

POST VR5-KET Image Data ANOVA Mean Cell ns

Jonathan Ramos

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```
library(ggplot2)
library(ggpubr)
library(car) # For levene.test() function
```

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

```
library(emmeans)
library(stringr)
library(MASS)
```

In this rmd file I will simply repeat the statistical procedures that were performed on the PRE-VR5 ketamine image data on this set of PRE-VR5_SAC ketamine image data.

EDA and ANOVA function

This function performs the same type of ANOVA as performed in graphpad prism. In addition, performs some exploratory data analysis to assess normality and homogeneity of variances (both quantitatively and qualitatively)

```
Sidak <- function(pvals)
  # takes a vector of p-values and corrects p-values according to
  # Sidaks method for multiple comparisons (1967)
  #
  # Jonathan Ramos 3/12/2024
  {
    adjusted <- c()
    j <- length(pvals)

    for (i in 1:j){
      adj_p <- 1-(1-pvals[i])^j
      adjusted <- c(adjusted, adj_p)
    }
    return(adjusted)
  }

eda_anova <- function(fname)
  # takes a filename, loads data from csv; data 4 columns:
  # react_treat, react, treat, and norm_int (response var)
  # react_treat is just react and treat in one string separated by "_"
  # builds factor cols for categorical cols (norm_int is numeric, all others are categorical)
  # then performs the following tasks:
  # checks assumptions of normality with qqplot and shapiro wilk tests
```

```

# checks assumptions of equal variances with box plot and levene test
# performs 2way ANOVA (2 by 2, react by treat)
# performs post hoc pairwise comparisons (emmeans of levels of react by treat
# and emmeans of levels of treat by react)
# prints out all statistical test results and returns plot objects
# for the two plots: the qqplots and the box plots
#
# Jonathan Ramos 3/12/2024

{
df <- read.csv(fname, header=TRUE, sep=",")
df$react_treat_factor <- as.factor(df$react_treat)
df$react_factor <- as.factor(df$react)
df$treat_factor <- as.factor(df$treat)

### check assumption of normality
# quantitative assessment
print(tapply(df$norm_int, df$react_treat_factor, shapiro.test))

# qualitative assessment
g <- ggqqplot(df, x="norm_int", facet.by=c("treat_factor", "react_factor"))

### check assumption of equal variances
# quantitative assessment
print(leveneTest(y = df$norm_int, group=df$react_treat_factor, center='mean'))

# qualitative assessment
f <- ggplot(df, aes(x=treat_factor, y=norm_int)) + geom_boxplot(aes(fill=treat_factor), alpha=0.5) +
  #geom_dotplot(binaxis = "y", stackdir = "center", dotsize=0.5) +
  facet_wrap(~react_factor) +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))

# run the ANOVA, display summary
df.lm <- lm(norm_int ~ treat_factor + react_factor + treat_factor*react_factor, contrasts=list(treat_
df.III.aov <- car::Anova(df.lm, type = 3)
print(df.III.aov)

# post hoc pairwise comparisons
emm <- emmeans(df.lm, ~ treat_factor * react_factor)
p1 <- pairs(emm, simple="treat_factor", adjust="tukey")
p2 <- pairs(emm, simple="react_factor", adjust="tukey")

# add col to summary dataframe containing sidak adjusted p-values
adjusted_p.value1 <- Sidak(summary(p1, adjust="tukey")$p.value)
s1 <- summary(p1)
s1['adjusted_p.value'] <- adjusted_p.value1

adjusted_p.value2 <- Sidak(summary(p2, adjust="tukey")$p.value)
s2 <- summary(p2)
s2['adjusted_p.value'] <- adjusted_p.value2

# display results
print(s1)

```

```

print(s2)

return(list(g, f))
}

eda_anova_1way <- function(fname)
# doc
{
df <- read.csv(fname, header=TRUE, sep=",")
df$treat_factor <- as.factor(df$treat)

df <- df[df$react == "VR5",c('norm_adj_mmbg','treat_factor','react')]

### check assumption of normality
# quantitative assessment
print(tapply(df$norm_adj_mmbg, df$treat_factor, shapiro.test))

# qualitative assessment
g <- ggqqplot(df, x="norm_adj_mmbg", facet.by=c("treat_factor"))
g

### check assumption of equal variances
# quantitative assessment
print(leveneTest(y=df$norm_adj_mmbg, group=df$treat_factor, center='mean'))

# qualitative assessment
f <- ggplot(df, aes(x=treat_factor, y=norm_adj_mmbg)) + geom_boxplot(aes(fill=treat_factor), alpha=0.5)
#geom_dotplot(binaxis = "y", stackdir = "center", dotsize=0.5, alpha=0.5)
theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
f

# run the ANOVA, display summary
# since this is just a one way ANOVA with only 2 levels, this is essentially just a t-test
# ANOVA is performed here for consistency
df.lm <- lm(norm_adj_mmbg ~ treat_factor, data=df)
df.III.aov <- car::Anova(df.lm, type = 3)
print(df.III.aov)

# now let's actually just do the t-test
print(t.test(df[df$treat_factor == "KET",]$norm_adj_mmbg, df[df$treat_factor == "SAL",]$norm_adj_mmbg))

# KS test
print(kruskal.test(norm_adj_mmbg ~ treat_factor, data=df))

# no post hoc is required for 1way ANOVA with 2 levels
# return figure objects only
return(list(g, f))
}

```

```

### this time with boxcox transformation first
eda_anova_1way_boxcox <- function(fname)
# doc
{
df <- read.csv(fname, header=TRUE, sep=",")
df$treat_factor <- as.factor(df$treat)
df <- df[df$react == "VR5",c('norm_adj_mmbg','treat_factor','react')]
print(df$coloc_stain_type)

norm.adj.mmbg <- c(df$norm_adj_mmbg)
norm.adj.mmbg <- norm.adj.mmbg + 0.00000001

# apply boxcox over range of lambdas
b <- boxcox(lm(norm.adj.mmbg ~ 1))

# Exact best lambda
lambda.best <- b$x[which.max(b$y)]
print("best lamda")
print(lambda.best)

boxcox.transformed <- c()
j <- length(norm.adj.mmbg)
for (i in 1:j){
  transformed.x <- (norm.adj.mmbg[i]^lambda.best-1)/lambda.best
  boxcox.transformed <- c(boxcox.transformed, transformed.x)
}
df$norm.adj.mmbg.boxcox <- boxcox.transformed

### check assumption of normality
# quantitative assessment
print(tapply(df$norm.adj.mmbg.boxcox, df$treat_factor, shapiro.test))

# qualitative assessment
g <- ggqqplot(df, x="norm.adj.mmbg.boxcox", facet.by=c("treat_factor"))
g

### check assumption of equal variances
# quantitative assessment
print(leveneTest(y=df$norm.adj.mmbg.boxcox, group=df$treat_factor, center='mean'))

# qualitative assessment
f <- ggplot(df, aes(x=treat_factor, y=norm.adj.mmbg.boxcox)) + geom_boxplot(aes(fill=treat_factor), a
  #geom_dotplot(binaxis = "y", stackdir = "center", dotsize=0.5, alpha=0.5)
theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
f

# run the ANOVA, display summary
# since this is just a one way ANOVA with only 2 levels, this is essentially just a t-test
# ANOVA is performed here for consistency
df.lm <- lm(norm.adj.mmbg.boxcox ~ treat_factor, data=df)
df.III.aov <- car::Anova(df.lm, type = 3)

```

```

print(df.III.aov)

# now let's actually just do the t-test
print(t.test(df[df$treat_factor == "KET"],$norm.adj.mmbg.boxcox, df[df$treat_factor == "SAL"],$norm.a

# KS test
print(kruskal.test(norm.adj.mmbg.boxcox ~ treat_factor, data=df))

# no post hoc is required for 1way ANOVA with 2 levels
# return figure objects only
return(list(g, f))
}

```

pulling out filenames

```

fnames <- list.files(path='NORM',pattern='NORM.csv', full.names=TRUE)
fnames

## [1] "NORM/KET-VR5_cFos_coloc_w_PV_NORM.csv"
## [2] "NORM/KET-VR5_cFos_coloc_w_WFA_NORM.csv"
## [3] "NORM/KET-VR5_PV_coloc_w_cFos_NORM.csv"
## [4] "NORM/KET-VR5_PV_coloc_w_WFA_NORM.csv"
## [5] "NORM/KET-VR5_single_cFos_NORM.csv"
## [6] "NORM/KET-VR5_single_PV_NORM.csv"
## [7] "NORM/KET-VR5_single_WFA_NORM.csv"
## [8] "NORM/KET-VR5_triple_cFos_NORM.csv"
## [9] "NORM/KET-VR5_triple_PV_NORM.csv"
## [10] "NORM/KET-VR5_triple_WFA_NORM.csv"
## [11] "NORM/KET-VR5_WFA_coloc_w_cFos_NORM.csv"
## [12] "NORM/KET-VR5_WFA_coloc_w_PV_NORM.csv"

```

single PV

```
i <- str_which(fnames, "single_PV")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_single_PV_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.95439, p-value = 1.861e-08
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.92737, p-value = 2.869e-13
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1    1e-04 0.9931
```

```
##          733
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##          Sum Sq Df    F value Pr(>F)
```

```
## (Intercept) 303.975  1 1148.8126 <2e-16 ***
```

```
## treat_factor  0.061  1    0.2292 0.6322
```

```
## Residuals    193.951 733
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -0.48011, df = 696.93, p-value = 0.6313
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.09318228 0.05656431
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.971607 0.989916
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

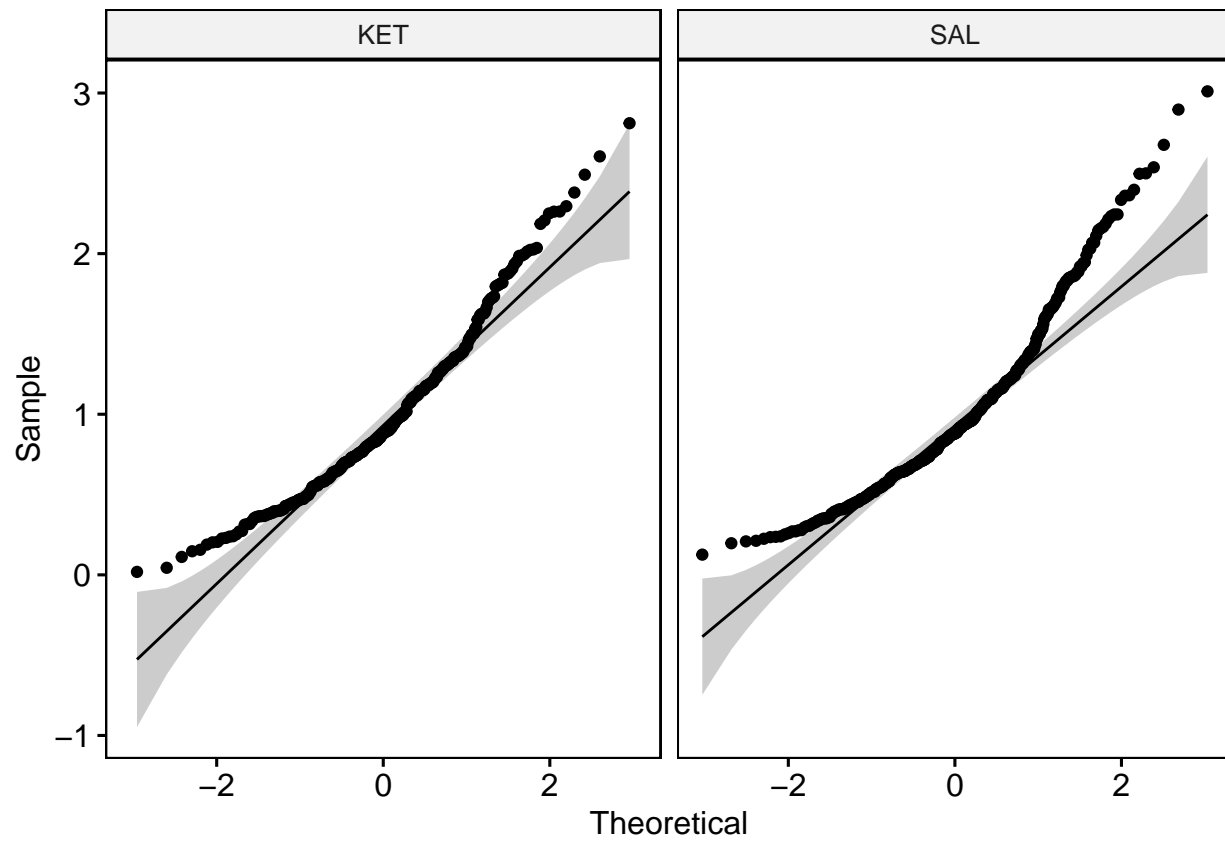
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 0.048198, df = 1, p-value = 0.8262
```

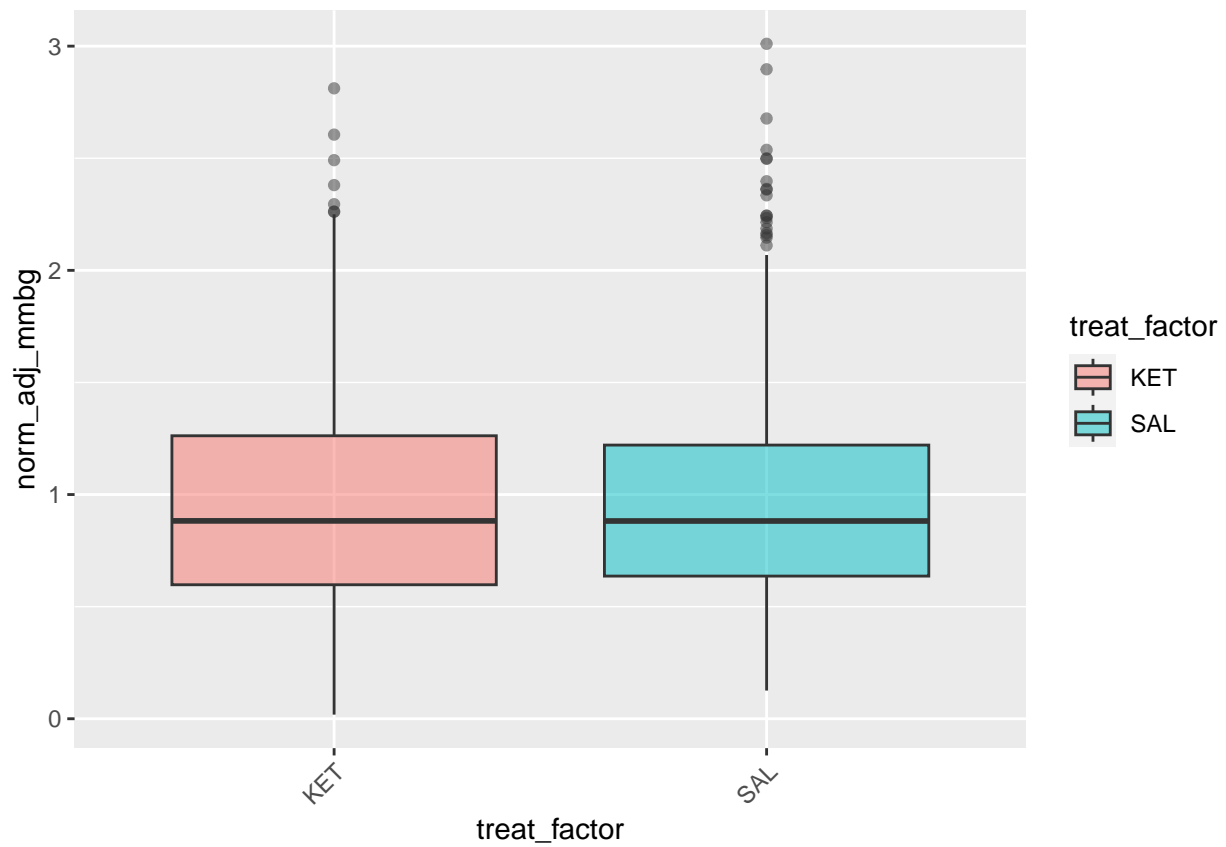
```
figs[1]
```

```
## [[1]]
```



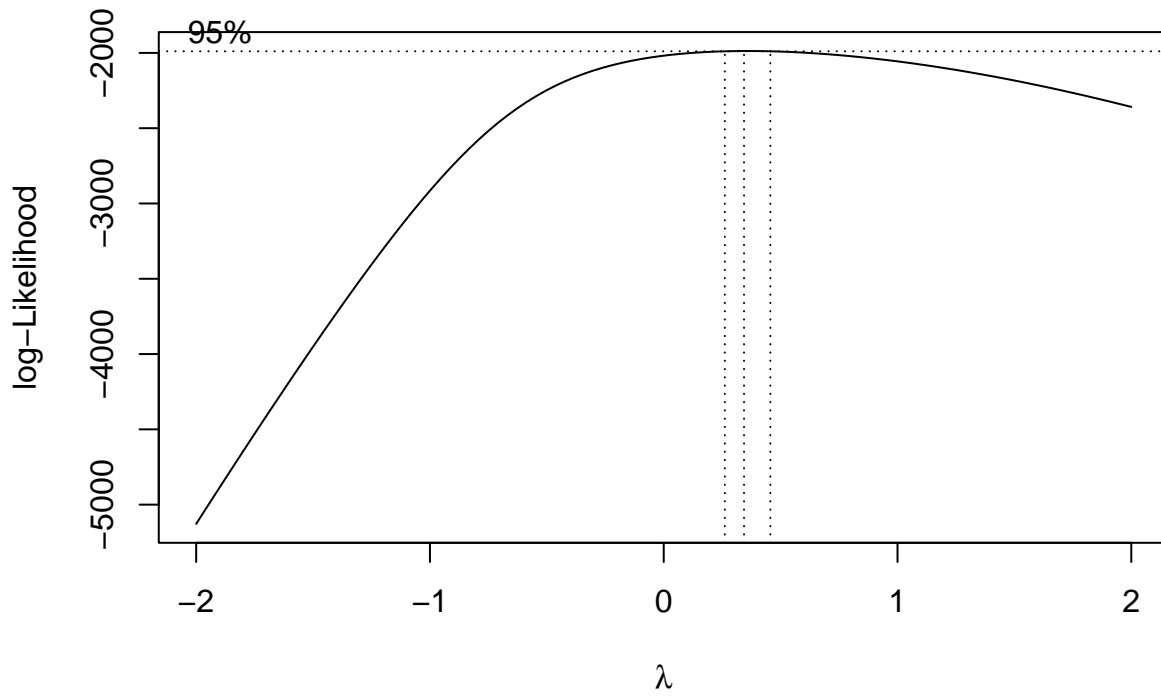
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

```
## [1] 0.3434343
```

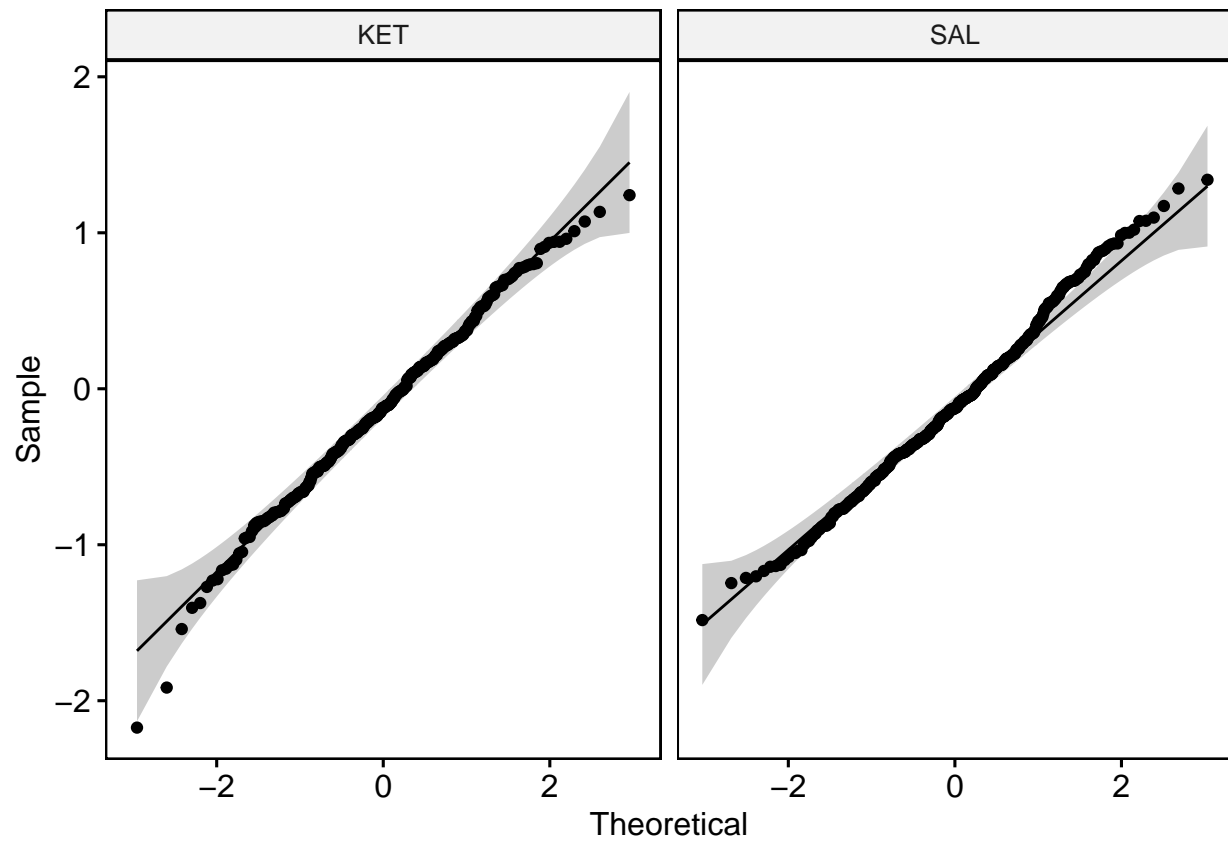


```

## $KET
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.99338, p-value = 0.169
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.99405, p-value = 0.1064
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.6278 0.4284
##      733
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##      Sum Sq Df F value    Pr(>F)
## (Intercept)  4.828  1 17.7575 2.822e-05 ***
## treat_factor  0.123  1  0.4509  0.5021
## Residuals    199.276 733
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -0.66727, df = 672.36, p-value = 0.5048
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1026249  0.0505651
## sample estimates:
##  mean of x  mean of y
## -0.1224443 -0.0964144
##
##
## Kruskal-Wallis rank sum test
##
## data:  norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 0.048198, df = 1, p-value = 0.8262
figs[1]

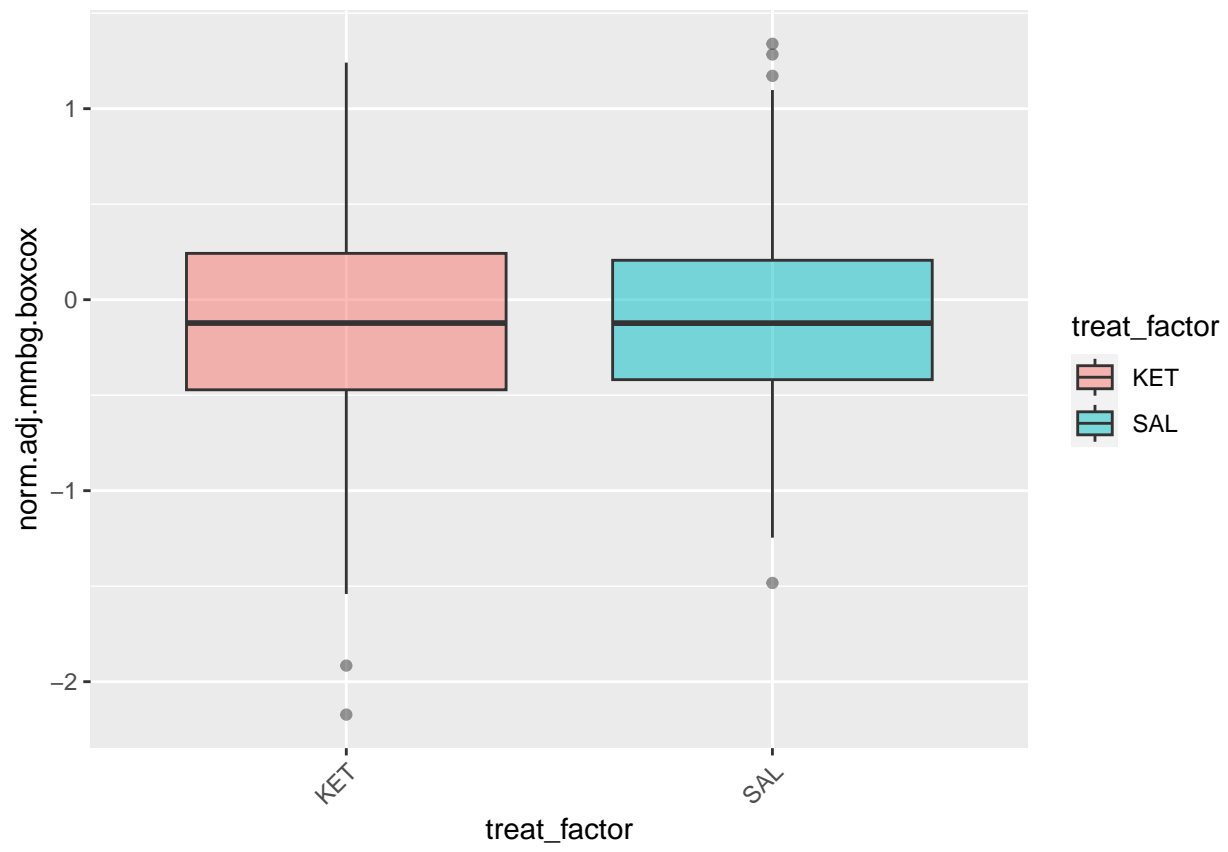
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



single WFA

```
i <- str_which(fnames, "single_WFA")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_single_WFA_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.9802, p-value = 2.873e-05
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.92259, p-value = 2.112e-13
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value    Pr(>F)
```

```
## group    1 12.388 0.0004568 ***
```

```
##          791
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##              Sum Sq Df   F value  Pr(>F)
```

```
## (Intercept) 319.38   1 1774.6337 < 2e-16 ***
```

```
## treat_factor  0.52   1   2.9139 0.08821 .
```

```
## Residuals    142.36 791
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = 1.7054, df = 738.91, p-value = 0.08855
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.007775929 0.110640912
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.8958081 0.8443756
```

```
##
```

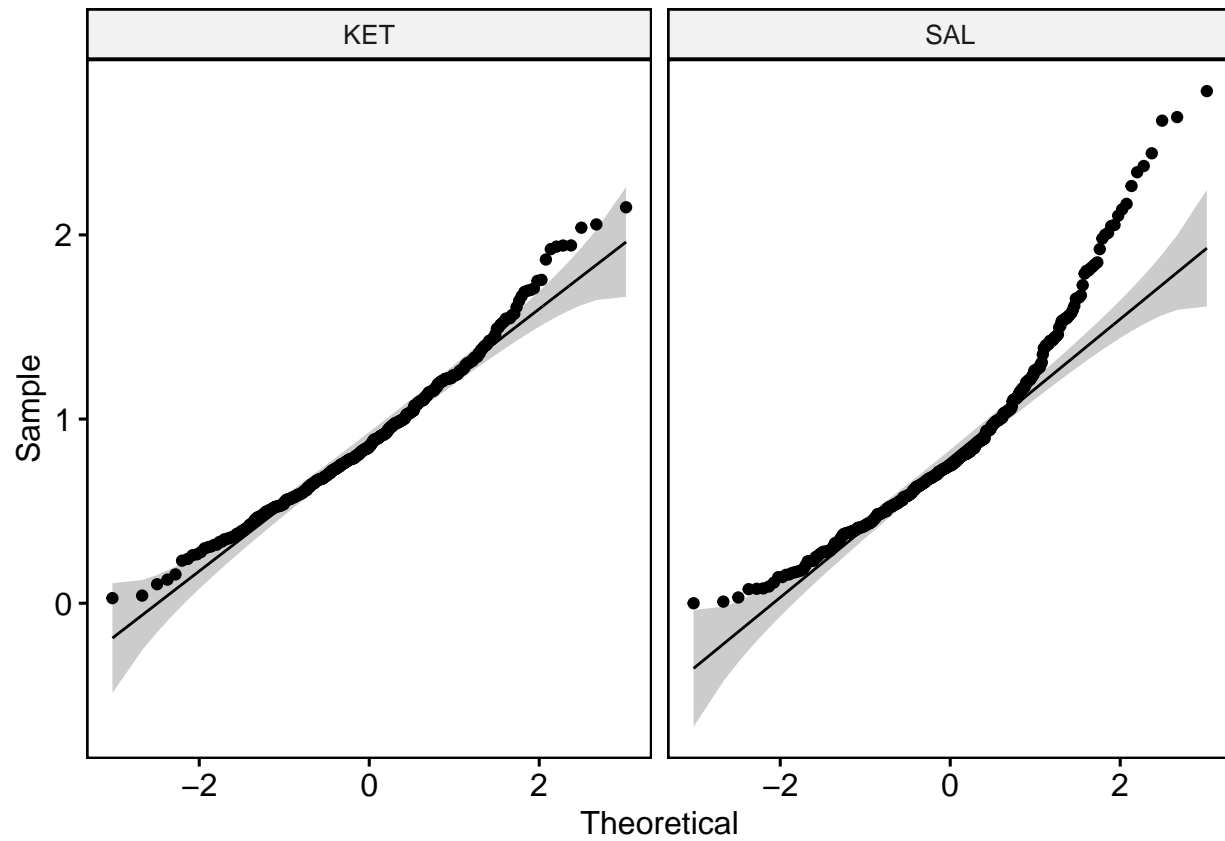
```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##  
## data: norm_adj_mmbg by treat_factor  
## Kruskal-Wallis chi-squared = 11.168, df = 1, p-value = 0.0008324
```

