

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

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Install packages needed.

We first create a vector of all the packages needed

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

Install packages not yet installed

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

Load all packages

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

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

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

## -----

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

```

## -----

##
## Attaching package: 'plyr'

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

##
## Attaching package: 'ggpubr'

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

## Loading required package: carData

##
## Attaching package: 'car'

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

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

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

## -- Conflicts ----- tidyverse_conflicts() --
## x plyr::arrange() masks dplyr::arrange()
## x purrr::compact() masks plyr::compact()
## x plyr::count() masks dplyr::count()
## x plyr::failwith() masks dplyr::failwith()
## x dplyr::filter() masks stats::filter()
## x plyr::id() masks dplyr::id()
## x dplyr::lag() masks stats::lag()
## x ggpubr::mutate() masks plyr::mutate(), dplyr::mutate()
## x car::recode() masks dplyr::recode()
## x plyr::rename() masks dplyr::rename()
## x purrr::some() masks car::some()
## x plyr::summarise() masks dplyr::summarise()
## x plyr::summarize() masks dplyr::summarize()

##
## Attaching package: 'reshape'

```

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

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

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

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

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

Change directory on mac/linux:

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

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

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

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

Step 1: Call the pdf command to start the plot

```
pdf(file = "/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output/ Figure1.pdf", # T
width = 7, # The width of the plot in inches
height = 5) # The height of the plot in inches
```

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

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

```
dev.off()
```

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

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

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

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

#ES4 = Repetition for 14 DOE

ES5 = First experiment for 7 DOE

#ES8 = Repetition for 7 DOE

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

ES13B = Repetition of ES13A

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

#ES14B = Repetition of ES14A

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

Run Shapiro-Wilk Tests to check for normality

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

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

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

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

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

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

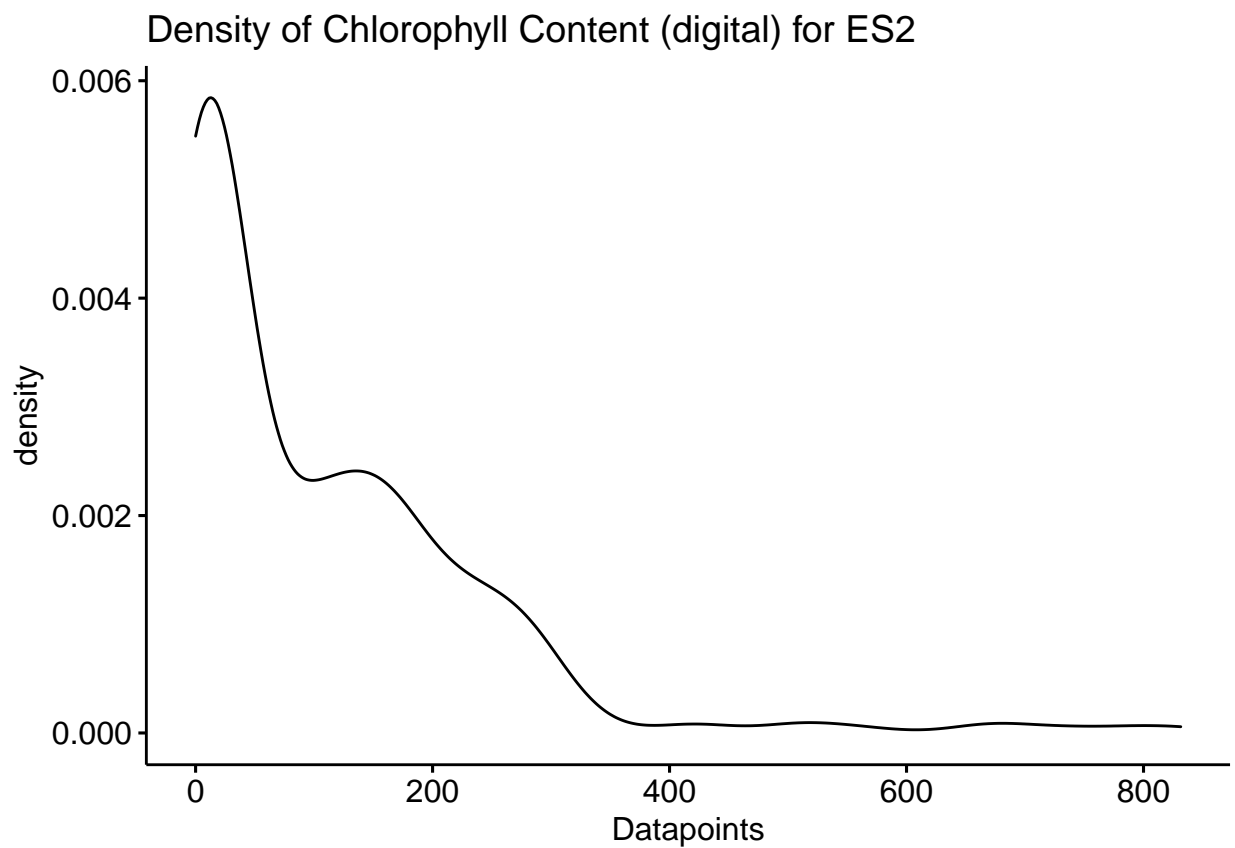
```
shapiro.test(ES14A$chl)
```

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

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

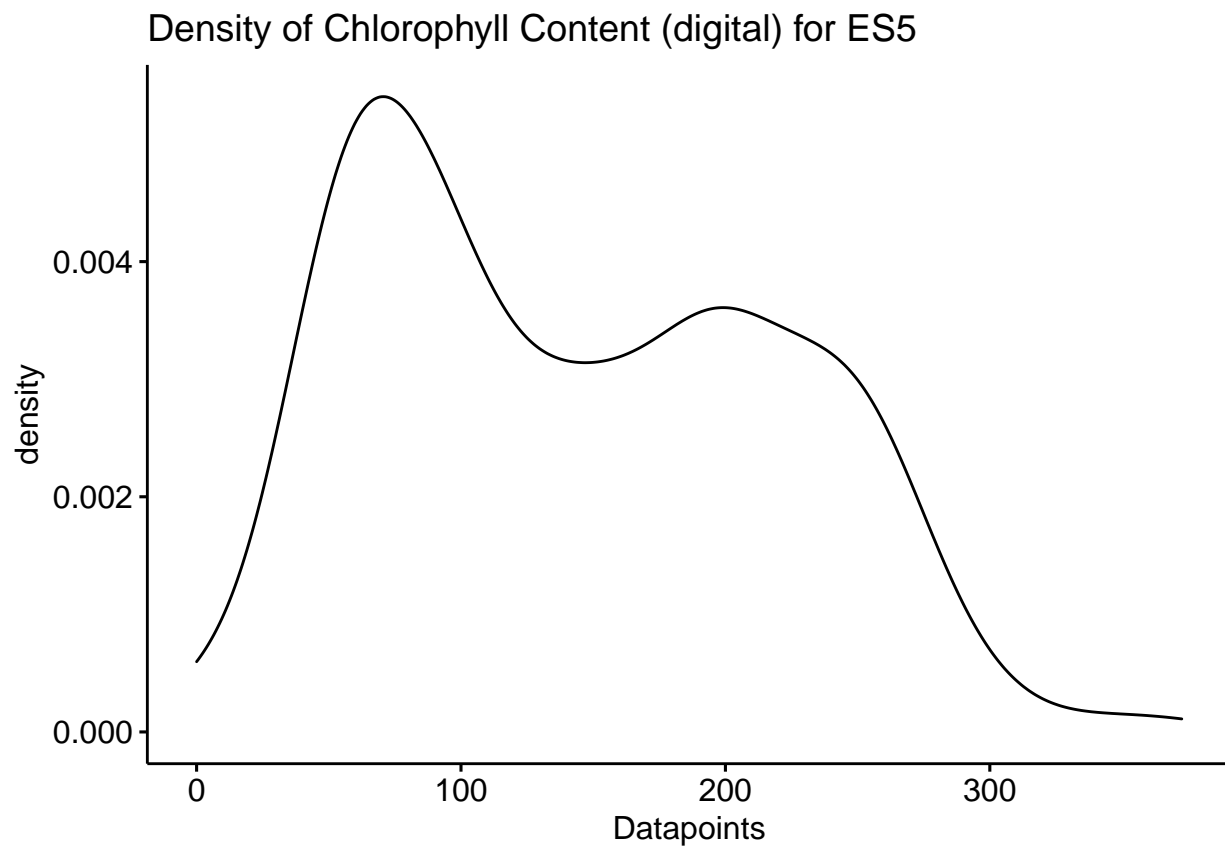
```
ggdensity(ES2$chl, main = "Density of Chlorophyll Content (digital) for ES2", xlab = "Datapoints")
```

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



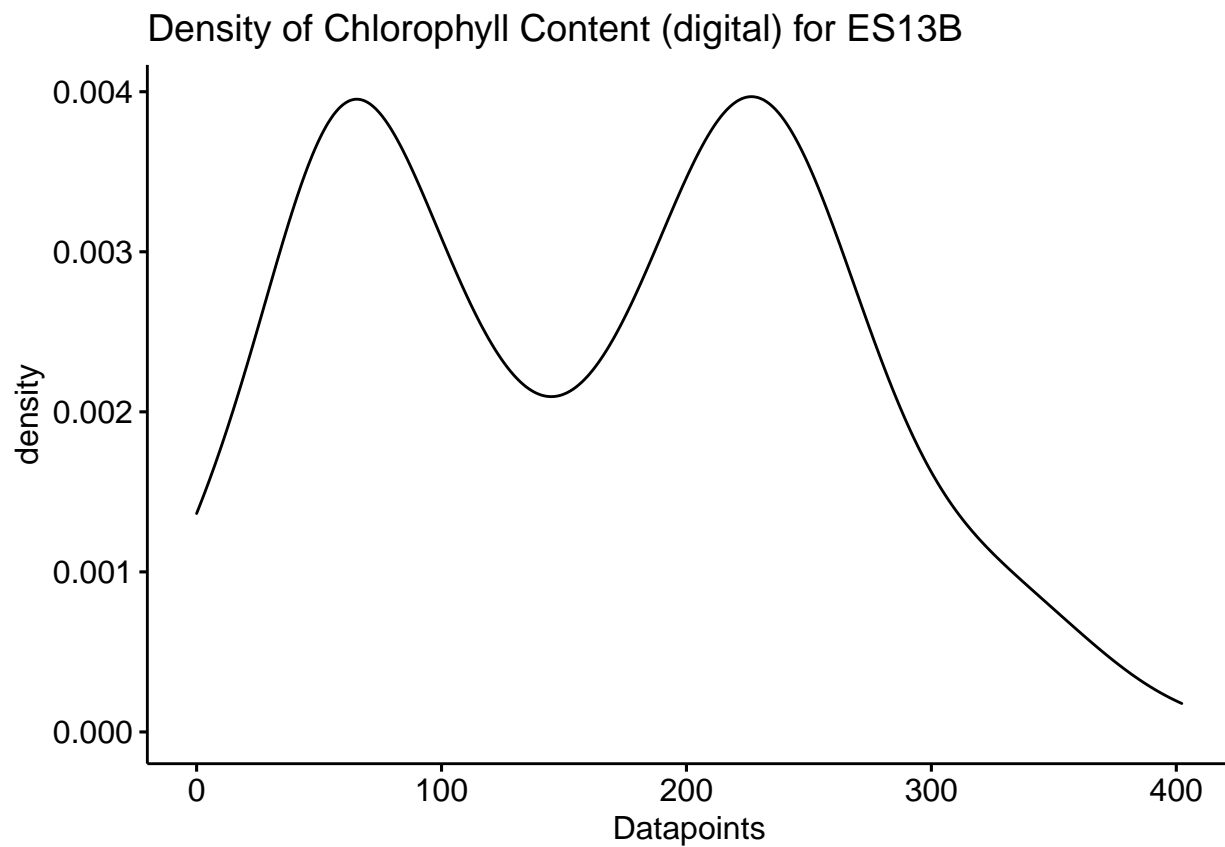
```
ggdensity(ES5$chl, main = "Density of Chlorophyll Content (digital) for ES5", xlab = "Datapoints")
```

