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", "tidyvers
```

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/donwloaded this repository to your "Documents" folder.

Change directory on mac/linux:

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

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

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

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

Step 1: Call the pdf command to start the plot

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

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:

```r
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 exporuse (DOE)

#ES4 = Repetetion for 14 DOE

ES5 = First experiment for 7 DOE

#ES8 = Repetition for 7 DOE

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

ES13B = Repetition of ES13A

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

#ES14B = Repetition of ES14A

```r
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

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

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

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

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

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

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

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

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

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

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

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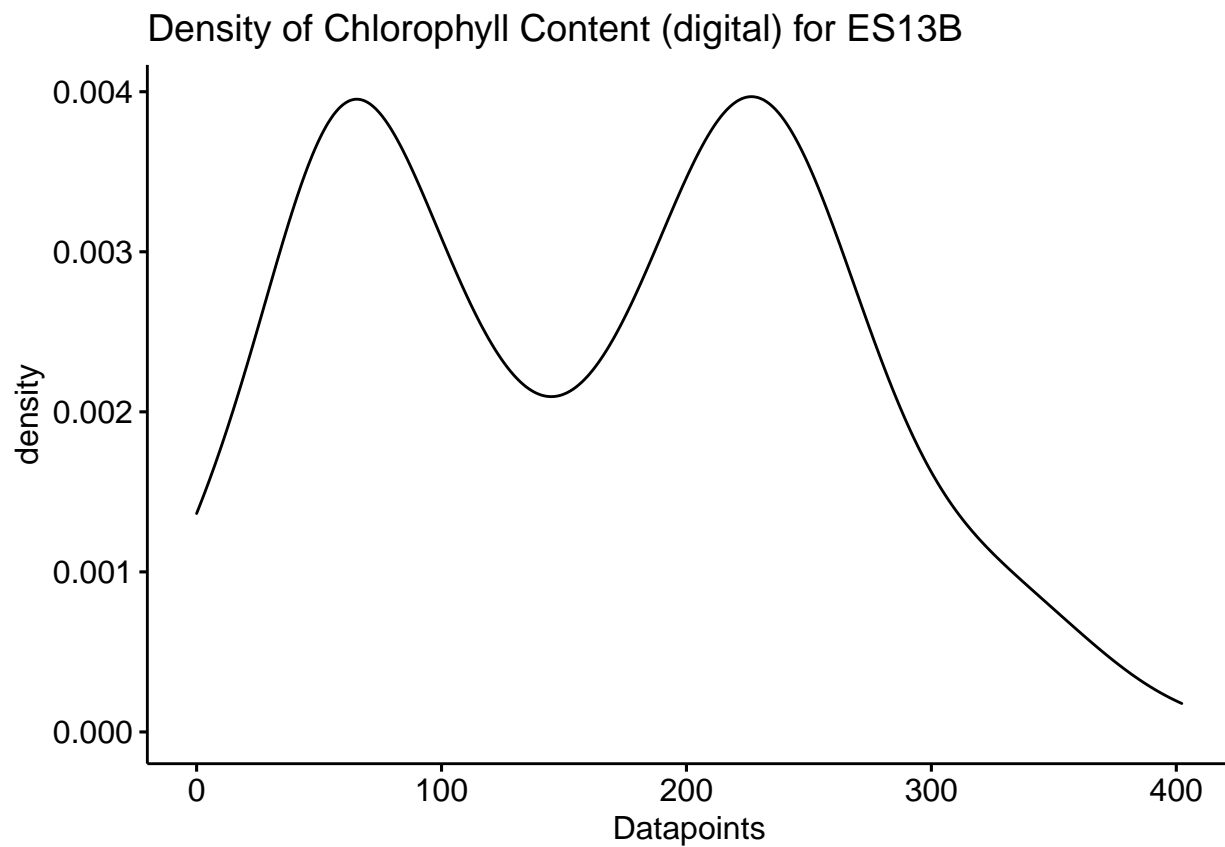

Density of Chlorophyll Content (digital) for ES2
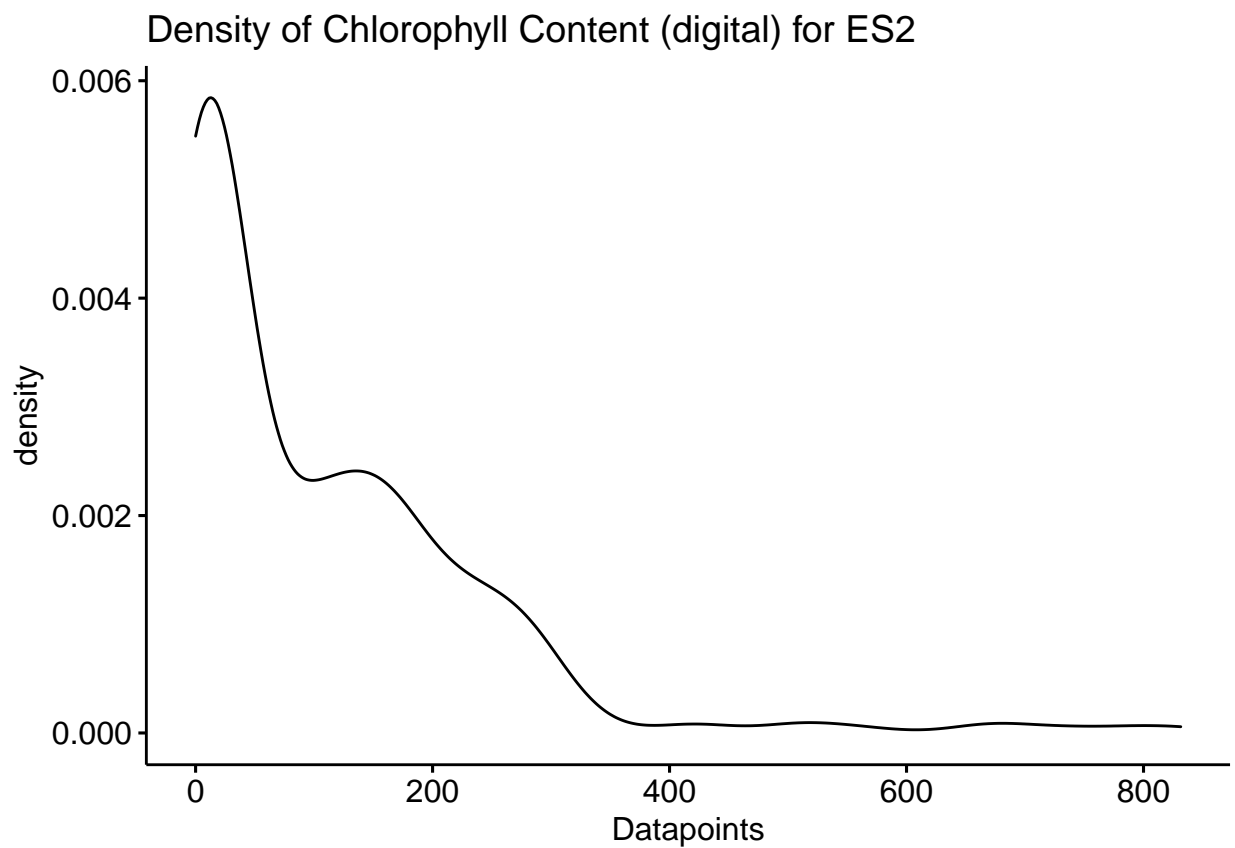
```
ggdensity(ES5$chl, main = "Density of Chlorophyll Content (digital) for ES5", xlab = "Datapoints")
```

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

Density of Chlorophyll Content (digital) for ES5
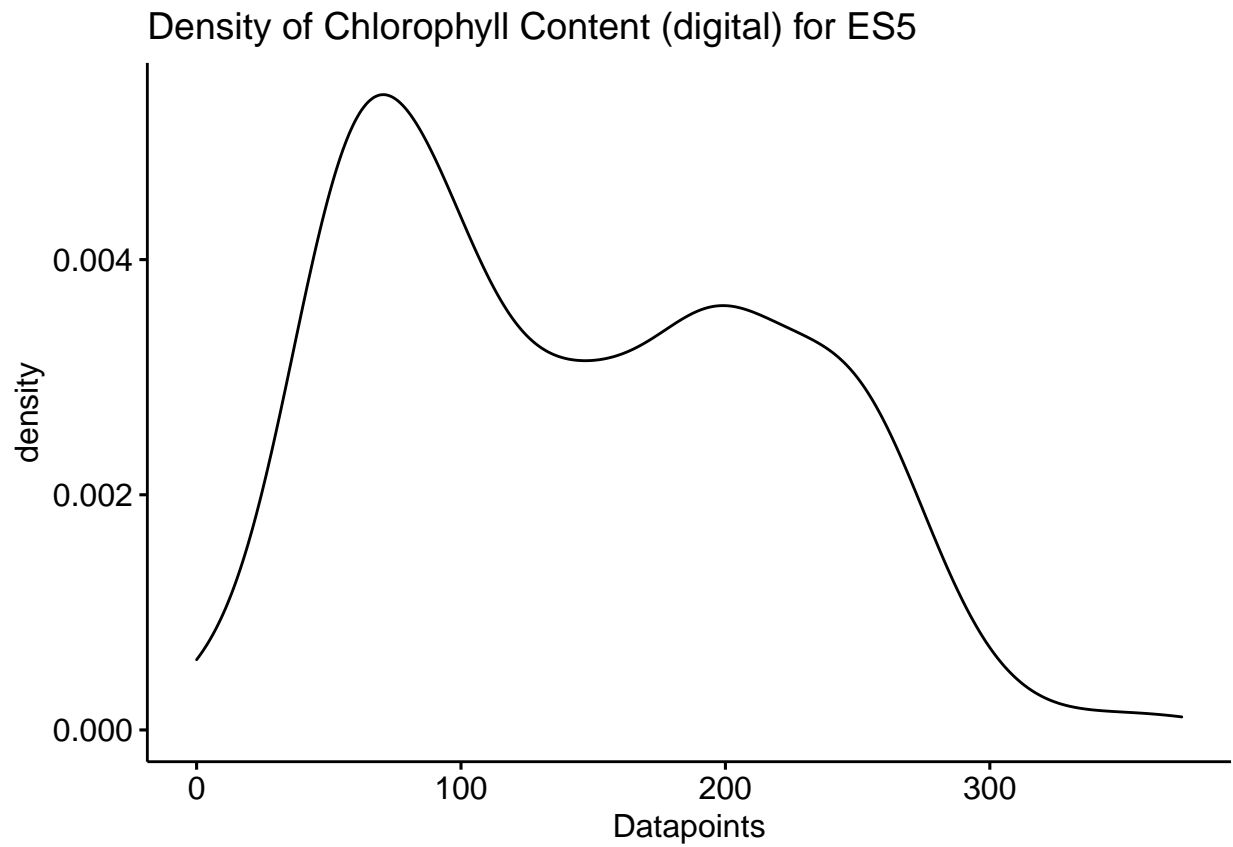

```r
ggdensity(ES13B$chl, main = "Density of Chlorophyll Content (digital) for ES13B", xlab = "Datapoints")
```

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

Density of Chlorophyll Content (digital) for ES13B


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

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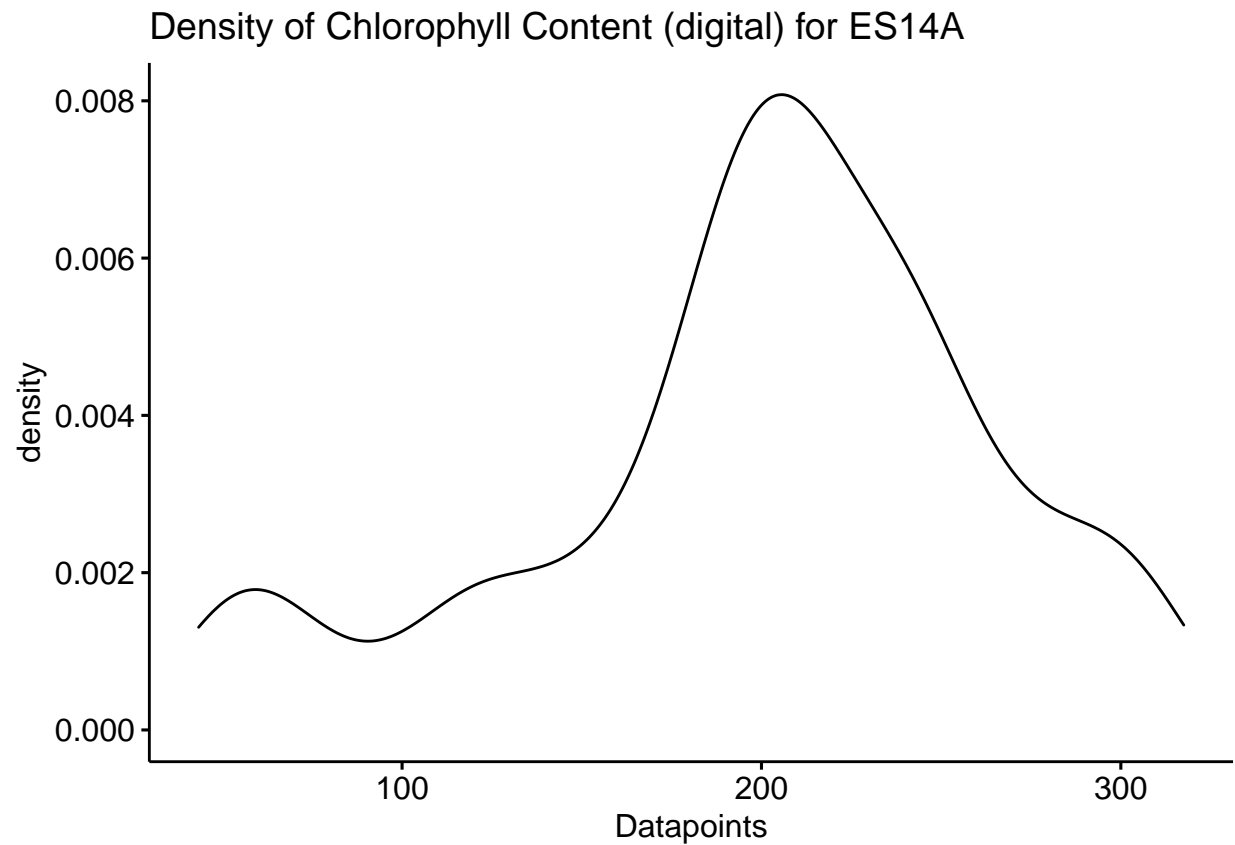
Density of Chlorophyll Content (digital) for ES14A

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

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

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

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

```r
ggqqplot(ES5$chl)
```

```
## 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).
```
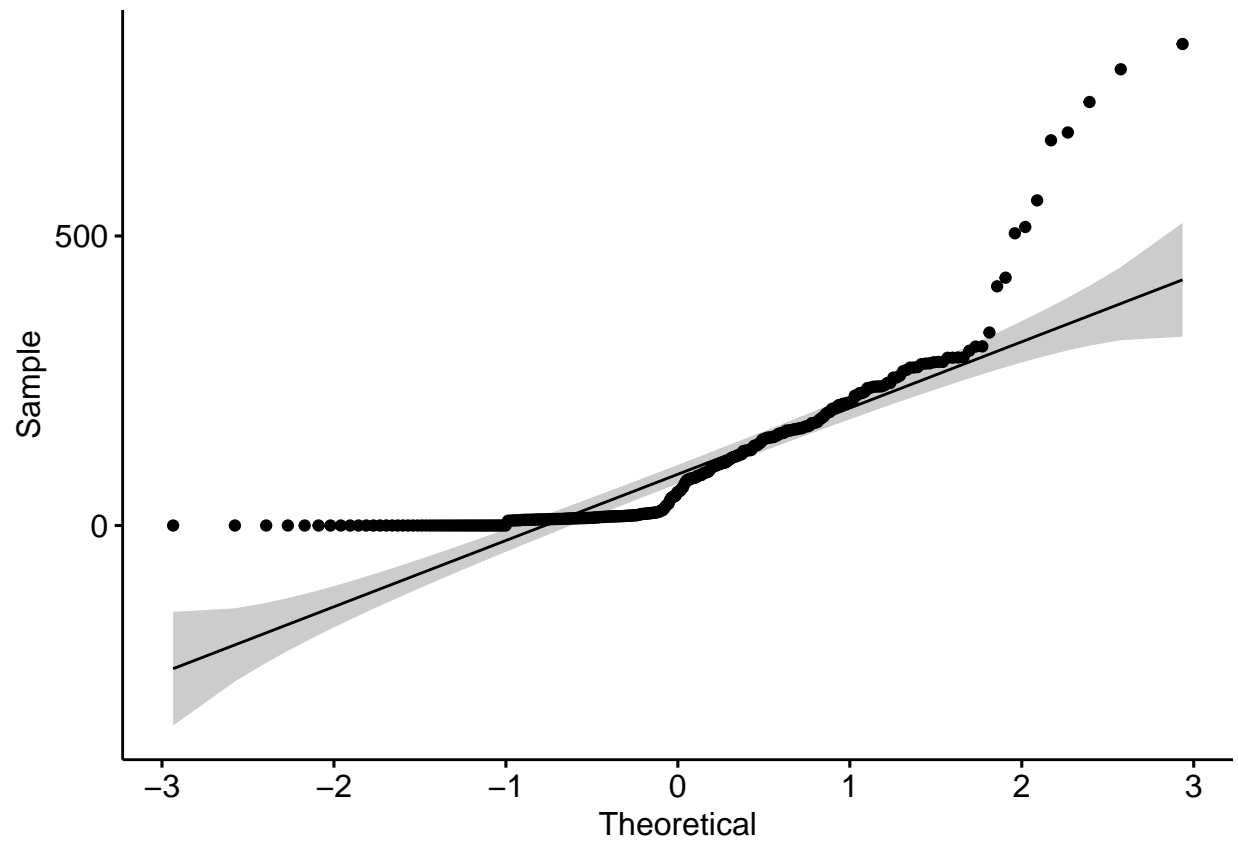
```
ggqqplot(ES13B$chl)
```

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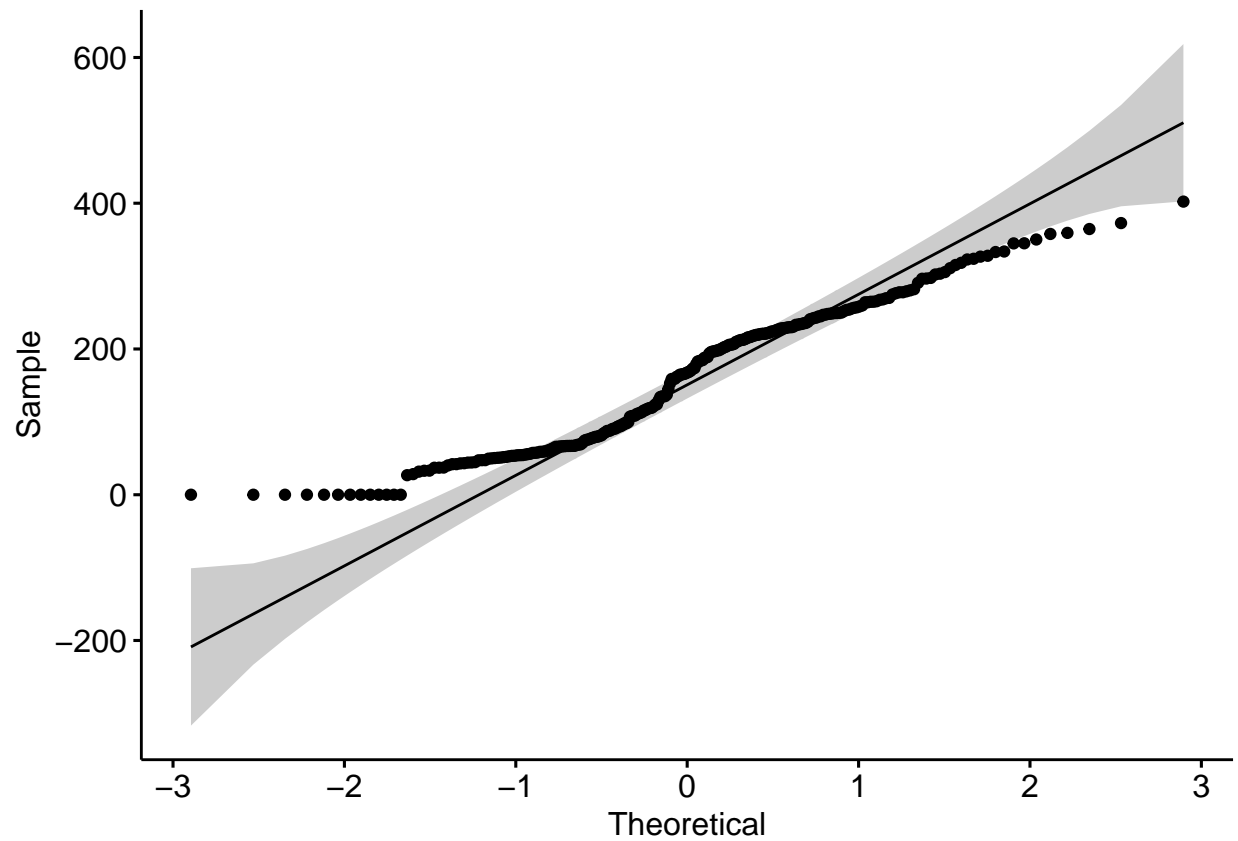
```
ggqqplot(ES14A$chl)
```

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

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

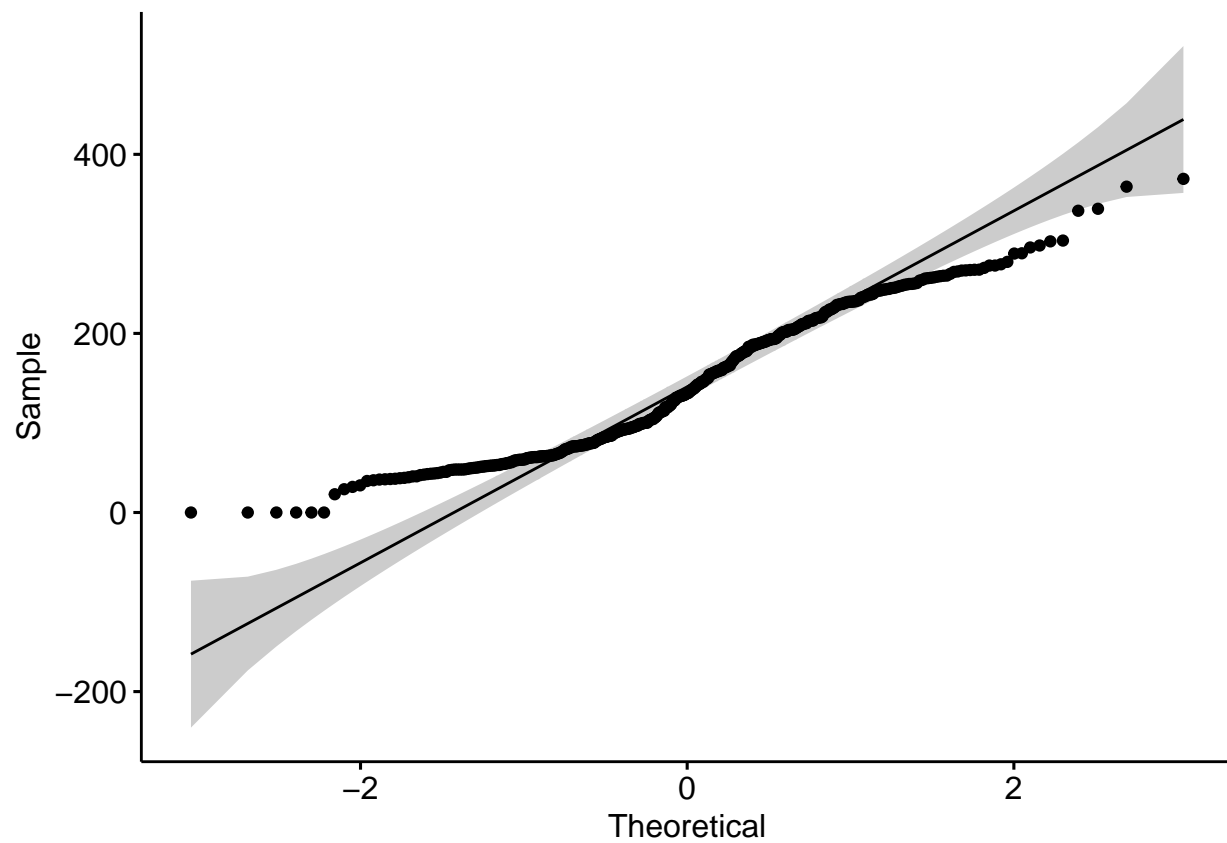## Warning: Removed 3 rows containing non-finite values (stat_qq_line).
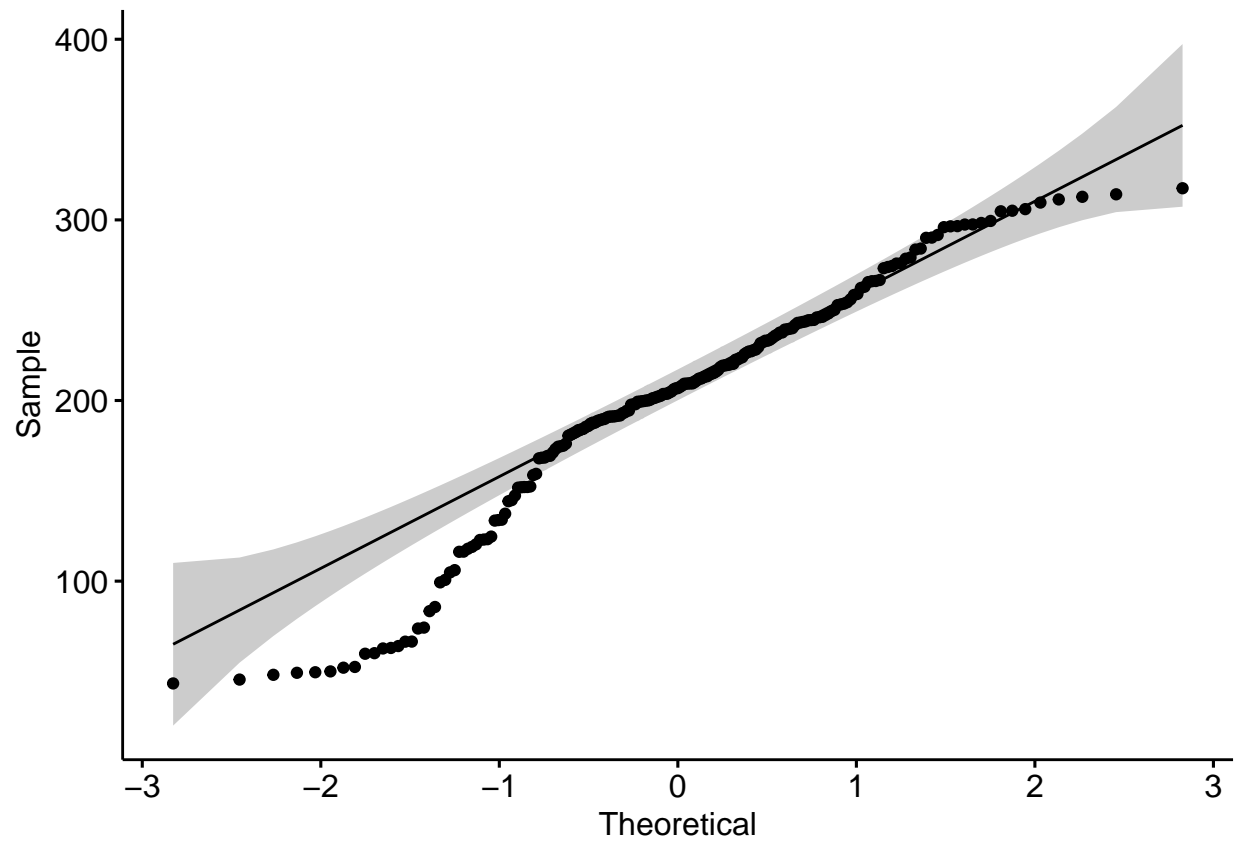
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2", xlab = "Datapoi
```

