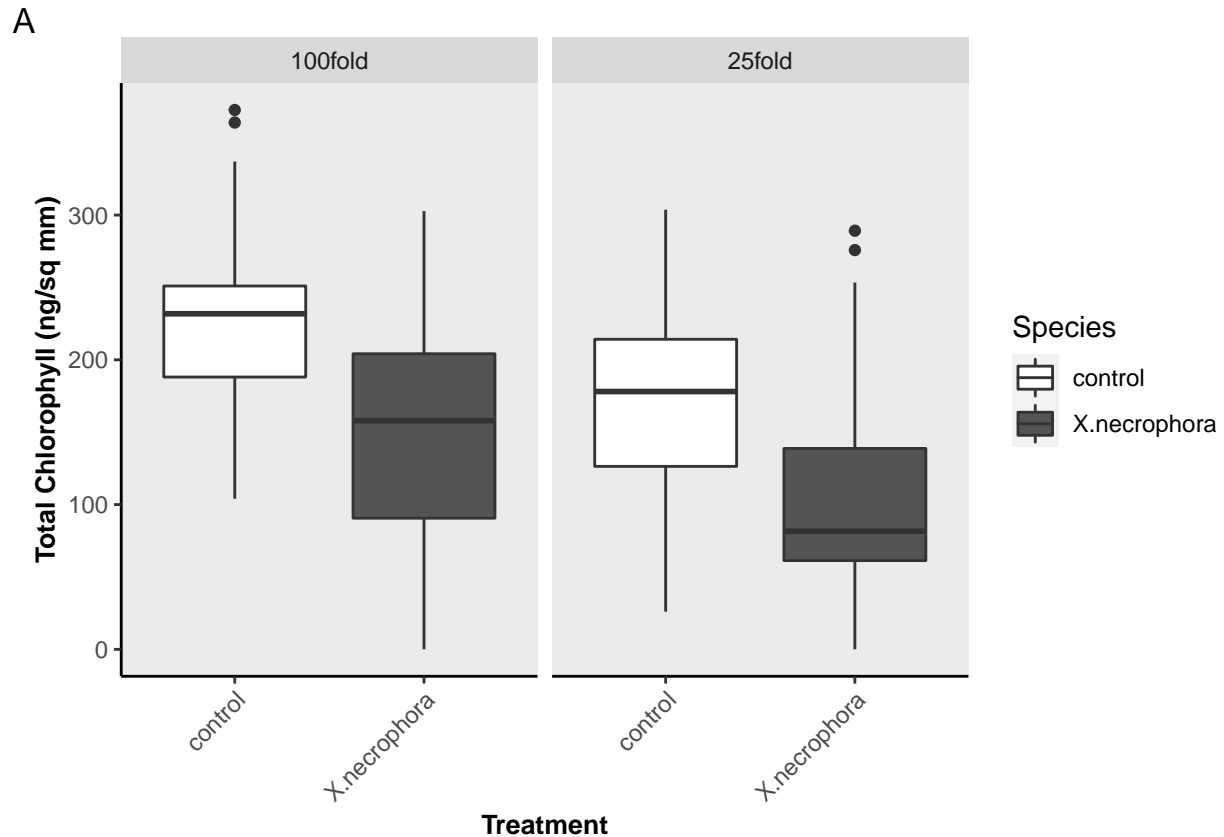
ES5.control <- ES5.control %>%
  add_column(Species = "control")

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

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

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

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

Individual plot for panel B

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

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

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

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

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

#plot for figure by species by dilution factor

#Reorganizing for plotting

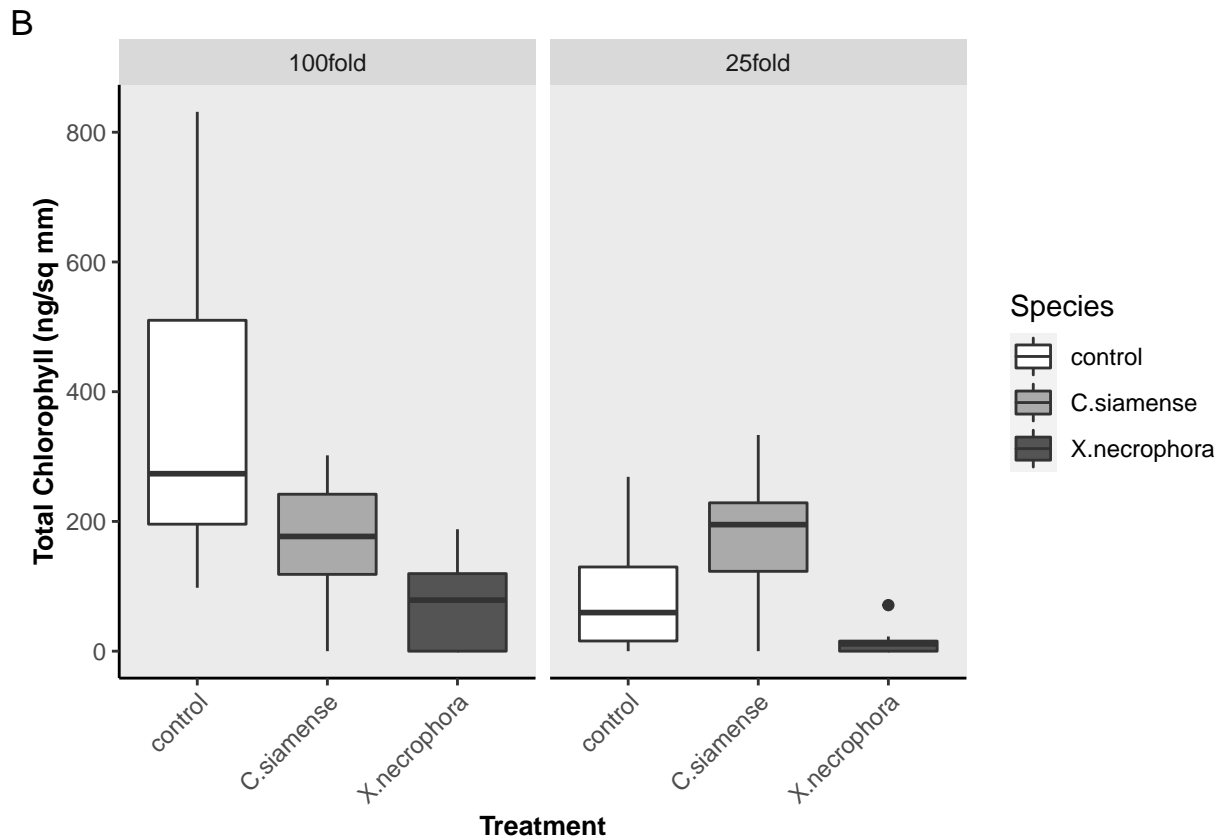
ES2.mod.v2$Species <- factor(ES2.mod.v2$Species,
  levels = c("control", "C.siamense", "X.necrophora"))
```

```

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).



Plot composite figure 1

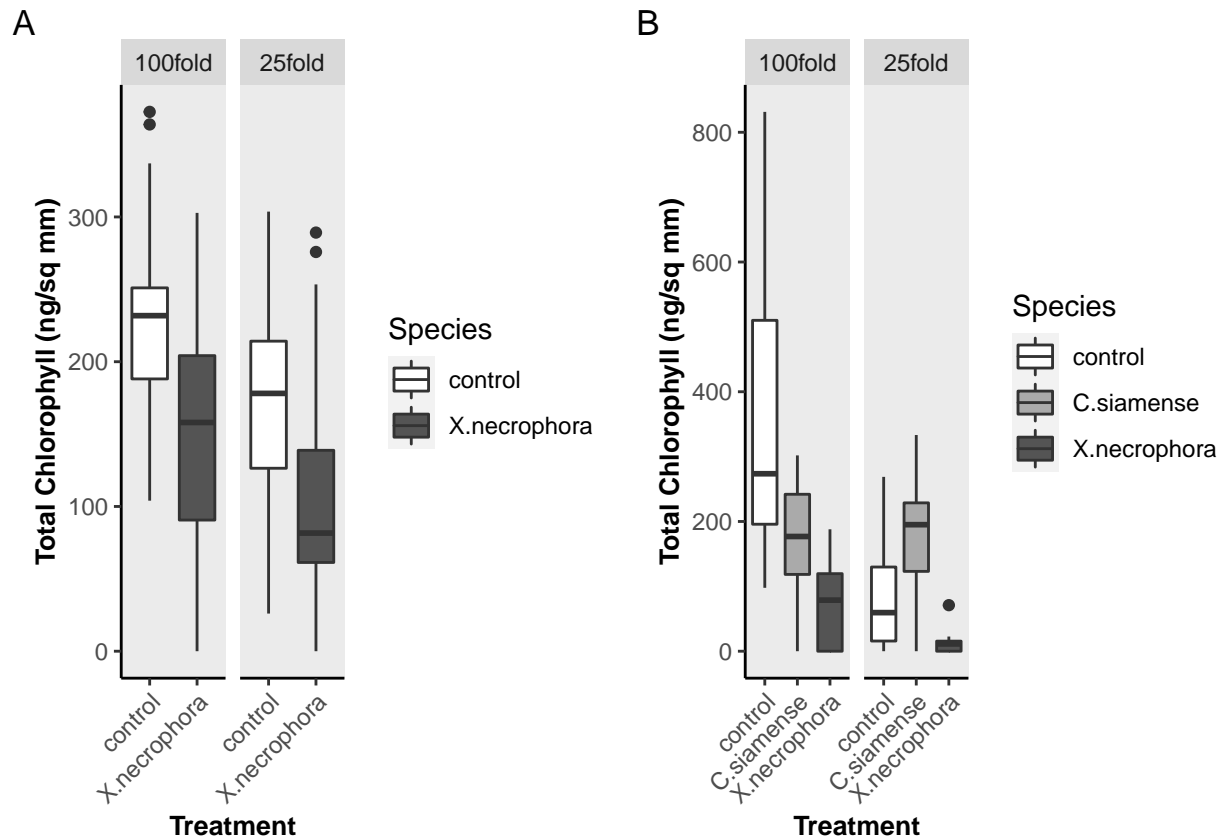
```

###Grid for composite figure 1 (updated 10/25/2021). Using ES2 and ES5 only.
gridExtra::grid.arrange(ES5.mod.ggplot, ES2.mod.v2.ggplot, ncol=2)

