

Block_report

2023-02-12

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

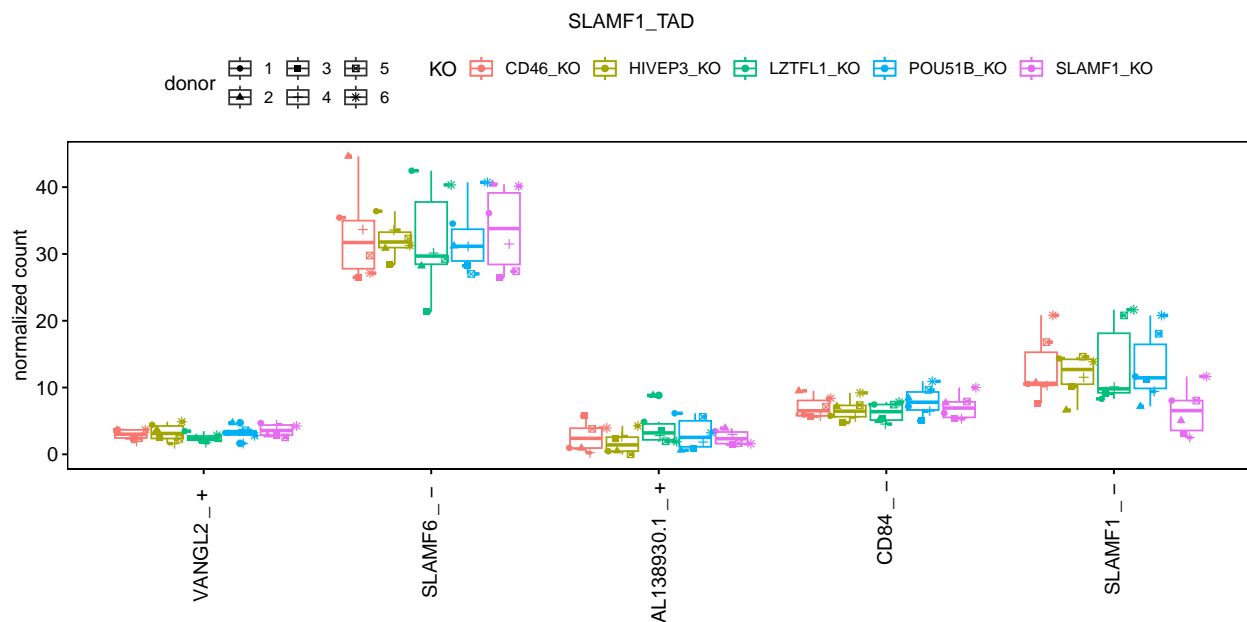
```
## Loading required package: ggplot2

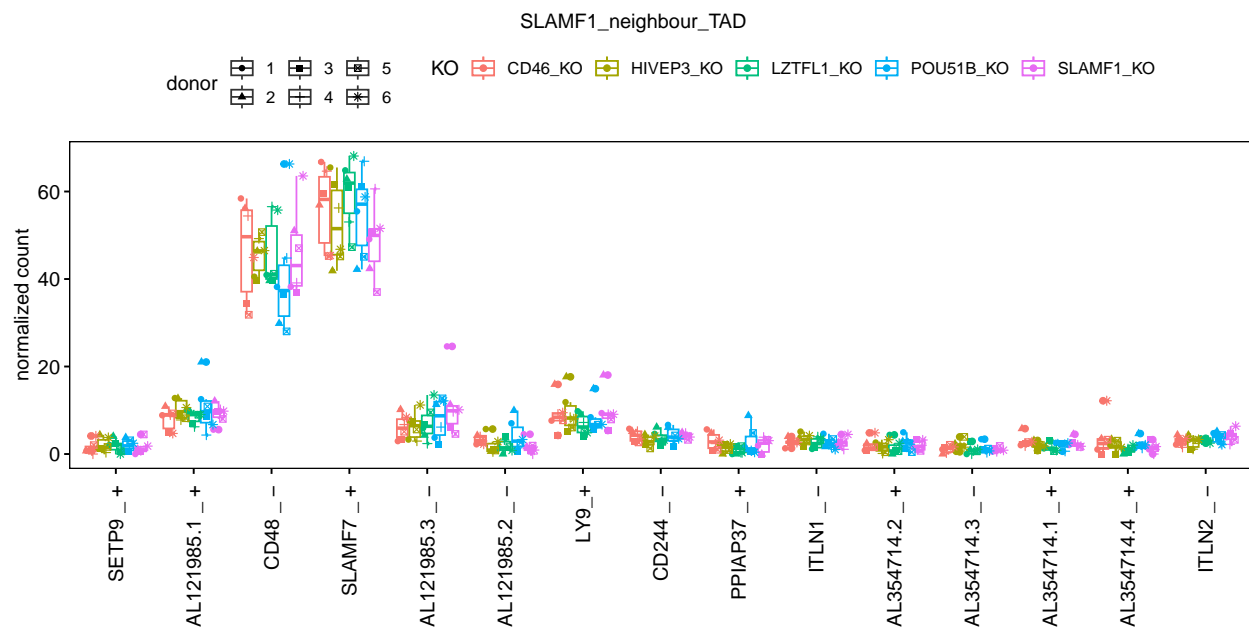
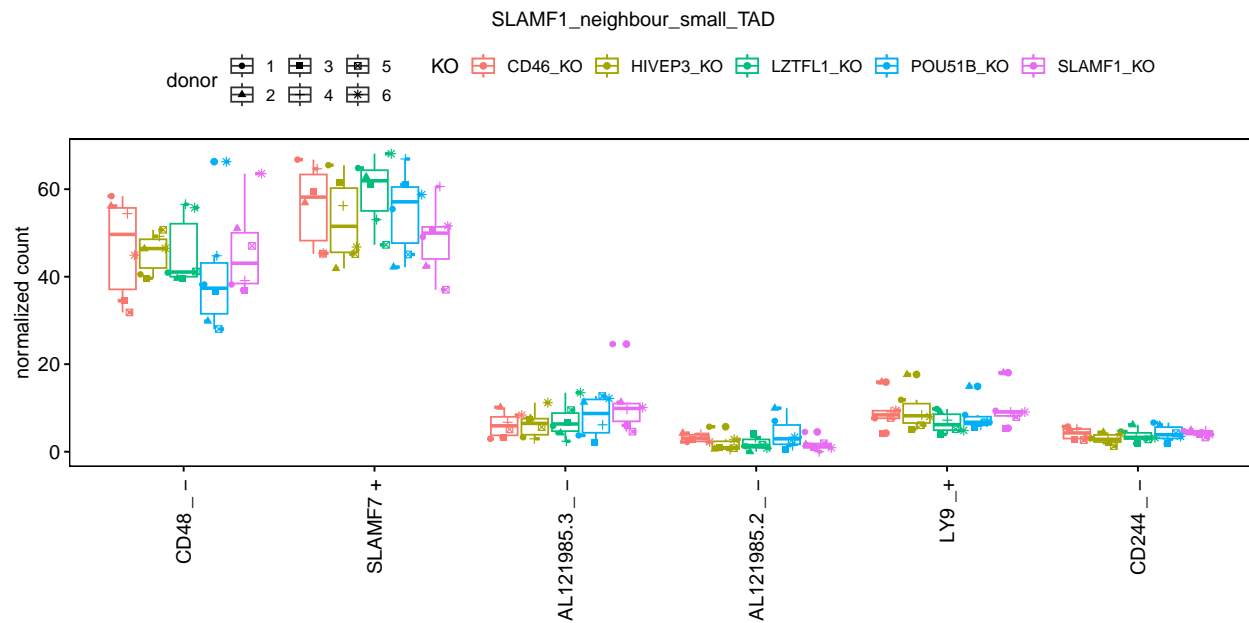
## -- Attaching packages ----- tidyverse 1.3.1 --

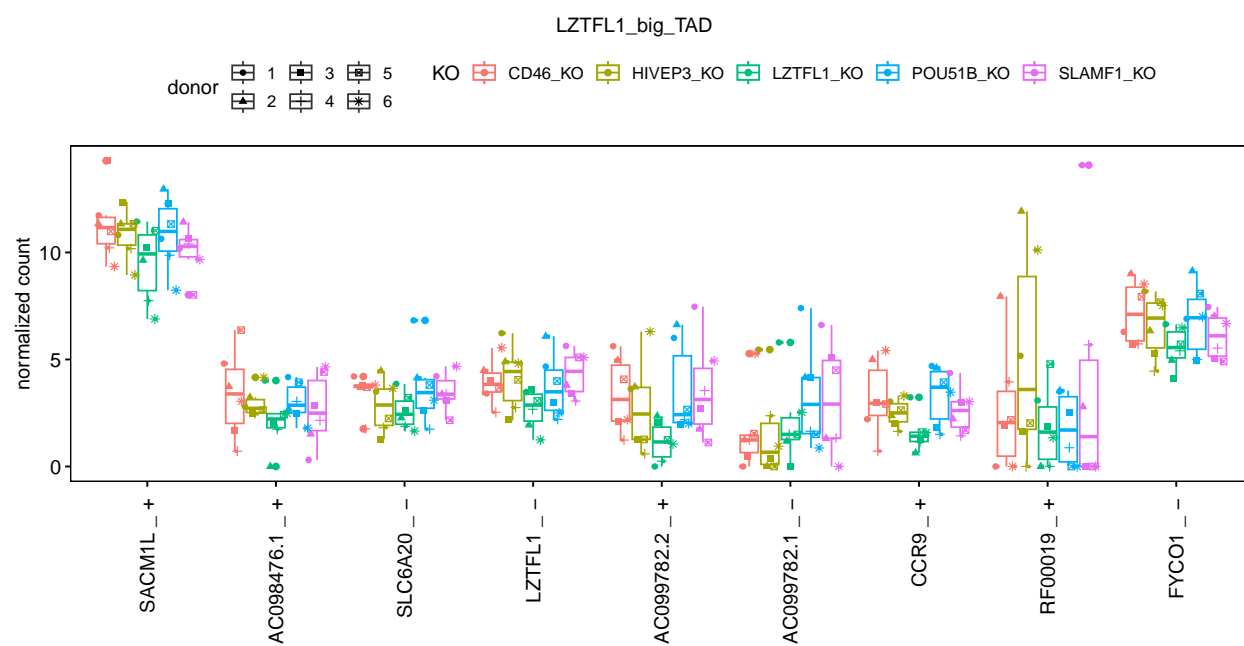
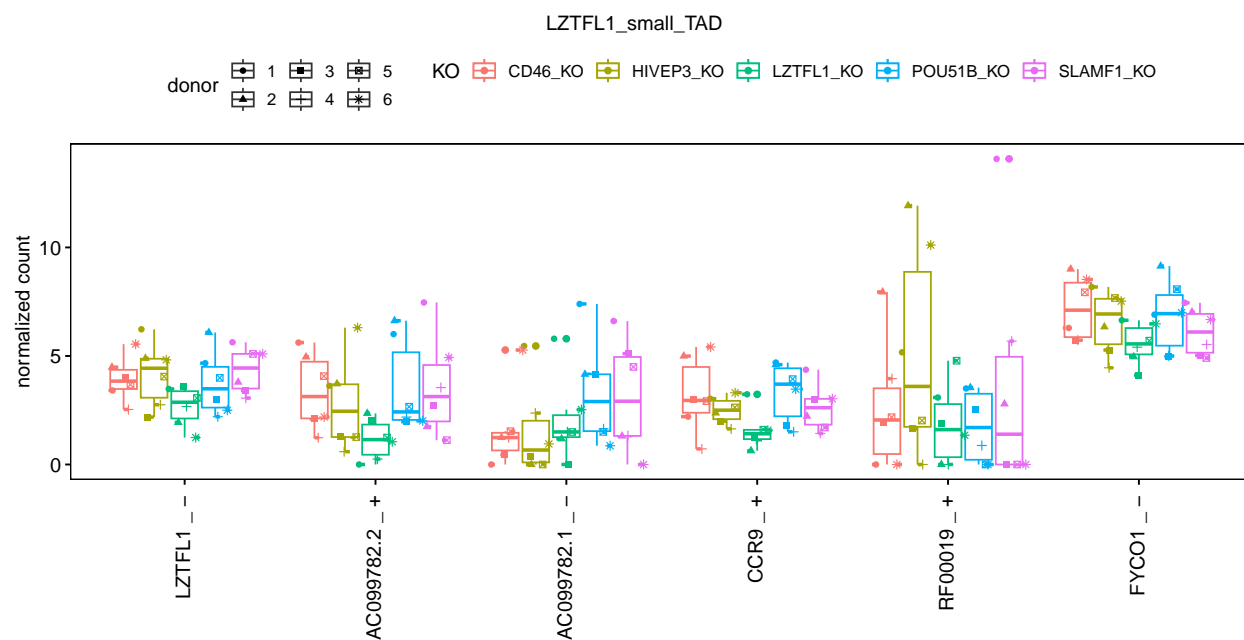
## v tibble 3.1.6      v dplyr 1.0.7
## v tidyr 1.1.4      v stringr 1.4.0
## v readr 2.1.0      v forcats 0.5.2
## v purrr 0.3.4

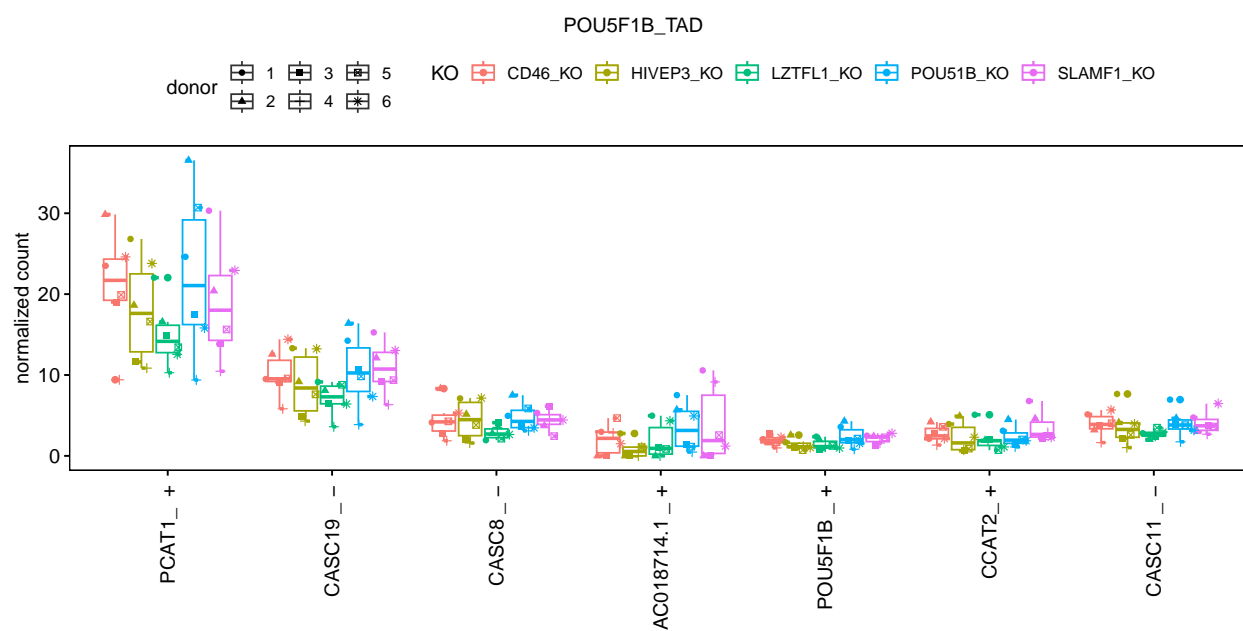
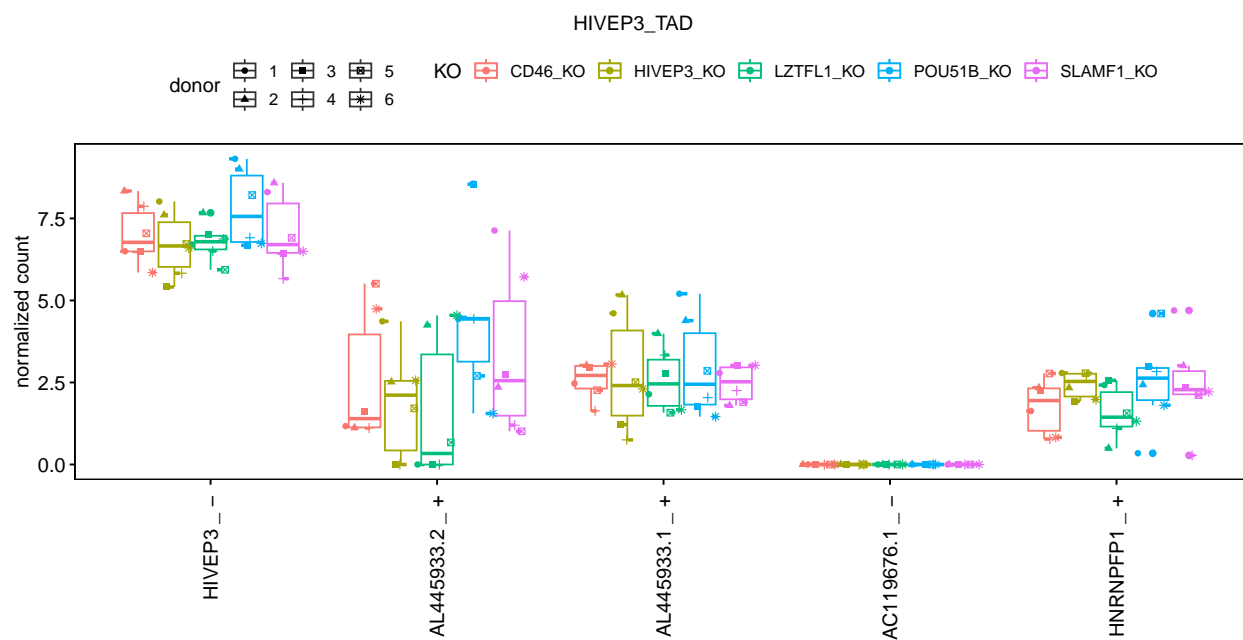