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



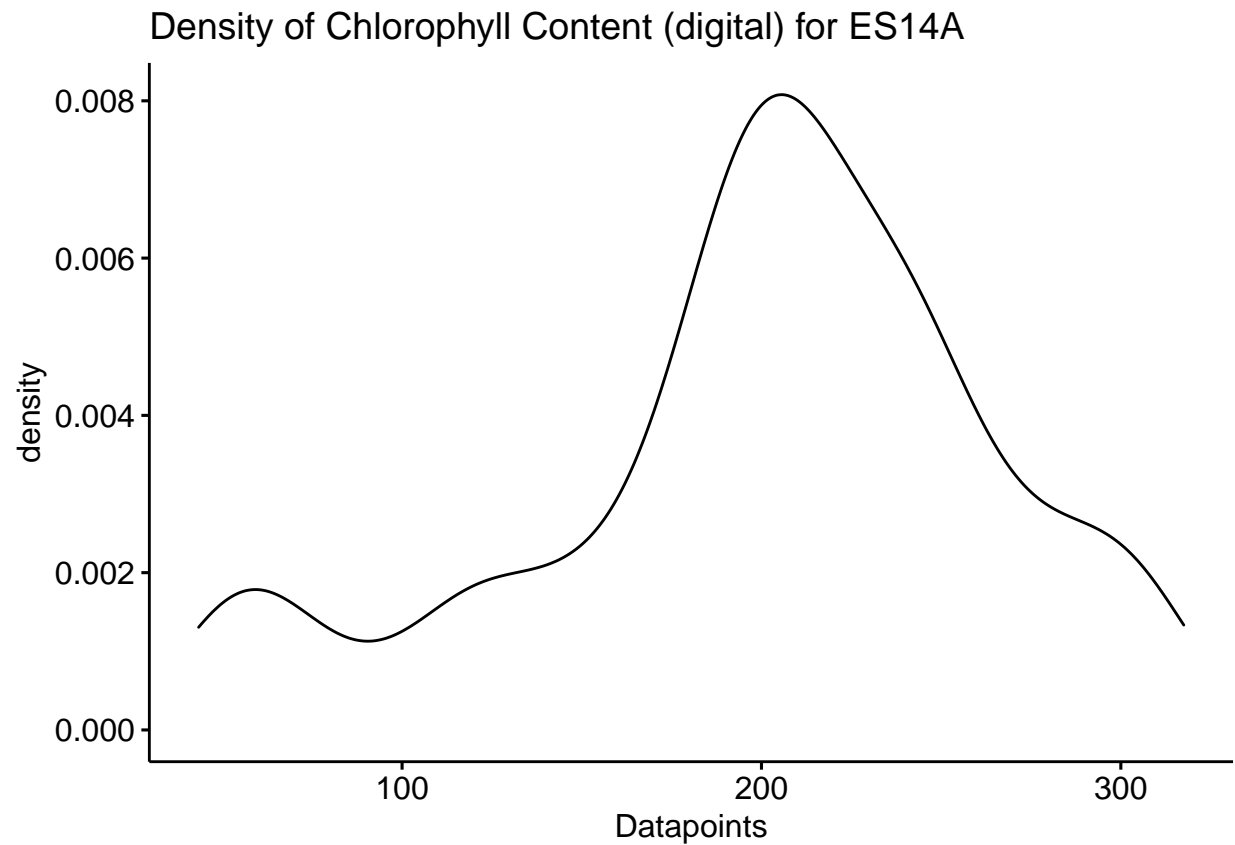
```
ggdensity(ES13B$chl, main = "Density of Chlorophyll Content (digital) for ES13B", xlab = "Datapoints")
```

