

KET PRE VR5 SAC NORM means

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

## Loading required package: carData

library(emmeans)
library(stringr)
library(MASS)
knitr::opts_chunk$set(fig.width=6, fig.height=4)
```

NORM intensities, grouped by rat

```
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_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=0.7) +
  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_means',pattern='NORM.csv', full.names=TRUE)
fnames

## [1] "NORM_means/KET-VR5_cFos_coloc_w_PV_NORM.csv"
## [2] "NORM_means/KET-VR5_cFos_coloc_w_WFA_NORM.csv"
## [3] "NORM_means/KET-VR5_PV_coloc_w_cFos_NORM.csv"
## [4] "NORM_means/KET-VR5_PV_coloc_w_WFA_NORM.csv"

```

```
## [5] "NORM_means/KET-VR5_single_cFos_NORM.csv"
## [6] "NORM_means/KET-VR5_single_PV_NORM.csv"
## [7] "NORM_means/KET-VR5_single_WFA_NORM.csv"
## [8] "NORM_means/KET-VR5_triple_cFos_NORM.csv"
## [9] "NORM_means/KET-VR5_triple_PV_NORM.csv"
## [10] "NORM_means/KET-VR5_triple_WFA_NORM.csv"
## [11] "NORM_means/KET-VR5_WFA_coloc_w_cFos_NORM.csv"
## [12] "NORM_means/KET-VR5_WFA_coloc_w_PV_NORM.csv"
```

single PV

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.86056, p-value = 0.2622
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.76813, p-value = 0.05627
```

```
##
```

```
##
```

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

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

```
## group 1      3.4 0.1148
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = 0.23354, df = 3.3946, p-value = 0.8287
```

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

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

```
## -0.2363387  0.2764882
```

```
## sample estimates:
```

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

```
## 1.0072263 0.9871515
```

```
##
```

```
##
```

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

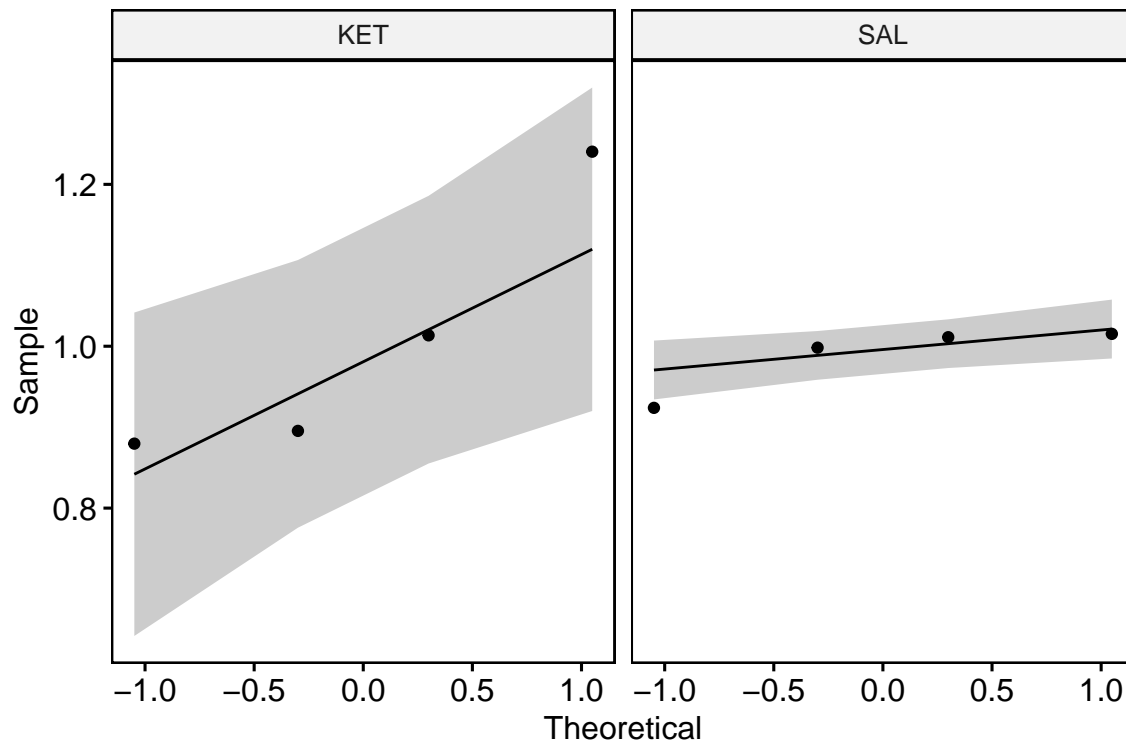
```
##
```

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

```
## Kruskal-Wallis chi-squared = 0.083333, df = 1, p-value = 0.7728
```

```
figs[1]
```

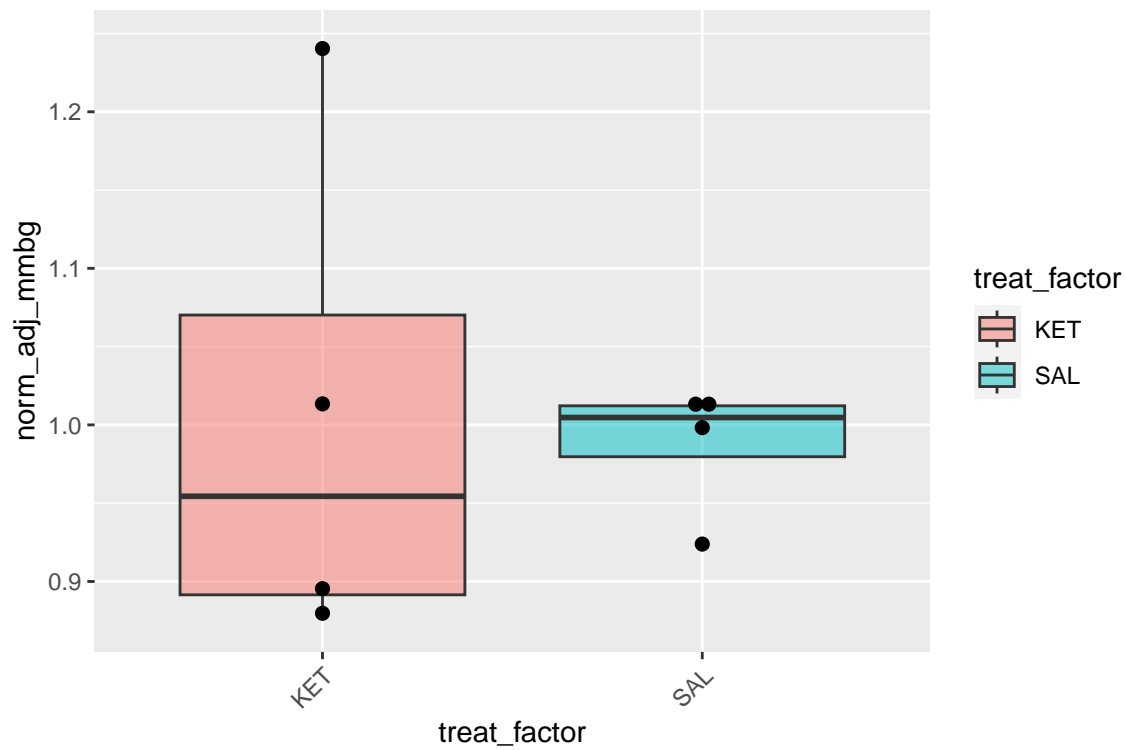
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



single WFA

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.79416, p-value = 0.09215
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.81332, p-value = 0.1283
```

```
##
```

```
##
```

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

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

```
## group 1  1.2109 0.3133
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -0.51293, df = 4.4475, p-value = 0.6324
```

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

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

```
## -0.6011072  0.4073495
```

```
## sample estimates:
```

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