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

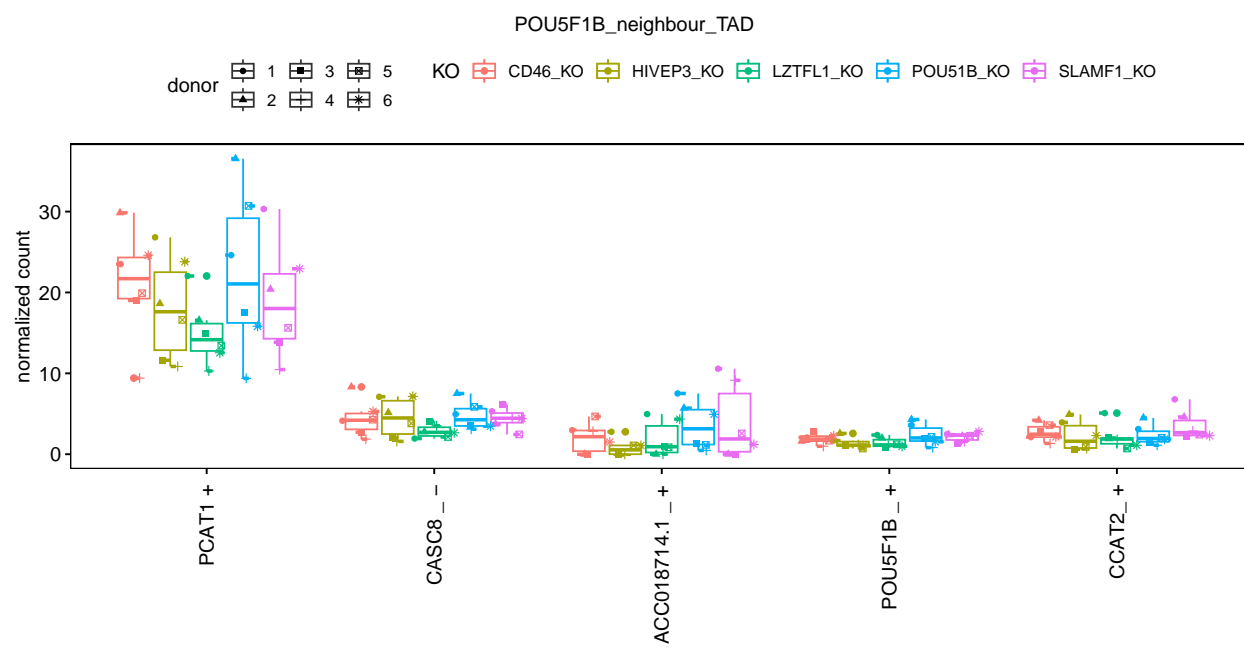
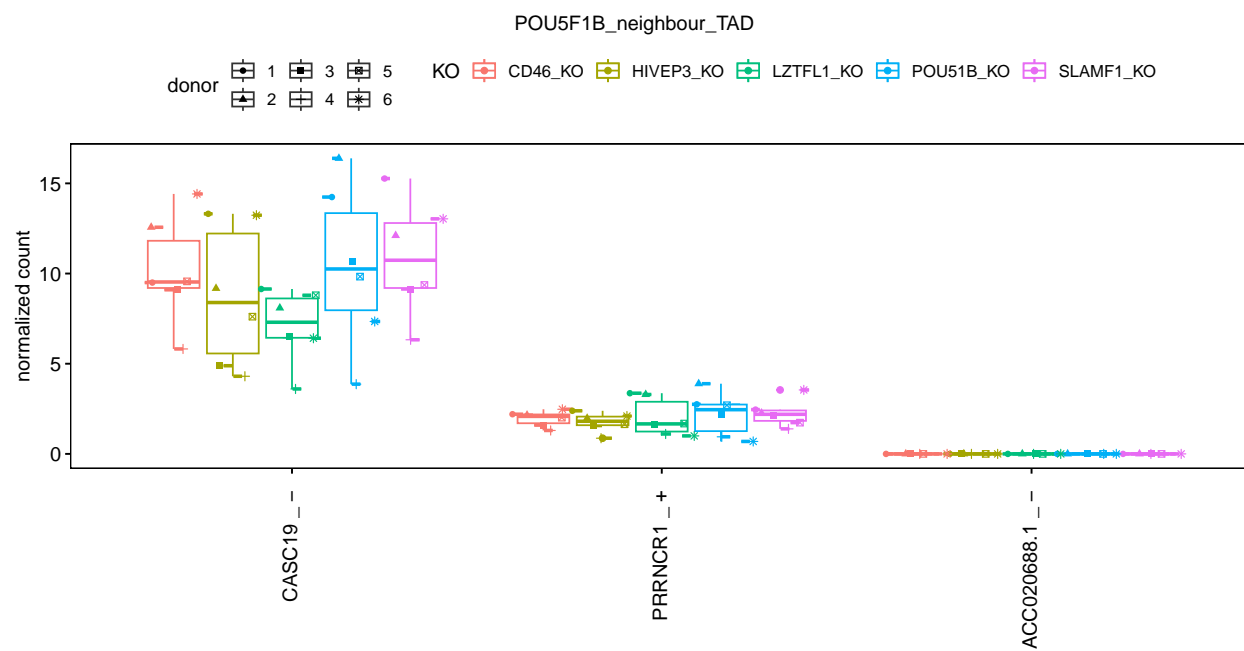
Overview of all KD regions/TADs

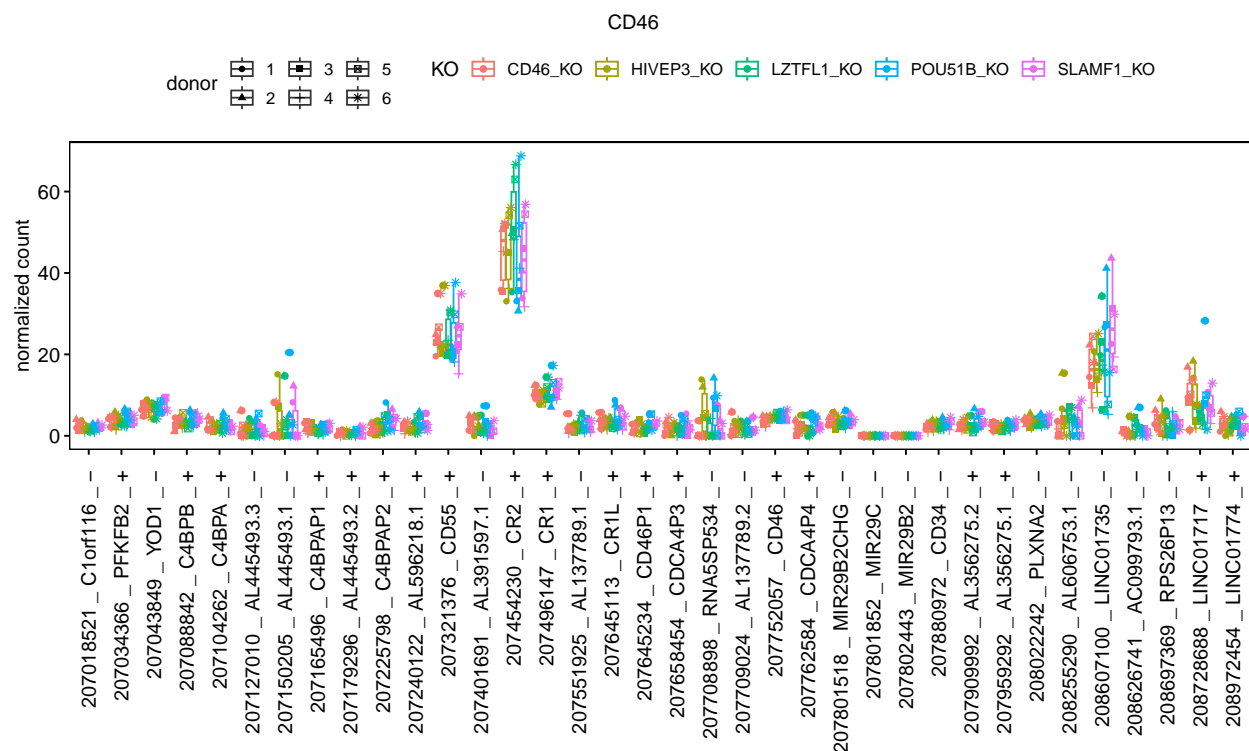
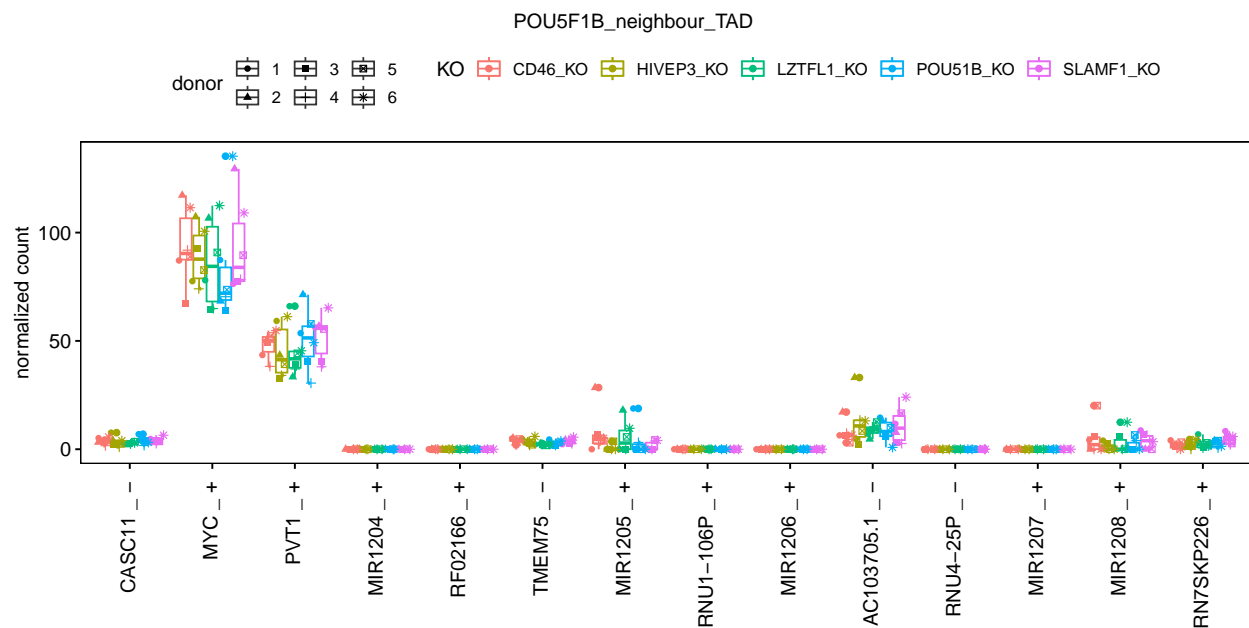








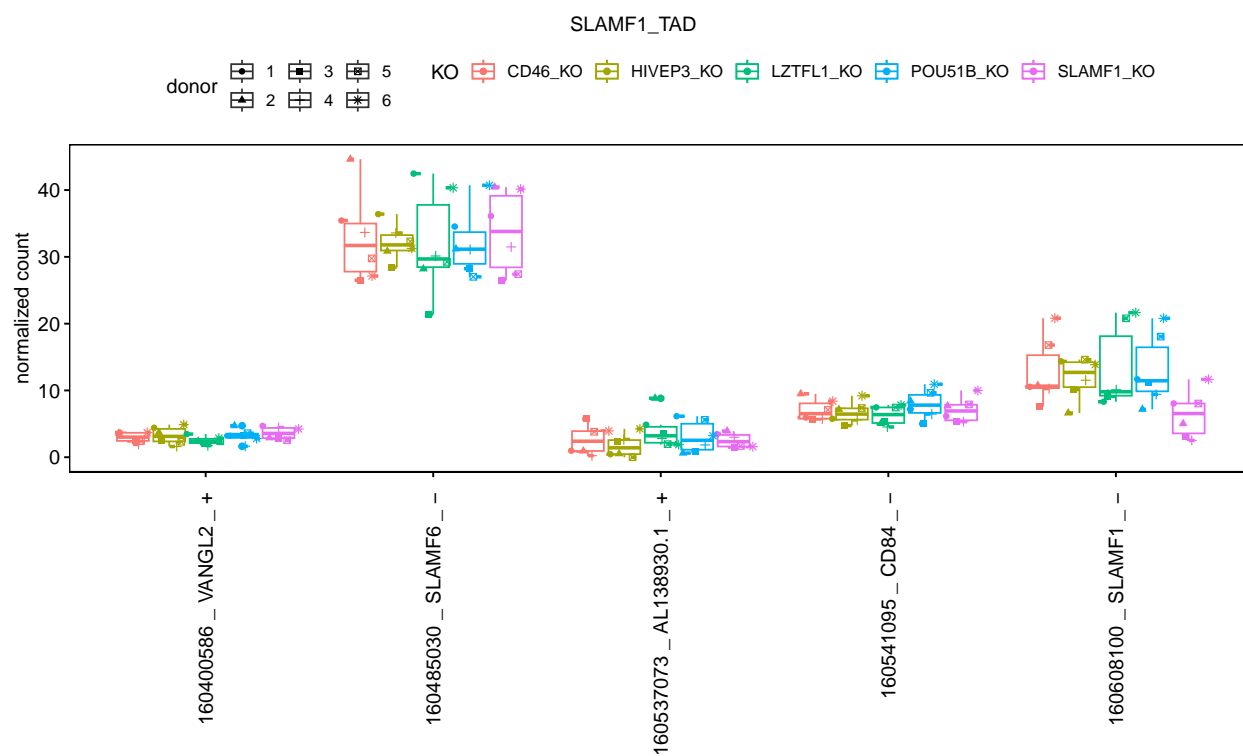




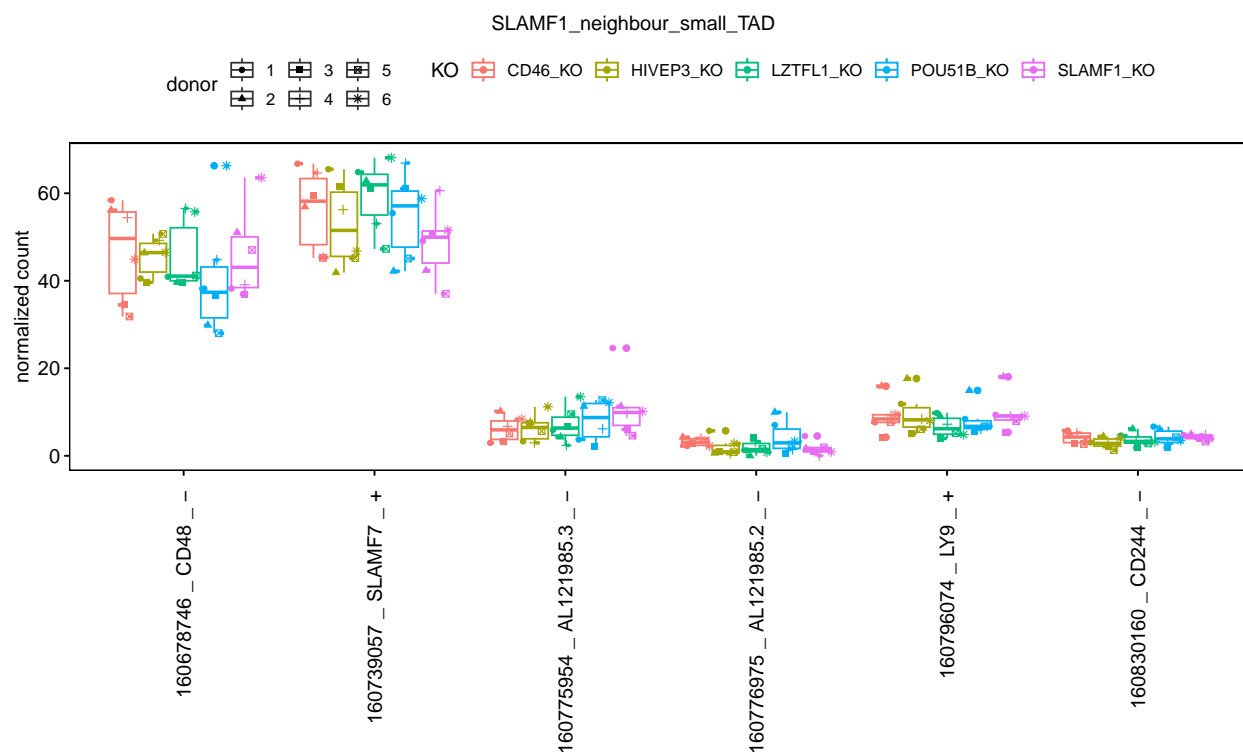
Removal of unsuccessful KDs

Removals based on the difference between KD and control samples per patient. Maybe provide deterministic “formula” to compute boolean vector keep/disregard?

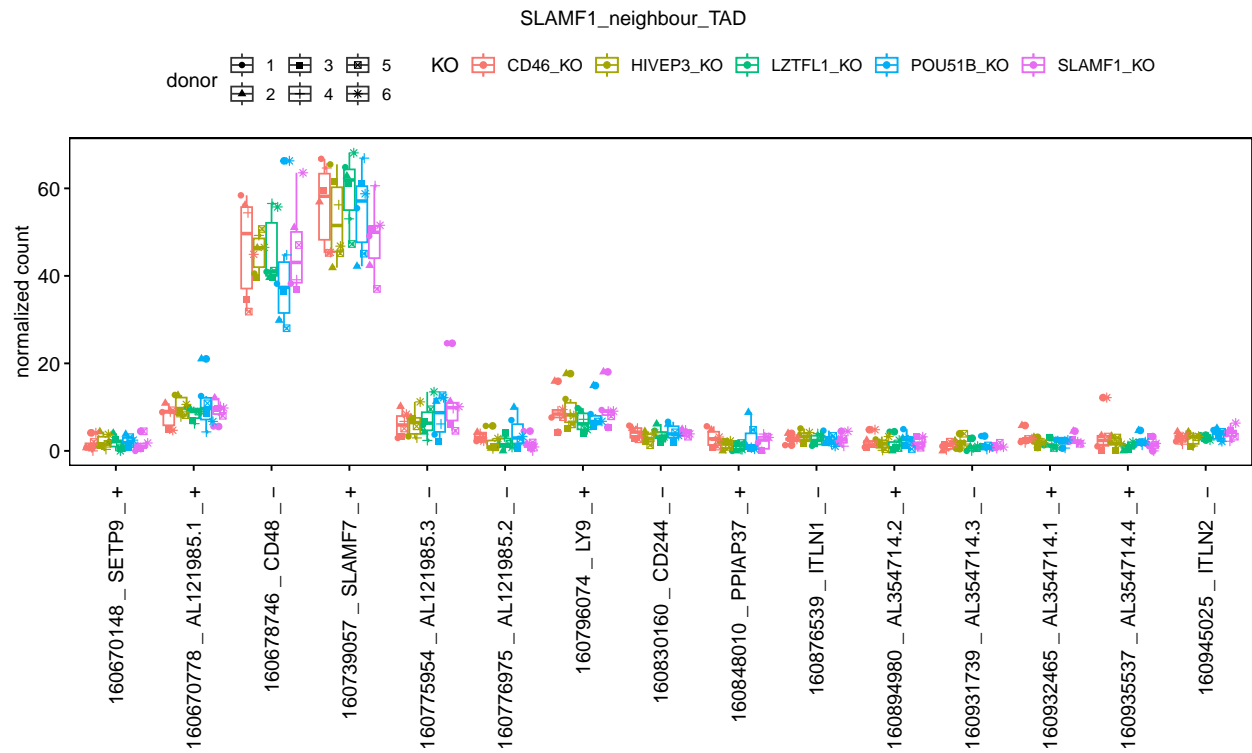
```
slamf1 <- df