Density of Chlorophyll Content (Digital) for ES2
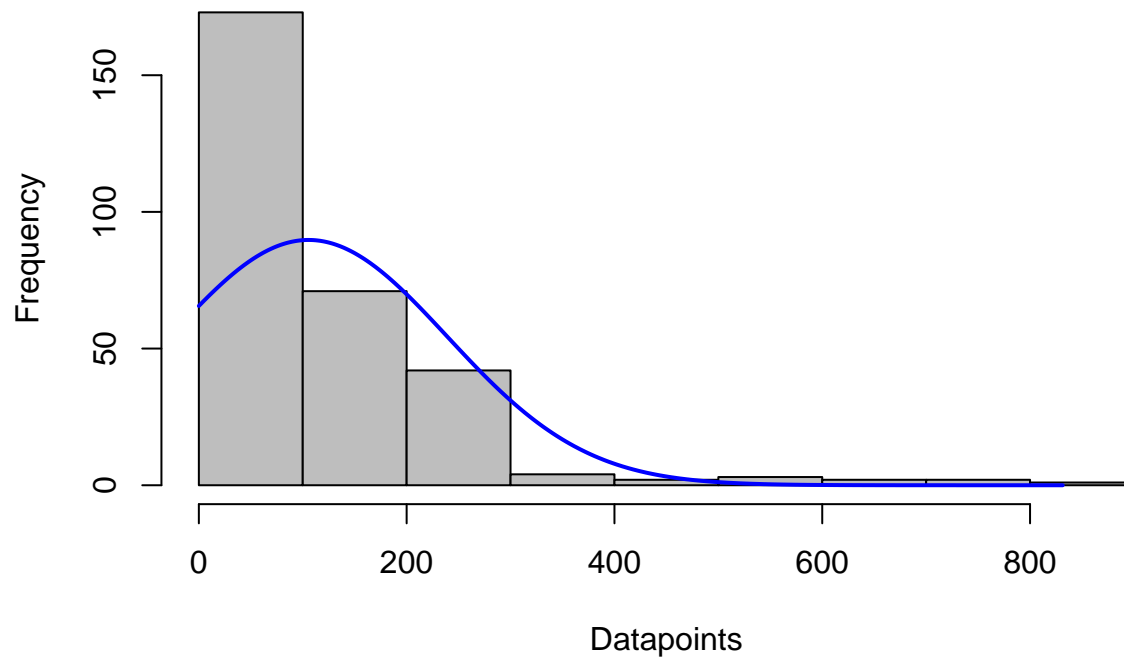

```
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5", xlab = "Datapoin
```

Density of Chlorophyll Content (Digital) for ES5
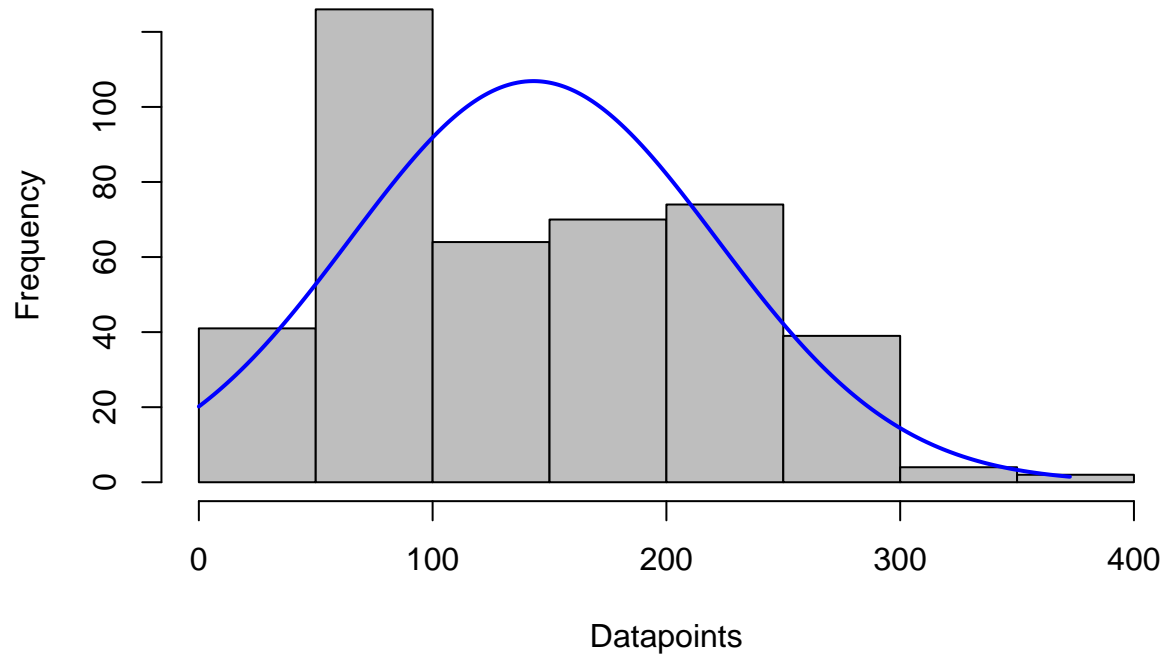

```r
plotNormalHistogram(ES13B$chl, main = "Density of Chlorophyll Content (Digital) for E13B", xlab = "Datap
```

Density of Chlorophyll Content (Digital) for E13B
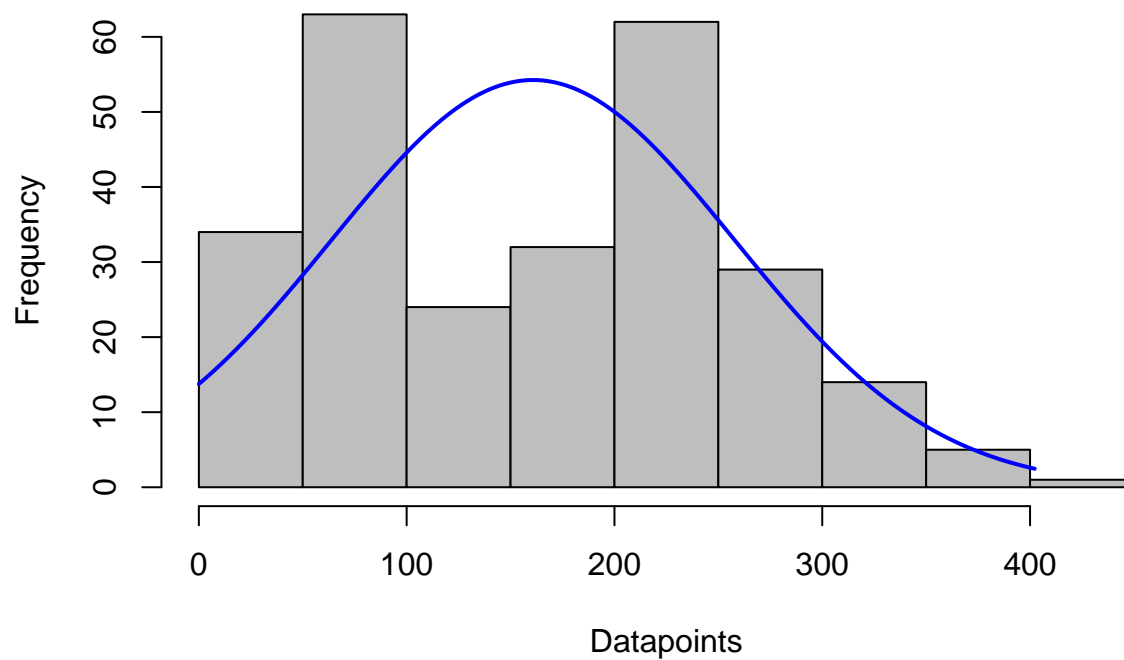

```
plotNormalHistogram(ES14A$chl, main = "Density of Chlorophyll Content (Digital) for E14A", xlab = "Datap
```

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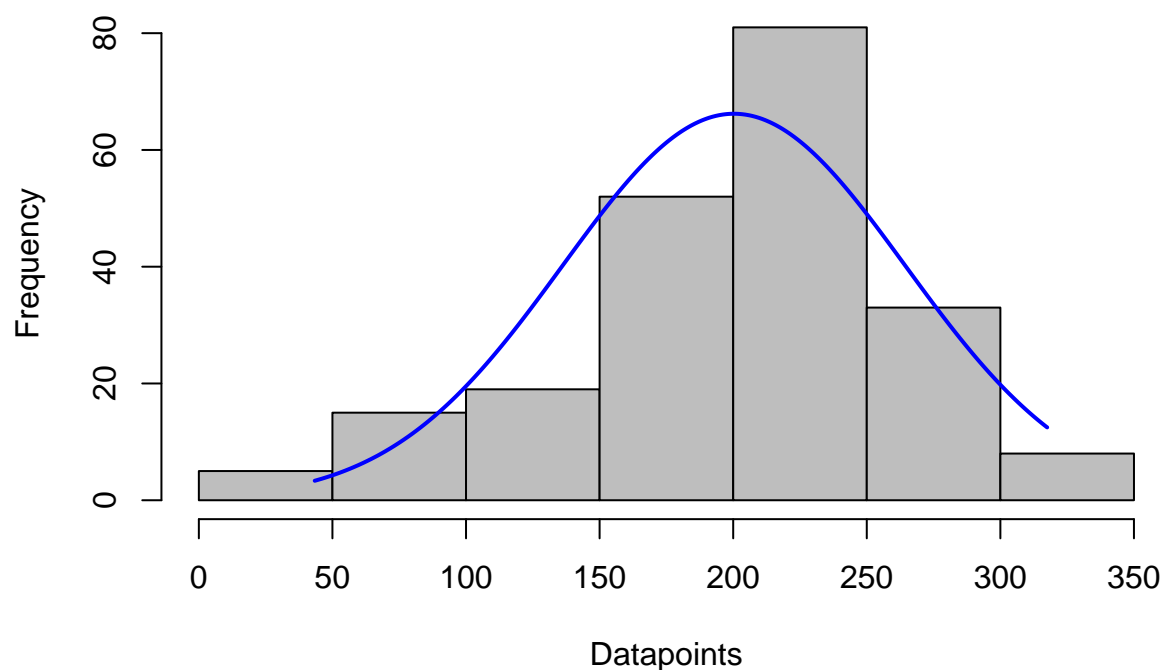
Use the Tukey's tranformation method to normalize the distribution and append to datasets

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

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

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

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

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

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

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

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

Append the transformed values to original datasets

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

Statistical analyses

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

ES2 dataset (untransformed data)

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

```
###############ES2 analysis###############################
ES2.chl.anova <- lm (ES2$chl ~ ES2$Treatment + ES2$Dilution + ES2$Condition + ES2$isoRep + ES2$techRep +
ES2.chl.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 (tukey trans) by Treament
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 (tukey trans) 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
```

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```
## 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"
```

```r
#Tukey's HSD for Variable chl (tukey trans) by isoRep
ES2.chl.isoRep.HSD.test <- HSD.test(ES2.chl.anova, 'ES2$isoRep', group = T)
ES2.chl.isoRep.HSD.test
```

```
## $statistics
##    MSerror  Df     Mean       CV
##   10102.73 276 105.3393 95.41771
##
## $parameters
##    test     name.t ntr StudentizedRange alpha
##   Tukey ES2$isoRep   2         2.784016  0.05
##
## $means
##               ES2$chl      std   r Min     Max     Q25    Q50      Q75
## isolateRep1  95.20639 127.0337 147   0 678.735 10.5195 24.386 138.3605
## isolateRep2 115.90342 140.6136 141   0 831.472 14.0000 85.555 171.1230
##
## $comparison
## NULL
##
## $groups
##               ES2$chl groups
## isolateRep2 115.90342      a
## isolateRep1  95.20639      a
##
## attr(,"class")
## [1] "group"
```

```r
#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=TR
```

```
##
## 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"
```

```r
#Complete ANOVA for ES2 by treatment by condition, by dilution
ES2.comp.HSD.group <- HSD.test(ES2.chl.anova, c("ES2$Treatment", "ES2$Condition", "ES2$Dilution"), group
```

```
##
## Study: ES2.chl.anova ~ c("ES2$Treatment", "ES2$Condition", "ES2$Dilution")
##
## HSD Test for ES2$chl
##
## Mean Square Error:  10102.73
##
## ES2$Treatment:ES2$Condition:ES2$Dilution,  means
##
##                                 ES2.chl        std  r     Min     Max
## control:Shaking:100fold      365.312600 219.329463 15 117.742 787.887
## control:Shaking:25fold        83.216056  81.789480 18   0.000 268.776
## control:Stationary:100fold   414.783000 240.691662  9  97.748 831.472
## control:Stationary:25fold     72.232400  73.372023 15   0.000 237.395
## DMCC2126:Shaking:100fold     107.106250  88.648073 12  10.433 281.899
## DMCC2126:Shaking:25fold       11.166278   8.588222 18   0.000  29.554
## DMCC2126:Stationary:100fold  141.064056  40.361686 18  58.992 207.739
## DMCC2126:Stationary:25fold    16.665333  14.486460  9   0.000  51.676
## DMCC2127:Shaking:100fold      27.384333  29.312311 12   0.000  87.367
## DMCC2127:Shaking:25fold       12.535833   6.846127 12   0.000  23.493
```

```
## DMCC2127:Stationary:100fold  84.257600  66.188284 15   0.000 167.994
## DMCC2127:Stationary:25fold   20.285333  32.415599 15   0.000 112.319
## DMCC2165:Shaking:100fold     37.540750  46.913463 12   0.000 150.248
## DMCC2165:Shaking:25fold      11.067600   6.311390 15   0.000  19.414
## DMCC2165:Stationary:100fold  80.062000  63.751126 12   0.000 187.945
## DMCC2165:Stationary:25fold    8.921222   6.912163 18   0.000  17.639
## DMCC2966:Shaking:100fold    223.958000  61.555261 18 128.523 301.867
## DMCC2966:Shaking:25fold     203.815933  41.016531 15 123.094 282.574
## DMCC2966:Stationary:100fold 107.479733  95.130285 15   0.000 289.798
## DMCC2966:Stationary:25fold  125.500533  95.202754 15   0.000 309.266
##
## Alpha: 0.05 ; DF Error: 276
## Critical Value of Studentized Range: 5.061243
##
## 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:Stationary:100fold  414.783000      a
## control:Shaking:100fold     365.312600      a
## DMCC2966:Shaking:100fold    223.958000      b
## DMCC2966:Shaking:25fold     203.815933     bc
## DMCC2126:Stationary:100fold 141.064056    bcd
## DMCC2966:Stationary:25fold  125.500533   bcde
## DMCC2966:Stationary:100fold 107.479733   bcde
## DMCC2126:Shaking:100fold    107.106250   bcde
## DMCC2127:Stationary:100fold  84.257600    cde
## control:Shaking:25fold       83.216056    cde
## DMCC2165:Stationary:100fold  80.062000    cde
## control:Stationary:25fold    72.232400     de
## DMCC2165:Shaking:100fold     37.540750     de
## DMCC2127:Shaking:100fold     27.384333     de
## DMCC2127:Stationary:25fold   20.285333     de
## DMCC2126:Stationary:25fold   16.665333     de
## DMCC2127:Shaking:25fold      12.535833     de
## DMCC2126:Shaking:25fold      11.166278      e
## DMCC2165:Shaking:25fold      11.067600      e
## DMCC2165:Stationary:25fold    8.921222      e
```

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$Condition:ES2$Dilution  20         5.061243  0.05
##
## $means
##                                 ES2$chl        std  r     Min     Max       Q25
## control:Shaking:100fold     365.312600 219.329463 15 117.742 787.887 234.01100
## control:Shaking:25fold       83.216056  81.789480 18   0.000 268.776  11.50550
```

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```
## control:Stationary:100fold 414.783000 240.691662  9  97.748 831.472 272.67000
## control:Stationary:25fold   72.232400  73.372023 15   0.000 237.395  19.04600
## DMCC2126:Shaking:100fold    107.106250  88.648073 12  10.433 281.899  52.75425
## DMCC2126:Shaking:25fold      11.166278   8.588222 18   0.000  29.554   2.47200
## DMCC2126:Stationary:100fold 141.064056  40.361686 18  58.992 207.739 124.20750
## DMCC2126:Stationary:25fold   16.665333  14.486460  9   0.000  51.676  10.37600
## DMCC2127:Shaking:100fold     27.384333  29.312311 12   0.000  87.367   8.01525
## DMCC2127:Shaking:25fold      12.535833   6.846127 12   0.000  23.493  11.11275
## DMCC2127:Stationary:100fold  84.257600  66.188284 15   0.000 167.994  18.08300
## DMCC2127:Stationary:25fold   20.285333  32.415599 15   0.000 112.319   0.00000
## DMCC2165:Shaking:100fold     37.540750  46.913463 12   0.000 150.248   0.00000
## DMCC2165:Shaking:25fold      11.067600   6.311390 15   0.000  19.414   9.55700
## DMCC2165:Stationary:100fold  80.062000  63.751126 12   0.000 187.945  19.12150
## DMCC2165:Stationary:25fold    8.921222   6.912163 18   0.000  17.639   0.00000
## DMCC2966:Shaking:100fold    223.958000  61.555261 18 128.523 301.867 169.69900
## DMCC2966:Shaking:25fold     203.815933  41.016531 15 123.094 282.574 172.80800
## DMCC2966:Stationary:100fold 107.479733  95.130285 15   0.000 289.798   0.00000
## DMCC2966:Stationary:25fold  125.500533  95.202754 15   0.000 309.266  48.06800
##                                 Q50       Q75
## control:Shaking:100fold     273.5930 510.07500
## control:Shaking:25fold       74.7350 117.59850
## control:Stationary:100fold  413.0270 561.43300
## control:Stationary:25fold    26.5490 133.90650
## DMCC2126:Shaking:100fold     86.9630 129.27900
## DMCC2126:Shaking:25fold      11.0480  16.28075
## DMCC2126:Stationary:100fold 152.6480 165.71925
## DMCC2126:Stationary:25fold   12.4910  17.61900
## DMCC2127:Shaking:100fold     16.4120  36.10000
## DMCC2127:Shaking:25fold      13.0145  16.20800
## DMCC2127:Stationary:100fold  85.5550 147.53650
## DMCC2127:Stationary:25fold    9.7160  15.58600
## DMCC2165:Shaking:100fold     20.7445  53.31675
## DMCC2165:Shaking:25fold      12.9490  14.88350
## DMCC2165:Stationary:100fold 103.5510 109.77625
## DMCC2165:Stationary:25fold   10.8535  13.96450
## DMCC2966:Shaking:100fold    231.8610 279.95400
## DMCC2966:Shaking:25fold     211.9050 228.78400
## DMCC2966:Stationary:100fold 108.5790 170.38100
## DMCC2966:Stationary:25fold  120.0120 195.54450
##
## $comparison
## NULL
##
## $groups
##                             ES2$chl groups
## control:Stationary:100fold 414.783000      a
## control:Shaking:100fold    365.312600      a
## DMCC2966:Shaking:100fold   223.958000      b
## DMCC2966:Shaking:25fold    203.815933     bc
## DMCC2126:Stationary:100fold 141.064056    bcd
## DMCC2966:Stationary:25fold 125.500533   bcde
## DMCC2966:Stationary:100fold 107.479733   bcde
## DMCC2126:Shaking:100fold   107.106250   bcde
## DMCC2127:Stationary:100fold 84.257600    cde
```