```
## 0.8368427 0.9337216
```

```
##
```

```
##
```

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

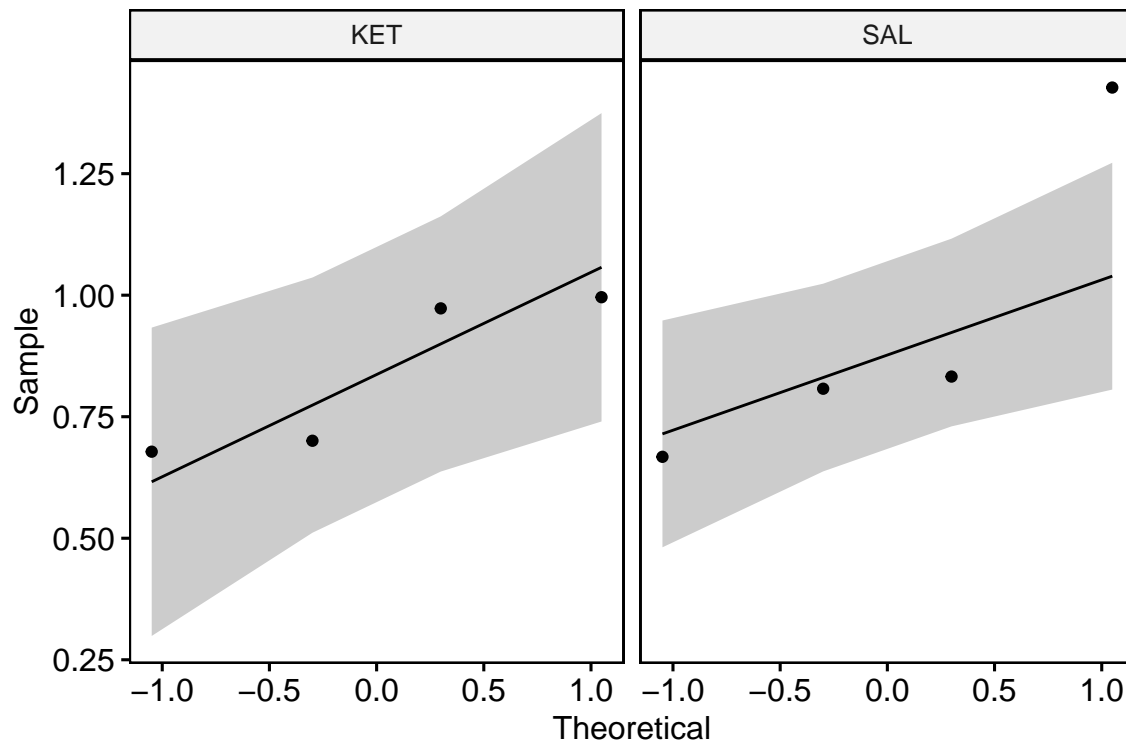
```
##
```

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

```
## Kruskal-Wallis chi-squared = 0, df = 1, p-value = 1
```

```
figs[1]
```

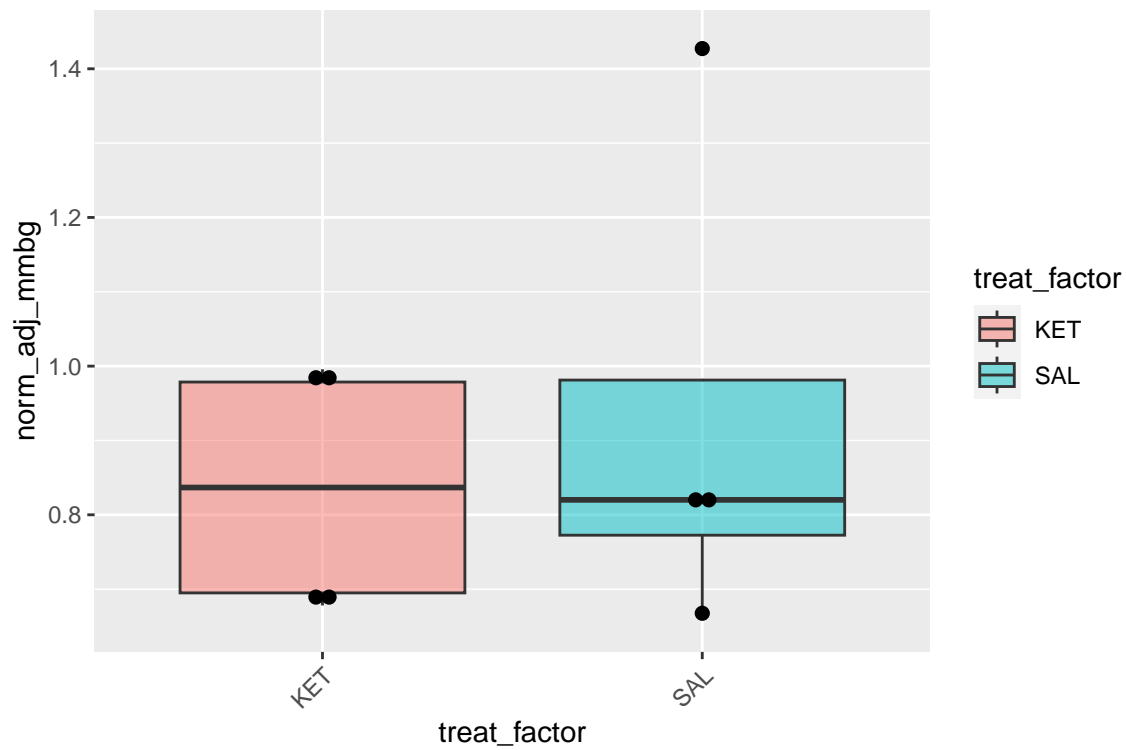
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



Single c-Fos

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.98066, p-value = 0.9059
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.987, p-value = 0.9416
```

```
##
```

```
##
```

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

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

```
## group 1  0.7226 0.4279
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -0.18416, df = 5.4443, p-value = 0.8606
```

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

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

```
## -0.2115231  0.1825922
```

```
## sample estimates:
```

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

```
## 1.049343  1.063809
```

```
##
```

```
##
```

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

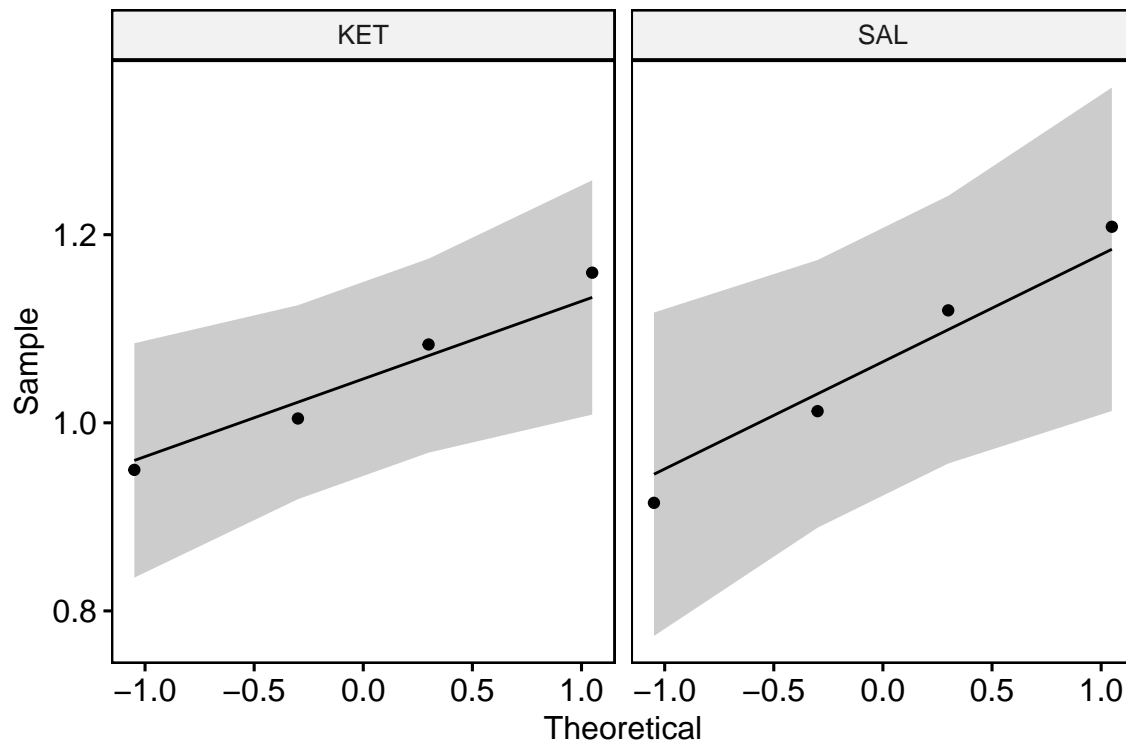
```
##
```

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

```
## Kruskal-Wallis chi-squared = 0.083333, df = 1, p-value = 0.7728
```

```
figs[1]
```