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



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

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

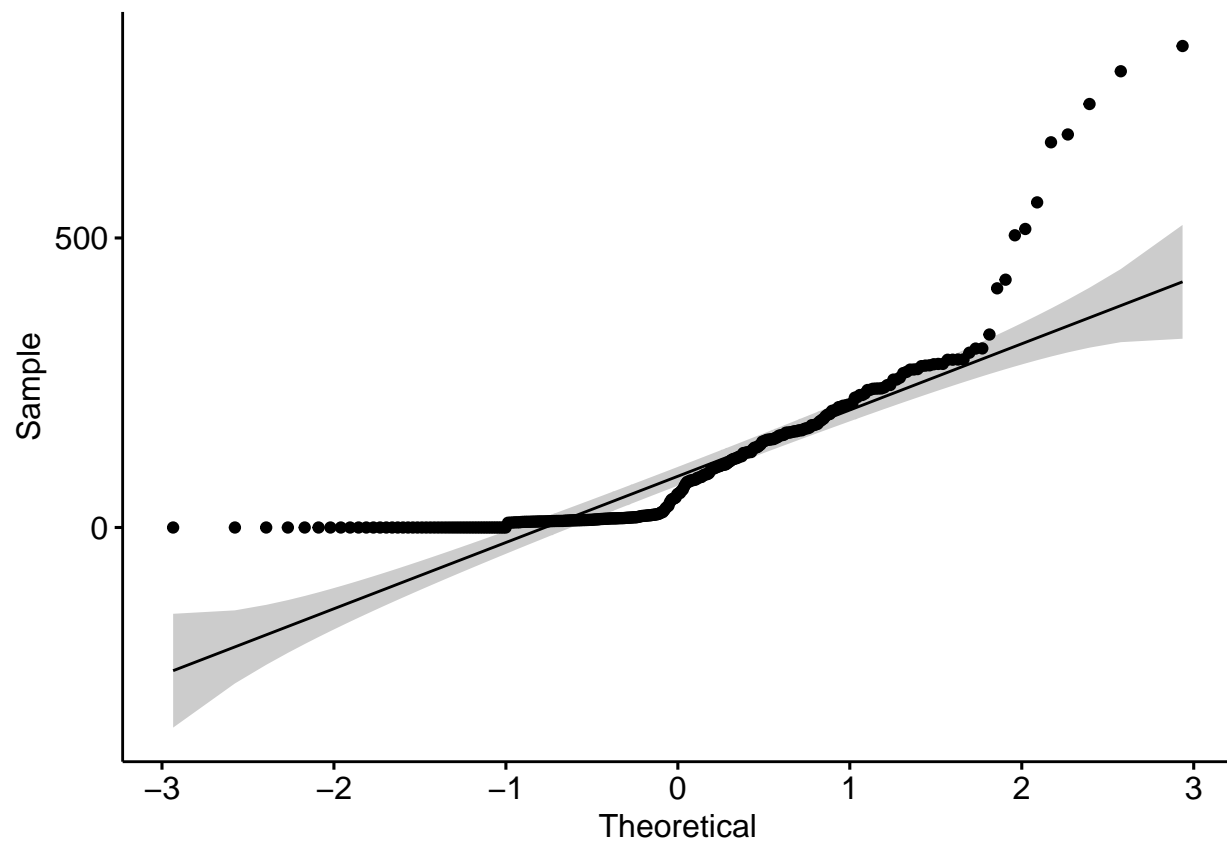


```
ggqqplot(ES2$chl)
```

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

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

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

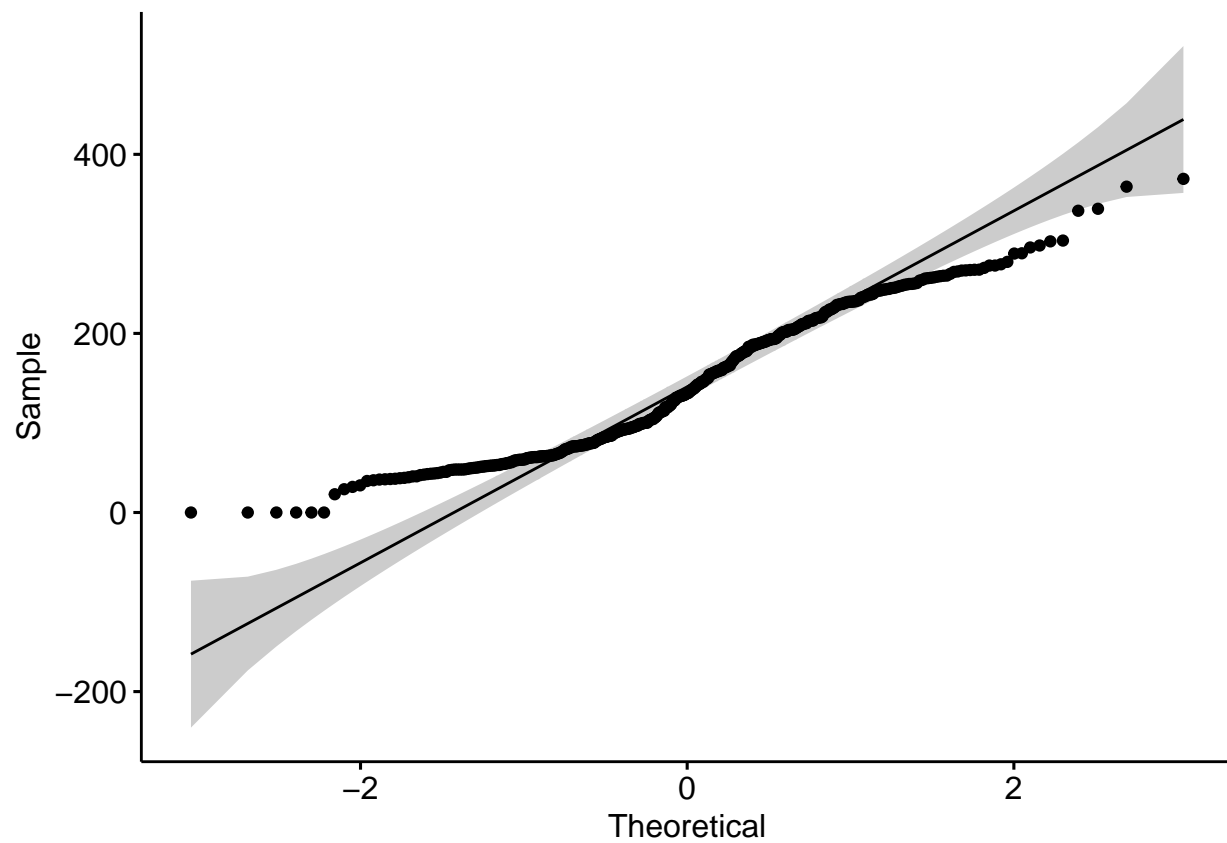



```
ggqqplot(ES5$ch1)
```

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

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

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

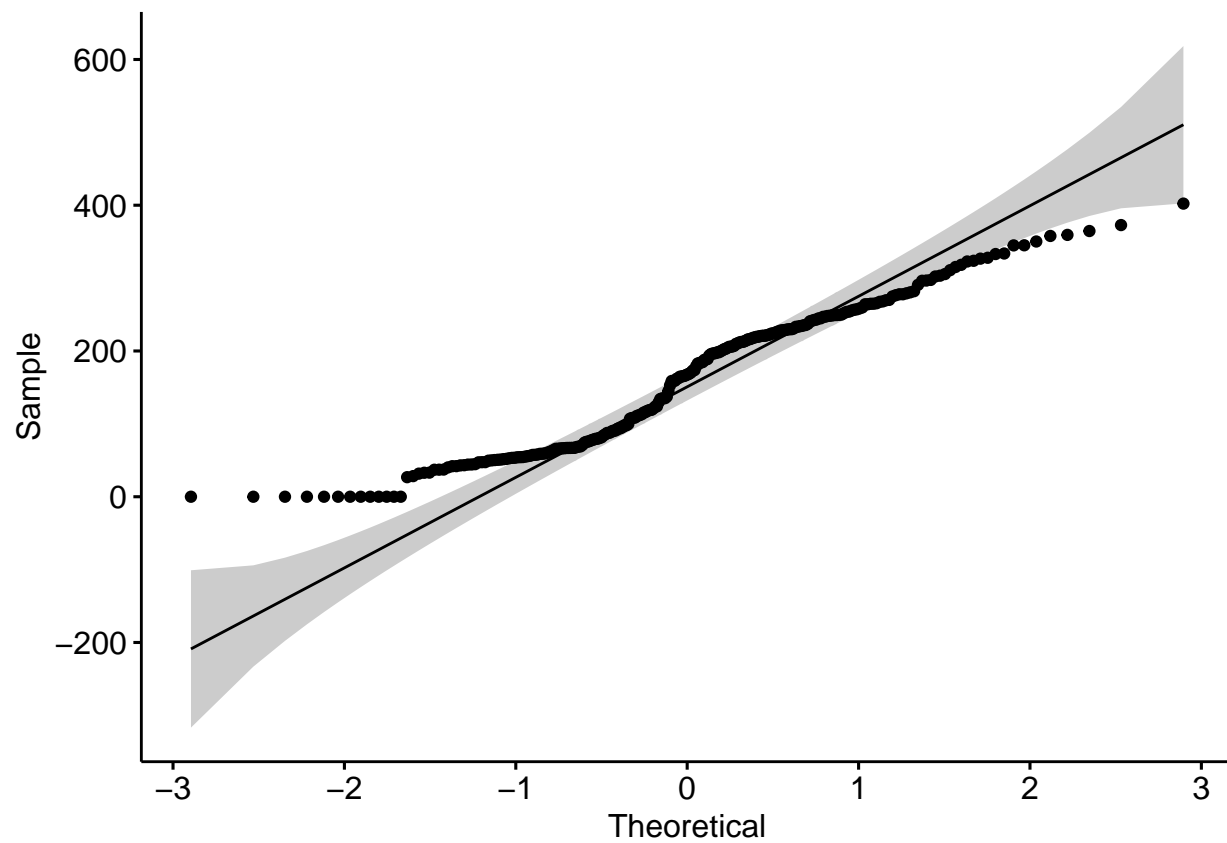


```
ggqqplot(ES13B$chl)
```

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

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

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

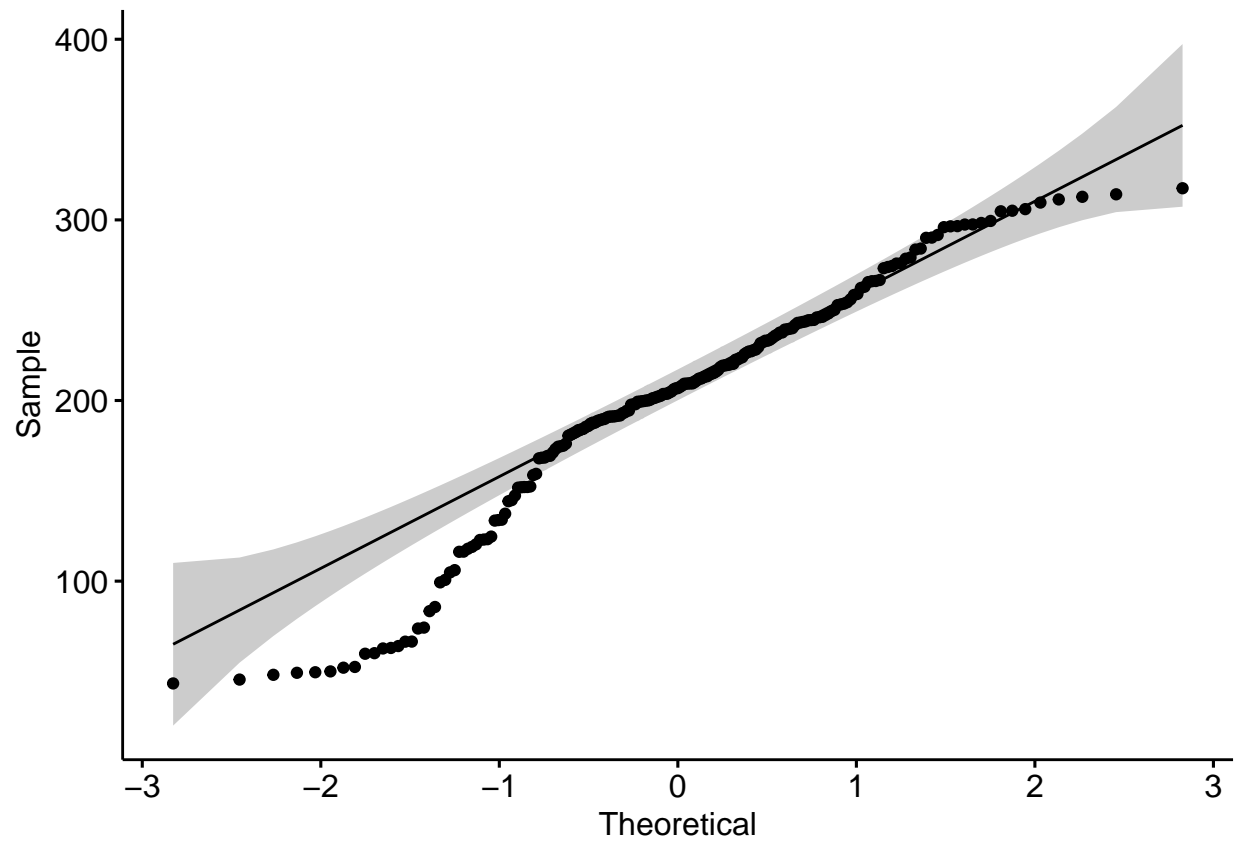


```
ggqqplot(ES14A$chl)
```

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

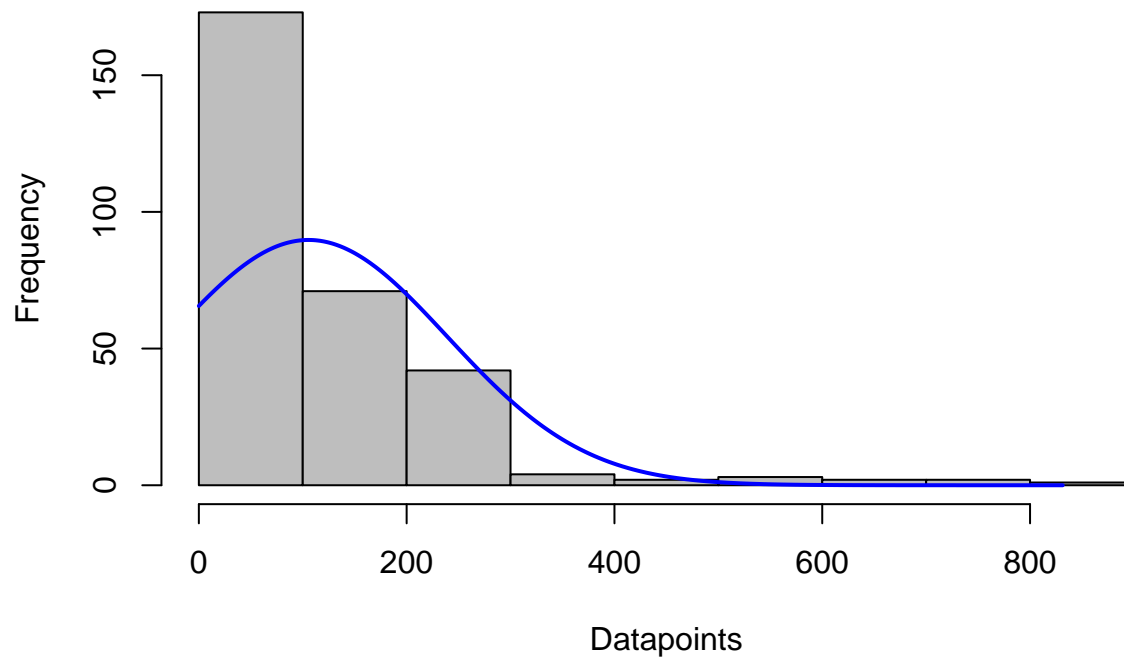
```
## Warning: Removed 3 rows containing non-finite values (stat_qq_line).
```

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



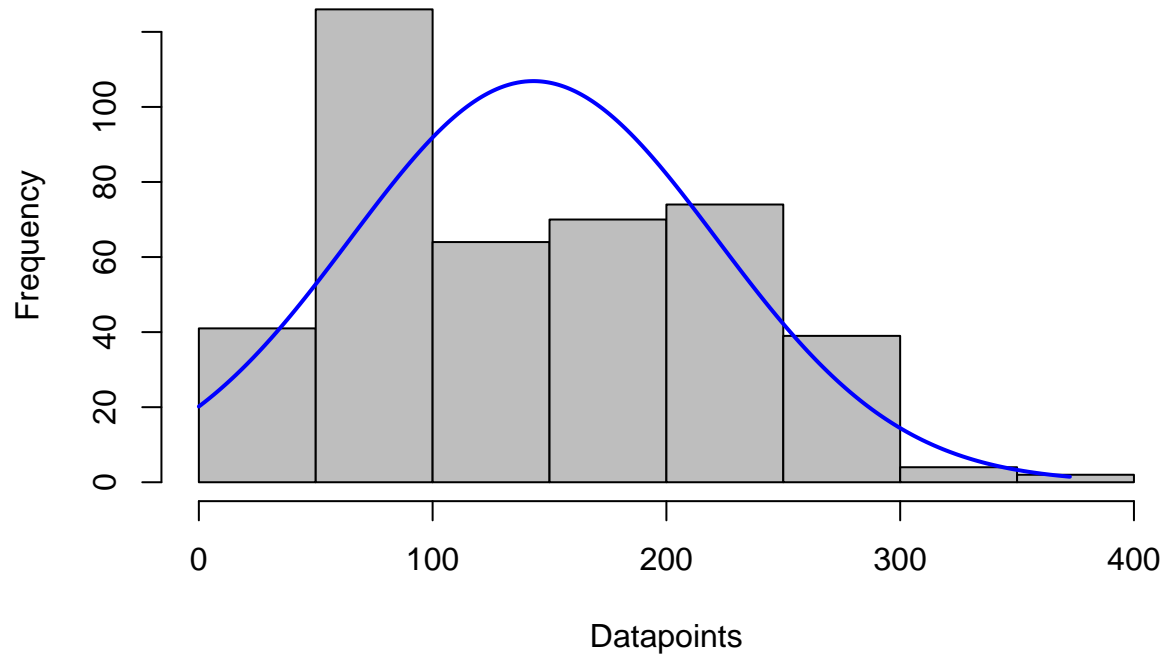
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2", xlab = "Datapoint", ylab = "Density", col = "black", lty = 1, lwd = 2, pch = 1, cex = 1.5, las = 1)
```

Density of Chlorophyll Content (Digital) for ES2



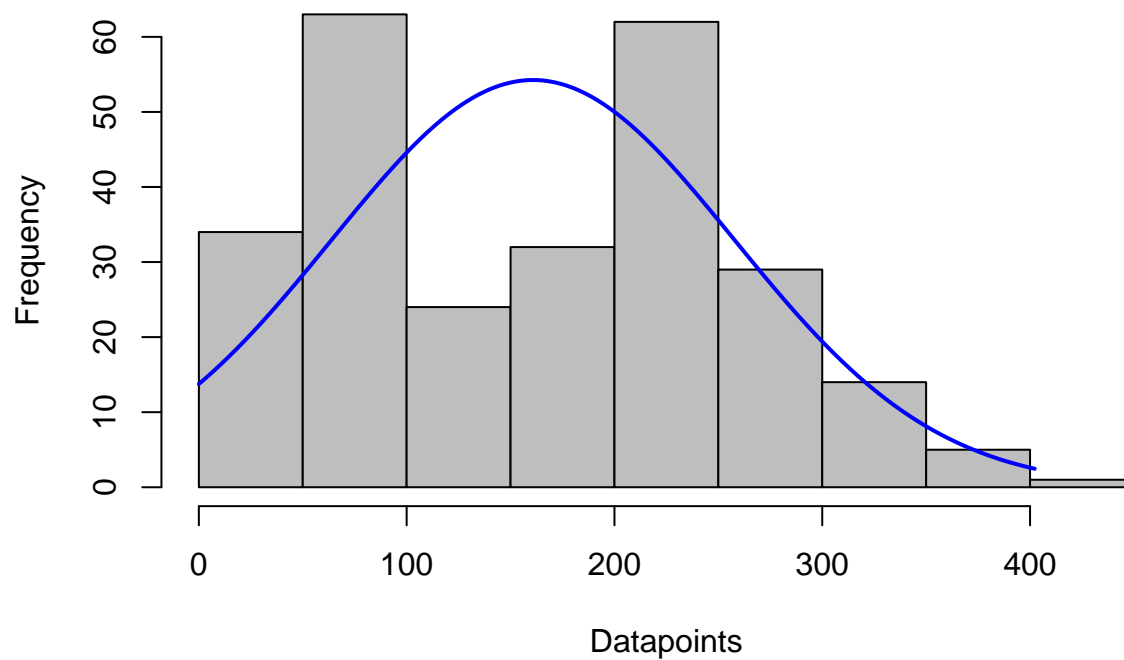
```
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5", xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for ES5