```
## control:Shaking:25fold         83.216056    cde
## DMCC2165:Stationary:100fold    80.062000    cde
## control:Stationary:25fold      72.232400     de
## DMCC2165:Shaking:100fold       37.540750     de
## DMCC2127:Shaking:100fold       27.384333     de
## DMCC2127:Stationary:25fold     20.285333     de
## DMCC2126:Stationary:25fold     16.665333     de
## DMCC2127:Shaking:25fold        12.535833     de
## DMCC2126:Shaking:25fold        11.166278      e
## DMCC2165:Shaking:25fold        11.067600      e
## DMCC2165:Stationary:25fold      8.921222      e
##
## 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.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"
```

```r
#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"
```

```
#Tukey's HSD for Variable chl (tukey trans) by isoRep
ES2.mod.chl.isoRep.HSD.test <- HSD.test(ES2.mod.chl.anova, 'ES2.mod$isoRep', group = T)
ES2.mod.chl.isoRep.HSD.test
```

```
## $statistics
##    MSerror  Df     Mean        CV
##   4.787063 276 4.479861 48.83937
##
## $parameters
##    test         name.t ntr StudentizedRange alpha
##   Tukey ES2.mod$isoRep   2         2.784016  0.05
##
## $means
##             ES2.mod$ES2_chl.tuk      std   r Min      Max      Q25      Q50
## isolateRep1            4.159075 2.958162 147   0 11.53155 2.416823 3.312666
## isolateRep2            4.814297 2.827923 141   0 12.44351 2.690283 5.303860
##                 Q75
## isolateRep1 6.351531
## isolateRep2 6.878451
##
## $comparison
## NULL
##
## $groups
##             ES2.mod$ES2_chl.tuk groups
## isolateRep2            4.814297      a
## isolateRep1            4.159075      b
##
## attr(,"class")
## [1] "group"
```

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

```
##
## 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_chl.tuk      std  r      Min       Max       Q25
## control:100fold           8.952842 2.033695 24 5.575585 12.443509 7.860042
## control:25fold            4.211675 2.459674 33 0.000000  8.147445 2.807281
## DMCC2126:100fold          5.904452 1.432971 30 2.409370  8.294402 5.211560
## DMCC2126:25fold           2.180805 1.263683 27 0.000000  4.390190 2.359361
## DMCC2127:100fold          3.720246 2.309541 27 0.000000  6.831014 2.547399
## DMCC2127:25fold           2.139470 1.622868 27 0.000000  5.873811 0.000000
## DMCC2165:100fold          3.677465 2.368645 24 0.000000  7.124617 2.700544
## DMCC2165:25fold           1.925497 1.211620 33 0.000000  3.041187 0.000000
## DMCC2966:100fold          6.114039 2.778697 33 0.000000  8.510026 5.991199
## DMCC2966:25fold           6.285168 2.210961 30 0.000000  8.587655 6.035946
##                       Q50       Q75
## control:100fold  8.279323 10.486003
## control:25fold   4.628247  6.200641
## DMCC2126:100fold 6.189452  6.705312
## DMCC2126:25fold  2.483657  2.863395
## DMCC2127:100fold 3.818594  5.417472
## DMCC2127:25fold  2.531540  2.807481
## DMCC2165:100fold 3.362478  5.745663
## DMCC2165:25fold  2.561469  2.745123
```

```
## DMCC2966:100fold 6.963949  7.832392
## DMCC2966:25fold  7.032779  7.590879
##
## $comparison
## NULL
##
## $groups
##                  ES2.mod$ES2_chl.tuk groups
## control:100fold             8.952842      a
## DMCC2966:25fold             6.285168      b
## DMCC2966:100fold            6.114039      b
## DMCC2126:100fold            5.904452     bc
## control:25fold             4.211675     cd
## DMCC2127:100fold            3.720246     de
## DMCC2165:100fold            3.677465     de
## DMCC2126:25fold             2.180805      e
## DMCC2127:25fold             2.139470      e
## DMCC2165:25fold             1.925497      e
##
## attr(,"class")
## [1] "group"
```

```
#Complete ANOVA for ES2.mod by treatment by condition, by dilution
ES2.mod.comp.HSD.group <- HSD.test(ES2.mod.chl.anova, c("ES2.mod$Treatment", "ES2.mod$Condition", "ES2.m

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

```
## $statistics
##    MSerror  Df     Mean       CV
##   4.787063 276 4.479861 48.83937
##
## $parameters
##    test                                                    name.t ntr
##    Tukey ES2.mod$Treatment:ES2.mod$Condition:ES2.mod$Dilution   20
##    StudentizedRange alpha
##            5.061243  0.05
##
## $means
##                            ES2.mod$ES2_chl.tuk       std  r      Min       Max
## control:Shaking:100fold              8.798267 1.9828967 15 5.978597 12.194780
## control:Shaking:25fold               4.289829 2.5912255 18 0.000000  8.147445
## control:Stationary:100fold           9.210468 2.2114466  9 5.575585 12.443509
## control:Stationary:25fold            4.117890 2.3786595 15 0.000000  7.776816
## DMCC2126:Shaking:100fold             5.267468 1.9475065 12 2.409370  8.294402
## DMCC2126:Shaking:25fold              1.990082 1.3058091 18 0.000000  3.560255
## DMCC2126:Stationary:100fold          6.329108 0.7558881 18 4.613679  7.397232
## DMCC2126:Stationary:25fold           2.562252 1.1493281  9 0.000000  4.390190
## DMCC2127:Shaking:100fold             2.718108 1.8775300 12 0.000000  5.345709
## DMCC2127:Shaking:25fold              2.287858 1.0938454 12 0.000000  3.266645
## DMCC2127:Stationary:100fold          4.521957 2.3636341 15 0.000000  6.831014
## DMCC2127:Stationary:25fold           2.020759 1.9791611 15 0.000000  5.873811
## DMCC2165:Shaking:100fold             2.818319 2.3433519 12 0.000000  6.550935
## DMCC2165:Shaking:25fold              2.131528 1.1204622 15 0.000000  3.041187
## DMCC2165:Stationary:100fold          4.536612 2.1515647 12 0.000000  7.124617
```

```
## DMCC2165:Stationary:25fold           1.753804 1.2887125 18 0.000000   2.933781
## DMCC2966:Shaking:100fold             7.538945 0.8254875 18 6.178283   8.510026
## DMCC2966:Shaking:25fold              7.310403 0.5695012 15 6.079094   8.301844
## DMCC2966:Stationary:100fold          4.404150 3.3283476 15 0.000000   8.380806
## DMCC2966:Stationary:25fold           5.259932 2.7475728 15 0.000000   8.587655
##                                 Q25       Q50       Q75
## control:Shaking:100fold    7.7274852 8.201898 10.359933
## control:Shaking:25fold     2.4878607 5.027823  5.972661
## control:Stationary:100fold 8.1915108 9.571763 10.739566
## control:Stationary:25fold  3.0157515 3.419937  6.273385
## DMCC2126:Shaking:100fold   4.2801750 5.335099  6.180383
## DMCC2126:Shaking:25fold    0.5903447 2.461623  2.846913
## DMCC2126:Stationary:100fold 6.0993511 6.589981  6.795896
## DMCC2126:Stationary:25fold 2.4044250 2.577650  2.932533
## DMCC2127:Shaking:100fold   1.8234010 2.839753  3.837417
## DMCC2127:Shaking:25fold    2.4670786 2.617529  2.841275
## DMCC2127:Stationary:100fold 2.9573845 5.303860  6.505797
## DMCC2127:Stationary:25fold 0.0000000 2.345891  2.800751
## DMCC2165:Shaking:100fold   0.0000000 3.114771  4.399467
## DMCC2165:Shaking:25fold    2.3281209 2.612694  2.752718
## DMCC2165:Stationary:100fold 3.0185079 5.697205  5.823266
## DMCC2165:Stationary:25fold 0.0000000 2.444908  2.687717
## DMCC2966:Shaking:100fold   6.8481012 7.707340  8.272894
## DMCC2966:Shaking:25fold    6.9031198 7.452517  7.669810
## DMCC2966:Stationary:100fold 0.0000000 5.799689  6.866089
## DMCC2966:Stationary:25fold 3.9450519 6.021563  7.231307
##
## $comparison
## NULL
##
## $groups
##                            ES2.mod$ES2_chl.tuk groups
## control:Stationary:100fold            9.210468      a
## control:Shaking:100fold               8.798267      a
## DMCC2966:Shaking:100fold              7.538945     ab
## DMCC2966:Shaking:25fold               7.310403    abc
## DMCC2126:Stationary:100fold           6.329108   abcd
## DMCC2126:Shaking:100fold              5.267468   bcde
## DMCC2966:Stationary:25fold            5.259932   bcde
## DMCC2165:Stationary:100fold           4.536612   cdef
## DMCC2127:Stationary:100fold           4.521957   cdef
## DMCC2966:Stationary:100fold           4.404150    def
## control:Shaking:25fold                4.289829    def
## control:Stationary:25fold             4.117890    def
## DMCC2165:Shaking:100fold              2.818319     ef
## DMCC2127:Shaking:100fold              2.718108     ef
## DMCC2126:Stationary:25fold            2.562252     ef
## DMCC2127:Shaking:25fold               2.287858     ef
## DMCC2165:Shaking:25fold               2.131528      f
## DMCC2127:Stationary:25fold            2.020759      f
## DMCC2126:Shaking:25fold               1.990082      f
## DMCC2165:Stationary:25fold            1.753804      f
##
## attr(,"class")
```

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

Run analyses for ES5

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

```
###############ES5 analysis###############################
ES5.chl.anova <- lm (ES5$chl ~ ES5$Treatment + ES5$Dilution + ES5$Condition + ES5$isoRep + ES5$techRep
ES5.chl.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.chl.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 (tukey trans) by Treament
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 (tukey trans) 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 (tukey trans) by isoRep
ES5.chl.isoRep.HSD.test <- HSD.test(ES5.chl.anova, 'ES5$isoRep', group = T)
ES5.chl.isoRep.HSD.test
```

```
## $statistics
##     MSerror  Df     Mean       CV
##    3997.188 408 143.1371 44.16975
##
## $parameters
##     test     name.t ntr StudentizedRange alpha
##    Tukey ES5$isoRep   3         3.326652  0.05
##
## $means
##               ES5$chl      std   r Min   Max    Q25    Q50    Q75
## isolateRep1 154.8617 76.00701 141  36 372.6 89.600 154.00 217.1
## isolateRep2 144.1152 78.24548 138   0 289.2 71.625 138.75 210.4
## isolateRep3 130.4553 79.49175 141   0 363.9 62.900 113.30 193.6
##
## $comparison
## NULL
##
## $groups
##               ES5$chl groups
## isolateRep1 154.8617      a
## isolateRep2 144.1152      ab
```

```
## isolateRep3 130.4553        b
##
## attr(,"class")
## [1] "group"
```

```r
#Complete ANOVA for ES5 by treatment by dilution
ES5.comp.HSD.group <- HSD.test(ES5.chl.anova, c("ES5$Treatment", "ES5$Dilution"), group=TRUE,console=TRU
```

```
##
## Study: ES5.chl.anova ~ c("ES5$Treatment", "ES5$Dilution")
##
## HSD Test for ES5$chl
##
## Mean Square Error:  3997.188
##
## ES5$Treatment:ES5$Dilution,  means
##
##                    ES5.chl      std  r   Min   Max
## control:100fold  220.39216 57.43989 51 104.0 372.6
## control:25fold   167.27843 70.26818 51  26.0 303.7
## DMCC2126:100fold 168.37843 66.33045 51  48.0 270.4
## DMCC2126:25fold   97.39259 63.59504 54  30.3 277.2
## DMCC2127:100fold 142.66852 78.80234 54  37.1 339.2
## DMCC2127:25fold  102.15556 66.60843 54   0.0 296.0
## DMCC2165:100fold 139.55741 78.49134 54   0.0 279.9
## DMCC2165:25fold  112.61373 66.16763 51  40.3 289.2
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.30873
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##                    ES5$chl groups
## control:100fold  220.39216      a
## DMCC2126:100fold 168.37843      b
## control:25fold   167.27843      b
## DMCC2127:100fold 142.66852     bc
## DMCC2165:100fold 139.55741     bc
## DMCC2165:25fold  112.61373     cd
## DMCC2127:25fold  102.15556      d
## DMCC2126:25fold   97.39259      d
```

```r
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$Dilution   8          4.30873  0.05
```

```
##
## $means
##                    ES5$chl      std  r   Min   Max     Q25    Q50     Q75
## control:100fold  220.39216 57.43989 51 104.0 372.6 188.100 231.80 251.000
## control:25fold   167.27843 70.26818 51  26.0 303.7 126.400 178.10 214.200
## DMCC2126:100fold 168.37843 66.33045 51  48.0 270.4 120.950 178.80 222.900
## DMCC2126:25fold   97.39259 63.59504 54  30.3 277.2  52.575  82.15 107.350
## DMCC2127:100fold 142.66852 78.80234 54  37.1 339.2  79.800 112.80 202.400
## DMCC2127:25fold  102.15556 66.60843 54   0.0 296.0  56.875  80.35 130.975
## DMCC2165:100fold 139.55741 78.49134 54   0.0 279.9  76.300 148.65 203.650
## DMCC2165:25fold  112.61373 66.16763 51  40.3 289.2  62.200  86.20 161.700
##
## $comparison
## NULL
##
## $groups
##                    ES5$chl groups
## control:100fold  220.39216      a
## DMCC2126:100fold 168.37843      b
## control:25fold   167.27843      b
## DMCC2127:100fold 142.66852     bc
## DMCC2165:100fold 139.55741     bc
## DMCC2165:25fold  112.61373     cd
## DMCC2127:25fold  102.15556      d
## DMCC2126:25fold   97.39259      d
##
## attr(,"class")
## [1] "group"
```

```r
#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
```

```
##
## 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.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
```

```r
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 isoRep
ES5.mod.chl.isoRep.HSD.test <- HSD.test(ES5.mod.chl.anova, 'ES5.mod$isoRep', group = T)
ES5.mod.chl.isoRep.HSD.test
```

```
## $statistics
##     MSerror  Df     Mean       CV
##    57.63529 408 24.21363 31.35338
##
## $parameters
##     test         name.t ntr StudentizedRange alpha
##    Tukey ES5.mod$isoRep   3         3.326652  0.05
##
## $means
##             ES5.mod$ES5_chl.tuk      std   r      Min      Max      Q25
## isolateRep1         25.74400 8.601144 141 10.27062 46.91458 18.57805
## isolateRep2         24.26394 9.528258 138  0.00000 39.79045 16.06130
## isolateRep3         22.63401 9.536132 141  0.00000 46.19961 14.76124
##                 Q50      Q75
## isolateRep1 26.41730 33.02394
## isolateRep2 24.68604 32.35779
## isolateRep3 21.63961 30.65409
##
```

```
## $comparison
## NULL
##
## $groups
##              ES5.mod$ES5_chl.tuk groups
## isolateRep1           25.74400      a
## isolateRep2           24.26394      ab
## isolateRep3           22.63401      b
##
## attr(,"class")
## [1] "group"
```

```
#Complete ANOVA for ES5.mod by treatment by dilution
ES5.mod.comp.HSD.group <- HSD.test(ES5.mod.chl.anova, c("ES5.mod$Treatment", "ES5.mod$Dilution"), group=
```

```
##
## Study: ES5.mod.chl.anova ~ c("ES5.mod$Treatment", "ES5.mod$Dilution")
##
## HSD Test for ES5.mod$ES5_chl.tuk
##
## Mean Square Error:  57.63529
##
## ES5.mod$Treatment:ES5.mod$Dilution,  means
##
##                  ES5.mod.ES5_chl.tuk       std  r       Min      Max
## control:100fold           33.08875  5.694754 51 20.467824 46.91458
## control:25fold            27.20249  8.178120 51  8.312519 41.07609
## DMCC2126:100fold          27.42587  7.586754 51 12.382456 38.08942
## DMCC2126:25fold           18.84674  7.624616 54  9.182009 38.70932
## DMCC2127:100fold          24.30329  8.849956 54 10.473529 44.13634
## DMCC2127:25fold           19.14544  8.753292 54  0.000000 40.39612
## DMCC2165:100fold          23.53701 10.140662 54  0.000000 38.95398
## DMCC2165:25fold           20.80779  7.827922 51 11.052188 39.79045
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.30873
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##                  ES5.mod$ES5_chl.tuk groups
## control:100fold          33.08875      a
## DMCC2126:100fold         27.42587      b
## control:25fold           27.20249      b
## DMCC2127:100fold         24.30329      bc
## DMCC2165:100fold         23.53701      bcd
## DMCC2165:25fold          20.80779      cde
## DMCC2127:25fold          19.14544      de
## DMCC2126:25fold          18.84674      e
```

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

```
## $statistics
```

```
##     MSerror Df    Mean       CV
##    57.63529 408 24.21363 31.35338
##
## $parameters
##    test                              name.t ntr StudentizedRange alpha
##    Tukey ES5.mod$Treatment:ES5.mod$Dilution   8           4.30873  0.05
##
## $means
##                    ES5.mod$ES5_chl.tuk      std  r       Min      Max      Q25
## control:100fold            33.08875  5.694754 51 20.467824 46.91458 30.08453
## control:25fold             27.20249  8.178120 51  8.312519 41.07609 23.23414
## DMCC2126:100fold           27.42587  7.586754 51 12.382456 38.08942 22.56815
## DMCC2126:25fold            18.84674  7.624616 54  9.182009 38.70932 13.13726
## DMCC2127:100fold           24.30329  8.849956 54 10.473529 44.13634 17.22704
## DMCC2127:25fold            19.14544  8.753292 54  0.000000 40.39612 13.82542
## DMCC2165:100fold           23.53701 10.140662 54  0.000000 38.95398 16.73550
## DMCC2165:25fold            20.80779  7.827922 51 11.052188 39.79045 14.65419
##                               Q50       Q75
## control:100fold           34.46067 36.29008
## control:25fold            29.03565 32.73653
## DMCC2126:100fold          29.10978 33.59217
## DMCC2126:25fold           17.55877 20.88640
## DMCC2127:100fold          21.57740 31.55186
## DMCC2127:25fold           17.30728 23.77782
## DMCC2165:100fold          25.80930 31.67917
## DMCC2165:25fold           18.11673 27.26771
##
## $comparison
## NULL
##
## $groups
##                    ES5.mod$ES5_chl.tuk groups
## control:100fold            33.08875      a
## DMCC2126:100fold           27.42587      b
## control:25fold             27.20249      b
## DMCC2127:100fold           24.30329      bc
## DMCC2165:100fold           23.53701      bcd
## DMCC2165:25fold            20.80779      cde
## DMCC2127:25fold            19.14544      de
## DMCC2126:25fold            18.84674      e
##
## attr(,"class")
## [1] "group"
```

```r
#Complete ANOVA for ES5.mod by treatment by condition, by dilution
ES5.mod.comp.HSD.group <- HSD.test(ES5.mod.chl.anova, c("ES5.mod$Treatment", "ES5.mod$Condition", "ES5.
```

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

ES5.mod.comp.HSD.group

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

```
##    StudentizedRange alpha
##           4.87582  0.05
##
## $means
##                              ES5.mod$ES5_chl.tuk       std  r       Min      Max
## control:Shaking:100fold              30.92160  6.877550 24 20.467824 46.19961
## control:Shaking:25fold               26.28822  7.584437 27  8.312519 36.10186
## control:Stationary:100fold           35.01510  3.511991 27 29.814226 46.91458
## control:Stationary:25fold            28.23105  8.847762 24 10.583319 41.07609
## DMCC2126:Shaking:100fold             26.63321  8.061394 24 12.382456 38.08942
## DMCC2126:Shaking:25fold              16.33068  4.334703 27  9.182009 24.92251
## DMCC2126:Stationary:100fold          28.13045  7.218510 27 12.994778 37.53790
## DMCC2126:Stationary:25fold           21.36280  9.304178 27 10.270619 38.70932
## DMCC2127:Shaking:100fold             18.70574  5.119409 27 10.473529 30.33414
## DMCC2127:Shaking:25fold              13.80400  6.101857 27  0.000000 22.40212
## DMCC2127:Stationary:100fold          29.90084  8.268740 27 16.549688 44.13634
## DMCC2127:Stationary:25fold           24.48688  7.726440 27 13.222435 40.39612
## DMCC2165:Shaking:100fold             24.56023  8.205647 27 10.418401 38.34533
## DMCC2165:Shaking:25fold              18.20998  5.258465 27 11.052188 28.65280
## DMCC2165:Stationary:100fold          22.51380 11.836979 27  0.000000 38.95398
## DMCC2165:Stationary:25fold           23.73032  9.225861 24 12.382456 39.79045
##                                  Q25      Q50      Q75
## control:Shaking:100fold      25.60774 29.95578 35.75395
## control:Shaking:25fold       23.23414 28.68481 31.88435
## control:Stationary:100fold   32.89985 34.77877 36.49626
## control:Stationary:25fold    22.97996 30.57655 35.12646
## DMCC2126:Shaking:100fold     18.24222 28.49017 32.10254
## DMCC2126:Shaking:25fold      12.72170 15.30503 19.21892
## DMCC2126:Stationary:100fold  23.96670 29.23662 34.36364
## DMCC2126:Stationary:25fold   13.75020 17.95239 28.49754
## DMCC2127:Shaking:100fold     15.79238 18.06204 22.03937
## DMCC2127:Shaking:25fold      11.94225 14.14409 18.38373
## DMCC2127:Stationary:100fold  21.18901 31.73483 36.13001
## DMCC2127:Stationary:25fold   16.98374 23.80439 29.93923
## DMCC2165:Shaking:100fold     17.06819 21.67684 31.48681
## DMCC2165:Shaking:25fold      14.32943 16.96287 19.24541
## DMCC2165:Stationary:100fold  14.61527 26.86130 31.84574
## DMCC2165:Stationary:25fold   16.28243 21.81134 30.38458
##
## $comparison
## NULL
##
## $groups
##                              ES5.mod$ES5_chl.tuk groups
## control:Stationary:100fold           35.01510      a
## control:Shaking:100fold              30.92160     ab
## DMCC2127:Stationary:100fold          29.90084     ab
## control:Stationary:25fold            28.23105    abc
## DMCC2126:Stationary:100fold          28.13045    abc
## DMCC2126:Shaking:100fold             26.63321     bc
## control:Shaking:25fold               26.28822     bc
## DMCC2165:Shaking:100fold             24.56023    bcd
## DMCC2127:Stationary:25fold           24.48688    bcd
## DMCC2165:Stationary:25fold           23.73032    bcd
```

```
## DMCC2165:Stationary:100fold          22.51380    cde
## DMCC2126:Stationary:25fold           21.36280    cde
## DMCC2127:Shaking:100fold             18.70574    def
## DMCC2165:Shaking:25fold              18.20998    def
## DMCC2126:Shaking:25fold              16.33068     ef
## DMCC2127:Shaking:25fold              13.80400      f
##
## attr(,"class")
## [1] "group"
```