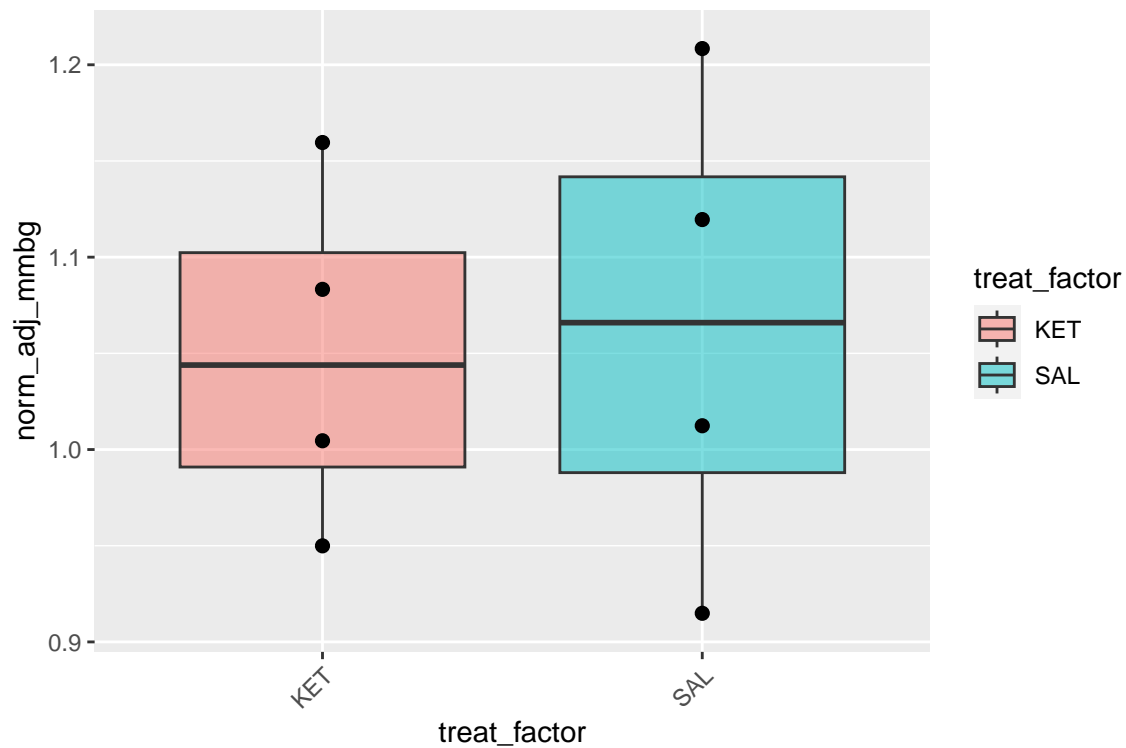
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



PV coloc w WFA

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.93051, p-value = 0.5974
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.99923, p-value = 0.9978
```

```
##
```

```
##
```

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

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

```
## group 1  1.8187 0.2261
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -0.002015, df = 3.9199, p-value = 0.9985
```

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

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

```
## -0.3790987  0.3785532
```

```
## sample estimates:
```

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

```
## 1.098372  1.098645
```

```
##
```

```
##
```

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

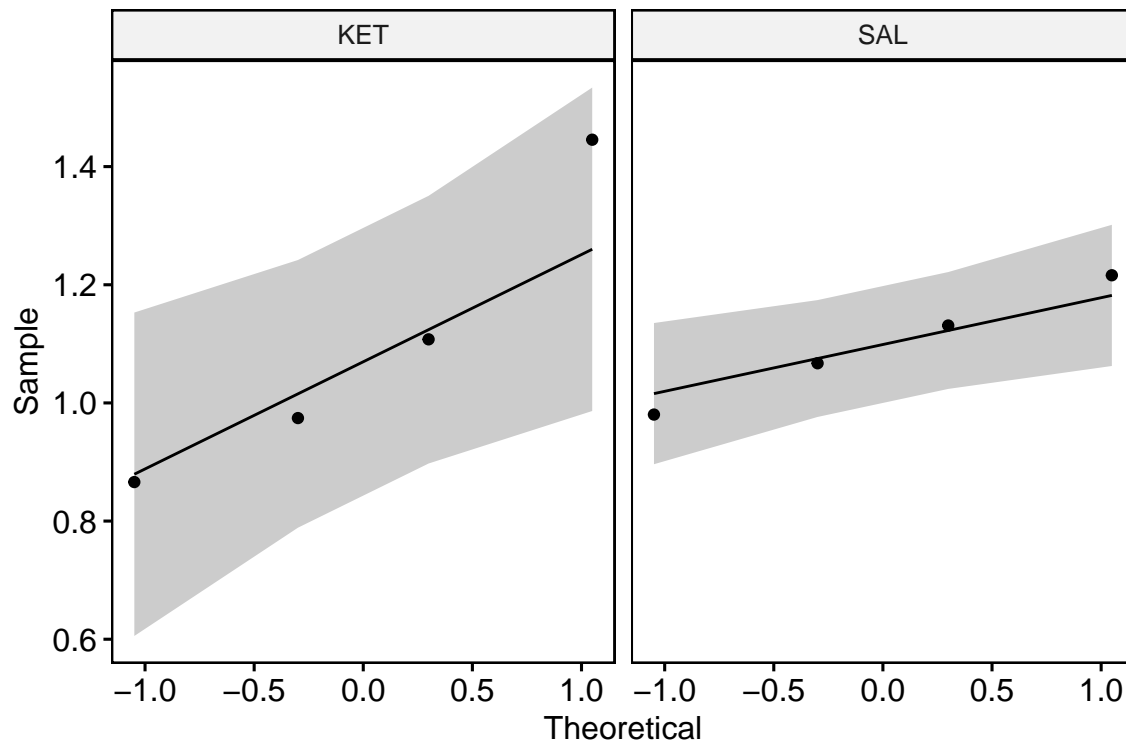
```
##
```

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

