

Exploratory Data Analysis

```
# Load packages and read Files
```

```
library(tidyverse)
```

```
library(data.table)
```

```
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)))
```

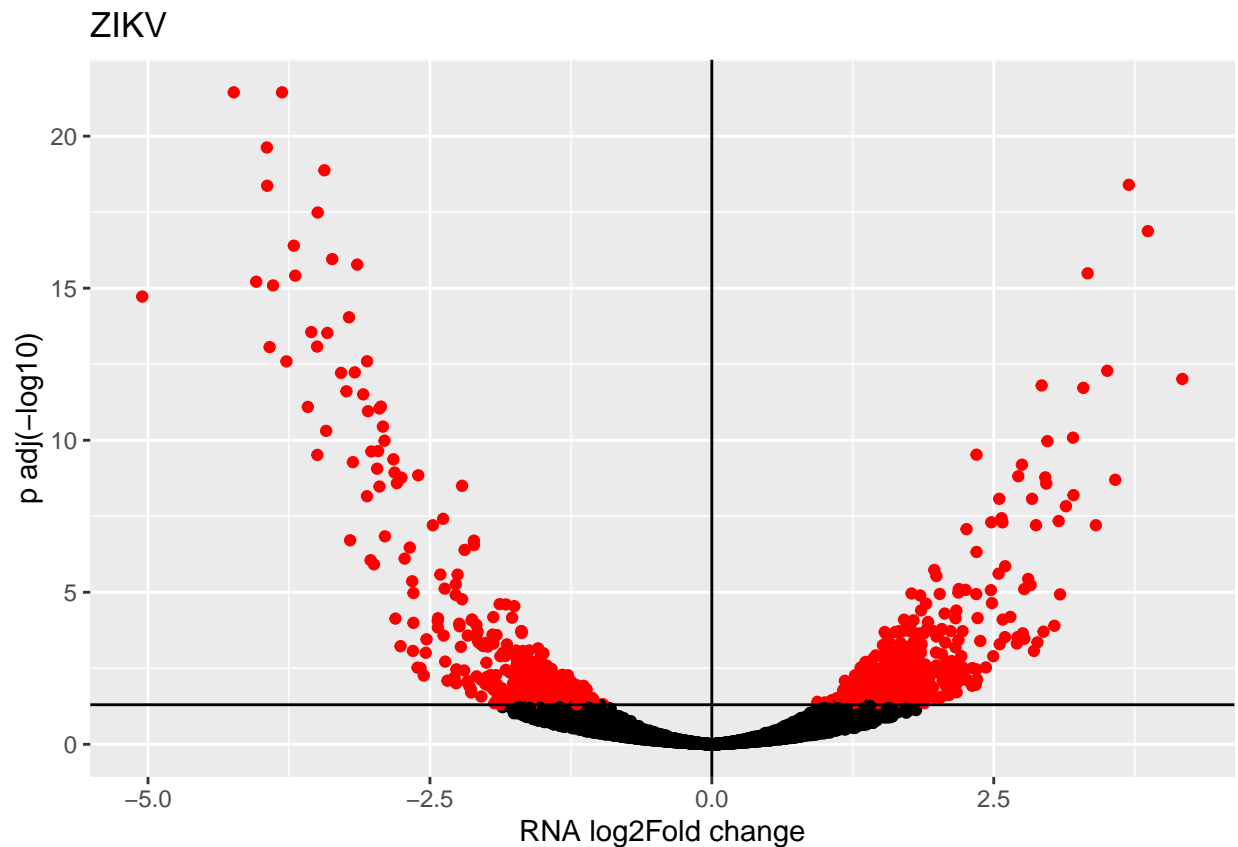
```
fig1b +
```

```
  geom_point(aes(colour = -log10(padj) > -log10(0.05)), show.legend = FALSE) +
```

```
  labs(title = "ZIKV") + xlab("RNA log2Fold change") + ylab("p adj(-log10)") +
```

```
  geom_vline(xintercept = 0) + geom_hline(yintercept = -log10(0.05)) +
```

```
  scale_color_manual(values = c('black', 'red'))
```



```
# 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 = "ZIKV") + xlab("RNA log2Fold change") + ylab("p adj(-log10)") +
  geom_vline(xintercept = 0) + geom_hline(yintercept = -log10(0.05)) +
  scale_color_manual(values = c('black', 'red'))
```