Run analyses for ES13B

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

```
#Statistical analysis
#####ES13B###
ES13B.chl.anova <- lm (ES13B$chl ~ ES13B$Treatment + ES13B$HostVariety + ES13B$isoRepNumber + ES13B$tecl
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:
```

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```
##                              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 Host variety
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
```

```
##
## 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 + ES13
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 Host variety
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_chl.tuk      std  r Min      Max      Q25      Q50
## AG4632                  46.00199 23.04112 54   0 96.69957 26.32493 44.64489
## DG47E80                 52.85715 24.31248 54   0 98.36929 34.08532 61.52054
## DG47X95                 53.96776 24.74253 48   0 95.60617 31.59813 58.99393
```

```
## Osage                       49.22977 28.48843 54    0 104.34627 25.98636 49.51131
## P5414LLS                    44.71323 23.92033 54    0  87.02381 23.82148 49.53890
##              Q75
## AG4632    63.64317
## DG47E80   68.39115
## DG47X95   73.50975
## Osage     71.73382
## P5414LLS 65.74587
##
## $comparison
## NULL
##
## $groups
##         ES13B.mod$ES13B_chl.tuk groups
## DG47X95                53.96776      a
## DG47E80                52.85715      a
## Osage                  49.22977      a
## AG4632                 46.00199      a
## P5414LLS               44.71323      a
##
## attr(,"class")
## [1] "group"
```

#Complete ANOVA for ES13B.mod
```
ES13B.mod.comp.HSD.group <- HSD.test(ES13B.mod.chl.anova, c("ES13B.mod$Treatment", "ES13B.mod$HostVariet
```

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

```
##                 ES13B.mod$ES13B_chl.tuk groups
## Control:Osage                  67.15363      a
## Control:DG47E80                66.70288      a
## Control:DG47X95                64.01404      a
## Control:P5414LLS               58.04351     ab
## Control:AG4632                 57.20904     ab
## DMCC2165:DG47X95               41.05111     bc
## DMCC2165:DG47E80               39.01143      c
## DMCC2165:AG4632                34.79495      c
## DMCC2165:P5414LLS              31.38296      c
## DMCC2165:Osage                 31.30592      c
```

ES13B.mod.comp.HSD.group

```
## $statistics
##     MSerror  Df     Mean       CV
##    436.2119 252 49.24912 42.40824
##
## $parameters
##     test                                 name.t ntr StudentizedRange alpha
##    Tukey ES13B.mod$Treatment:ES13B.mod$HostVariety  10         4.514628  0.05
##
## $means
##                  ES13B.mod$ES13B_chl.tuk      std  r      Min       Max
## Control:AG4632                  57.20904 22.03662 27  0.00000  96.69957
## Control:DG47E80                 66.70288 17.20548 27 35.38176  98.36929
## Control:DG47X95                 64.01404 17.93361 27 24.66777  95.60617
## Control:Osage                   67.15363 26.52535 27  0.00000 104.34627
## Control:P5414LLS                58.04351 11.99680 27 34.39165  76.51943
## DMCC2165:AG4632                 34.79495 18.32309 27  0.00000  78.61163
## DMCC2165:DG47E80                39.01143 22.59966 27  0.00000  76.18307
## DMCC2165:DG47X95                41.05111 26.62931 21  0.00000  93.72814
## DMCC2165:Osage                  31.30592 16.83924 27  0.00000  84.32030
## DMCC2165:P5414LLS               31.38296 25.56143 27  0.00000  87.02381
##                        Q25      Q50      Q75
## Control:AG4632     47.05388 62.96010 68.61805
## Control:DG47E80    62.26497 67.17475 78.30087
## Control:DG47X95    56.17982 65.54711 77.85944
## Control:Osage      65.40652 71.46612 76.90405
## Control:P5414LLS   51.98765 59.22541 67.22892
## DMCC2165:AG4632    22.34657 29.72913 43.18888
## DMCC2165:DG47E80   20.43572 33.65317 61.08024
## DMCC2165:DG47X95   19.88940 30.28659 60.68214
## DMCC2165:Osage     24.95960 26.04835 30.23822
## DMCC2165:P5414LLS  15.75931 23.21526 36.18682
##
## $comparison
## NULL
##
## $groups
##                 ES13B.mod$ES13B_chl.tuk groups
## Control:Osage                  67.15363      a
## Control:DG47E80                66.70288      a
## Control:DG47X95                64.01404      a
```

```
## Control:P5414LLS              58.04351     ab
## Control:AG4632                57.20904     ab
## DMCC2165:DG47X95              41.05111     bc
## DMCC2165:DG47E80              39.01143      c
## DMCC2165:AG4632               34.79495      c
## DMCC2165:P5414LLS             31.38296      c
## DMCC2165:Osage                31.30592      c
##
## attr(,"class")
## [1] "group"
```

Run analyses for ES14A

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

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

```r
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
```

```r
#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
```

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```
##
## $groups
##           ES14A$chl groups
## Control    220.1037      a
## DMCC2165   180.9794      b
##
## attr(,"class")
## [1] "group"
```

```
#Tukey's HSD for Variable chl by Host
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,console
```

```
##
## 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$Host + ES14A.mod$is
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 Host
```
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_chl.tuk groups
## Peanut               14333.182      a
## Tomato                9575.703      b
## Cotton                8224.039      b
## Soybean               7661.688      b
```

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

```
#Complete ANOVA for ES14A.mod
ES14A.mod.comp.HSD.group <- HSD.test(ES14A.mod.chl.anova, c("ES14A.mod$Treatment", "ES14A.mod$Host"), g
```

```
##
## Study: ES14A.mod.chl.anova ~ c("ES14A.mod$Treatment", "ES14A.mod$Host")
##
## HSD Test for ES14A.mod$ES14A_chl.tuk
##
## Mean Square Error:  14465471
##
## ES14A.mod$Treatment:ES14A.mod$Host,  means
##
##                 ES14A.mod.ES14A_chl.tuk      std  r      Min      Max
## Control:Cotton                  9103.740 3172.165 27 3121.3676 14110.73
## Control:Peanut                 13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean                12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato                 10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton                 7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut                15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean                3195.045 3010.793 27  667.0663 10153.43
## DMCC2165:Tomato                 8613.327 2039.245 27 3745.4797 12440.10
##
## Alpha: 0.05 ; DF Error: 202
## Critical Value of Studentized Range: 4.331714
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##                 ES14A.mod$ES14A_chl.tuk groups
## DMCC2165:Peanut               15330.007      a
## Control:Peanut                13336.356     ab
## Control:Soybean               12128.331     bc
## Control:Tomato                10658.376    bcd
## Control:Cotton                 9103.740    cde
## DMCC2165:Tomato                8613.327     de
## DMCC2165:Cotton                7344.338      e
## DMCC2165:Soybean               3195.045      f
```

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

```
## $statistics
##    MSerror  Df    Mean       CV
##   14465471 202 9953.906 38.20962
##
## $parameters
##    test                          name.t ntr StudentizedRange alpha
##    Tukey ES14A.mod$Treatment:ES14A.mod$Host   8         4.331714  0.05
##
```

```
## $means
##                   ES14A.mod$ES14A_chl.tuk       std  r       Min      Max
## Control:Cotton                   9103.740 3172.165 27 3121.3676 14110.73
## Control:Peanut                  13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean                 12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato                  10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton                  7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut                 15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean                 3195.045 3010.793 27  667.0663 10153.43
## DMCC2165:Tomato                  8613.327 2039.245 27 3745.4797 12440.10
##                        Q25        Q50        Q75
## Control:Cotton    7235.4241   9415.107 11840.543
## Control:Peanut   10983.3242  13169.695 16057.689
## Control:Soybean   9787.4152  11674.646 16090.596
## Control:Tomato    9595.2157  10503.255 11629.391
## DMCC2165:Cotton   5421.6757   7809.559  9207.086
## DMCC2165:Peanut  13422.7747  14940.064 17699.067
## DMCC2165:Soybean   921.2485   1394.263  5240.336
## DMCC2165:Tomato   7629.0246   8616.978  9828.773
##
## $comparison
## NULL
##
## $groups
##                   ES14A.mod$ES14A_chl.tuk groups
## DMCC2165:Peanut                 15330.007      a
## Control:Peanut                  13336.356     ab
## Control:Soybean                 12128.331     bc
## Control:Tomato                  10658.376    bcd
## Control:Cotton                   9103.740    cde
## DMCC2165:Tomato                  8613.327     de
## DMCC2165:Cotton                  7344.338      e
## DMCC2165:Soybean                 3195.045      f
##
## attr(,"class")
## [1] "group"
```

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 = Spec
  #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(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
  facet_wrap(~ Dilution)
ES5.mod.ggplot #+ stat_compare_means(aes(group = Dilution), label = "p.signif", na.rm = TRUE)
```

`## Warning: Removed 8 rows containing non-finite values (stat_boxplot).`
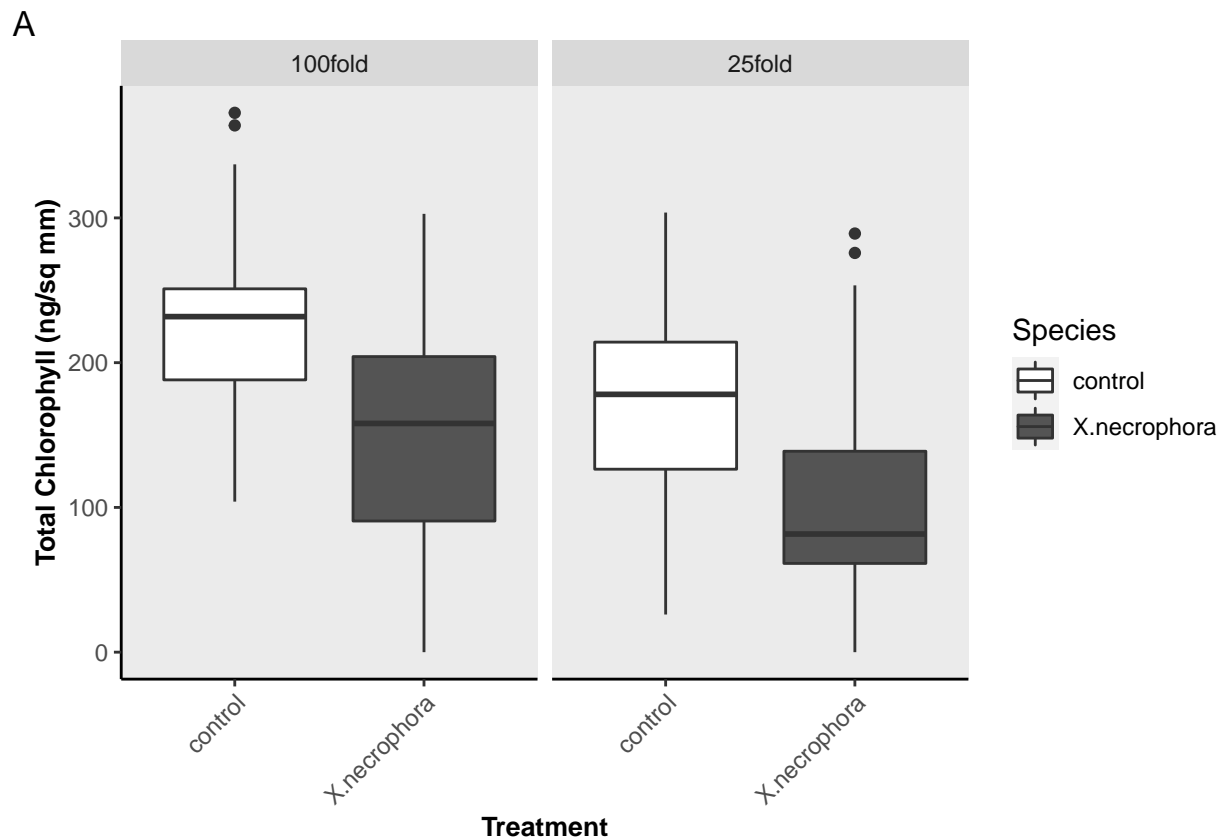
Individual plot for panel B

```
##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,                     # Relevel group factor
                       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 = Sp
 # 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(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
  facet_wrap(~ Dilution)
ES2.mod.v2.ggplot #+ stat_compare_means(aes(group = Dilution), label = "p.signif", na.rm = TRUE)
```

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

B
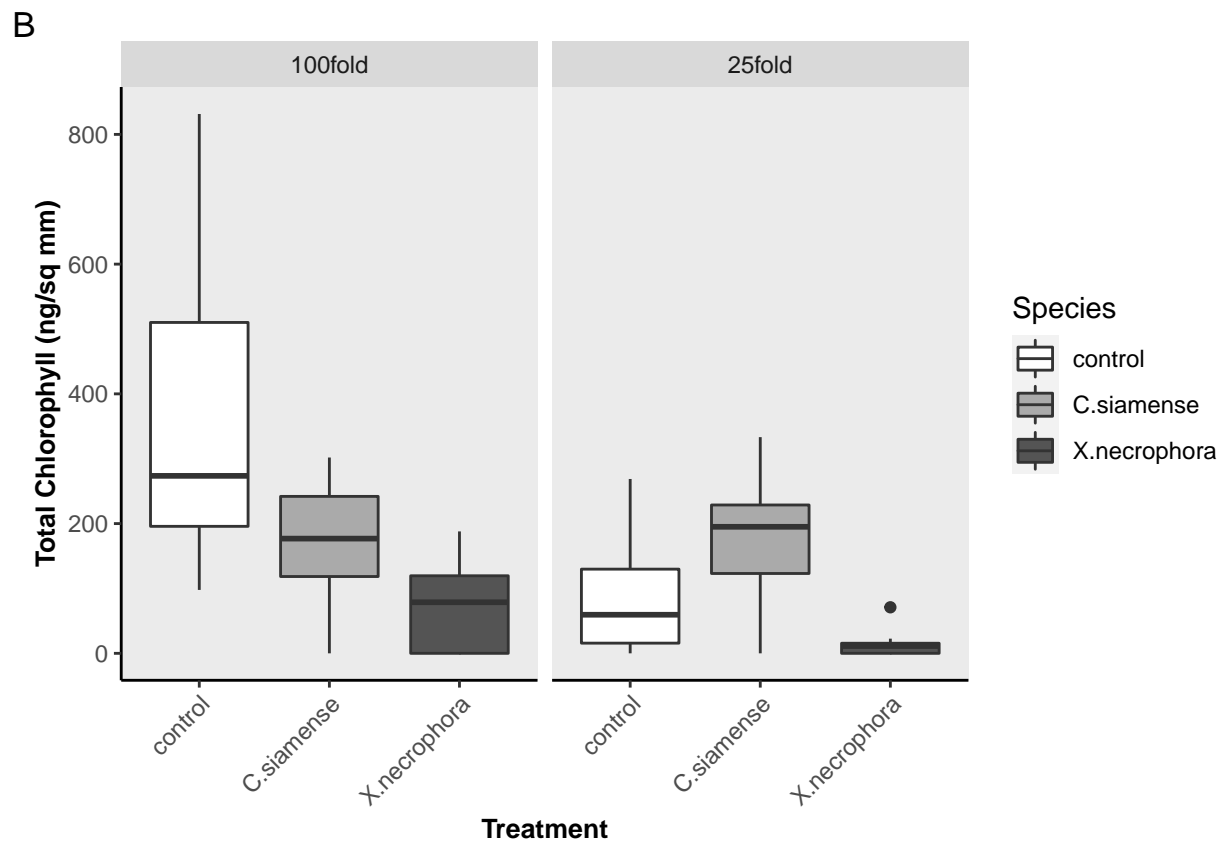
Plot composite figure 1

```
###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) #+ ggtitle("Digital chlorophyll cont
```

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

```
## Warning: Removed 32 rows containing non-finite values (stat_boxplot).
```
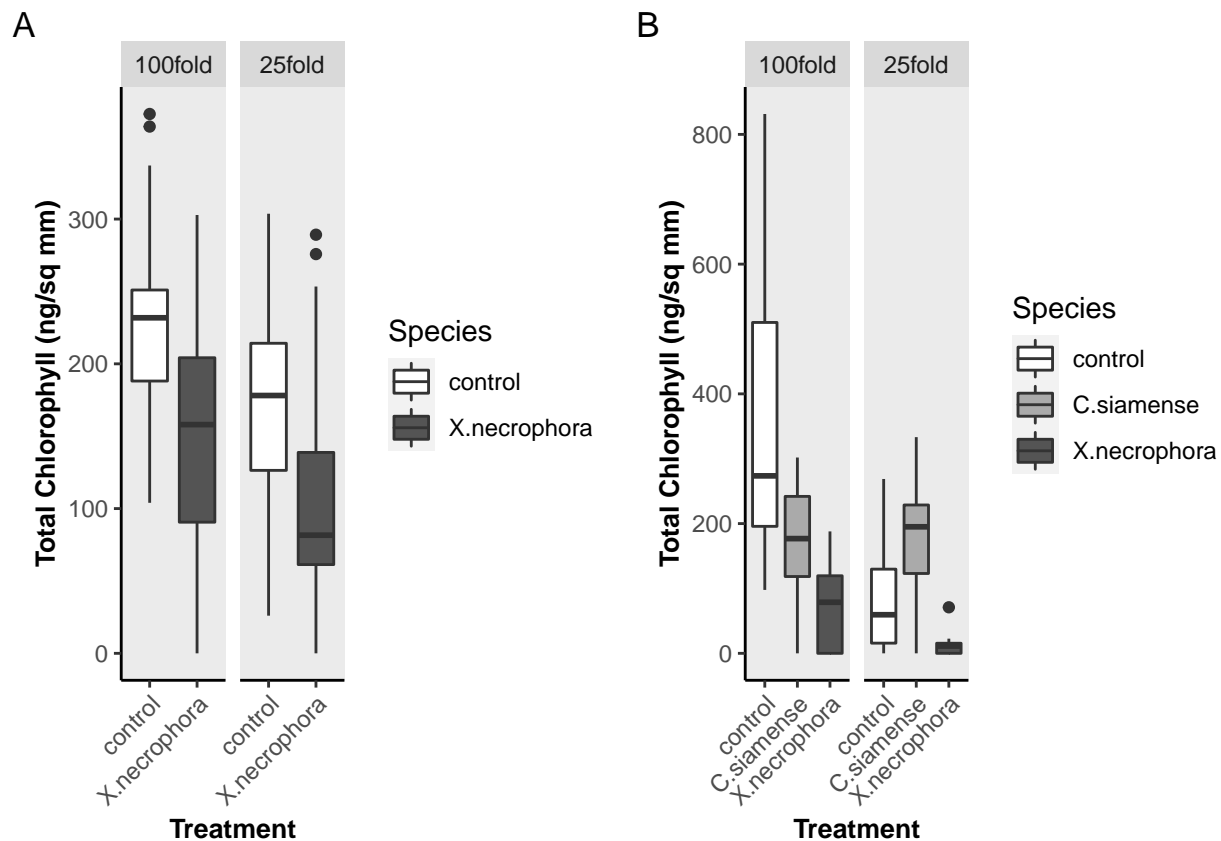
Plotting individual plots and composite figure 3

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=Hos
  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(si
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_l
ES13B.ByHosCult
```

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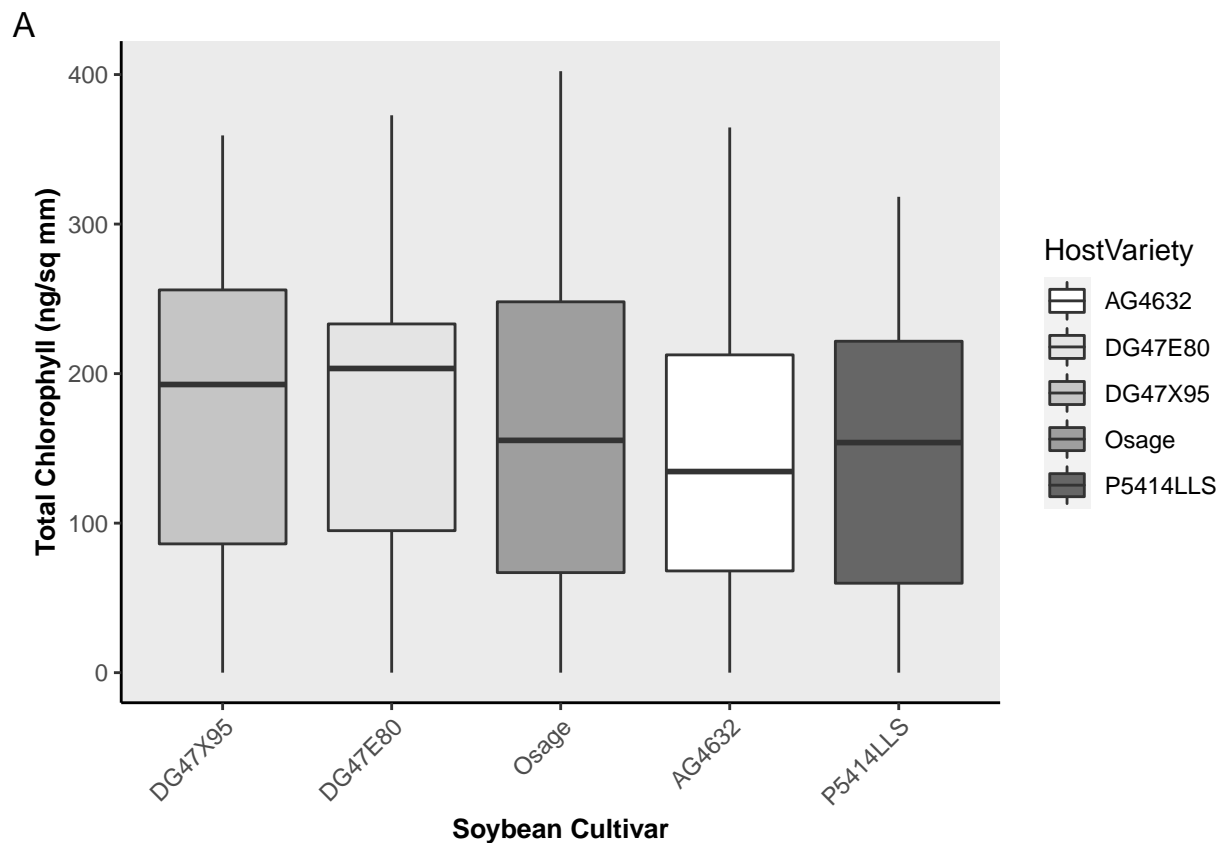
A

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 = ch
    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
    theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element
ES13B.ggplot.ByCultByTreat
```

