

DGEs_mouse_donortreatment_plots

Purpose:

To plot the murine genes (with donor and treatment serving as factors in the design) as volcano plots. This includes the July 2018 samples.

Required libraries

```
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(ggplot2)
library(ggrepel)
library(stringr)
```

Visualizing the DGE output by volcano plots.

```
##The location of the DGE files just generated so that they can be read in
DGE_files <- "Mouse DGEs_donortreatment"
DGE_R <- basename(Sys.glob(file.path(DGE_files, "*.txt")))
DGE_R

## [1] "2018-10-16mouse_donor_treatmentMousegenes-HBV_vs_mock_d28_analysis_results.txt"
## [2] "2018-10-16mouse_donor_treatmentMousegenes-HBV_vs_mock_d8_analysis_results.txt"
## [3] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_HBV_d28_analysis_results.txt"
## [4] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_HBV_d8_analysis_results.txt"
## [5] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_mock_d28_analysis_results.txt"
## [6] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_mock_d8_analysis_results.txt"

##Function to read in the DGE files
exptDGEs <- function(files) {
  d <- read.delim(files, header = TRUE)
}

##Read in all the files
all_DGEs <- lapply(file.path(DGE_files, DGE_R), exptDGEs)
names(all_DGEs) <- sub(".txt", "", DGE_R)
names(all_DGEs)

## [1] "2018-10-16mouse_donor_treatmentMousegenes-HBV_vs_mock_d28_analysis_results"
## [2] "2018-10-16mouse_donor_treatmentMousegenes-HBV_vs_mock_d8_analysis_results"
## [3] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_HBV_d28_analysis_results"
## [4] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_HBV_d8_analysis_results"
## [5] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_mock_d28_analysis_results"
## [6] "2018-10-16mouse_donor_treatmentMousegenes-coinf_vs_mock_d8_analysis_results"
```

```

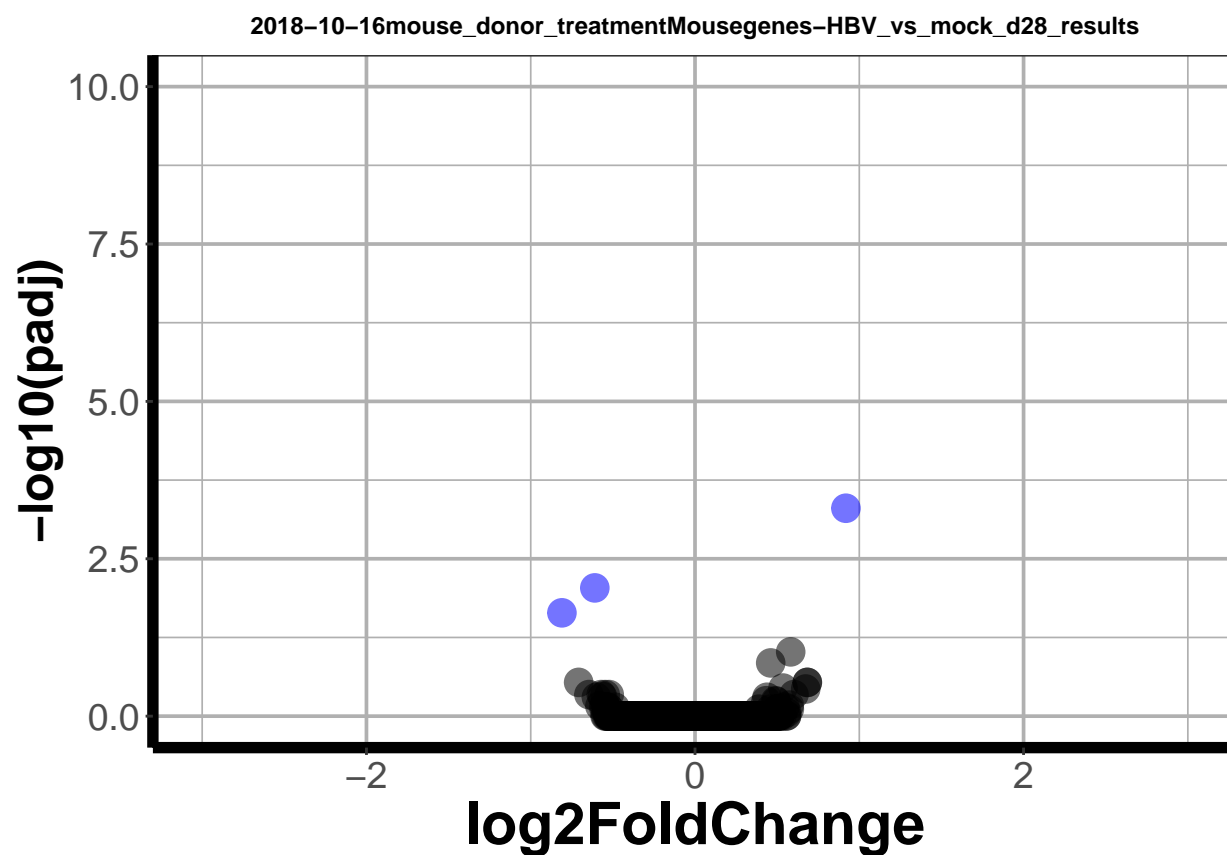
##Function to generate the volcano plots; here all the axes labels are intact
##and HBV genes are labeled for reference when making paper's figures.
for(i in 1:6) {
  index <- all_DGEs[[i]]
  output_name <- str_replace(names(all_DGEs[i]), "^[0-9]*--[0-9]*--[0-9]*\\s", "") %>%
    str_replace("_*\\s*analysis", "")
  index$filleffect <- with(index, factor(ifelse(padj > 0.05, 0, 1)))
  print(ggplot(data=index, aes(x=log2FoldChange, y=-log10(padj), color =filleffect)) +
    geom_point(aes(colour=filleffect, alpha=0.4, size=1)) +
    scale_colour_manual(values = c("black", "blue")) +
    theme(legend.position = "none") +
    ggtitle(output_name) +
    xlim(c(-3, 3)) + ylim(c(0, 10)) +
    theme_bw() +
    theme(legend.position = "none",
      axis.title.x = element_text(face = "bold", size = 22),
      axis.text = element_text(size = 14),
      plot.title = element_text(size = 9, hjust = 0.5, face = "bold"),
      panel.grid.major = element_line(size = 0.65,
        color = "gray69"),
      panel.grid.minor = element_line(size = 0.3, color = "gray69"),
      axis.line = element_line(size = 2),
      axis.title.y = element_text(face = "bold", size = 18)))

  ggsave(file.path("Mouse DGEs_donortreatment", paste(Sys.Date(), output_name,
    "donortreatmentDGEs_unfiltered_labeled.png")), units = 'in', height = 10,
    width = 10, dpi = 300, device = "png")
}