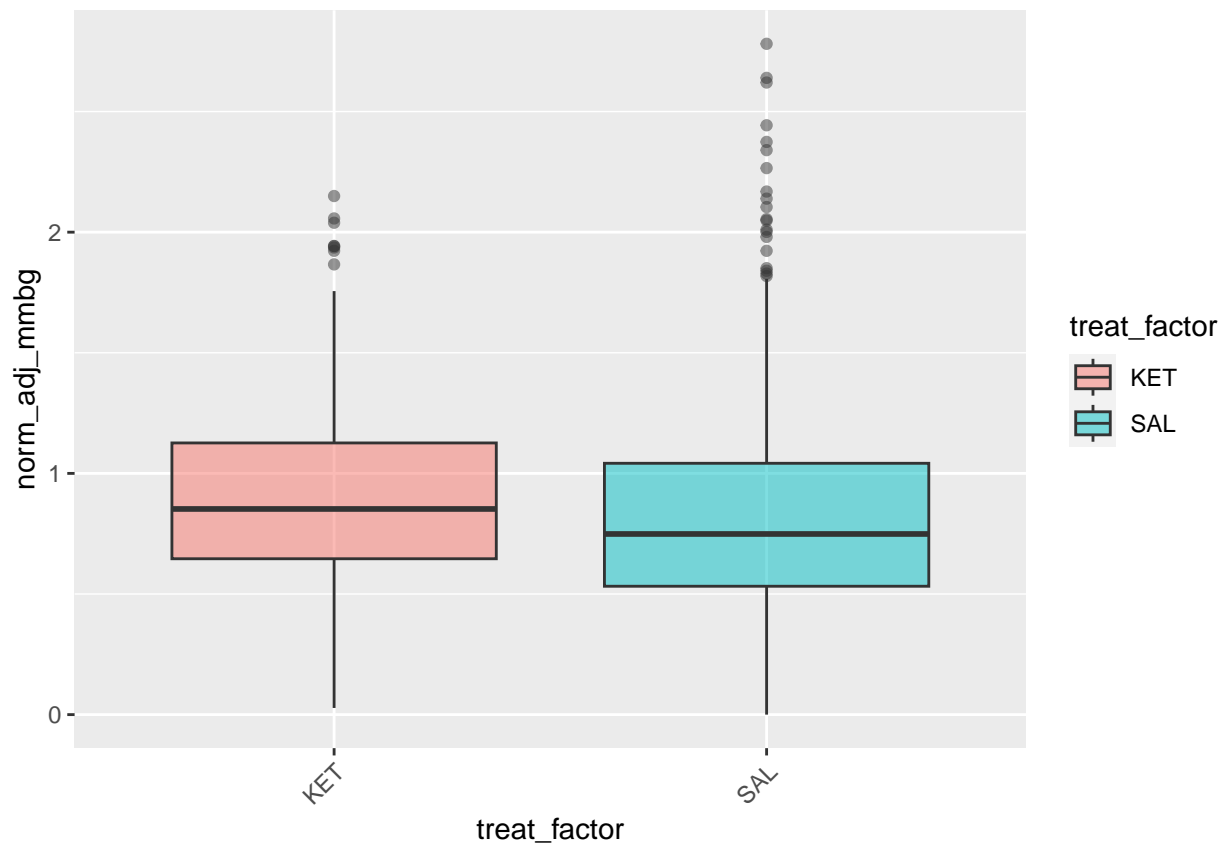
```
figs[1]
```

```
## [[1]]
```



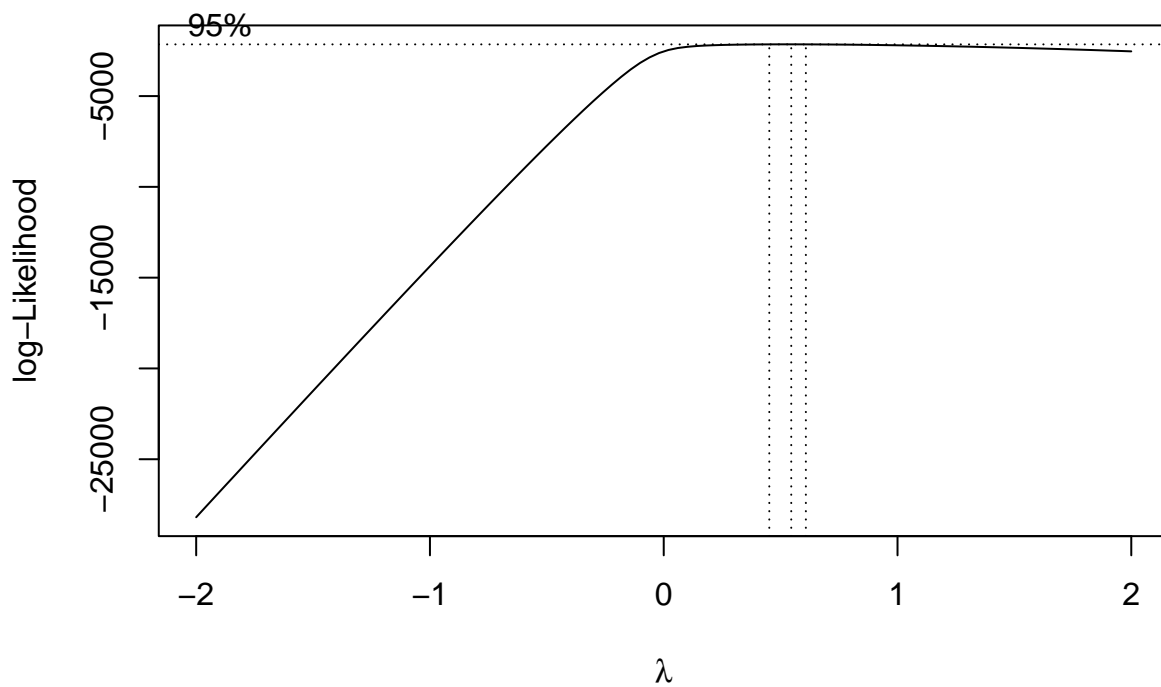
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

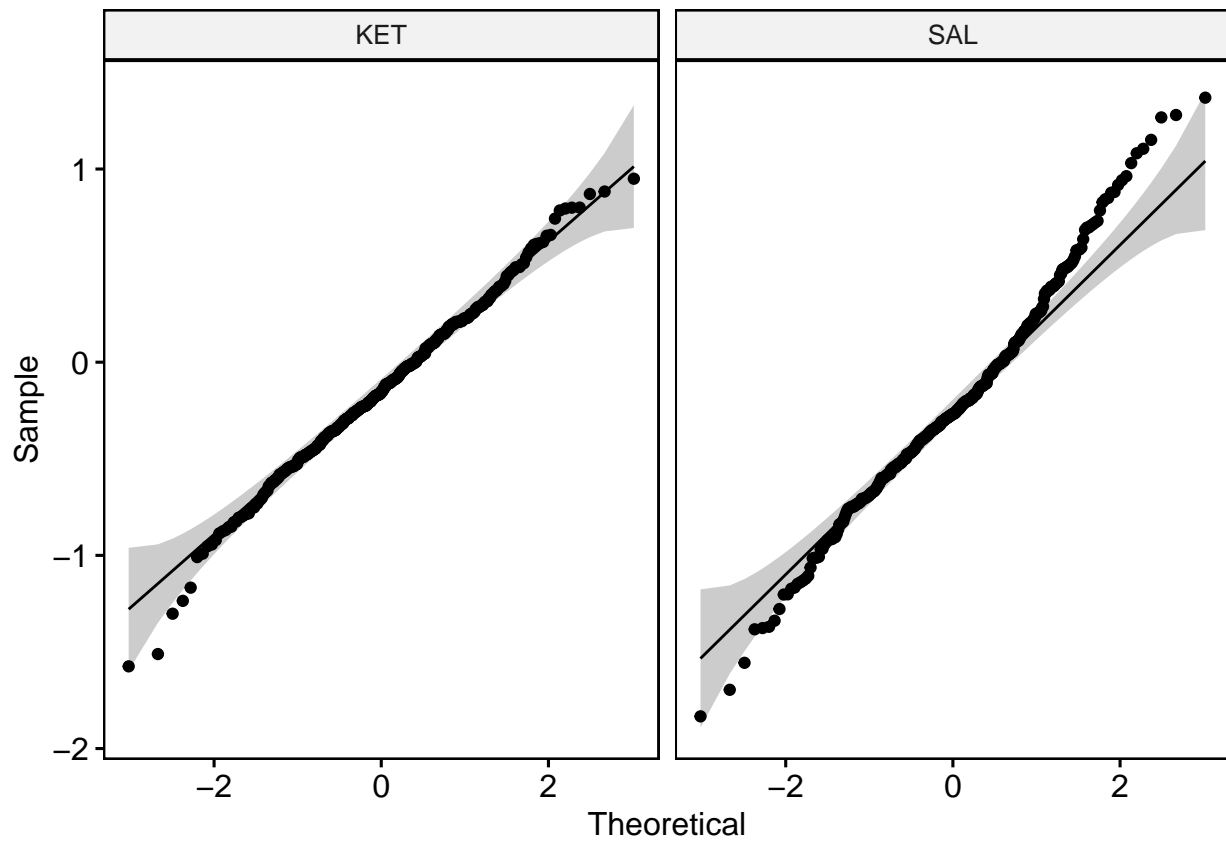
```
## [1] 0.5454545
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99431, p-value = 0.1451
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.98674, p-value = 0.001137
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value    Pr(>F)
## group 1  13.314 0.0002807 ***
##      791
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##              Sum Sq Df F value    Pr(>F)
## (Intercept)   8.344  1 40.6295 3.124e-10 ***
## treat_factor   1.335  1   6.5003  0.01097 *
## Residuals    162.437 791
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 2.5472, df = 743.26, p-value = 0.01106
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.01881421 0.14530004
## sample estimates:
## mean of x mean of y
## -0.1447885 -0.2268456
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 11.168, df = 1, p-value = 0.0008324
figs[1]

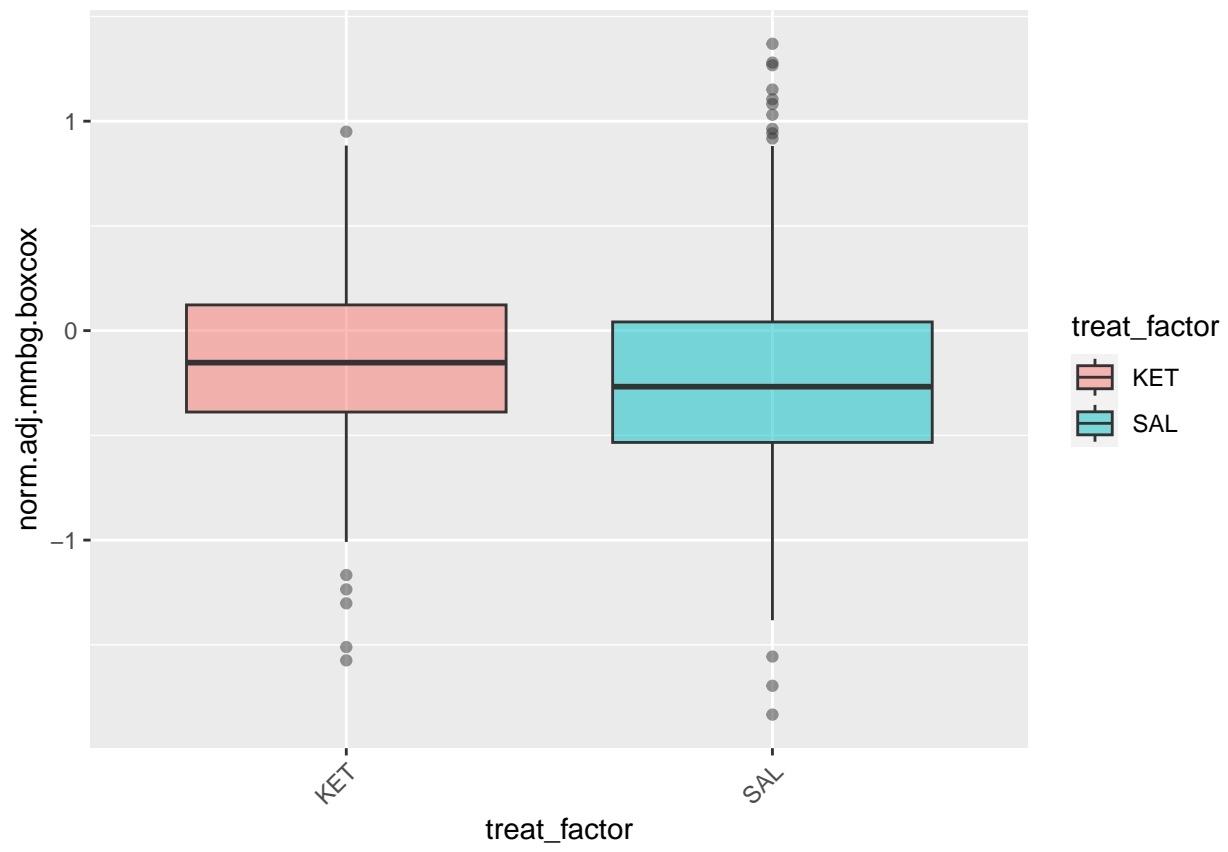
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```

Single c-Fos

```
i <- str_which(fnames, "single_cFos")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_single_cFos_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.84536, p-value < 2.2e-16
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.84617, p-value < 2.2e-16
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1  1.4207 0.2333
```

```
##          4620
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##          Sum Sq   Df    F value    Pr(>F)
```

```
## (Intercept) 2601.54    1 8431.6331 < 2e-16 ***
```

```
## treat_factor   1.81    1   5.8814 0.01534 *
```

```
## Residuals    1425.48 4620
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -2.429, df = 4603.1, p-value = 0.01518
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.07169374 -0.00765307
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 1.036830 1.076504
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

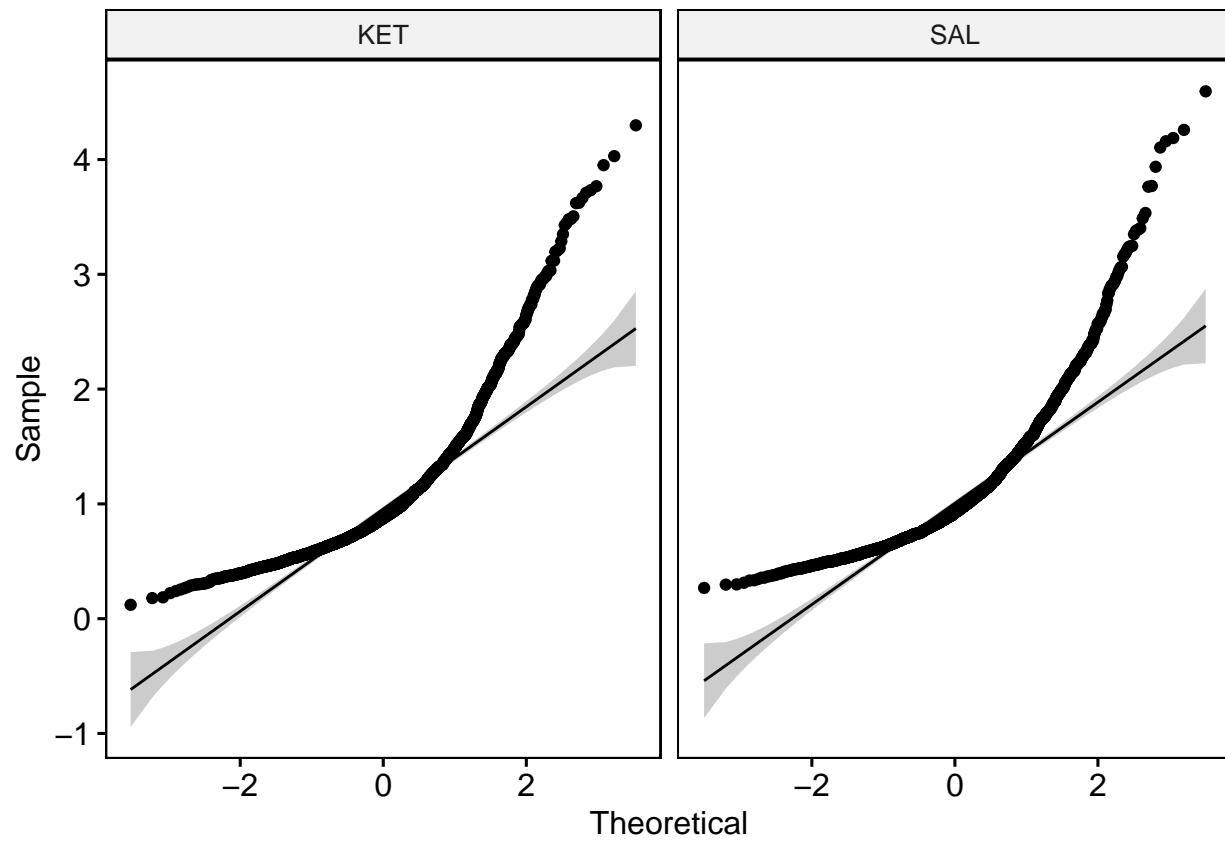
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 17.037, df = 1, p-value = 3.665e-05
```

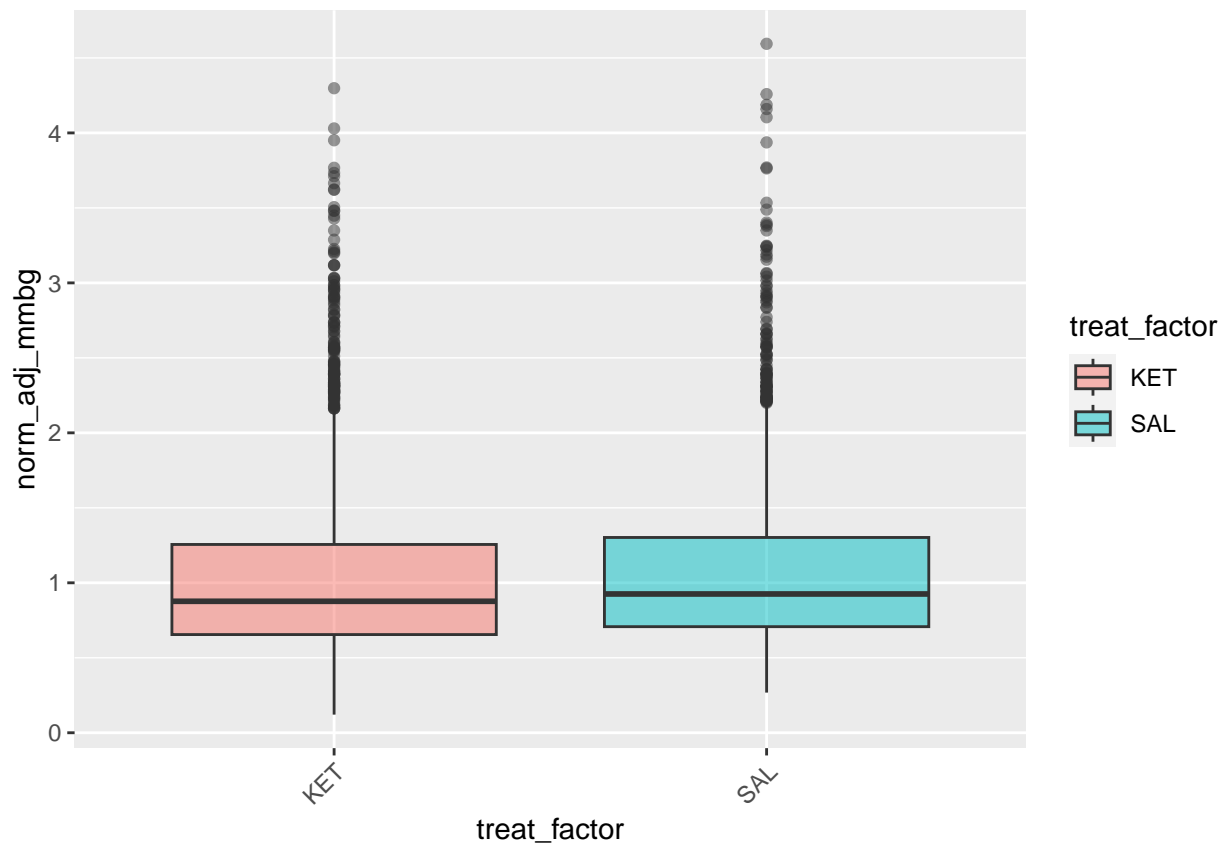
```
figs[1]
```

```
## [[1]]
```



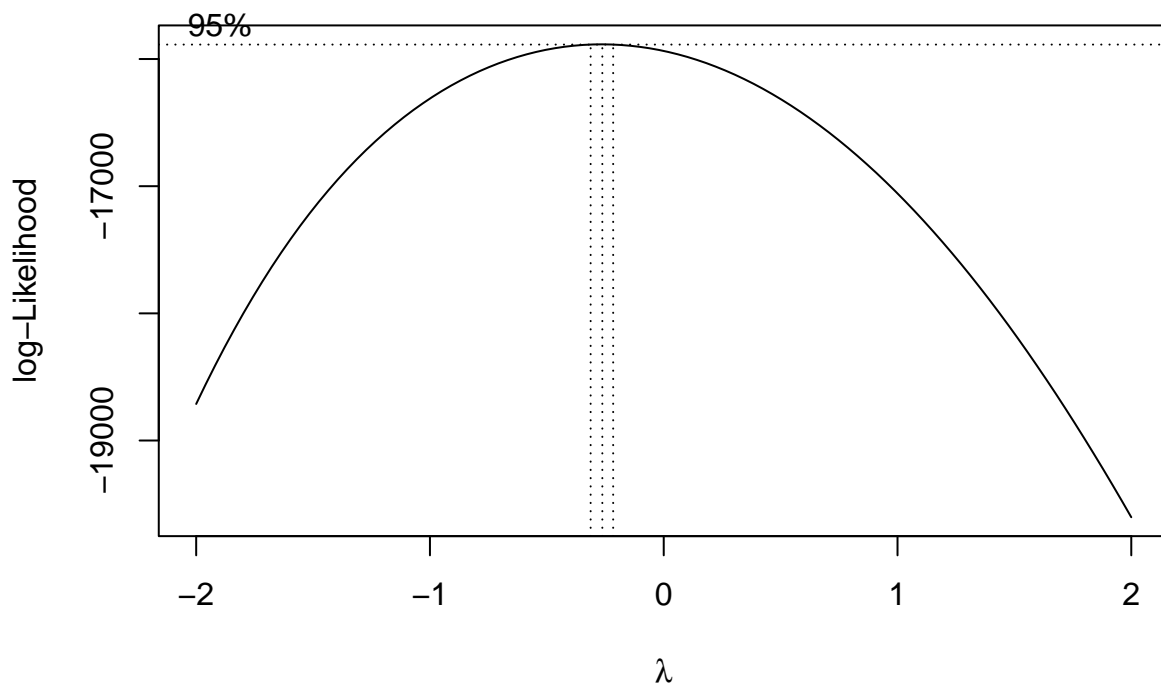
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

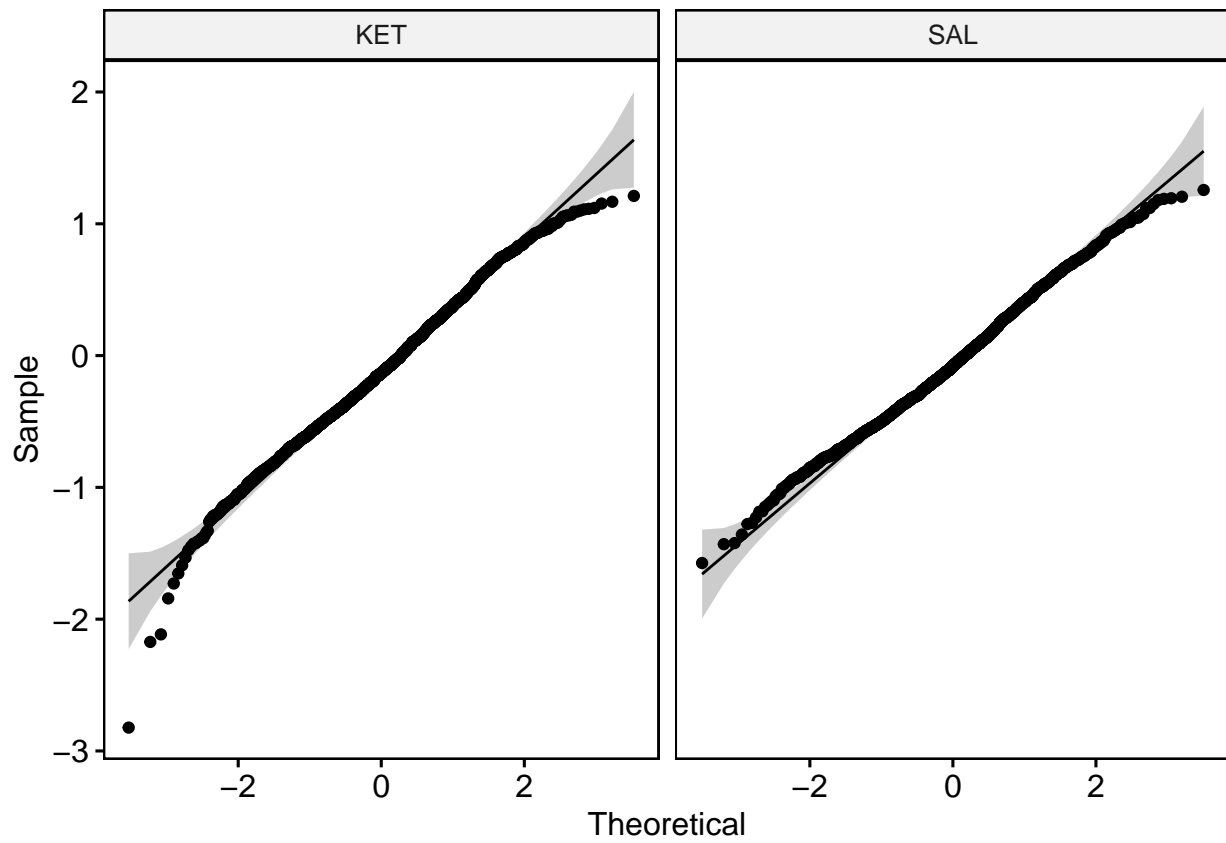
```
## [1] -0.2626263
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99474, p-value = 1.421e-07
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99632, p-value = 3.428e-05
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value    Pr(>F)
## group  1 16.018 6.372e-05 ***
##      4620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##           Sum Sq   Df F value    Pr(>F)
## (Intercept)  32.58    1 151.717 < 2.2e-16 ***
## treat_factor   4.20    1  19.575 9.894e-06 ***
## Residuals    992.24 4620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -4.4459, df = 4619.7, p-value = 8.958e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.08701482 -0.03375832
## sample estimates:
##  mean of x   mean of y
## -0.11603709 -0.05565052
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 17.037, df = 1, p-value = 3.665e-05
figs[1]