```
## Kruskal-Wallis chi-squared = 0.33333, df = 1, p-value = 0.5637
```

```
figs[1]
```

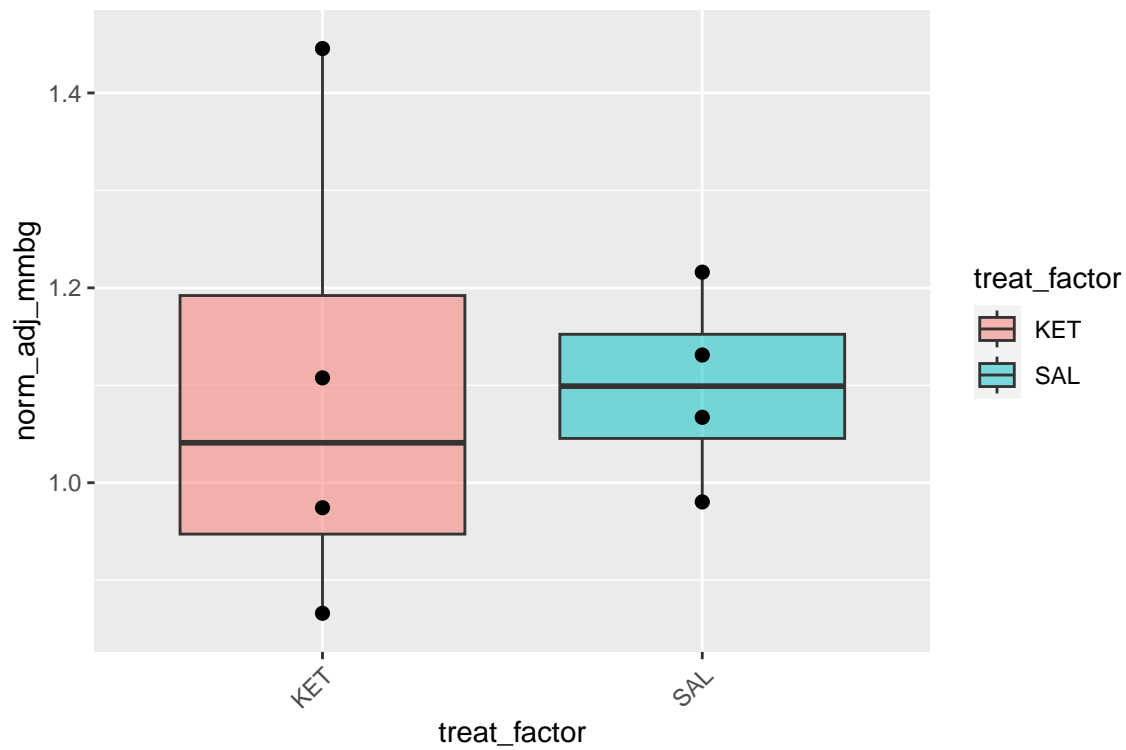
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



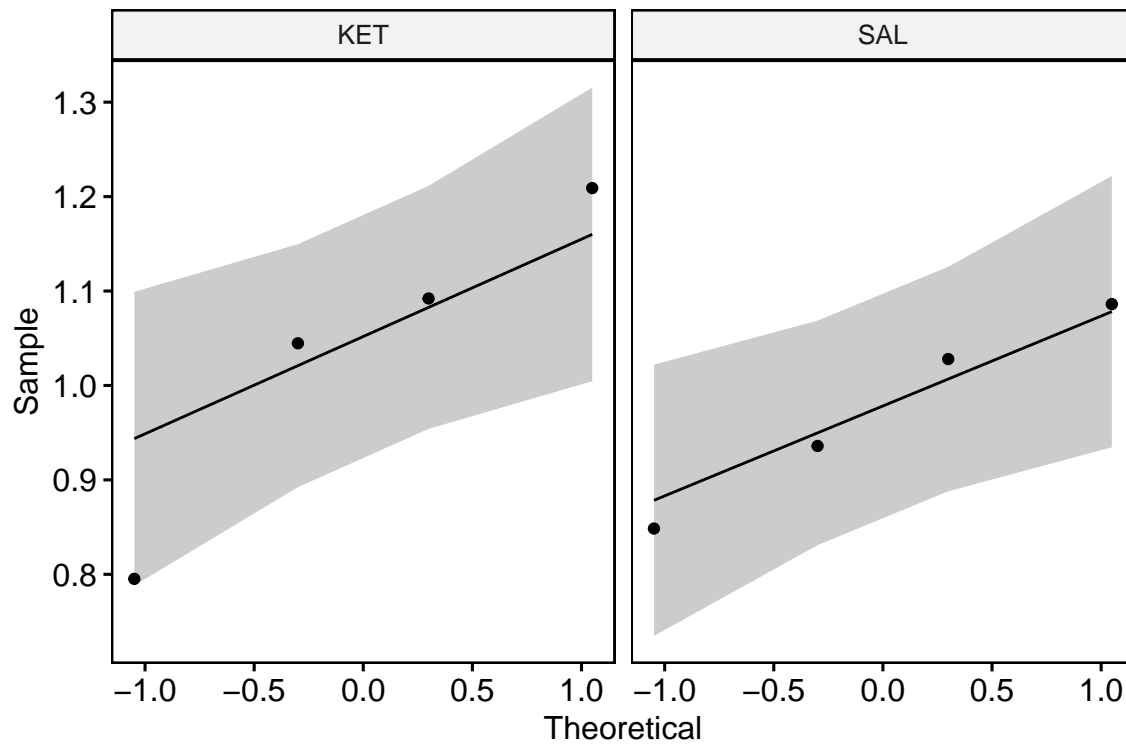
PV coloc w cFos

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

## [1] "NORM_means/KET-VR5_PV_coloc_w_cFos_NORM.csv"
figs <- eda_anova_1way(f)

## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.93739, p-value = 0.6385
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.97623, p-value = 0.8796
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.4345 0.5343
##      6
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = 0.59686, df = 4.907, p-value = 0.5771
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.2020048  0.3232730
## sample estimates:
## mean of x mean of y
##  1.035257  0.974623
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 0.75, df = 1, p-value = 0.3865
figs[1]

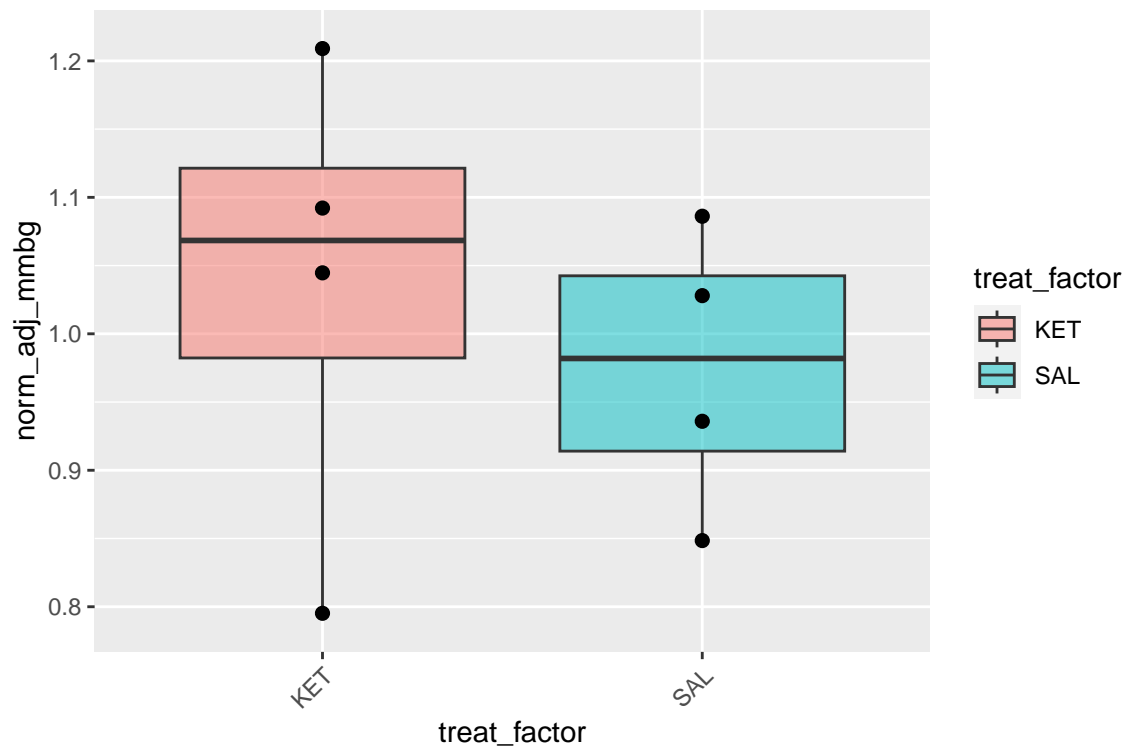
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with  
## `binwidth`.
```



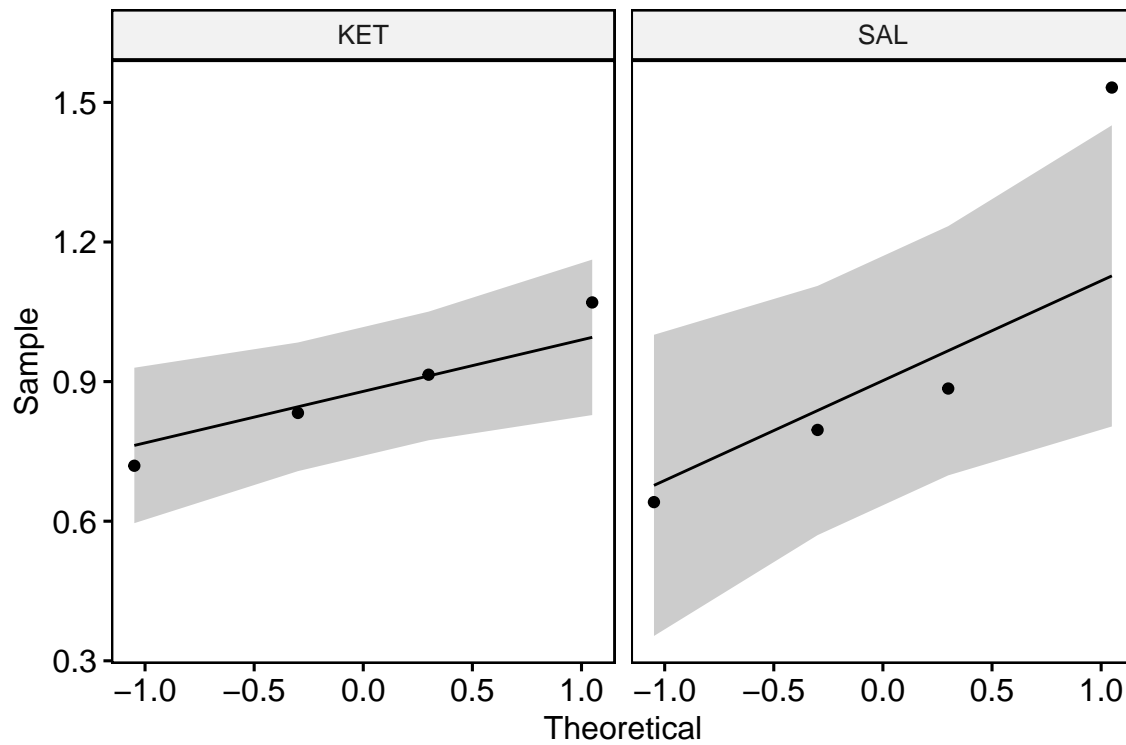
WFA coloc w PV

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

## [1] "NORM_means/KET-VR5_WFA_coloc_w_PV_NORM.csv"
figs <- eda_anova_1way(f)

## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.99326, p-value = 0.9735
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.85251, p-value = 0.2344
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  2.3698 0.1746
##      6
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = -0.37873, df = 3.8339, p-value = 0.7249
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.6710372  0.5123601
## sample estimates:
## mean of x mean of y
## 0.8841805 0.9635191
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 0.083333, df = 1, p-value = 0.7728
figs[1]