```

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

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



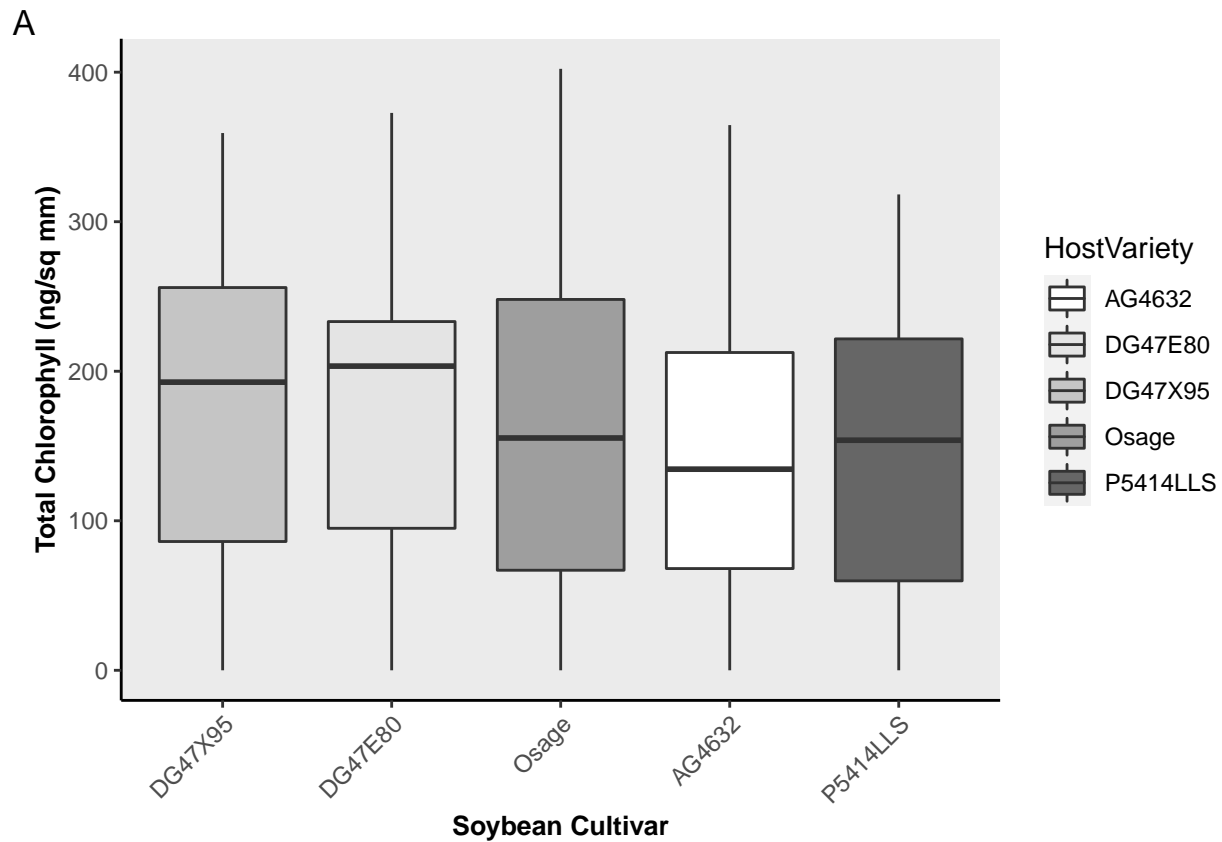
Plotting individual plots and composite figure 3

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
```

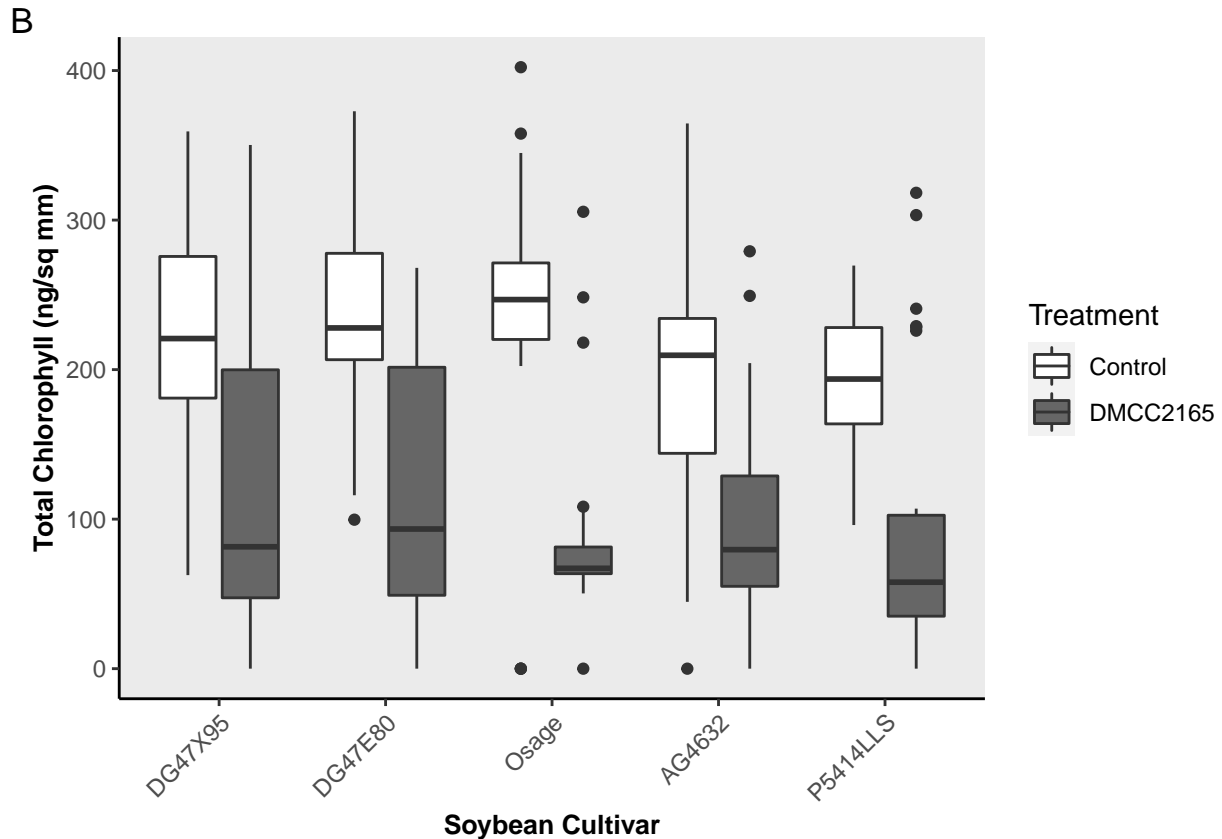
```
## Warning: Removed 6 rows containing non-finite values (stat_boxplot).
```



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
```

