Statistical analyses and plotting for Xylaria necrophora secondary metabolites experiments

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Install and load required packages

```
library(agricolae)
library(dplyr)
```

```
##
## 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
```

```
library(plyr)
```

```
## ------------------------------------------------------------------------------

## 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
```

```
require(ggplot2)
```

```
## Loading required package: ggplot2
```

```r
library(readr)
library("ggpubr")
```

```
##
## Attaching package: 'ggpubr'
```

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

```r
library("car")
```

```
## Loading required package: carData
```

```
##
## Attaching package: 'car'
```

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

```r
library(rcompanion)
#install.packages("tidyverse")
library(tidyverse)
```

```
## -- 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()
```

```r
library(reshape)
```

```
##
## 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 where the directory where the output files will be saved. In this case, we assume you have cloned/donwloaded this repository to your "Documents" folder.

Change directory on mac/linux: setwd("/Users/YOURUSERNAME/Documents/X.necrophora.secondaryMetabolites/output

Change directory on Windows (Windows 10 in this example) setwd("C:/Users/YOURUSERNAME/Documents/X.necrophora

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

Loading digital chl datasets (only one repetition of each experiment for illustration purposes) ES2 = First experiment for 14 Days of exporuse (DOE) #ES4 = Repetetion for 14 DOE

ES5 = First experiment for 7 DOE #ES8 = Repetition for 7 DOE

#ES13A = Experiment testing potentially resistant cultivars (7DOE) ES13B = Repetition of ES13A

ES14A = Experiment testing effects among plant species (7DOE) #ES14B = Repetition of ES14A

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

Run Shapiro-Wilk Tests to check for normality

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

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

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

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

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