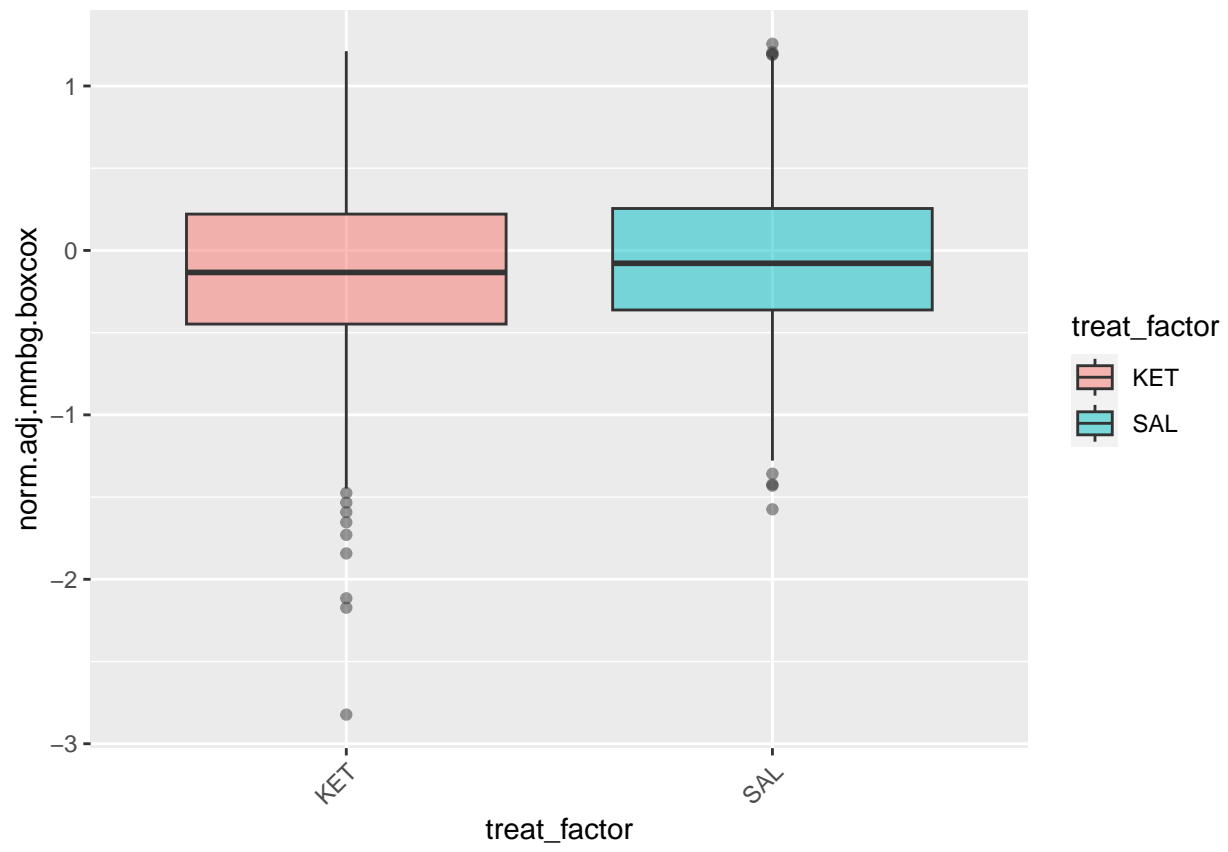
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



Single c-Fos

```
i <- str_which(fnames, "single_cFos")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_single_cFos_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.84536, p-value < 2.2e-16
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.84617, p-value < 2.2e-16
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1  1.4207 0.2333
```

```
##          4620
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##          Sum Sq   Df    F value    Pr(>F)
```

```
## (Intercept) 2601.54    1 8431.6331 < 2e-16 ***
```

```
## treat_factor   1.81    1   5.8814 0.01534 *
```

```
## Residuals    1425.48 4620
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -2.429, df = 4603.1, p-value = 0.01518
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.07169374 -0.00765307
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 1.036830 1.076504
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
```

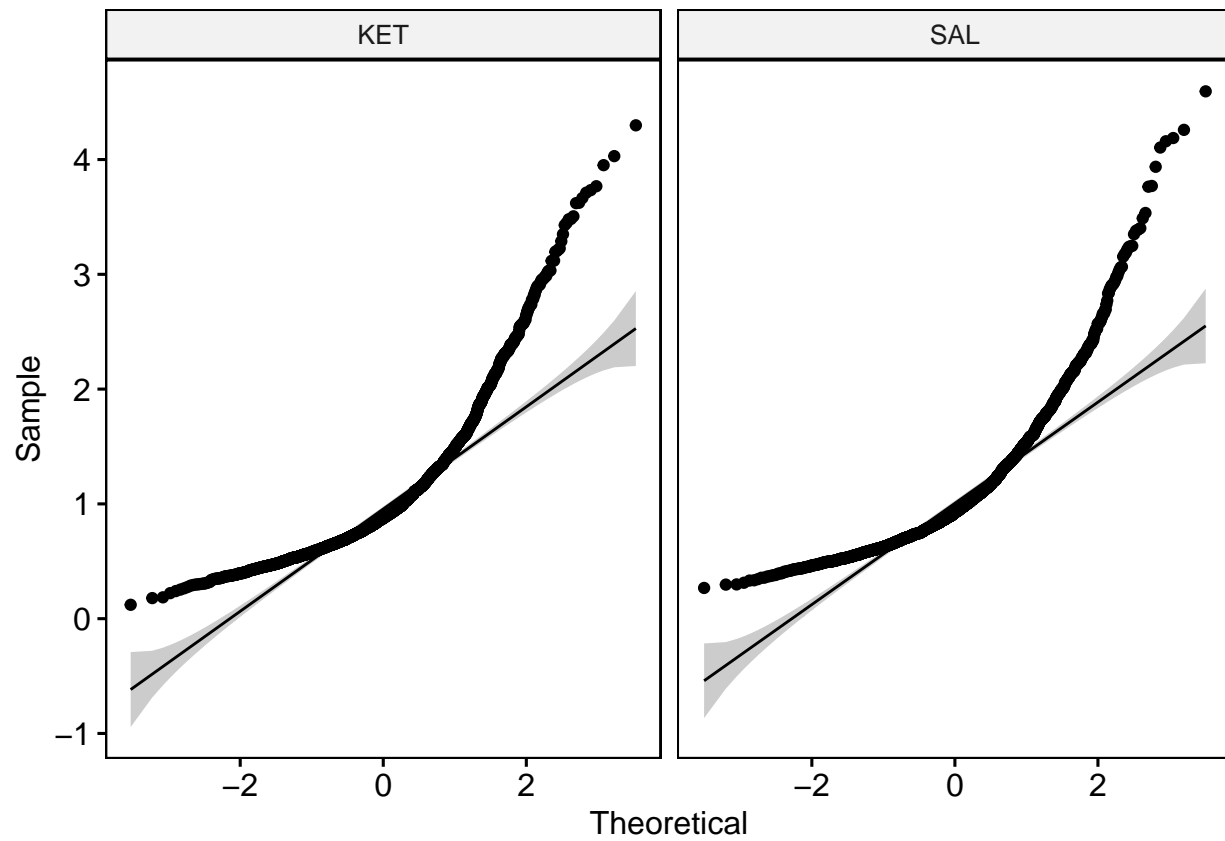
```
## data: norm_adj_mmbg by treat_factor
```



```
## Kruskal-Wallis chi-squared = 17.037, df = 1, p-value = 3.665e-05
```

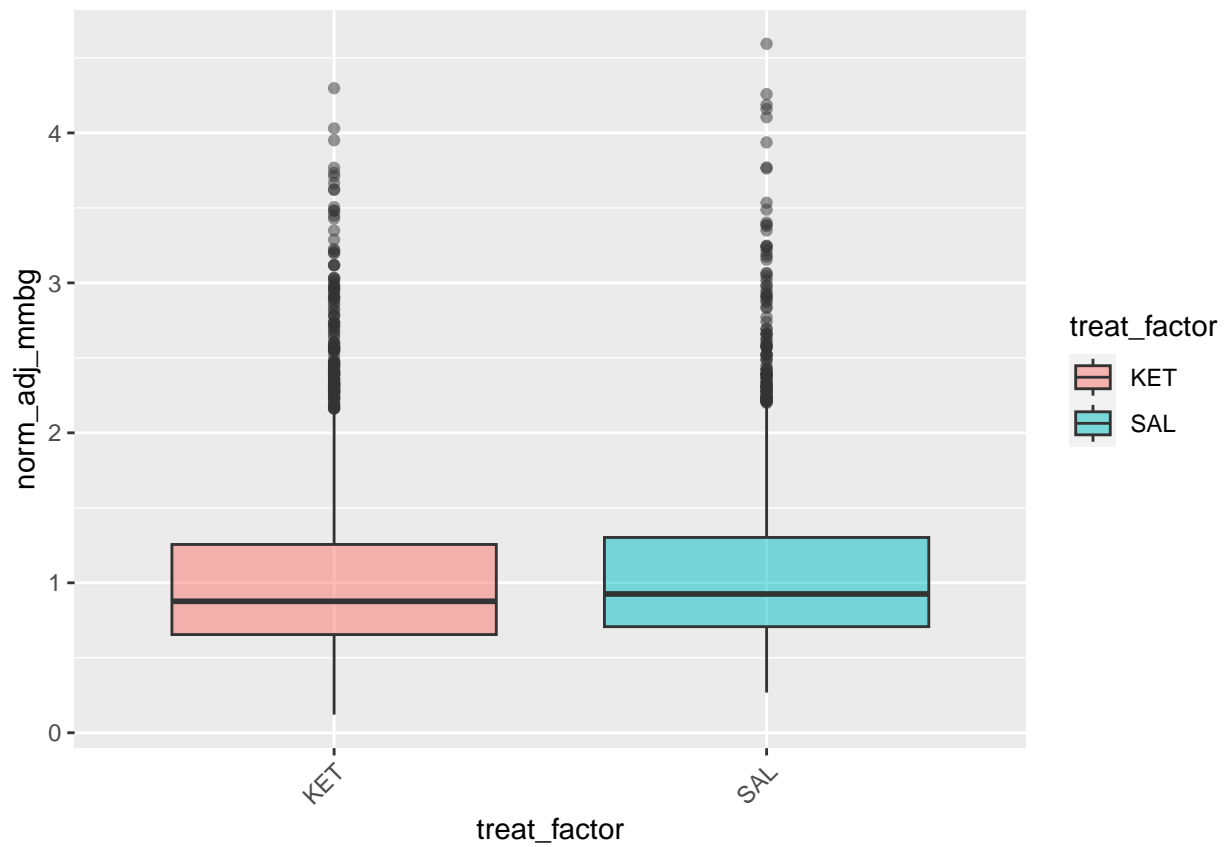
```
figs[1]
```

```
## [[1]]
```



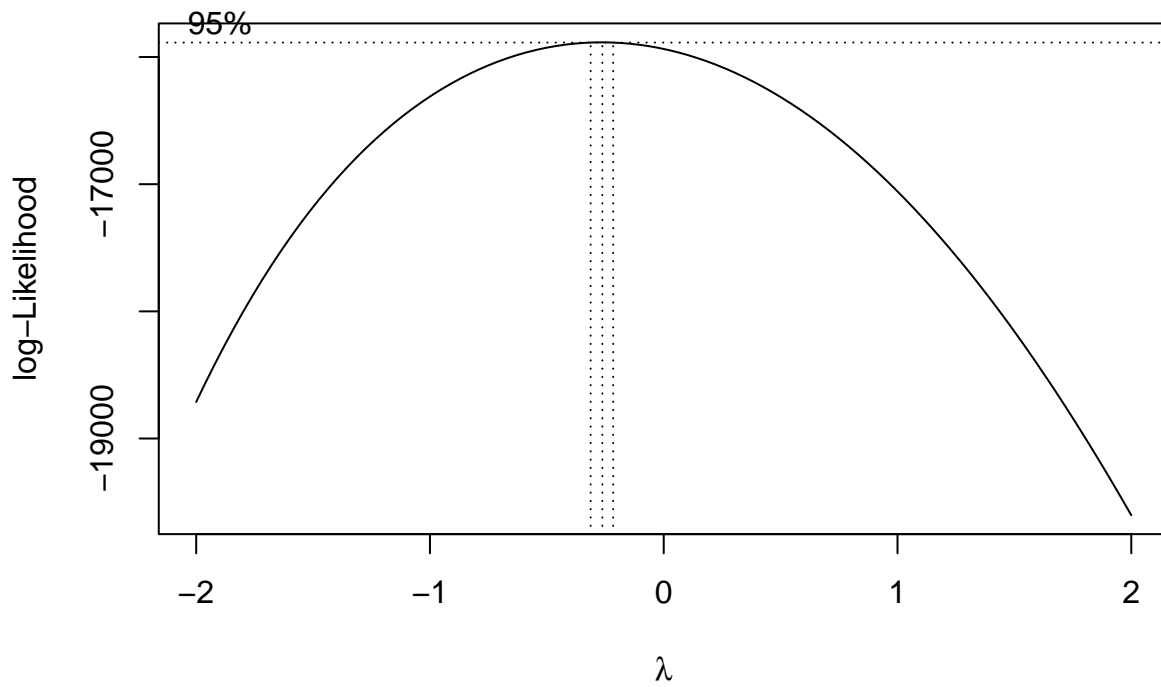
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

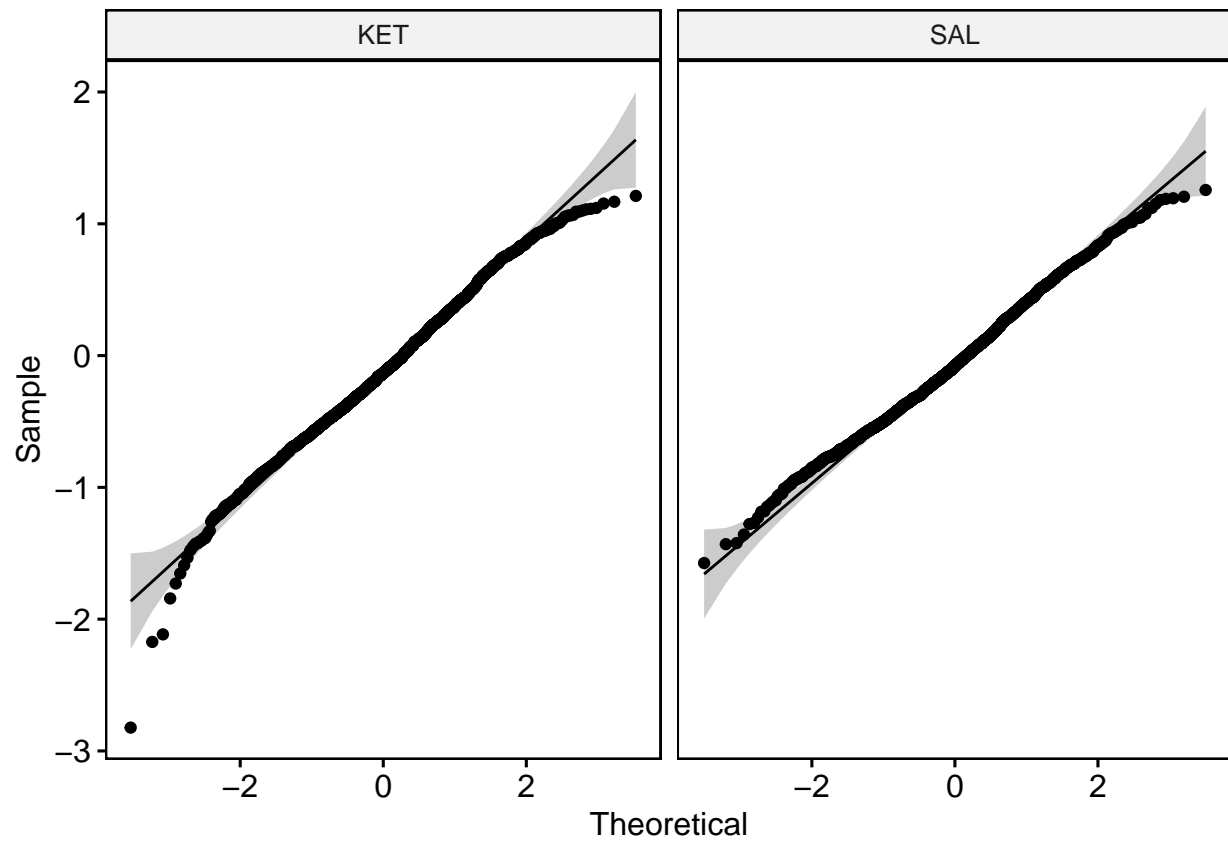
```
## [1] -0.2626263
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99474, p-value = 1.421e-07
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99632, p-value = 3.428e-05
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value    Pr(>F)
## group  1  16.018 6.372e-05 ***
##      4620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##           Sum Sq   Df F value    Pr(>F)
## (Intercept)  32.58    1 151.717 < 2.2e-16 ***
## treat_factor   4.20    1  19.575 9.894e-06 ***
## Residuals    992.24 4620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -4.4459, df = 4619.7, p-value = 8.958e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.08701482 -0.03375832
## sample estimates:
##  mean of x   mean of y
## -0.11603709 -0.05565052
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 17.037, df = 1, p-value = 3.665e-05
figs[1]

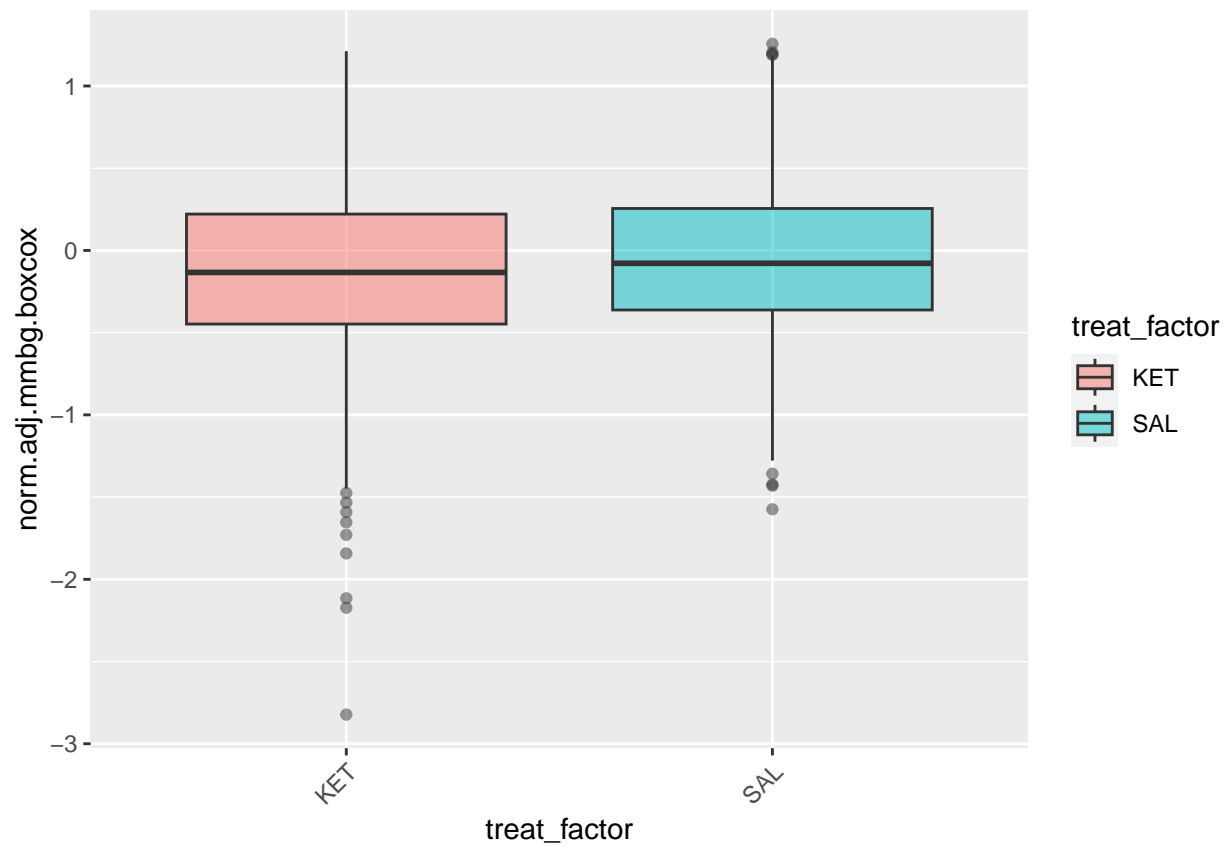
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



PV coloc w WFA

```
i <- str_which(fnames, "PV_coloc_w_WFA")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_PV_coloc_w_WFA_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.96259, p-value = 0.003747
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.92828, p-value = 1.176e-06
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1  0.1105 0.7399
```

```
##          251
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##          Sum Sq Df F value Pr(>F)
```

```
## (Intercept) 122.399  1 415.6615 <2e-16 ***
```

```
## treat_factor  0.005  1  0.0181 0.8929
```

```
## Residuals    73.912 251
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -0.13555, df = 237.7, p-value = 0.8923
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.1441739  0.1256107
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 1.059684 1.068966
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

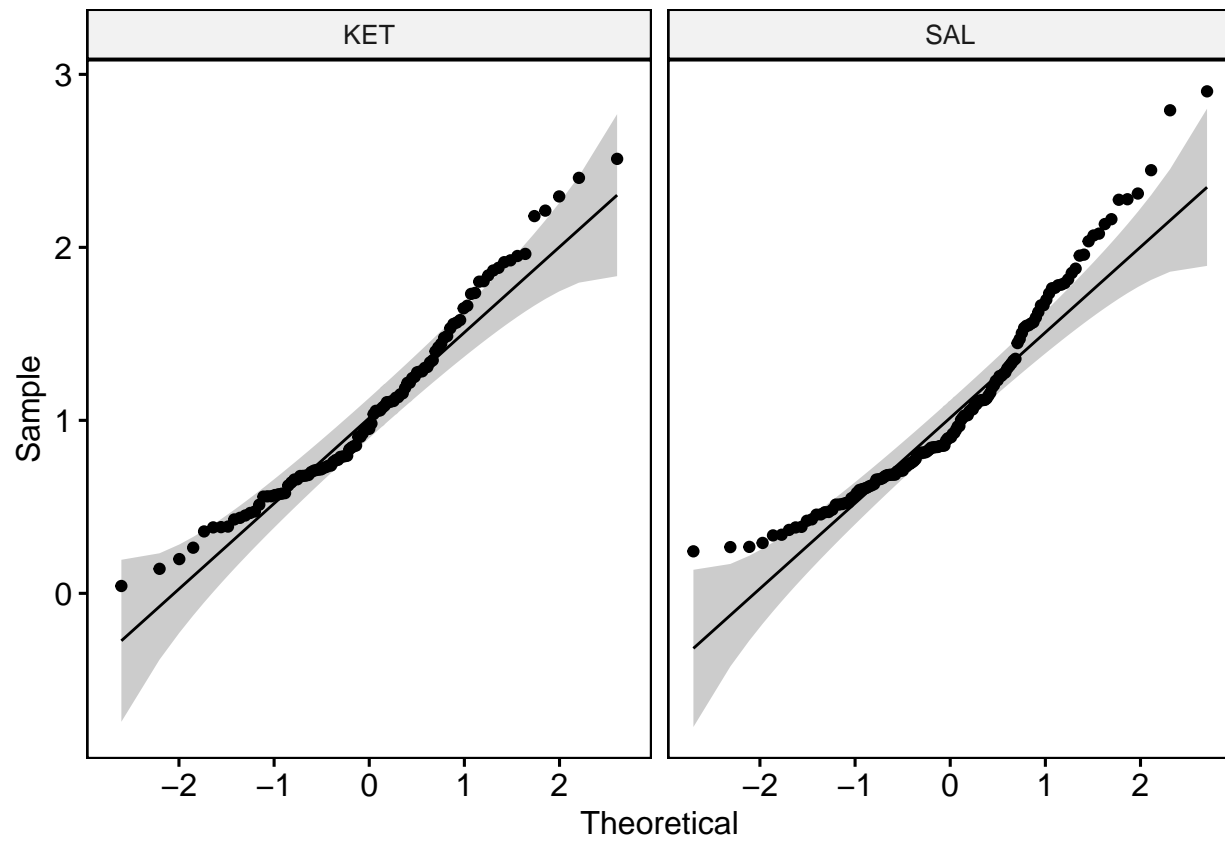
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 0.013512, df = 1, p-value = 0.9075
```

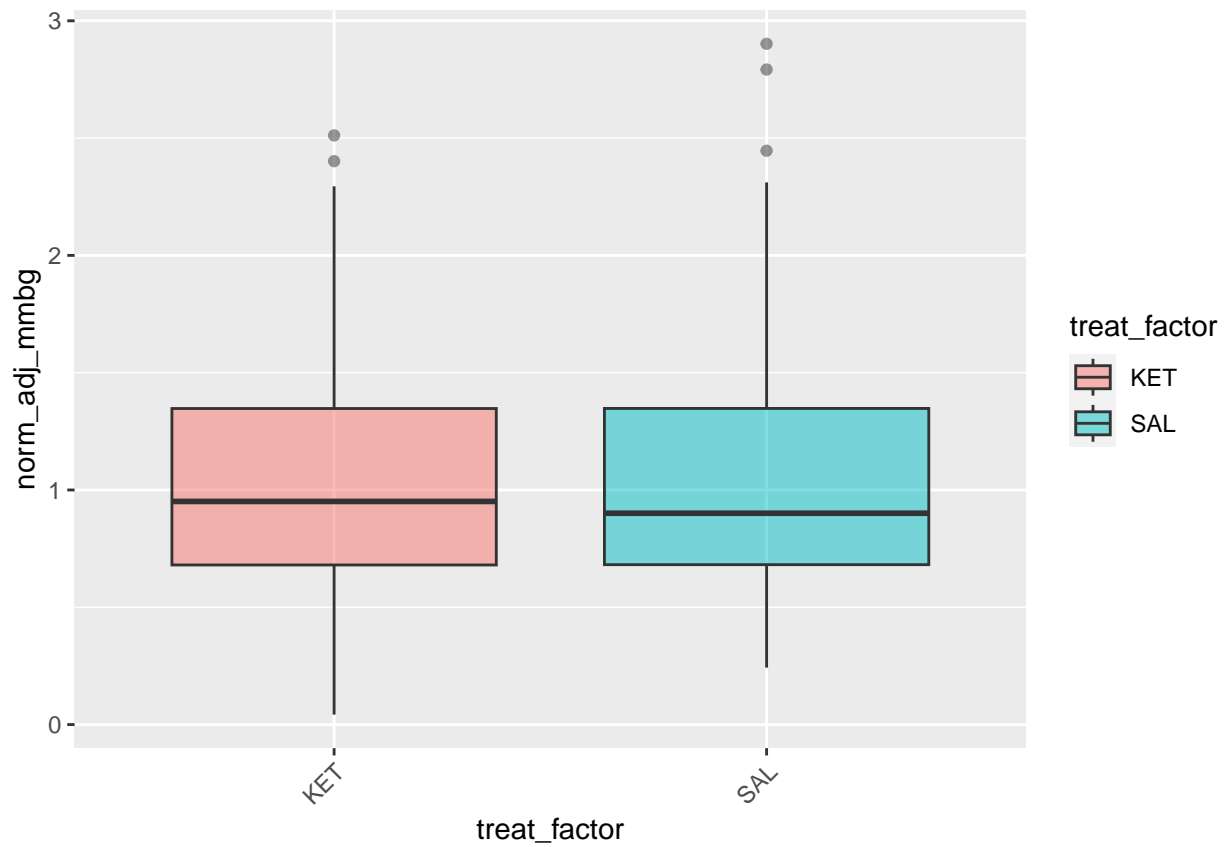
```
figs[1]
```

```
## [[1]]
```



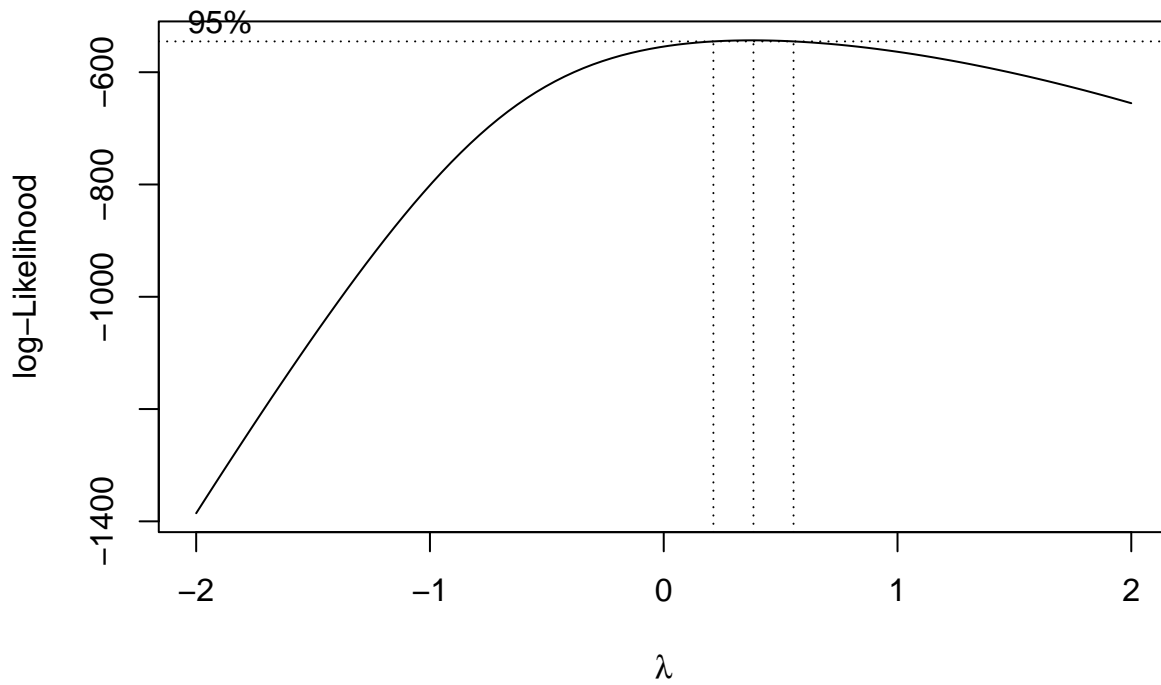
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