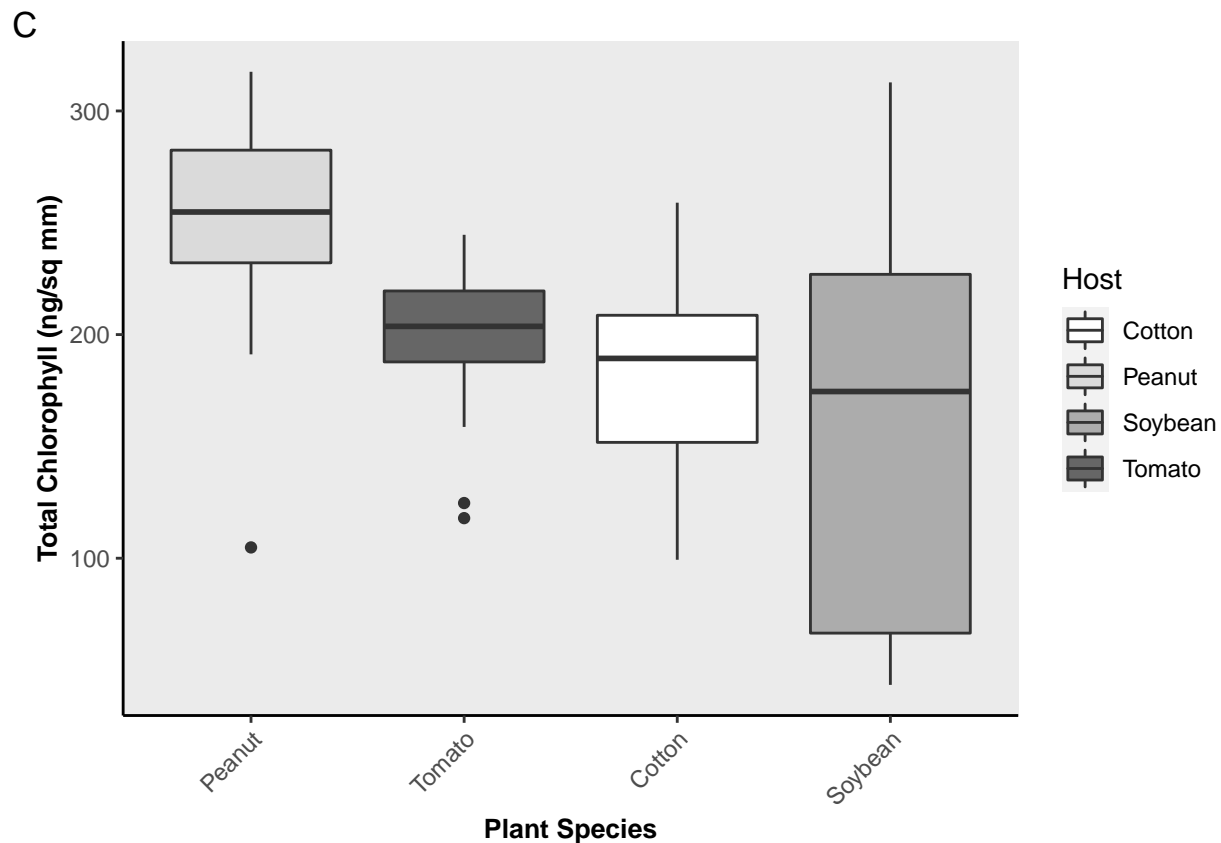
```
## Warning: Removed 6 rows containing non-finite values (stat_boxplot).
```



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
```

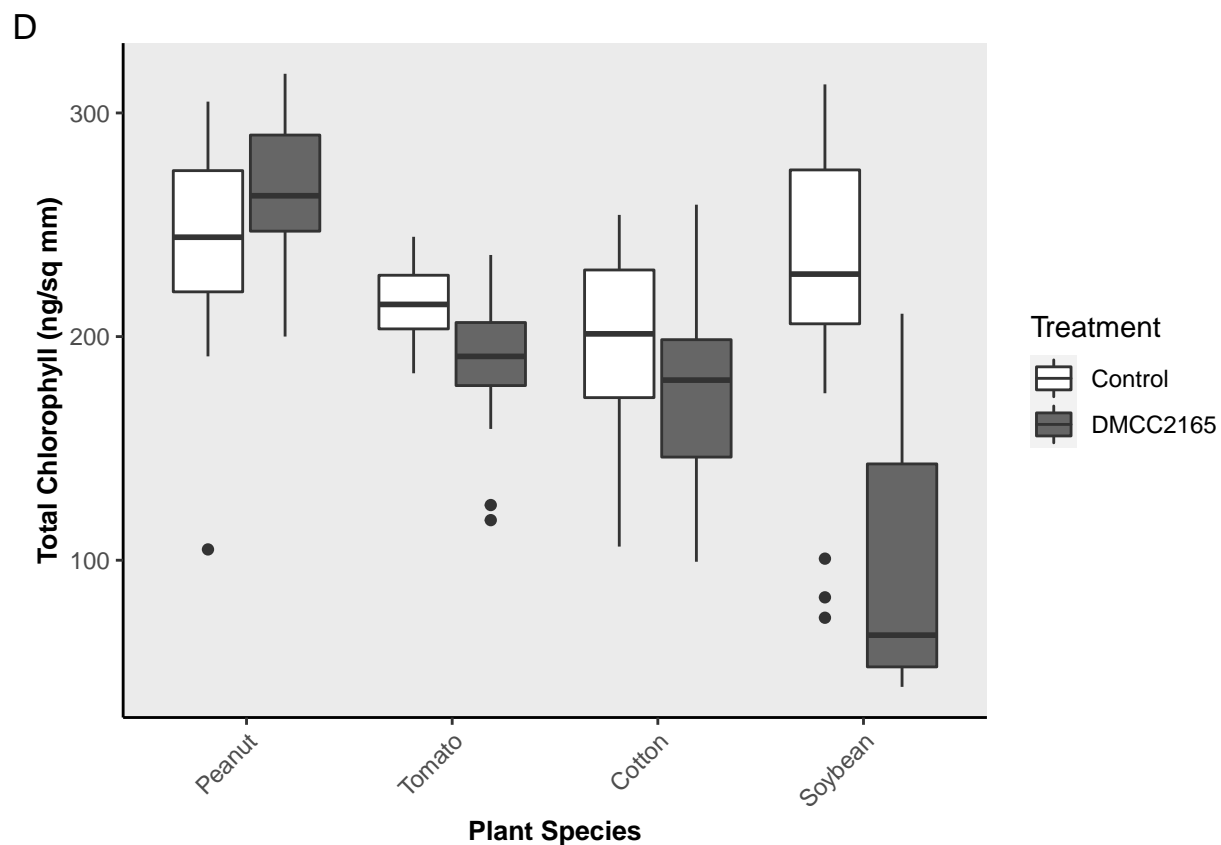
```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```



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 3

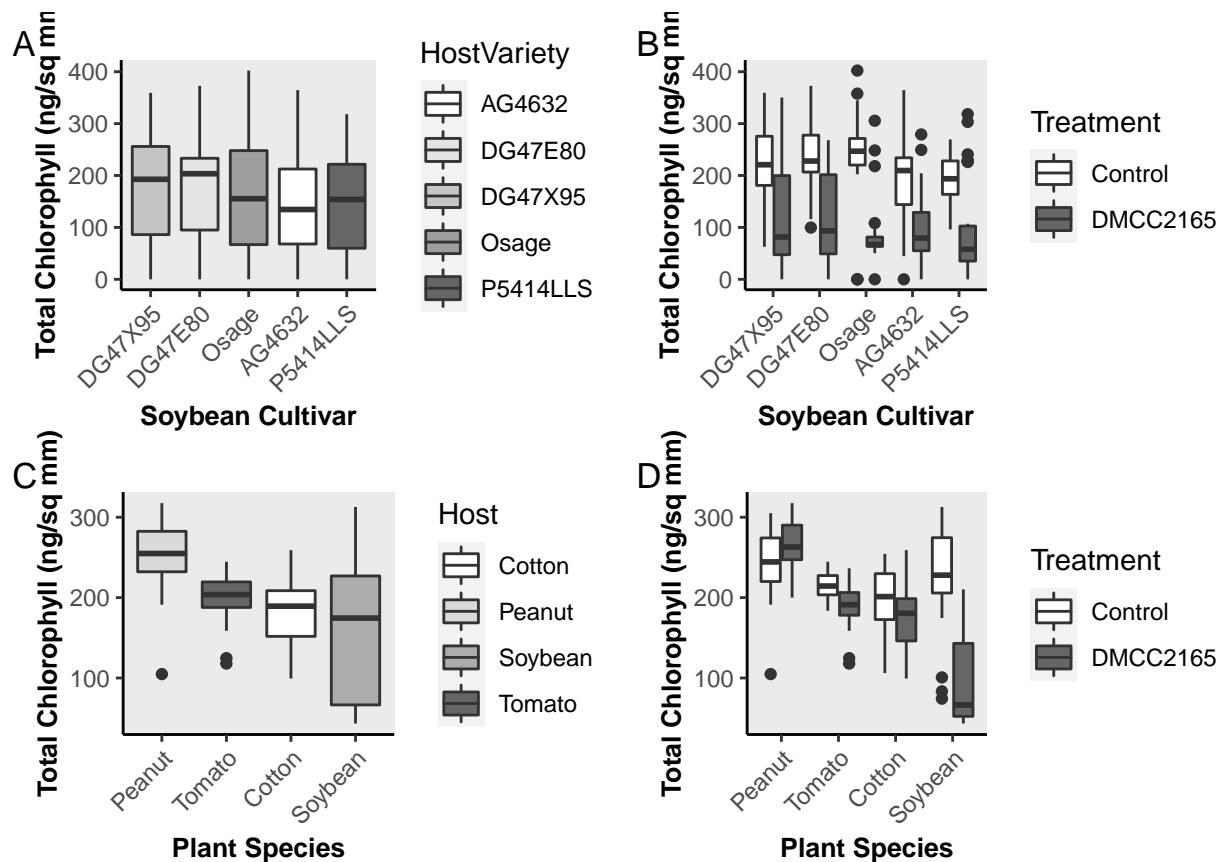
```
###Grid for composite figure 3 (08/16/2021). Using ES13B and ES14 only.
gridExtra::grid.arrange(ES13B.ByHosCult,
  ES13B.ggplot.ByCultByTreat ,
  ES14A.ggplot.ByHost,
  ES14A.ggplot.ByHostByTreat, ncol=2)
```