```
##
##  Shapiro-Wilk normality test
##
## data:  ES13B$chl
## W = 0.95496, p-value = 2.7e-07
```
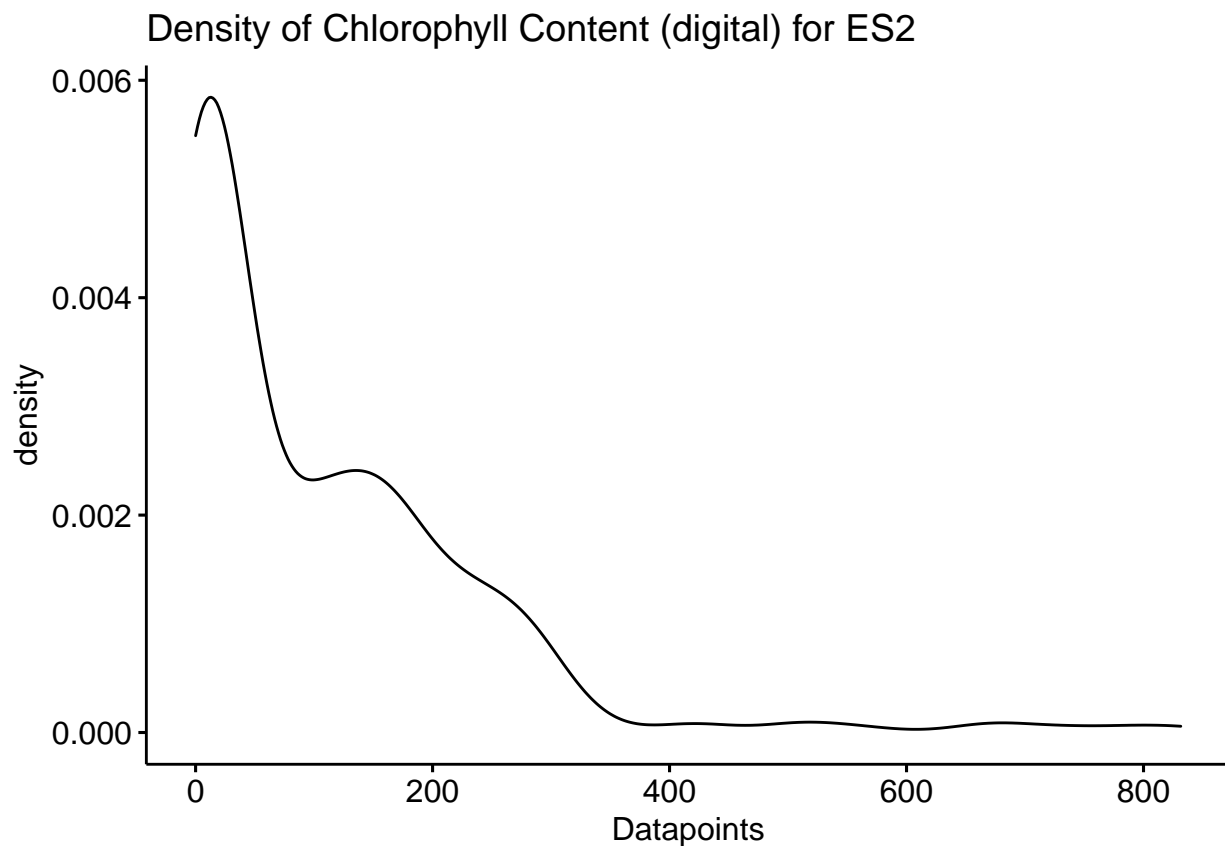
```
shapiro.test(ES14A$chl)
```

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

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

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

Density of Chlorophyll Content (digital) for ES5
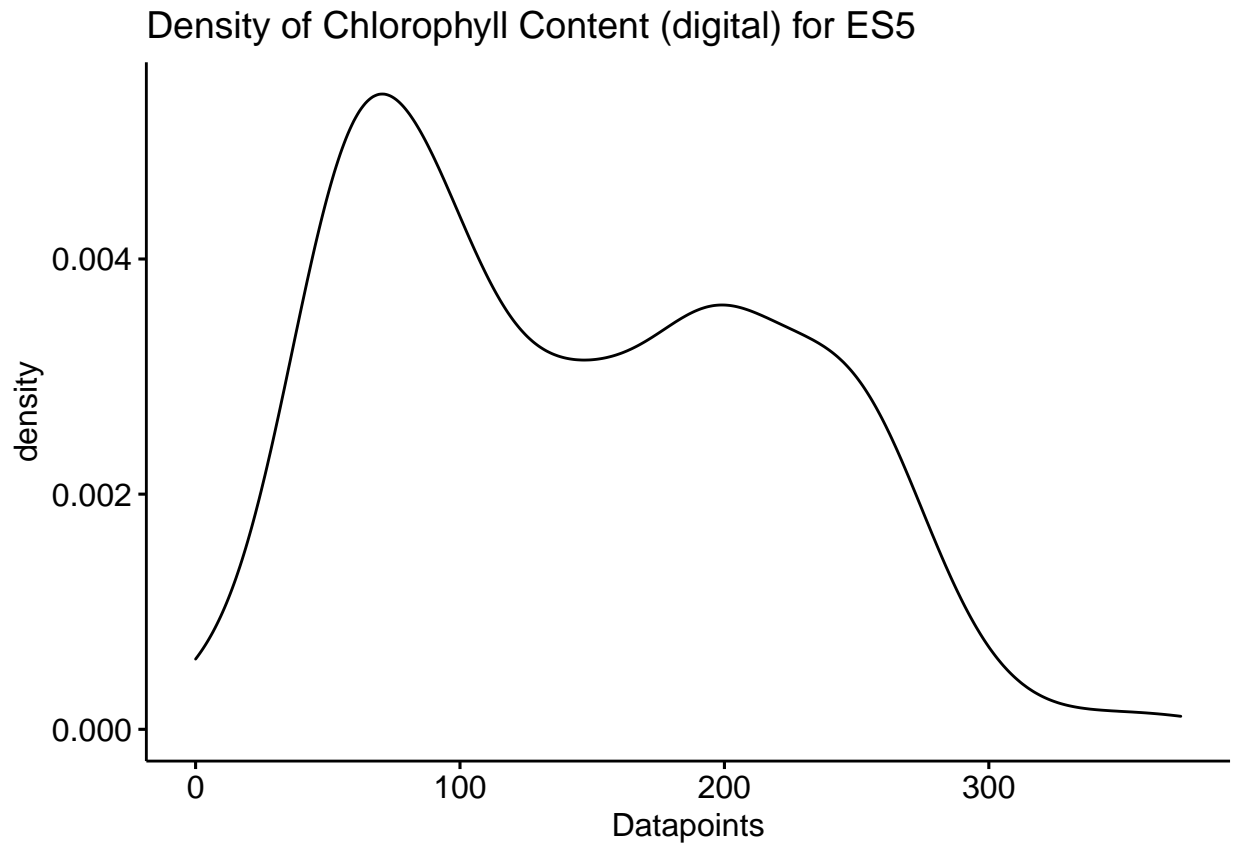
```r
ggdensity(ES13B$chl, main = "Density of Chlorophyll Content (digital) for ES13B", xlab = "Datapoints")
```

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

Density of Chlorophyll Content (digital) for ES13B


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

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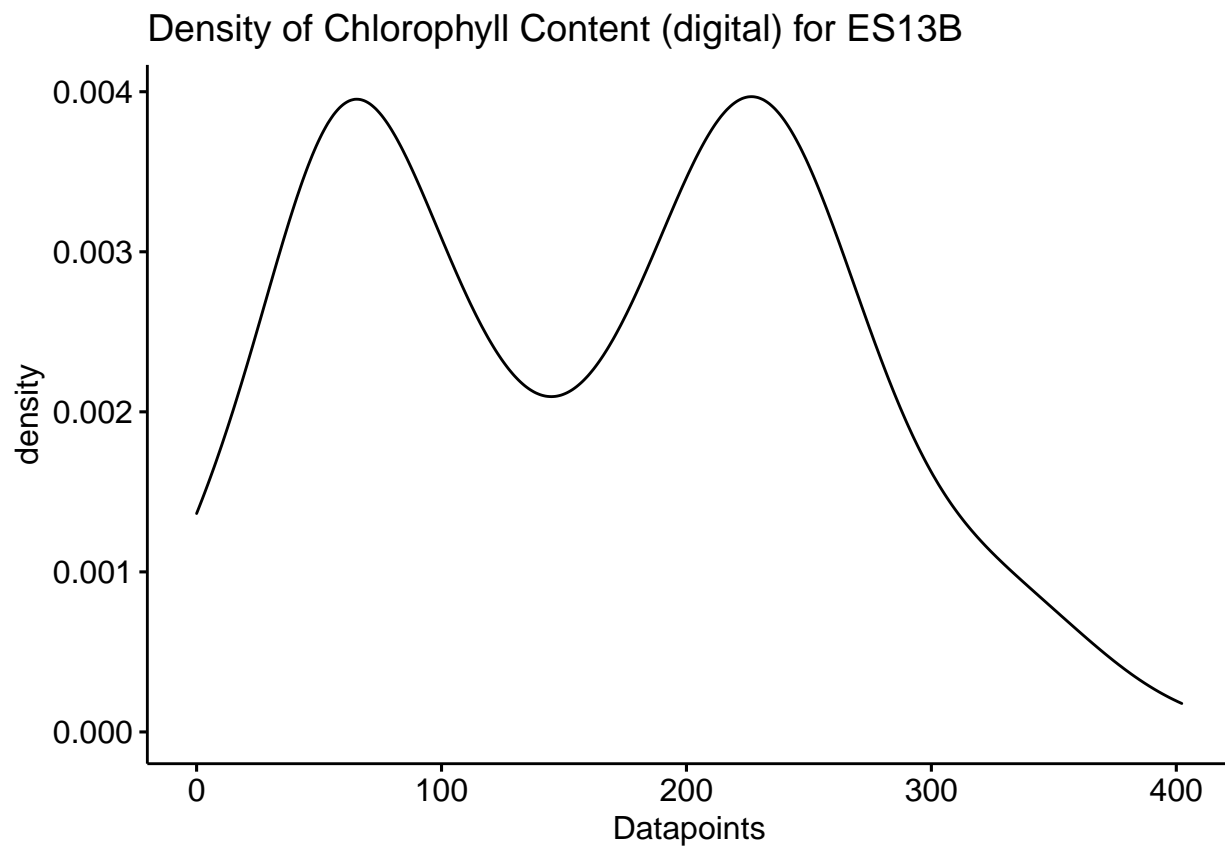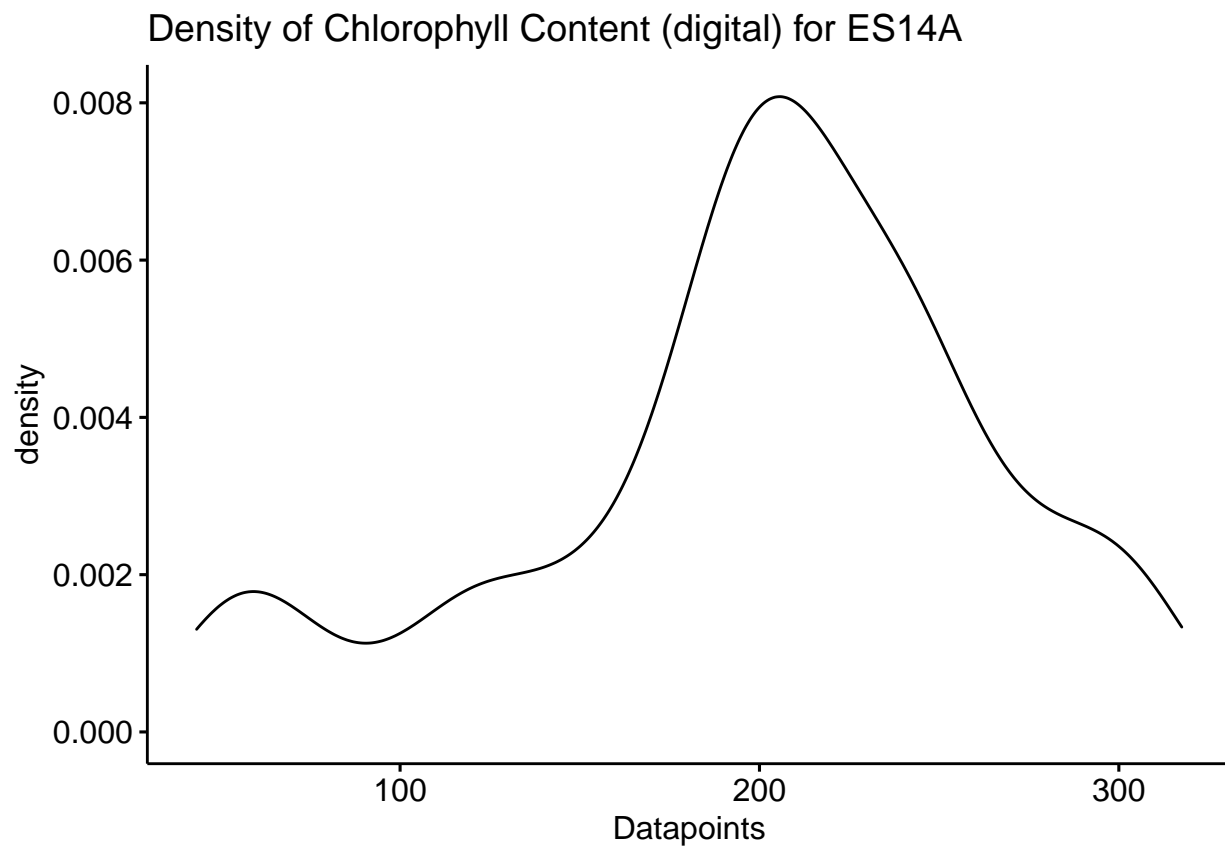
Density of Chlorophyll Content (digital) for ES14A


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

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

