

Figure-4E.R

sokole

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# This Script Generates Figure 4E
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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 files
Peak.Counts <- read.csv("./ERS_count.matrix.normalized.csv")
colnames(Peak.Counts)[1] <- "Peaks"

# Extract DAP of interest
DAP.of.interest <- "chr9-95008034-95008434"
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("_T.*", "", Peak.Counts$Islet)
Peak.Counts$Islet <- gsub("_D.*", "", Peak.Counts$Islet)

# Making a column on inferred genotype
Peak.Counts$Inferred_Genotype <- Peak.Counts$Islet
Peak.Counts$Inferred_Genotype <- gsub("Islet_144", "TC", Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_146", "TT", Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_151", "TT", Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_147", "TT", Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_148", "TC", Peak.Counts$Inferred_Genotype)
Peak.Counts$Inferred_Genotype <- gsub("Islet_153", "TC", Peak.Counts$Inferred_Genotype)

# Making a column on treatment
Peak.Counts$Treatment <- rownames(Peak.Counts)
Peak.Counts$Treatment <- gsub(".*T", "T", Peak.Counts$Treatment)
Peak.Counts$Treatment <- gsub(".*D", "D", Peak.Counts$Treatment)

# Factor and levels
Peak.Counts$Inferred_Genotype <- factor(Peak.Counts$Inferred_Genotype, levels = c("T", "C", "TT"))
Peak.Counts$Peak <- "ERS-specific CRE"

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

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

```

Treatment  DMSO  Thapsigargin