```
## [1] 0.3838384
```

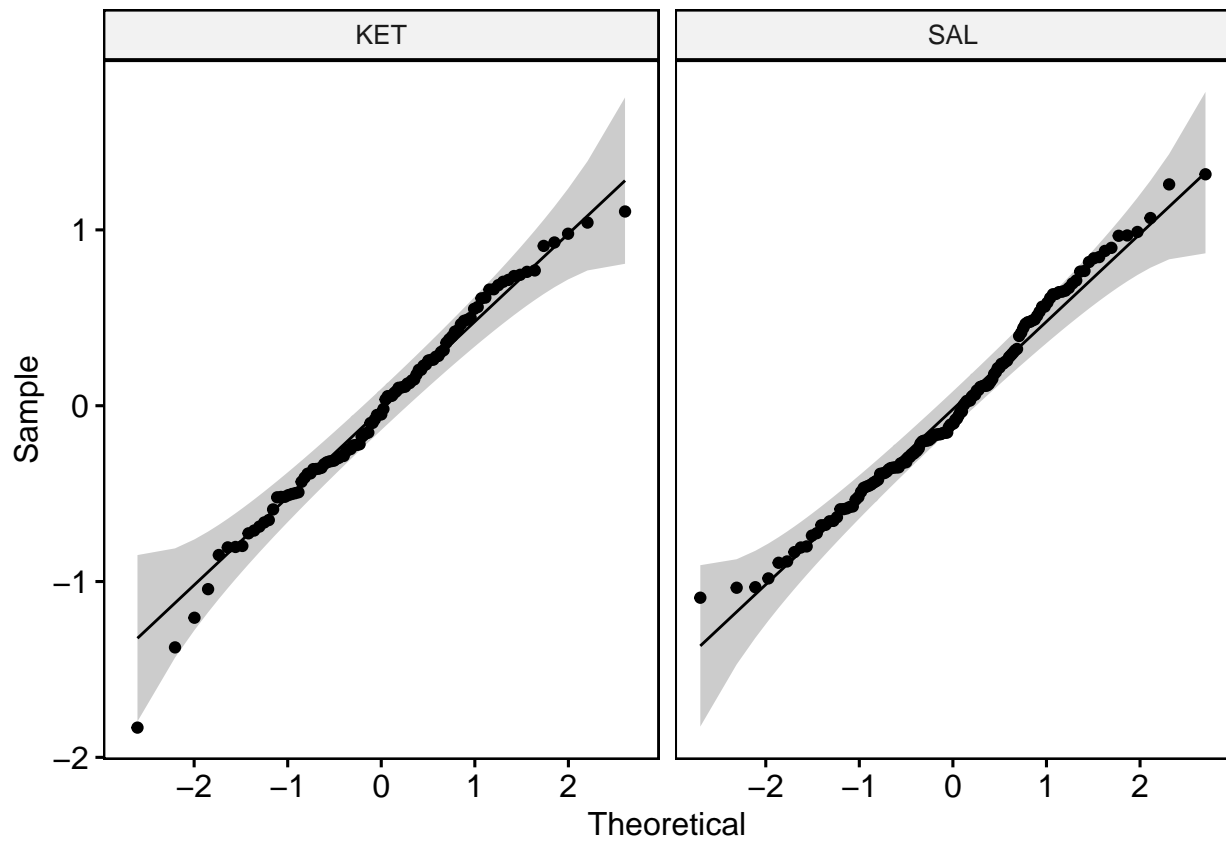


```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.98611, p-value = 0.3207
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.98498, p-value = 0.1182
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.0527 0.8186
##      251
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##      Sum Sq Df F value Pr(>F)
## (Intercept)  0.076  1  0.2743 0.6009
## treat_factor  0.011  1  0.0395 0.8427
## Residuals    69.098 251
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -0.19765, df = 227.99, p-value = 0.8435
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1451815  0.1187113
## sample estimates:
##  mean of x  mean of y
## -0.02631898 -0.01308387
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 0.013512, df = 1, p-value = 0.9075
figs[1]

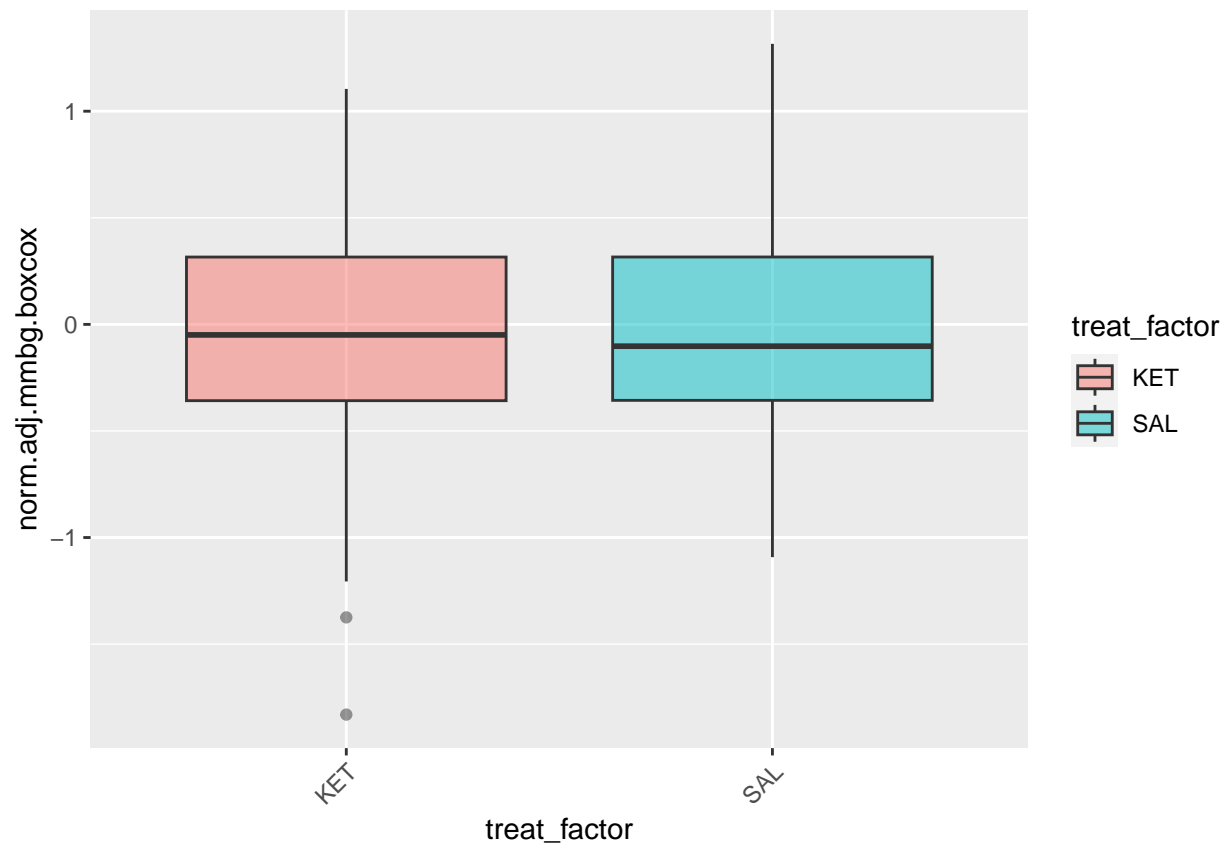
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



PV coloc w cFos

```
i <- str_which(fnames, "PV_coloc_w_cFos")
f <- fnames[i]
print(f)

## [1] "NORM/KET-VR5_PV_coloc_w_cFos_NORM.csv"

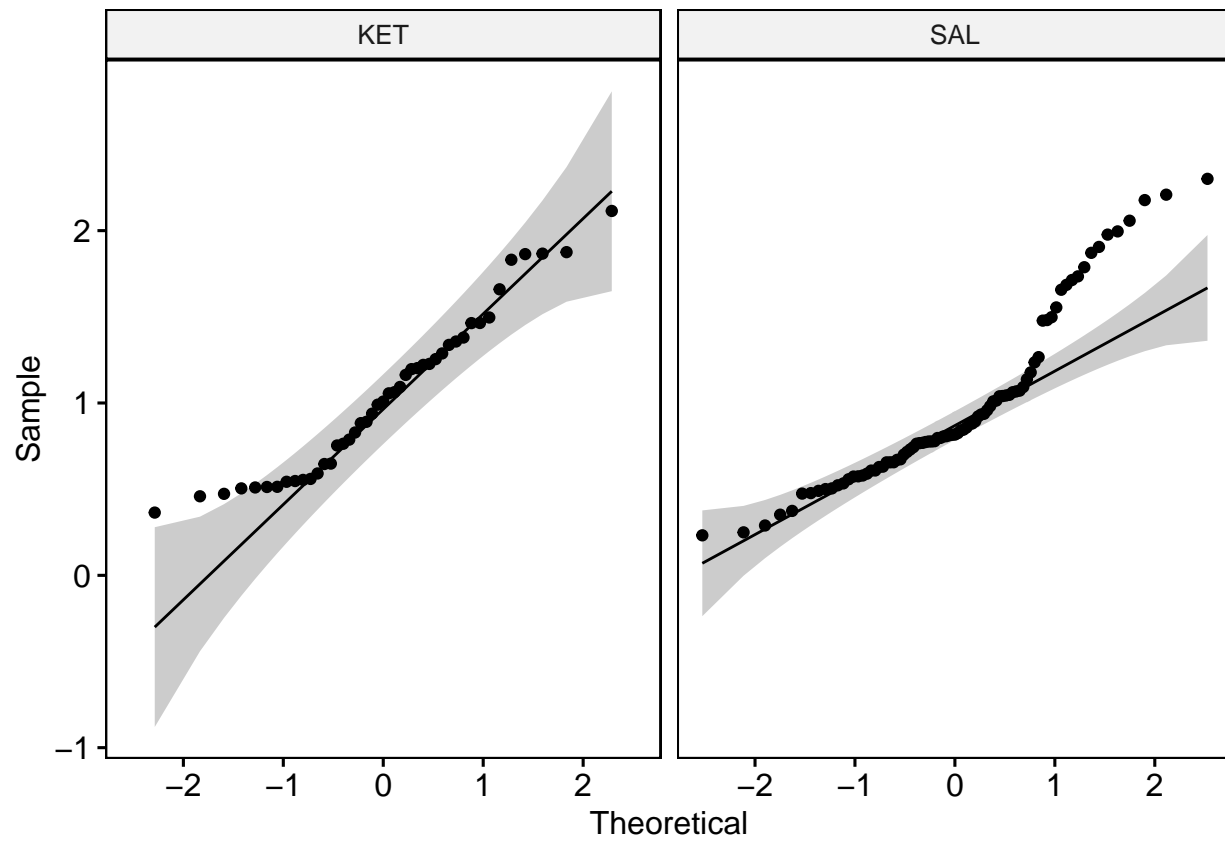
figs <- eda_anova_1way(f)

## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.94189, p-value = 0.02525
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.89164, p-value = 2.446e-06
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group  1  0.0409 0.8401
##      130
## Anova Table (Type III tests)
##
## Response: norm_adj_mmbg
##              Sum Sq Df F value Pr(>F)
## (Intercept)  48.544  1 212.791 <2e-16 ***
## treat_factor  0.124  1   0.542 0.4629
## Residuals    29.657 130
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = 0.74826, df = 93.184, p-value = 0.4562
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1067771  0.2359059
## sample estimates:
## mean of x mean of y
## 1.0386310 0.9740666
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 0.7343, df = 1, p-value = 0.3915
```

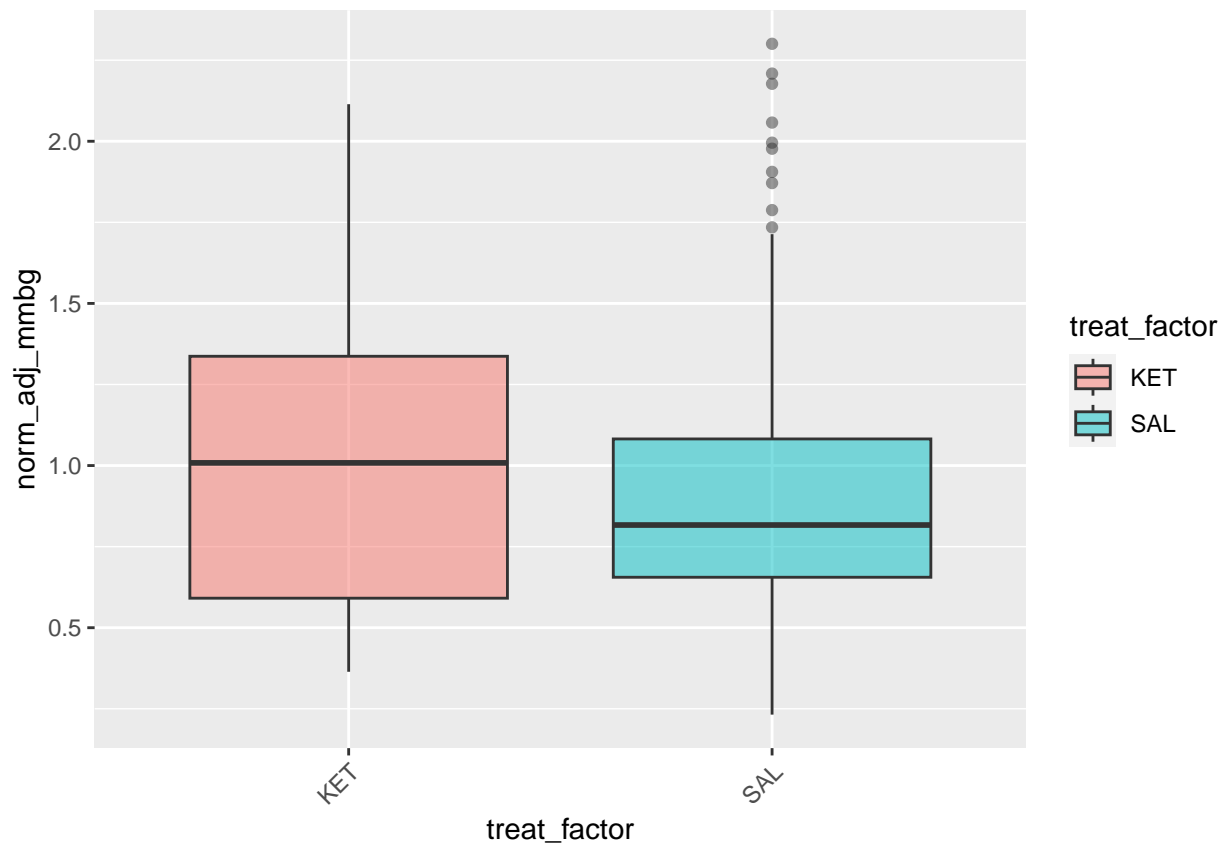
```
figs[1]
```

```
## [[1]]
```



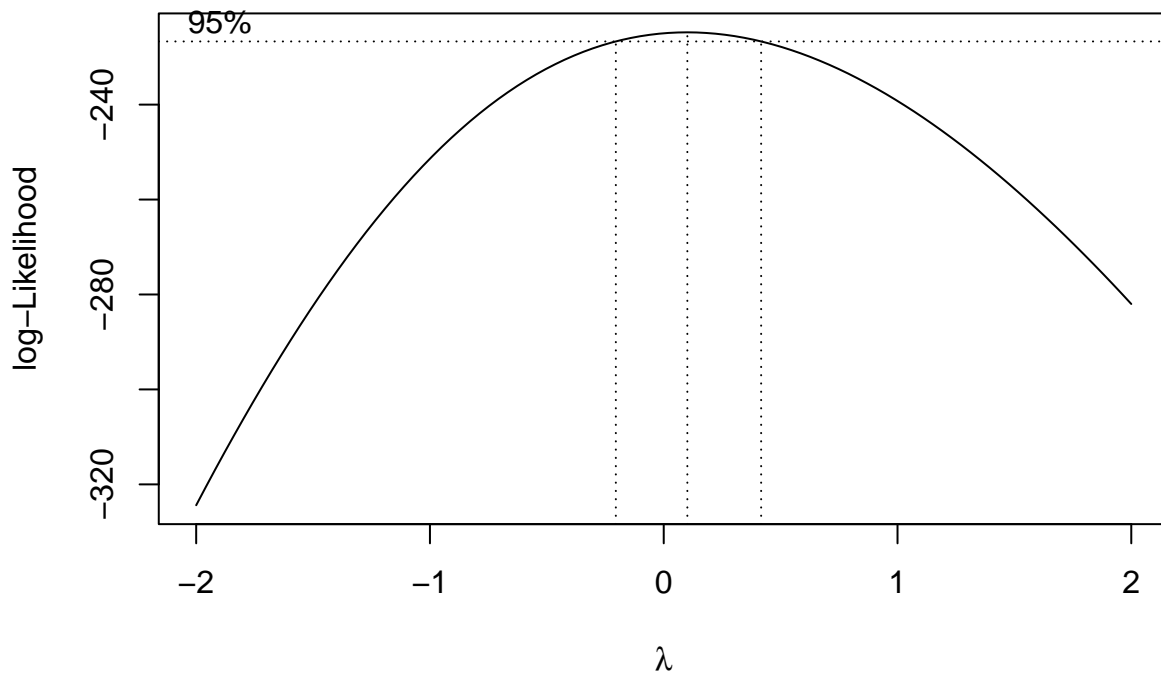
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

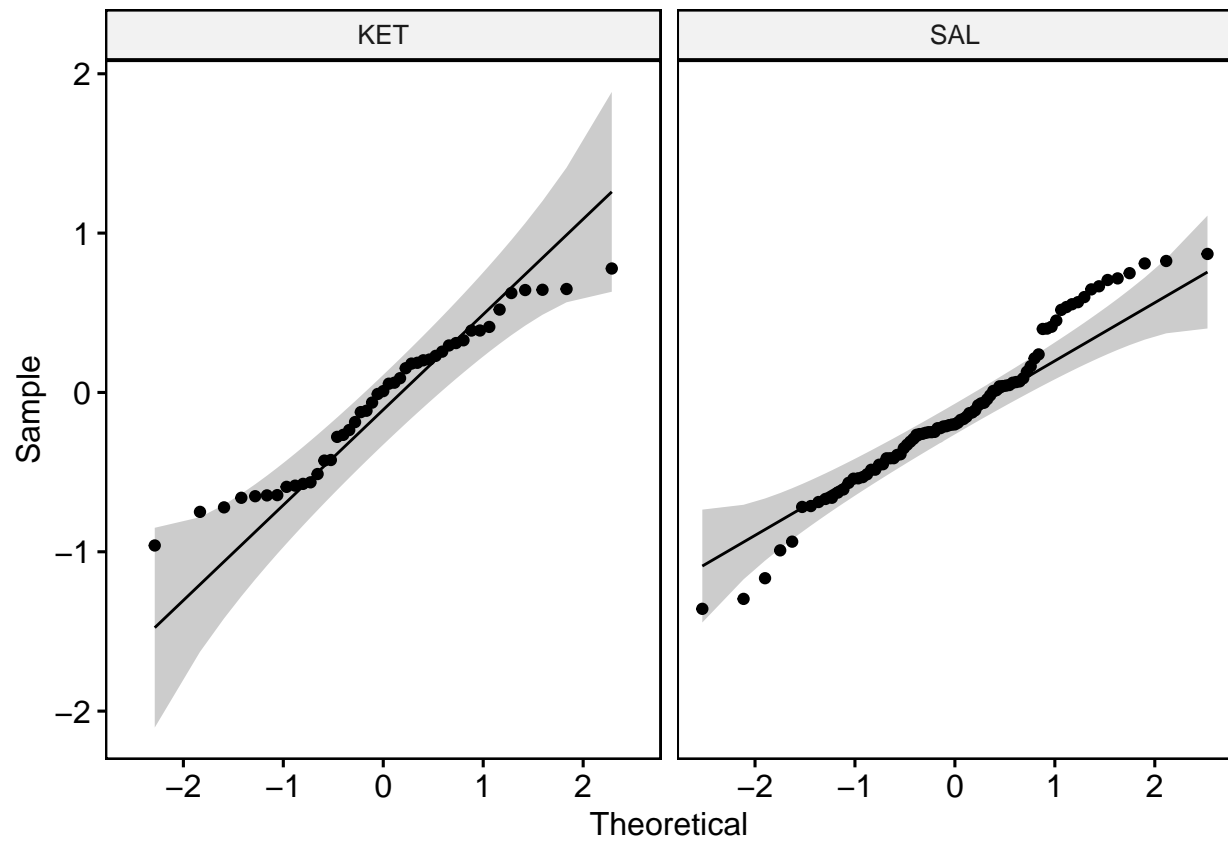
```
## [1] 0.1010101
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.9573, p-value = 0.09637
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.97355, p-value = 0.07151
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.2364 0.6276
##      130
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##              Sum Sq Df F value Pr(>F)
## (Intercept)  0.1270  1  0.5643 0.4539
## treat_factor  0.1723  1  0.7652 0.3833
## Residuals    29.2677 130
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 0.88602, df = 92.284, p-value = 0.3779
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.09462061  0.24705147
## sample estimates:
##  mean of x   mean of y
## -0.05313441 -0.12934983
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 0.7343, df = 1, p-value = 0.3915
figs[1]

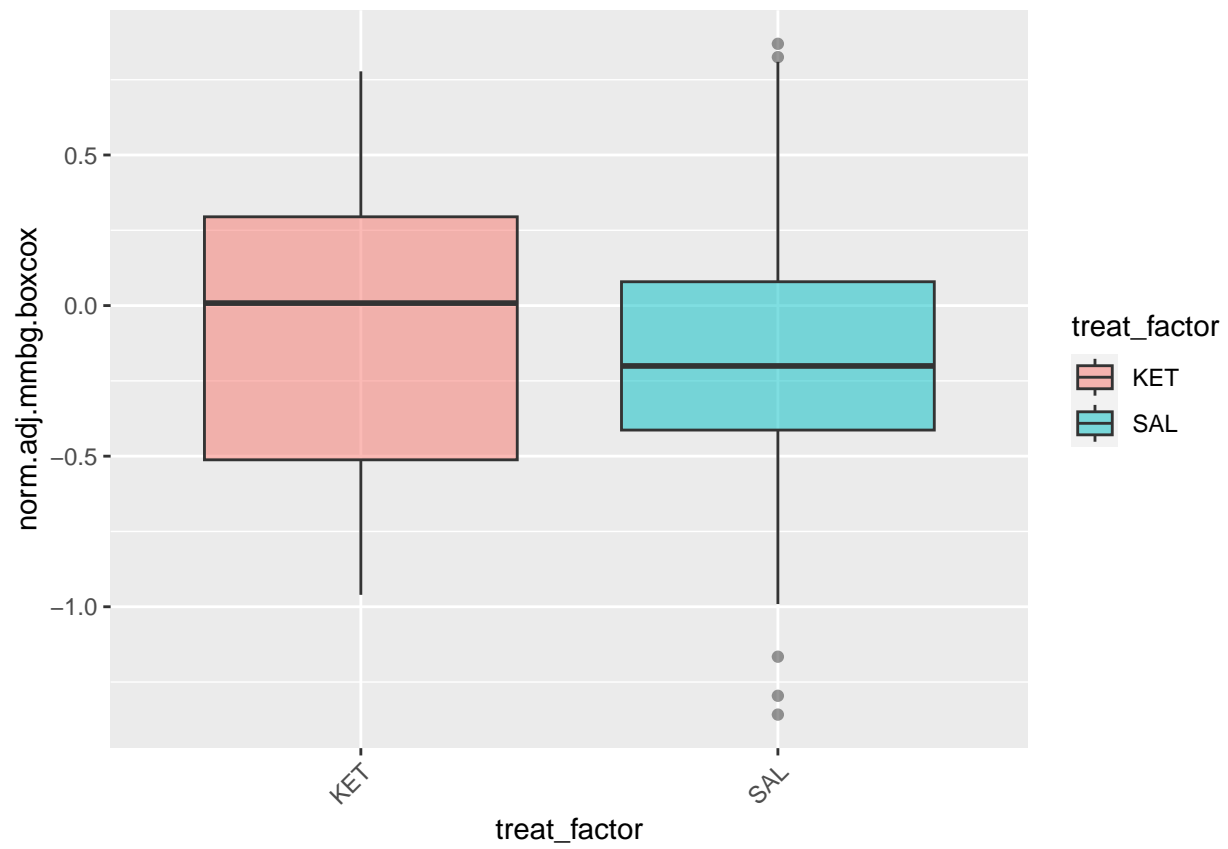
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```

WFA coloc w PV

```
i <- str_which(fnames, "WFA_coloc_w_PV")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_WFA_coloc_w_PV_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.9735, p-value = 0.02953
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.89414, p-value = 1.272e-08
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1  0.6287 0.4286
```

```
##          248
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##          Sum Sq Df F value Pr(>F)
```

```
## (Intercept) 87.569  1 435.6000 <2e-16 ***
```

```
## treat_factor  0.188  1  0.9363 0.3342
```

```
## Residuals    49.856 248
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = 0.98956, df = 245.06, p-value = 0.3234
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.05486627  0.16565440
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.9004574 0.8450634
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

