10302021-qpCR-Figures

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```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```
```
## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.6      v dplyr   1.0.7
## v tidyr   1.1.4      v stringr 1.4.0
## v readr   2.1.0      v forcats 0.5.1
```
```
## -- Conflicts ------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```
```
library(ggplot2)
library(ggthemes)
library(forcats)
library(ggpubr)
```

```r
pomc <- read.csv("../data/08202021-POMC-final.csv", fileEncoding = 'UTF-8-BOM')
pomc <- pomc %>% mutate(Time = as.factor(Time)) %>%
  mutate(Time = fct_relevel(Time, c("8am", "4pm", "12am"))) %>%
  mutate(Time = fct_recode(Time,
                           "08:00" = "8am",
                           "16:00" = "4pm",
                           "00:00" = "12am")) %>%
  filter(Relative.GE < 3) #remove mouse with high relative GE (data not normal)

#p-values from SigmaPlot
pomc_stats <- tibble::tribble(
  ~group1, ~group2, ~group3, ~p.adj,
  "08:00", "16:00", "00:00", "0.865"
)


pomc_plot <- ggplot(pomc, aes(x=Time, y=Relative.GE)) +
  geom_point() +
  stat_summary(fun = 'mean', geom="bar", aes(alpha=0.5), fill="darkorange") +
  stat_summary(fun.data = mean_se, geom = "errorbar", width=.1, alpha=0.5) +
  theme_few() +
  theme(legend.position = "none") +
  labs(y="Relative Gene Expression",
       title = "Figure 3",
       subtitle = "Expression of POMC mRNA") +
  geom_bracket(xmin="08:00", xmax="00:00", label=pomc_stats$p.adj, data=pomc_stats, y.position=2.5) +
```

```r
  scale_y_continuous(expand = expansion(mult = c(0, 0.1)))


ggsave(filename="../figures/pomc_fig_w_bars_orange.png", plot=pomc_plot, height=3, width=3)

mcko <- read.csv("../data/08162021-McKO-totalret-final.csv", fileEncoding = 'UTF-8-BOM')
mcko <- mcko %>%
  mutate(Genotype = fct_relevel(Genotype, c("WT", "McKO")))

#p-values from SigmaPlot
mcko_stats <- tibble::tribble(
  ~group1, ~group2, ~p.adj,
  "WT", "McKO", "<0.001"
)

mcko_plot <- mcko %>%
  ggplot(aes(x=Genotype, y=Relative.GE)) +
  geom_point() +
  stat_summary(fun = 'mean', geom="bar", aes(alpha=0.5), fill="darkorange") +
  stat_summary(fun.data = mean_se, geom = "errorbar", width=.1, alpha=0.5) +
  theme_few() +
  theme(legend.position = "none") +
  labs(y="Relative Gene Expression",
       title="Expression of MOR mRNA") +
  stat_pvalue_manual(mcko_stats,
    y.position = 1.5, step.increase = 0.1,
    label = "p.adj") +
  scale_y_continuous(expand = expansion(mult = c(0, 0.1)))
ggsave(filename="../figures/mcko_fig_bars_orange.png", plot=mcko_plot, height=4, width=3)
```