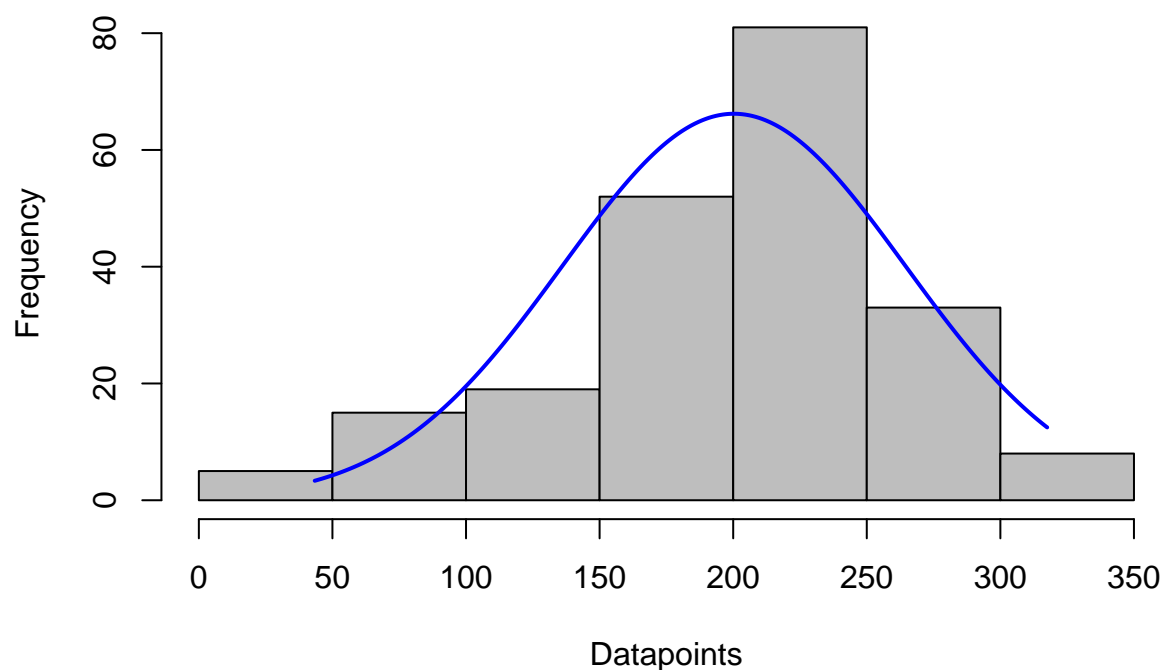
```
plotNormalHistogram(ES13B$chl, main = "Density of Chlorophyll Content (Digital) for E13B", xlab = "Datapoints")
```

Density of Chlorophyll Content (Digital) for E13B



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

Density of Chlorophyll Content (Digital) for E14A



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

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

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

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

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



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

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

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

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

Append the transformed values to original datasets

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

Statistical analyses

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

ES2 dataset (untransformed data)

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

```
#####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
```

```
## 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"
```

```
#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"
```

```
#Complete ANOVA for ES2 by treatment by dilution
```

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

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

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

ES2.comp.HSD.group

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

```

##                               Q75
## control:100fold  527.0058
## control:25fold   129.7670
## DMCC2126:100fold 159.8775
## DMCC2126:25fold   16.5335
## DMCC2127:100fold  90.5650
## DMCC2127:25fold   15.6860
## DMCC2165:100fold 105.9032
## DMCC2165:25fold   14.7740
## DMCC2966:100fold 241.9460
## DMCC2966:25fold   222.5877
##
## $comparison
## NULL
##
## $groups
##                               ES2$chl groups
## control:100fold  383.864000      a
## DMCC2966:100fold 171.013333      b
## DMCC2966:25fold  164.658233      b
## DMCC2126:100fold 127.480933     bc
## control:25fold    78.223485      cd
## DMCC2127:100fold  58.980593      cd
## DMCC2165:100fold  58.801375      cd
## DMCC2127:25fold   16.841111      d
## DMCC2126:25fold   12.999296      d
## DMCC2165:25fold    9.896848      d
##
## attr("class")
## [1] "group"

#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

```

```

## 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_ch1.tuk groups
## control      6.207956      a
## DMCC2966      6.195529      a
## DMCC2126      4.140619      b
## DMCC2127      2.929858      c
## DMCC2165      2.663168      c
##
## attr("class")
## [1] "group"
```

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

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

```
## $statistics
##      MSerror Df      Mean      CV
##      4.787063 276 4.479861 48.83937
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##      Tukey ES2.mod$Dilution 2      2.784016 0.05
##
## $means
##      ES2.mod$ES2_ch1.tuk      std      r Min      Max      Q25      Q50
## 100fold      5.670079 2.877306 138    0 12.443509 3.837417 6.189452
## 25fold      3.384861 2.482893 150    0  8.587655 2.358352 2.806307
##              Q75
## 100fold 7.383524
## 25fold  5.616963
##
## $comparison
## NULL
##
## $groups
##      ES2.mod$ES2_ch1.tuk groups
## 100fold      5.670079      a
## 25fold      3.384861      b
##
## attr("class")
```

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

```
#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 = T)
```

```
##
```

```
## 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_ch1.tuk groups
## control:100fold      8.952842      a
## DMCC2966:25fold      6.285168      b
## DMCC2966:100fold     6.114039      b
## DMCC2126:100fold     5.904452     bc
## control:25fold       4.211675     cd
## DMCC2127:100fold     3.720246     de
## DMCC2165:100fold     3.677465     de
## DMCC2126:25fold      2.180805      e
## DMCC2127:25fold      2.139470      e
## DMCC2165:25fold      1.925497      e

```

ES2.mod.comp.HSD.group

```

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

```

```
## DMCC2966:100fold 6.963949 7.832392
## DMCC2966:25fold 7.032779 7.590879
##
## $comparison
## NULL
##
## $groups
##          ES2.mod$ES2_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.mod$Dilution"))
```

```
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_ch1.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$sampleNumber)
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"

#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=TRUE)

##
## 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

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"
```

```
#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$ES5_ch1.tuk ~ ES5.mod$Treatment + ES5.mod$Dilution +
##     ES5.mod$Condition + ES5.mod$isoRep + ES5.mod$techRep + ES5.mod$sampleNumber)
##
## Coefficients:
##             (Intercept)      ES5.mod$TreatmentDMCC2126
##                   30.278                      -7.067
## ES5.mod$TreatmentDMCC2127      ES5.mod$TreatmentDMCC2165
##                   -8.357                      -7.928
## ES5.mod$Dilution25fold      ES5.mod$ConditionStationary
##                   -5.443                      4.789
## ES5.mod$isoRepisolateRep2      ES5.mod$isoRepisolateRep3
##                   -1.403                      -2.930
## ES5.mod$techRepstemRep2      ES5.mod$techRepstemRep3
##                   -1.392                      2.517
## ES5.mod$sampleNumbersample2      ES5.mod$sampleNumbersample3
##                   1.050                      2.548
```

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

```
##
## Call:
## lm(formula = ES5.mod$ES5_ch1.tuk ~ ES5.mod$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 Treatment
```

```
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_ch1.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.ch1.anova, c("ES5.mod$Treatment", "ES5.mod$Dilution"), group

##
## Study: ES5.mod.ch1.anova ~ c("ES5.mod$Treatment", "ES5.mod$Dilution")
##
## HSD Test for ES5.mod$ES5_ch1.tuk
##
## Mean Square Error:  57.63529
##
## ES5.mod$Treatment:ES5.mod$Dilution,  means
##
##      ES5.mod.ES5_ch1.tuk      std  r      Min      Max
## control:100fold      33.08875  5.694754  51  20.467824  46.91458
## control:25fold      27.20249  8.178120  51   8.312519  41.07609
## DMCC2126:100fold      27.42587  7.586754  51  12.382456  38.08942
## DMCC2126:25fold      18.84674  7.624616  54   9.182009  38.70932
## DMCC2127:100fold      24.30329  8.849956  54  10.473529  44.13634
## DMCC2127:25fold      19.14544  8.753292  54   0.000000  40.39612
## DMCC2165:100fold      23.53701 10.140662  54   0.000000  38.95398
## DMCC2165:25fold      20.80779  7.827922  51  11.052188  39.79045
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.30873
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##      ES5.mod$ES5_ch1.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_ch1.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_ch1.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"

```

```
#Complete ANOVA for ES5.mod by treatment by condition, by dilution
```

```
ES5.mod.comp.HSD.group <- HSD.test(ES5.mod.ch1.anova, c("ES5.mod$Treatment", "ES5.mod$Condition", "ES5.mod$Dilution"))
```

```

##
## Study: ES5.mod.ch1.anova ~ c("ES5.mod$Treatment", "ES5.mod$Condition", "ES5.mod$Dilution")
##
## HSD Test for ES5.mod$ES5_ch1.tuk
##
## Mean Square Error: 57.63529
##