plotTAD(slamf1, "1:160420210-160615210(5)", "SLAMF1_TAD")
```



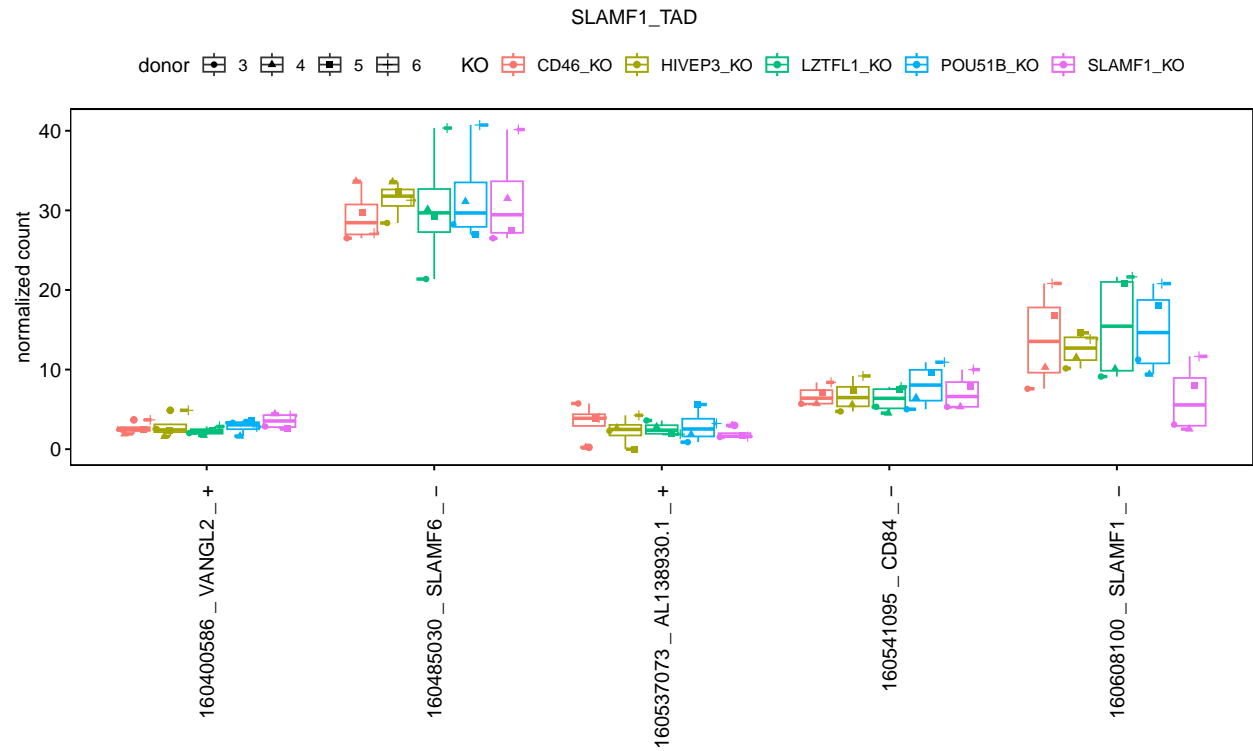
```
plotTAD(slamf1, "1:160705210-160835210(6)", "SLAMF1_neighbour_small_TAD")
```



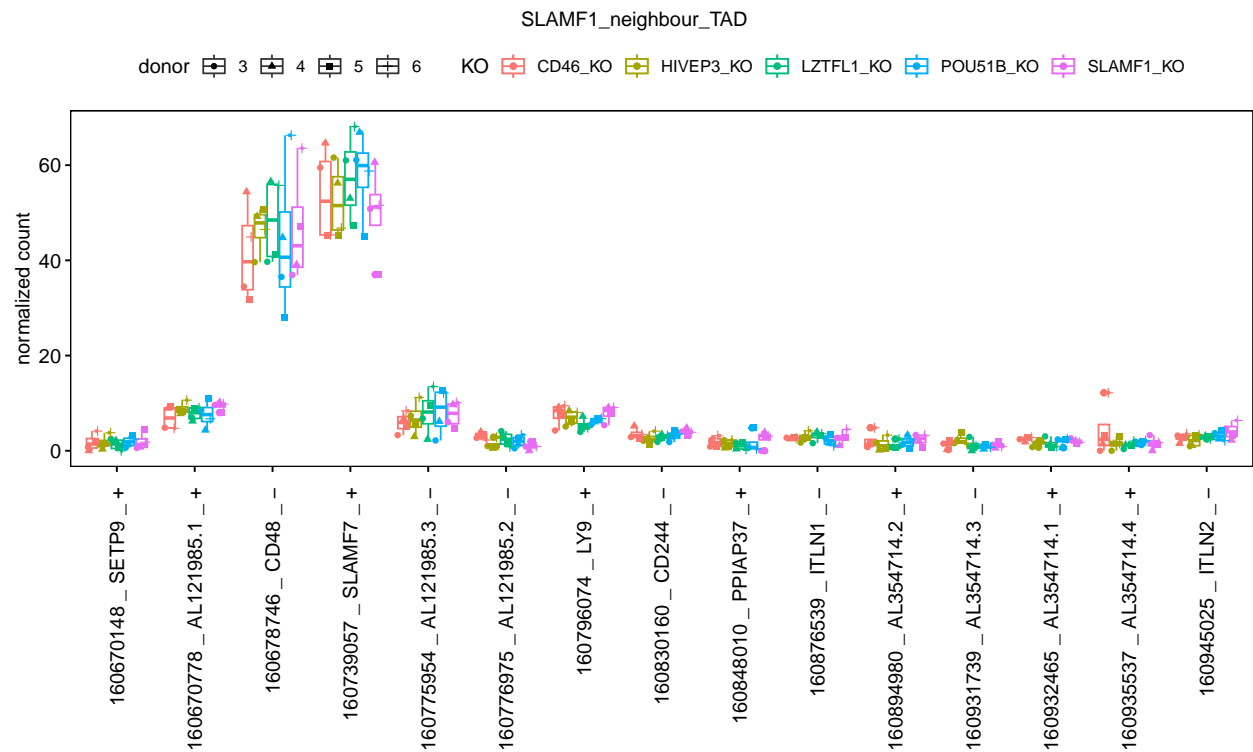
```
plotTAD(slamf1, "1:160670210-160995210(15)", "SLAMF1_neighbour_TAD")
```



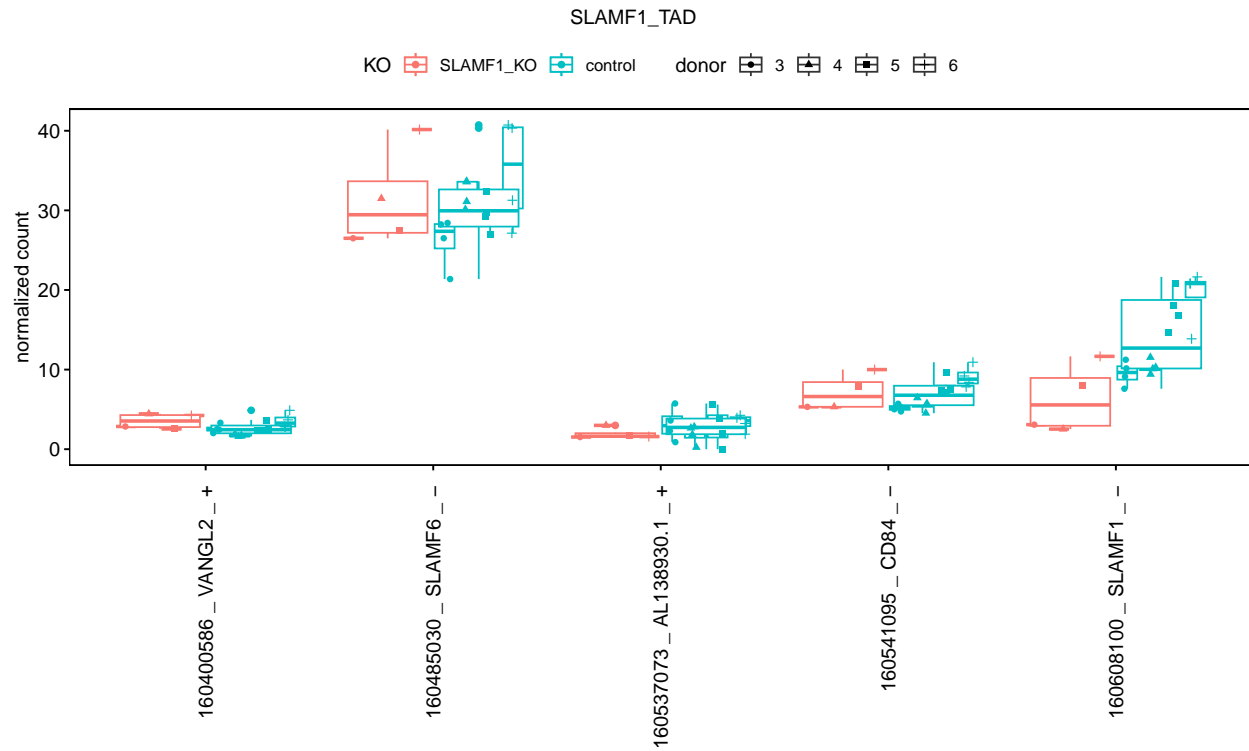
```
slamf1 <- slamf1[slamf1$donor != 1,]
slamf1 <- slamf1[slamf1$donor != 2,]
plotTAD(slamf1, "1:160420210-160615210(5)", "SLAMF1_TAD")
```

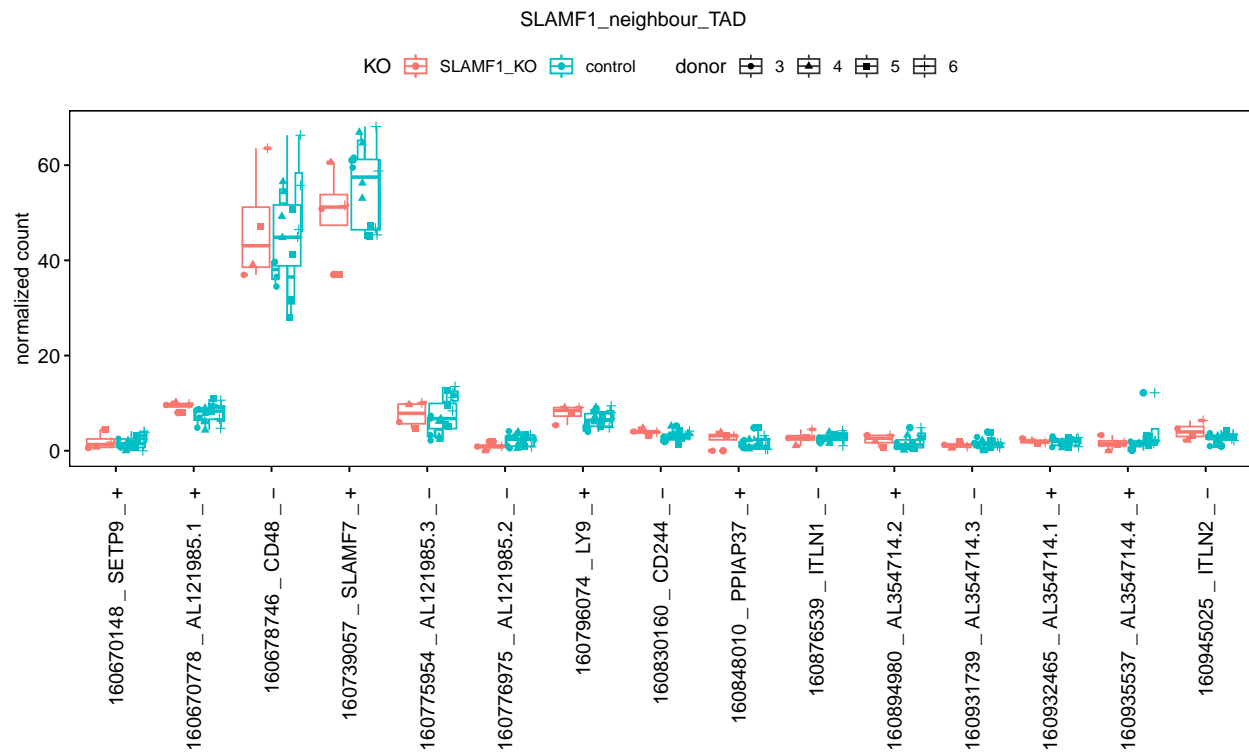
```
plotTAD(slamf1, "1:160670210-160995210(15)", "SLAMF1_neighbour_TAD")
```