```

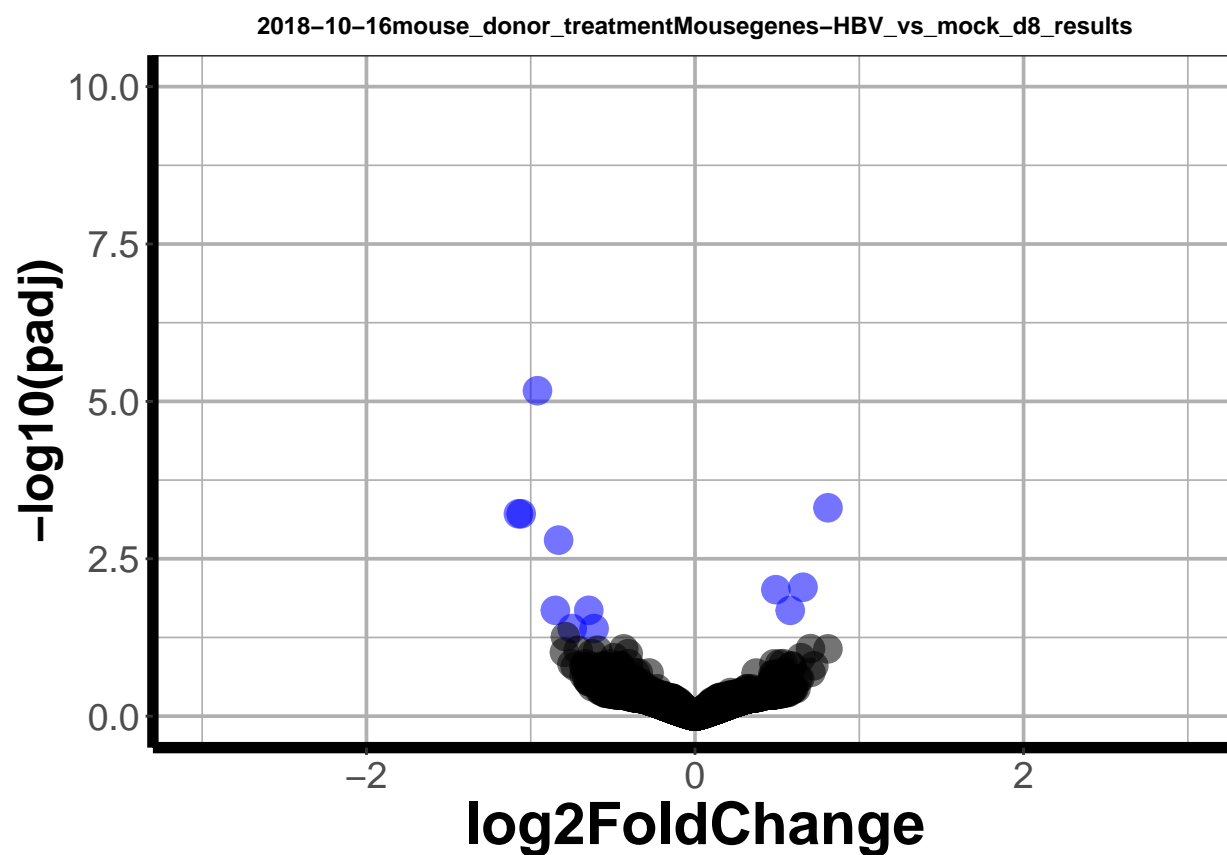
Warning: Removed 30927 rows containing missing values (geom_point).