```

```
## ES5.mod$Treatment:ES5.mod$Condition:ES5.mod$Dilution, means
##
##
## ES5.mod.ES5_ch1.tuk      std  r      Min      Max
## control:Shaking:100fold    30.92160  6.877550  24  20.467824  46.19961
## control:Shaking:25fold     26.28822  7.584437  27   8.312519  36.10186
## control:Stationary:100fold  35.01510  3.511991  27  29.814226  46.91458
## control:Stationary:25fold   28.23105  8.847762  24  10.583319  41.07609
## DMCC2126:Shaking:100fold    26.63321  8.061394  24  12.382456  38.08942
## DMCC2126:Shaking:25fold     16.33068  4.334703  27   9.182009  24.92251
## DMCC2126:Stationary:100fold  28.13045  7.218510  27  12.994778  37.53790
## DMCC2126:Stationary:25fold   21.36280  9.304178  27  10.270619  38.70932
## DMCC2127:Shaking:100fold    18.70574  5.119409  27  10.473529  30.33414
## DMCC2127:Shaking:25fold     13.80400  6.101857  27   0.000000  22.40212
## DMCC2127:Stationary:100fold  29.90084  8.268740  27  16.549688  44.13634
## DMCC2127:Stationary:25fold   24.48688  7.726440  27  13.222435  40.39612
## DMCC2165:Shaking:100fold    24.56023  8.205647  27  10.418401  38.34533
## DMCC2165:Shaking:25fold     18.20998  5.258465  27  11.052188  28.65280
## DMCC2165:Stationary:100fold  22.51380 11.836979  27   0.000000  38.95398
## DMCC2165:Stationary:25fold   23.73032  9.225861  24  12.382456  39.79045
##
## Alpha: 0.05 ; DF Error: 408
## Critical Value of Studentized Range: 4.87582
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
## ES5.mod$ES5_ch1.tuk groups
## control:Stationary:100fold    35.01510    a
## control:Shaking:100fold       30.92160   ab
## DMCC2127:Stationary:100fold    29.90084   ab
## control:Stationary:25fold      28.23105  abc
## DMCC2126:Stationary:100fold    28.13045  abc
## DMCC2126:Shaking:100fold       26.63321   bc
## control:Shaking:25fold         26.28822   bc
## DMCC2165:Shaking:100fold       24.56023  bcd
## DMCC2127:Stationary:25fold     24.48688  bcd
## DMCC2165:Stationary:25fold     23.73032  bcd
## DMCC2165:Stationary:100fold    22.51380  cde
## DMCC2126:Stationary:25fold     21.36280  cde
## DMCC2127:Shaking:100fold       18.70574  def
## DMCC2165:Shaking:25fold        18.20998  def
## DMCC2126:Shaking:25fold        16.33068   ef
## DMCC2127:Shaking:25fold        13.80400    f
```

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

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

```

## StudentizedRange alpha
##      4.87582  0.05
##
## $means
##               ES5.mod$ES5_ch1.tuk      std  r      Min      Max
## control:Shaking:100fold      30.92160  6.877550 24 20.467824 46.19961
## control:Shaking:25fold      26.28822  7.584437 27  8.312519 36.10186
## control:Stationary:100fold    35.01510  3.511991 27 29.814226 46.91458
## control:Stationary:25fold    28.23105  8.847762 24 10.583319 41.07609
## DMCC2126:Shaking:100fold    26.63321  8.061394 24 12.382456 38.08942
## DMCC2126:Shaking:25fold     16.33068  4.334703 27  9.182009 24.92251
## DMCC2126:Stationary:100fold  28.13045  7.218510 27 12.994778 37.53790
## DMCC2126:Stationary:25fold   21.36280  9.304178 27 10.270619 38.70932
## DMCC2127:Shaking:100fold    18.70574  5.119409 27 10.473529 30.33414
## DMCC2127:Shaking:25fold     13.80400  6.101857 27  0.000000 22.40212
## DMCC2127:Stationary:100fold  29.90084  8.268740 27 16.549688 44.13634
## DMCC2127:Stationary:25fold   24.48688  7.726440 27 13.222435 40.39612
## DMCC2165:Shaking:100fold    24.56023  8.205647 27 10.418401 38.34533
## DMCC2165:Shaking:25fold     18.20998  5.258465 27 11.052188 28.65280
## DMCC2165:Stationary:100fold  22.51380 11.836979 27  0.000000 38.95398
## DMCC2165:Stationary:25fold   23.73032  9.225861 24 12.382456 39.79045
##
##               Q25      Q50      Q75
## control:Shaking:100fold    25.60774 29.95578 35.75395
## control:Shaking:25fold     23.23414 28.68481 31.88435
## control:Stationary:100fold  32.89985 34.77877 36.49626
## control:Stationary:25fold   22.97996 30.57655 35.12646
## DMCC2126:Shaking:100fold   18.24222 28.49017 32.10254
## DMCC2126:Shaking:25fold    12.72170 15.30503 19.21892
## DMCC2126:Stationary:100fold 23.96670 29.23662 34.36364
## DMCC2126:Stationary:25fold  13.75020 17.95239 28.49754
## DMCC2127:Shaking:100fold   15.79238 18.06204 22.03937
## DMCC2127:Shaking:25fold     11.94225 14.14409 18.38373
## DMCC2127:Stationary:100fold 21.18901 31.73483 36.13001
## DMCC2127:Stationary:25fold  16.98374 23.80439 29.93923
## DMCC2165:Shaking:100fold   17.06819 21.67684 31.48681
## DMCC2165:Shaking:25fold     14.32943 16.96287 19.24541
## DMCC2165:Stationary:100fold 14.61527 26.86130 31.84574
## DMCC2165:Stationary:25fold  16.28243 21.81134 30.38458
##
## $comparison
## NULL
##
## $groups
##               ES5.mod$ES5_ch1.tuk groups
## control:Stationary:100fold      35.01510      a
## control:Shaking:100fold          30.92160      ab
## DMCC2127:Stationary:100fold      29.90084      ab
## control:Stationary:25fold        28.23105      abc
## DMCC2126:Stationary:100fold      28.13045      abc
## DMCC2126:Shaking:100fold         26.63321      bc
## control:Shaking:25fold           26.28822      bc
## DMCC2165:Shaking:100fold         24.56023      bcd
## DMCC2127:Stationary:25fold        24.48688      bcd
## DMCC2165:Stationary:25fold        23.73032      bcd

```

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

Run analyses for ES13B

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

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

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

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

```
##
## Call:
## lm(formula = ES13B$chl ~ ES13B$Treatment + ES13B$HostVariety +
##     ES13B$isoRepNumber + ES13B$techRepNumber + ES13B$SampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -219.035  -47.751   -4.823   42.506  237.651
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      187.9400    17.1352  10.968  <2e-16 ***
## ES13B$TreatmentDMCC2165 -105.4678    9.9569 -10.592  <2e-16 ***
## ES13B$HostVarietyDG47E80   27.8736   15.5401   1.794   0.0741 .
## ES13B$HostVarietyDG47X95   26.3892   16.0431   1.645   0.1012
## ES13B$HostVarietyOsage     16.1981   15.5401   1.042   0.2983
## ES13B$HostVarietyP5414LLS  -3.8273   15.5401  -0.246   0.8057
## ES13B$IsoRepNumberisoRep2  -7.3121   12.2504  -0.597   0.5511
## ES13B$IsoRepNumberisoRep3   1.4292   12.1499   0.118   0.9065
## ES13B$techRepNumbertechRep2 29.6658   12.1499   2.442   0.0153 *
## ES13B$techRepNumbertechRep3  8.0253   12.1499   0.661   0.5095
## ES13B$SampleNumbersample2   0.7302   12.1733   0.060   0.9522
## ES13B$SampleNumbersample3   1.9473   12.1733   0.160   0.8730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 80.75 on 252 degrees of freedom
## (6 observations deleted due to missingness)
## Multiple R-squared:  0.337, Adjusted R-squared:  0.308
## F-statistic: 11.64 on 11 and 252 DF, p-value: < 2.2e-16
```

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

```
## Analysis of Variance Table
##
## Response: ES13B$chl
##               Df Sum Sq Mean Sq F value Pr(>F)
## ES13B$Treatment    1  745236   745236 114.2939 < 2e-16 ***
## ES13B$HostVariety   4   44757    11189   1.7160 0.14689
## ES13B$IsoRepNumber   2    3558     1779   0.2728 0.76144
## ES13B$techRepNumber  2   41380    20690   3.1731 0.04355 *
## ES13B$SampleNumber  2     170        85   0.0131 0.98702
## Residuals          252 1643127    6520
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

```
## $statistics
##      MSerror Df      Mean      CV
##    6520.345 252 160.8255 50.20887
##
## $parameters
##      test      name.t ntr StudentizedRange alpha
##    Tukey ES13B$Treatment    2          2.785184 0.05
##
## $means
##      ES13B$chl      std      r Min      Max      Q25      Q50      Q75
## Control    212.7620 79.79142 135    0 402.241 166.577 220.922 257.822
## DMCC2165   106.4733 82.90892 129    0 350.226  51.563  71.243 161.827
##
```

```
## $comparison
## NULL
##
## $groups
##      ES13B$chl groups
## Control    212.7620      a
## DMCC2165   106.4733      b
##
## attr("class")
## [1] "group"

#Tukey's HSD for Variable chl by 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
## Usage     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
## Usage     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$HostVariety + ES13B.mod$isoRepNumber + ES13B.mod$techRepNumber + ES13B.mod$SampleNumber)
ES13B.mod.chl.anova

##
## Call:
## lm(formula = ES13B.mod$ES13B_chl.tuk ~ ES13B.mod$Treatment +
##     ES13B.mod$HostVariety + ES13B.mod$isoRepNumber + ES13B.mod$techRepNumber +
##     ES13B.mod$SampleNumber)
##
## Coefficients:
##             (Intercept)          ES13B.mod$TreatmentDMCC2165
##                   56.4659                      -27.1569
## ES13B.mod$HostVarietyDG47E80 ES13B.mod$HostVarietyDG47X95
##                   6.8552                      6.4268
```

```
##      ES13B.mod$HostVarietyUsage      ES13B.mod$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$HostVarietyDG47X95     6.4268      4.1496   1.549  0.1227
## ES13B.mod$HostVarietyUsage       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_ch1.tuk groups
## DG47X95          53.96776      a
## DG47E80          52.85715      a
## Osage            49.22977      a
## AG4632           46.00199      a
## P5414LLS         44.71323      a
##
## attr("class")
## [1] "group"
```

```
#Complete ANOVA for ES13B.mod
```

```
ES13B.mod.comp.HSD.group <- HSD.test(ES13B.mod.ch1.anova, c("ES13B.mod$Treatment", "ES13B.mod$HostVariety"))
```

```
##
## Study: ES13B.mod.ch1.anova ~ c("ES13B.mod$Treatment", "ES13B.mod$HostVariety")
##
## HSD Test for ES13B.mod$ES13B_ch1.tuk
##
## Mean Square Error:  436.2119
##
## ES13B.mod$Treatment:ES13B.mod$HostVariety,  means
##
##      ES13B.mod.ES13B_ch1.tuk      std  r      Min      Max
## Control:AG4632          57.20904 22.03662 27  0.00000 96.69957
## Control:DG47E80          66.70288 17.20548 27 35.38176 98.36929
## Control:DG47X95          64.01404 17.93361 27 24.66777 95.60617
## Control:Osage            67.15363 26.52535 27  0.00000 104.34627
## Control:P5414LLS         58.04351 11.99680 27 34.39165 76.51943
## DMCC2165:AG4632          34.79495 18.32309 27  0.00000 78.61163
## DMCC2165:DG47E80          39.01143 22.59966 27  0.00000 76.18307
## DMCC2165:DG47X95          41.05111 26.62931 21  0.00000 93.72814
## DMCC2165:Osage           31.30592 16.83924 27  0.00000 84.32030
## DMCC2165:P5414LLS        31.38296 25.56143 27  0.00000 87.02381
##
## Alpha: 0.05 ; DF Error: 252
## Critical Value of Studentized Range: 4.514628
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
```