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

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

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

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

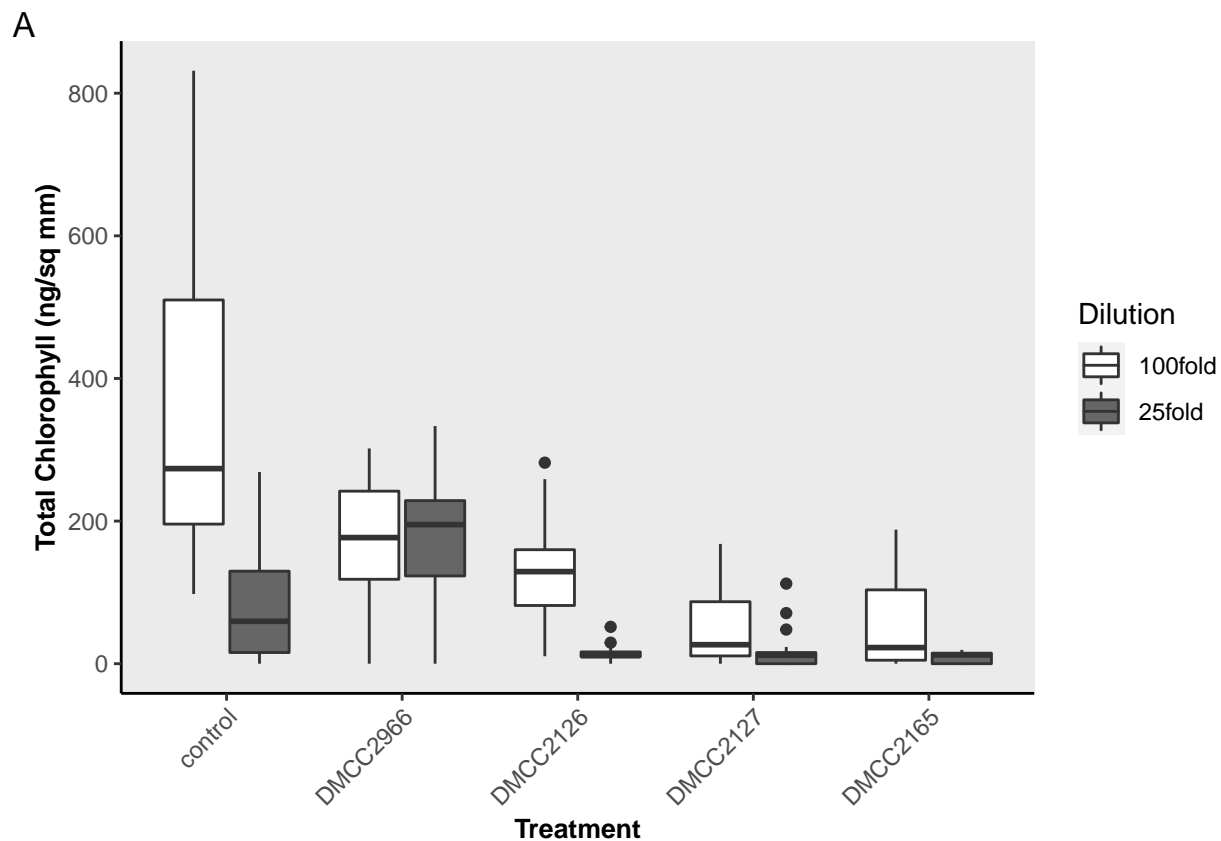


Supplementary Materials/Figures

Plotting Supplementary Figure 1

```
#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 = "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"))
ES2.mod.ggplot.v2
```

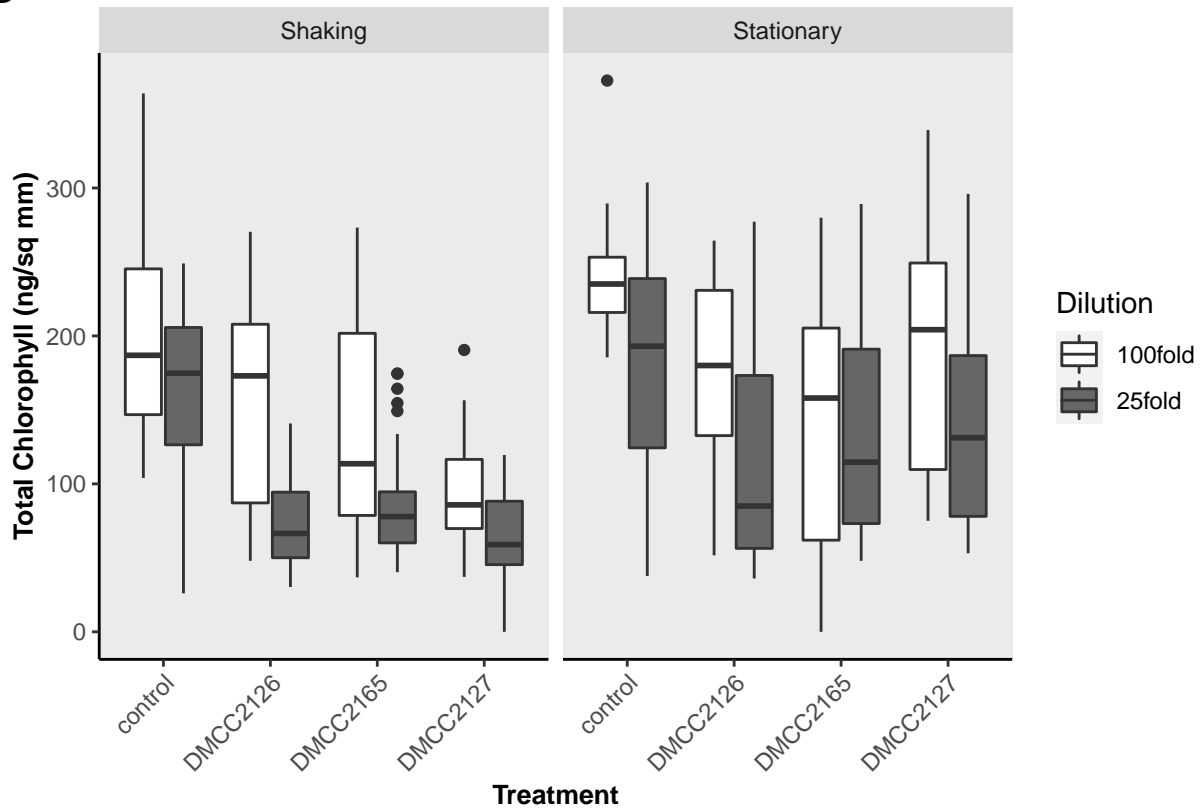
```
## Warning: Removed 60 rows containing non-finite values (stat_boxplot).
```

```
#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 = "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(~ Condition)
ES5.mod.ggplot.v2
```

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

B

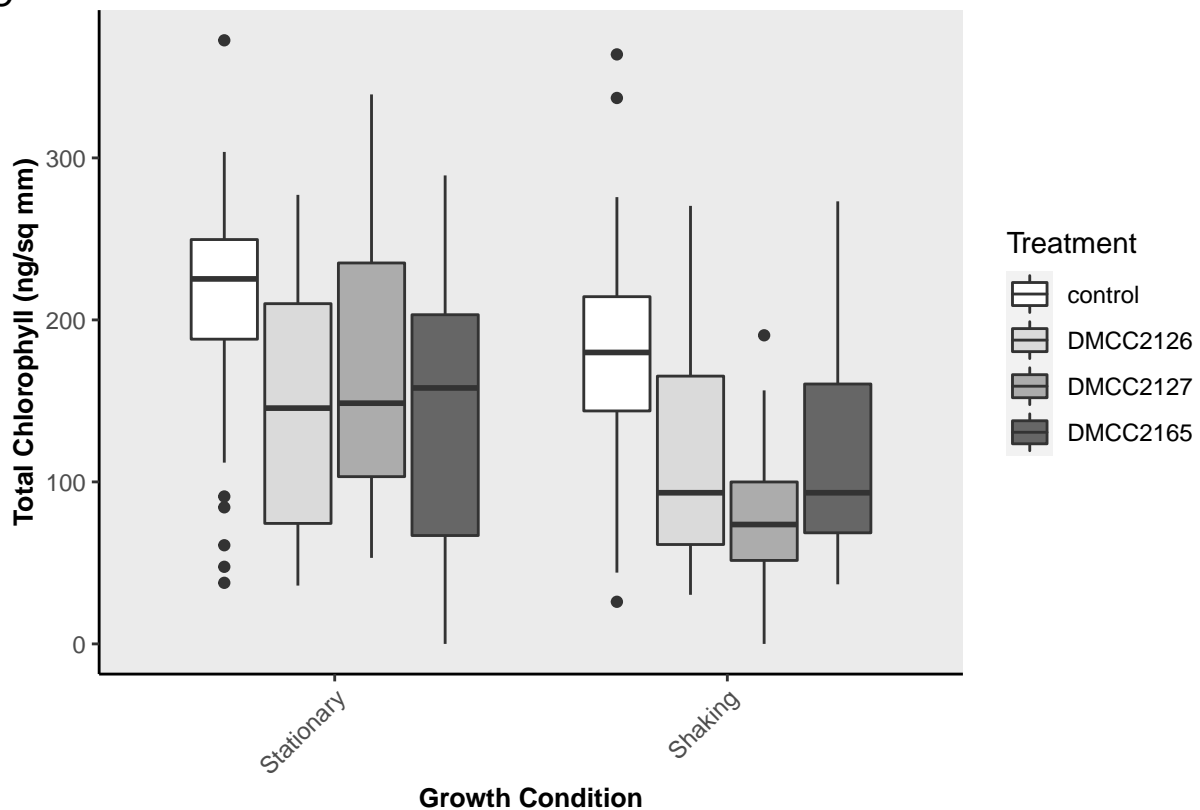


```
#ES5 by conditions (side by side)
ES5.mod.ggplot.v3 <- ggplot(ES5.mod, aes(x = reorder(Condition, -chl, na.rm = TRUE),
                                              y = chl, fill=Treatment)) +

  geom_boxplot() +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "C") +
  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).
```