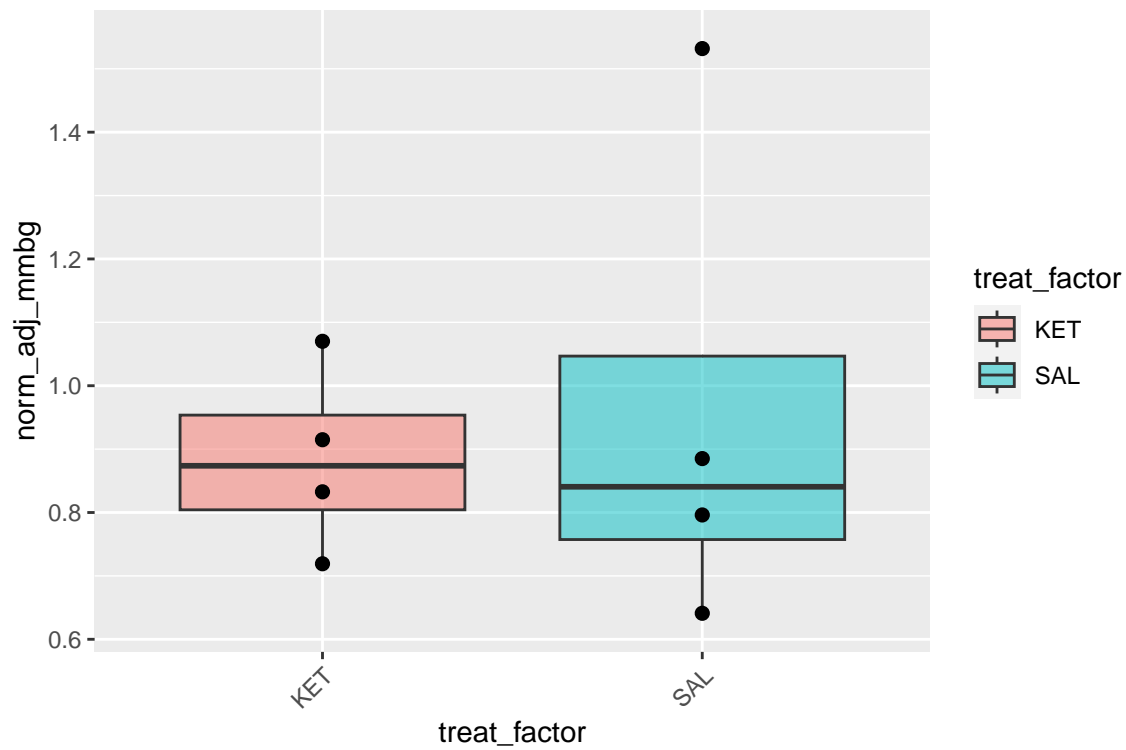
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with  
## `binwidth`.
```



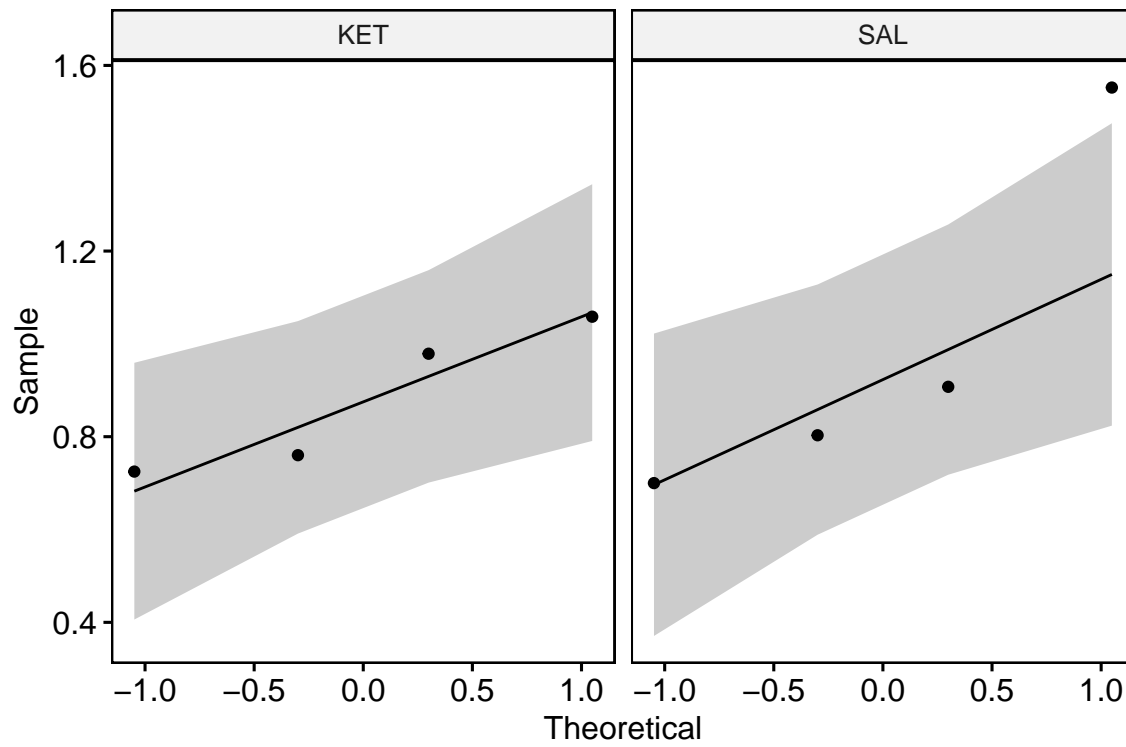
WFA coloc w cFos

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

## [1] "NORM_means/KET-VR5_WFA_coloc_w_cFos_NORM.csv"
figs <- eda_anova_1way(f)

## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.88176, p-value = 0.3462
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.82294, p-value = 0.1501
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  1.8735 0.2201
##      6
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = -0.528, df = 4.0522, p-value = 0.6251
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.6863533  0.4660778
## sample estimates:
## mean of x mean of y
## 0.8805976 0.9907353
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 0, df = 1, p-value = 1
figs[1]

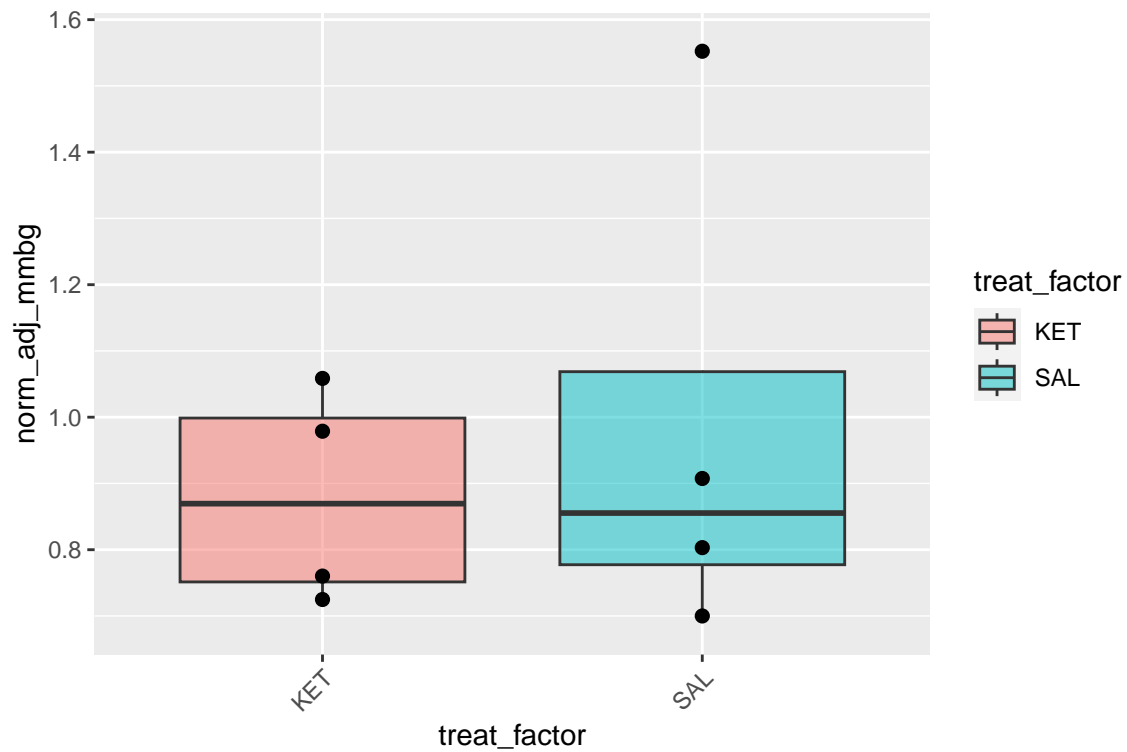
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with  
## `binwidth`.
```