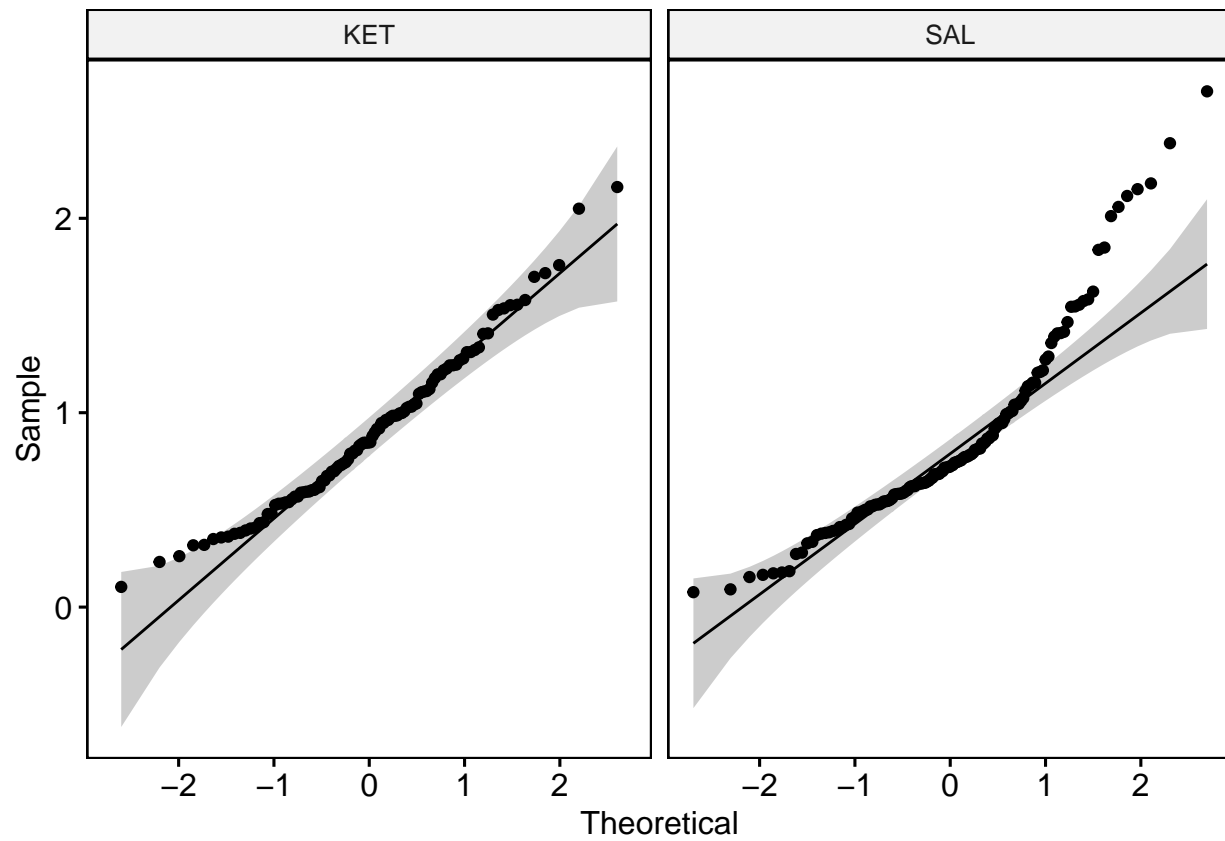
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 2.897, df = 1, p-value = 0.08874
```

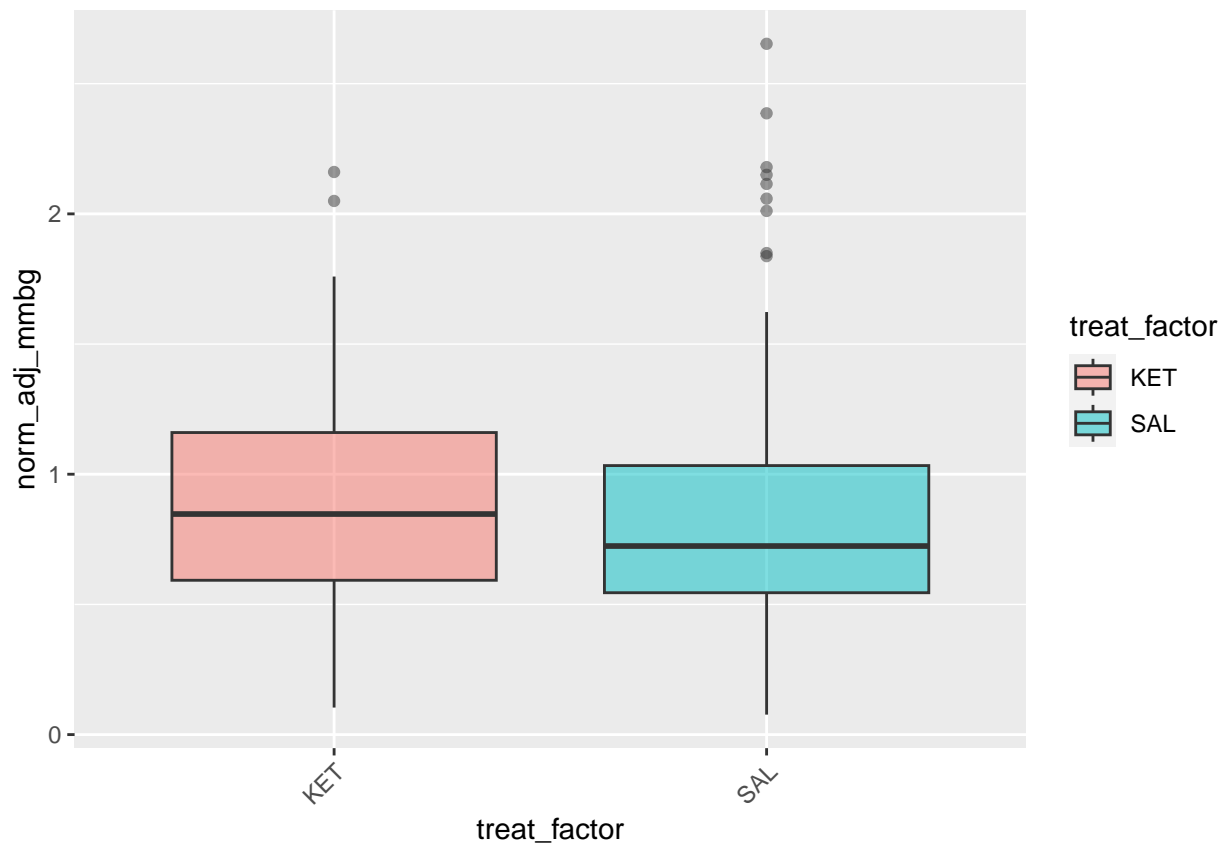
```
figs[1]
```

```
## [[1]]
```



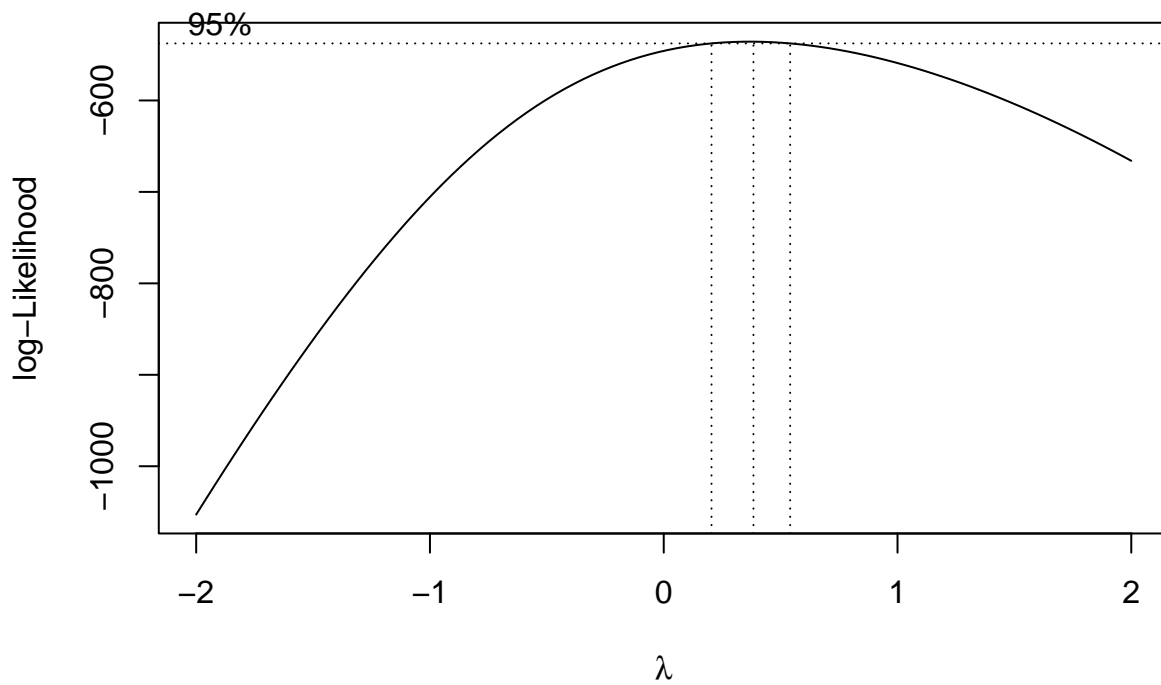
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

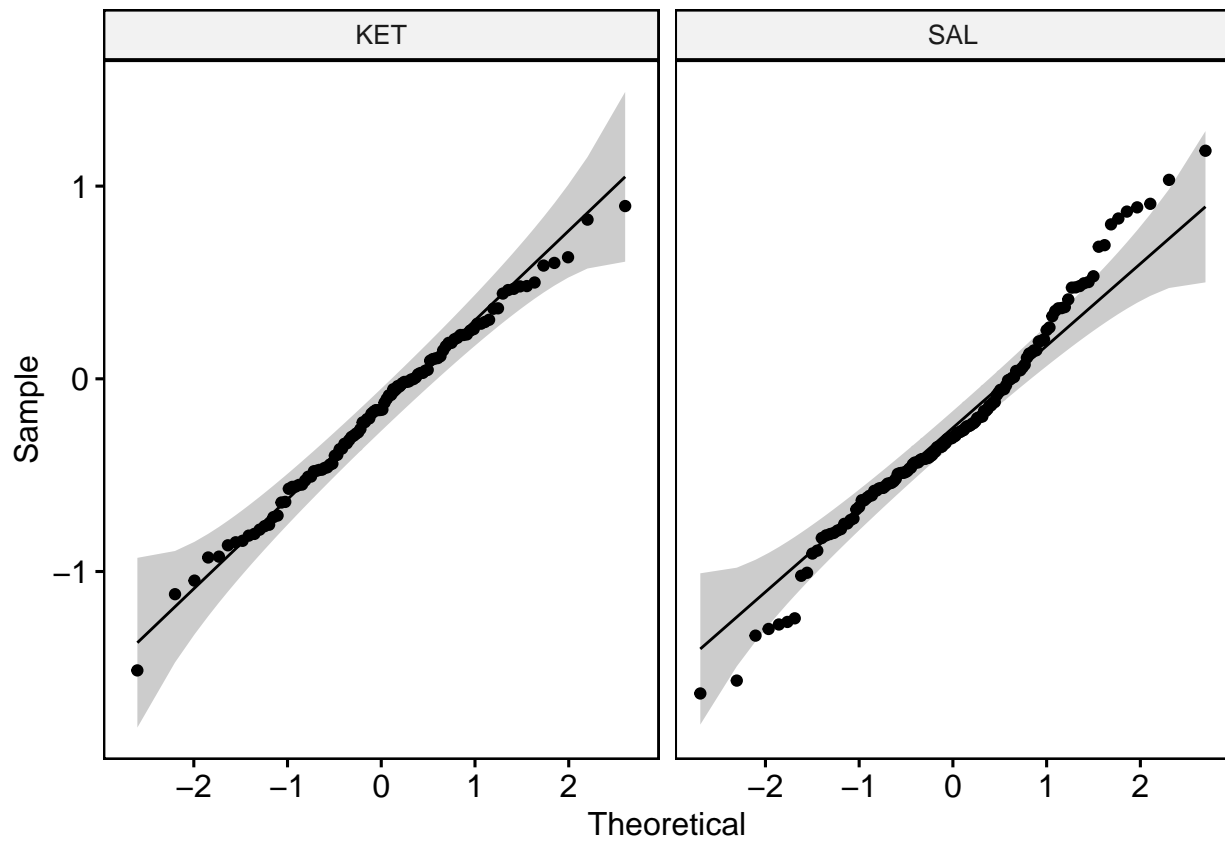
```
## [1] 0.3838384
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.99435, p-value = 0.94
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.97877, p-value = 0.02629
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.3597 0.5492
##      248
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##      Sum Sq Df F value    Pr(>F)
## (Intercept)  2.974  1 12.6760 0.0004439 ***
## treat_factor  0.427  1  1.8218 0.1783355
## Residuals    58.177 248
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 1.3746, df = 243.2, p-value = 0.1705
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03613565  0.20306712
## sample estimates:
## mean of x mean of y
## -0.1659316 -0.2493973
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 2.897, df = 1, p-value = 0.08874
figs[1]

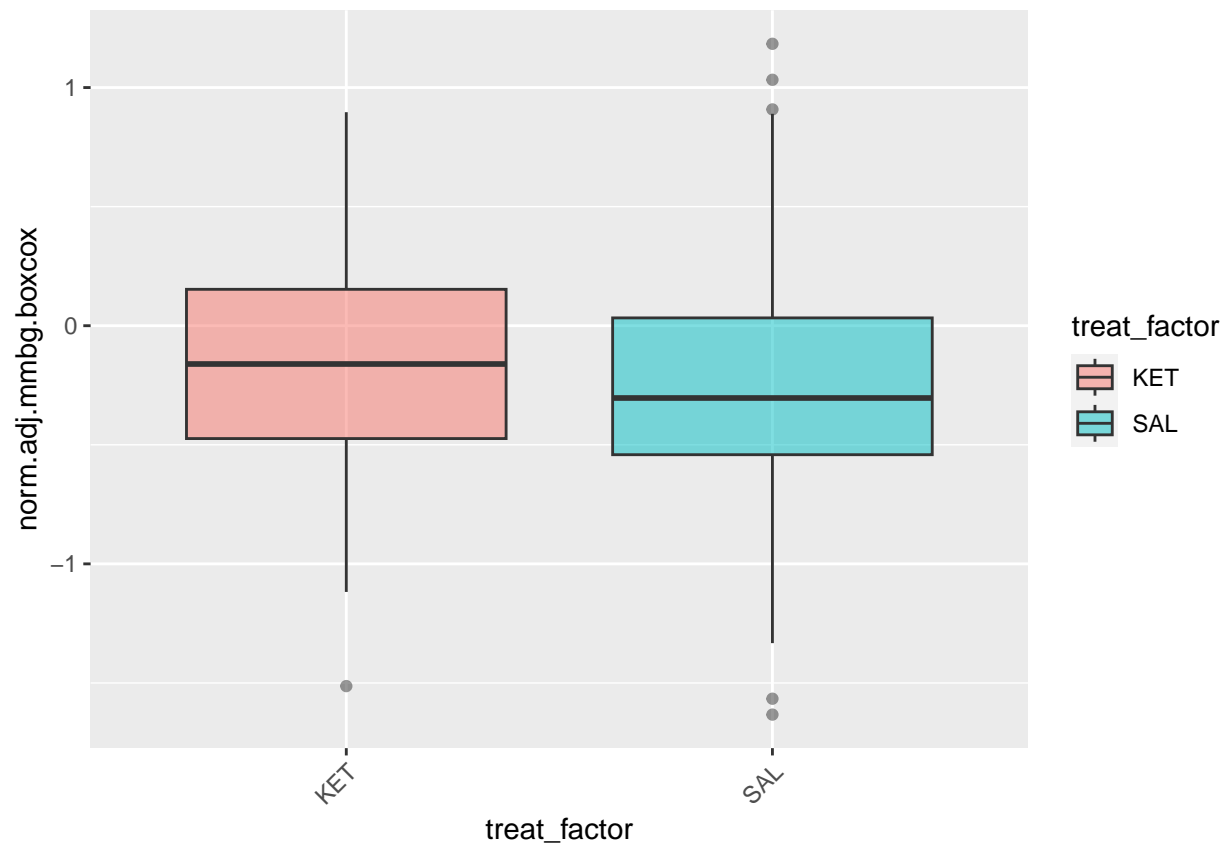
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



WFA coloc w cFos

```
i <- str_which(fnames, "WFA_coloc_w_cFos")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_WFA_coloc_w_cFos_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.96465, p-value = 0.01977
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.93795, p-value = 0.000254
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value    Pr(>F)
```

```
## group    1  8.4342 0.004154 **
```

```
##          176
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##              Sum Sq Df F value Pr(>F)
```

```
## (Intercept)  74.850  1 390.554 <2e-16 ***
```

```
## treat_factor   0.202  1   1.055 0.3058
```

```
## Residuals    33.730 176
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = 1.0462, df = 159.25, p-value = 0.297
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.05989867  0.19484519
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.9383939 0.8709207
```

```
##
```

```
##
```

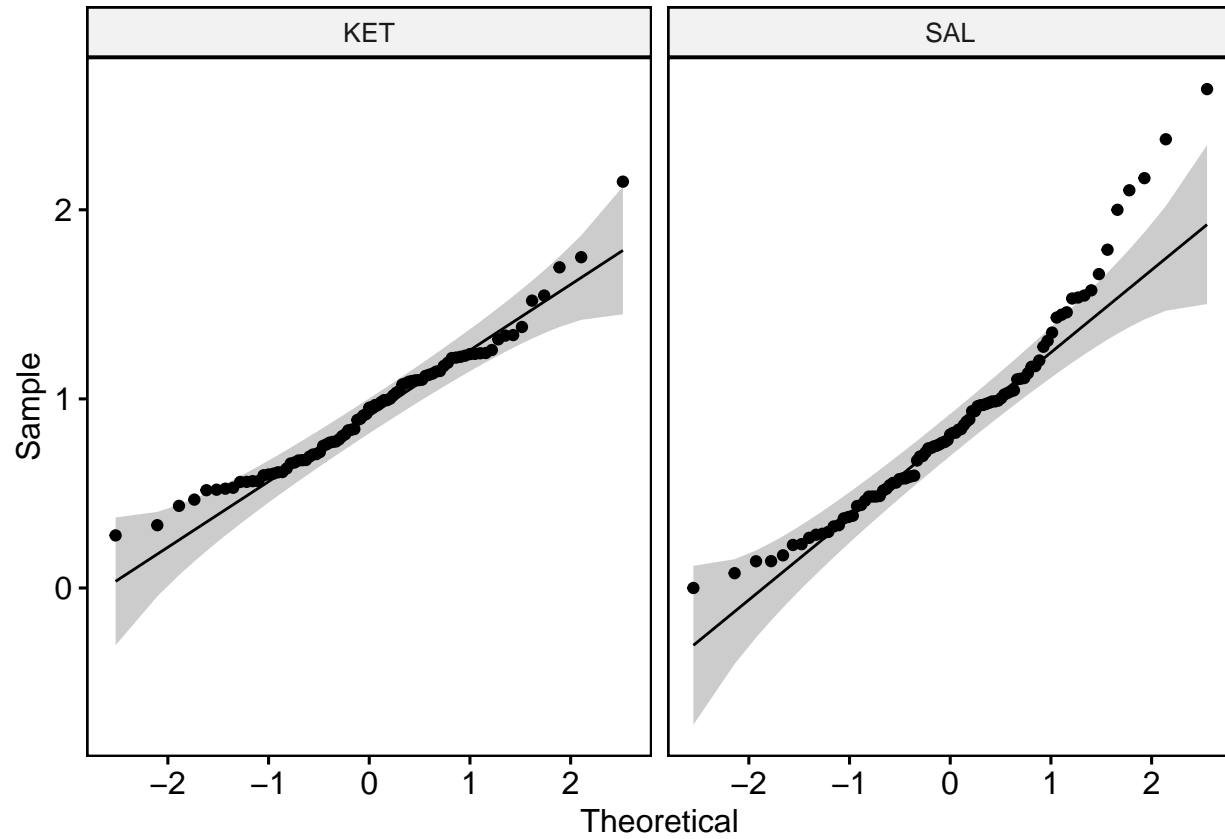
```
## Kruskal-Wallis rank sum test
```



```
##
## data: norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 3.7334, df = 1, p-value = 0.05333
```

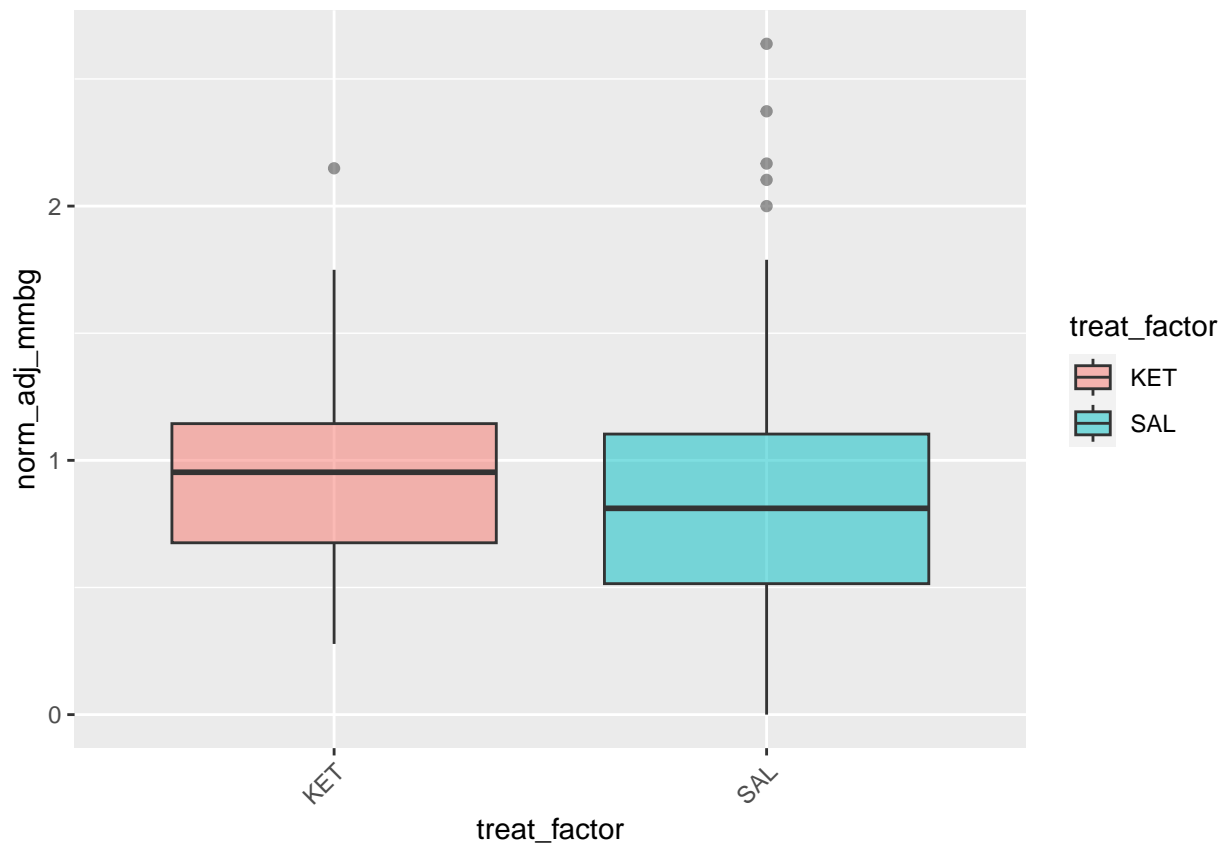
```
figs[1]
```

```
## [[1]]
```



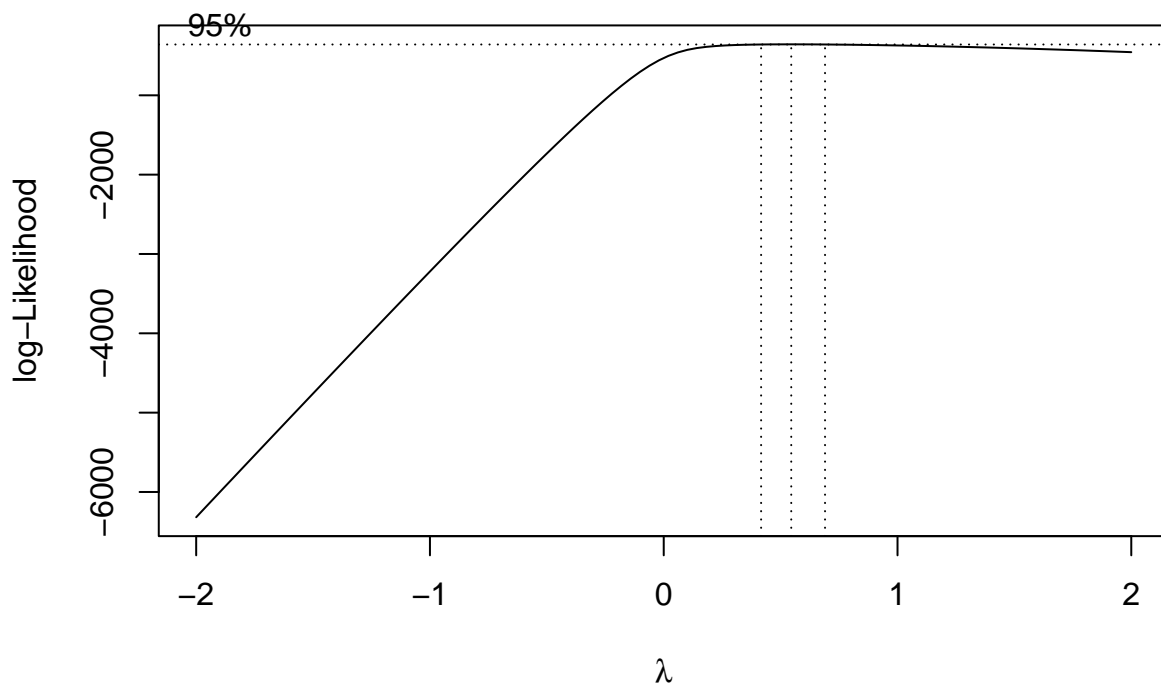
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

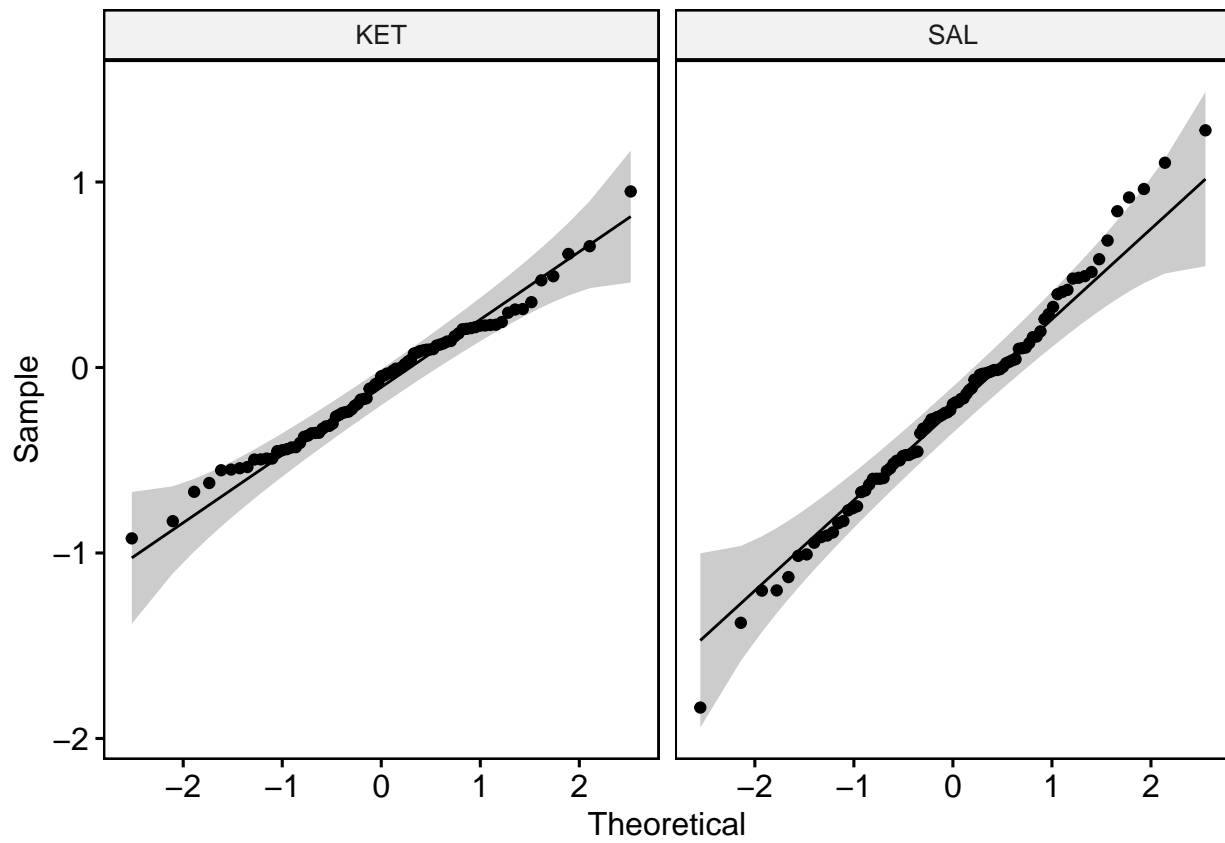
```
## [1] 0.5454545
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.98688, p-value = 0.5478
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.99225, p-value = 0.8689
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value    Pr(>F)
## group  1 11.531 0.0008459 ***
##      176
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##              Sum Sq Df F value    Pr(>F)
## (Intercept)  0.688   1  3.1655 0.07694 .
## treat_factor  0.646   1  2.9717 0.08649 .
## Residuals    38.252 176
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 1.7593, df = 154.94, p-value = 0.0805
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.01481082  0.25600309
## sample estimates:
##  mean of x   mean of y
## -0.08996608 -0.21056221
##
##
## Kruskal-Wallis rank sum test
##
## data:  norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 3.7334, df = 1, p-value = 0.05333
figs[1]

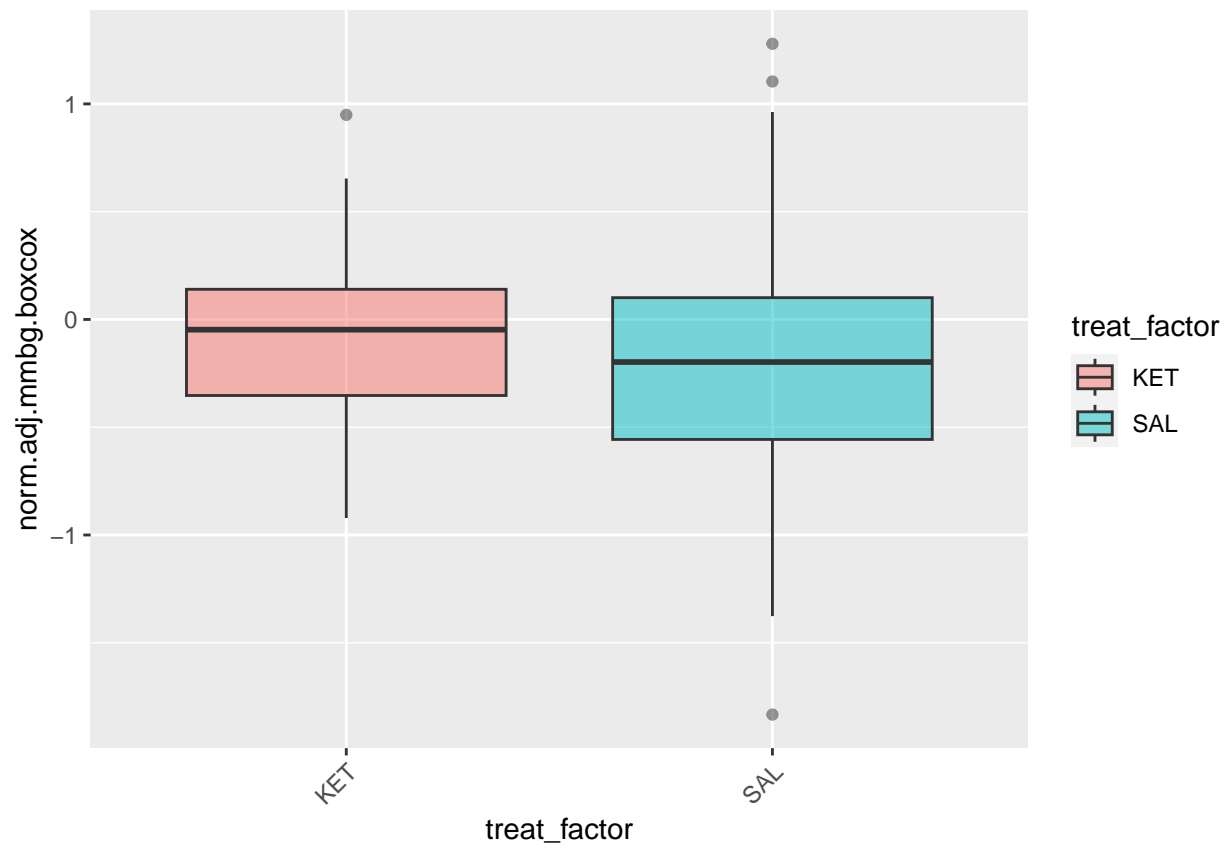
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



cFos coloc w PV