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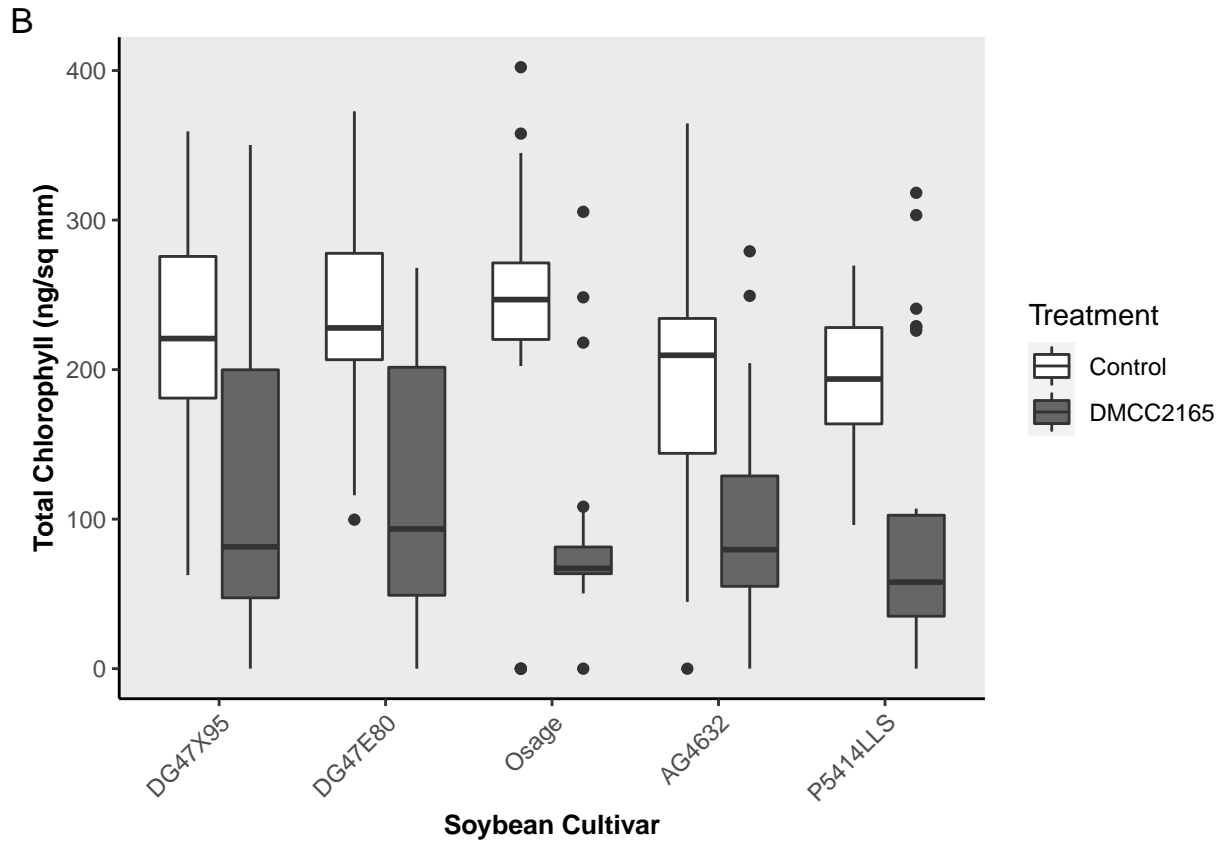
B

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)]
    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
    theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element
  #stat_summary(fun.data = give.n, geom = "text", position = position_dodge(width = 0.75), size = 3) # 
ES14A.ggplot.ByHost
```

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

C
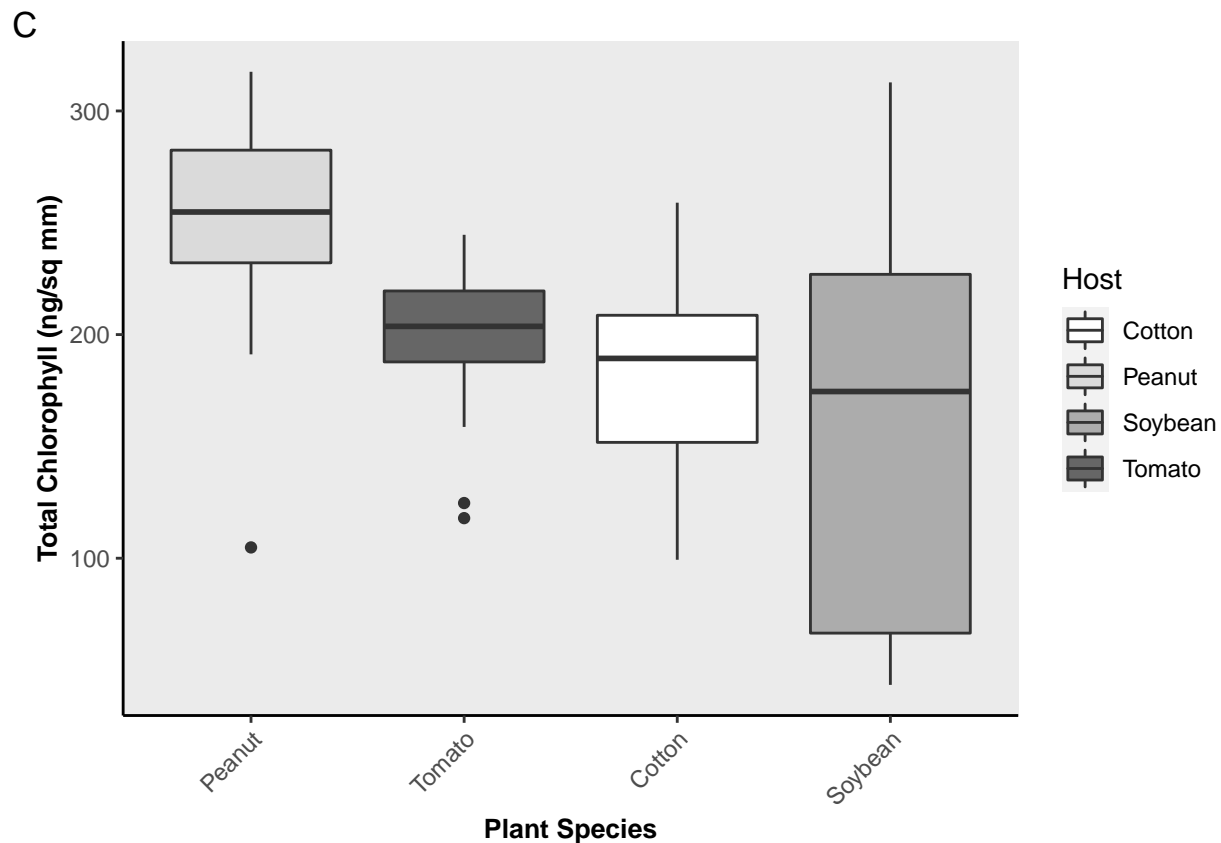
Panel D

```
###Plot by host by treatment w/ outliers
ES14A.ggplot.ByHostByTreat <- ggplot(ES14A.mod, aes(x = reorder(Host, -chl, na.rm = TRUE), y = chl, fill
    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
    theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element
  #stat_summary(fun.data = give.n, geom = "text", position = position_dodge(width = 0.75), size = 3) #
ES14A.ggplot.ByHostByTreat
```

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

D
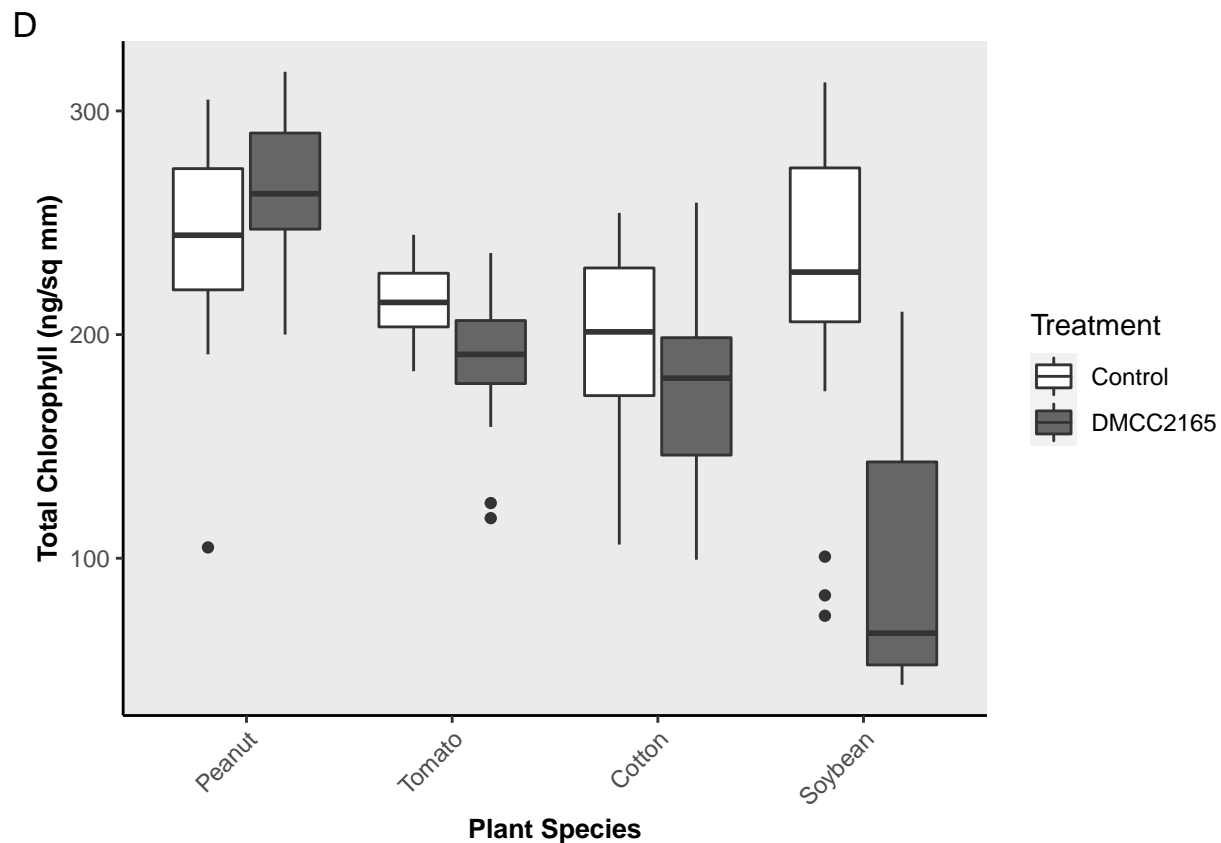
Composite figure 3

```
###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.
```

```
## 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).
```
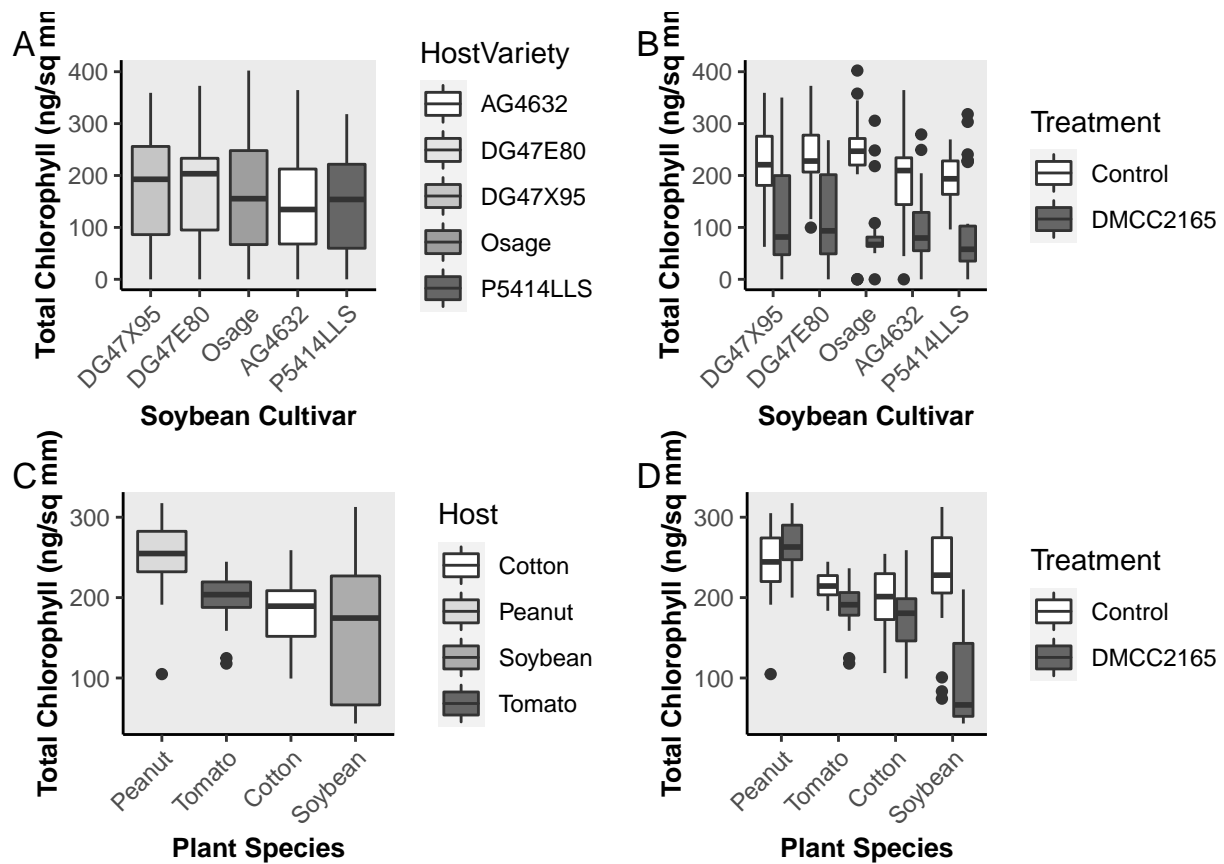
Supplementary Materials/Figures

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 = Dil
  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(si
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_b
  #facet_wrap(~ Condition)
ES2.mod.ggplot.v2 #+ stat_compare_means(aes(group = Dilution), label = "p.signif", na.rm = TRUE)
```

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

A
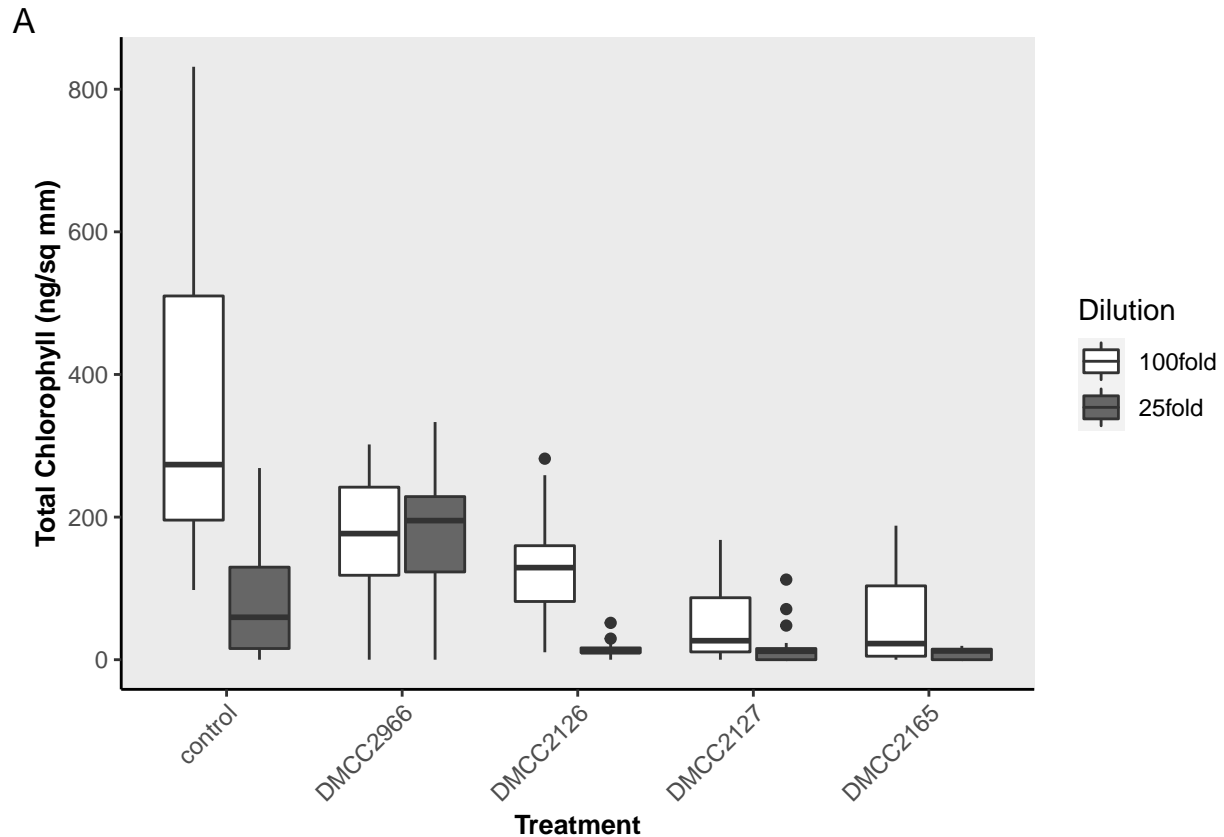

```r
#ES5 by treatment by dilution, no title
ES5.mod.ggplot.v2 <- ggplot(ES5.mod, aes(x = reorder(Treatment, -chl, na.rm = TRUE), y = chl, fill = Di
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "B") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
  facet_wrap(~ Condition)
ES5.mod.ggplot.v2 #+ stat_compare_means(aes(group = Dilution), label = "p.signif", na.rm = TRUE)
```

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

B
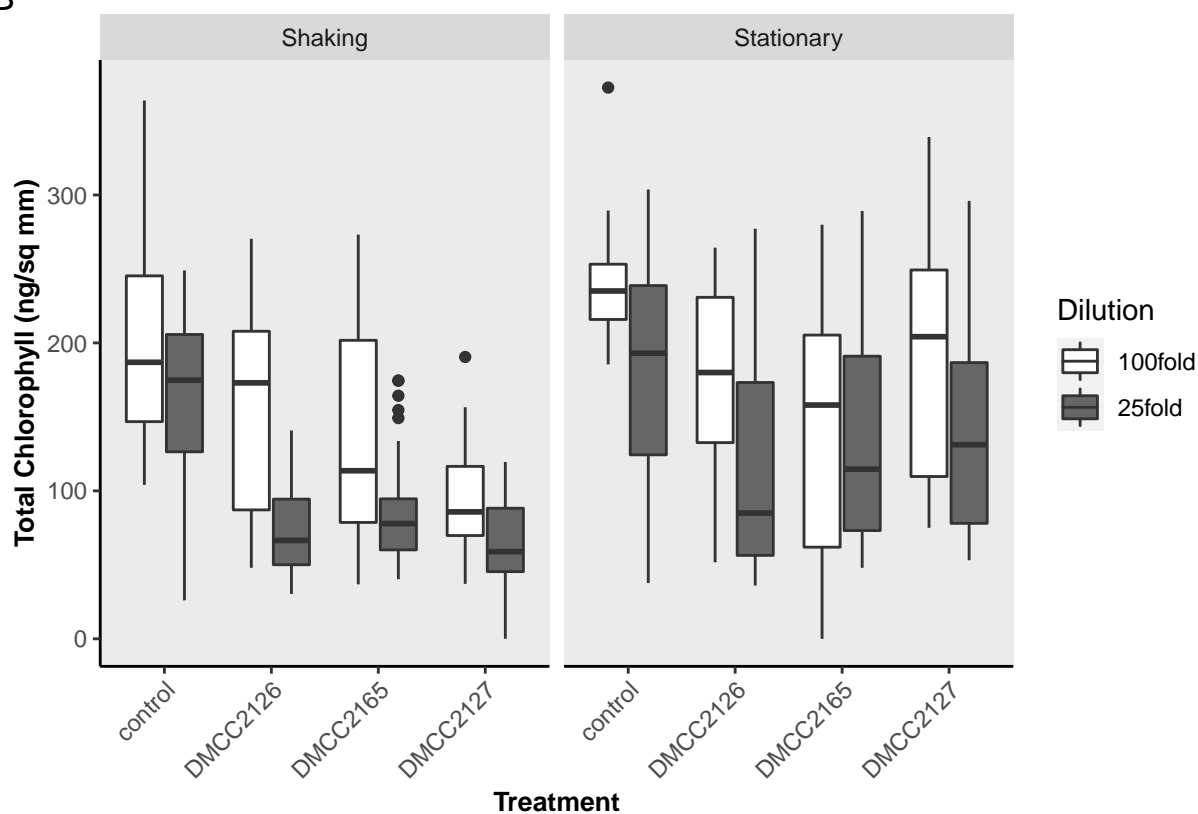

```
#ES5 by conditions (side by side)
ES5.mod.ggplot.v3 <- ggplot(ES5.mod, aes(x = reorder(Condition, -chl, na.rm = TRUE), y = chl, fill=Treat
  scale_fill_grey(start =1, end = 0.4) + labs(tag = "C") +
  xlab("Growth Condition") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
#facet_wrap(~ Condition)
ES5.mod.ggplot.v3 #+ stat_compare_means(aes(group = Condition), label = "p.signif", na.rm = TRUE)
```

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

C

Total Chlorophyll (ng/sq mm)