```
slamf1[slamf1$KO != "SLAMF1_KO",]$KO <- "control"
plotTADcontrol(slamf1, "1:160420210-160615210(5)", "SLAMF1_TAD")
```

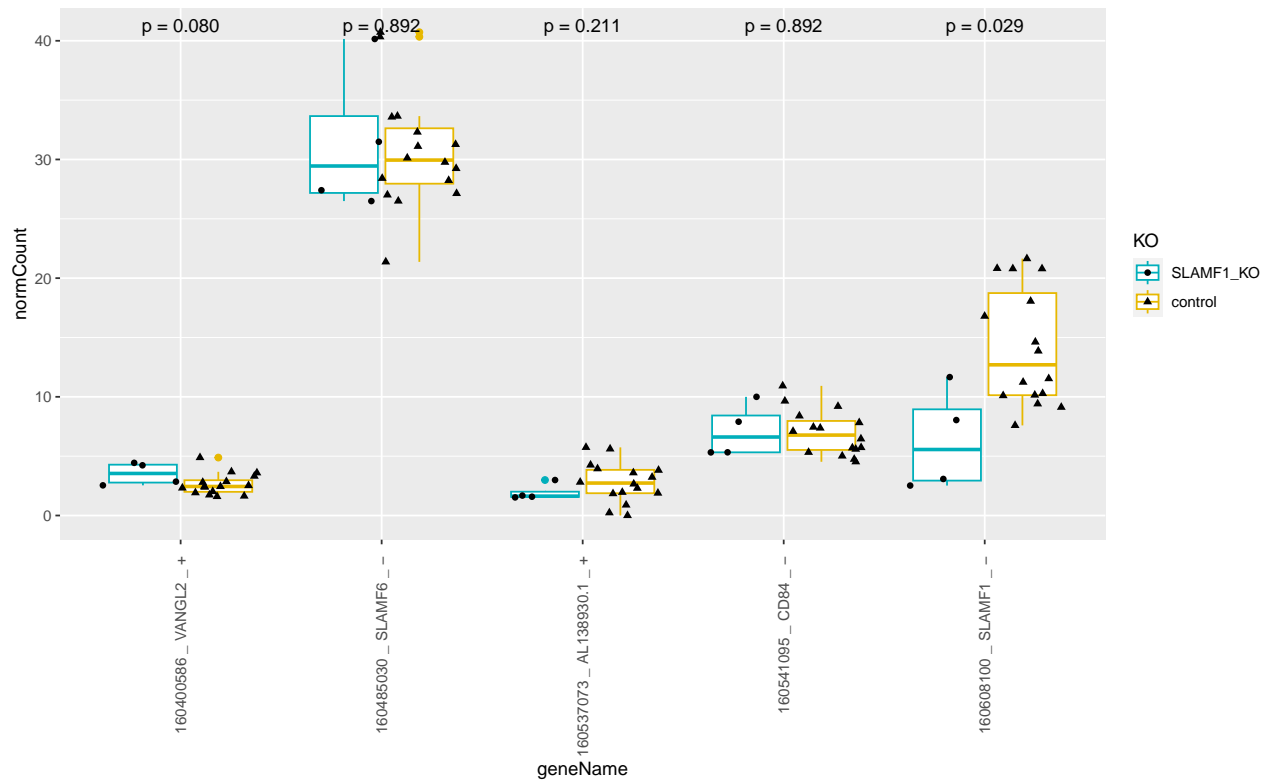