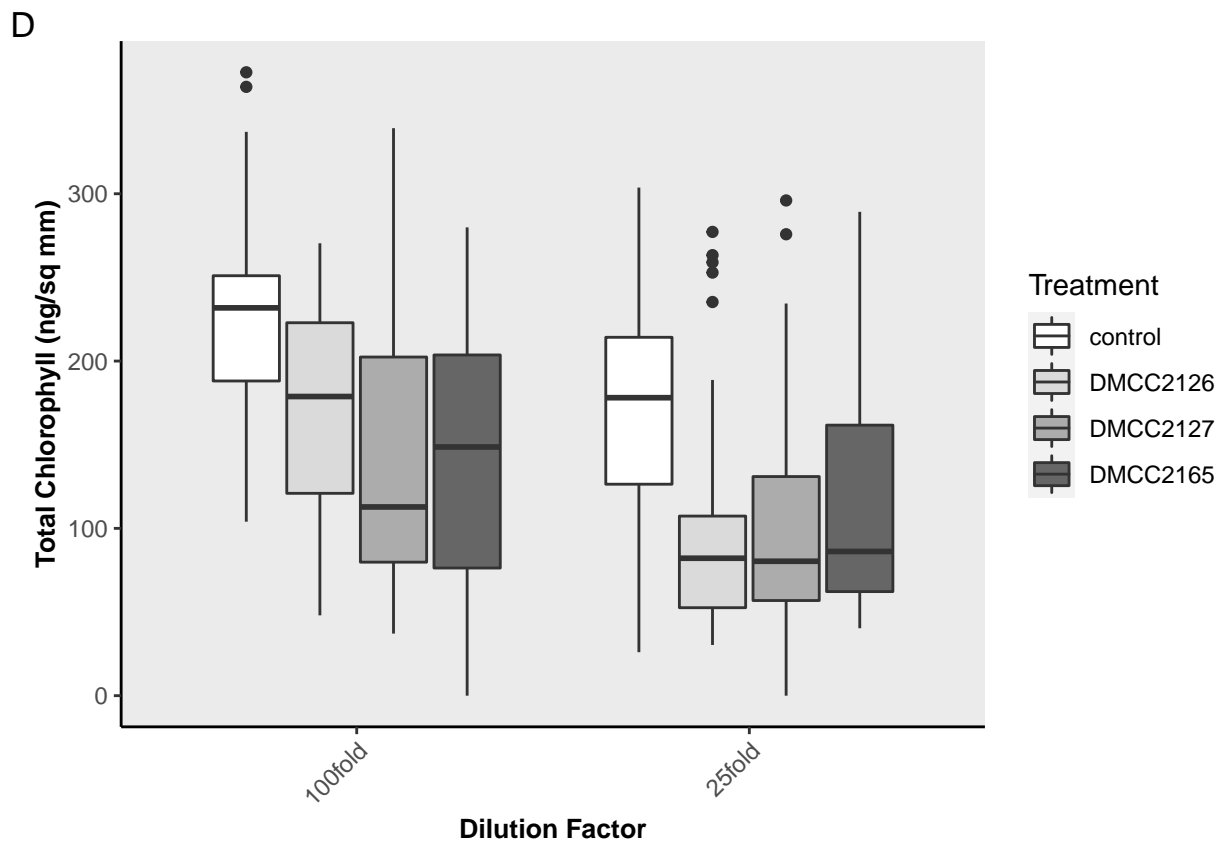
C



```
#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 = "D") +
  xlab("Dilution Factor") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"),
        axis.title.x = element_text(size=10, face = "bold"),
        axis.title.y = element_text(size = 10, face = "bold"),
        axis.text.x = element_text(angle = 45, hjust = 1)) +
  theme(panel.border = element_blank(),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        axis.line = element_line(colour = "black"))
ES5.mod.ggplot.v4
```

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



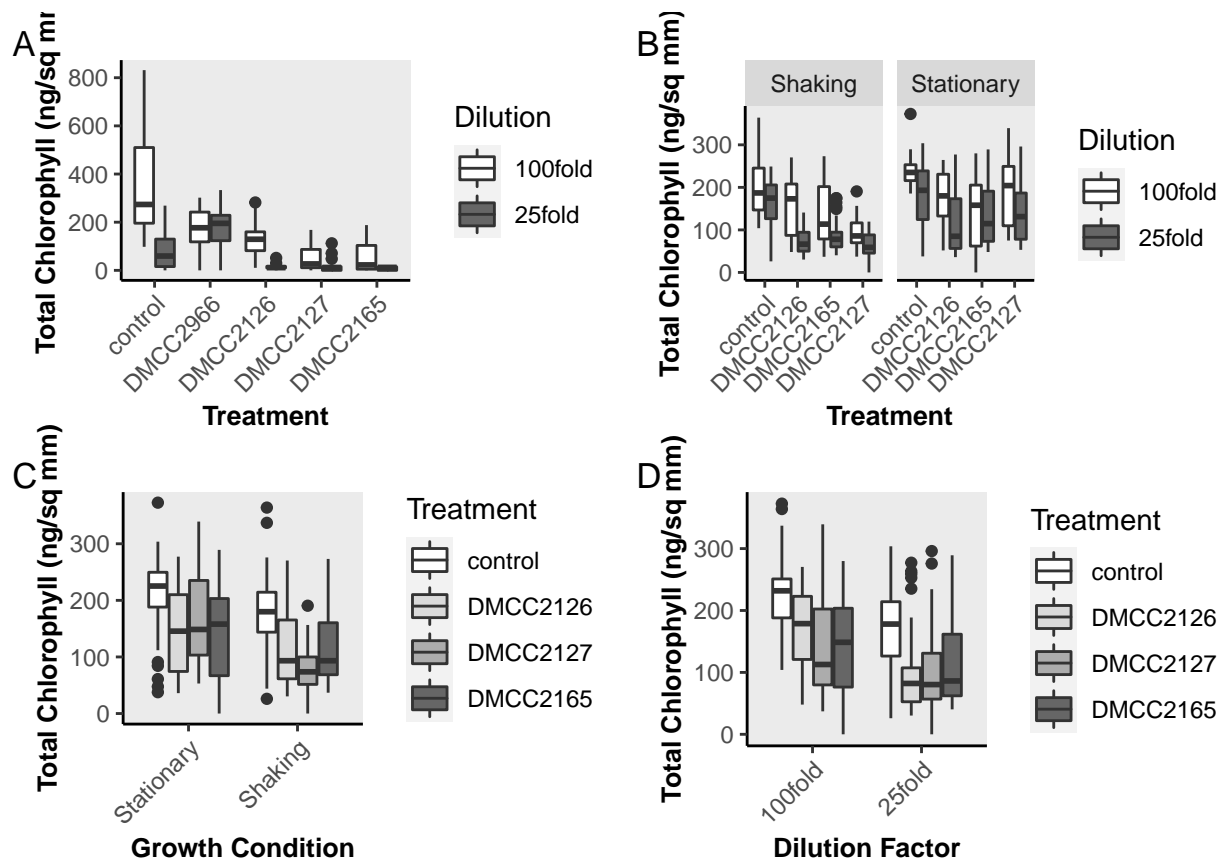
```
###Grid for supplementary figure 1 (updated 08/25/2021). Using ES2 and ES5 only.
gridExtra::grid.arrange(ES2.mod.ggplot.v2,
  ES5.mod.ggplot.v2,
  ES5.mod.ggplot.v3,ES5.mod.ggplot.v4, ncol=2)
```