```
i <- str_which(fnames, "cFos_coloc_w_PV")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_cFos_coloc_w_PV_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.84964, p-value = 3.584e-05
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.9195, p-value = 4.522e-05
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##          Df F value Pr(>F)
```

```
## group    1  0.5998 0.4401
```

```
##          130
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##              Sum Sq Df F value Pr(>F)
```

```
## (Intercept) 40.074  1 218.3137 <2e-16 ***
```

```
## treat_factor  0.186  1   1.0124 0.3162
```

```
## Residuals    23.863 130
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -0.9952, df = 86.451, p-value = 0.3224
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.23726289  0.07894879
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.9436824 1.0228394
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

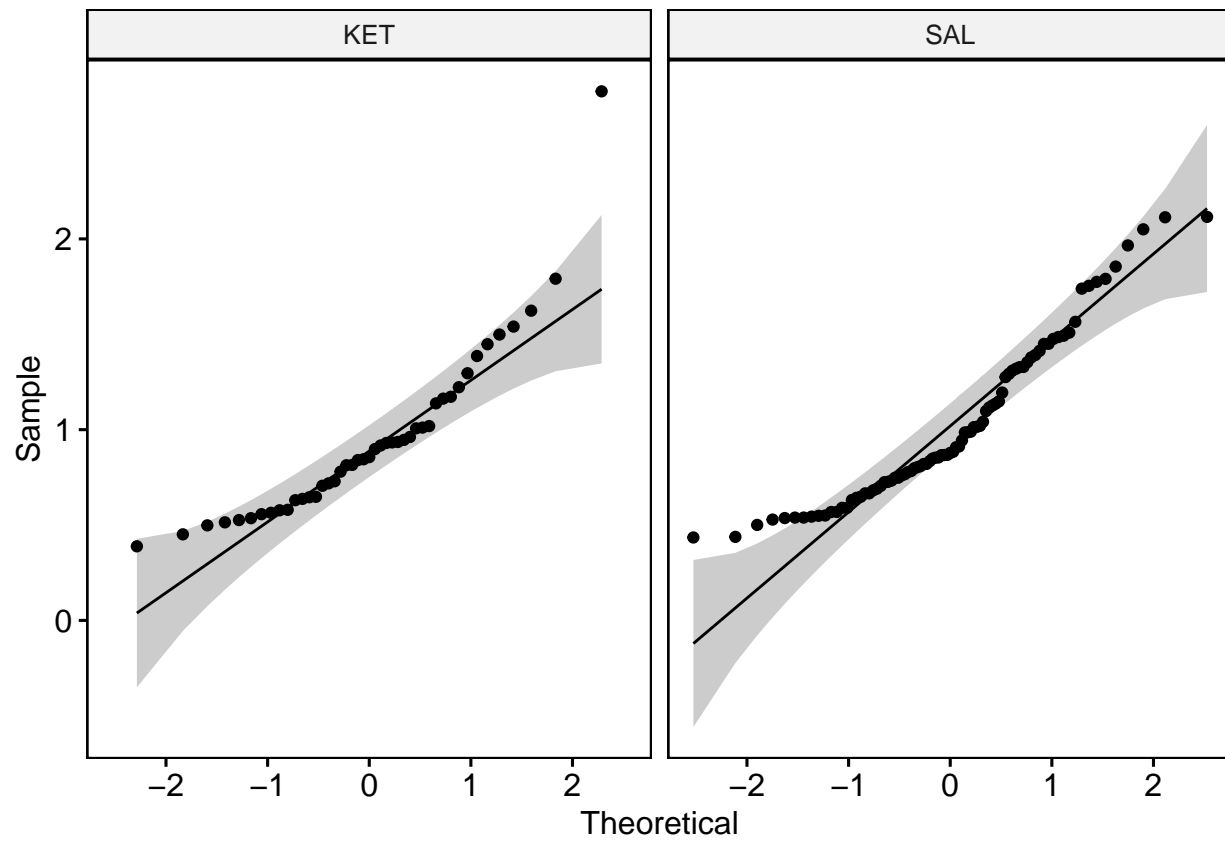
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 1.2351, df = 1, p-value = 0.2664
```

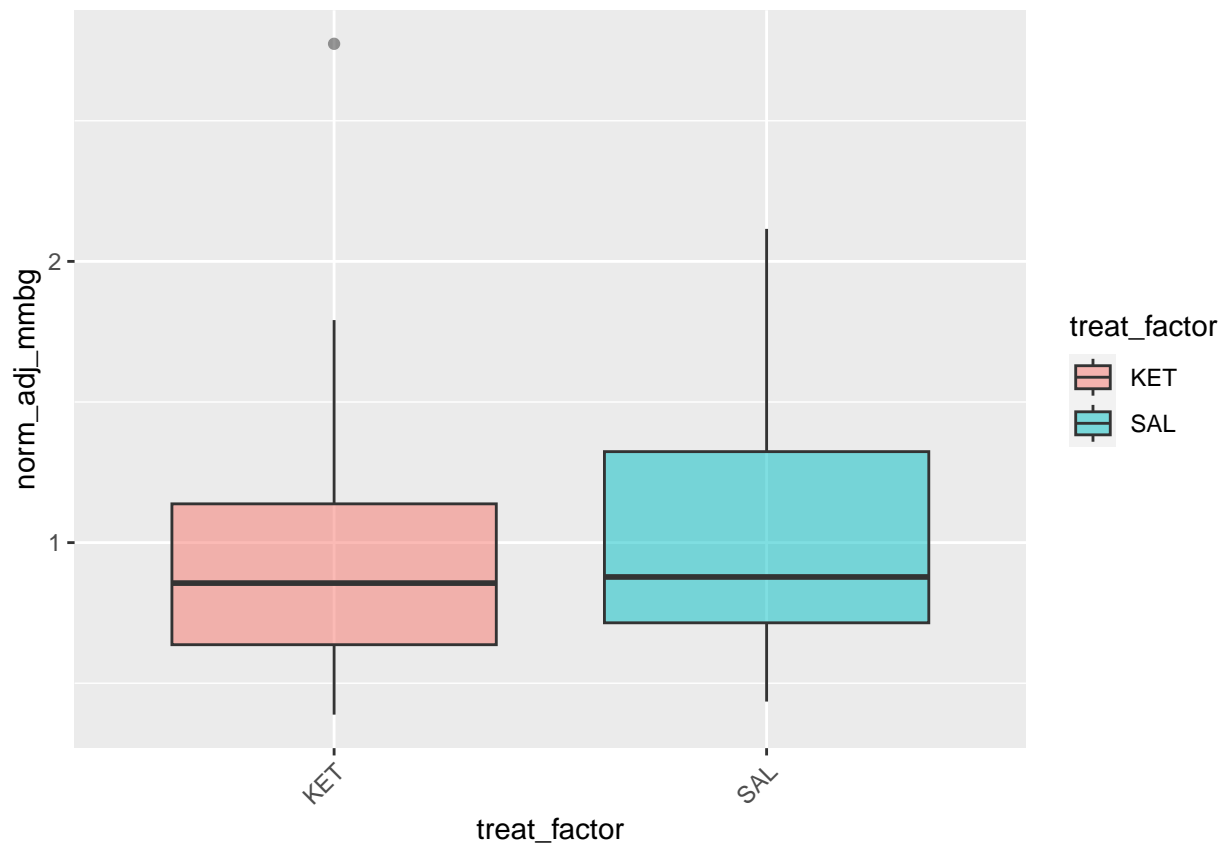
```
figs[1]
```

```
## [[1]]
```

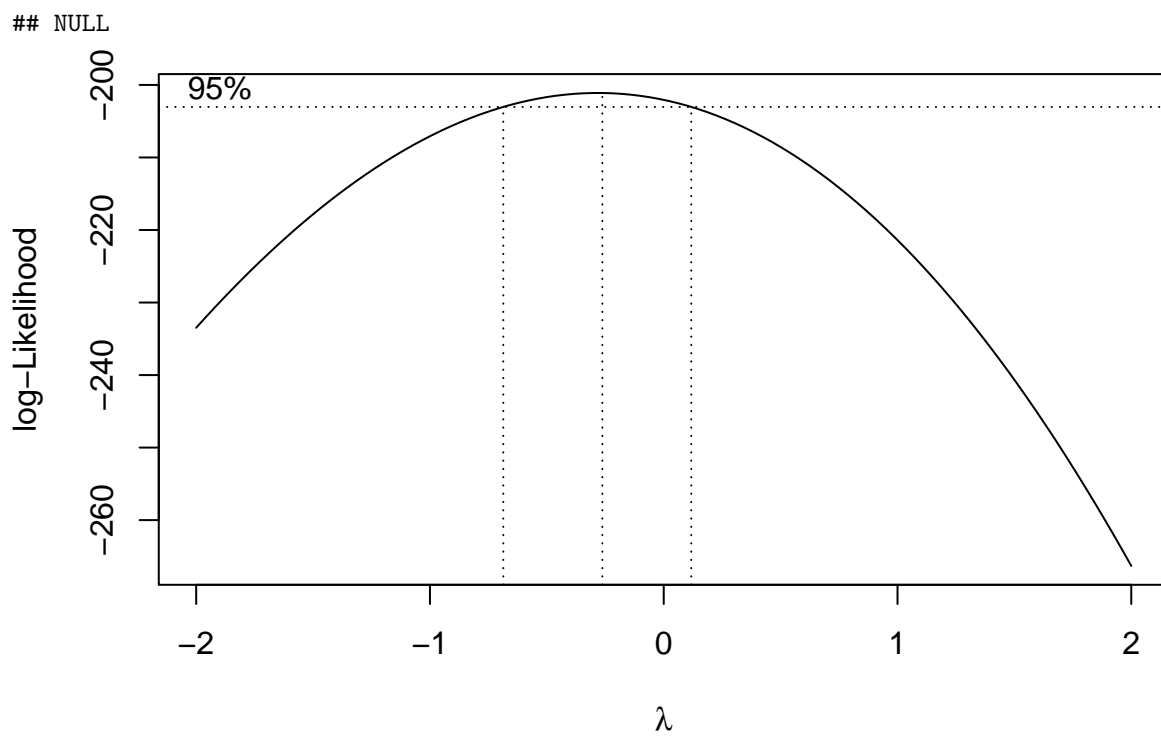


```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```



```
## [1] "best lamda"
## [1] -0.2626263
```

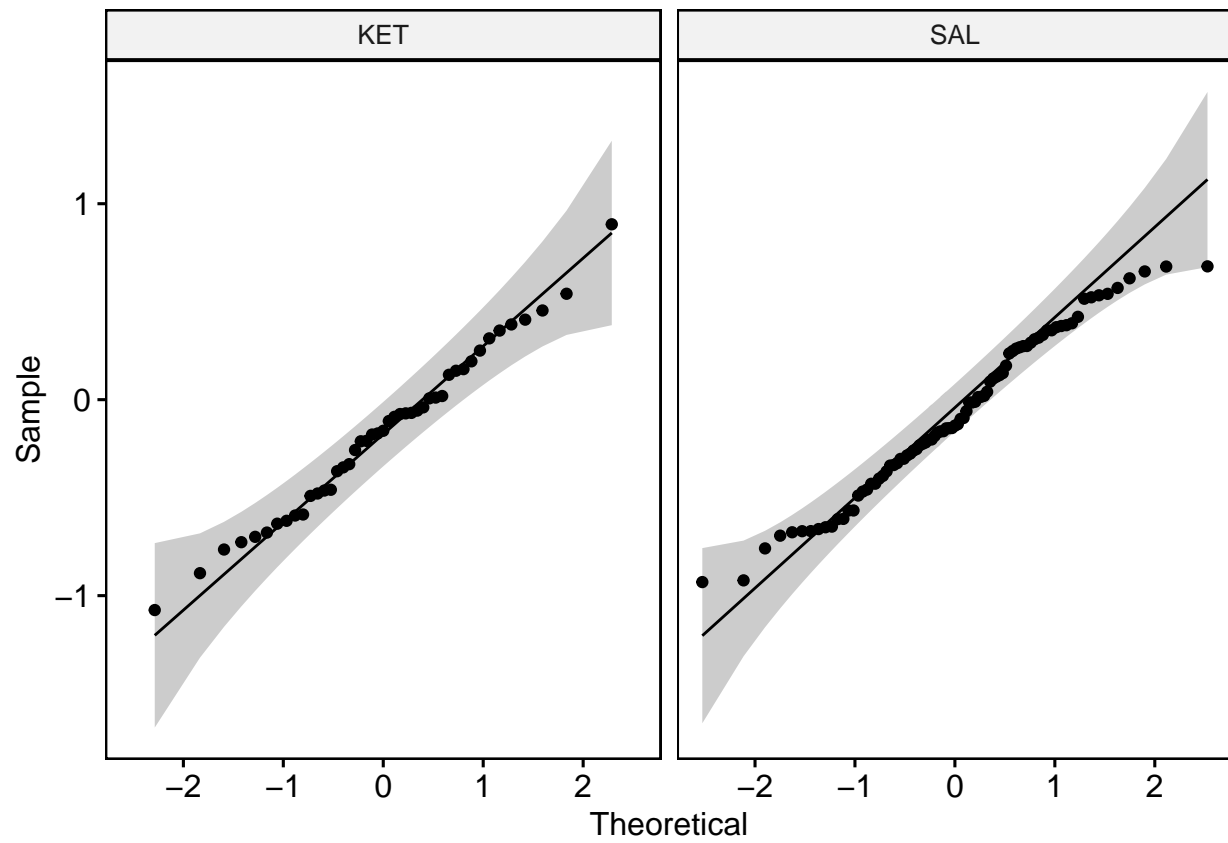


```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.9909, p-value = 0.9759
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.97742, p-value = 0.1321
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.0093 0.9234
##      130
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##      Sum Sq Df F value    Pr(>F)
## (Intercept)  1.2898  1  7.6916 0.006364 **
## treat_factor  0.2419  1  1.4428 0.231868
## Residuals    21.7994 130
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -1.1878, df = 86.399, p-value = 0.2382
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.24146802  0.06083094
## sample estimates:
##  mean of x  mean of y
## -0.1692986 -0.0789801
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 1.2351, df = 1, p-value = 0.2664
figs[1]

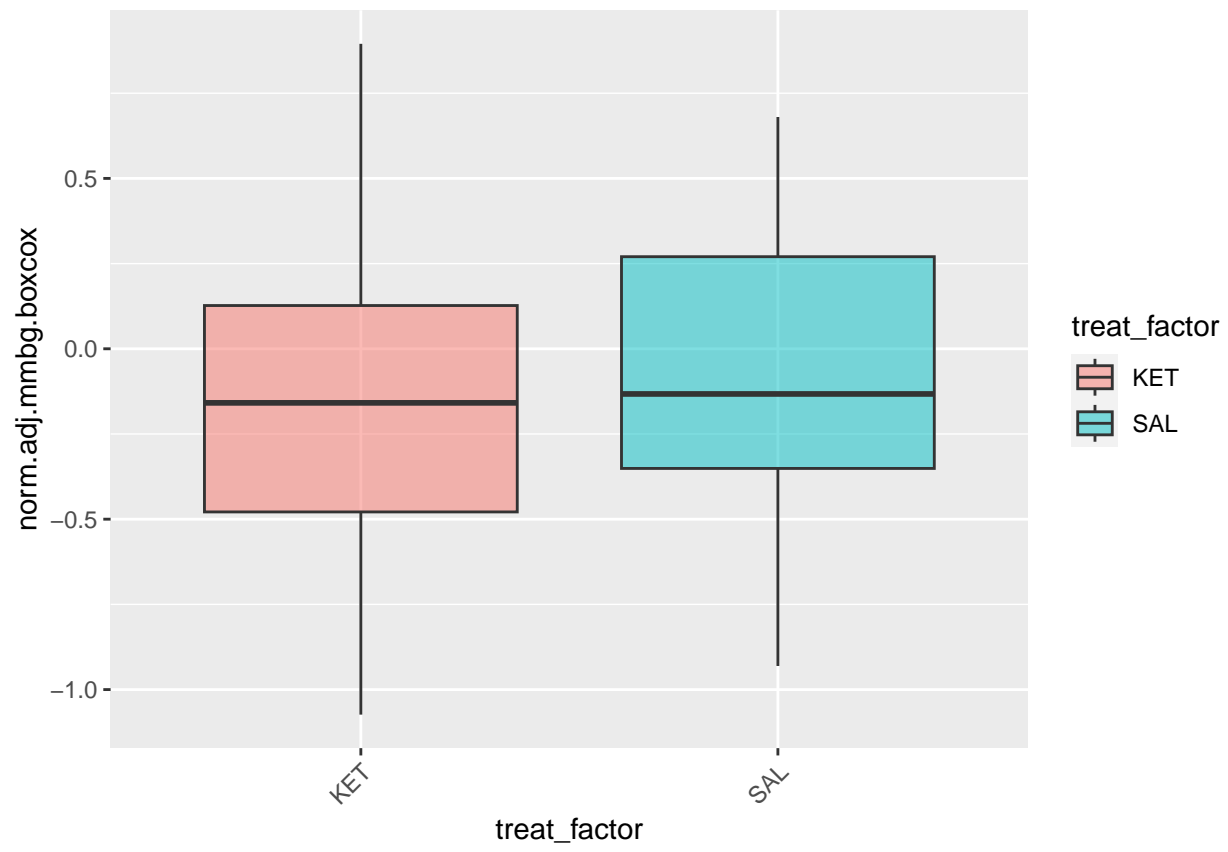
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



cFos coloc w WFA

```
i <- str_which(fnames, "cFos_coloc_w_WFA")
f <- fnames[i]
print(f)
```

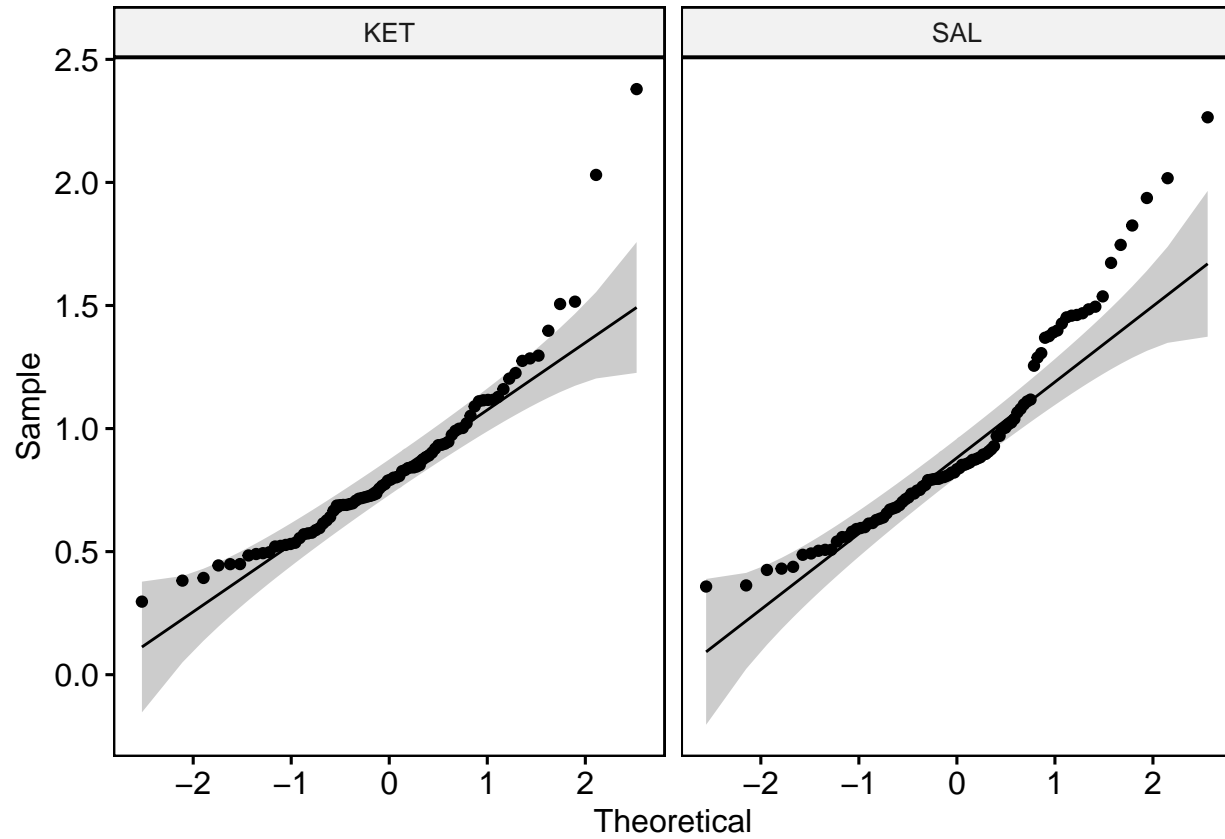
```
## [1] "NORM/KET-VR5_cFos_coloc_w_WFA_NORM.csv"
figs <- eda_anova_1way(f)
```

```
## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.87841, p-value = 7.985e-07
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.90886, p-value = 6.214e-06
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group  1  2.862 0.09243 .
##      179
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Anova Table (Type III tests)
##
## Response: norm_adj_mmbg
##              Sum Sq Df F value    Pr(>F)
## (Intercept)  60.825  1 454.7264 < 2e-16 ***
## treat_factor   0.396  1   2.9597 0.08709 .
## Residuals    23.944 179
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = -1.733, df = 178.62, p-value = 0.08483
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.20029655  0.01299002
## sample estimates:
## mean of x mean of y
## 0.8409950 0.9346483
##
##
##  Kruskal-Wallis rank sum test
```

```
##
## data: norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 2.2584, df = 1, p-value = 0.1329
```

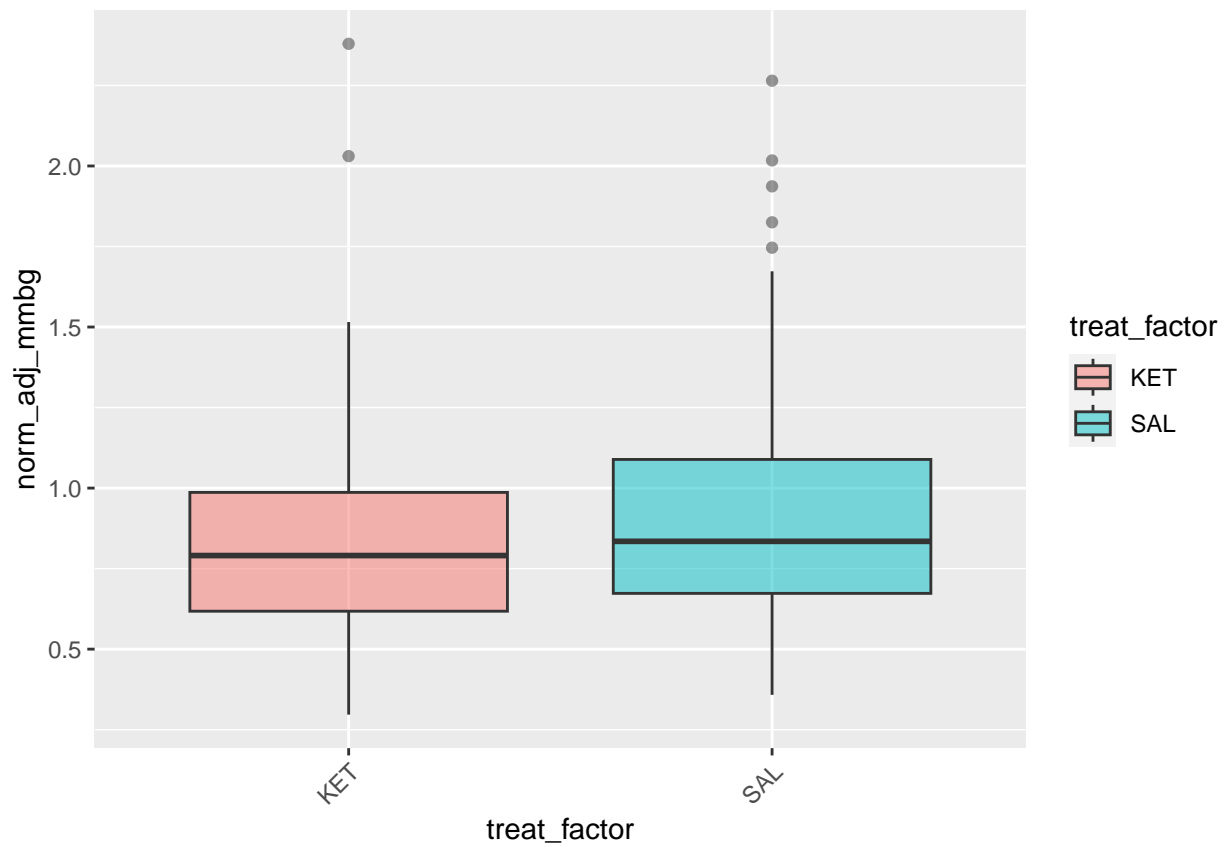
```
figs[1]
```