```
## ES13B.mod$ES13B_ch1.tuk groups
## Control:Osage 67.15363 a
## Control:DG47E80 66.70288 a
## Control:DG47X95 64.01404 a
## Control:P5414LLS 58.04351 ab
## Control:AG4632 57.20904 ab
## DMCC2165:DG47X95 41.05111 bc
## DMCC2165:DG47E80 39.01143 c
## DMCC2165:AG4632 34.79495 c
## DMCC2165:P5414LLS 31.38296 c
## DMCC2165:Osage 31.30592 c
```

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

```
## $statistics
## MSerror Df Mean CV
## 436.2119 252 49.24912 42.40824
##
## $parameters
## test name.t ntr StudentizedRange alpha
## Tukey ES13B.mod$Treatment:ES13B.mod$HostVariety 10 4.514628 0.05
##
## $means
## ES13B.mod$ES13B_ch1.tuk std r Min Max
## Control:AG4632 57.20904 22.03662 27 0.00000 96.69957
## Control:DG47E80 66.70288 17.20548 27 35.38176 98.36929
## Control:DG47X95 64.01404 17.93361 27 24.66777 95.60617
## Control:Osage 67.15363 26.52535 27 0.00000 104.34627
## Control:P5414LLS 58.04351 11.99680 27 34.39165 76.51943
## DMCC2165:AG4632 34.79495 18.32309 27 0.00000 78.61163
## DMCC2165:DG47E80 39.01143 22.59966 27 0.00000 76.18307
## DMCC2165:DG47X95 41.05111 26.62931 21 0.00000 93.72814
## DMCC2165:Osage 31.30592 16.83924 27 0.00000 84.32030
## DMCC2165:P5414LLS 31.38296 25.56143 27 0.00000 87.02381
## Q25 Q50 Q75
## Control:AG4632 47.05388 62.96010 68.61805
## Control:DG47E80 62.26497 67.17475 78.30087
## Control:DG47X95 56.17982 65.54711 77.85944
## Control:Osage 65.40652 71.46612 76.90405
## Control:P5414LLS 51.98765 59.22541 67.22892
## DMCC2165:AG4632 22.34657 29.72913 43.18888
## DMCC2165:DG47E80 20.43572 33.65317 61.08024
## DMCC2165:DG47X95 19.88940 30.28659 60.68214
## DMCC2165:Osage 24.95960 26.04835 30.23822
## DMCC2165:P5414LLS 15.75931 23.21526 36.18682
##
## $comparison
## NULL
##
## $groups
## ES13B.mod$ES13B_ch1.tuk groups
## Control:Osage 67.15363 a
## Control:DG47E80 66.70288 a
## Control:DG47X95 64.01404 a
```

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

Run analyses for ES14A

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

```
#####ES14A###
```

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

```
##
## Call:
## lm(formula = ES14A$chl ~ ES14A$Treatment + ES14A$Host + ES14A$isoRepNumber +
##     ES14A$techRepNumber + ES14A$LeafSampleNumber)
##
## Coefficients:
##              (Intercept)              ES14A$TreatmentDMCC2165
##                   204.803                   -39.317
##              ES14A$HostPeanut              ES14A$HostSoybean
##                   71.821                   -20.797
##              ES14A$HostTomato              ES14A$isoRepNumberisoRep2
##                   20.597                   8.076
##              ES14A$isoRepNumberisoRep3      ES14A$techRepNumbertechRep2
##                   10.061                   -3.623
##              ES14A$techRepNumbertechRep3      ES14A$LeafSampleNumbersample2
##                   -2.447                   -2.221
##              ES14A$LeafSampleNumbersample3
##                   -17.082
```

```
summary(ES14A.chl.anova)
```

```
##
## Call:
## lm(formula = ES14A$chl ~ ES14A$Treatment + ES14A$Host + ES14A$isoRepNumber +
##     ES14A$techRepNumber + ES14A$LeafSampleNumber)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -152.26  -25.67    3.28   28.37  140.22
##
## Coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)                204.803    11.492    17.821 < 2e-16 ***
## ES14A$TreatmentDMCC2165    -39.317     6.956    -5.652 5.34e-08 ***
## ES14A$HostPeanut           71.821     9.760     7.359 4.58e-12 ***
## ES14A$HostSoybean          -20.797     9.760    -2.131 0.0343 *
## ES14A$HostTomato           20.597     9.914     2.078 0.0390 *
## ES14A$IsoRepNumberisoRep2    8.076     8.552     0.944 0.3461
## ES14A$IsoRepNumberisoRep3   10.061     8.452     1.190 0.2353
## ES14A$techRepNumbertechRep2 -3.623     8.552    -0.424 0.6723
## ES14A$techRepNumbertechRep3 -2.447     8.552    -0.286 0.7751
## ES14A$LeafSampleNumbersample2 -2.221     8.512    -0.261 0.7944
## ES14A$LeafSampleNumbersample3 -17.082     8.512    -2.007 0.0461 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 50.71 on 202 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.4051, Adjusted R-squared:  0.3756
## F-statistic: 13.75 on 10 and 202 DF,  p-value: < 2.2e-16
```

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

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

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

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

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



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

```
#Tukey's HSD for Variable chl by 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, consol
```

```
##
## Study: ES14A.chl.anova ~ c("ES14A$Treatment", "ES14A$Host")
##
## HSD Test for ES14A$chl
##
## Mean Square Error: 2571.854
##
## ES14A$Treatment:ES14A$Host, means
##
```

```

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

```

ES14A.comp.HSD.group

```

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

```

```
## DMCC2165:Soybean 143.0605
## DMCC2165:Tomato 206.2940
##
## $comparison
## NULL
##
## $groups
##          ES14A$chl groups
## DMCC2165:Peanut 265.62833      a
## Control:Peanut  243.47885     ab
## Control:Soybean 226.62589     abc
## Control:Tomato  215.70517     bc
## Control:Cotton  194.11622     cd
## DMCC2165:Tomato 189.69526     cd
## DMCC2165:Cotton 171.34937     d
## DMCC2165:Soybean 97.24481     e
##
## attr(,"class")
## [1] "group"
```

Same analysis as above using Tukey's normalized data.

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

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

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

```
##
## Call:
## lm(formula = ES14A.mod$ES14A_chl.tuk ~ ES14A.mod$Treatment +
```

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

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

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

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

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

```
## $statistics
##      MSerror Df      Mean      CV
##  14465471 202 9953.906 38.20962
##
## $parameters
##      test              name.t ntr StudentizedRange alpha
```

```
## Tukey ES14A.mod$Treatment 2 2.788514 0.05
##
## $means
## ES14A.mod$ES14A_chl.tuk std r Min Max Q25
## Control 11325.224 3958.923 105 1687.6965 20150.01 9294.444
## DMCC2165 8620.679 5150.335 108 667.0663 20680.22 4821.441
## Q50 Q75
## Control 11009.769 13177.60
## DMCC2165 8538.763 11666.87
##
## $comparison
## NULL
##
## $groups
## ES14A.mod$ES14A_chl.tuk groups
## Control 11325.224 a
## DMCC2165 8620.679 b
##
## attr("class")
## [1] "group"
```

#Tukey's HSD for Variable chl by 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_ch1.tuk      std      r      Min      Max
## Control:Cotton           9103.740 3172.165 27 3121.3676 14110.73
## Control:Peanut          13336.356 3754.679 27 3057.3977 19300.87
## Control:Soybean         12128.331 5109.049 27 1687.6965 20150.01
## Control:Tomato          10658.376 1512.759 24 8038.0704 13187.45
## DMCC2165:Cotton          7344.338 2712.946 27 2785.4532 14551.29
## DMCC2165:Peanut         15330.007 3094.045 27 9318.2997 20680.22
## DMCC2165:Soybean         3195.045 3010.793 27  667.0663 10153.43
## DMCC2165:Tomato          8613.327 2039.245 27 3745.4797 12440.10
##               Q25      Q50      Q75
## Control:Cotton      7235.4241 9415.107 11840.543
## Control:Peanut     10983.3242 13169.695 16057.689
## Control:Soybean      9787.4152 11674.646 16090.596
## Control:Tomato       9595.2157 10503.255 11629.391
## DMCC2165:Cotton      5421.6757 7809.559 9207.086
## DMCC2165:Peanut     13422.7747 14940.064 17699.067
## DMCC2165:Soybean      921.2485 1394.263 5240.336
## DMCC2165:Tomato      7629.0246 8616.978 9828.773
##
## $comparison
## NULL
##
## $groups
##               ES14A.mod$ES14A_ch1.tuk groups
## DMCC2165:Peanut          15330.007      a
## Control:Peanut           13336.356     ab
## Control:Soybean          12128.331     bc
## Control:Tomato           10658.376    bcd
## Control:Cotton            9103.740    cde
## DMCC2165:Tomato           8613.327     de
## DMCC2165:Cotton           7344.338      e
## DMCC2165:Soybean          3195.045      f
##
## attr(,"class")
## [1] "group"
```

Plotting individual plots and composite figures

Individual plots for figure 1

Extract the information needed for panel “A”