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

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

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

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

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

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

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

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

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

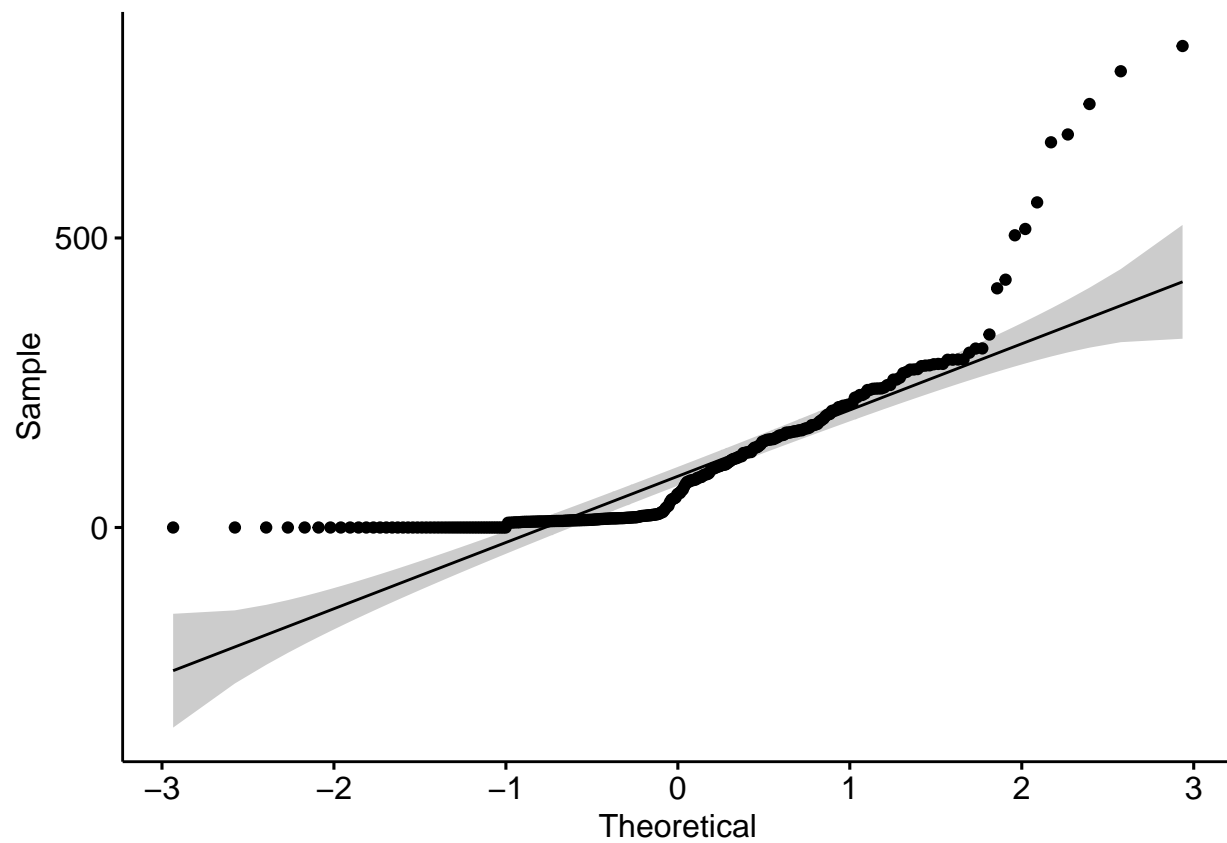## Warning: Removed 6 rows containing non-finite values (stat_qq_line).

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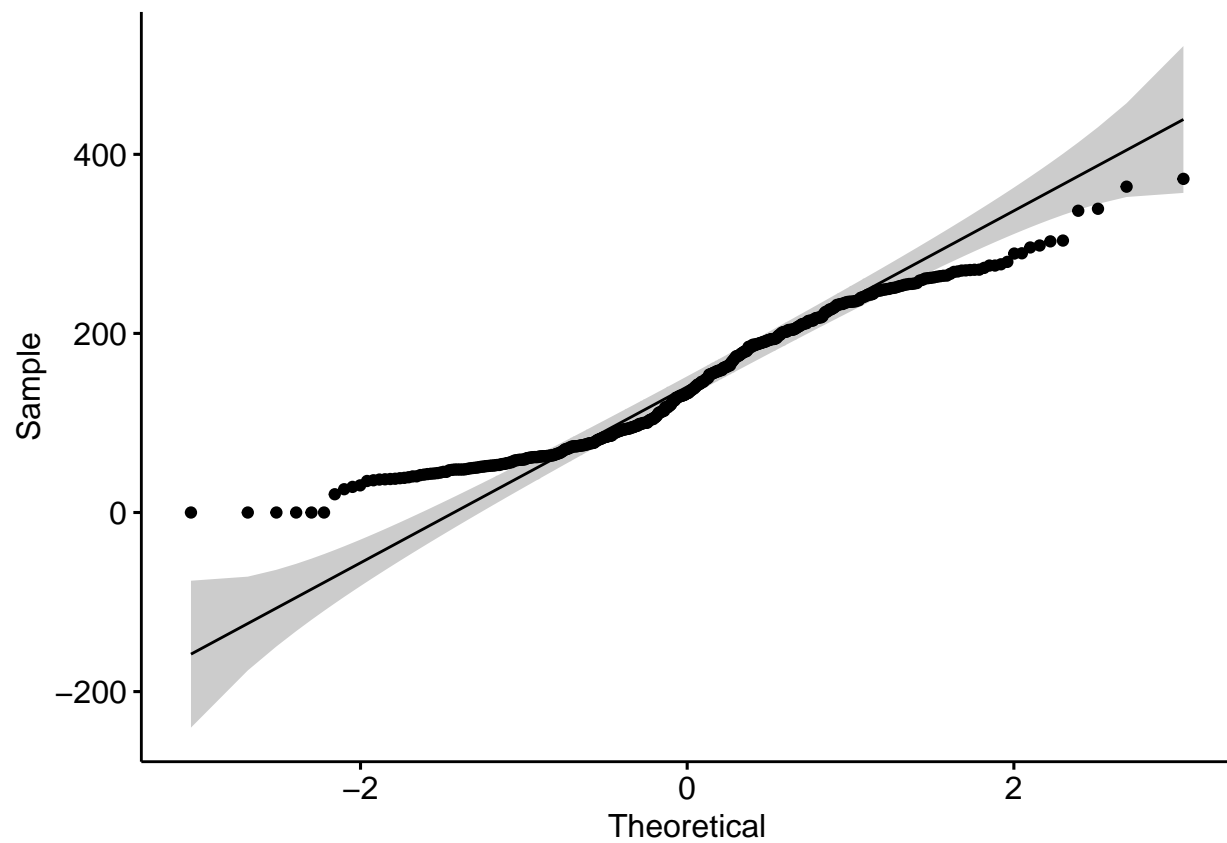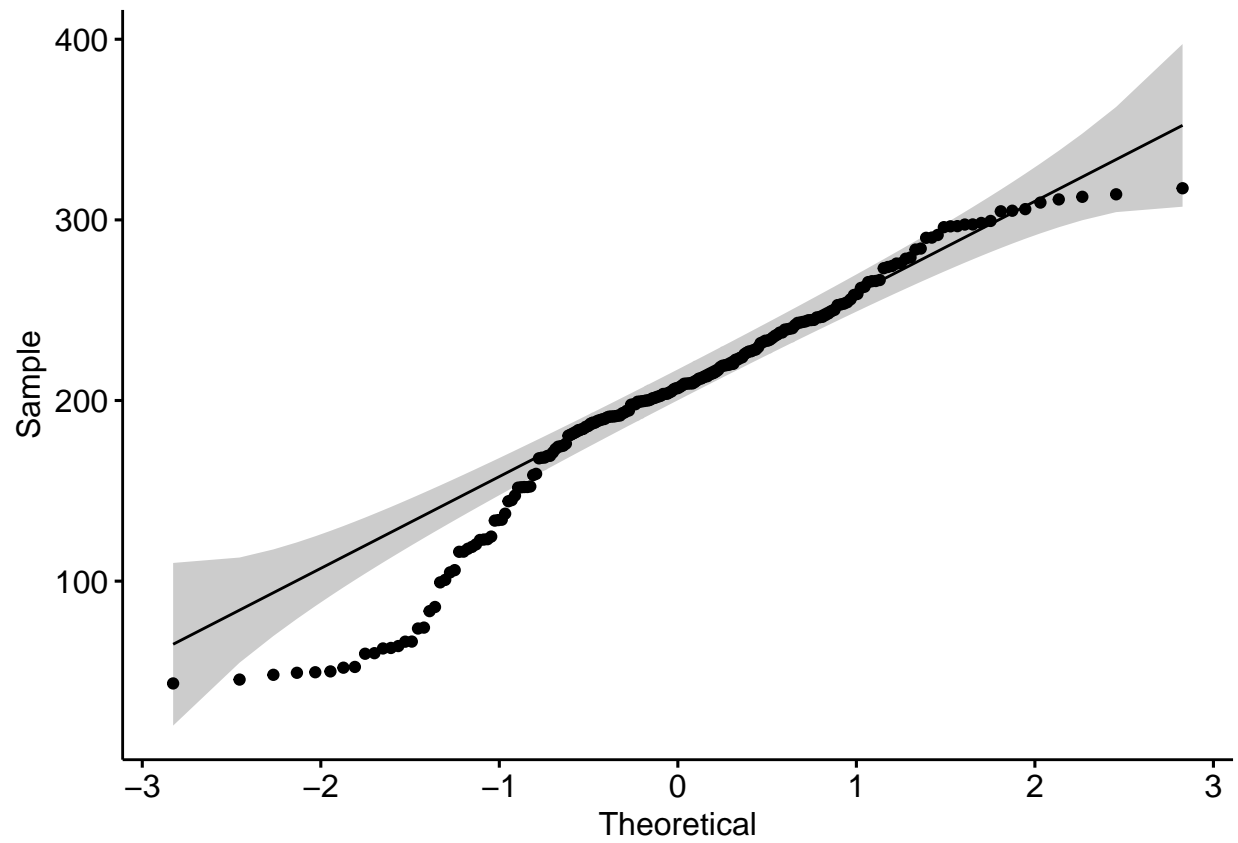
```
plotNormalHistogram(ES2$chl, main = "Density of Chlorophyll Content (Digital) for ES2", xlab = "Datapoin
```
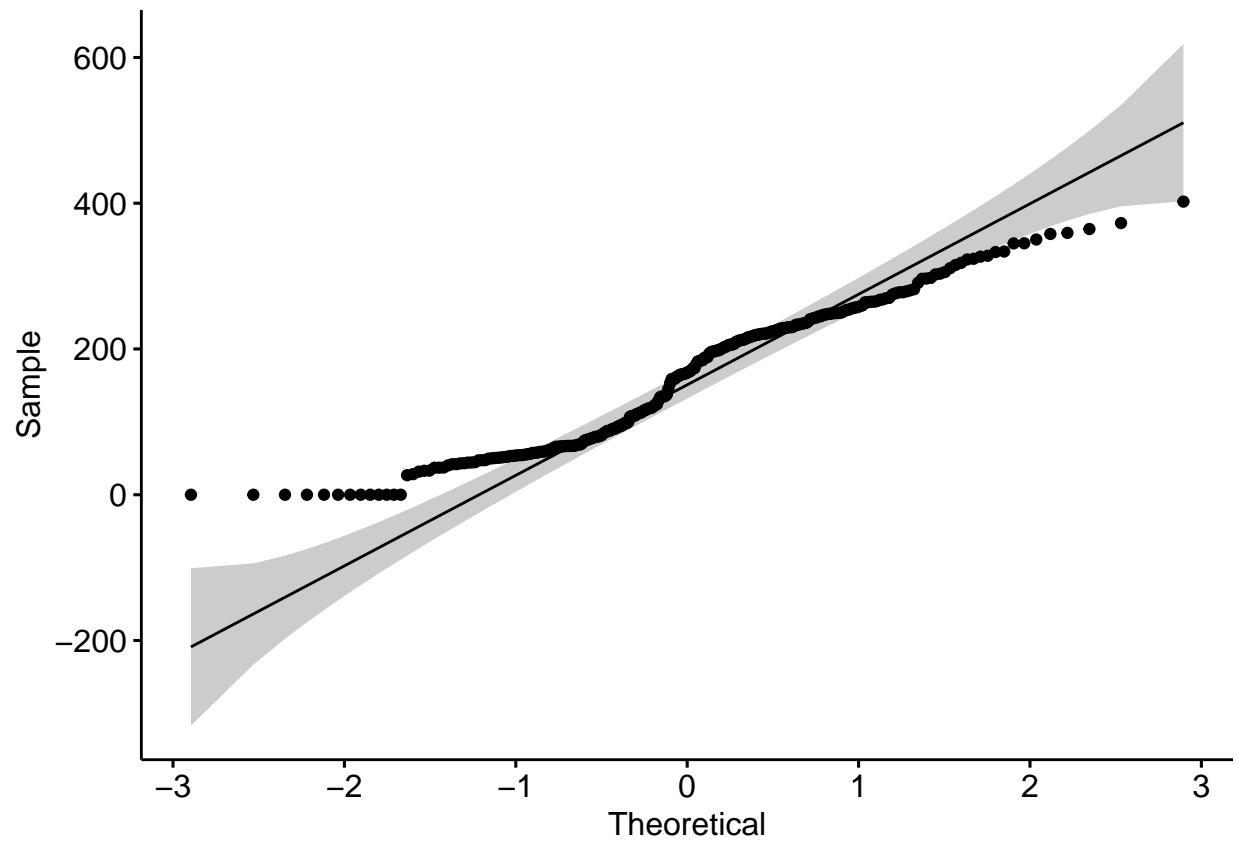
Density of Chlorophyll Content (Digital) for ES2
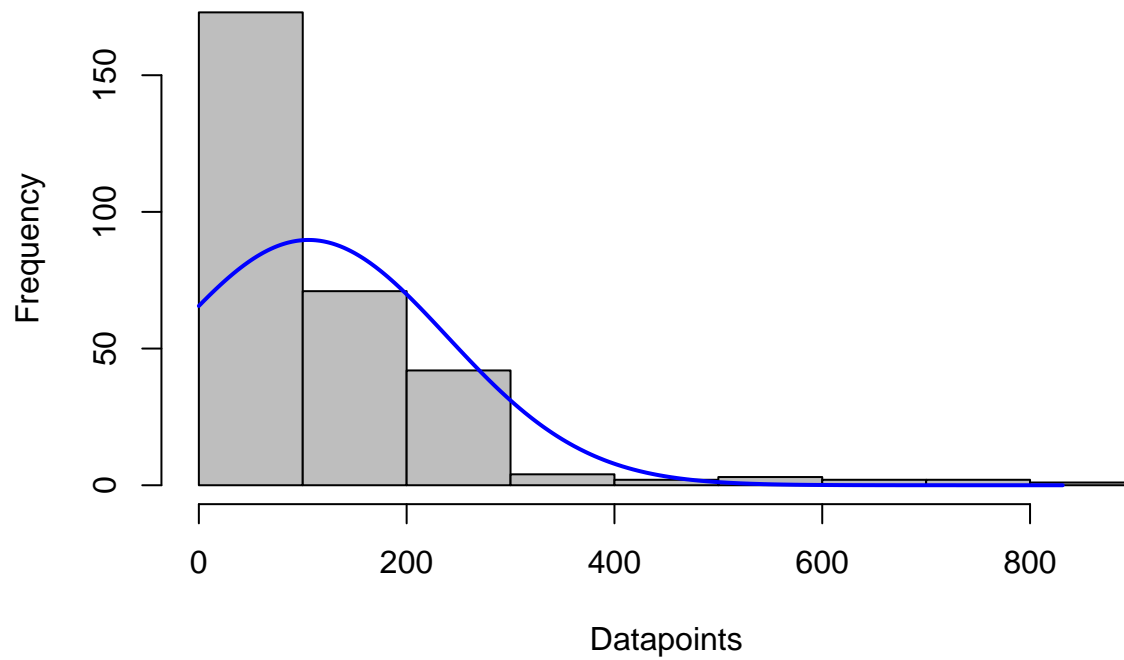