```
plotTADcontrol(slamf1, "1:160670210-160995210(15)", "SLAMF1_neighbour_TAD")
```

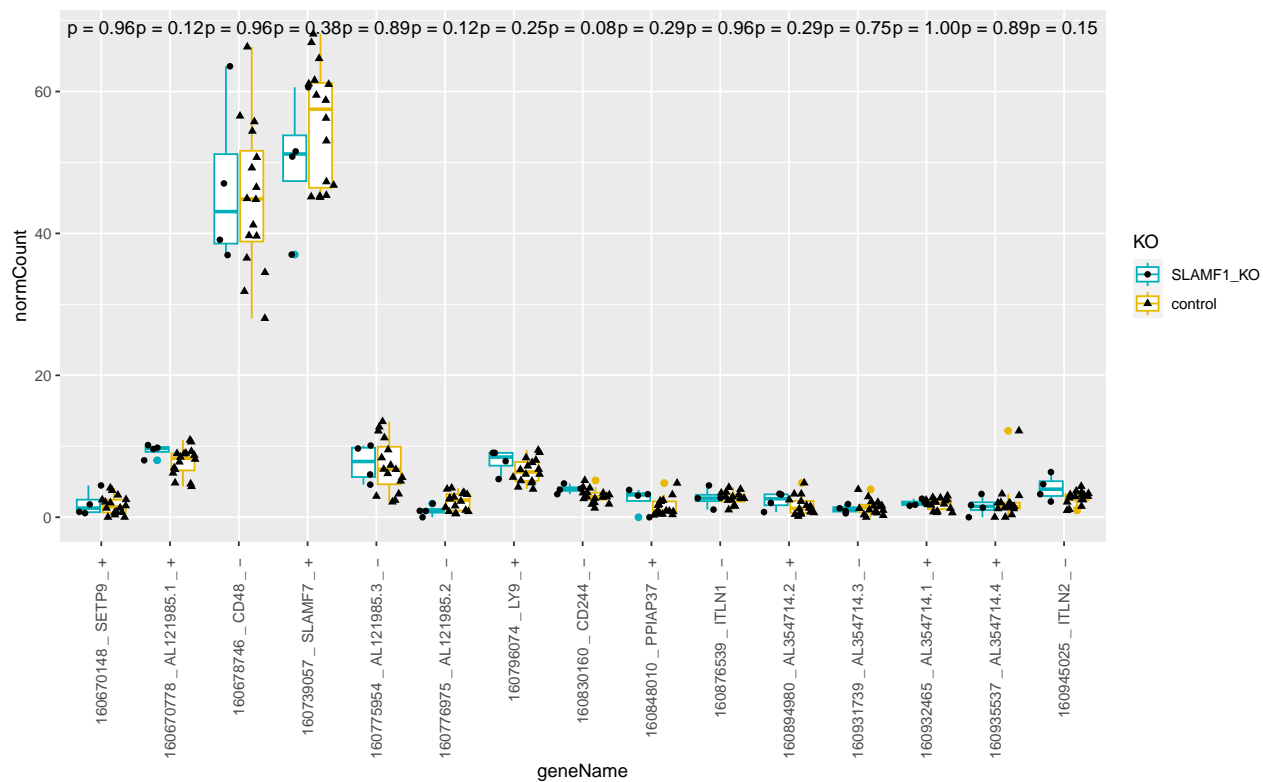


