

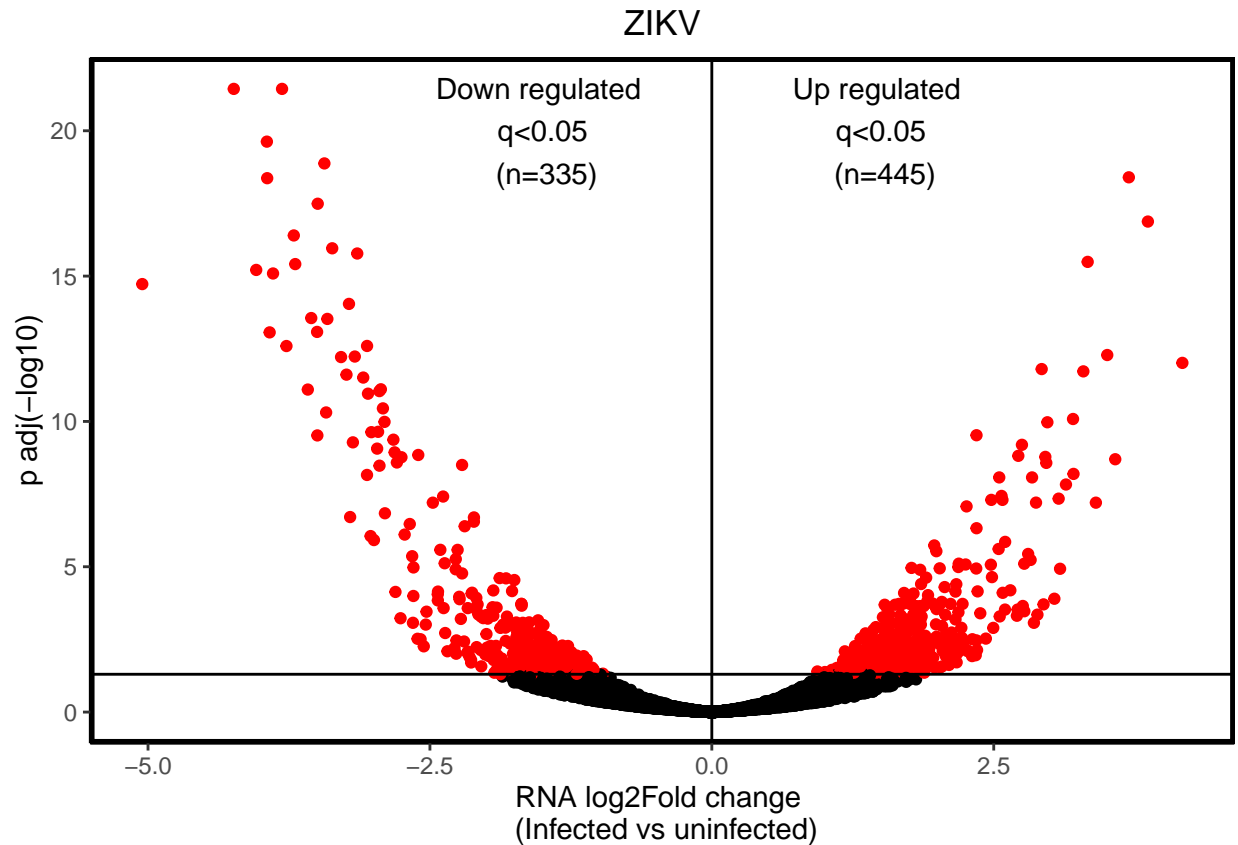
## Exploratory Data Analysis

```
# Load packages and read Files
library(tidyverse)
library(data.table)
library(scales)
library(metR)

df.ZIKV <- fread("GSE207347_A1B1_vs_A2B2_ZIKV_ribodiff_name.txt.gz")
df.DENV <- fread("GSE207347_A1B1_vs_A3B3_DENV_ribodiff_name.txt.gz")
df.ZIKV_DE <- fread("GSE207347_ZIKV_DESeq2_result_name.txt.gz")
df.DENV_DE <- fread("GSE207347_DENV_DESeq2_result_name.txt.gz")

# Figure 1 B
fig1b <- ggplot(subset(df.ZIKV_DE, !is.na(padj)),
                 aes(log2FoldChange, -log10(padj)))

fig1b +
  geom_point(aes(colour = -log10(padj) > -log10(0.05)), show.legend = FALSE) +
  labs(title = "ZIKV") + ylab("p adj(-log10)") +
  xlab("RNA log2Fold change \n (Infected vs uninfected)") +
  geom_vline(xintercept = 0) + geom_hline(yintercept = -log10(0.05)) +
  scale_color_manual(values = c('black', 'red')) +
  annotate("text", x = -1.5, y = 20,
           label = "Down regulated \n q<0.05 \n (n=335)",
           col = "black") +
  annotate("text", x = 1.5, y = 20,
           label = "Up regulated \n q<0.05 \n (n=445)",
           col = "black") +
  theme(panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        panel.background = element_blank(),
        plot.title = element_text(hjust = 0.5),
        axis.line = element_line(colour = "black"),
        panel.border = element_rect(colour = "black",
                                     fill = NA, linewidth = 1.5))
```



```
df.ZIKV_DE.sub <- subset(df.ZIKV_DE, !is.na(padj))
# Count of Up regulated with q < 0.05
(df.ZIKV_DE.sub$log2FoldChange > 0 & df.ZIKV_DE.sub$padj < 0.05) %>% sum()
```

```
## [1] 445
```

```
# Count of Down regulated with q < 0.05
(df.ZIKV_DE.sub$log2FoldChange < 0 & df.ZIKV_DE.sub$padj < 0.05) %>% sum()
```

```
## [1] 335
```