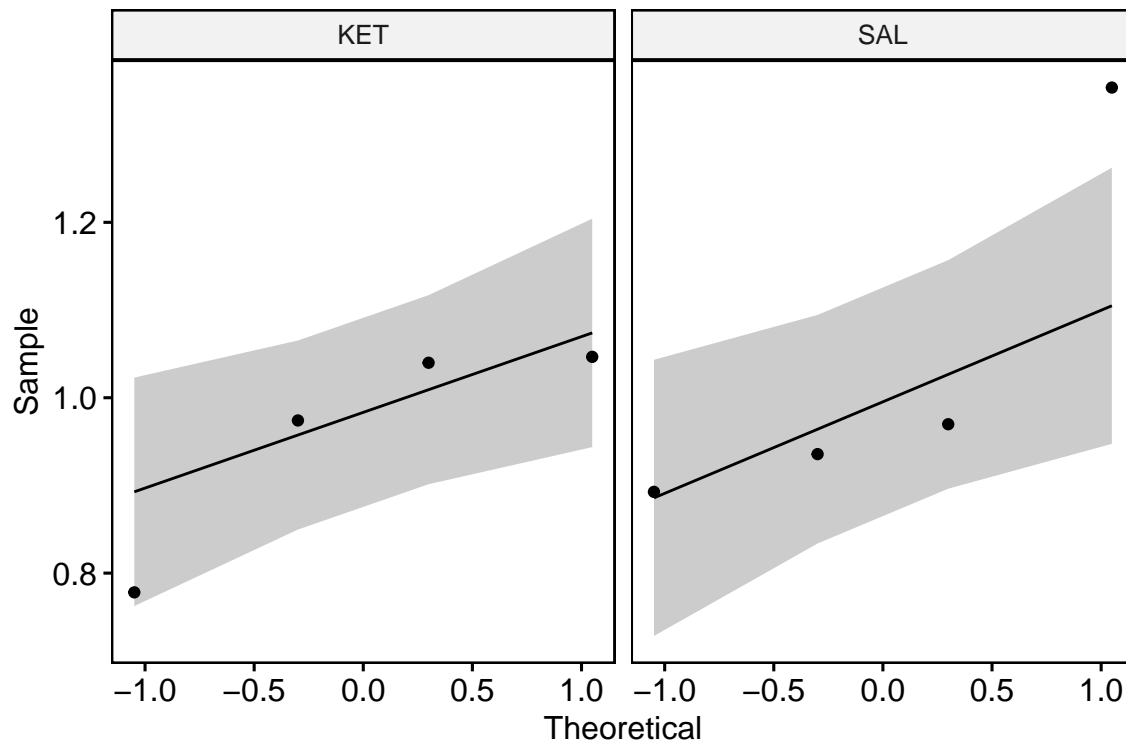
cFos coloc w PV

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

```
## [1] "NORM_means/KET-VR5_cFos_coloc_w_PV_NORM.csv"
figs <- eda_anova_1way(f)
```

```
## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.8102, p-value = 0.1218
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.76539, p-value = 0.05326
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  1.0707 0.3407
##      6
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = -0.6339, df = 4.8588, p-value = 0.5548
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.3986195  0.2420183
## sample estimates:
## mean of x mean of y
## 0.9596533 1.0379539
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 0.083333, df = 1, p-value = 0.7728
figs[1]

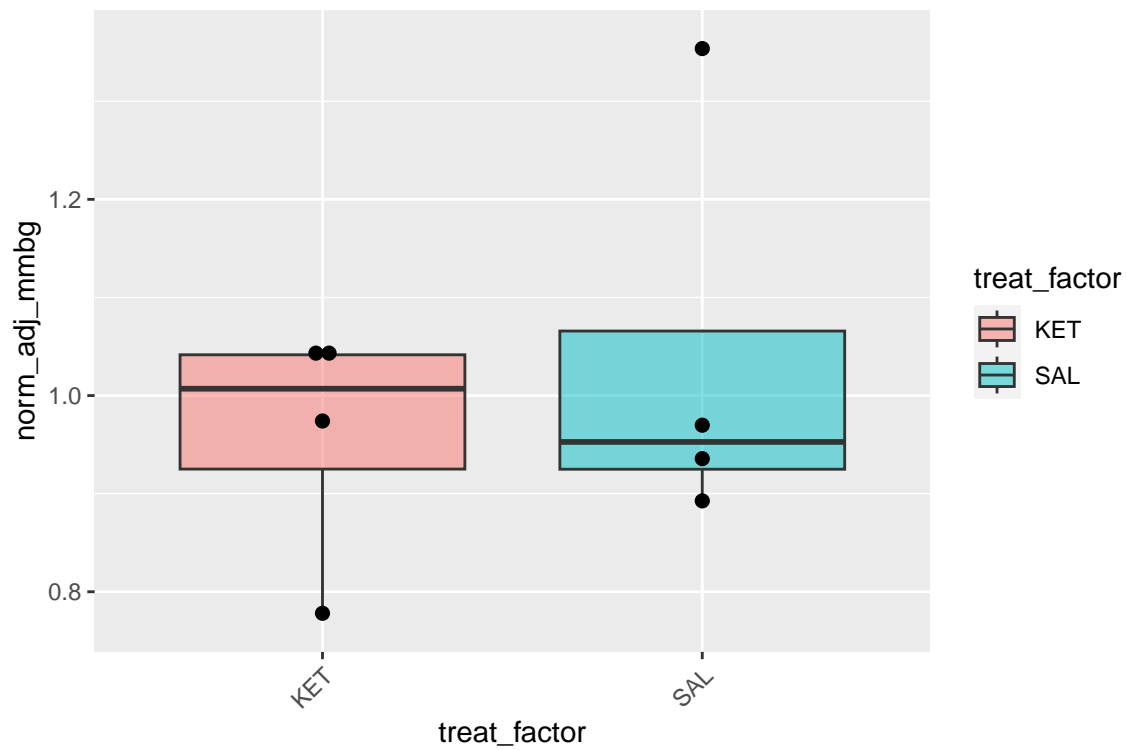
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



cFos coloc w WFA

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

```
## [1] "NORM_means/KET-VR5_cFos_coloc_w_WFA_NORM.csv"
```

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.97656, p-value = 0.8816
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.93658, p-value = 0.6336
```

```
##
```

```
##
```

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

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

```
## group 1  0.1136 0.7475
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -1.8017, df = 5.4732, p-value = 0.1264
```

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

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

```
## -0.36186642  0.05910286
```

```
## sample estimates:
```

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

```
## 0.8174022 0.9687840
```

```
##
```

```
##
```

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

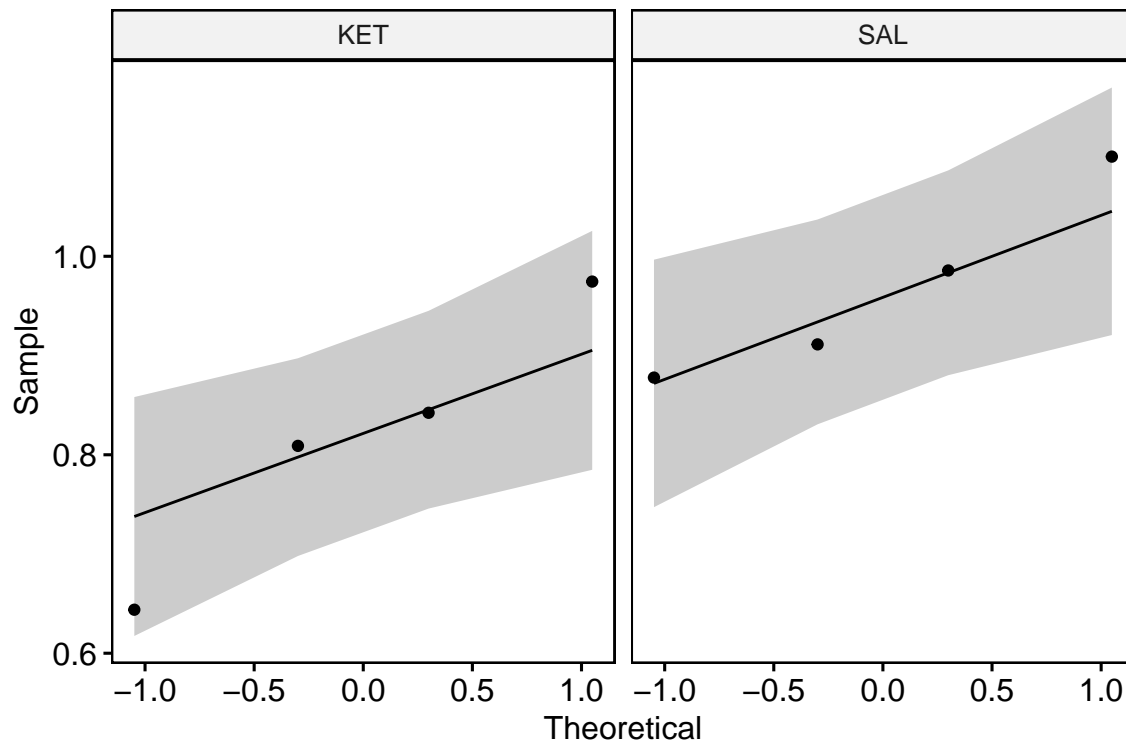
```
##
```

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

```
## Kruskal-Wallis chi-squared = 3, df = 1, p-value = 0.08326
```

```
figs[1]
```