```
slamf1_1 <- slamf1[slamf1$TAD == "1:160420210-160615210(5)",]
ggplot(slamf1_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
```

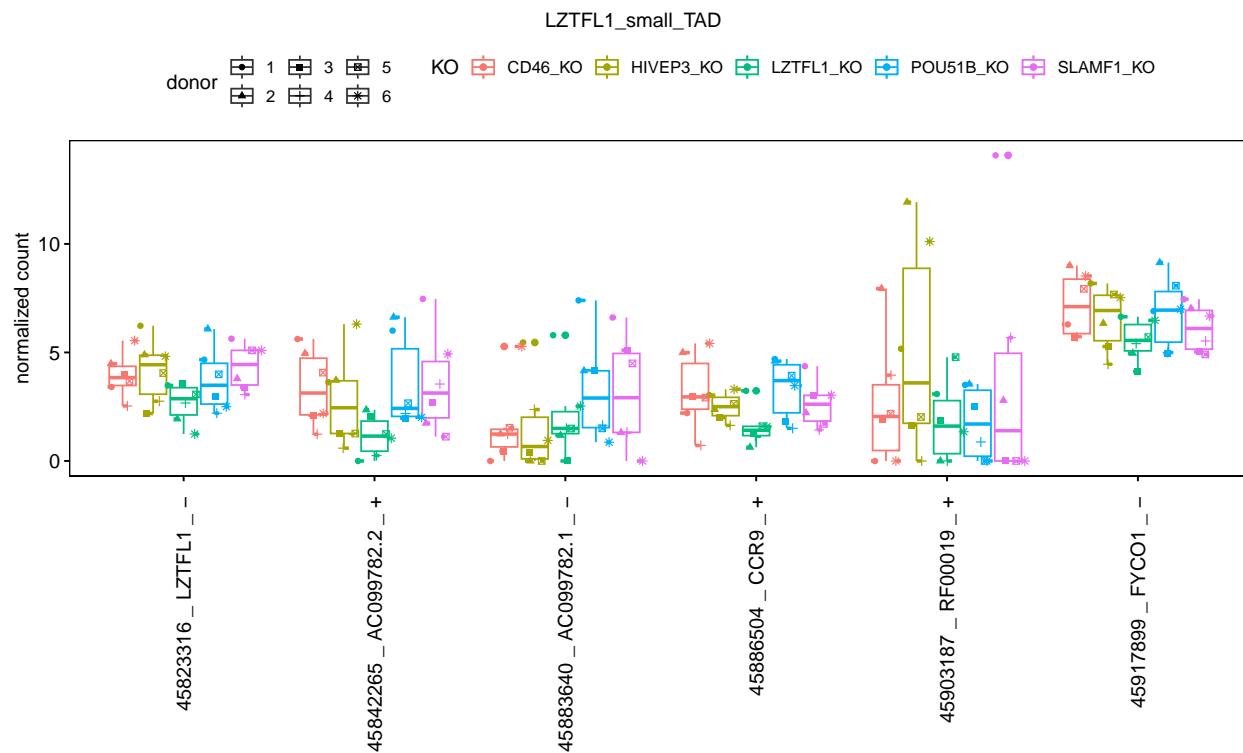
```
scale_color_manual(values = c("#00AFBB", "#E7B800")) +
stat_compare_means(aes(group = KO), label = "p.format") + rotate_x_text(angle = 90) + geom_point(aes(s
```



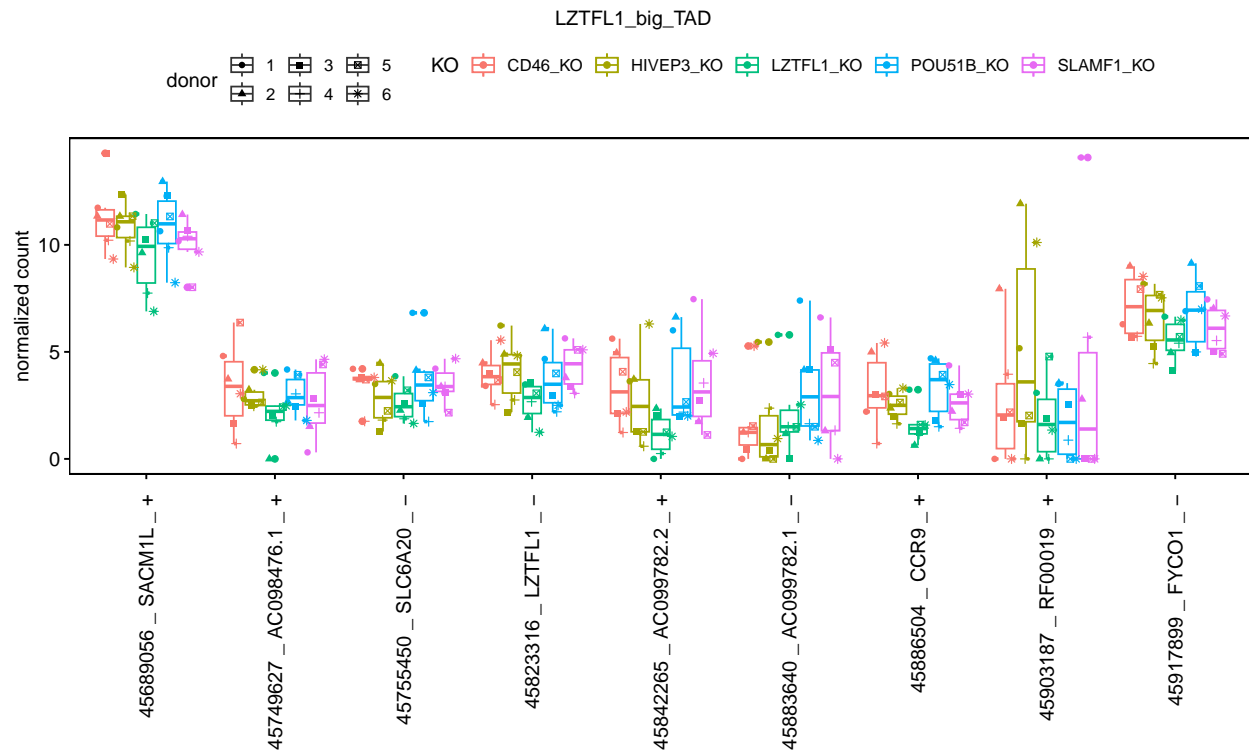
```
slamf1_2 <- slamf1[slamf1$TAD == "1:160670210-160995210(15)",]
ggplot(slamf1_2, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.format") + rotate_x_text(angle = 90) + geom_point(aes(s
```



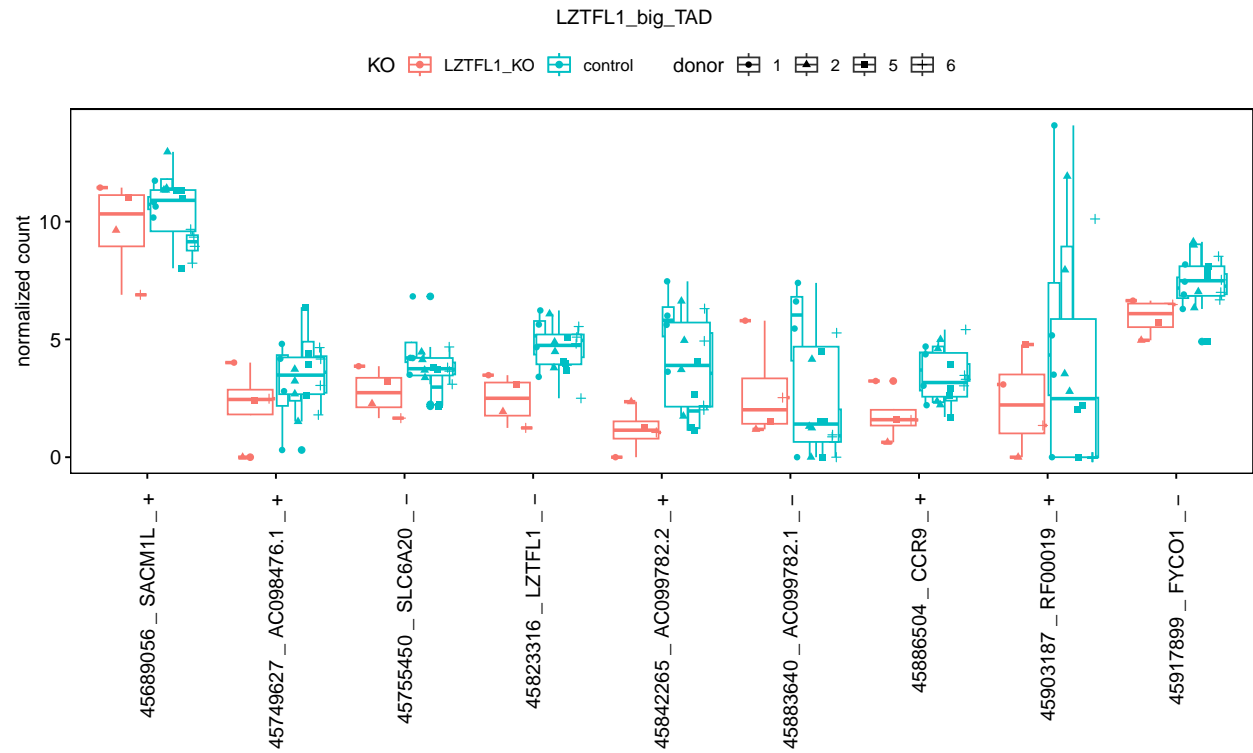
```
lztfl1 <- df
plotTAD(lztfl1, "3:45833508-45933508(6)", "LZTFL1_small_TAD")
```



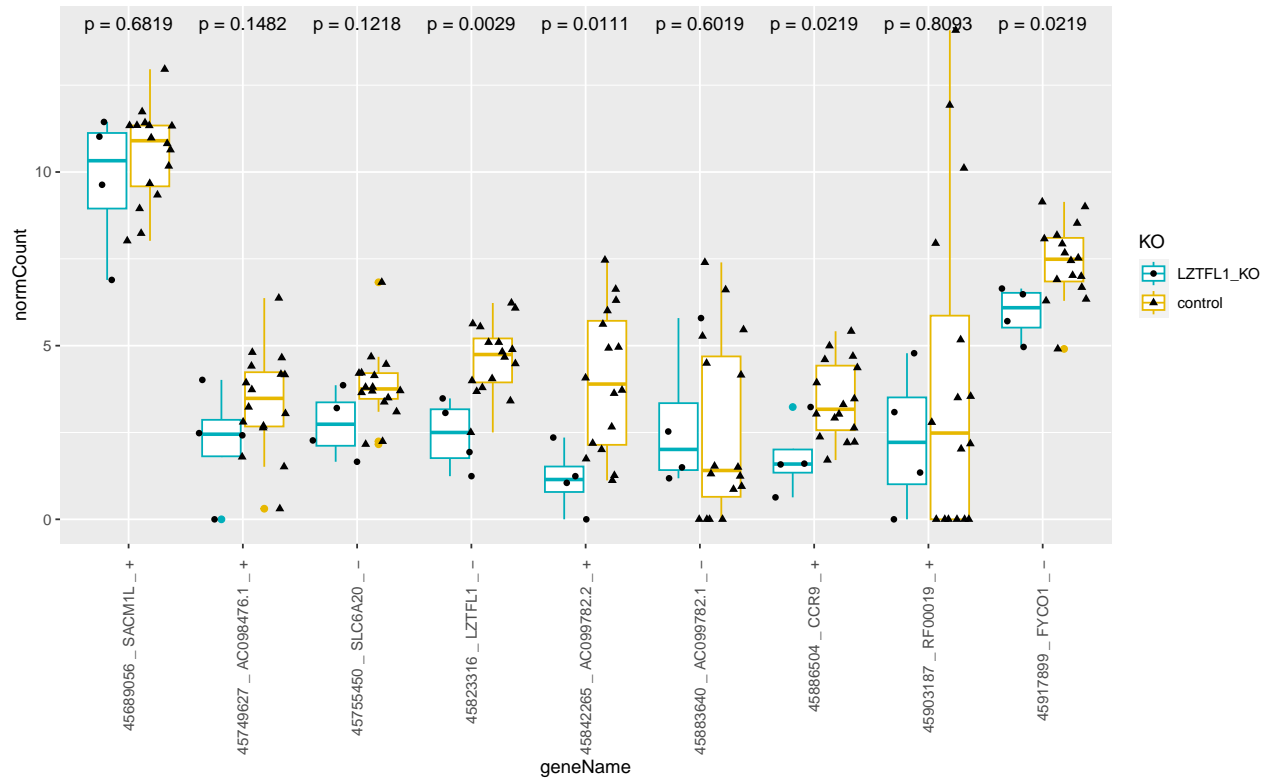
```
plotTAD(lztf11, "3:45743508-45933508(9)", "LZTFL1_big_TAD")
```



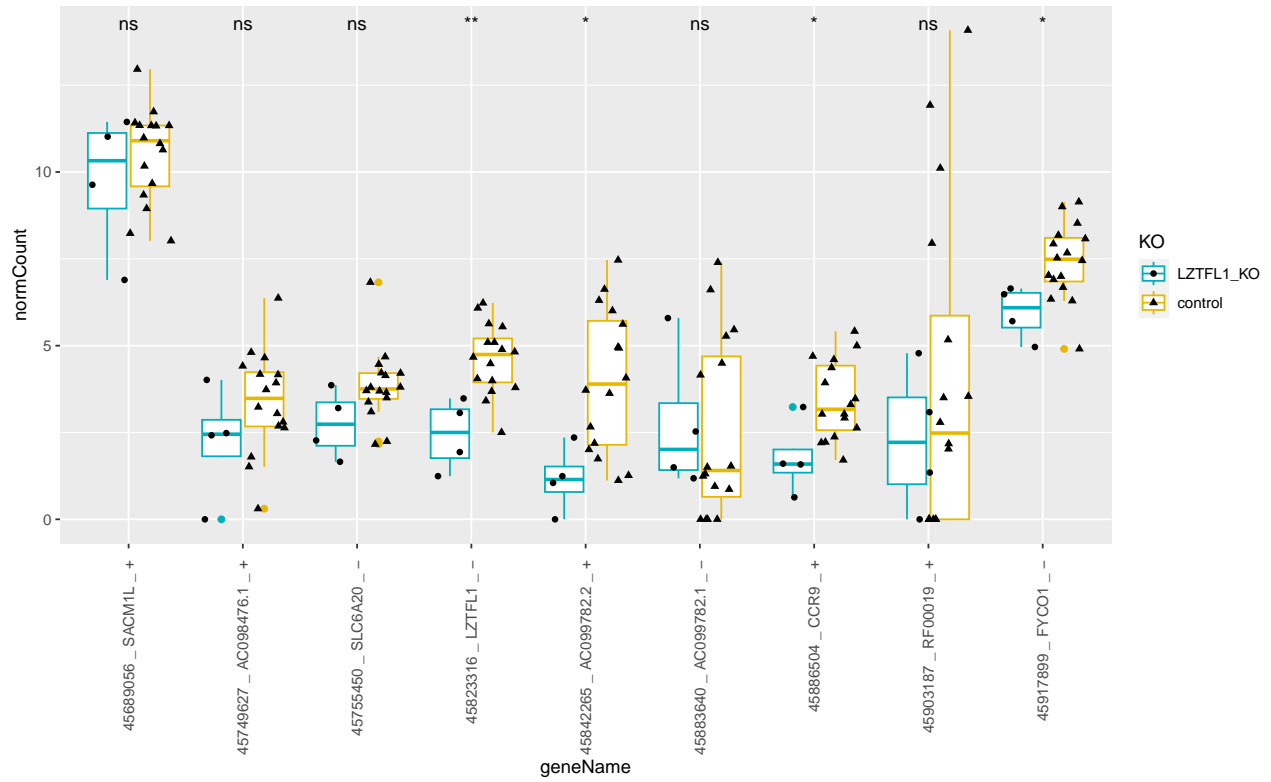
```