Warning: Removed 30927 rows containing missing values (geom_point).



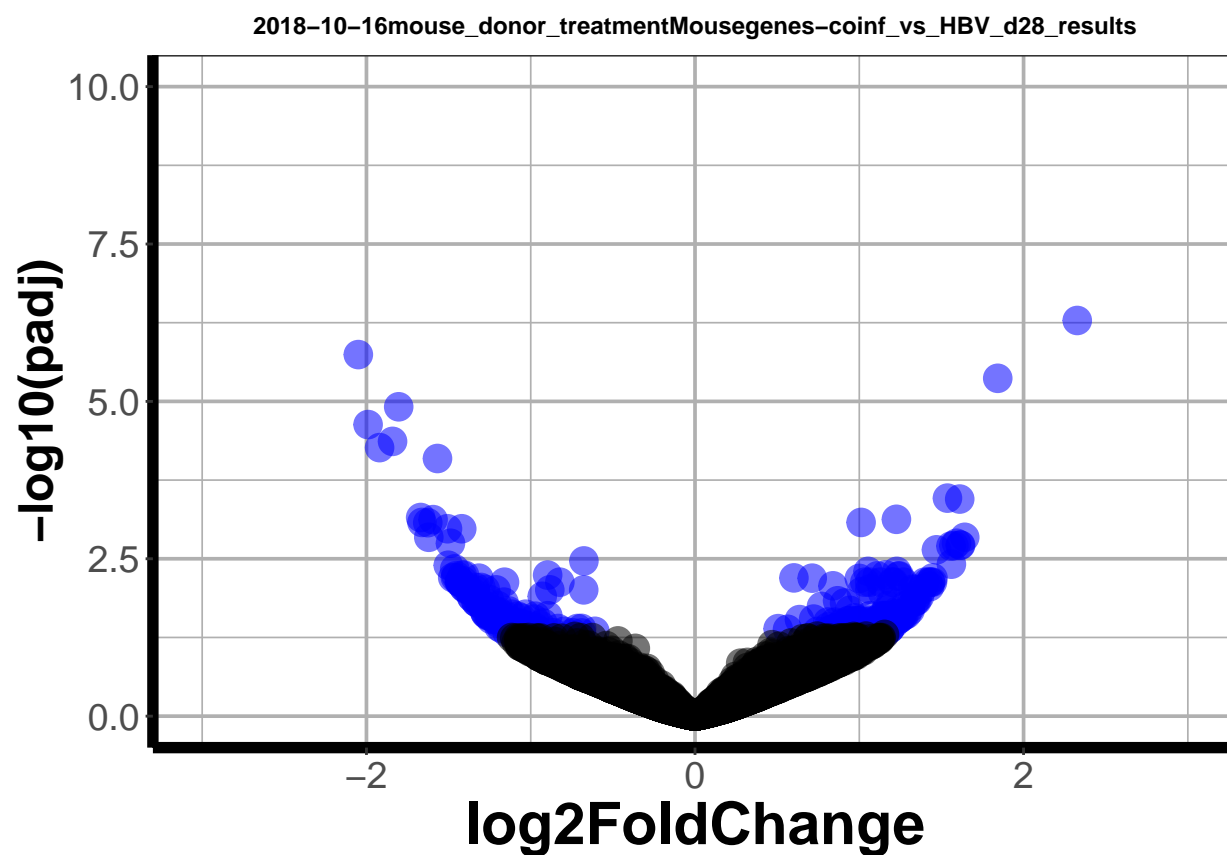
Warning: Removed 42341 rows containing missing values (geom_point).