```
plotNormalHistogram(ES5$chl, main = "Density of Chlorophyll Content (Digital) for ES5", xlab = "Datapoi
```

Density of Chlorophyll Content (Digital) for ES5


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

Density of Chlorophyll Content (Digital) for E13B
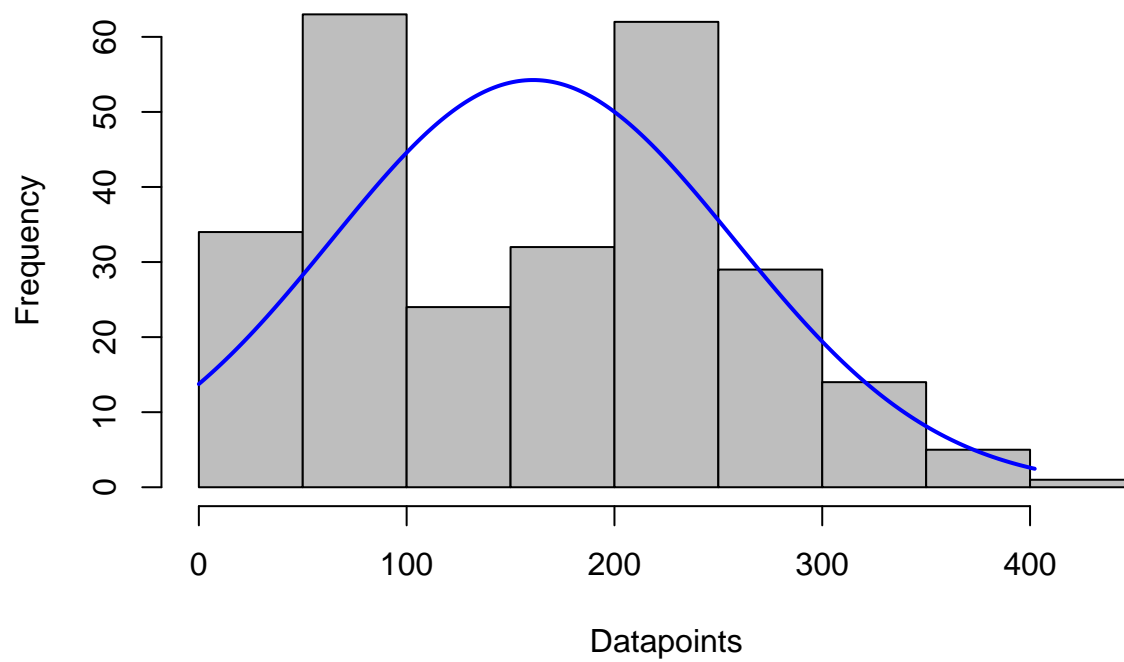