lztf11 <- lztf11[lztf11$donor != 3,]
lztf11 <- lztf11[lztf11$donor != 4,]
lztf11[lztf11$KO != "LZTFL1_KO",]$KO <- "control"
plotTADcontrol(lztf11, "3:45743508-45933508(9)", "LZTFL1_big_TAD")
```



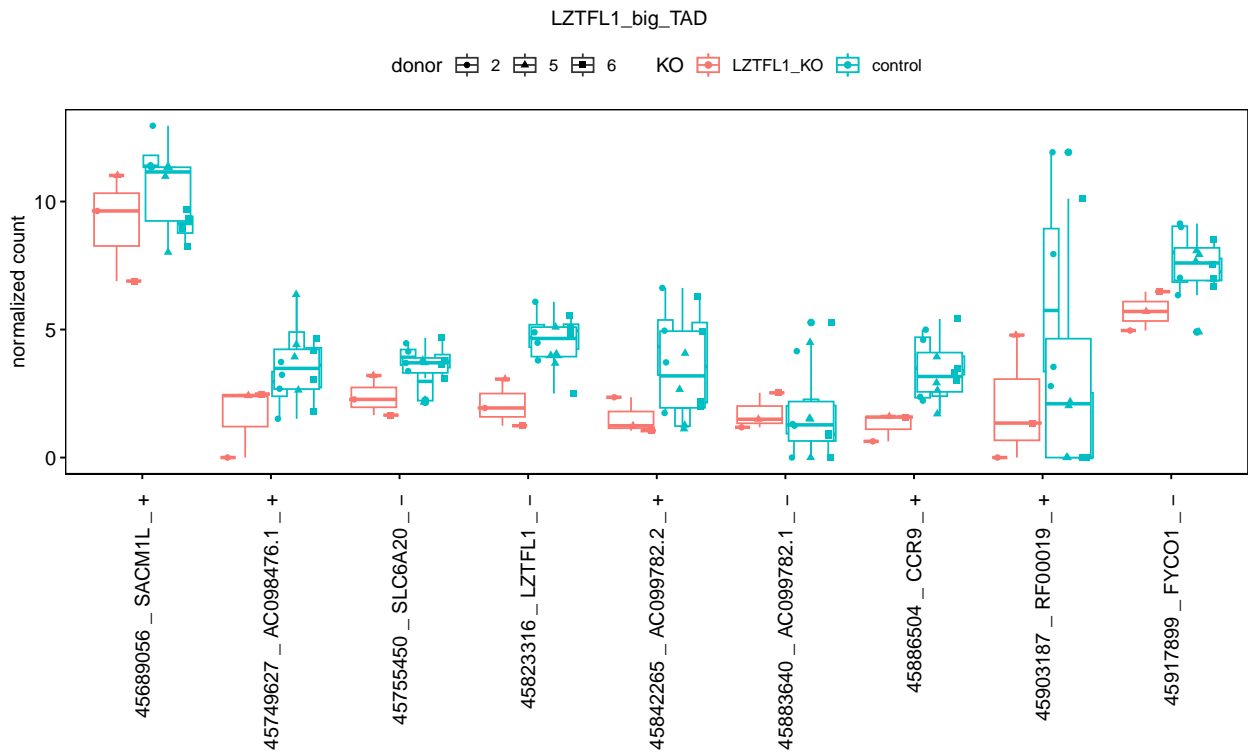
```
lztfl1_1 <- lztfl1[lztfl1$TAD == "3:45743508-45933508(9)",]
ggplot(lztfl1_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO)) +
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.format") + rotate_x_text(angle = 90) + geom_point(aes(
```



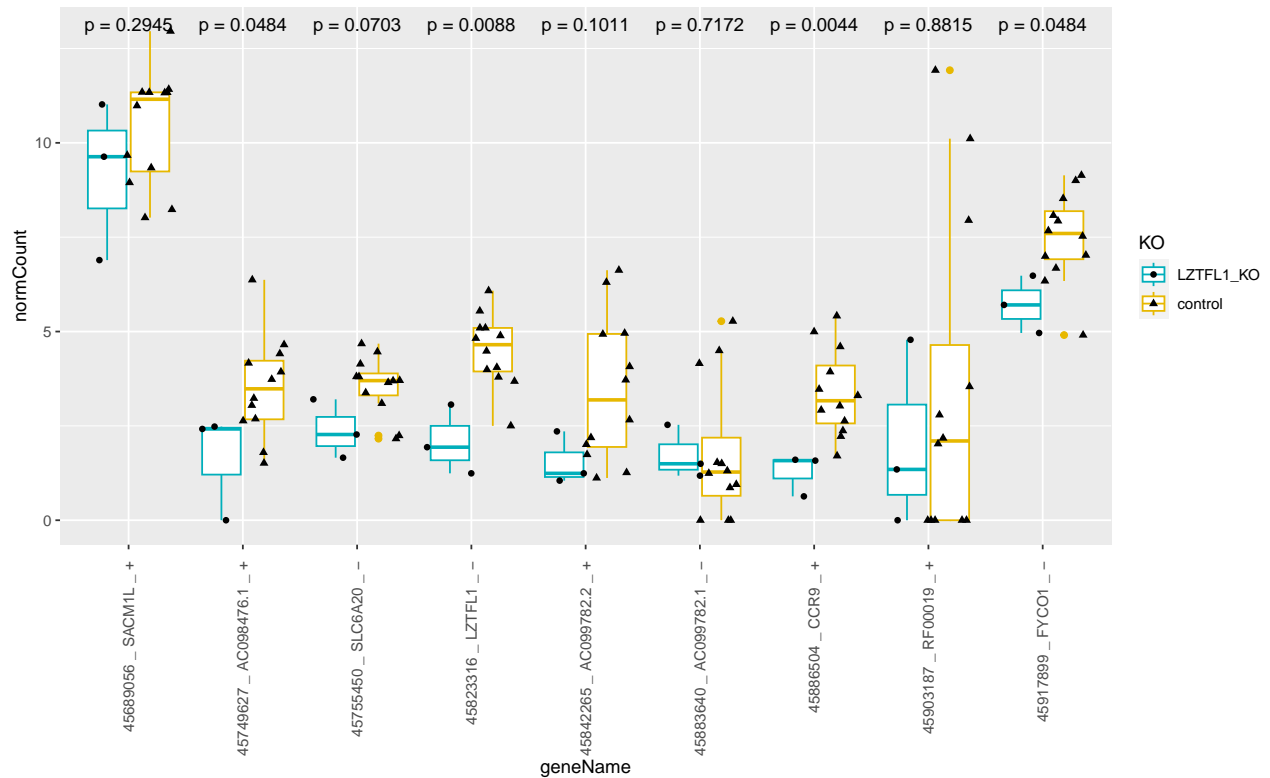
```
ggplot(lztf1l_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.signif") + rotate_x_text(angle = 90) + geom_point(aes(
```



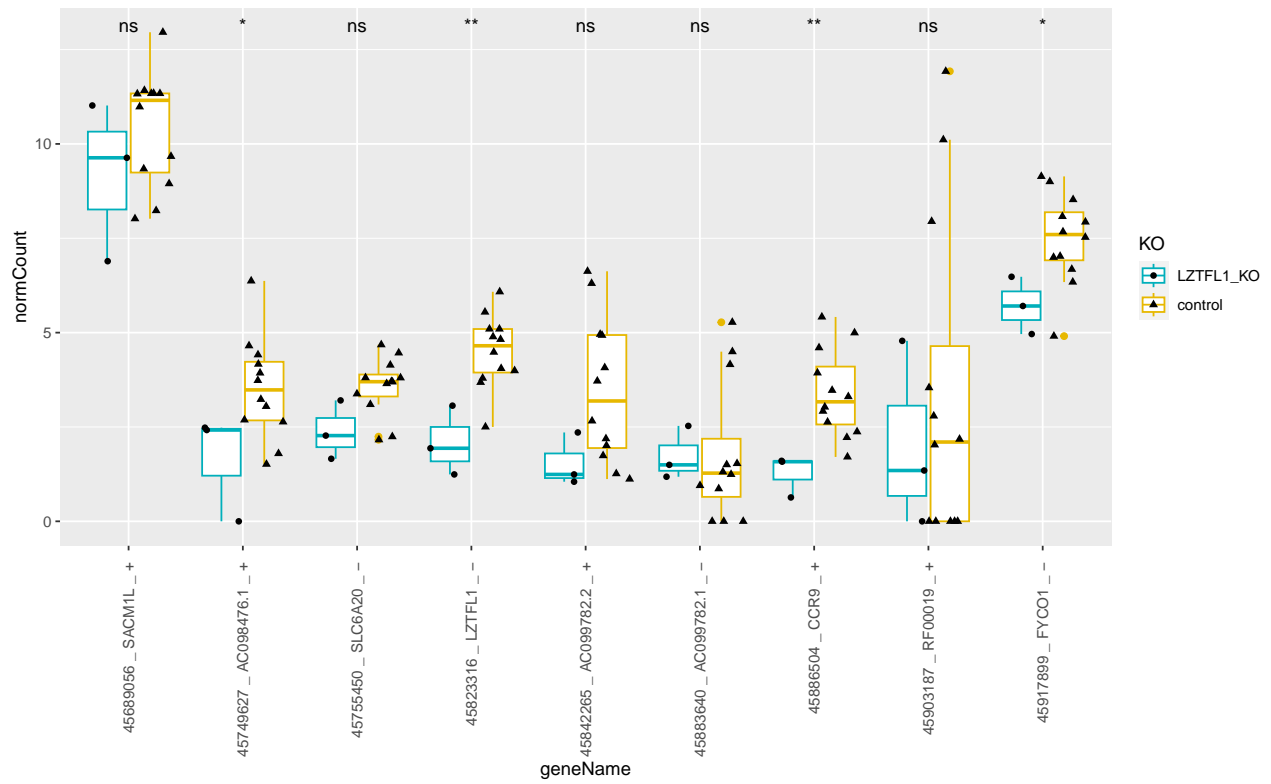
```
# remove also donor 1
lztfl1 <- lztfl1[lztfl1$donor != 1,]
plotTADcontrol(lztfl1, "3:45743508-45933508(9)", "LZTFL1_big_TAD")
```



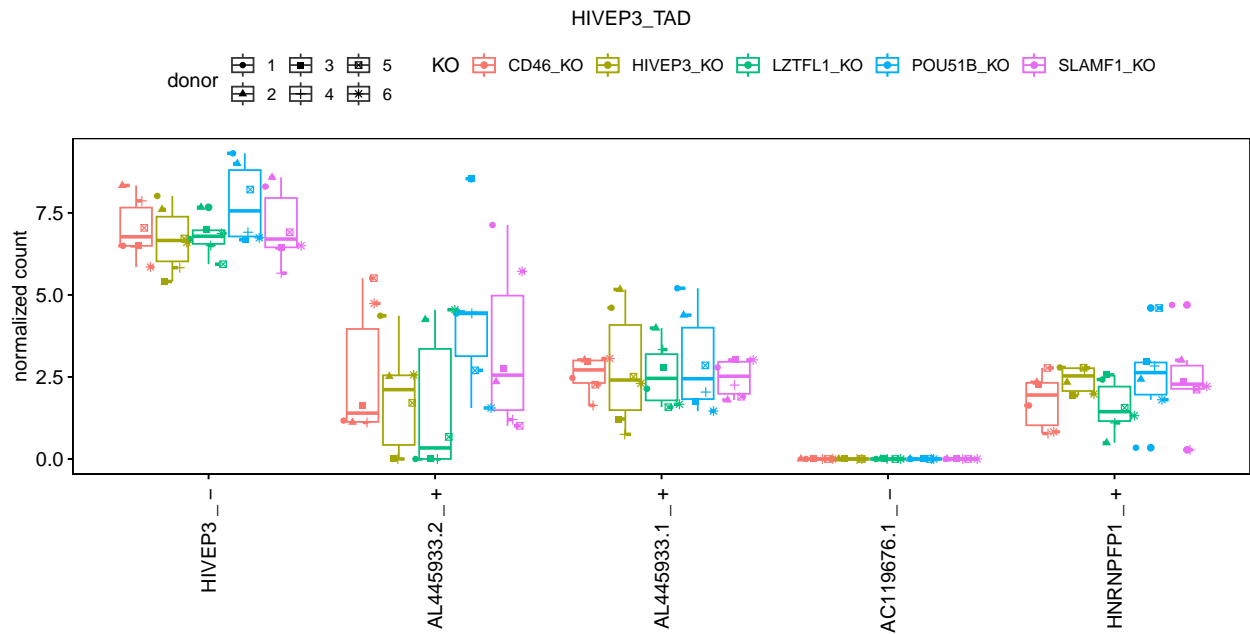