```
## [[1]]
```



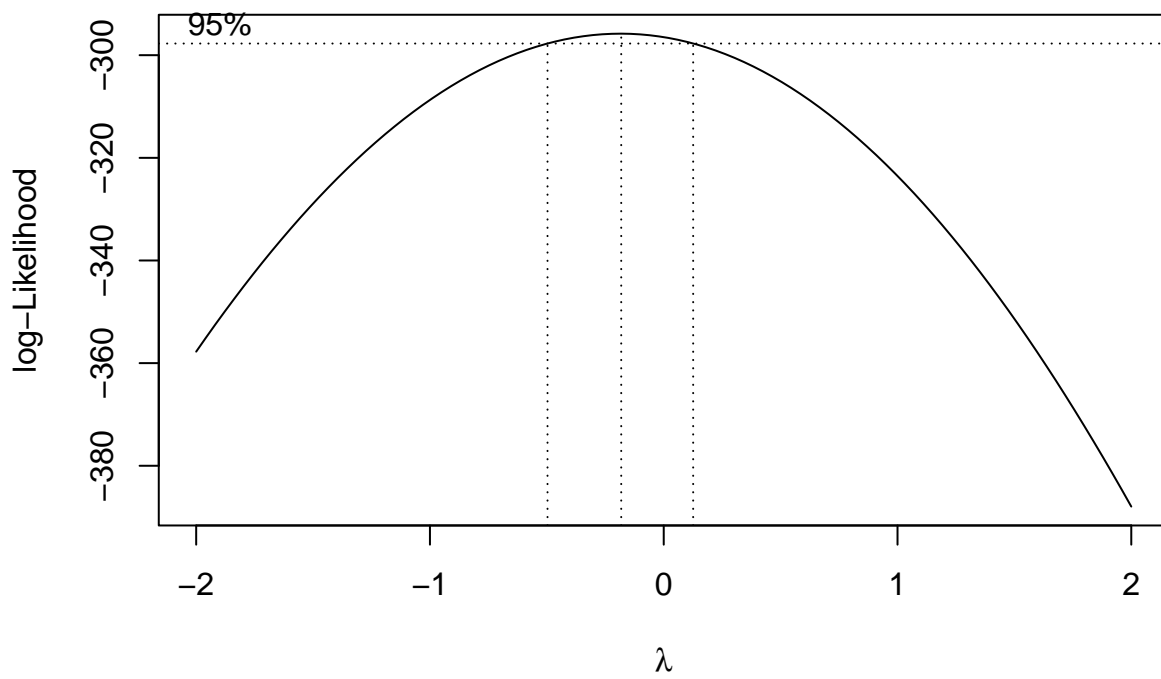
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

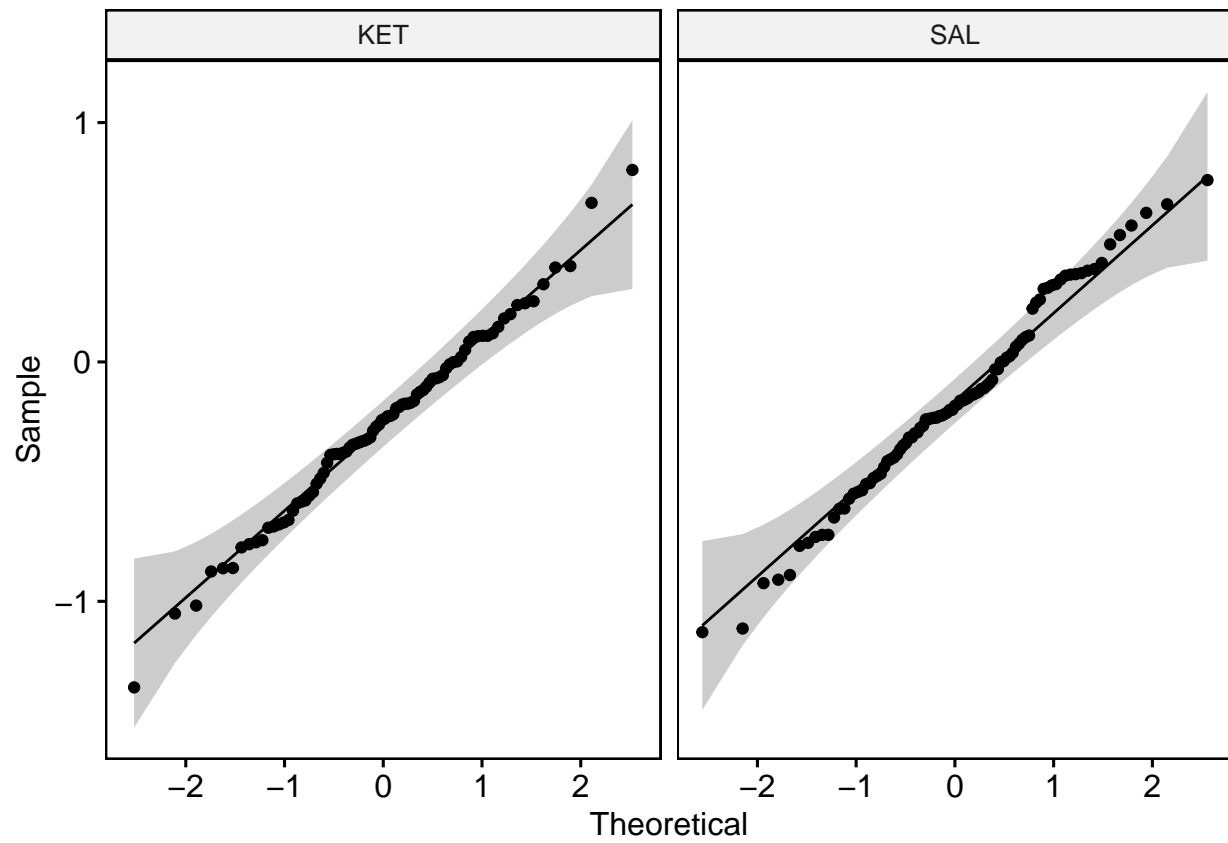
```
## [1] -0.1818182
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.99374, p-value = 0.958
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.9876, p-value = 0.5172
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group  1  0.2458 0.6207
##      179
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##      Sum Sq Df F value    Pr(>F)
## (Intercept)  5.7854  1 37.3249 6.08e-09 ***
## treat_factor  0.4235  1  2.7321  0.1001
## Residuals    27.7450 179
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -1.6576, df = 178.67, p-value = 0.09915
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.21216726  0.01844849
## sample estimates:
##  mean of x  mean of y
## -0.2593677 -0.1625083
##
##
## Kruskal-Wallis rank sum test
##
## data:  norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 2.2584, df = 1, p-value = 0.1329
figs[1]

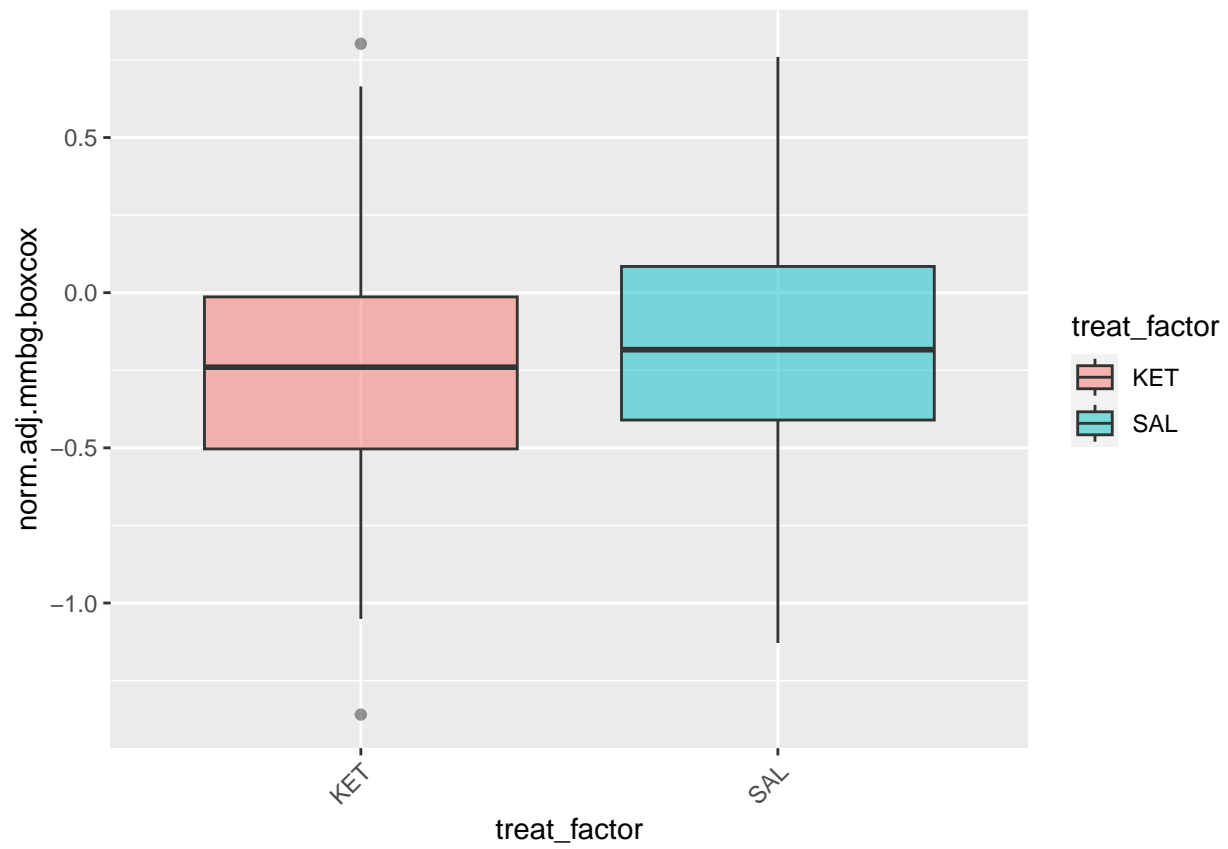
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```

triple PV

```
i <- str_which(fnames, "triple_PV")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_triple_PV_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.95945, p-value = 0.4782
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.91277, p-value = 0.003125
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##      Df F value Pr(>F)
```

```
## group 1  0.3207 0.5732
```

```
##      63
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##           Sum Sq Df  F value Pr(>F)
```

```
## (Intercept)  32.927  1 137.3894 <2e-16 ***
```

```
## treat_factor  0.163  1   0.6804 0.4126
```

```
## Residuals    15.099 63
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = 0.84639, df = 45.516, p-value = 0.4018
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.1459600  0.3576666
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 1.223393  1.117539
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

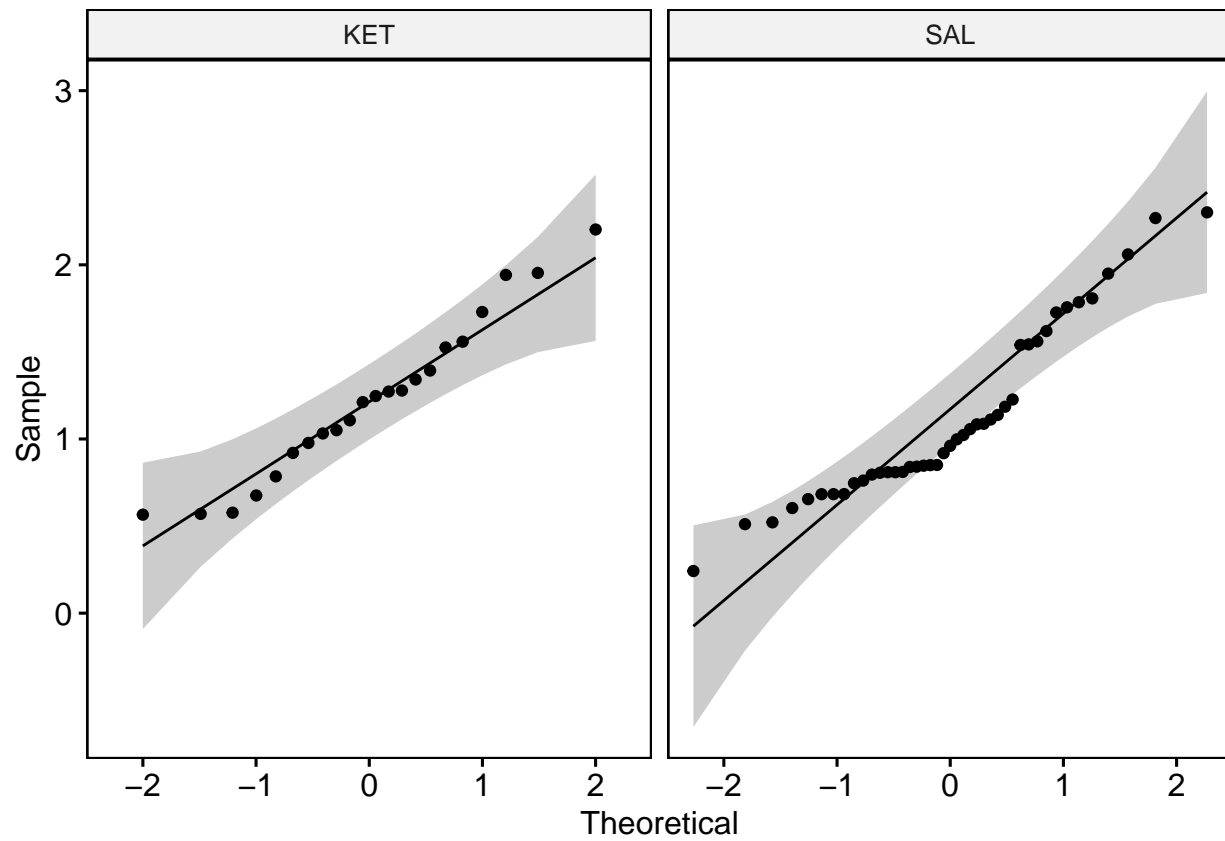
```
##
```

```
## data: norm_adj_mmbg by treat_factor
```

```
## Kruskal-Wallis chi-squared = 1.0525, df = 1, p-value = 0.3049
```

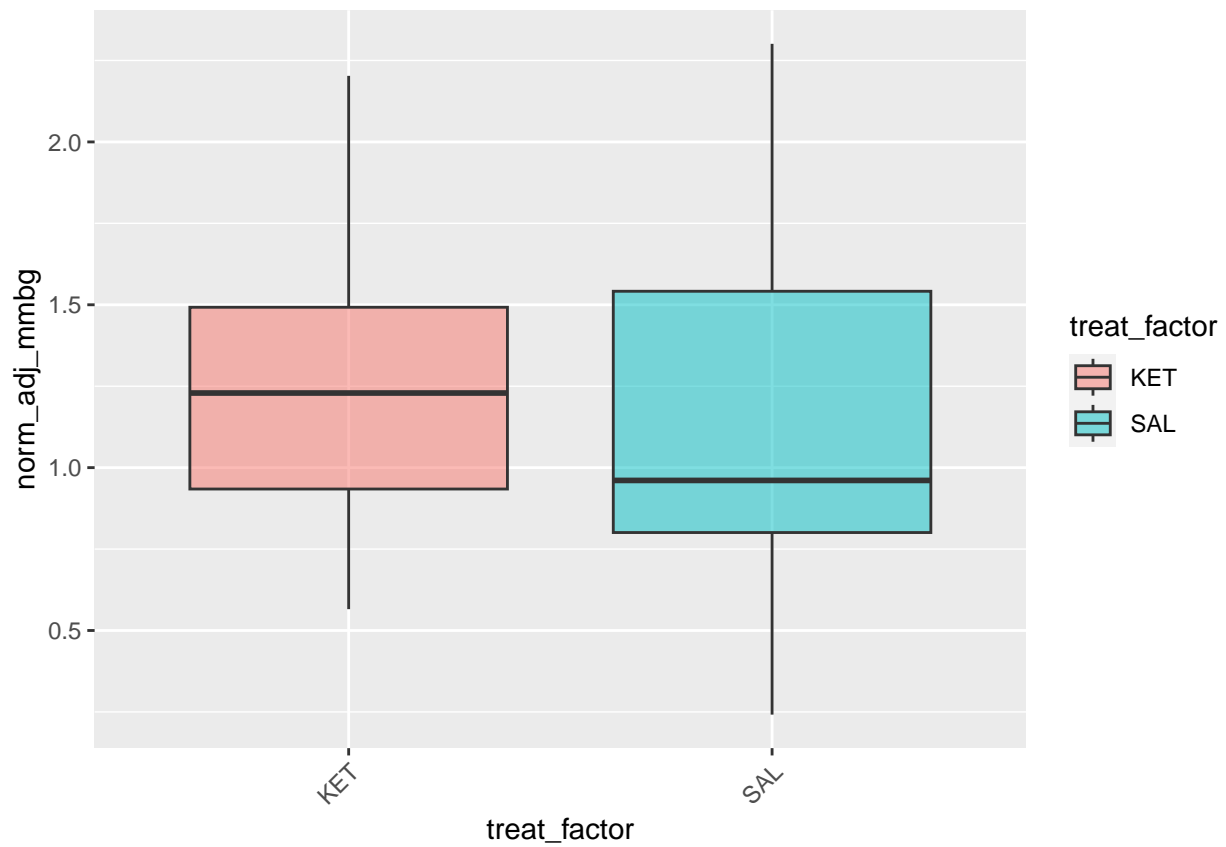
```
figs[1]
```

```
## [[1]]
```

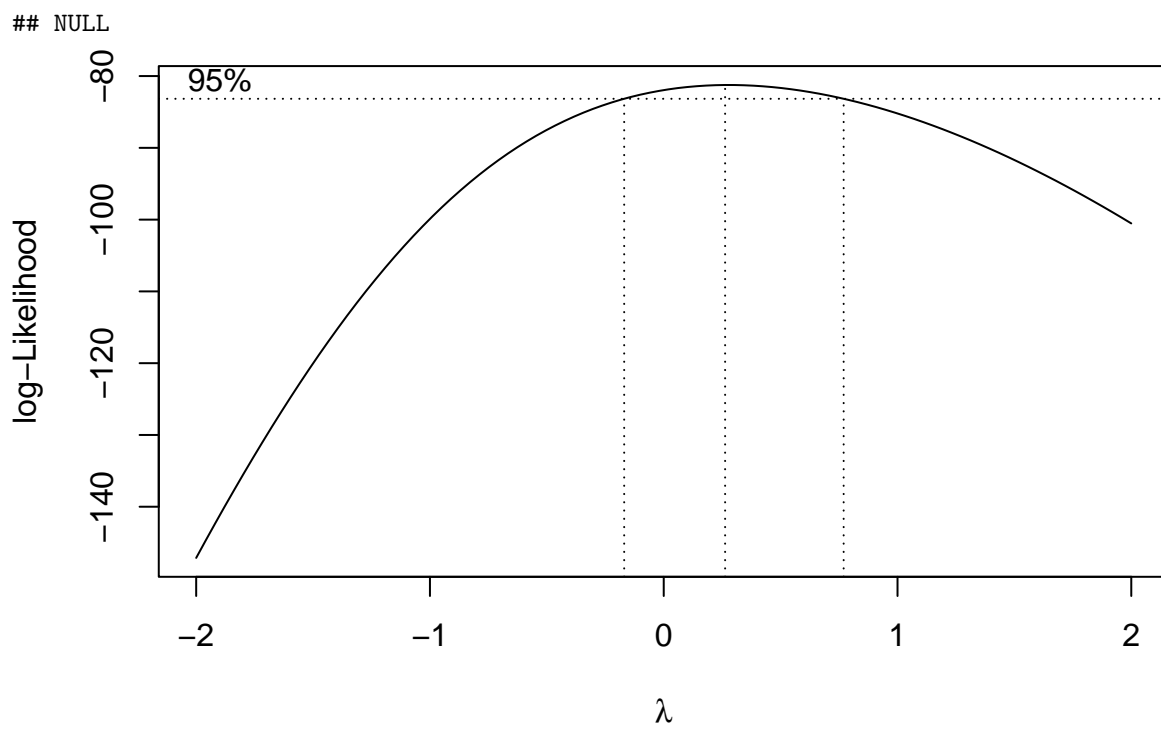


```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```



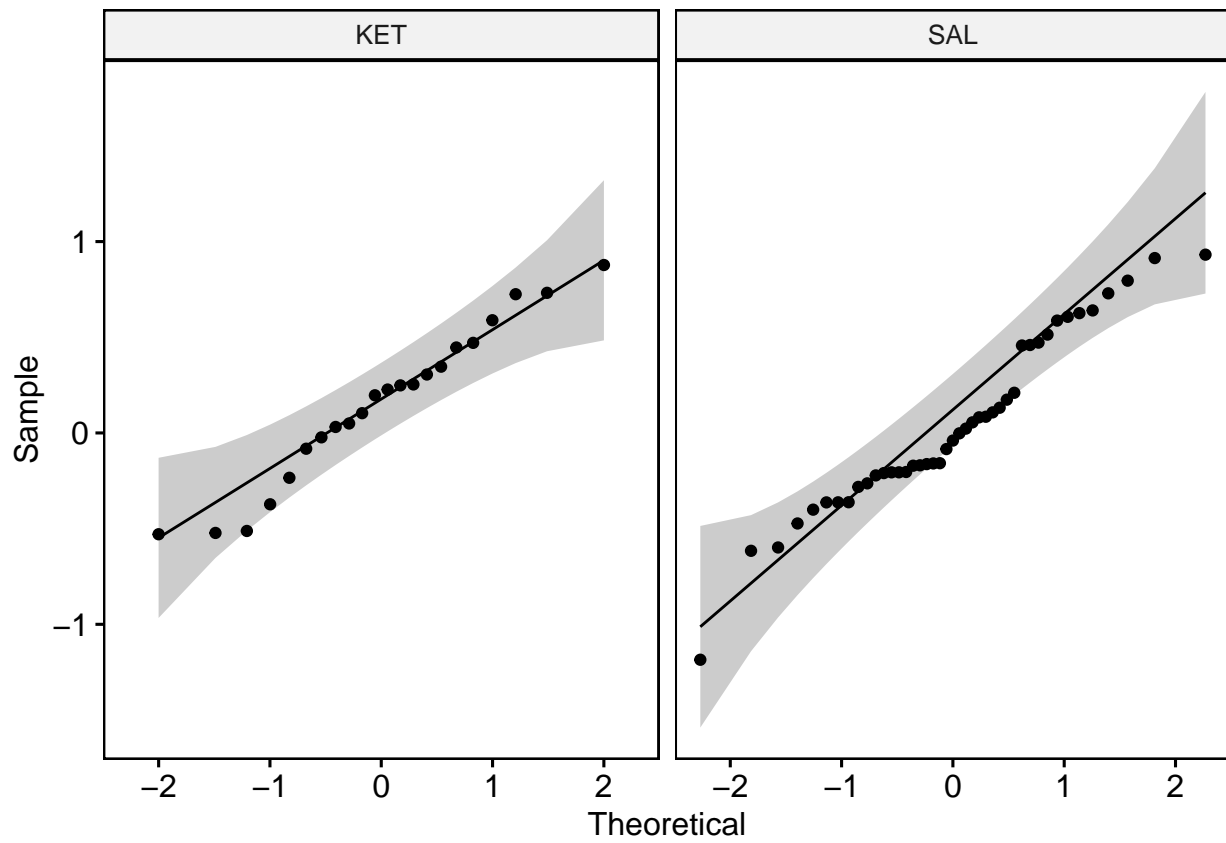
```
## [1] "best lamda"
## [1] 0.2626263
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.96181, p-value = 0.5267
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.95927, p-value = 0.1304
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.2839  0.596
##      63
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##              Sum Sq Df F value Pr(>F)
## (Intercept)  0.5029  1  2.5685 0.1140
## treat_factor  0.1814  1  0.9267 0.3394
## Residuals    12.3349 63
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 0.99624, df = 46.593, p-value = 0.3243
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1138634  0.3371698
## sample estimates:
##  mean of x  mean of y
## 0.15119116 0.03953798
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 1.0525, df = 1, p-value = 0.3049
figs[1]

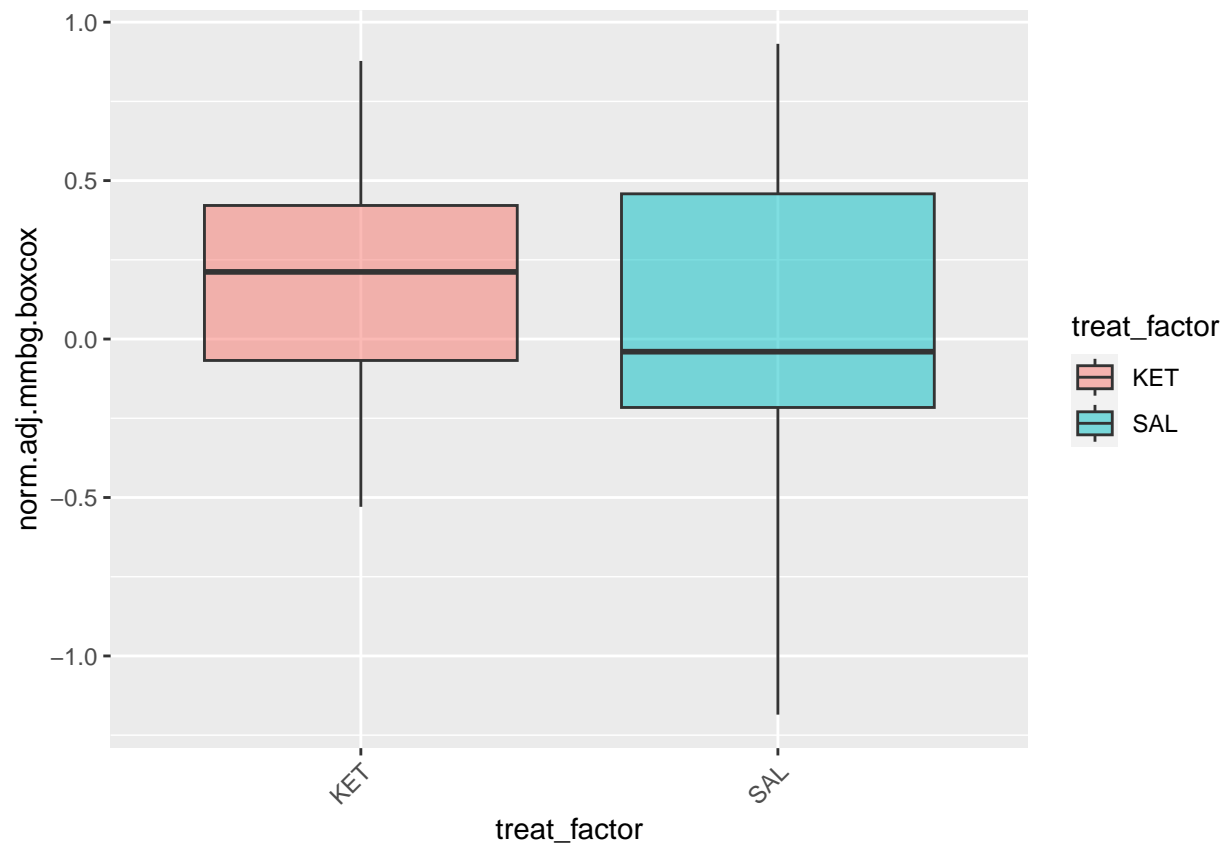
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



triple WFA

```
i <- str_which(fnames, "triple_WFA")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_triple_WFA_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.95014, p-value = 0.3427
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.87181, p-value = 0.0001941
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##      Df F value Pr(>F)
```

```
## group 1  1.2004 0.2775
```

```
##      62
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##           Sum Sq Df F value    Pr(>F)
```

```
## (Intercept) 24.774  1 81.2543 7.029e-13 ***
```

```
## treat_factor  0.053  1  0.1737    0.6783
```

```
## Residuals    18.903 62
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = 0.45799, df = 50.888, p-value = 0.6489
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.2073251  0.3298700
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 1.086138  1.024866
```

```
##
```

```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
```

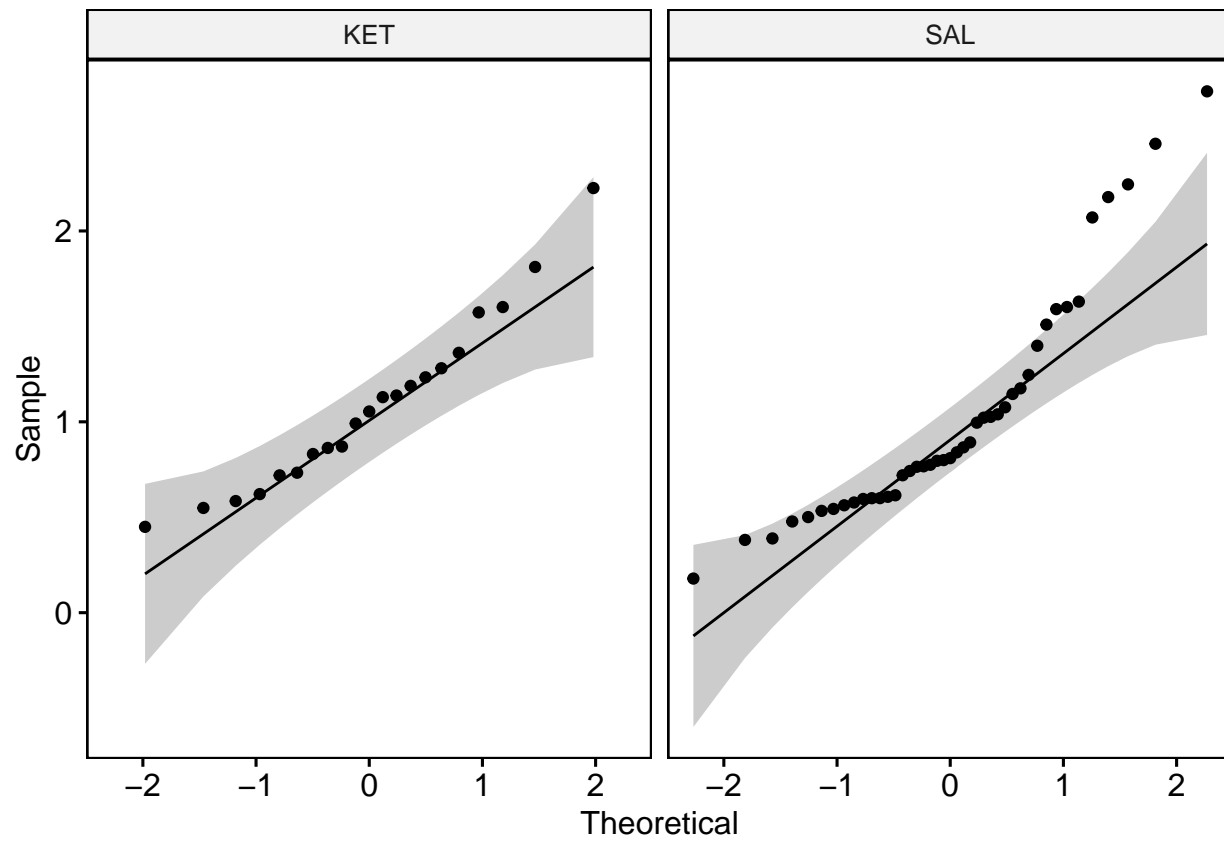
```
## data: norm_adj_mmbg by treat_factor
```