Treatment
- control
- DMCC2126
- DMCC2127
- DMCC2165

Growth Condition
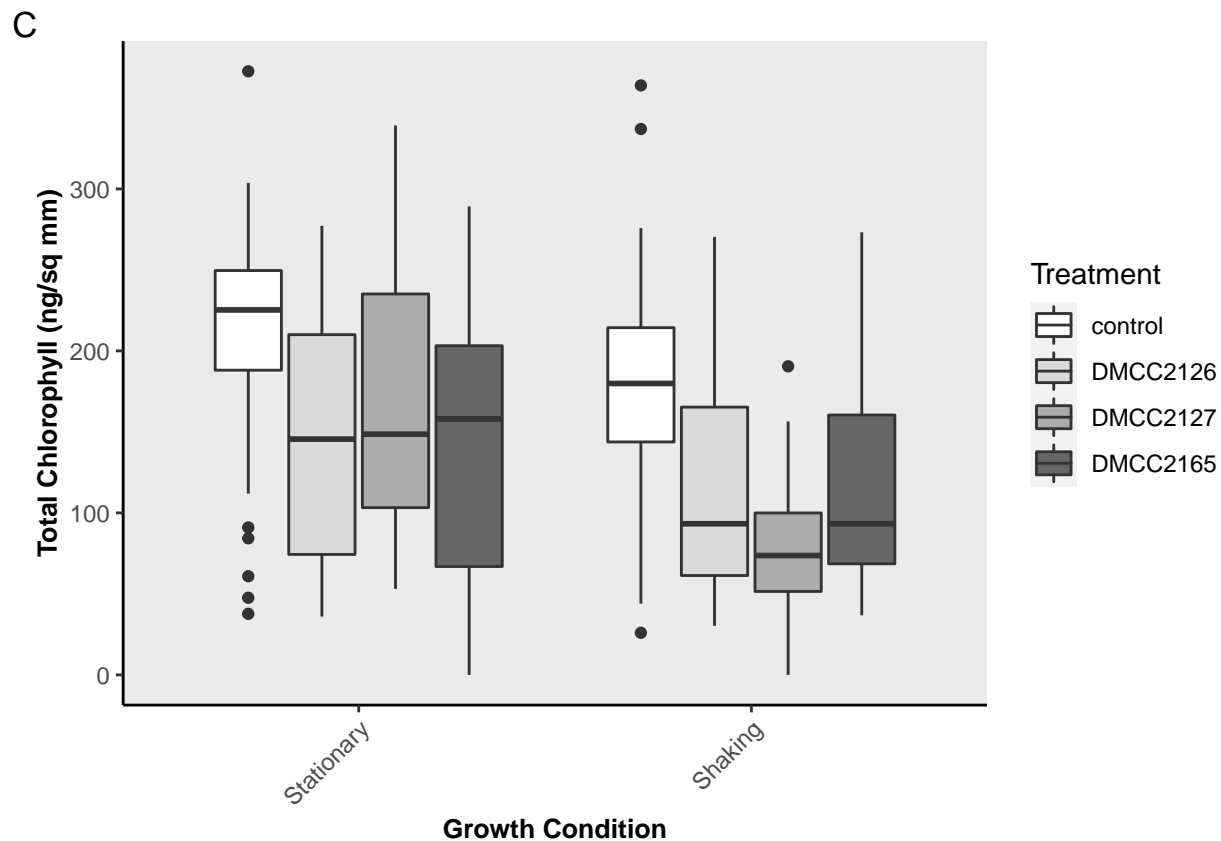
```
#ES5 by dilutions (side by side)
ES5.mod.ggplot.v4 <- ggplot(ES5.mod, aes(x = reorder(Dilution, -chl, na.rm = TRUE), y = chl, fill=Treat
  scale_fill_grey(start =1, end = 0.4) + labs(tag = "D") +
  xlab("Dilution Factor") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
#facet_wrap(~ Condition)
ES5.mod.ggplot.v4 #+ stat_compare_means(aes(group = Condition), label = "p.signif", na.rm = TRUE)
```

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

D

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 chemic

ES10.digital <- read.csv("../raw_data/ES10.digital.chl.csv", header = T)
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 measuremen
ES10.digital.sum <- aggregate(ES10.digital$chl,list(ES10.digital$ExpCode),sum)
```

```r
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')
ES10.chem.dig
```

```
##      ExpCode No ExpNo ExtractionType Treatment                          Species
## 1  ES10_01  1  ES10        Chemical   Control                          Control
## 2  ES10_02  2  ES10        Chemical   Control                          Control
## 3  ES10_03  3  ES10        Chemical   Control                          Control
## 4  ES10_04  4  ES10        Chemical   Control                          Control
## 5  ES10_05  5  ES10        Chemical   Control                          Control
## 6  ES10_06  6  ES10        Chemical   Control                          Control
## 7  ES10_07  7  ES10        Chemical   Control                          Control
## 8  ES10_08  8  ES10        Chemical   Control                          Control
## 9  ES10_09  9  ES10        Chemical   Control                          Control
## 10 ES10_10 10  ES10        Chemical   Control                          Control
## 11 ES10_11 11  ES10        Chemical   Control                          Control
## 12 ES10_12 12  ES10        Chemical   Control                          Control
## 13 ES10_13 13  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 14 ES10_14 14  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 15 ES10_15 15  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 16 ES10_16 16  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 17 ES10_17 17  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 18 ES10_18 18  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 19 ES10_19 19  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 20 ES10_20 20  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 21 ES10_21 21  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 22 ES10_22 22  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 23 ES10_23 23  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 24 ES10_24 24  ES10        Chemical   DMCC2165         X.necrophora_DMCC2165_LA
## 25 ES10_25 25  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 26 ES10_26 26  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 27 ES10_27 27  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 28 ES10_28 28  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 29 ES10_29 29  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 30 ES10_30 30  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 31 ES10_31 31  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 32 ES10_32 32  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 33 ES10_33 33  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 34 ES10_34 34  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 35 ES10_35 35  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 36 ES10_36 36  ES10        Chemical   DMCC3828 X.necrophora_DMCC3828_Martinique
## 37 ES10_37 37  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 38 ES10_38 38  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 39 ES10_39 39  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 40 ES10_40 40  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 41 ES10_41 41  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 42 ES10_42 42  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 43 ES10_43 43  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 44 ES10_44 44  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 45 ES10_45 45  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
## 46 ES10_46 46  ES10        Chemical   DMCC3830         X.cf.venustula_DMCC3830_LA
```

```
## 47 ES10_47 47   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 48 ES10_48 48   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 49 ES10_49 49   ES10      Chemical   Control                             Control
## 50 ES10_50 50   ES10      Chemical   Control                             Control
## 51 ES10_51 51   ES10      Chemical   Control                             Control
## 52 ES10_52 52   ES10      Chemical   Control                             Control
## 53 ES10_53 53   ES10      Chemical   Control                             Control
## 54 ES10_54 54   ES10      Chemical   Control                             Control
## 55 ES10_57 57   ES10      Chemical   Control                             Control
## 56 ES10_58 58   ES10      Chemical   Control                             Control
## 57 ES10_59 59   ES10      Chemical   Control                             Control
## 58 ES10_60 60   ES10      Chemical   Control                             Control
## 59 ES10_61 61   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 60 ES10_62 62   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 61 ES10_63 63   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 62 ES10_64 64   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 63 ES10_65 65   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 64 ES10_66 66   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 65 ES10_67 67   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 66 ES10_68 68   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 67 ES10_69 69   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 68 ES10_70 70   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 69 ES10_71 71   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 70 ES10_72 72   ES10      Chemical  DMCC2165          X.necrophora_DMCC2165_LA
## 71 ES10_73 73   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 72 ES10_74 74   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 73 ES10_75 75   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 74 ES10_76 76   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 75 ES10_77 77   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 76 ES10_78 78   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 77 ES10_79 79   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 78 ES10_80 80   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 79 ES10_81 81   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 80 ES10_82 82   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 81 ES10_83 83   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 82 ES10_84 84   ES10      Chemical  DMCC3828 X.necrophora_DMCC3828_Martinique
## 83 ES10_85 85   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 84 ES10_86 86   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 85 ES10_87 87   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 86 ES10_88 88   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 87 ES10_89 89   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 88 ES10_90 90   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 89 ES10_91 91   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 90 ES10_92 92   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 91 ES10_93 93   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 92 ES10_94 94   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 93 ES10_95 95   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
## 94 ES10_96 96   ES10      Chemical  DMCC3830         X.cf.venustula_DMCC3830_LA
##     Condition Dilution techRepNumber isoRepNumber HostVariety
## 1    shaking  100fold      techRep1       isoRep1     AG4632
## 2    shaking  100fold      techRep2       isoRep1     AG4632
## 3    shaking  100fold      techRep3       isoRep1     AG4632
## 4    shaking  100fold      techRep1       isoRep2     AG4632
## 5    shaking  100fold      techRep2       isoRep2     AG4632
```

```
## 6    shaking   100fold    techRep3    isoRep2    AG4632
## 7    shaking   100fold    techRep1    isoRep3    AG4632
## 8    shaking   100fold    techRep2    isoRep3    AG4632
## 9    shaking   100fold    techRep3    isoRep3    AG4632
## 10   shaking   100fold    techRep1    isoRep4    AG4632
## 11   shaking   100fold    techRep2    isoRep4    AG4632
## 12   shaking   100fold    techRep3    isoRep4    AG4632
## 13   shaking   100fold    techRep1    isoRep1    AG4632
## 14   shaking   100fold    techRep2    isoRep1    AG4632
## 15   shaking   100fold    techRep3    isoRep1    AG4632
## 16   shaking   100fold    techRep1    isoRep2    AG4632
## 17   shaking   100fold    techRep2    isoRep2    AG4632
## 18   shaking   100fold    techRep3    isoRep2    AG4632
## 19   shaking   100fold    techRep1    isoRep3    AG4632
## 20   shaking   100fold    techRep2    isoRep3    AG4632
## 21   shaking   100fold    techRep3    isoRep3    AG4632
## 22   shaking   100fold    techRep1    isoRep4    AG4632
## 23   shaking   100fold    techRep2    isoRep4    AG4632
## 24   shaking   100fold    techRep3    isoRep4    AG4632
## 25   shaking   100fold    techRep1    isoRep1    AG4632
## 26   shaking   100fold    techRep2    isoRep1    AG4632
## 27   shaking   100fold    techRep3    isoRep1    AG4632
## 28   shaking   100fold    techRep1    isoRep2    AG4632
## 29   shaking   100fold    techRep2    isoRep2    AG4632
## 30   shaking   100fold    techRep3    isoRep2    AG4632
## 31   shaking   100fold    techRep1    isoRep3    AG4632
## 32   shaking   100fold    techRep2    isoRep3    AG4632
## 33   shaking   100fold    techRep3    isoRep3    AG4632
## 34   shaking   100fold    techRep1    isoRep4    AG4632
## 35   shaking   100fold    techRep2    isoRep4    AG4632
## 36   shaking   100fold    techRep3    isoRep4    AG4632
## 37   shaking   100fold    techRep1    isoRep1    AG4632
## 38   shaking   100fold    techRep2    isoRep1    AG4632
## 39   shaking   100fold    techRep3    isoRep1    AG4632
## 40   shaking   100fold    techRep1    isoRep2    AG4632
## 41   shaking   100fold    techRep2    isoRep2    AG4632
## 42   shaking   100fold    techRep3    isoRep2    AG4632
## 43   shaking   100fold    techRep1    isoRep3    AG4632
## 44   shaking   100fold    techRep2    isoRep3    AG4632
## 45   shaking   100fold    techRep3    isoRep3    AG4632
## 46   shaking   100fold    techRep1    isoRep4    AG4632
## 47   shaking   100fold    techRep2    isoRep4    AG4632
## 48   shaking   100fold    techRep3    isoRep4    AG4632
## 49   shaking    25fold    techRep1    isoRep1    AG4632
## 50   shaking    25fold    techRep2    isoRep1    AG4632
## 51   shaking    25fold    techRep3    isoRep1    AG4632
## 52   shaking    25fold    techRep1    isoRep2    AG4632
## 53   shaking    25fold    techRep2    isoRep2    AG4632
## 54   shaking    25fold    techRep3    isoRep2    AG4632
## 55   shaking    25fold    techRep3    isoRep3    AG4632
## 56   shaking    25fold    techRep1    isoRep4    AG4632
## 57   shaking    25fold    techRep2    isoRep4    AG4632
## 58   shaking    25fold    techRep3    isoRep4    AG4632
## 59   shaking    25fold    techRep1    isoRep1    AG4632
```

```
## 60    shaking    25fold    techRep2    isoRep1    AG4632
## 61    shaking    25fold    techRep3    isoRep1    AG4632
## 62    shaking    25fold    techRep1    isoRep2    AG4632
## 63    shaking    25fold    techRep2    isoRep2    AG4632
## 64    shaking    25fold    techRep3    isoRep2    AG4632
## 65    shaking    25fold    techRep1    isoRep3    AG4632
## 66    shaking    25fold    techRep2    isoRep3    AG4632
## 67    shaking    25fold    techRep3    isoRep3    AG4632
## 68    shaking    25fold    techRep1    isoRep4    AG4632
## 69    shaking    25fold    techRep2    isoRep4    AG4632
## 70    shaking    25fold    techRep3    isoRep4    AG4632
## 71    shaking    25fold    techRep1    isoRep1    AG4632
## 72    shaking    25fold    techRep2    isoRep1    AG4632
## 73    shaking    25fold    techRep3    isoRep1    AG4632
## 74    shaking    25fold    techRep1    isoRep2    AG4632
## 75    shaking    25fold    techRep2    isoRep2    AG4632
## 76    shaking    25fold    techRep3    isoRep2    AG4632
## 77    shaking    25fold    techRep1    isoRep3    AG4632
## 78    shaking    25fold    techRep2    isoRep3    AG4632
## 79    shaking    25fold    techRep3    isoRep3    AG4632
## 80    shaking    25fold    techRep1    isoRep4    AG4632
## 81    shaking    25fold    techRep2    isoRep4    AG4632
## 82    shaking    25fold    techRep3    isoRep4    AG4632
## 83    shaking    25fold    techRep1    isoRep1    AG4632
## 84    shaking    25fold    techRep2    isoRep1    AG4632
## 85    shaking    25fold    techRep3    isoRep1    AG4632
## 86    shaking    25fold    techRep1    isoRep2    AG4632
## 87    shaking    25fold    techRep2    isoRep2    AG4632
## 88    shaking    25fold    techRep3    isoRep2    AG4632
## 89    shaking    25fold    techRep1    isoRep3    AG4632
## 90    shaking    25fold    techRep2    isoRep3    AG4632
## 91    shaking    25fold    techRep3    isoRep3    AG4632
## 92    shaking    25fold    techRep1    isoRep4    AG4632
## 93    shaking    25fold    techRep2    isoRep4    AG4632
## 94    shaking    25fold    techRep3    isoRep4    AG4632
##                                    TreatmentCode X645nm_without_adj
## 1     ES10_Control_isoRep1_techRep1_100fold_AG4632               0.33
## 2     ES10_Control_isoRep1_techRep2_100fold_AG4632               0.10
## 3     ES10_Control_isoRep1_techRep3_100fold_AG4632               0.15
## 4     ES10_Control_isoRep2_techRep1_100fold_AG4632               0.24
## 5     ES10_Control_isoRep2_techRep2_100fold_AG4632               0.44
## 6     ES10_Control_isoRep2_techRep3_100fold_AG4632               0.29
## 7     ES10_Control_isoRep3_techRep1_100fold_AG4632               0.30
## 8     ES10_Control_isoRep3_techRep2_100fold_AG4632               0.29
## 9     ES10_Control_isoRep3_techRep3_100fold_AG4632               0.19
## 10    ES10_Control_isoRep4_techRep1_100fold_AG4632               0.41
## 11    ES10_Control_isoRep4_techRep2_100fold_AG4632               0.22
## 12    ES10_Control_isoRep4_techRep3_100fold_AG4632               0.41
## 13 ES10_DMCC2165_isoRep1_techRep1_100fold_AG4632               0.27
## 14 ES10_DMCC2165_isoRep1_techRep2_100fold_AG4632               0.09
## 15 ES10_DMCC2165_isoRep1_techRep3_100fold_AG4632               0.38
## 16 ES10_DMCC2165_isoRep2_techRep1_100fold_AG4632               0.30
## 17 ES10_DMCC2165_isoRep2_techRep2_100fold_AG4632               0.12
## 18 ES10_DMCC2165_isoRep2_techRep3_100fold_AG4632               0.04
```

```
## 19 ES10_DMCC2165_isoRep3_techRep1_100fold_AG4632          0.08
## 20 ES10_DMCC2165_isoRep3_techRep2_100fold_AG4632          0.30
## 21 ES10_DMCC2165_isoRep3_techRep3_100fold_AG4632          0.12
## 22 ES10_DMCC2165_isoRep4_techRep1_100fold_AG4632          0.42
## 23 ES10_DMCC2165_isoRep4_techRep2_100fold_AG4632          0.15
## 24 ES10_DMCC2165_isoRep4_techRep3_100fold_AG4632          0.39
## 25 ES10_DMCC3828_isoRep1_techRep1_100fold_AG4632          0.32
## 26 ES10_DMCC3828_isoRep1_techRep2_100fold_AG4632          0.27
## 27 ES10_DMCC3828_isoRep1_techRep3_100fold_AG4632          0.20
## 28 ES10_DMCC3828_isoRep2_techRep1_100fold_AG4632          0.34
## 29 ES10_DMCC3828_isoRep2_techRep2_100fold_AG4632          0.25
## 30 ES10_DMCC3828_isoRep2_techRep3_100fold_AG4632          0.49
## 31 ES10_DMCC3828_isoRep3_techRep1_100fold_AG4632          0.37
## 32 ES10_DMCC3828_isoRep3_techRep2_100fold_AG4632          0.27
## 33 ES10_DMCC3828_isoRep3_techRep3_100fold_AG4632          0.36
## 34 ES10_DMCC3828_isoRep4_techRep1_100fold_AG4632          0.39
## 35 ES10_DMCC3828_isoRep4_techRep2_100fold_AG4632          0.40
## 36 ES10_DMCC3828_isoRep4_techRep3_100fold_AG4632          0.39
## 37 ES10_DMCC3830_isoRep1_techRep1_100fold_AG4632          0.04
## 38 ES10_DMCC3830_isoRep1_techRep2_100fold_AG4632          0.12
## 39 ES10_DMCC3830_isoRep1_techRep3_100fold_AG4632          0.12
## 40 ES10_DMCC3830_isoRep2_techRep1_100fold_AG4632          0.11
## 41 ES10_DMCC3830_isoRep2_techRep2_100fold_AG4632          0.23
## 42 ES10_DMCC3830_isoRep2_techRep3_100fold_AG4632          0.05
## 43 ES10_DMCC3830_isoRep3_techRep1_100fold_AG4632          0.08
## 44 ES10_DMCC3830_isoRep3_techRep2_100fold_AG4632          0.02
## 45 ES10_DMCC3830_isoRep3_techRep3_100fold_AG4632          0.45
## 46 ES10_DMCC3830_isoRep4_techRep1_100fold_AG4632          0.25
## 47 ES10_DMCC3830_isoRep4_techRep2_100fold_AG4632          0.10
## 48 ES10_DMCC3830_isoRep4_techRep3_100fold_AG4632          0.05
## 49   ES10_Control_isoRep1_techRep1_25fold_AG4632          0.41
## 50   ES10_Control_isoRep1_techRep2_25fold_AG4632          0.32
## 51   ES10_Control_isoRep1_techRep3_25fold_AG4632          0.38
## 52   ES10_Control_isoRep2_techRep1_25fold_AG4632          0.19
## 53   ES10_Control_isoRep2_techRep2_25fold_AG4632          0.41
## 54   ES10_Control_isoRep2_techRep3_25fold_AG4632          0.38
## 55   ES10_Control_isoRep3_techRep3_25fold_AG4632          0.38
## 56   ES10_Control_isoRep4_techRep1_25fold_AG4632          0.28
## 57   ES10_Control_isoRep4_techRep2_25fold_AG4632          0.38
## 58   ES10_Control_isoRep4_techRep3_25fold_AG4632          0.62
## 59  ES10_DMCC2165_isoRep1_techRep1_25fold_AG4632          0.09
## 60  ES10_DMCC2165_isoRep1_techRep2_25fold_AG4632          0.11
## 61  ES10_DMCC2165_isoRep1_techRep3_25fold_AG4632          0.23
## 62  ES10_DMCC2165_isoRep2_techRep1_25fold_AG4632          0.23
## 63  ES10_DMCC2165_isoRep2_techRep2_25fold_AG4632          0.02
## 64  ES10_DMCC2165_isoRep2_techRep3_25fold_AG4632          0.03
## 65  ES10_DMCC2165_isoRep3_techRep1_25fold_AG4632          0.27
## 66  ES10_DMCC2165_isoRep3_techRep2_25fold_AG4632          0.19
## 67  ES10_DMCC2165_isoRep3_techRep3_25fold_AG4632          0.11
## 68  ES10_DMCC2165_isoRep4_techRep1_25fold_AG4632          0.29
## 69  ES10_DMCC2165_isoRep4_techRep2_25fold_AG4632          0.14
## 70  ES10_DMCC2165_isoRep4_techRep3_25fold_AG4632          0.20
## 71   ES10_DMCC3828_isoRep1_techRep1_25fold_AG4632         0.18
## 72   ES10_DMCC3828_isoRep1_techRep2_25fold_AG4632         0.15
```