```
lztfl1_1 <- lztfl1[lztfl1$TAD == "3:45743508-45933508(9)",]
ggplot(lztfl1_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.format") + rotate_x_text(angle = 90) + geom_point(aes(
```



```
ggplot(lztfl1_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.signif") + rotate_x_text(angle = 90) + geom_point(aes(
```



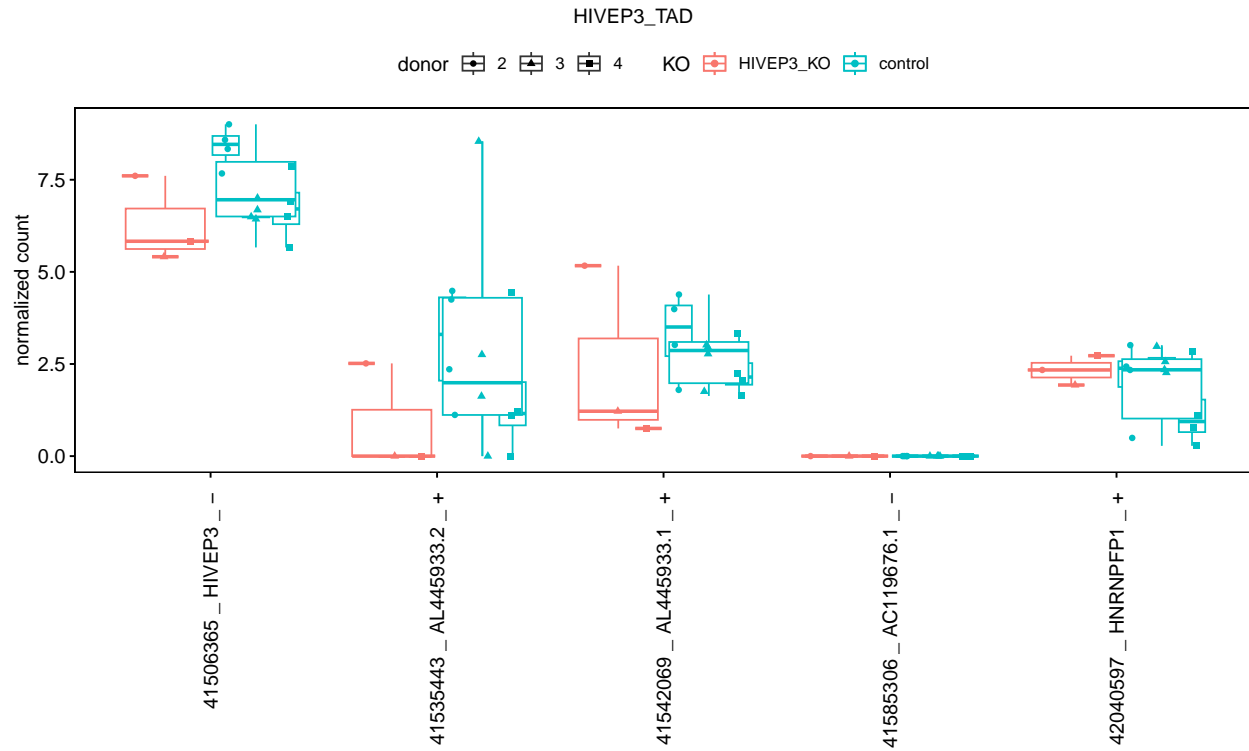
```
hivep1 <- df
plotTAD(hivep1, "1:41519329-42059329(5)", "HIVEP3_TAD")
```



```

hivep1 <- hivep1[hivep1$donor != 1,]
hivep1 <- hivep1[hivep1$donor != 5,]
hivep1 <- hivep1[hivep1$donor != 6,]
hivep1[hivep1$KO != "HIVEP3_KO",]$KO <- "control"
plotTAD(hivep1, "1:41519329-42059329(5)", "HIVEP3_TAD")

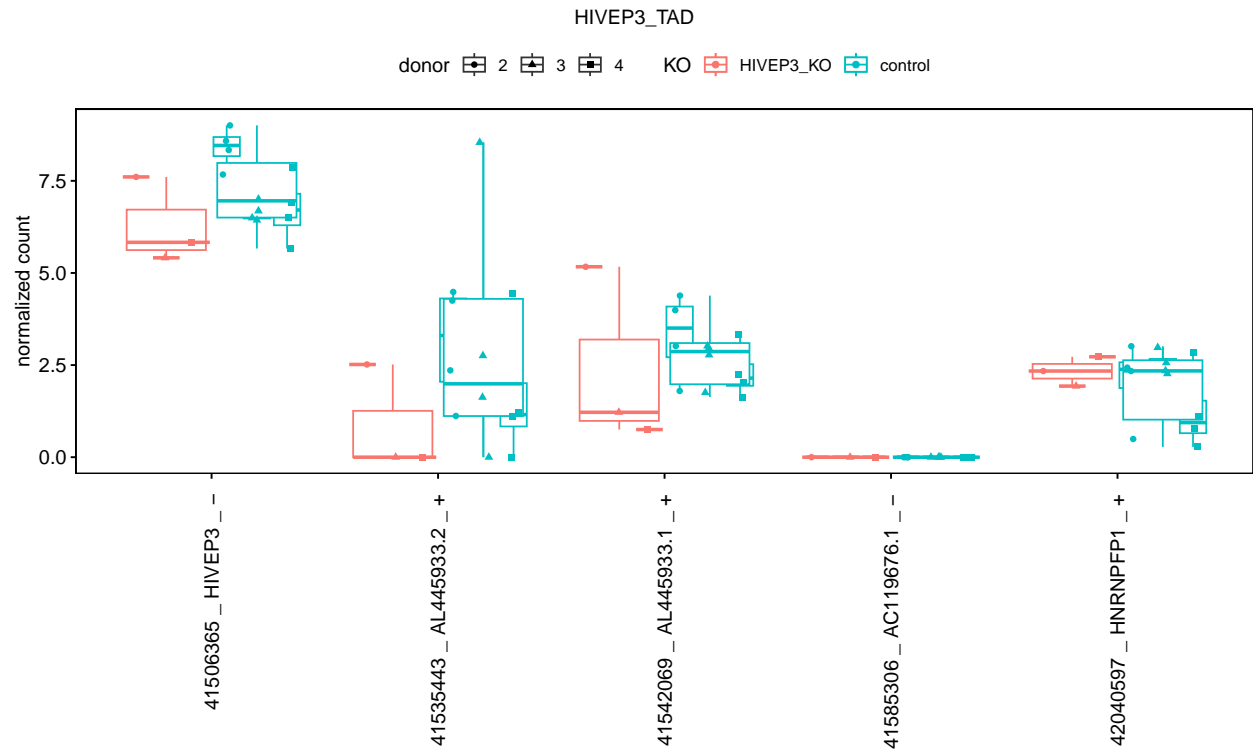
```



```

plotTADcontrol(hivep1, "1:41519329-42059329(5)", "HIVEP3_TAD")

```



```
hivep1_1 <- hivep1[hivep1$TAD == "1:41519329-42059329(5)",]
ggplot(hivep1_1, aes(geneName, normCount)) +
  geom_boxplot(aes(color = KO))+
  scale_color_manual(values = c("#00AFBB", "#E7B800")) +
  stat_compare_means(aes(group = KO), label = "p.format") + rotate_x_text(angle = 90) + geom_point(aes(
```