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

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

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

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



Plotting Supplementary Figure 2

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

Loading datasets for composite figure

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

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

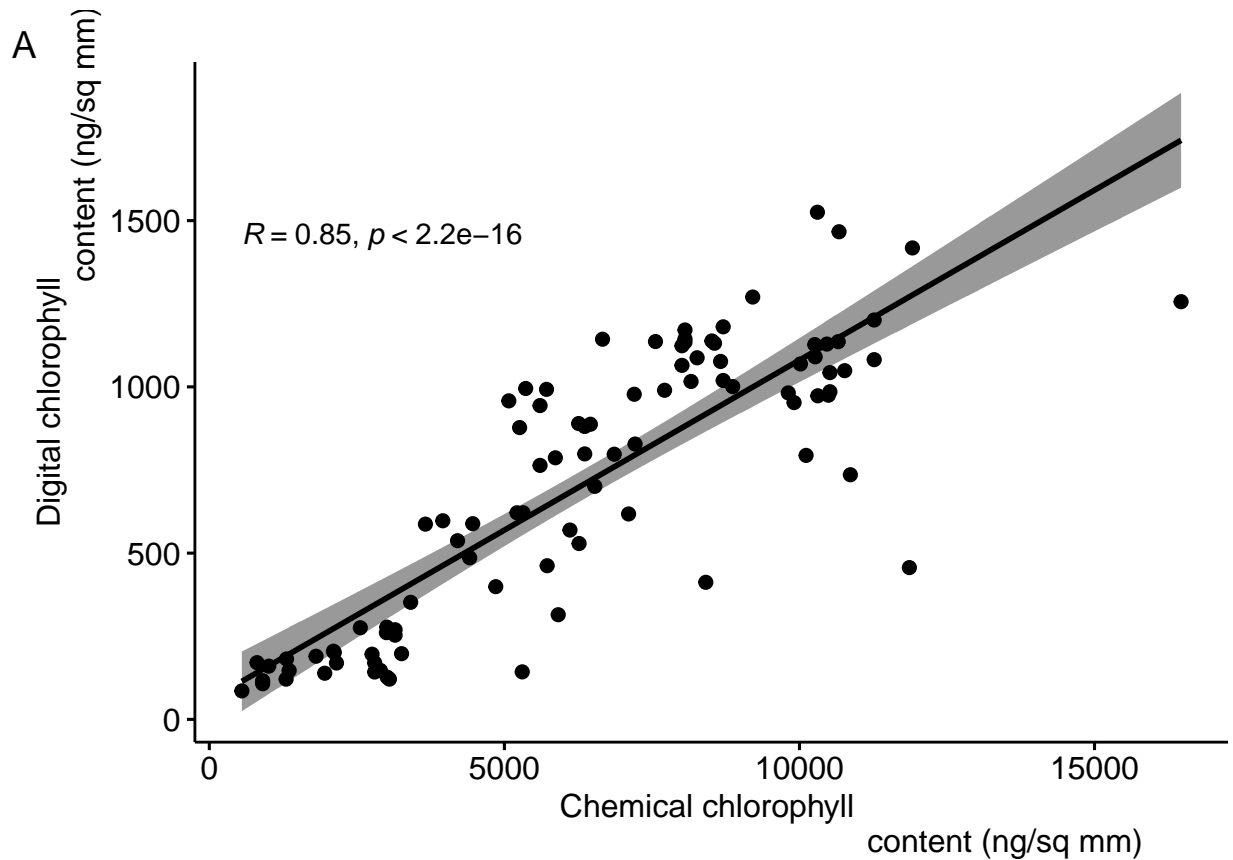
BiomassAndpH.metadata <- read.csv("../raw_data/FilteringTreatments.metadata.csv",
                                     header = T)
```

Summarizing and aggregating datasets

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

Plotting Supplementary Figure 2 panel A

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

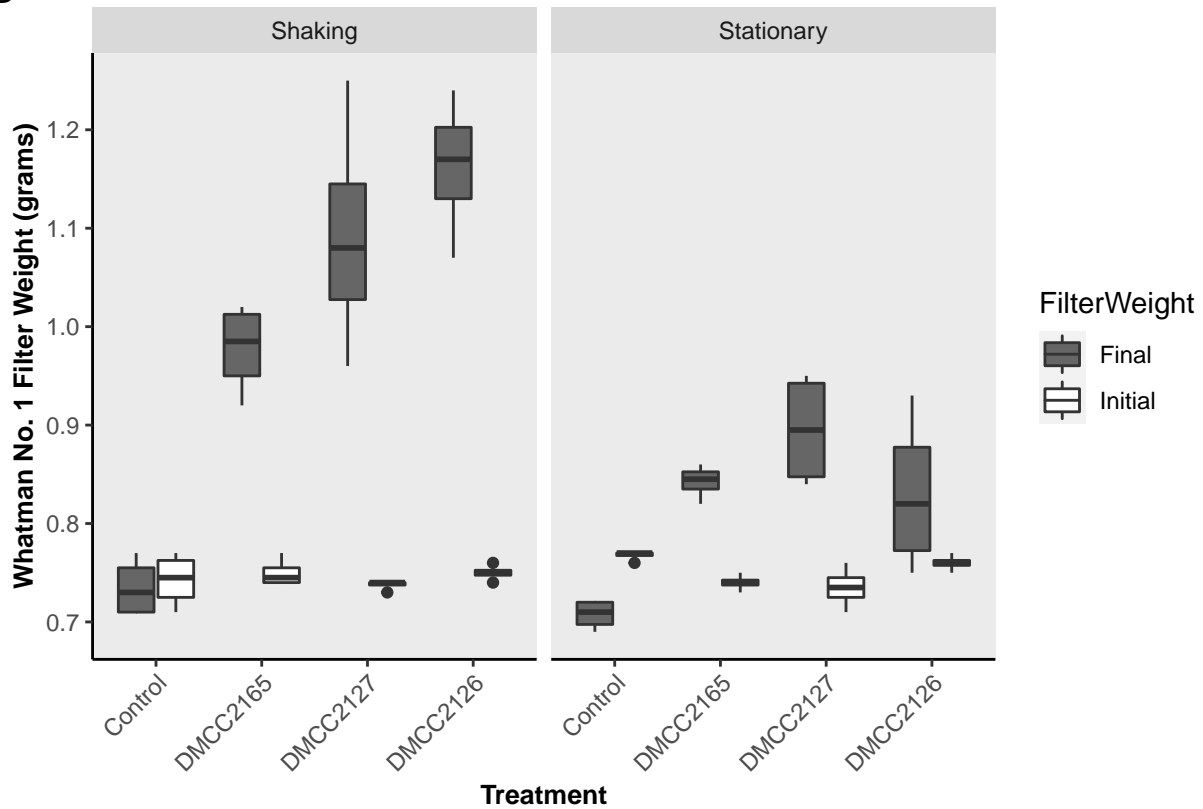


Plotting Biomass by Treatment by Condition

(Supplementary Figure 2, Panel B)

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

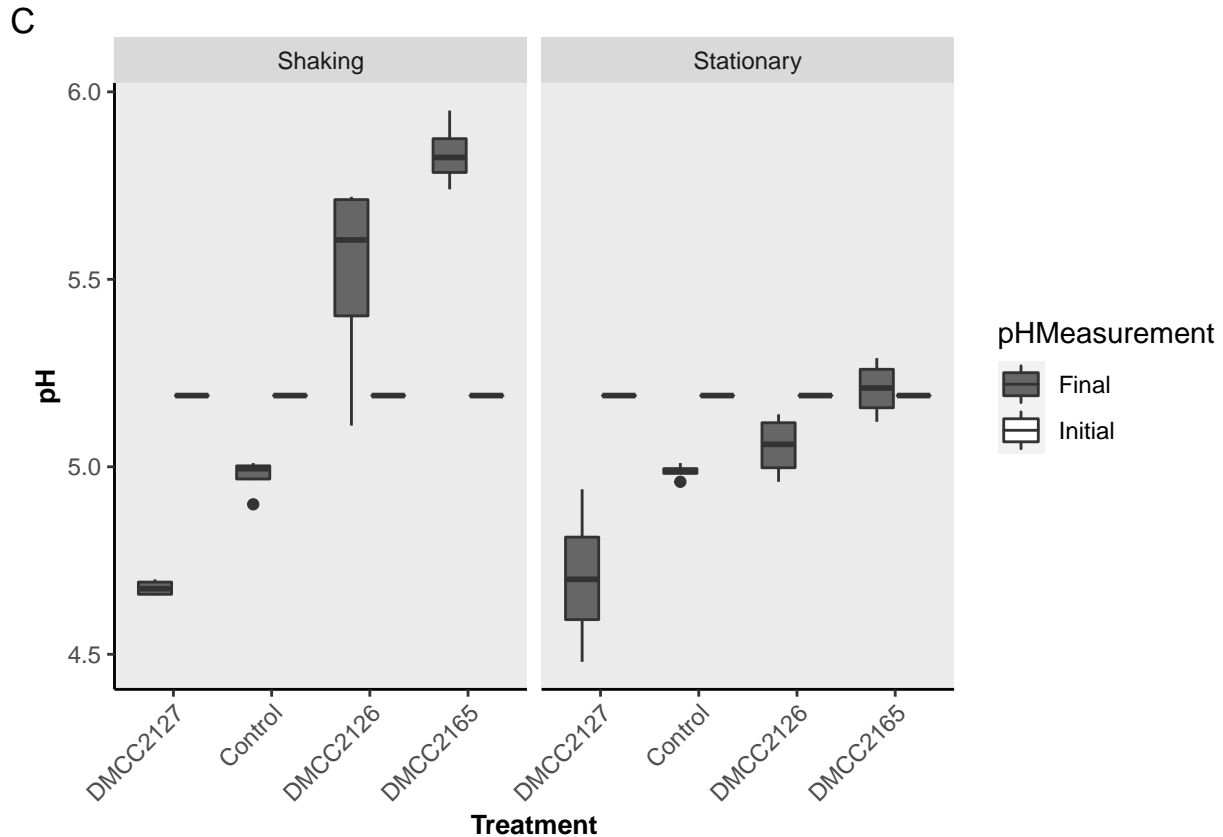
B



Supplementary figure 2 panel C

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

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

Supplementary figure 2 panel D

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

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

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

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

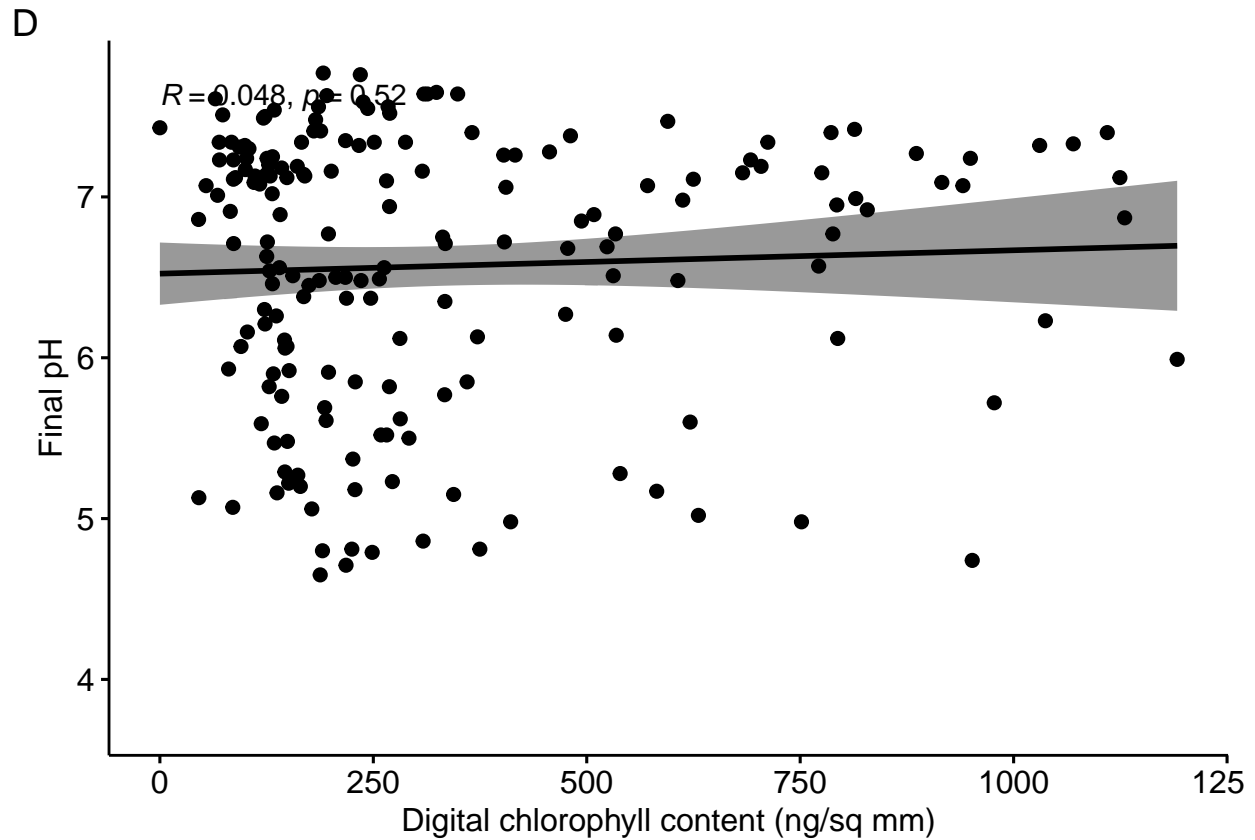
FinalpHvsChl.reg

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

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

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

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



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

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

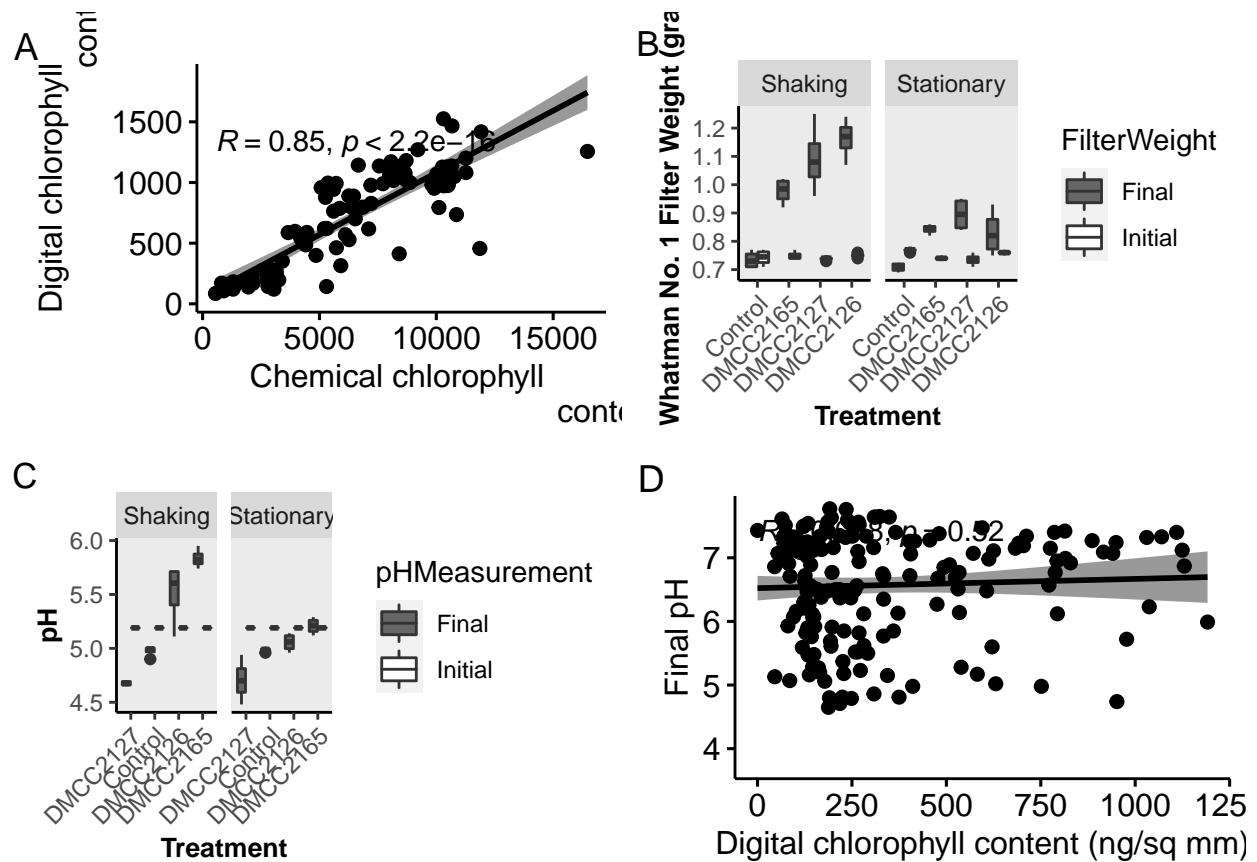
```
## 'geom_smooth()' using formula 'y ~ x'
```

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

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

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

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



Plotting Supplementary Figure 3

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)
```