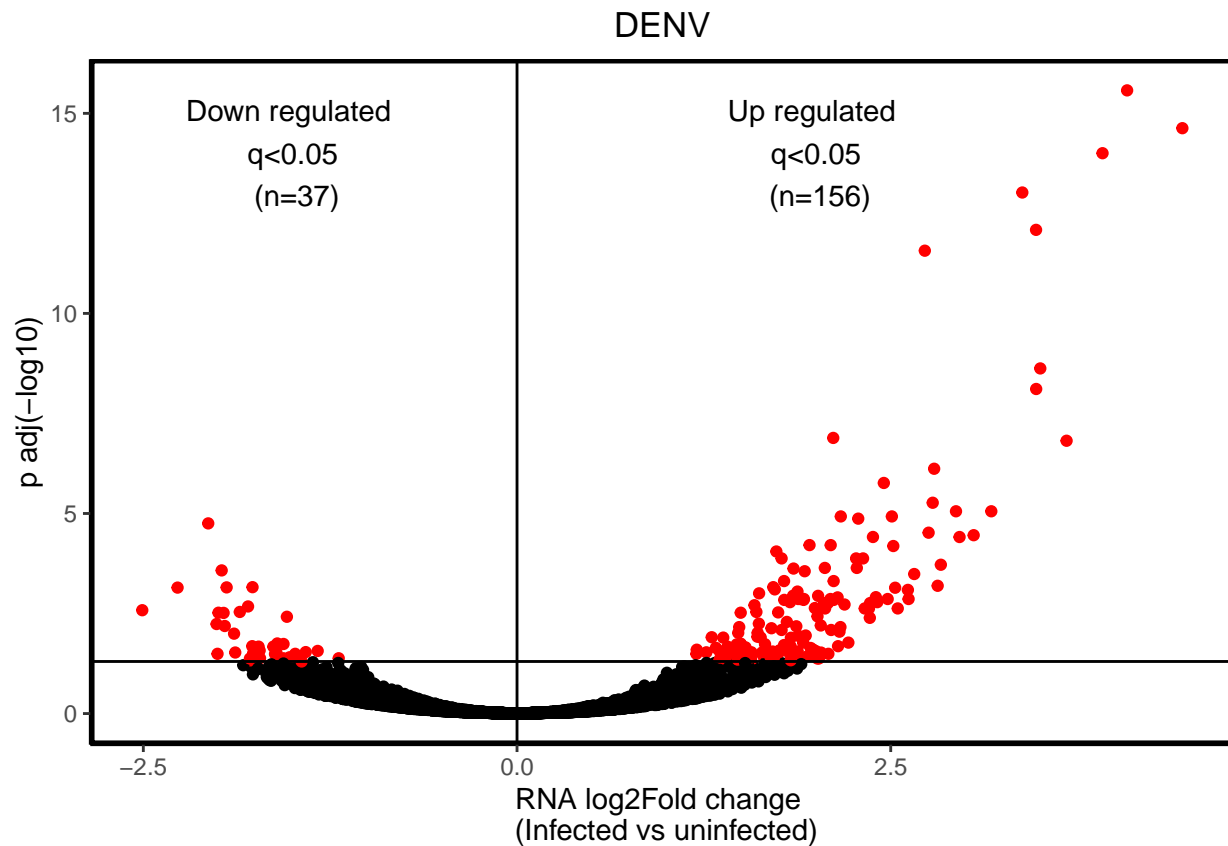
```
# Figure 1 C
fig1c <- ggplot(subset(df.DENV_DE, !is.na(padj)),
  aes(log2FoldChange, -log10(padj)))

fig1c +
  geom_point(aes(colour = -log10(padj) > -log10(0.05)), show.legend = FALSE) +
  labs(title = "DENV") + ylab("p adj(-log10)") +
  xlab("RNA log2Fold change \n (Infected vs uninfected)") +
  geom_vline(xintercept = 0) + geom_hline(yintercept = -log10(0.05)) +
  scale_color_manual(values = c('black', 'red')) +
  annotate("text", x = -1.5, y = 14,
    label = "Down regulated \n q<0.05 \n (n=37)",
    col = "black") +
```

```

annotate("text", x = 2, y = 14,
        label = "Up regulated \n q<0.05 \n (n=156)",
        col = "black") +
theme(panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      panel.background = element_blank(),
      plot.title = element_text(hjust = 0.5),
      axis.line = element_line(colour = "black"),
      panel.border = element_rect(colour = "black",
                                fill = NA, linewidth = 1.5))