```
## 73  ES10_DMCC3828_isoRep1_techRep3_25fold_AG4632                    0.30
## 74  ES10_DMCC3828_isoRep2_techRep1_25fold_AG4632                    0.32
## 75  ES10_DMCC3828_isoRep2_techRep2_25fold_AG4632                    0.11
## 76  ES10_DMCC3828_isoRep2_techRep3_25fold_AG4632                    0.40
## 77  ES10_DMCC3828_isoRep3_techRep1_25fold_AG4632                    0.12
## 78  ES10_DMCC3828_isoRep3_techRep2_25fold_AG4632                    0.31
## 79  ES10_DMCC3828_isoRep3_techRep3_25fold_AG4632                    0.29
## 80  ES10_DMCC3828_isoRep4_techRep1_25fold_AG4632                    0.18
## 81  ES10_DMCC3828_isoRep4_techRep2_25fold_AG4632                    0.24
## 82  ES10_DMCC3828_isoRep4_techRep3_25fold_AG4632                    0.36
## 83  ES10_DMCC3830_isoRep1_techRep1_25fold_AG4632                    0.21
## 84  ES10_DMCC3830_isoRep1_techRep2_25fold_AG4632                    0.09
## 85  ES10_DMCC3830_isoRep1_techRep3_25fold_AG4632                    0.23
## 86  ES10_DMCC3830_isoRep2_techRep1_25fold_AG4632                    0.27
## 87  ES10_DMCC3830_isoRep2_techRep2_25fold_AG4632                    0.08
## 88  ES10_DMCC3830_isoRep2_techRep3_25fold_AG4632                    0.20
## 89  ES10_DMCC3830_isoRep3_techRep1_25fold_AG4632                    0.31
## 90  ES10_DMCC3830_isoRep3_techRep2_25fold_AG4632                    0.22
## 91  ES10_DMCC3830_isoRep3_techRep3_25fold_AG4632                    0.06
## 92  ES10_DMCC3830_isoRep4_techRep1_25fold_AG4632                    0.02
## 93  ES10_DMCC3830_isoRep4_techRep2_25fold_AG4632                    0.03
## 94  ES10_DMCC3830_isoRep4_techRep3_25fold_AG4632                    0.21
##     X646nm_without_adj X663nm_without_adj X645nm X646nm X663nm Volume
## 1                 0.34               0.72  0.330  0.340  0.720    1.0
## 2                 0.11               0.23  0.100  0.110  0.230    1.0
## 3                 0.16               0.41  0.150  0.160  0.410    1.0
## 4                 0.25               0.58  0.240  0.250  0.580    1.0
## 5                 0.46               1.00  0.440  0.460  1.000    1.0
## 6                 0.31               0.70  0.290  0.310  0.700    1.0
## 7                 0.32               0.74  0.300  0.320  0.740    1.0
## 8                 0.31               0.68  0.290  0.310  0.680    1.0
## 9                 0.20               0.45  0.190  0.200  0.450    1.0
## 10                0.42               0.91  0.410  0.420  0.910    1.0
## 11                0.22               0.46  0.220  0.220  0.460    1.0
## 12                0.42               0.87  0.410  0.420  0.870    1.0
## 13                0.29               0.67  0.270  0.290  0.670    1.0
## 14                0.10               0.25  0.090  0.100  0.250    1.0
## 15                0.40               0.90  0.380  0.400  0.900    1.0
## 16                0.31               0.68  0.300  0.310  0.680    1.0
## 17                0.13               0.34  0.120  0.130  0.340    1.0
## 18                0.04               0.14  0.040  0.040  0.140    1.0
## 19                0.08               0.18  0.080  0.080  0.180    1.0
## 20                0.31               0.67  0.300  0.310  0.670    1.0
## 21                0.13               0.24  0.120  0.130  0.240    1.0
## 22                0.43               0.91  0.378  0.387  0.819    0.9
## 23                0.16               0.40  0.150  0.160  0.400    1.0
## 24                0.41               0.92  0.390  0.410  0.920    1.0
## 25                0.33               0.74  0.320  0.330  0.740    1.0
## 26                0.29               0.64  0.270  0.290  0.640    1.0
## 27                0.21               0.51  0.200  0.210  0.510    1.0
## 28                0.36               0.76  0.340  0.360  0.760    1.0
## 29                0.27               0.63  0.250  0.270  0.630    1.0
## 30                0.51               1.09  0.392  0.408  0.872    0.8
## 31                0.39               0.85  0.370  0.390  0.850    1.0
```

```
## 32            0.28          0.58  0.270  0.280  0.580   1.0
## 33            0.38          0.82  0.360  0.380  0.820   1.0
## 34            0.40          0.85  0.390  0.400  0.850   1.0
## 35            0.41          0.83  0.400  0.410  0.830   1.0
## 36            0.40          0.86  0.390  0.400  0.860   1.0
## 37            0.05          0.12  0.040  0.050  0.120   1.0
## 38            0.12          0.22  0.120  0.120  0.220   1.0
## 39            0.12          0.24  0.120  0.120  0.240   1.0
## 40            0.12          0.29  0.110  0.120  0.290   1.0
## 41            0.24          0.53  0.230  0.240  0.530   1.0
## 42            0.05          0.11  0.050  0.050  0.110   1.0
## 43            0.08          0.19  0.080  0.080  0.190   1.0
## 44            0.02          0.05  0.020  0.020  0.050   1.0
## 45            0.46          0.99  0.450  0.460  0.990   1.0
## 46            0.26          0.59  0.250  0.260  0.590   1.0
## 47            0.11          0.23  0.100  0.110  0.230   1.0
## 48            0.06          0.18  0.050  0.060  0.180   1.0
## 49            0.43          0.96  0.410  0.430  0.960   1.0
## 50            0.33          0.72  0.320  0.330  0.720   1.0
## 51            0.40          0.90  0.380  0.400  0.900   1.0
## 52            0.20          0.47  0.190  0.200  0.470   1.0
## 53            0.43          0.96  0.410  0.430  0.960   1.0
## 54            0.40          0.93  0.380  0.400  0.930   1.0
## 55            0.40          0.89  0.380  0.400  0.890   1.0
## 56            0.29          0.57  0.280  0.290  0.570   1.0
## 57            0.39          0.88  0.380  0.390  0.880   1.0
## 58            0.64          1.37  0.620  0.640  1.370   1.0
## 59            0.10          0.30  0.090  0.100  0.300   1.0
## 60            0.12          0.25  0.110  0.120  0.250   1.0
## 61            0.24          0.55  0.230  0.240  0.550   1.0
## 62            0.24          0.58  0.207  0.216  0.522   0.9
## 63            0.03          0.09  0.020  0.030  0.090   1.0
## 64            0.03          0.09  0.030  0.030  0.090   1.0
## 65            0.28          0.61  0.243  0.252  0.549   0.9
## 66            0.19          0.40  0.190  0.190  0.400   1.0
## 67            0.12          0.32  0.110  0.120  0.320   1.0
## 68            0.31          0.72  0.290  0.310  0.720   1.0
## 69            0.15          0.34  0.140  0.150  0.340   1.0
## 70            0.22          0.46  0.200  0.220  0.460   1.0
## 71            0.19          0.47  0.180  0.190  0.470   1.0
## 72            0.16          0.36  0.150  0.160  0.360   1.0
## 73            0.31          0.68  0.300  0.310  0.680   1.0
## 74            0.34          0.72  0.320  0.340  0.720   1.0
## 75            0.11          0.27  0.110  0.110  0.270   1.0
## 76            0.41          0.80  0.200  0.205  0.400   0.5
## 77            0.13          0.24  0.120  0.130  0.240   1.0
## 78            0.33          0.78  0.310  0.330  0.780   1.0
## 79            0.31          0.67  0.290  0.310  0.670   1.0
## 80            0.19          0.49  0.180  0.190  0.490   1.0
## 81            0.25          0.54  0.240  0.250  0.540   1.0
## 82            0.38          0.86  0.360  0.380  0.860   1.0
## 83            0.23          0.56  0.210  0.230  0.560   1.0
## 84            0.09          0.24  0.090  0.090  0.240   1.0
## 85            0.24          0.55  0.230  0.240  0.550   1.0
```

```
## 86                  0.28               0.59  0.216  0.224  0.472     0.8
## 87                  0.09               0.20  0.072  0.081  0.180     0.9
## 88                  0.21               0.43  0.200  0.210  0.430     1.0
## 89                  0.32               0.72  0.310  0.320  0.720     1.0
## 90                  0.23               0.53  0.220  0.230  0.530     1.0
## 91                  0.07               0.18  0.060  0.070  0.180     1.0
## 92                  0.02               0.10  0.020  0.020  0.100     1.0
## 93                  0.03               0.11  0.030  0.030  0.110     1.0
## 94                  0.22               0.52  0.210  0.220  0.520     1.0
##     ChlorophyllA ChlorophyllB FinalpH     ChlSource relative_chl
## 1            NA           NA   7.47 Chl_Chem_Arnon     12.44040
## 2            NA           NA   7.51 Chl_Chem_Arnon      3.86460
## 3            NA           NA   7.55 Chl_Chem_Arnon      6.31820
## 4            NA           NA   7.45 Chl_Chem_Arnon      9.49960
## 5            NA           NA   7.50 Chl_Chem_Arnon     16.90800
## 6            NA           NA   7.54 Chl_Chem_Arnon     11.47200
## 7            NA           NA   7.46 Chl_Chem_Arnon     11.99480
## 8            NA           NA   7.45 Chl_Chem_Arnon     11.31160
## 9            NA           NA   7.54 Chl_Chem_Arnon      7.44700
## 10           NA           NA   7.44 Chl_Chem_Arnon     15.58020
## 11           NA           NA   7.38 Chl_Chem_Arnon      8.13320
## 12           NA           NA   7.46 Chl_Chem_Arnon     15.25940
## 13           NA           NA   7.58 Chl_Chem_Arnon     10.82740
## 14           NA           NA   7.49 Chl_Chem_Arnon      3.82300
## 15           NA           NA   7.44 Chl_Chem_Arnon     14.89400
## 16           NA           NA   7.41 Chl_Chem_Arnon     11.51360
## 17           NA           NA   7.46 Chl_Chem_Arnon      5.15080
## 18           NA           NA   7.53 Chl_Chem_Arnon      1.93080
## 19           NA           NA   7.54 Chl_Chem_Arnon      3.05960
## 20           NA           NA   7.45 Chl_Chem_Arnon     11.43340
## 21           NA           NA   7.56 Chl_Chem_Arnon      4.34880
## 22           NA           NA   7.49 Chl_Chem_Arnon     14.20398
## 23           NA           NA   7.54 Chl_Chem_Arnon      6.23800
## 24           NA           NA   7.51 Chl_Chem_Arnon     15.25640
## 25           NA           NA   7.44 Chl_Chem_Arnon     12.39880
## 26           NA           NA   7.41 Chl_Chem_Arnon     10.58680
## 27           NA           NA   7.53 Chl_Chem_Arnon      8.13020
## 28           NA           NA   7.47 Chl_Chem_Arnon     12.96320
## 29           NA           NA   7.51 Chl_Chem_Arnon     10.10260
## 30           NA           NA   7.36 Chl_Chem_Arnon     14.91184
## 31           NA           NA   7.39 Chl_Chem_Arnon     14.29100
## 32           NA           NA   7.51 Chl_Chem_Arnon     10.10560
## 33           NA           NA   7.43 Chl_Chem_Arnon     13.84840
## 34           NA           NA   7.39 Chl_Chem_Arnon     14.69500
## 35           NA           NA   7.46 Chl_Chem_Arnon     14.73660
## 36           NA           NA   7.47 Chl_Chem_Arnon     14.77520
## 37           NA           NA   6.65 Chl_Chem_Arnon      1.77040
## 38           NA           NA   7.17 Chl_Chem_Arnon      4.18840
## 39           NA           NA   7.52 Chl_Chem_Arnon      4.34880
## 40           NA           NA   7.61 Chl_Chem_Arnon      4.54780
## 41           NA           NA   7.54 Chl_Chem_Arnon      8.89660
## 42           NA           NA   7.56 Chl_Chem_Arnon      1.89220
## 43           NA           NA   7.59 Chl_Chem_Arnon      3.13980
## 44           NA           NA   7.49 Chl_Chem_Arnon      0.80500
```

```
## 45        NA           NA    7.62 Chl_Chem_Arnon   17.02980
## 46        NA           NA    7.50 Chl_Chem_Arnon    9.78180
## 47        NA           NA    7.60 Chl_Chem_Arnon    3.86460
## 48        NA           NA    7.58 Chl_Chem_Arnon    2.45360
## 49        NA           NA    7.10 Chl_Chem_Arnon   15.98120
## 50        NA           NA    7.07 Chl_Chem_Arnon   12.23840
## 51        NA           NA    6.67 Chl_Chem_Arnon   14.89400
## 52        NA           NA    5.84 Chl_Chem_Arnon    7.60740
## 53        NA           NA    7.18 Chl_Chem_Arnon   15.98120
## 54        NA           NA    6.93 Chl_Chem_Arnon   15.13460
## 55        NA           NA    6.11 Chl_Chem_Arnon   14.81380
## 56        NA           NA    5.76 Chl_Chem_Arnon   10.22740
## 57        NA           NA    6.33 Chl_Chem_Arnon   14.73360
## 58        NA           NA    6.39 Chl_Chem_Arnon   23.51140
## 59        NA           NA    7.28 Chl_Chem_Arnon    4.22400
## 60        NA           NA    7.36 Chl_Chem_Arnon    4.22700
## 61        NA           NA    6.49 Chl_Chem_Arnon    9.05700
## 62        NA           NA    6.59 Chl_Chem_Arnon    8.36784
## 63        NA           NA    6.93 Chl_Chem_Arnon    1.12580
## 64        NA           NA    7.19 Chl_Chem_Arnon    1.32780
## 65        NA           NA    7.33 Chl_Chem_Arnon    9.31158
## 66        NA           NA    6.76 Chl_Chem_Arnon    7.04600
## 67        NA           NA    6.73 Chl_Chem_Arnon    4.78840
## 68        NA           NA    7.08 Chl_Chem_Arnon   11.63240
## 69        NA           NA    7.28 Chl_Chem_Arnon    5.55480
## 70        NA           NA    7.04 Chl_Chem_Arnon    7.72920
## 71        NA           NA    5.34 Chl_Chem_Arnon    7.40540
## 72        NA           NA    7.02 Chl_Chem_Arnon    5.91720
## 73        NA           NA    7.15 Chl_Chem_Arnon   11.51360
## 74        NA           NA    6.79 Chl_Chem_Arnon   12.23840
## 75        NA           NA    6.66 Chl_Chem_Arnon    4.38740
## 76        NA           NA    7.39 Chl_Chem_Arnon    7.24800
## 77        NA           NA    6.64 Chl_Chem_Arnon    4.34880
## 78        NA           NA    7.09 Chl_Chem_Arnon   12.51760
## 79        NA           NA    6.92 Chl_Chem_Arnon   11.23140
## 80        NA           NA    4.98 Chl_Chem_Arnon    7.56580
## 81        NA           NA    5.13 Chl_Chem_Arnon    9.17880
## 82        NA           NA    6.75 Chl_Chem_Arnon   14.16920
## 83        NA           NA    7.24 Chl_Chem_Arnon    8.73320
## 84        NA           NA    4.91 Chl_Chem_Arnon    3.74280
## 85        NA           NA    6.87 Chl_Chem_Arnon    9.05700
## 86        NA           NA    6.30 Chl_Chem_Arnon    8.14864
## 87        NA           NA    6.24 Chl_Chem_Arnon    2.89800
## 88        NA           NA    6.50 Chl_Chem_Arnon    7.48860
## 89        NA           NA    6.72 Chl_Chem_Arnon   12.03640
## 90        NA           NA    6.64 Chl_Chem_Arnon    8.69460
## 91        NA           NA    6.52 Chl_Chem_Arnon    2.65560
## 92        NA           NA    6.59 Chl_Chem_Arnon    1.20600
## 93        NA           NA    7.07 Chl_Chem_Arnon    1.48820
## 94        NA           NA    5.41 Chl_Chem_Arnon    8.41240
##                          chl_perSqMill        chl  dig.chl
## 1  Chl_Chem_Arnon_ngPerSquareMillm  8707.8460 1180.589
## 2  Chl_Chem_Arnon_ngPerSquareMillm  2802.1301  142.418
## 3  Chl_Chem_Arnon_ngPerSquareMillm  4463.5723  588.507
```

```
## 4  Chl_Chem_Arnon_ngPerSquareMillm  6662.7913 1143.303
## 5  Chl_Chem_Arnon_ngPerSquareMillm 11914.2079 1417.862
## 6  Chl_Chem_Arnon_ngPerSquareMillm  8163.1960 1016.298
## 7  Chl_Chem_Arnon_ngPerSquareMillm  8516.0397 1138.089
## 8  Chl_Chem_Arnon_ngPerSquareMillm  8060.4198 1144.063
## 9  Chl_Chem_Arnon_ngPerSquareMillm  5258.2897  877.566
## 10 Chl_Chem_Arnon_ngPerSquareMillm 10862.5500  735.656
## 11 Chl_Chem_Arnon_ngPerSquareMillm  5604.2603  943.735
## 12 Chl_Chem_Arnon_ngPerSquareMillm 10656.9976 1135.953
## 13 Chl_Chem_Arnon_ngPerSquareMillm  7714.4492  989.773
## 14 Chl_Chem_Arnon_ngPerSquareMillm  2757.6151  196.006
## 15 Chl_Chem_Arnon_ngPerSquareMillm 10516.5794 1042.858
## 16 Chl_Chem_Arnon_ngPerSquareMillm  8060.4198 1134.488
## 17 Chl_Chem_Arnon_ngPerSquareMillm  3661.9818  587.132
## 18 Chl_Chem_Arnon_ngPerSquareMillm  1308.5985  181.670
## 19 Chl_Chem_Arnon_ngPerSquareMillm  2103.3159  204.928
## 20 Chl_Chem_Arnon_ngPerSquareMillm  8009.0317 1123.632
## 21 Chl_Chem_Arnon_ngPerSquareMillm  3148.1008  253.272
## 22 Chl_Chem_Arnon_ngPerSquareMillm  9908.8571  952.713
## 23 Chl_Chem_Arnon_ngPerSquareMillm  4412.1842  485.929
## 24 Chl_Chem_Arnon_ngPerSquareMillm 10766.6468 1048.696
## 25 Chl_Chem_Arnon_ngPerSquareMillm  8663.3310 1076.474
## 26 Chl_Chem_Arnon_ngPerSquareMillm  7560.2849 1136.319
## 27 Chl_Chem_Arnon_ngPerSquareMillm  5713.9096  992.504
## 28 Chl_Chem_Arnon_ngPerSquareMillm  9207.9809 1270.165
## 29 Chl_Chem_Arnon_ngPerSquareMillm  7214.3143  828.085
## 30 Chl_Chem_Arnon_ngPerSquareMillm 10490.5257  974.839
## 31 Chl_Chem_Arnon_ngPerSquareMillm 10112.3476  793.915
## 32 Chl_Chem_Arnon_ngPerSquareMillm  7104.6650  617.725
## 33 Chl_Chem_Arnon_ngPerSquareMillm  9810.8920  981.841
## 34 Chl_Chem_Arnon_ngPerSquareMillm 10259.6388 1127.208
## 35 Chl_Chem_Arnon_ngPerSquareMillm 10304.1539 1525.224
## 36 Chl_Chem_Arnon_ngPerSquareMillm 10311.0270  973.135
## 37 Chl_Chem_Arnon_ngPerSquareMillm  1353.1135  146.843
## 38 Chl_Chem_Arnon_ngPerSquareMillm  2898.0333  147.320
## 39 Chl_Chem_Arnon_ngPerSquareMillm  3000.8095  260.796
## 40 Chl_Chem_Arnon_ngPerSquareMillm  3257.7500  197.593
## 41 Chl_Chem_Arnon_ngPerSquareMillm  6258.5595  889.677
## 42 Chl_Chem_Arnon_ngPerSquareMillm  1301.7254  120.989
## 43 Chl_Chem_Arnon_ngPerSquareMillm  2154.7040  169.459
## 44 Chl_Chem_Arnon_ngPerSquareMillm   551.5230   85.574
## 45 Chl_Chem_Arnon_ngPerSquareMillm 11862.8198  456.400
## 46 Chl_Chem_Arnon_ngPerSquareMillm  6861.4706  797.425
## 47 Chl_Chem_Arnon_ngPerSquareMillm  2802.1301  170.111
## 48 Chl_Chem_Arnon_ngPerSquareMillm  1808.7334  189.849
## 49 Chl_Chem_Arnon_ngPerSquareMillm 11266.7818 1081.829
## 50 Chl_Chem_Arnon_ngPerSquareMillm  8560.5547 1131.232
## 51 Chl_Chem_Arnon_ngPerSquareMillm 10516.5794  985.416
## 52 Chl_Chem_Arnon_ngPerSquareMillm  5361.0659  995.133
## 53 Chl_Chem_Arnon_ngPerSquareMillm 11266.7818 1201.098
## 54 Chl_Chem_Arnon_ngPerSquareMillm 10670.7437 1466.543
## 55 Chl_Chem_Arnon_ngPerSquareMillm 10465.1913 1128.730
## 56 Chl_Chem_Arnon_ngPerSquareMillm  7200.5682  977.741
## 57 Chl_Chem_Arnon_ngPerSquareMillm 10266.5119 1090.271
```

```
## 58 Chl_Chem_Arnon_ngPerSquareMillm 16466.8103 1256.168
## 59 Chl_Chem_Arnon_ngPerSquareMillm  3014.5556  126.845
## 60 Chl_Chem_Arnon_ngPerSquareMillm  3052.1976  121.045
## 61 Chl_Chem_Arnon_ngPerSquareMillm  6361.3357  798.341
## 62 Chl_Chem_Arnon_ngPerSquareMillm  5863.9500  786.717
## 63 Chl_Chem_Arnon_ngPerSquareMillm   904.3667  116.206
## 64 Chl_Chem_Arnon_ngPerSquareMillm   904.3667  107.098
## 65 Chl_Chem_Arnon_ngPerSquareMillm  6532.9464  700.884
## 66 Chl_Chem_Arnon_ngPerSquareMillm  4854.0579  399.120
## 67 Chl_Chem_Arnon_ngPerSquareMillm  3411.9143  352.021
## 68 Chl_Chem_Arnon_ngPerSquareMillm  8265.9722 1087.415
## 69 Chl_Chem_Arnon_ngPerSquareMillm  3956.5643  597.260
## 70 Chl_Chem_Arnon_ngPerSquareMillm  5604.2603  763.795
## 71 Chl_Chem_Arnon_ngPerSquareMillm  5213.7746  621.323
## 72 Chl_Chem_Arnon_ngPerSquareMillm  4206.6317  537.292
## 73 Chl_Chem_Arnon_ngPerSquareMillm  8060.4198 1171.064
## 74 Chl_Chem_Arnon_ngPerSquareMillm  8707.8460 1019.121
## 75 Chl_Chem_Arnon_ngPerSquareMillm  3007.6826  277.418
## 76 Chl_Chem_Arnon_ngPerSquareMillm  5074.9948  957.892
## 77 Chl_Chem_Arnon_ngPerSquareMillm  3148.1008  269.519
## 78 Chl_Chem_Arnon_ngPerSquareMillm  8868.8834 1000.809
## 79 Chl_Chem_Arnon_ngPerSquareMillm  8009.0317 1064.669
## 80 Chl_Chem_Arnon_ngPerSquareMillm  5316.5508  621.491
## 81 Chl_Chem_Arnon_ngPerSquareMillm  6457.2389  887.573
## 82 Chl_Chem_Arnon_ngPerSquareMillm 10016.4445 1068.920
## 83 Chl_Chem_Arnon_ngPerSquareMillm  6265.4326  528.825
## 84 Chl_Chem_Arnon_ngPerSquareMillm  2558.9357  275.559
## 85 Chl_Chem_Arnon_ngPerSquareMillm  6361.3357  880.857
## 86 Chl_Chem_Arnon_ngPerSquareMillm  5724.8425  462.062
## 87 Chl_Chem_Arnon_ngPerSquareMillm  2118.0450  201.495
## 88 Chl_Chem_Arnon_ngPerSquareMillm  5302.8047  142.843
## 89 Chl_Chem_Arnon_ngPerSquareMillm  8413.2635  412.206
## 90 Chl_Chem_Arnon_ngPerSquareMillm  6111.2683  569.367
## 91 Chl_Chem_Arnon_ngPerSquareMillm  1956.0246  138.725
## 92 Chl_Chem_Arnon_ngPerSquareMillm   808.4635  170.577
## 93 Chl_Chem_Arnon_ngPerSquareMillm  1007.1429  160.033
## 94 Chl_Chem_Arnon_ngPerSquareMillm  5912.5889  314.680
```