```
plotNormalHistogram(ES14A$chl, main = "Density of Chlorophyll Content (Digital) for E14A", xlab = "Datap
```

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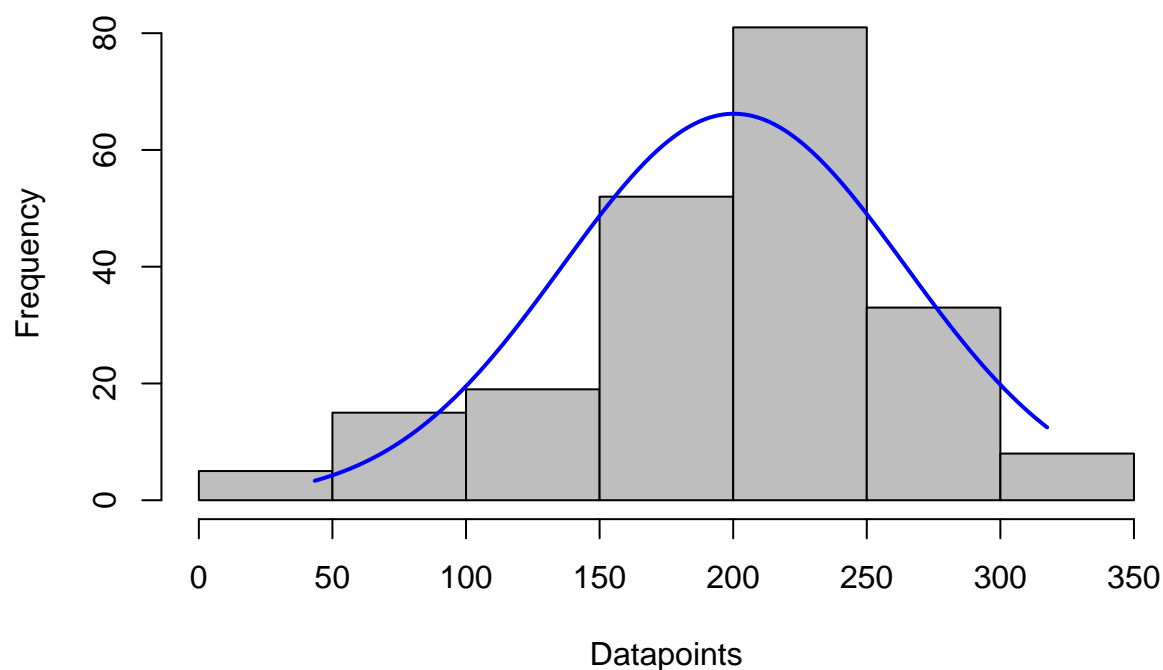
Use the Tukey's tranformation method to normalize the distribution and append to datasets

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