Warning: Removed 42341 rows containing missing values (geom_point).



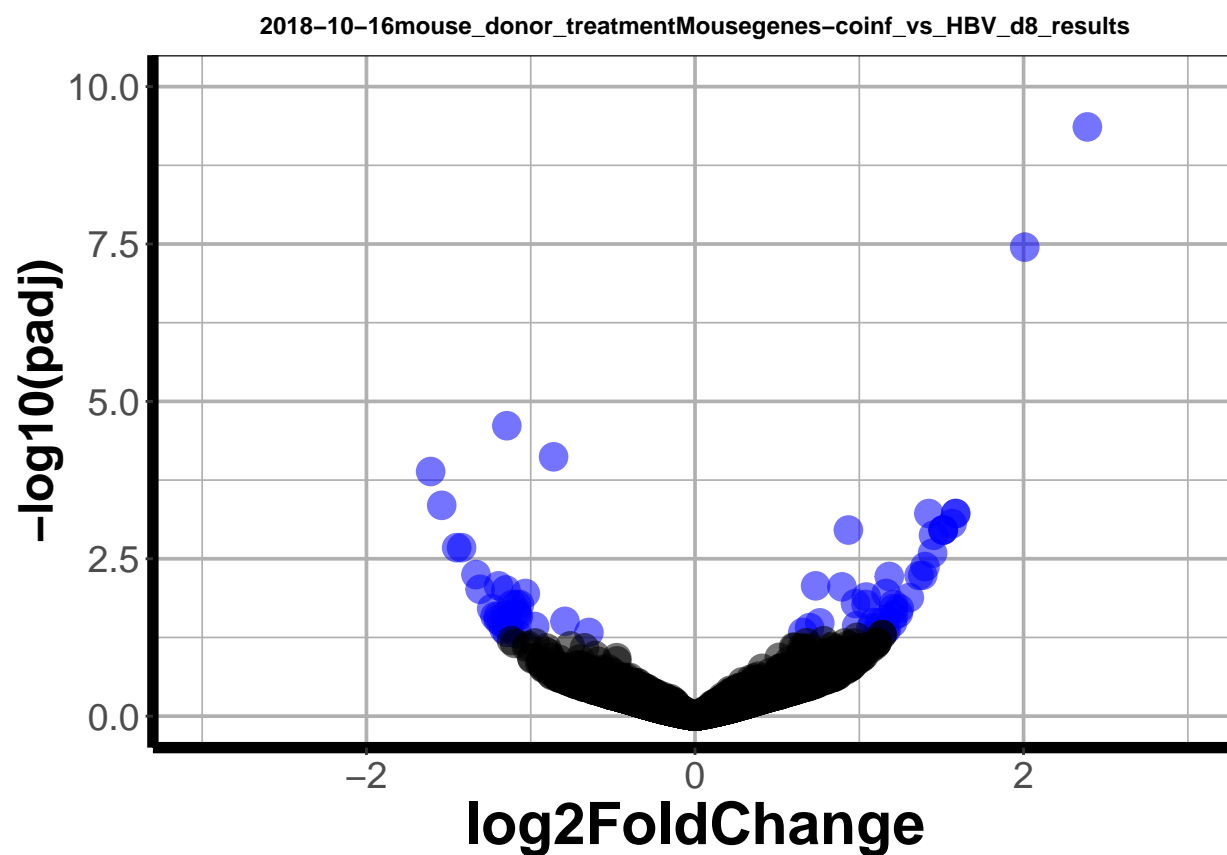
Warning: Removed 39667 rows containing missing values (geom_point).