```
## Kruskal-Wallis chi-squared = 1.0746, df = 1, p-value = 0.2999
```

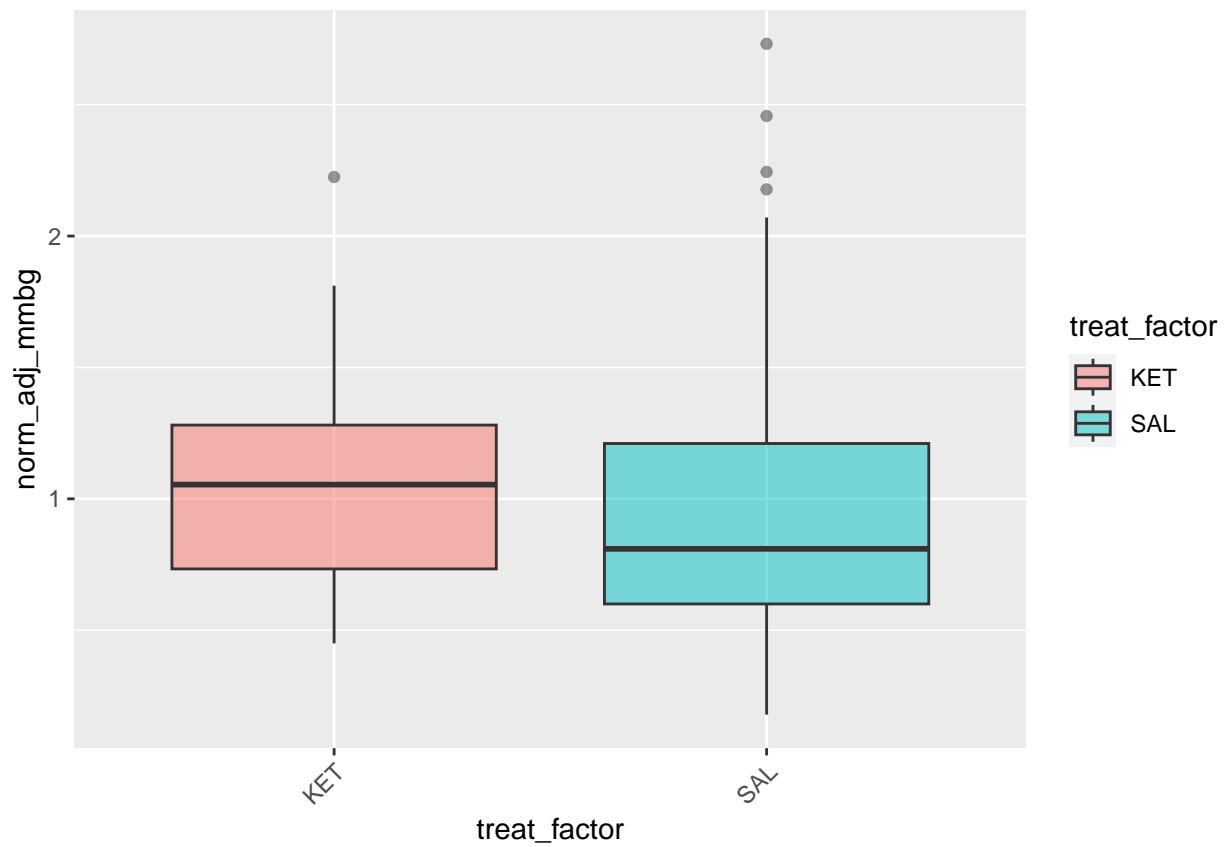
```
figs[1]
```

```
## [[1]]
```



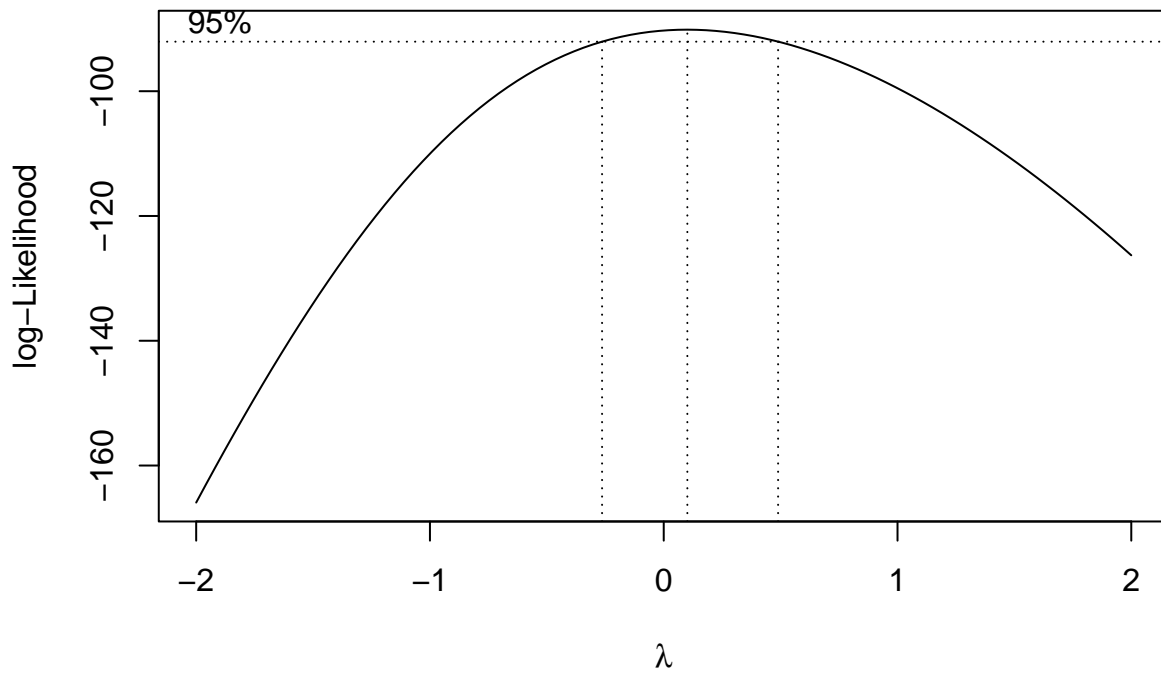
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

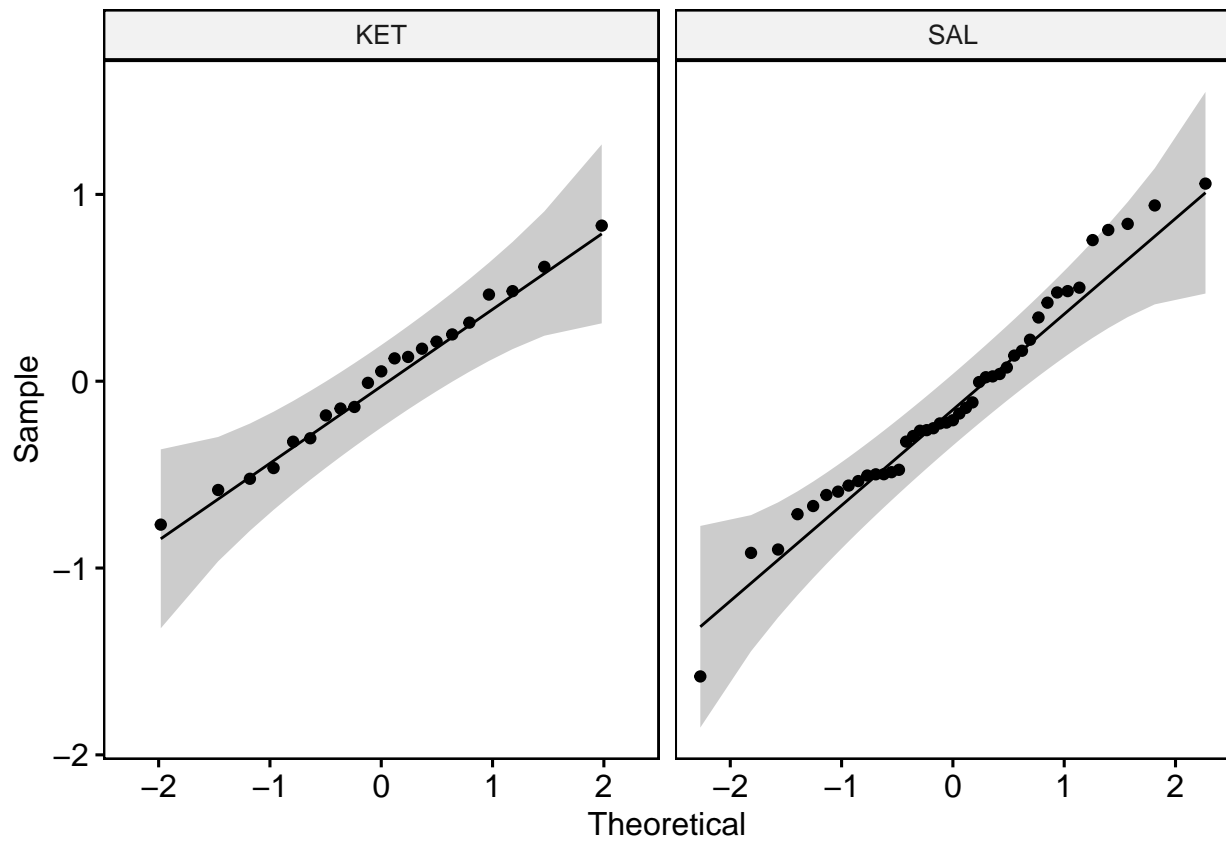
```
## [1] 0.1010101
```

```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.98898, p-value = 0.9959
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.97437, p-value = 0.442
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  1.3315  0.253
##      62
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##              Sum Sq Df F value Pr(>F)
## (Intercept)  0.0020  1  0.0076 0.9310
## treat_factor  0.2009  1  0.7671 0.3845
## Residuals    16.2394 62
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = 0.96347, df = 51.038, p-value = 0.3399
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1293147  0.3679747
## sample estimates:
##    mean of x    mean of y
##  0.009708107 -0.109621871
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 1.0746, df = 1, p-value = 0.2999
figs[1]

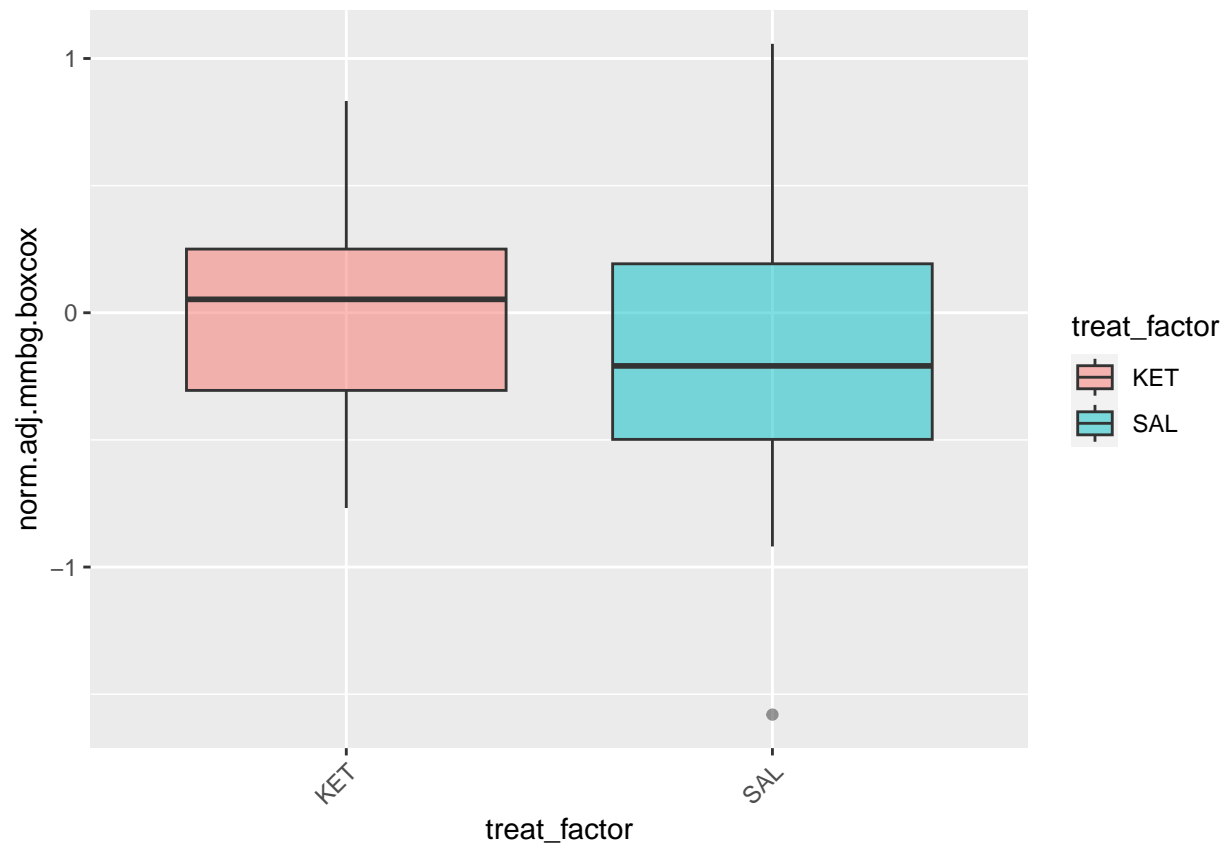
## [[1]]

```



```
figs[2]
```

```
## [[1]]
```



triple cFos

```
i <- str_which(fnames, "triple_cFos")
f <- fnames[i]
print(f)
```

```
## [1] "NORM/KET-VR5_triple_cFos_NORM.csv"
```

```
figs <- eda_anova_1way(f)
```

```
## $KET
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.9433, p-value = 0.2314
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: X[[i]]
```

```
## W = 0.94398, p-value = 0.03606
```

```
##
```

```
##
```

```
## Levene's Test for Homogeneity of Variance (center = "mean")
```

```
##      Df F value Pr(>F)
```

```
## group 1  5.0957 0.02746 *
```

```
##      63
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Anova Table (Type III tests)
```

```
##
```

```
## Response: norm_adj_mmbg
```

```
##           Sum Sq Df F value    Pr(>F)
```

```
## (Intercept) 13.2010  1 119.2685 3.597e-16 ***
```

```
## treat_factor  0.6048  1   5.4643  0.0226 *
```

```
## Residuals    6.9730 63
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
```

```
## t = -2.6355, df = 57.675, p-value = 0.01077
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## -0.35870430 -0.04900407
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 0.7746262 0.9784803
```

```
##
```

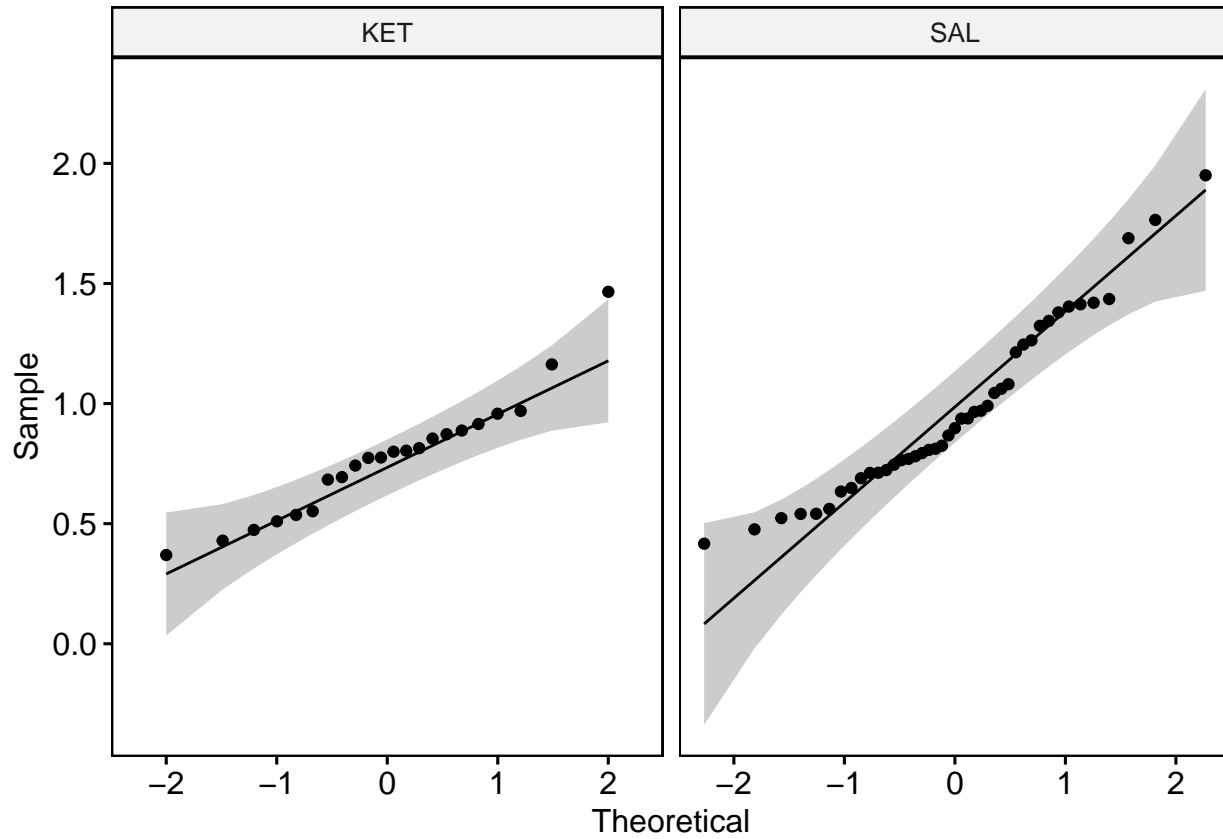
```
##
```

```
## Kruskal-Wallis rank sum test
```

```
##
## data: norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 4.0969, df = 1, p-value = 0.04296
```

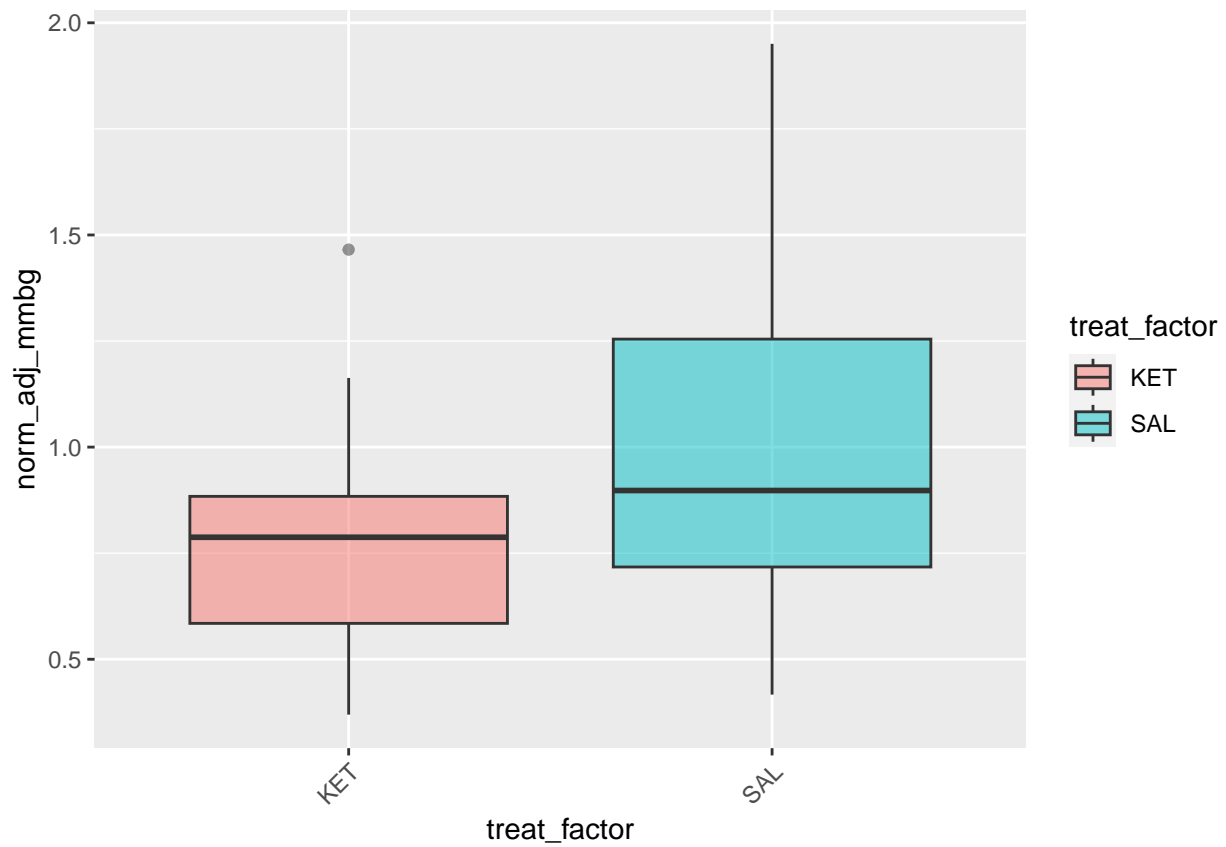
```
figs[1]
```

```
## [[1]]
```



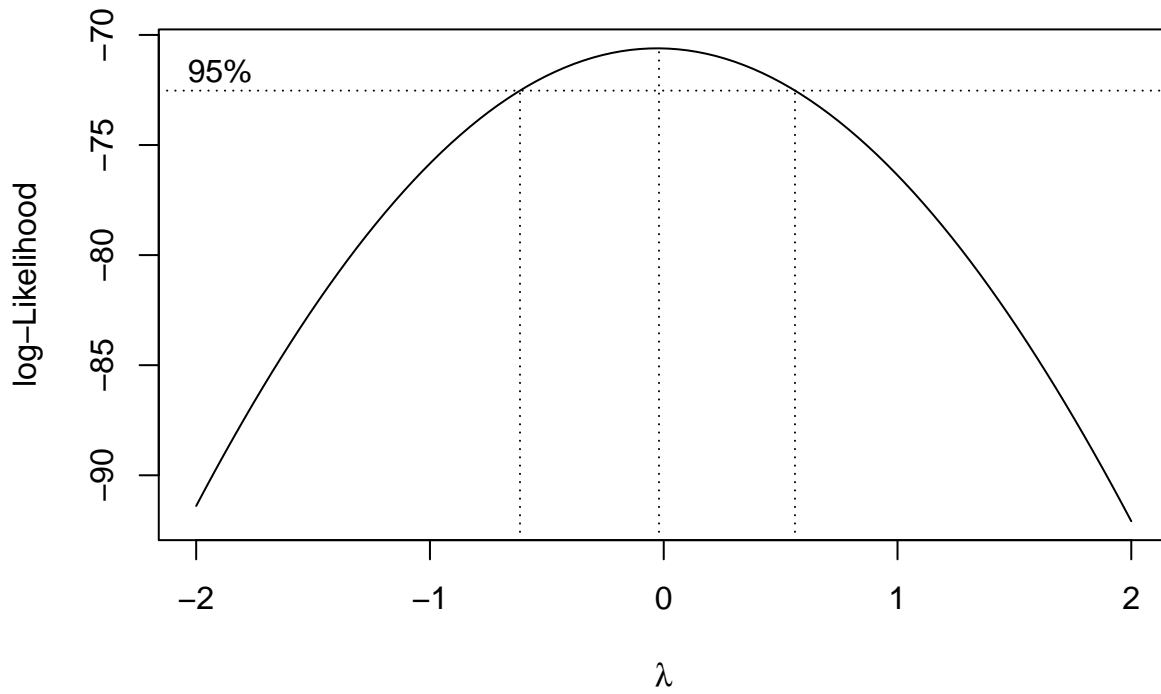
```
figs[2]
```

```
## [[1]]
```



```
figs <- eda_anova_1way_boxcox(f)
```

```
## NULL
```



```
## [1] "best lamda"
```

```
## [1] -0.02020202
```

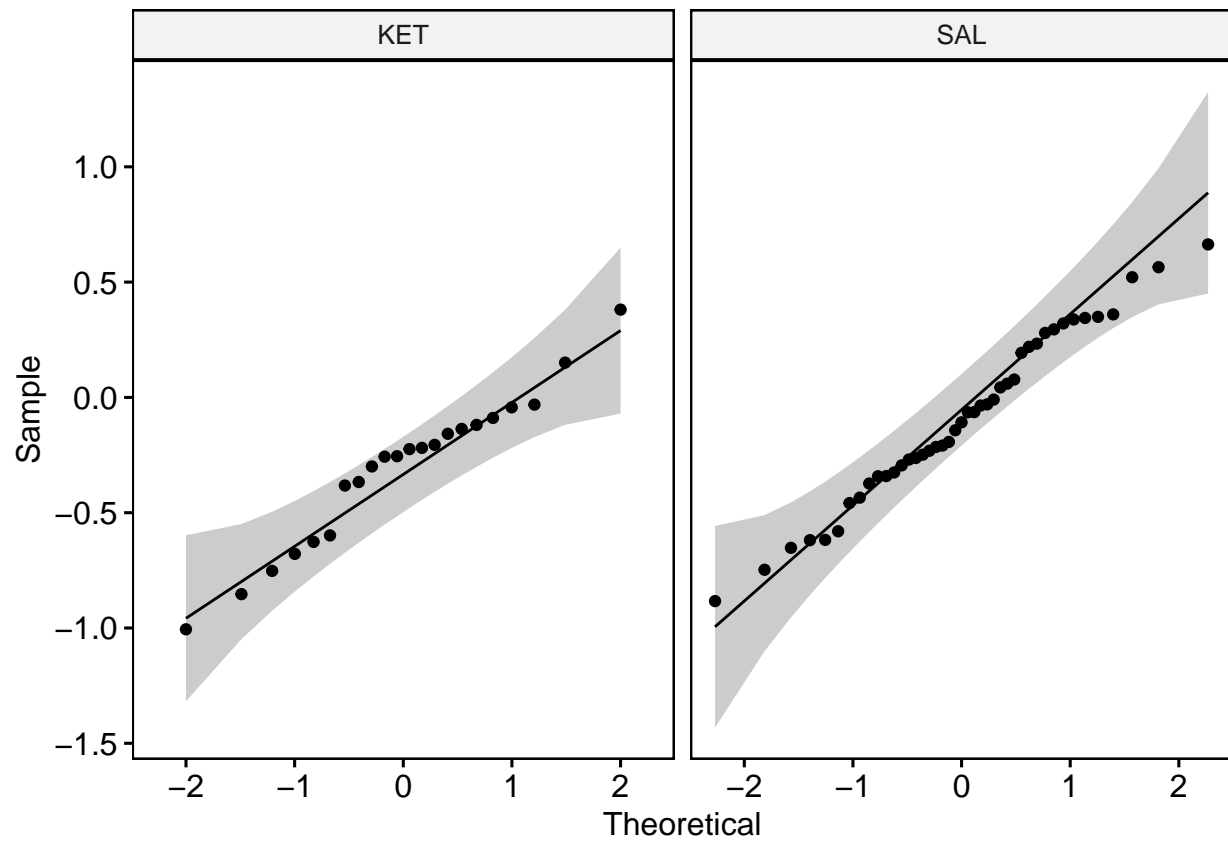


```

## $KET
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.96353, p-value = 0.5638
##
##
## $SAL
##
## Shapiro-Wilk normality test
##
## data: X[[i]]
## W = 0.98325, p-value = 0.7745
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1    0.854 0.3589
##      63
## Anova Table (Type III tests)
##
## Response: norm.adj.mmbg.boxcox
##           Sum Sq Df F value    Pr(>F)
## (Intercept)  2.0828  1   16.097 0.0001623 ***
## treat_factor  0.6869  1    5.309 0.0245253 *
## Residuals    8.1516 63
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Welch Two Sample t-test
##
## data: df[df$treat_factor == "KET", ]$norm.adj.mmbg.boxcox and df[df$treat_factor == "SAL", ]$norm.a
## t = -2.3938, df = 47.086, p-value = 0.02071
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.39982329 -0.03468546
## sample estimates:
##  mean of x   mean of y
## -0.30769080 -0.09043642
##
##
## Kruskal-Wallis rank sum test
##
## data: norm.adj.mmbg.boxcox by treat_factor
## Kruskal-Wallis chi-squared = 4.0969, df = 1, p-value = 0.04296
figs[1]

## [[1]]

```



```
figs[2]
```

```
## [[1]]
```