```
##
##      lambda      W Shapiro.p.value
## 416  0.375 0.9449        3.664e-09
##
## if (lambda >  0){TRANS = x ^ lambda}
## if (lambda == 0){TRANS = log(x)}
## if (lambda <  0){TRANS = -1 * x ^ lambda}
```
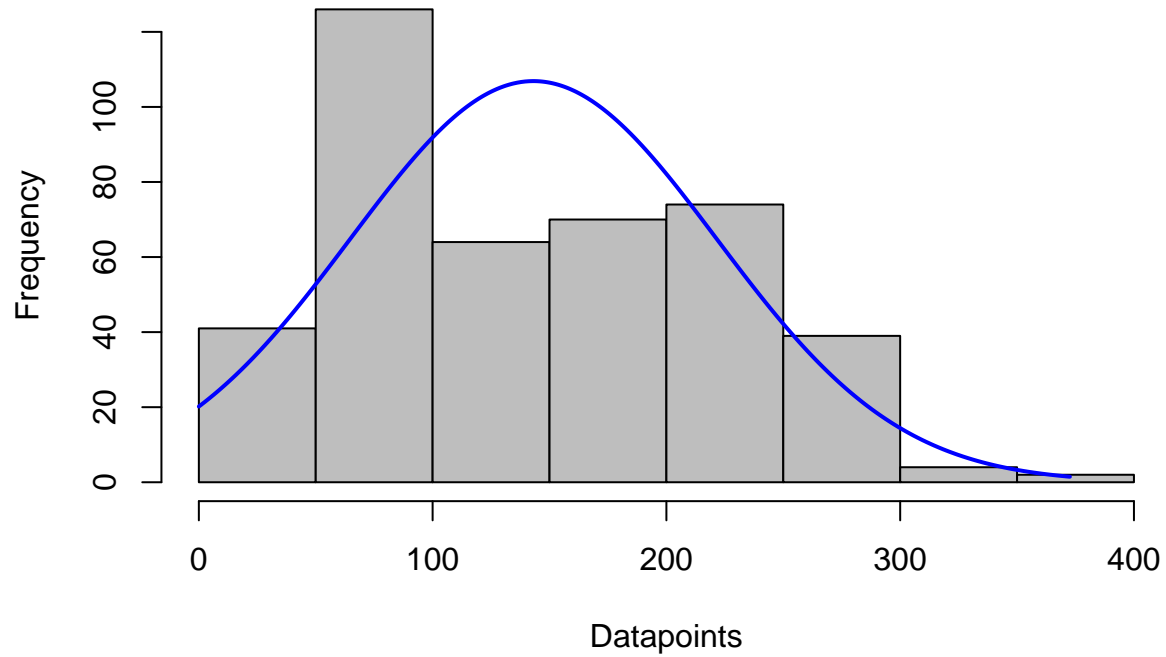
```
ES5_chl.tuk = transformTukey(ES5$chl, plotit=FALSE)
```

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

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

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

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

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

Append the transformed values to original datasets

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

Statistical analyses with raw chlorophyll content (untransformed data) for the experiment ran using cell free culture filtrates 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
```

```r
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
```

```r
#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"
```

```r
#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=TRU
                                              main="ES2 - Xylaria Chl Contnent (Tukey's Ladder Transfo
```

```
##
## Study: ES2 - Xylaria Chl Contnent (Tukey's Ladder Transformed Data) by treatment  by dilution at 14 I
##
## 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
                               main="ES2 - Xylaria Chl Contnent (Tukey's Ladder Transfo
```

```
##
## Study: ES2 - Xylaria Chl Contnent (Tukey's Ladder Transformed Data) by treatment  by dilution at 14 
##
## 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
##
```