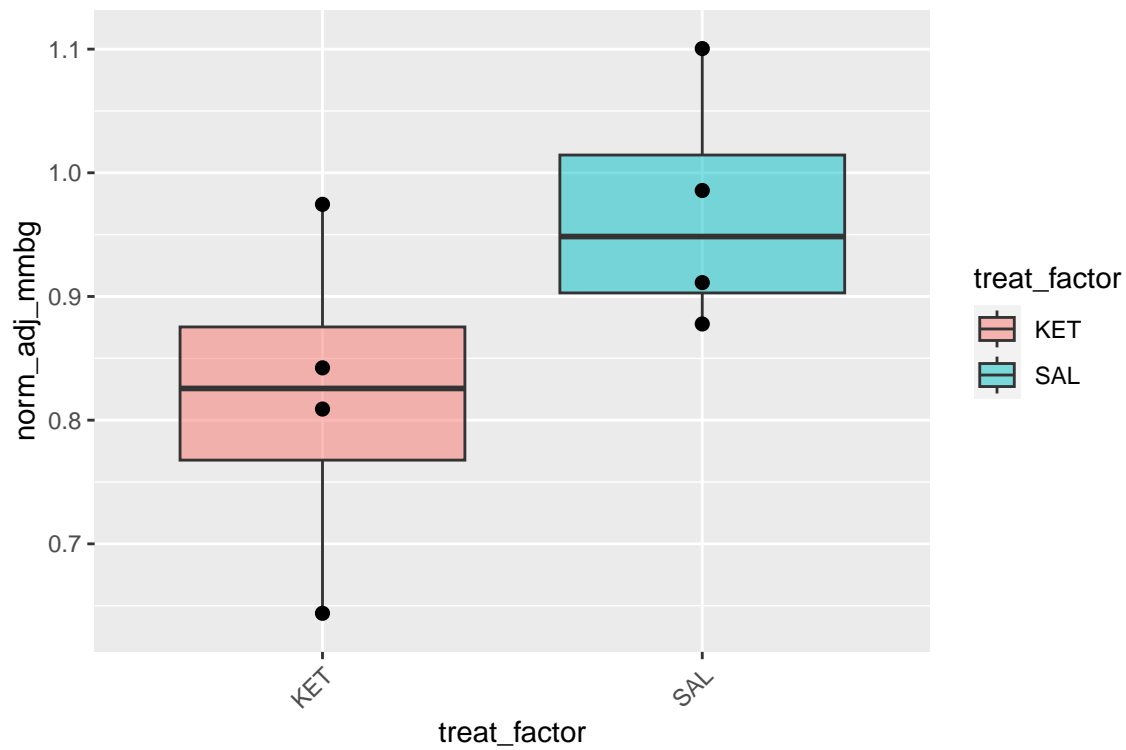
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



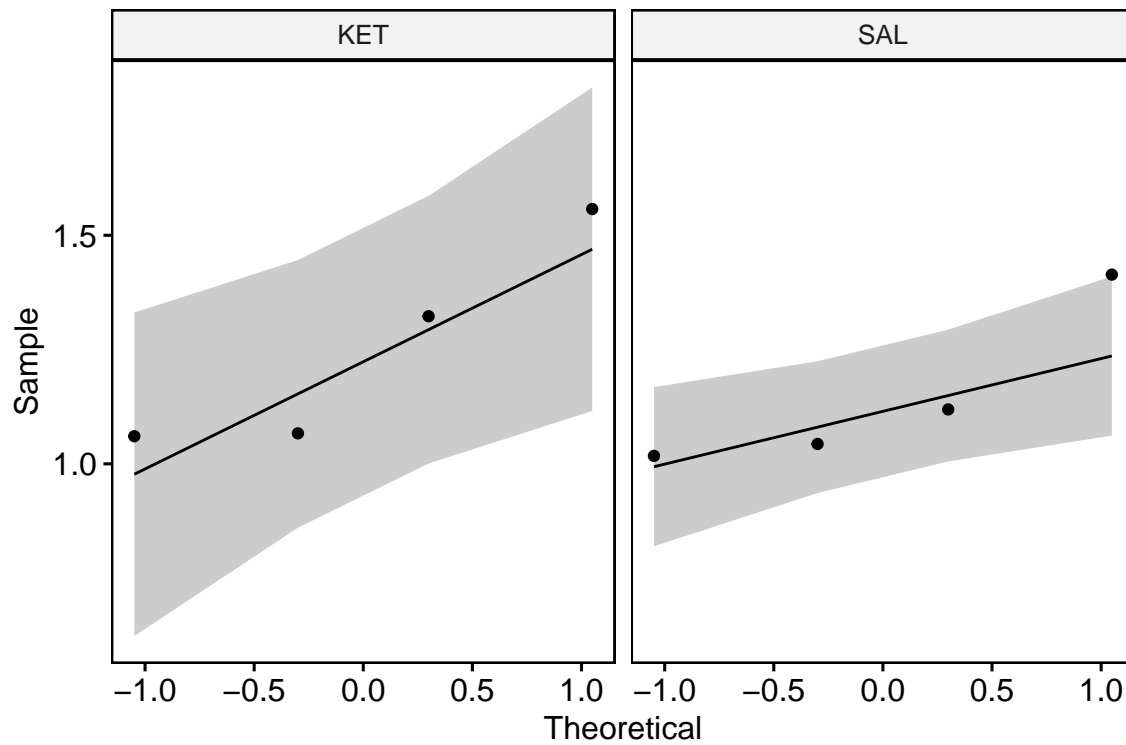
triple PV

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

## [1] "NORM_means/KET-VR5_triple_PV_NORM.csv"
figs <- eda_anova_1way(f)

## $KET
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.8716, p-value = 0.304
##
##
## $SAL
##
##  Shapiro-Wilk normality test
##
## data:  X[[i]]
## W = 0.8164, p-value = 0.135
##
##
## Levene's Test for Homogeneity of Variance (center = "mean")
##      Df F value Pr(>F)
## group 1  0.6551 0.4492
##      6
##
##  Welch Two Sample t-test
##
## data:  df[df$treat_factor == "KET", ]$norm_adj_mmbg and df[df$treat_factor == "SAL", ]$norm_adj_mmbg
## t = 0.69071, df = 5.6207, p-value = 0.5172
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.268984  0.475786
## sample estimates:
## mean of x mean of y
##  1.251871  1.148470
##
##
##  Kruskal-Wallis rank sum test
##
## data:  norm_adj_mmbg by treat_factor
## Kruskal-Wallis chi-squared = 0.75, df = 1, p-value = 0.3865
figs[1]

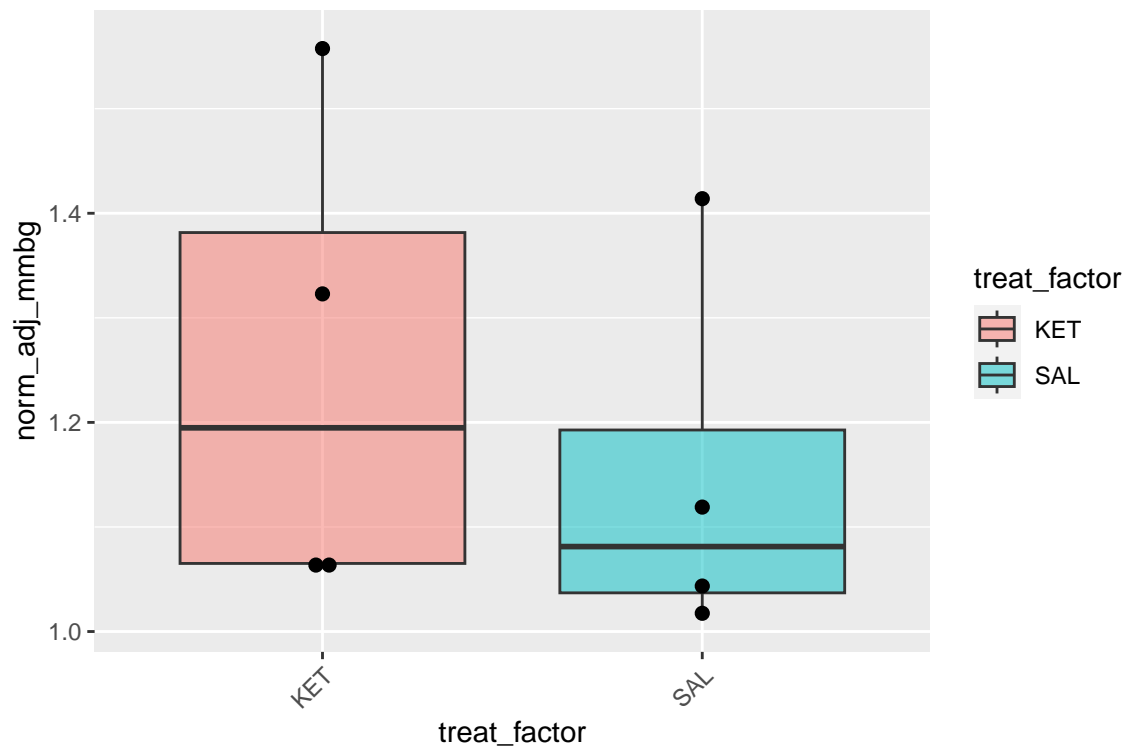
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



triple WFA

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.79507, p-value = 0.09367
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.93625, p-value = 0.6316
```

```
##
```

```
##
```

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

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

```
## group 1  0.6778 0.4418
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -0.12461, df = 4.7469, p-value = 0.9059
```

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

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

```
## -0.8350187  0.7589848
```

```
## sample estimates:
```

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