```



```

df.DENV_DE.sub <- subset(df.DENV_DE, !is.na(padj))
# Count of Up regulated with q < 0.05
(df.DENV_DE.sub$log2FoldChange > 0 & df.DENV_DE.sub$padj < 0.05) %>% sum()

```

```
## [1] 156
```

```

# Count of Down regulated with q < 0.05
(df.DENV_DE.sub$log2FoldChange < 0 & df.DENV_DE.sub$padj < 0.05) %>% sum()

```

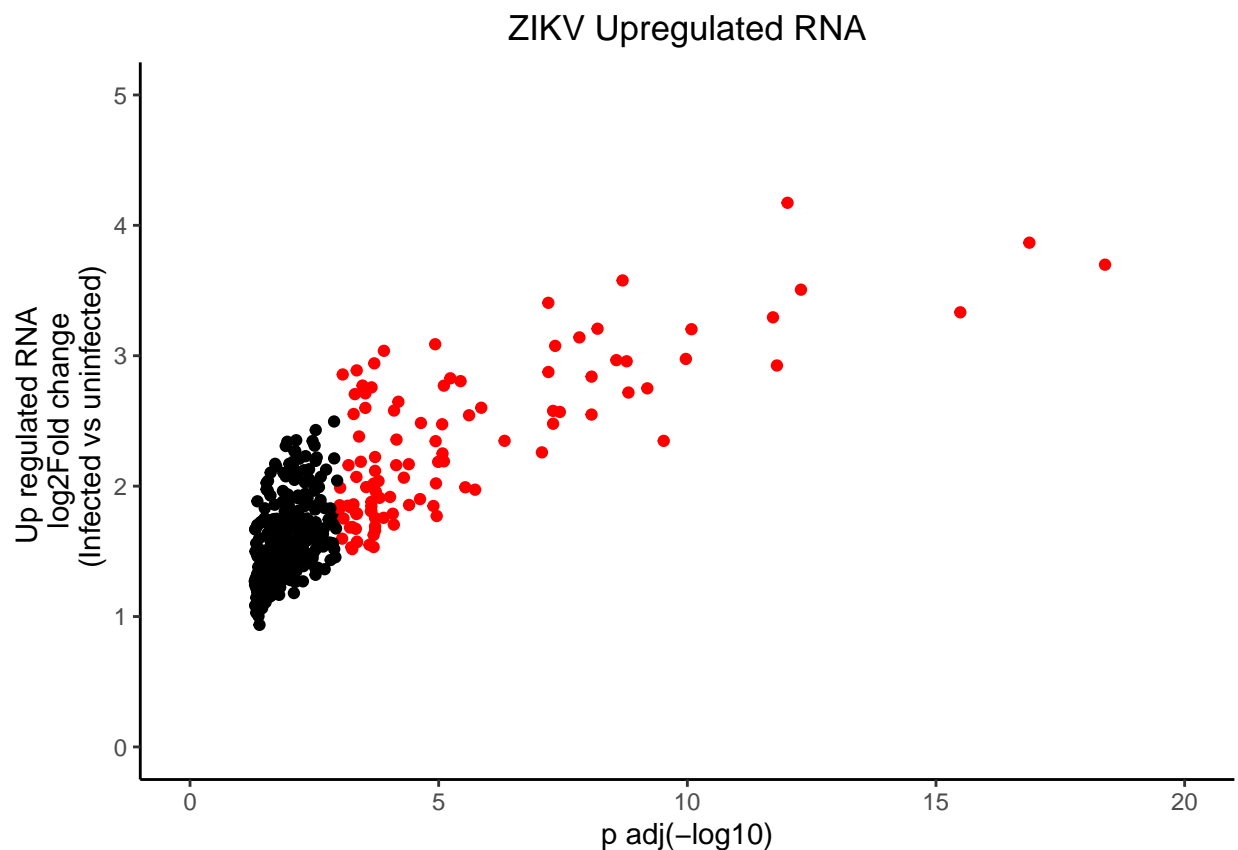
```
## [1] 37
```

# Figure 2 A

```
ZIKV.up <- df.ZIKV_DE.sub$log2FoldChange > 0 & df.ZIKV_DE.sub$padj < 0.05
df.ZIKV_DE.up <- df.ZIKV_DE.sub[ZIKV.up,]

fig2a <- ggplot(subset(df.ZIKV_DE.up, !is.na(padj)),
  aes(x = -log10(padj), y = log2FoldChange))

fig2a +
  geom_point(aes(colour = -log10(padj) > -log10(0.001)), show.legend = FALSE) +
  xlim(0, 20) + ylim(0, 5) + labs(title = "ZIKV Upregulated RNA") +
  xlab("p adj(-log10)") +
  ylab("Up regulated RNA \n log2Fold change \n (Infected vs uninfected)") +
  scale_color_manual(values = c('black', 'red')) +
  theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.background = element_blank(),
    plot.title = element_text(hjust = 0.5),
    axis.line = element_line(colour = "black"))
```



```
# Count of q < 0.001
sum(df.ZIKV_DE.up$padj < 0.001)
```