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```
## 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 transformed dataset

```
###############ES2 analysis#############################
ES2.mod.chl.anova <- lm (ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution + ES2.mod$Condition
ES2.mod.chl.anova
```

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

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

```
##
## Call:
## lm(formula = ES2.mod$ES2_chl.tuk ~ ES2.mod$Treatment + ES2.mod$Dilution +
##     ES2.mod$Condition + ES2.mod$isoRep + ES2.mod$techRep + ES2.mod$sampleNumber)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -7.1829 -1.1889  0.4416  1.2936  4.5838
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  7.52662    0.44329  16.979  < 2e-16 ***
## ES2.mod$TreatmentDMCC2126   -2.19660    0.41262  -5.323 2.11e-07 ***
## ES2.mod$TreatmentDMCC2127   -3.39025    0.41803  -8.110 1.67e-14 ***
## ES2.mod$TreatmentDMCC2165   -3.45003    0.41254  -8.363 3.06e-15 ***
## ES2.mod$TreatmentDMCC2966   -0.21011    0.40229  -0.522  0.60190
## ES2.mod$Dilution25fold      -2.34945    0.26117  -8.996  < 2e-16 ***
## ES2.mod$ConditionStationary -0.09975    0.26000  -0.384  0.70152
## ES2.mod$isoRepisolateRep2    0.73788    0.26043   2.833  0.00495 **
## ES2.mod$techRepStem2        -0.70265    0.33340  -2.108  0.03597 *
## ES2.mod$techRepStem3        -0.27113    0.30518  -0.888  0.37510
## ES2.mod$sampleNumbersample2 -0.03389    0.31425  -0.108  0.91420
```

```
## ES2.mod$sampleNumbersample3 -0.09430    0.31539  -0.299  0.76518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.188 on 276 degrees of freedom
##   (72 observations deleted due to missingness)
## Multiple R-squared:  0.4559, Adjusted R-squared:  0.4342
## F-statistic: 21.02 on 11 and 276 DF,  p-value: < 2.2e-16
```

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

```
## Analysis of Variance Table
##
## Response: ES2.mod$ES2_chl.tuk
##                      Df  Sum Sq Mean Sq F value    Pr(>F)
## ES2.mod$Treatment     4  680.08  170.02 35.5165 < 2.2e-16 ***
## ES2.mod$Dilution      1  367.55  367.55 76.7802 < 2.2e-16 ***
## ES2.mod$Condition     1    0.63    0.63  0.1326  0.716072
## ES2.mod$isoRep        1   36.95   36.95  7.7190  0.005839 **
## ES2.mod$techRep       2   21.22   10.61  2.2166  0.110912
## ES2.mod$sampleNumber  2    0.44    0.22  0.0456  0.955457
## Residuals           276 1321.23    4.79
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

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

```
## 
## $groups
##          ES2.mod$ES2_chl.tuk groups
## control            6.207956      a
## DMCC2966           6.195529      a
## DMCC2126           4.140619      b
## DMCC2127           2.929858      c
## DMCC2165           2.663168      c
## 
## attr(,"class")
## [1] "group"
```

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

```
## $statistics
##    MSerror  Df     Mean       CV
##   4.787063 276 4.479861 48.83937
## 
## $parameters
##    test           name.t ntr StudentizedRange alpha
##    Tukey ES2.mod$Dilution   2         2.784016  0.05
## 
## $means
##          ES2.mod$ES2_chl.tuk      std   r Min       Max      Q25      Q50
## 100fold            5.670079 2.877306 138   0 12.443509 3.837417 6.189452
## 25fold             3.384861 2.482893 150   0  8.587655 2.358352 2.806307
##              Q75
## 100fold 7.383524
## 25fold  5.616963
## 
## $comparison
## NULL
## 
## $groups
##          ES2.mod$ES2_chl.tuk groups
## 100fold            5.670079      a
## 25fold             3.384861      b
## 
## attr(,"class")
## [1] "group"
```

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

```
## $statistics
##    MSerror  Df     Mean       CV
##   4.787063 276 4.479861 48.83937
## 
## $parameters
##    test           name.t ntr StudentizedRange alpha
```

```
##   Tukey ES2.mod$isoRep   2          2.784016  0.05
##
## $means
##              ES2.mod$ES2_chl.tuk      std  r Min      Max      Q25      Q50
## isolateRep1            4.159075 2.958162 147   0 11.53155 2.416823 3.312666
## isolateRep2            4.814297 2.827923 141   0 12.44351 2.690283 5.303860
##              Q75
## isolateRep1 6.351531
## isolateRep2 6.878451
##
## $comparison
## NULL
##
## $groups
##              ES2.mod$ES2_chl.tuk groups
## isolateRep2            4.814297      a
## isolateRep1            4.159075      b
##
## attr(,"class")
## [1] "group"
```

```
#Complete ANOVA for ES2.mod by treatment by dilution
ES2.mod.comp.HSD.group <- HSD.test(ES2.mod.chl.anova, c("ES2.mod$Treatment", "ES2.mod$Dilution"), group=
                                   main="ES2.mod - Xylaria Chl Contnent (Tukey's Ladder Tra
```

```
##
## Study: ES2.mod - Xylaria Chl Contnent (Tukey's Ladder Transformed Data) by treatment  by dilution at
##
## HSD Test for ES2.mod$ES2_chl.tuk
##
## Mean Square Error:  4.787063
##
## ES2.mod$Treatment:ES2.mod$Dilution,  means
##
##                  ES2.mod.ES2_chl.tuk      std  r      Min       Max
## control:100fold          8.952842 2.033695 24 5.575585 12.443509
## control:25fold           4.211675 2.459674 33 0.000000  8.147445
## DMCC2126:100fold         5.904452 1.432971 30 2.409370  8.294402
## DMCC2126:25fold          2.180805 1.263683 27 0.000000  4.390190
## DMCC2127:100fold         3.720246 2.309541 27 0.000000  6.831014
## DMCC2127:25fold          2.139470 1.622868 27 0.000000  5.873811
## DMCC2165:100fold         3.677465 2.368645 24 0.000000  7.124617
## DMCC2165:25fold          1.925497 1.211620 33 0.000000  3.041187
## DMCC2966:100fold         6.114039 2.778697 33 0.000000  8.510026
## DMCC2966:25fold          6.285168 2.210961 30 0.000000  8.587655
##
## Alpha: 0.05 ; DF Error: 276
## Critical Value of Studentized Range: 4.511094
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Treatments with the same letter are not significantly different.
##
##                  ES2.mod$ES2_chl.tuk groups
```

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

ES2.mod.comp.HSD.group