```
##  1.112876  1.150893
```

```
##
```

```
##
```

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

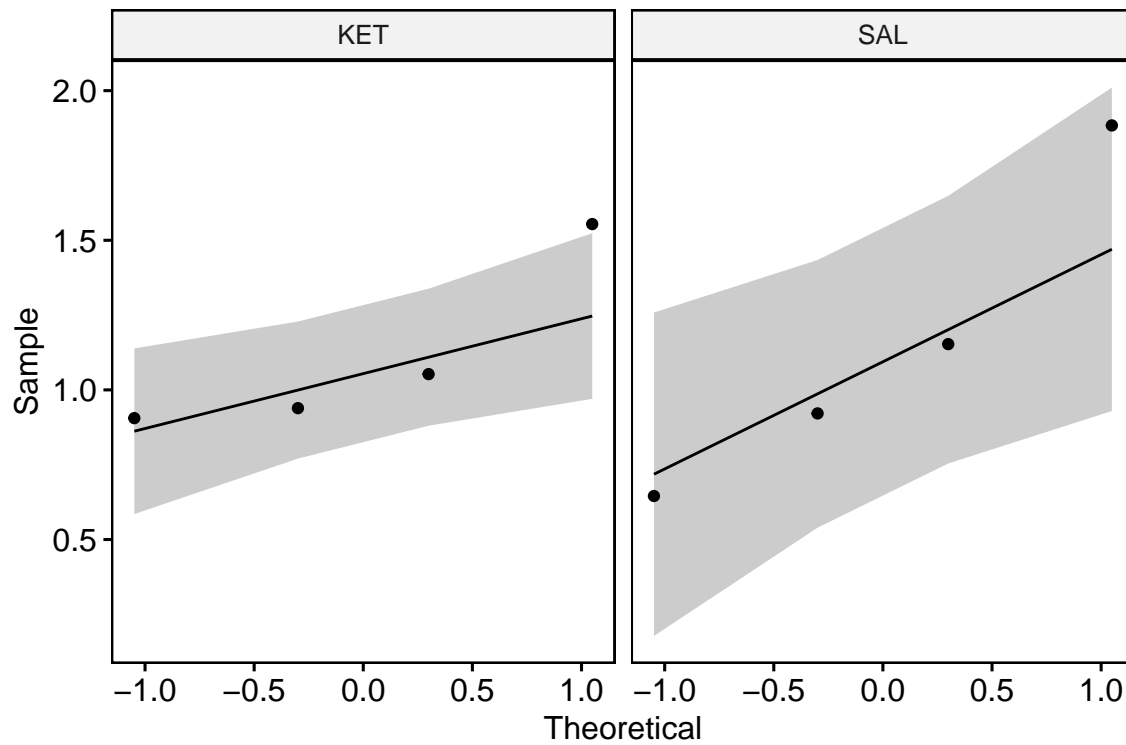
```
##
```

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

```
## Kruskal-Wallis chi-squared = 0, df = 1, p-value = 1
```

```
figs[1]
```

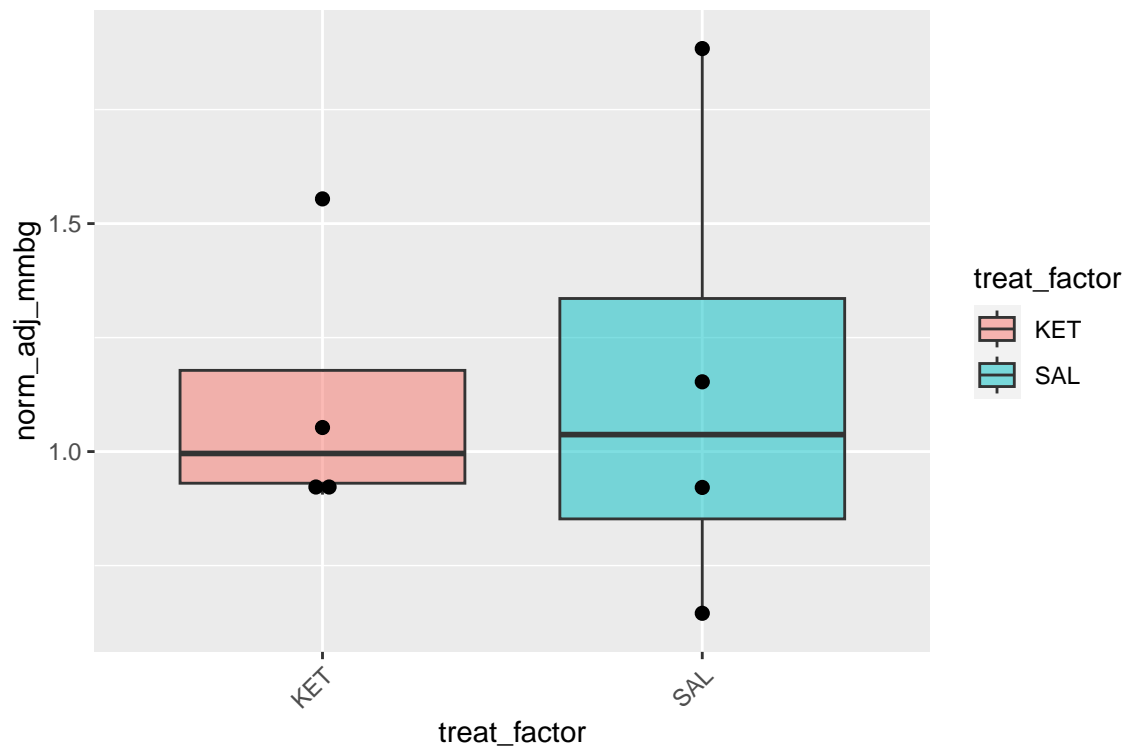
```
## [[1]]
```



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```



triple cFos

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

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

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

```
## $KET
```

```
##
```

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

```
##
```

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

```
## W = 0.88815, p-value = 0.3746
```

```
##
```

```
##
```

```
## $SAL
```

```
##
```

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

```
##
```

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

```
## W = 0.93308, p-value = 0.6126
```

```
##
```

```
##
```

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

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

```
## group 1  0.2505 0.6346
```

```
##      6
```

```
##
```

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

```
##
```

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

```
## t = -2.3483, df = 5.9442, p-value = 0.05758
```

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

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

```
## -0.450226955  0.009766906
```

```
## sample estimates:
```

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

```
## 0.7870625 1.0072925
```

```
##
```

```
##
```

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

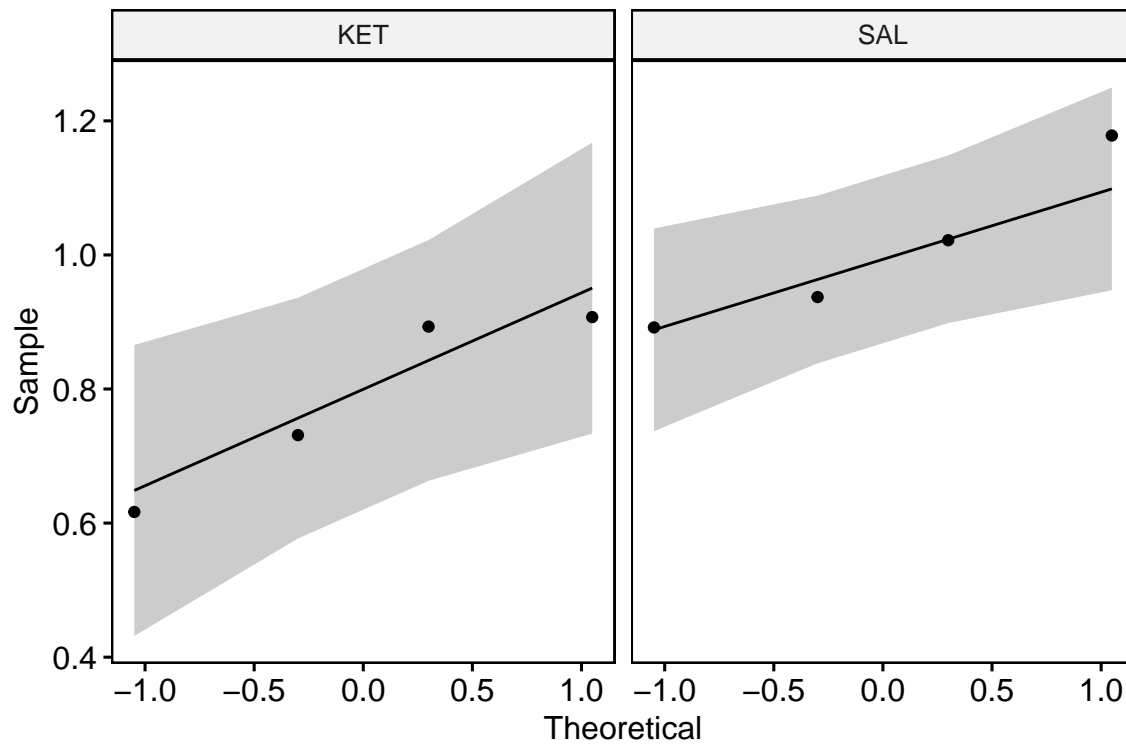
```
##
```

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

```
## Kruskal-Wallis chi-squared = 3, df = 1, p-value = 0.08326
```

```
figs[1]
```

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



```
figs[2]
```

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

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## `binwidth`.
```

