Figure-S4E.R

sokole

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```
# This Script Generates Figure S4E
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# Empty the environment & suppress warnings
rm(list = ls())
options(warn=-1)

#Loading Libraries
library(tidyverse)
```
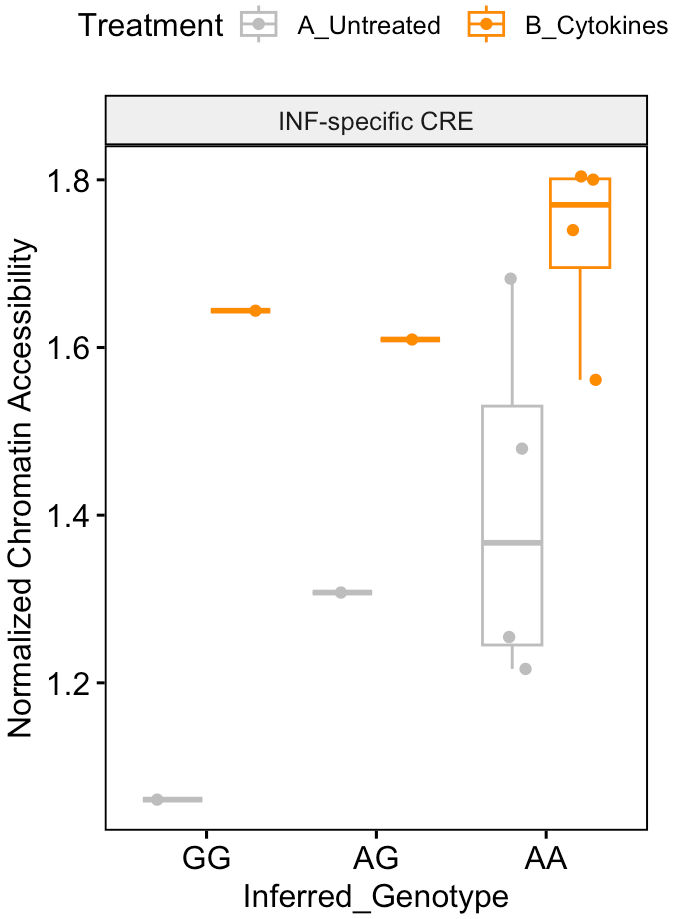

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.4     ✔ readr     2.1.5
## ✔ forcats   1.0.0     ✔ stringr   1.5.1
## ✔ ggplot2   3.5.1     ✔ tibble    3.2.1
## ✔ lubridate 1.9.3     ✔ tidyr     1.3.1
## ✔ purrr     1.0.2
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
to become errors
```

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


# Loading file
Peak.Counts <- read.csv("./INF_count.matrix.normalized.csv")
colnames(Peak.Counts)[1] <- "Peaks"

# Extract DAP of interest
DAP.of.interest <- "chr3-15816818-15817218"
Peak.Counts <- Peak.Counts[Peak.Counts$Peaks %in% DAP.of.interest,]
Peak.Counts <- Peak.Counts[-c(1)]
Peak.Counts <- as.data.frame(t(Peak.Counts))
colnames(Peak.Counts) <- "Counts"

# Making a column on islets
Peak.Counts$Islet <- rownames(Peak.Counts)
Peak.Counts$Islet <- gsub("_C.*","",Peak.Counts$Islet)
Peak.Counts$Islet <- gsub("_U.*","",Peak.Counts$Islet)

# Making a column on inferred genotype
Peak.Counts$Inferred_Genotype <- Peak.Counts$Islet
Peak.Counts$Inferred_Genotype <- gsub("Islet_106","AA",Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_125","AA",Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_151","GG",Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_152","AA",Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_153","AG",Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_99","AA",Peak.Counts$Inferred_Genotype)

# Making a column on treatment
Peak.Counts$Treatment <- rownames(Peak.Counts)
Peak.Counts$Treatment <- gsub(".*C","B_C",Peak.Counts$Treatment)
Peak.Counts$Treatment <- gsub(".*U","A_U",Peak.Counts$Treatment)

# Factor and levels
Peak.Counts$Inferred_Genotype <- factor(Peak.Counts$Inferred_Genotype, levels = c("G
G","AG","AA"))
Peak.Counts$Peak <- "INF-specific CRE"

# Plotting the dot-and-boxplots
bxp.1 <- ggboxplot(
  Peak.Counts, x = "Inferred_Genotype", y = "Counts", color = "Treatment",
  palette = c("grey","darkorange"), add = "jitter", size=0.5, facet.by = "Peak",
) + ylab("Normalized Chromatin Accessibility")

# View
ggarrange(bxp.1,ncol=2,nrow=1)
```


Treatment
A_Untreated
B_Cytokines
INF-specific CRE
Normalized Chromatin Accessibility
1.8
1.6
1.4
1.2
GG
AG
AA
Inferred_Genotype