```r
#Pearson correlations for ES10
cor(ES10.chem.dig$chl, ES10.chem.dig$dig.chl, method="pearson")
```
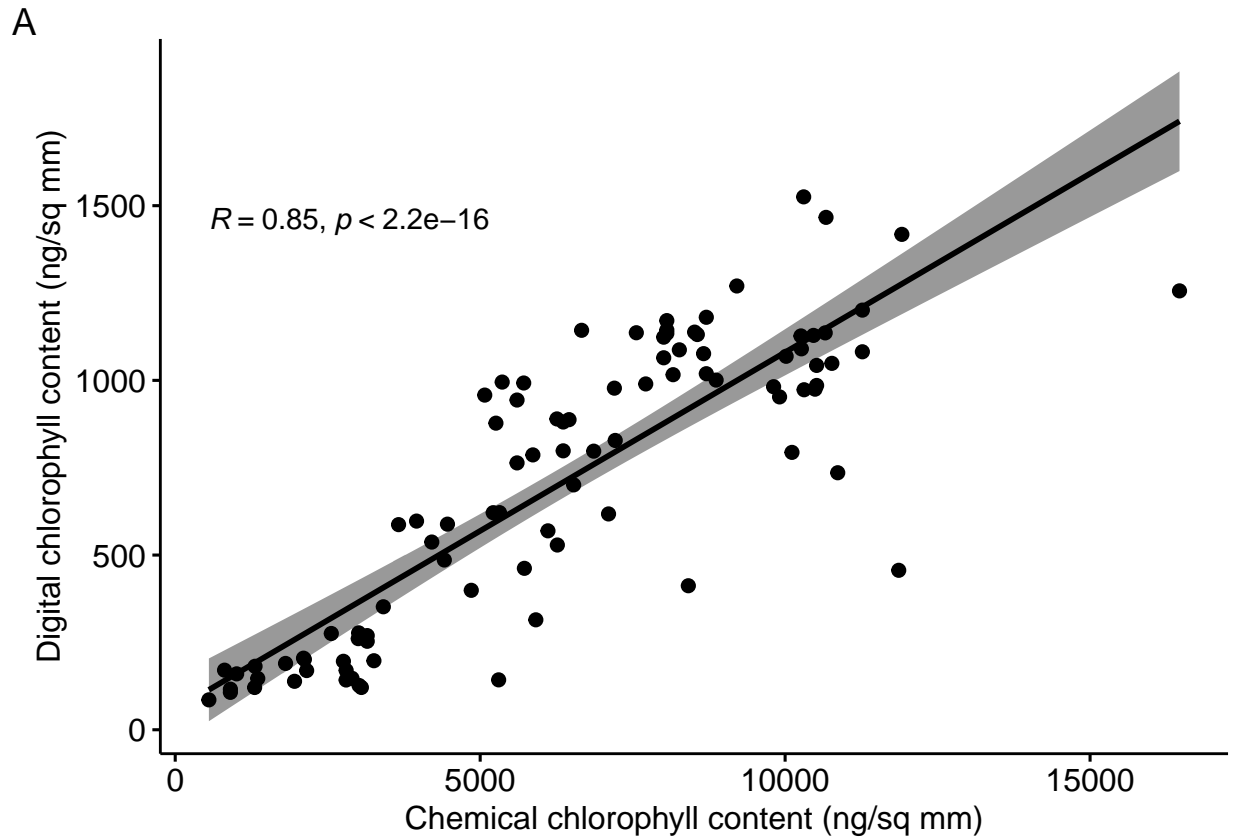
```
## [1] 0.8450695
```

Plotting supplementary figure 1 panel A

```r
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
ES10.chem.dig.ggplot
```

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

A

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

Digital chlorophyll content (ng/sq mm)

Chemical chlorophyll content (ng/sq mm)

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)
  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(s
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
  facet_wrap(~ Condition)
BiomassAndpH.metadata.ggplot.B #+ stat_compare_means(aes(group = Condition), label = "p.signif", na.rm
```

B
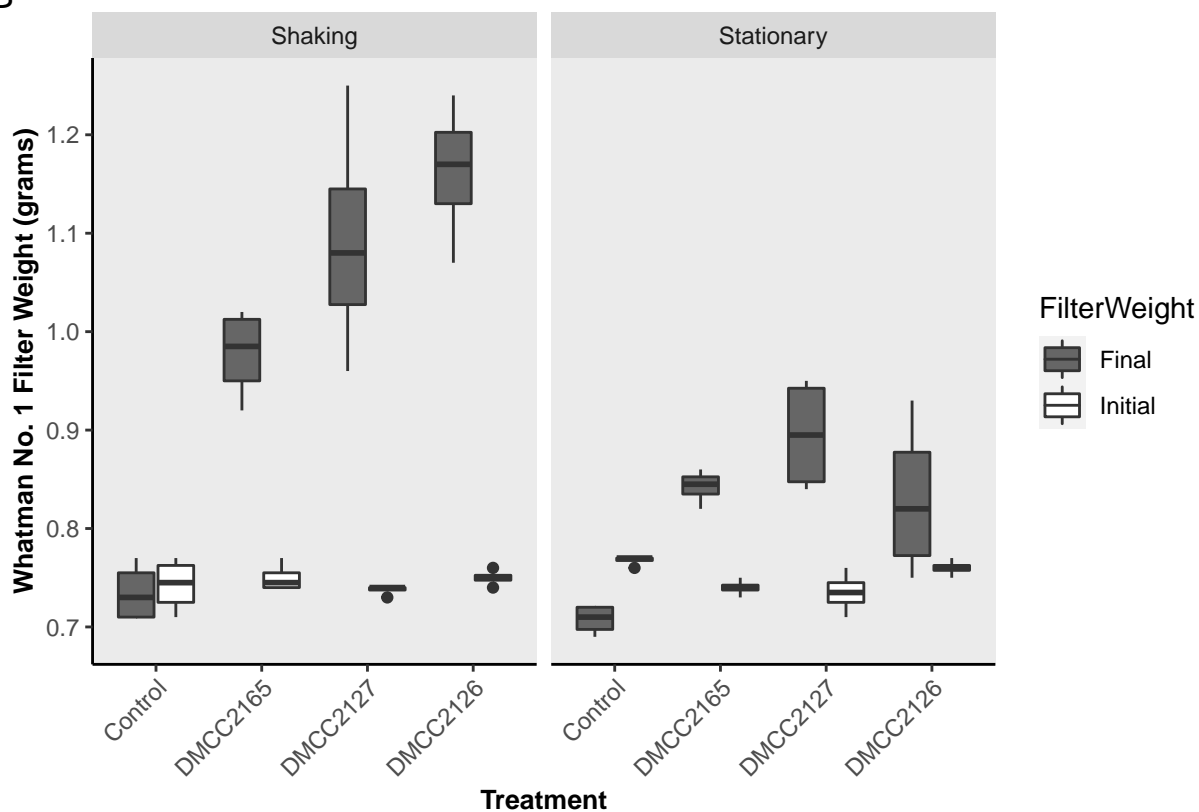
Supplementary figure 2 panel C

```
#ES5 by dilutions (side by side)
BiomassAndpH.metadata.pH.ggplot.C <- ggplot(BiomassAndpH.metadata, aes(x = reorder(Isolate, +pH), y = pl
  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(s:
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_l
  facet_wrap(~ Condition)
BiomassAndpH.metadata.pH.ggplot.C #+ stat_compare_means(aes(group = Condition), label = "p.signif", na.v
```

C
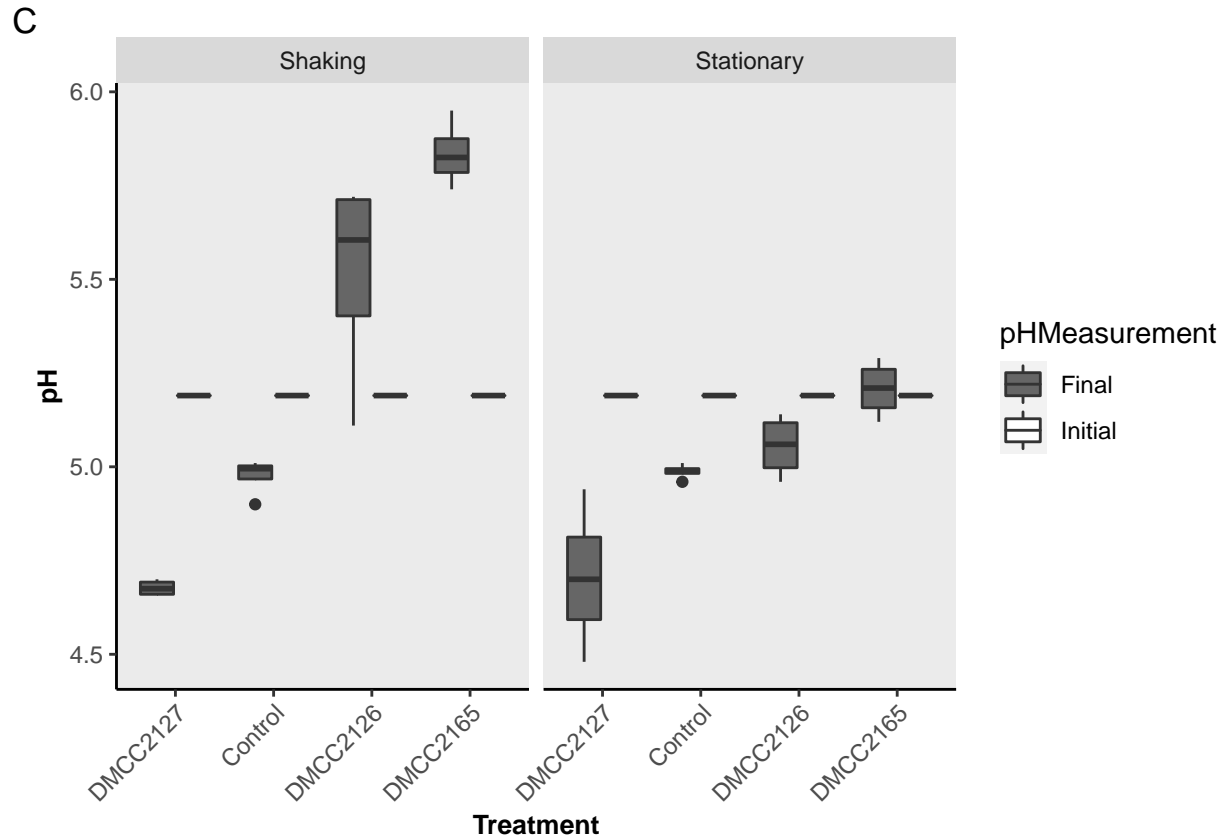
Supplementary figure 2 panel D

```r
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
FinalpHvsChl.reg
```
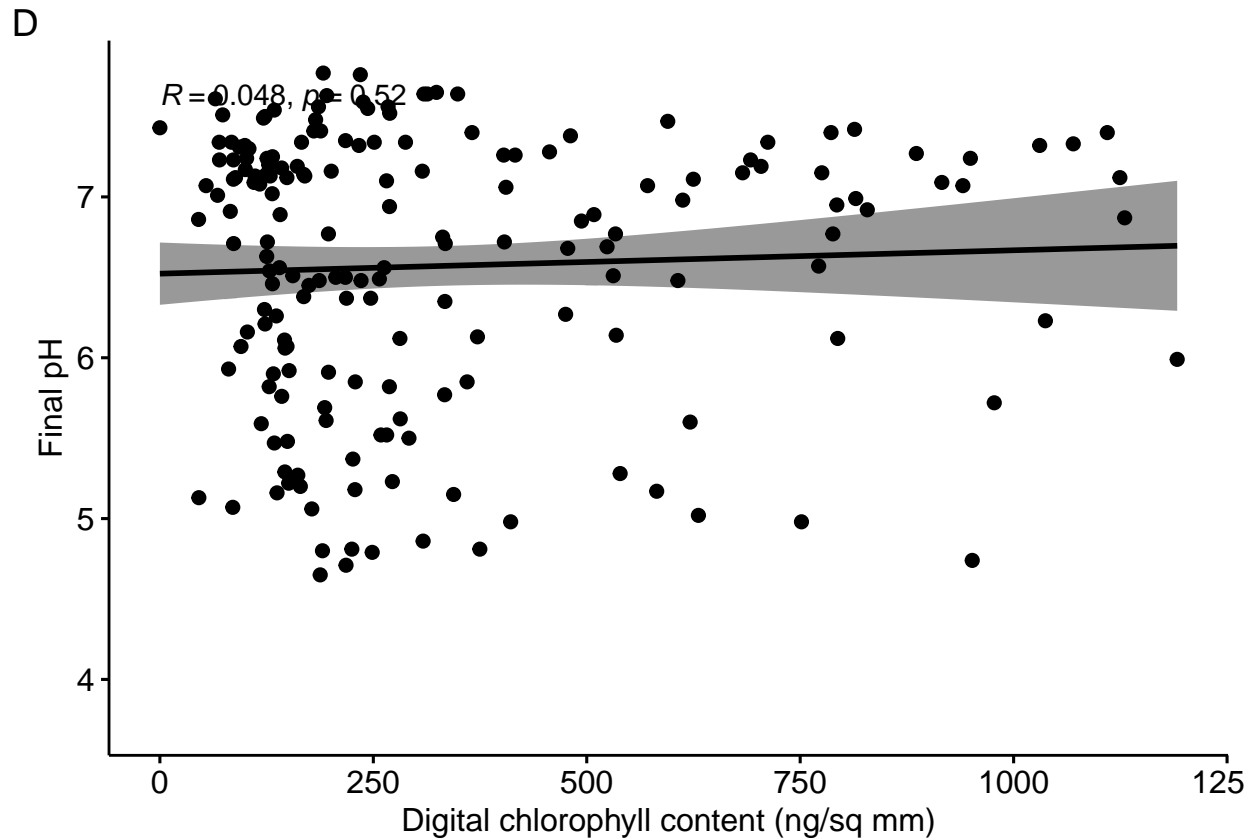
`geom_smooth()` using formula 'y ~ x'

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

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

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

D

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

```
gridExtra::grid.arrange(ES10.chem.dig.ggplot, BiomassAndpH.metadata.ggplot.B, BiomassAndpH.metadata.pH.g
```
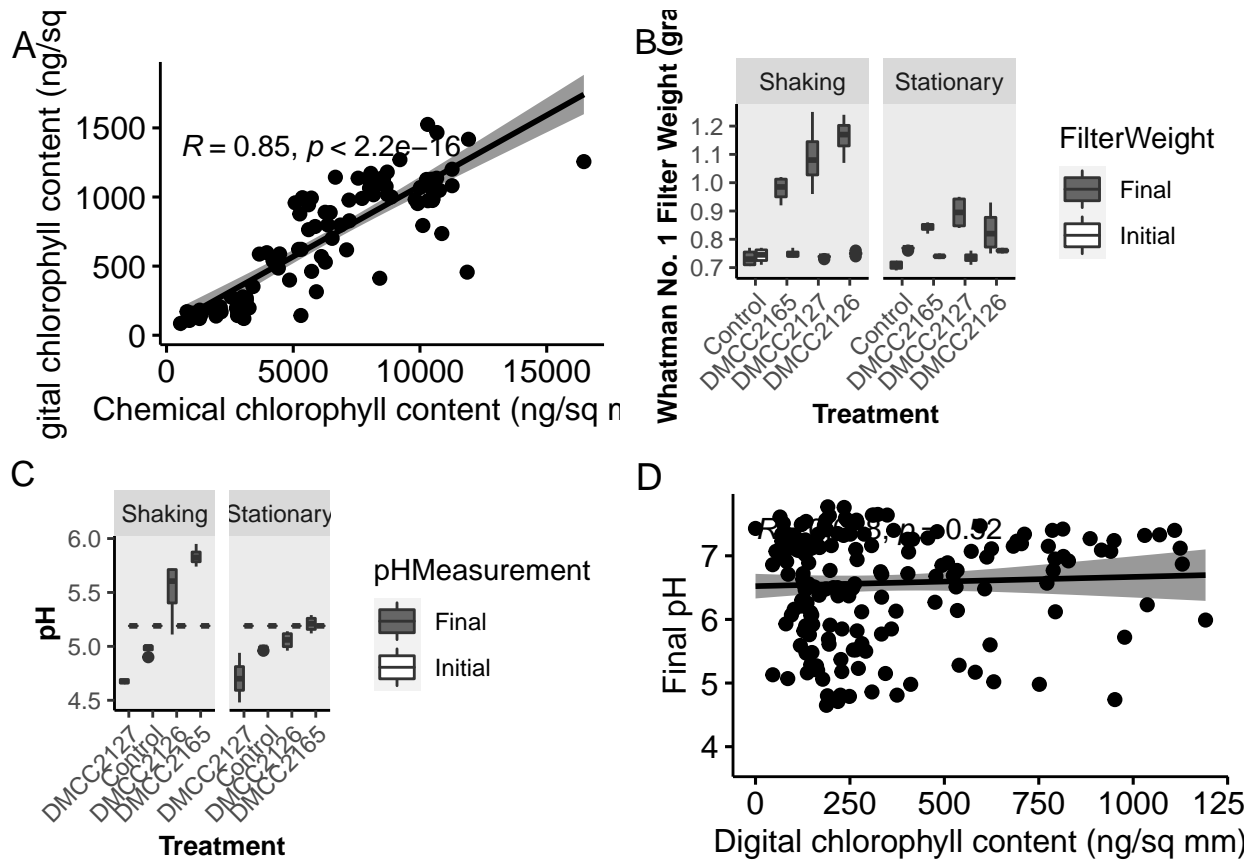
```
## 'geom_smooth()' using formula 'y ~ x'
## 'geom_smooth()' using formula 'y ~ x'
```

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

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

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

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
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
```

```r
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
```

```r
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 ***
## ES2.root.noNAs$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"
```

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

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

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

```
## $statistics
##    MSerror Df     Mean         CV
##    156.086 59 26.46406 47.20907
##
## $parameters
##    test                                              name.t ntr
##    Tukey ES2.root.noNAs$Isolate:ES2.root.noNAs$Concentration   9
##    StudentizedRange alpha
##            4.55324  0.05
```

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

Comparison after normalization of data

```
# 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.no
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$Concent
ES2.root.noNAs.mod.Concentration.HSD.test
```

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

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

#Tukey's HSD for Variable Isolate

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

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

```
## 
## $groups
##          ES2.root.noNAs.mod$ES2.root.tuk groups
## DMCC2966                          10.122508       a
## Control                            7.870193      ab
## DMCC2126                           7.431287      ab
## DMCC2165                           6.279095       b
## DMCC2127                           4.788109       b
## 
## attr(,"class")
## [1] "group"
```
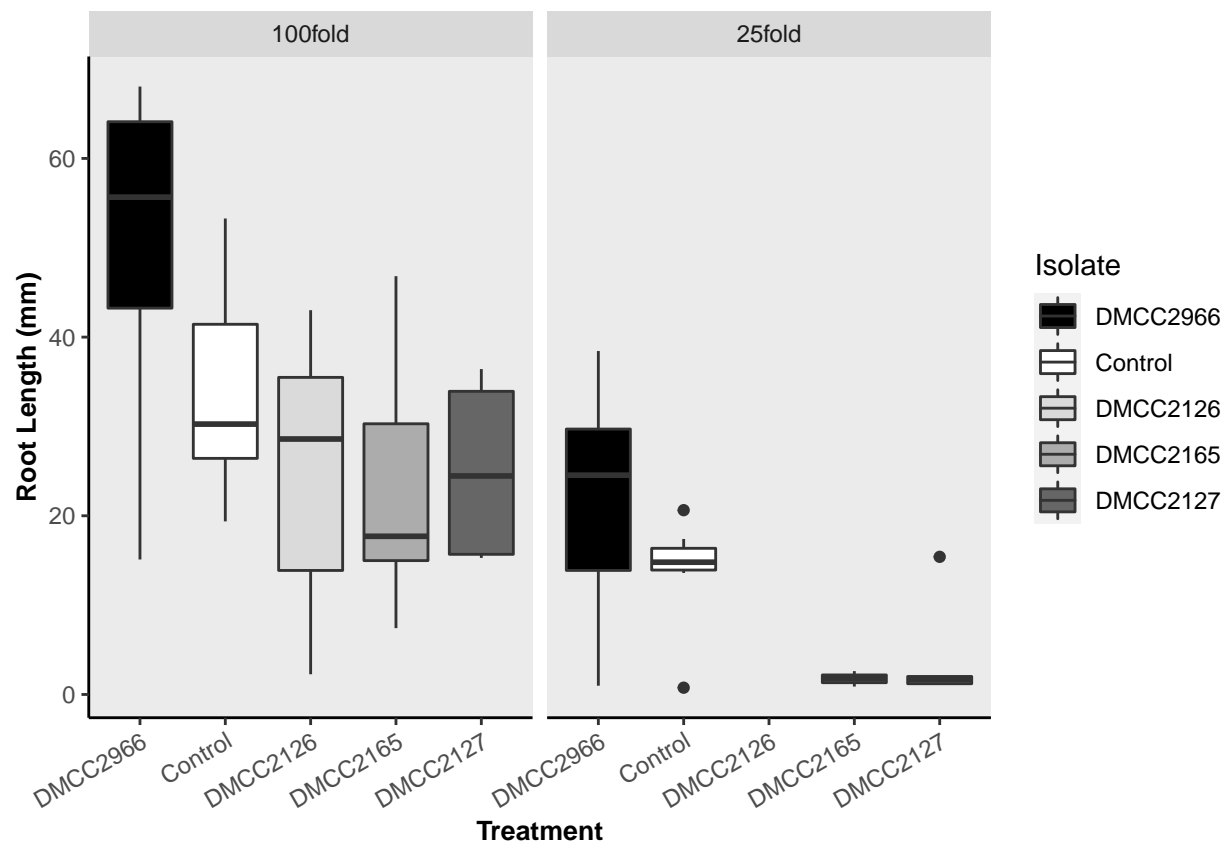
```
#Tukey's HSD for Treatment and concentration
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test <- HSD.test(ES2.root.noNAs.mod.lm, c('ES2.root.noNAs.mod$
ES2.root.noNAs.mod.leafsec.treat.dil.HSD.test
```

```
## $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 obse
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 = Isola
  #scale_fill_grey(start = 1, end = 0.4) +
  #scale_fill_manual(values = c("Control"="green", "DMCC2966"="green", "DMCC2126"="gold", "DMCC2165"="g
  #ggtitle("Root Length at 14 Days After Exposure") +
  scale_fill_manual(values = c("#000000", "#FFFFFF", "#DADADA", "#ACACAC","#666666")) +
  xlab("Treatment") + ylab("Root Length (mm)") + theme(plot.title = element_text(size = 14, hjust = 0.5
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_
  facet_wrap(~ Concentration)
ES2.root.noNAs.mod.ggplot.plate
```

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