```
## $statistics
##     MSerror  Df     Mean        CV
##    4.787063 276 4.479861 48.83937
##
## $parameters
##     test                              name.t ntr StudentizedRange alpha
##    Tukey ES2.mod$Treatment:ES2.mod$Dilution  10         4.511094  0.05
##
## $means
##                 ES2.mod$ES2_chl.tuk      std  r      Min       Max      Q25
## control:100fold            8.952842 2.033695 24 5.575585 12.443509 7.860042
## control:25fold             4.211675 2.459674 33 0.000000  8.147445 2.807281
## DMCC2126:100fold           5.904452 1.432971 30 2.409370  8.294402 5.211560
## DMCC2126:25fold            2.180805 1.263683 27 0.000000  4.390190 2.359361
## DMCC2127:100fold           3.720246 2.309541 27 0.000000  6.831014 2.547399
## DMCC2127:25fold            2.139470 1.622868 27 0.000000  5.873811 0.000000
## DMCC2165:100fold           3.677465 2.368645 24 0.000000  7.124617 2.700544
## DMCC2165:25fold            1.925497 1.211620 33 0.000000  3.041187 0.000000
## DMCC2966:100fold           6.114039 2.778697 33 0.000000  8.510026 5.991199
## DMCC2966:25fold            6.285168 2.210961 30 0.000000  8.587655 6.035946
##                     Q50       Q75
## control:100fold 8.279323 10.486003
## control:25fold  4.628247  6.200641
## DMCC2126:100fold 6.189452  6.705312
## DMCC2126:25fold 2.483657  2.863395
## DMCC2127:100fold 3.818594  5.417472
## DMCC2127:25fold 2.531540  2.807481
## DMCC2165:100fold 3.362478  5.745663
## DMCC2165:25fold 2.561469  2.745123
## DMCC2966:100fold 6.963949  7.832392
## DMCC2966:25fold 7.032779  7.590879
##
## $comparison
## NULL
##
## $groups
##                 ES2.mod$ES2_chl.tuk groups
## control:100fold            8.952842      a
## DMCC2966:25fold            6.285168       b
## DMCC2966:100fold           6.114039       b
## DMCC2126:100fold           5.904452      bc
```

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

```
#Complete ANOVA for ES2.mod by treatment by condition, by dilution
ES2.mod.comp.HSD.group <- HSD.test(ES2.mod.chl.anova, c("ES2.mod$Treatment", "ES2.mod$Condition", "ES2.m
                                   main="ES2.mod - Xylaria Chl Contnent (Tukey's Ladder Tran
```

```
##
## Study: ES2.mod - Xylaria Chl Contnent (Tukey's Ladder Transformed Data) by treatment  by dilution at
##
## HSD Test for ES2.mod$ES2_chl.tuk
##
## Mean Square Error:  4.787063
##
## ES2.mod$Treatment:ES2.mod$Condition:ES2.mod$Dilution,  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
##
## 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.mod$ES2_chl.tuk groups
## control:Stationary:100fold            9.210468      a
```

```
## control:Shaking:100fold                8.798267       a
## DMCC2966:Shaking:100fold               7.538945      ab
## DMCC2966:Shaking:25fold                7.310403      abc
## DMCC2126:Stationary:100fold            6.329108     abcd
## DMCC2126:Shaking:100fold               5.267468     bcde
## DMCC2966:Stationary:25fold             5.259932     bcde
## DMCC2165:Stationary:100fold            4.536612     cdef
## DMCC2127:Stationary:100fold            4.521957     cdef
## DMCC2966:Stationary:100fold            4.404150      def
## control:Shaking:25fold                 4.289829      def
## control:Stationary:25fold              4.117890      def
## DMCC2165:Shaking:100fold               2.818319       ef
## DMCC2127:Shaking:100fold               2.718108       ef
## DMCC2126:Stationary:25fold             2.562252       ef
## DMCC2127:Shaking:25fold                2.287858       ef
## DMCC2165:Shaking:25fold                2.131528        f
## DMCC2127:Stationary:25fold             2.020759        f
## DMCC2126:Shaking:25fold                1.990082        f
## DMCC2165:Stationary:25fold             1.753804        f
```

ES2.mod.comp.HSD.group

```
## $statistics
##    MSerror  Df     Mean        CV
##   4.787063 276 4.479861 48.83937
##
## $parameters
##    test                                                   name.t ntr
##    Tukey ES2.mod$Treatment:ES2.mod$Condition:ES2.mod$Dilution   20
##    StudentizedRange alpha
##          5.061243  0.05
##
## $means
##                              ES2.mod$ES2_chl.tuk      std  r       Min        Max
## control:Shaking:100fold               8.798267 1.9828967 15 5.978597  12.194780
## control:Shaking:25fold                4.289829 2.5912255 18 0.000000   8.147445
## control:Stationary:100fold            9.210468 2.2114466  9 5.575585  12.443509
## control:Stationary:25fold             4.117890 2.3786595 15 0.000000   7.776816
## DMCC2126:Shaking:100fold              5.267468 1.9475065 12 2.409370   8.294402
## DMCC2126:Shaking:25fold               1.990082 1.3058091 18 0.000000   3.560255
## DMCC2126:Stationary:100fold           6.329108 0.7558881 18 4.613679   7.397232
## DMCC2126:Stationary:25fold            2.562252 1.1493281  9 0.000000   4.390190
## DMCC2127:Shaking:100fold              2.718108 1.8775300 12 0.000000   5.345709
## DMCC2127:Shaking:25fold               2.287858 1.0938454 12 0.000000   3.266645
## DMCC2127:Stationary:100fold           4.521957 2.3636341 15 0.000000   6.831014
## DMCC2127:Stationary:25fold            2.020759 1.9791611 15 0.000000   5.873811
## DMCC2165:Shaking:100fold              2.818319 2.3433519 12 0.000000   6.550935
## DMCC2165:Shaking:25fold               2.131528 1.1204622 15 0.000000   3.041187
## DMCC2165:Stationary:100fold           4.536612 2.1515647 12 0.000000   7.124617
## DMCC2165:Stationary:25fold            1.753804 1.2887125 18 0.000000   2.933781
## DMCC2966:Shaking:100fold              7.538945 0.8254875 18 6.178283   8.510026
## DMCC2966:Shaking:25fold               7.310403 0.5695012 15 6.079094   8.301844
## DMCC2966:Stationary:100fold           4.404150 3.3283476 15 0.000000   8.380806
## DMCC2966:Stationary:25fold            5.259932 2.7475728 15 0.000000   8.587655
```

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