Statistical analyses for root lenght

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

##
## Call:
## lm(formula = ES2.root.noNAs$Length ~ ES2.root.noNAs$Isolate +
##     ES2.root.noNAs$Condition + ES2.root.noNAs$Concentration,
##     na.action = na.exclude)
```

```
##
## Coefficients:
##              (Intercept)      ES2.root.noNas$IsolateDMCC2126
##                  38.608                      -10.916
##      ES2.root.noNas$IsolateDMCC2127      ES2.root.noNas$IsolateDMCC2165
##                  -8.786                      -12.099
##      ES2.root.noNas$IsolateDMCC2966      ES2.root.noNas$ConditionStationary
##                  13.649                      -6.885
##      ES2.root.noNas$Concentration25fold
##                  -25.132
```

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

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

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

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

#Tukey's HSD for Variable Condition

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

```
## $statistics  
##   MSerror Df      Mean      CV  
##   156.086 59 26.46406 47.20907  
##  
## $parameters  
##      test                name.t ntr StudentizedRange alpha  
##   Tukey ES2.root.noNAs$Condition  2          2.829835  0.05  
##  
## $means  
##           ES2.root.noNAs$Length      std r   Min   Max   Q25   Q50   Q75  
## Shaking                27.54116 19.14552 37 0.759 67.578 14.983 24.544 36.420  
## Stationary              25.08983 18.19797 29 0.982 68.045 13.602 17.404 38.714  
##  
## $comparison  
## NULL  
##  
## $groups  
##           ES2.root.noNAs$Length groups  
## Shaking                27.54116      a  
## Stationary              25.08983      a  
##  
## attr(,"class")  
## [1] "group"
```

#Tukey's HSD for Variable Concentration

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