Warning: Removed 39667 rows containing missing values (geom_point).



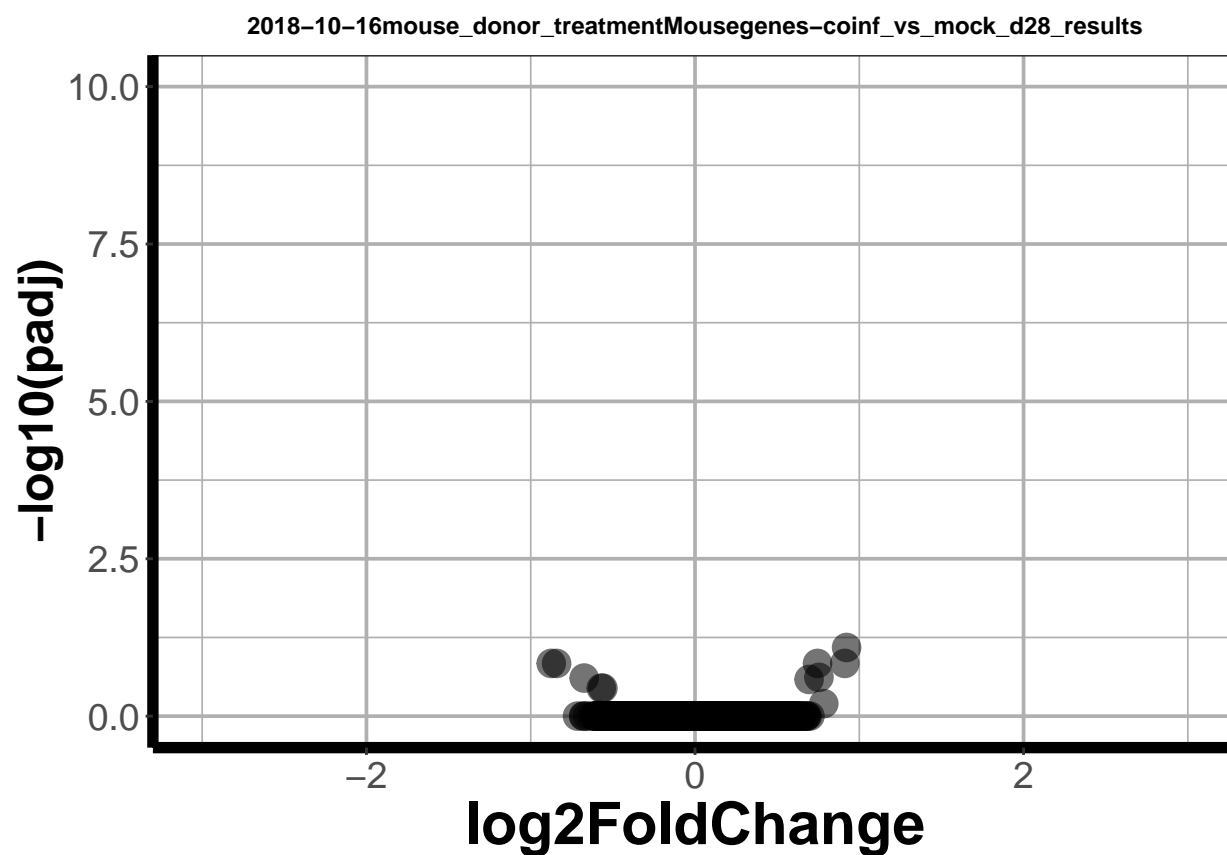
```
## Warning: Removed 38615 rows containing missing values (geom_point).
```

```
## Warning: Removed 38615 rows containing missing values (geom_point).
```