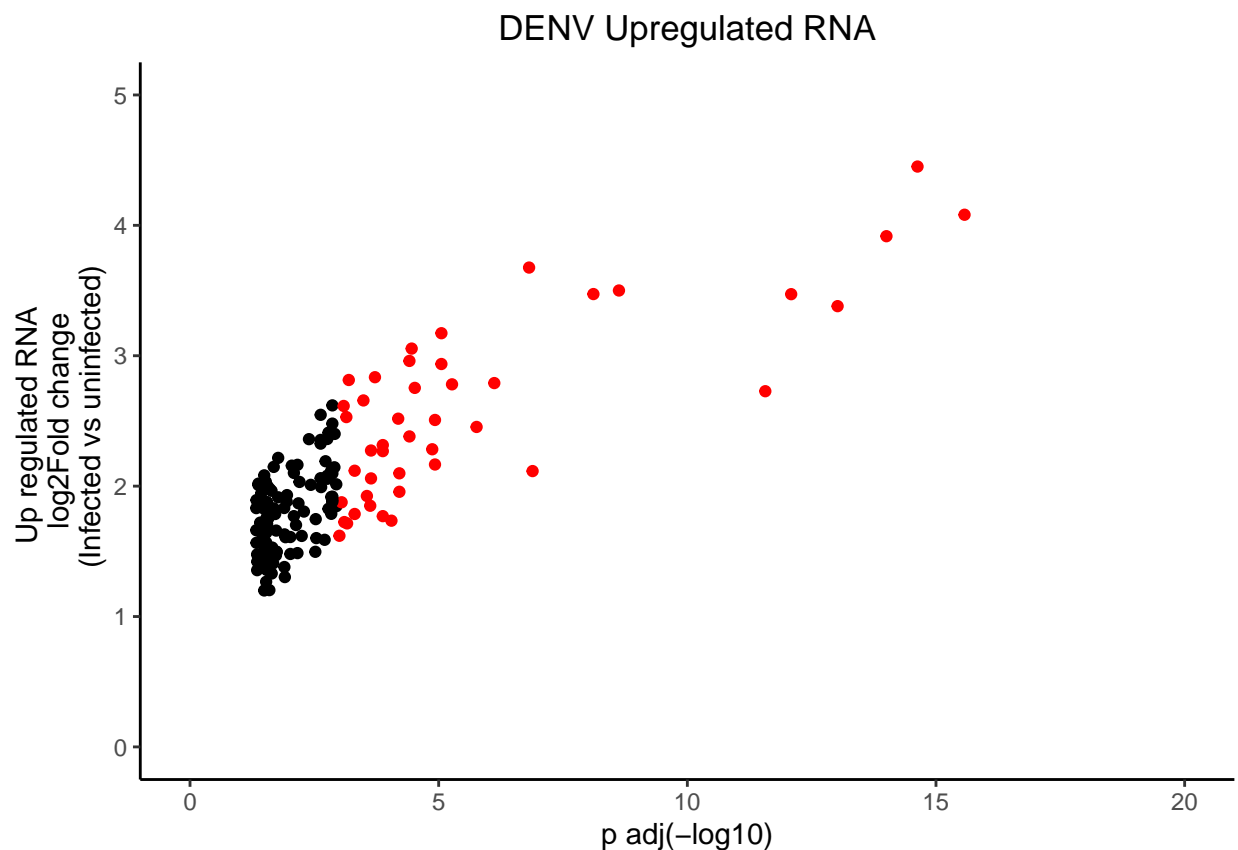
```
## [1] 104
```

*# Figure 2 B*

```
DENV.up <- df.DENV_DE.sub$log2FoldChange > 0 & df.DENV_DE.sub$padj < 0.05
df.DENV_DE.up <- df.DENV_DE.sub[DENV.up,]

fig2b <- ggplot(subset(df.DENV_DE.up, !is.na(padj)),
  aes(x = -log10(padj), y = log2FoldChange))

fig2b +
  geom_point(aes(colour = -log10(padj) > -log10(0.001)), show.legend = FALSE) +
  xlim(0, 20) + ylim(0, 5) + labs(title = "DENV Upregulated RNA") +
  xlab("p adj(-log10)") +
  ylab("Up regulated RNA \n log2Fold change \n (Infected vs uninfected)") +
  scale_color_manual(values = c('black', 'red')) +
  theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.background = element_blank(),
    plot.title = element_text(hjust = 0.5),
    axis.line = element_line(colour = "black"))
```



```
# Count of q < 0.001
sum(df.DENV_DE.up$padj < 0.001)
```

```
## [1] 44
```