```
## $statistics
##      MSerror Df      Mean      CV
##    156.086 59 26.46406 47.20907
##
## $parameters
##      test              name.t ntr
##    Tukey ES2.root.noNAs$Isolate:ES2.root.noNAs$Concentration    9
##      StudentizedRange alpha
```

```
##          4.55324  0.05
##
## $means
##          ES2.root.noNAs$Length      std  r      Min      Max      Q25
## Control:100fold          34.51244 12.257238 9 19.375 53.277 26.42600
## Control:25fold           13.82357  6.234620 7  0.759 20.628 13.92700
## DMCC2126:100fold         23.86656 15.081139 9  2.261 43.013 13.88100
## DMCC2127:100fold         25.15625 11.174660 4 15.283 36.420 15.68650
## DMCC2127:25fold           4.29120  6.223480 5  1.131 15.405  1.20100
## DMCC2165:100fold         22.60056 12.426130 9  7.425 46.821 14.98300
## DMCC2165:25fold           1.75000  1.223295 2  0.885  2.615  1.31750
## DMCC2966:100fold         50.63417 17.328417 12 15.108 68.045 43.24375
## DMCC2966:25fold          20.87289 13.073765 9  0.982 38.442 13.88400
##          Q50      Q75
## Control:100fold  30.2620 41.43500
## Control:25fold   14.8050 16.35950
## DMCC2126:100fold 28.5940 35.49300
## DMCC2127:100fold 24.4610 33.93075
## DMCC2127:25fold   1.7050  2.01400
## DMCC2165:100fold 17.7060 30.29700
## DMCC2165:25fold   1.7500  2.18250
## DMCC2966:100fold 55.6675 64.10850
## DMCC2966:25fold  24.5440 29.70700
##
## $comparison
## NULL
##
## $groups
##          ES2.root.noNAs$Length groups
## DMCC2966:100fold          50.63417      a
## Control:100fold           34.51244     ab
## DMCC2127:100fold          25.15625     bc
## DMCC2126:100fold          23.86656     bc
## DMCC2165:100fold          22.60056     bc
## DMCC2966:25fold           20.87289     bc
## Control:25fold            13.82357      c
## DMCC2127:25fold           4.29120      c
## DMCC2165:25fold           1.75000      c
##
## attr("class")
## [1] "group"
```

Comparison after normalization of data

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

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

```

## if (lambda == 0){TRANS = log(x)}
## if (lambda < 0){TRANS = -1 * x ^ lambda}

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

#ES2 longest root statistical analysis after normalization
ES2.root.noNAs.mod.lm <- lm (ES2.root.noNAs.mod$ES2.root.tuk ~ ES2.root.noNAs.mod$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

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

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

```



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

```
## Analysis of Variance Table
##
## Response: ES2.root.noNAs.mod$ES2.root.tuk
##              Df Sum Sq Mean Sq F value    Pr(>F)
## ES2.root.noNAs.mod$Isolate      4 221.55    55.39   7.6175 5.116e-05 ***
## ES2.root.noNAs.mod$Condition     1  12.18    12.18   1.6751   0.2006
## ES2.root.noNAs.mod$Concentration  1 403.79   403.79  55.5332 4.637e-10 ***
## Residuals                      59 429.00     7.27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#Tukey's HSD for Variable Condition

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

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

#Tukey's HSD for Variable Concentration

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

```
## $statistics
##      MSerror Df      Mean      CV
```

```
## 7.271182 59 7.841521 34.38763
##
## $parameters
## test name.t ntr StudentizedRange alpha
## Tukey ES2.root.noNAs.mod$Concentration 2 2.829835 0.05
##
## $means
## ES2.root.noNAs.mod$ES2.root.tuk std r Min Max Q25
## 100fold 9.428687 3.551457 43 1.6993990 15.53522 6.247133
## 25fold 4.874211 3.204748 23 0.8359054 10.71825 1.495429
## Q50 Q75
## 100fold 9.332817 12.224510
## 25fold 5.623663 6.777533
##
## $comparison
## NULL
##
## $groups
## ES2.root.noNAs.mod$ES2.root.tuk groups
## 100fold 9.428687 a
## 25fold 4.874211 b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable Isolate

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

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

```
##
## $groups
##      ES2.root.noNAs.mod$ES2.root.tuk groups
## DMCC2966      10.122508      a
## Control      7.870193      ab
## DMCC2126      7.431287      ab
## DMCC2165      6.279095      b
## DMCC2127      4.788109      b
##
## attr(,"class")
## [1] "group"

#Tukey's HSD for Treatment and concentration
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, c('ES2.root.noNAs.mod$',
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test

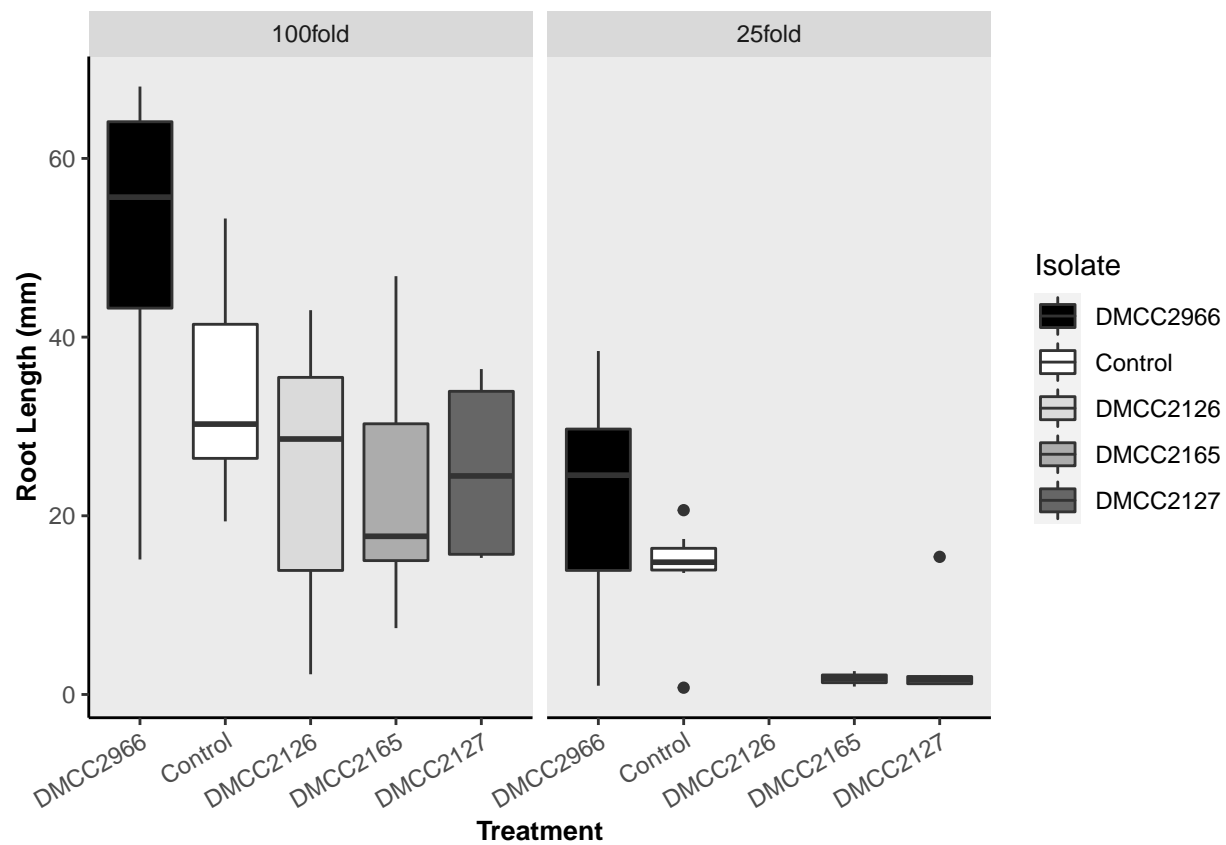
## $statistics
##      MSerror Df      Mean      CV
##      7.271182 59 7.841521 34.38763
##
## $parameters
##      test                                     name.t ntr
##      Tukey ES2.root.noNAs.mod$Isolate:ES2.root.noNAs.mod$Concentration 9
##      StudentizedRange alpha
##      4.55324 0.05
##
##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

```
## Control:100fold          9.866162      ab
## DMCC2127:100fold        7.994262     abc
## DMCC2126:100fold        7.431287     bc
## DMCC2165:100fold        7.364275     bc
## DMCC2966:25fold         6.785744     bc
## Control:25fold          5.303948      c
## DMCC2127:25fold         2.223187      c
## DMCC2165:25fold         1.395787      c
##
## attr(,"class")
## [1] "group"
```

Plotting Supplementary Figure 3

```
#Plate for Supp Figure 3 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"="gold")) +
  #ggtitle("Root Length at 14 Days After Exposure") +
  scale_fill_manual(values = c("#000000", "#FFFFFF", "#DADADA", "#ACACAC", "#666666")) +
  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()