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

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

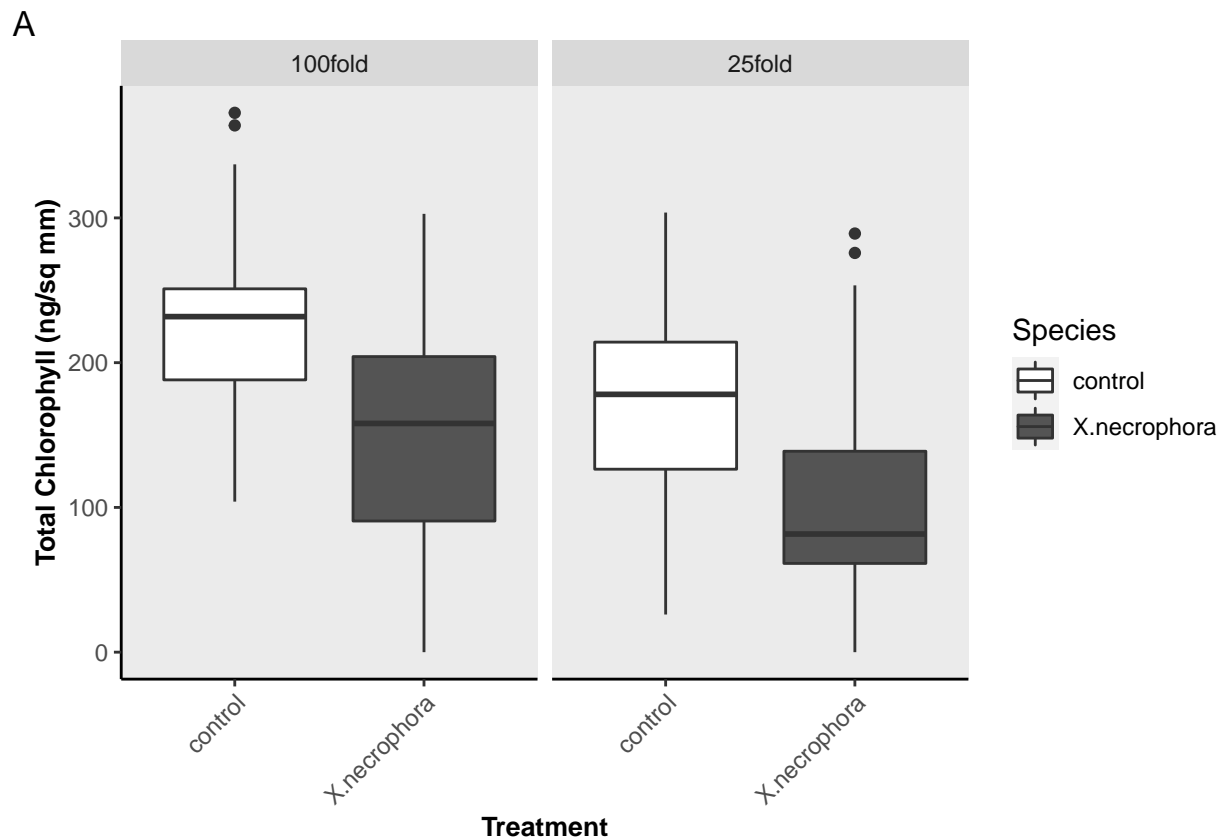
ES5.Xn <- ES5.Xn %>%
  add_column(Species = "X.necrophora")
```

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

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

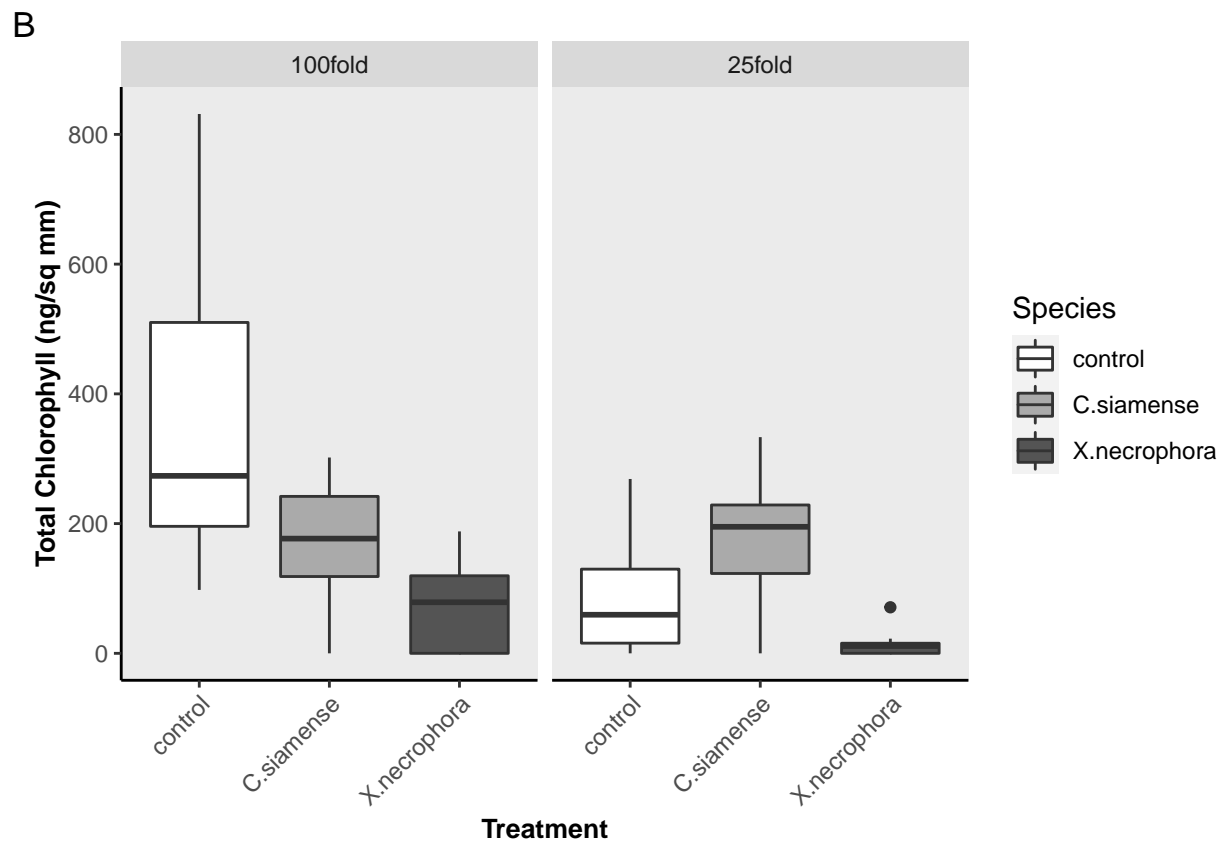
#Reorganizing for plotting

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 = Species))
# scale_fill_grey("control" = 1, "C.siamense" = 0.7, "X.necrophora" = 0.4)
scale_fill_manual(values = c("#FFFFFF", "#AAAAAA", "#545454")) + labs(tag = "B") +
  xlab("Treatment") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(size = 12, hjust = 0.1, face = "bold"),
        theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank()),
        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).

```

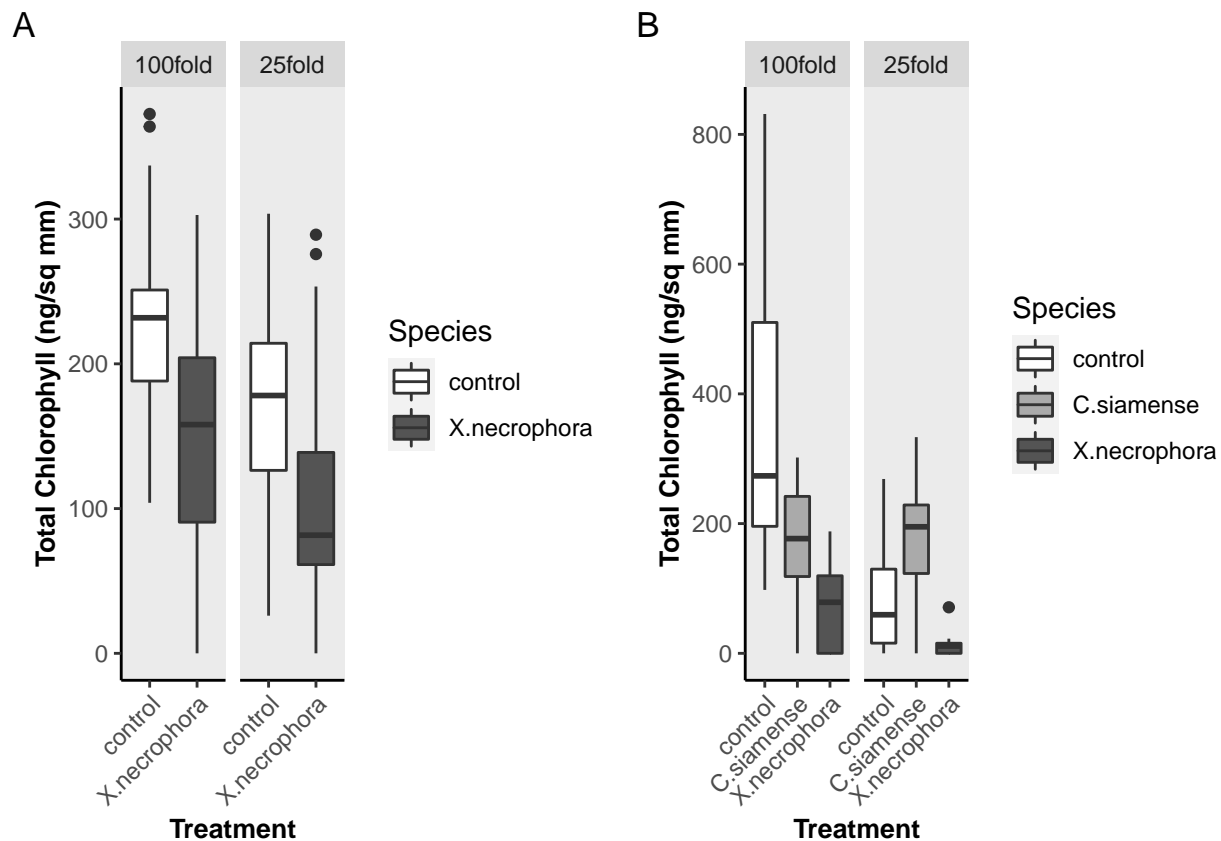


Plot composite figure 1

```
###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).
```