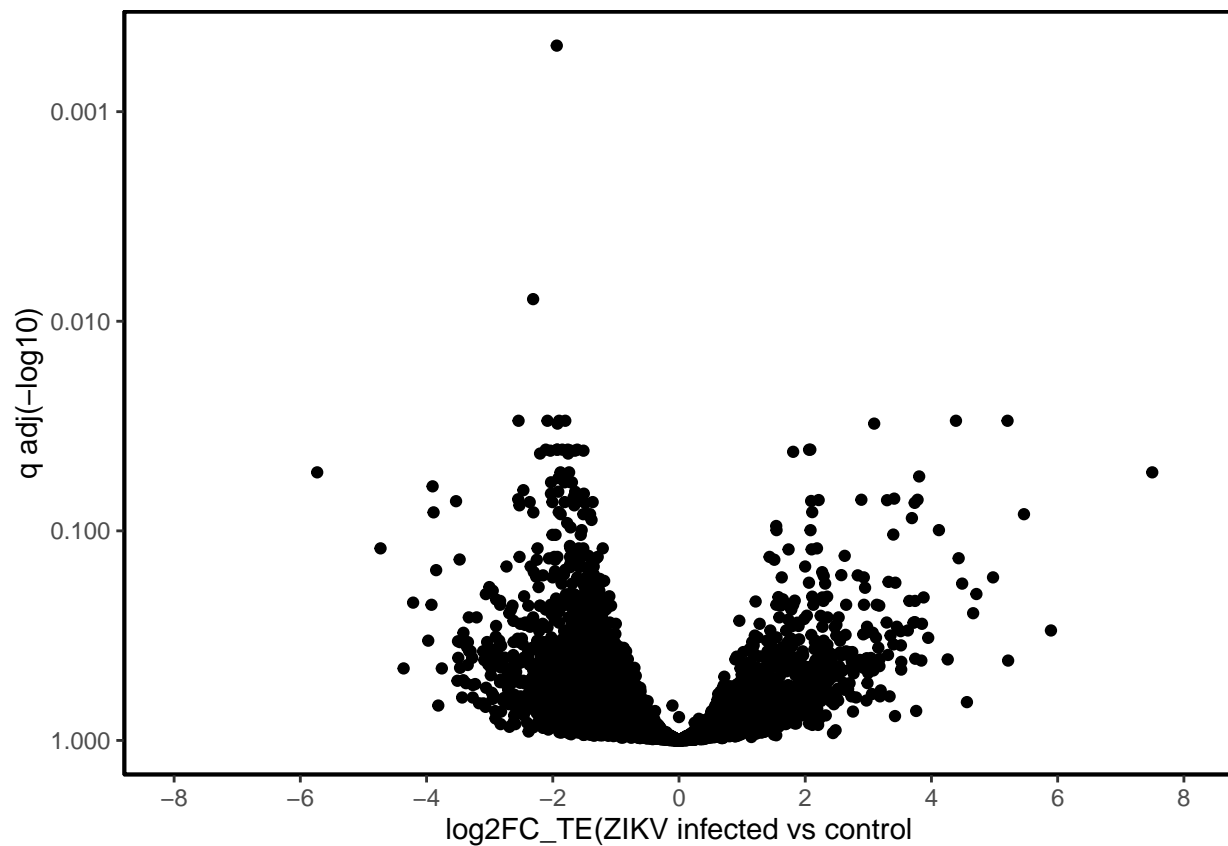
*# Figure 3 A*

```
colnames(df.ZIKV)[7] <- "log2FC_TE_DrugTreated_vs_Control"

df.ZIKV.sub <- subset(df.ZIKV, !is.na(padj))

fig3a <- ggplot(df.ZIKV.sub,
  aes(x = log2FC_TE_DrugTreated_vs_Control, y = padj))

fig3a +
  geom_point() +
  scale_y_continuous(trans = reverselog_trans(base = 10),
    breaks = c(1, 0.1, 0.01, 0.001)) +
  scale_x_continuous(limits = c(-8, 8),
    breaks = seq(-8, 8, 2)) +
  xlab("log2FC_TE(ZIKV infected vs control)") +
  ylab("q adj(-log10)") +
  theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.background = element_blank(),
    plot.title = element_text(hjust = 0.5),
    axis.line = element_line(colour = "black"),
    panel.border = element_rect(colour = "black",
      fill = NA, linewidth = 1))
```



# Figure 3 B

```
colnames(df.DENV)[7] <- "log2FC_TE_DrugTreated_vs_Control"

df.DENV.sub <- subset(df.DENV, !is.na(padj))

fig3b <- ggplot(df.DENV.sub,
  aes(x = log2FC_TE_DrugTreated_vs_Control, y = padj))

fig3b +
  geom_point() +
  scale_y_continuous(trans = reverselog_trans(base = 10),
    labels = trans_format("log10", math_format(10^.x)),
    breaks = trans_breaks("log10", function(x) 10^x)) +
  scale_x_continuous(limits = c(-8, 8),
    breaks = seq(-8, 8, 2)) +
  xlab("log2FC_TE(DENV infected vs control)") +
  ylab("q adj(-log10)") +
  theme(panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    panel.background = element_blank(),
    plot.title = element_text(hjust = 0.5),
    axis.line = element_line(colour = "black"),
    panel.border = element_rect(colour = "black",
      fill = NA, linewidth = 1))
```