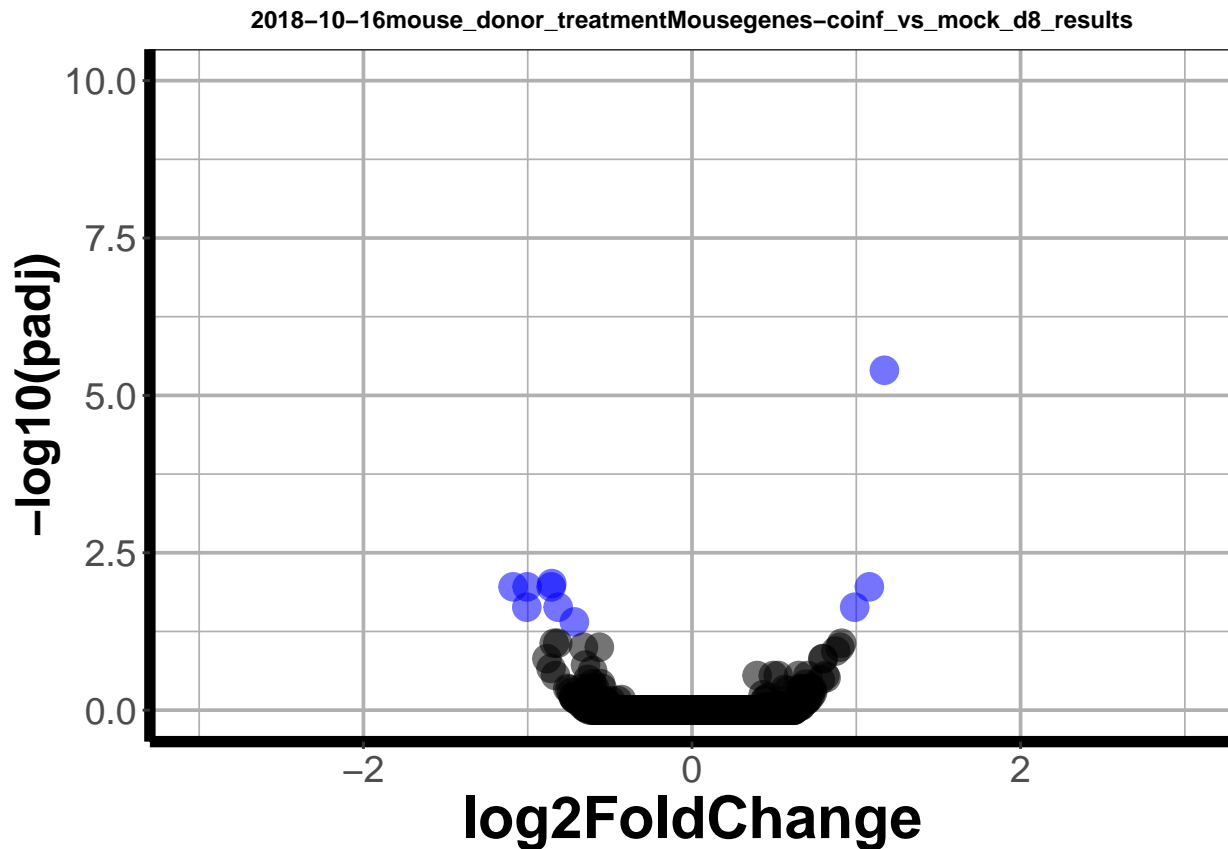
```
## Warning: Removed 31195 rows containing missing values (geom_point).
```

```
## Warning: Removed 31195 rows containing missing values (geom_point).
```



Warning: Removed 36148 rows containing missing values (geom_point).

Warning: Removed 36148 rows containing missing values (geom_point).



Session Info

```
sessionInfo()
```

```
## R version 3.3.3 (2017-03-06)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: macOS Sierra 10.12.6
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] stringr_1.3.1 ggrepel_0.8.0 ggplot2_3.0.0 dplyr_0.7.6
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.18      rstudioapi_0.7    knitr_1.20        bindr_0.1.1
## [5] magrittr_1.5      munsell_0.5.0     tidyselect_0.2.4  colorspace_1.3-2
## [9] R6_2.2.2          rlang_0.2.1       plyr_1.8.4        tools_3.3.3
## [13] grid_3.3.3        gtable_0.2.0      withr_2.1.2       htmltools_0.3.6
## [17] lazyeval_0.2.1    yaml_2.2.0        assertthat_0.2.0  rprojroot_1.3-2
## [21] digest_0.6.15     tibble_1.4.2      crayon_1.3.4      bindrcpp_0.2.2
## [25] purrr_0.2.5       glue_1.3.0        evaluate_0.11     rmarkdown_1.10
## [29] labeling_0.3      stringi_1.2.4     pillar_1.3.0      scales_0.5.0
## [33] backports_1.1.2   pkgconfig_2.0.1
```