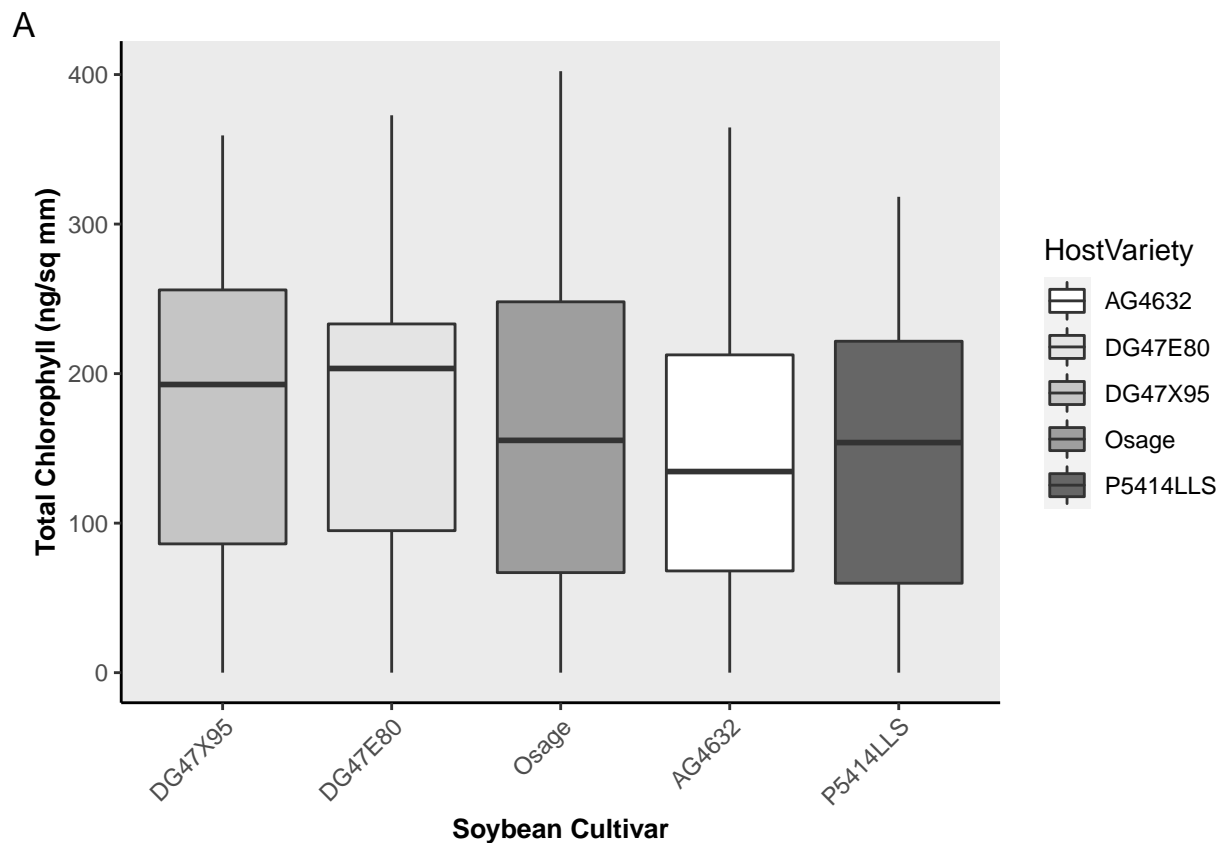


Plotting individual plots and composite figure 3

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=HostVariety)) +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "A") +
  xlab("Soybean Cultivar") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(size = 12, face = "bold"),
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank()))
ES13B.ByHosCult
```

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

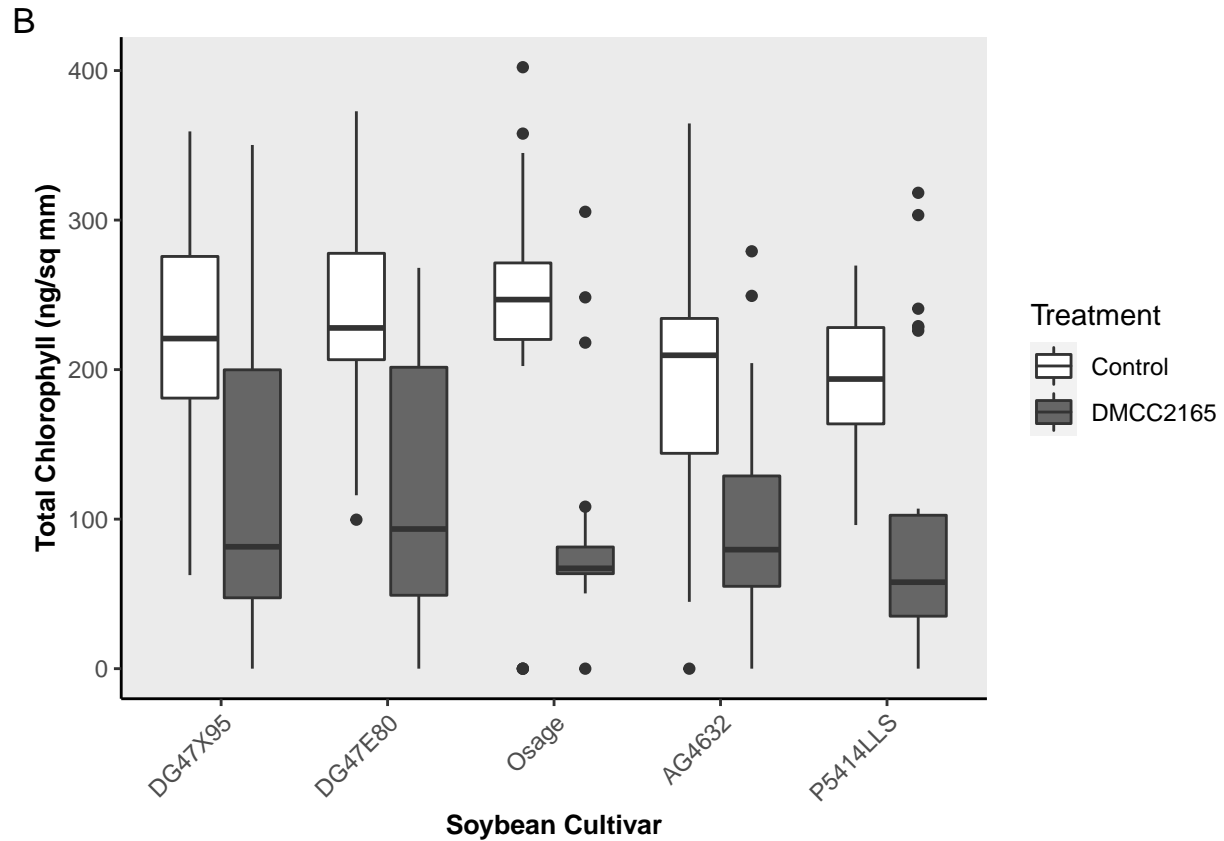


```
#stat_summary(fun.data = give.n, geom = "text", position = position_dodge(width = 0.75), size = 3) # +
```

Individual panel B

```
###Plot by variety by treatment w/ outliers
ES13B.ggplot.ByCultByTreat <- ggplot(ES13B.mod, aes(x = reorder(HostVariety, -chl, na.rm = TRUE), y = chl)) +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "B") +
  xlab("Soybean Cultivar") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(size = 12, face = "bold"),
        theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank()))
ES13B.ggplot.ByCultByTreat
```

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

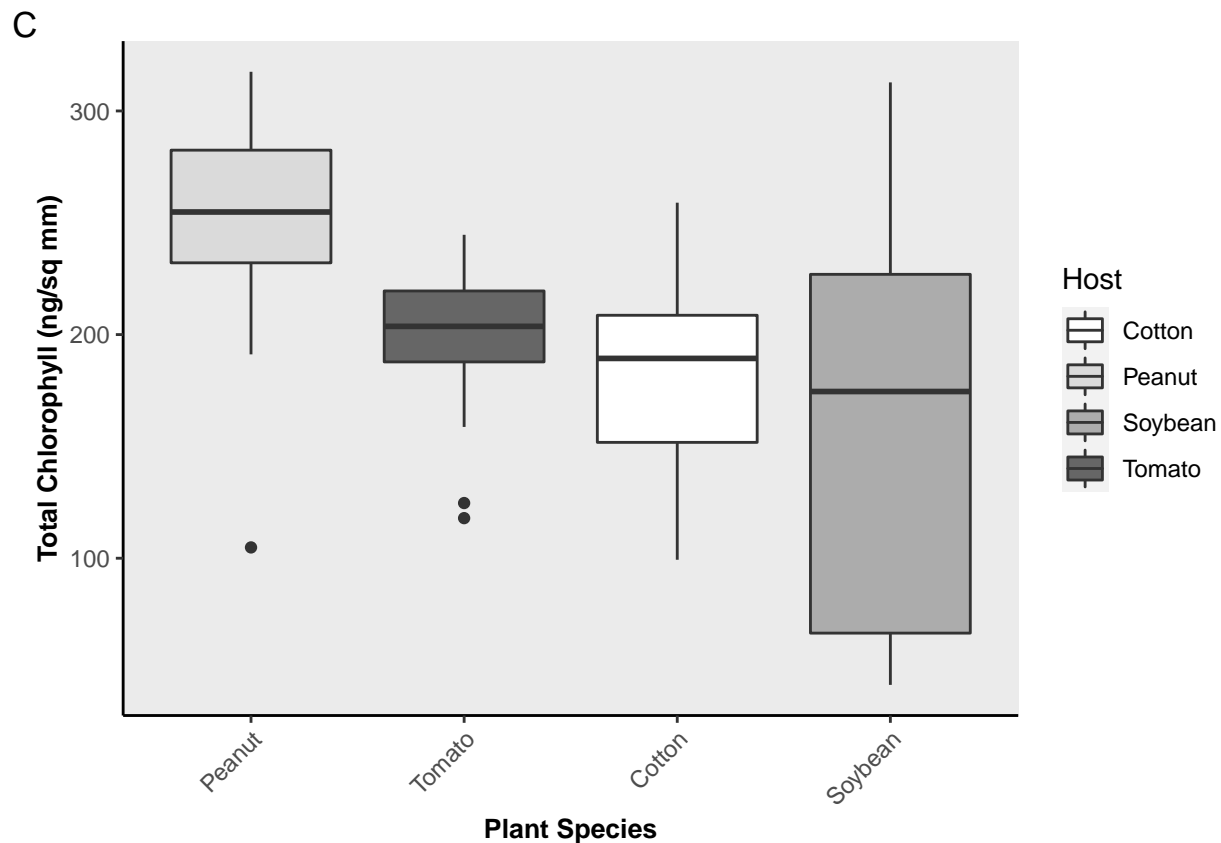


```
#stat_summary(fun.data = give.n, geom = "text", position = position_dodge(width = 0.75), size = 3) # +
```

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 = elemen
  #stat_summary(fun.data = give.n, geom = "text", position = position_dodge(width = 0.75), size = 3) #
ES14A.ggplot.ByHost
```

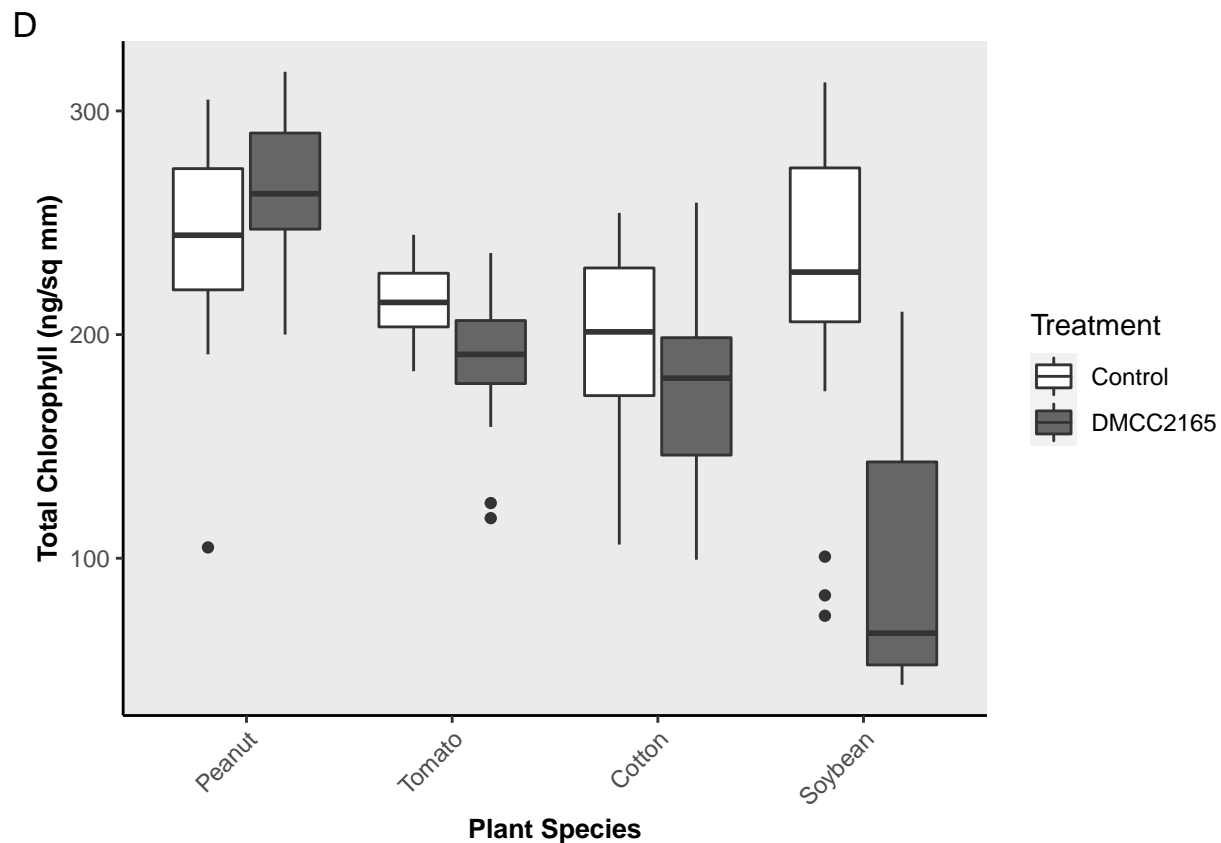
```
## Warning: Removed 3 rows containing non-finite values (stat_boxplot).
```



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 = Host)) +
  scale_fill_grey(start = 1, end = 0.4) + labs(tag = "D") +
  xlab("Plant Species") + ylab("Total Chlorophyll (ng/sq mm)") +
  theme(plot.title = element_text(size = 12, hjust = 0.1, face = "bold"), axis.title.x = element_text(size = 12, face = "bold"),
  theme(panel.border = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank())
  #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).
```



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.ByHost)
```

```
## 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).
```

