

# ELT2\_repression\_microscopy

Rtpw

8/4/2022

```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5      v purrr 0.3.4
## v tibble 3.1.6       v dplyr 1.0.8
## v tidyr 1.2.0        v stringr 1.4.0
## v readr 2.1.2        v forcats 0.5.1

## Warning: package 'tidyr' was built under R version 4.1.2
## Warning: package 'readr' was built under R version 4.1.2
## Warning: package 'dplyr' was built under R version 4.1.2

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

input_df <- read_csv("../01_input/ELT2_Repression_Microscopy_All_Data.csv") %>% mutate(gene = fct_relev
                                                                RNAi = fct_relevel(RNAi, c
separate(Label, sep = ":", into = c("Label", "type", "channel"))

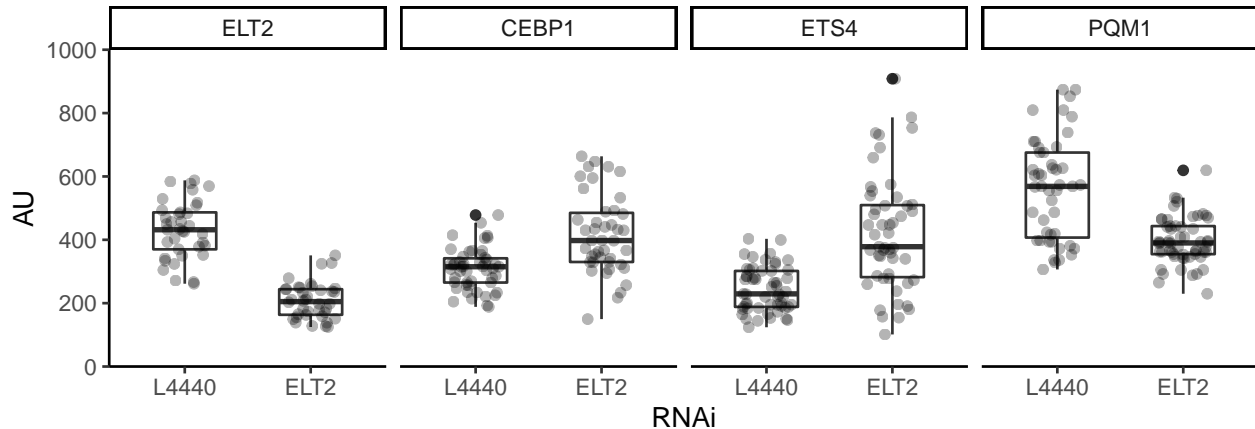
## Rows: 1886 Columns: 12
## -- Column specification -----
## Delimiter: ","
## chr (4): Label, gene, type, RNAi
## dbl (8): val, Area, Mean, Min, Max, IntDen, RawIntDen, rep
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.

analysis_df <- input_df %>%
  group_by(Label, type) %>%
  summarise(mean_background = mean(Mean)) %>%
  filter(type == "background") %>%
  select(-type) %>%
  right_join(input_df, by = "Label") %>%
  filter(type == "intestine") %>%
  mutate(AU = (IntDen - (mean_background*Area))/Area)

## `summarise()` has grouped output by 'Label'. You can override using the
## `.groups` argument.

gfp_plot <- analysis_df %>%
  ggplot(aes(x = RNAi, y = AU)) +
  geom_boxplot(width = 0.5) +
```

```
geom_jitter(alpha = 0.3, width = 0.2, size = 2, aes(stroke = 0)) +
facet_grid(. ~ gene) +
scale_y_continuous(limits = c(0,1000), breaks = seq(0,1000, by = 200), expand = c(0,0))+
theme_classic()
gfp_plot
```



Save the plot

```
ggsave(gfp_plot, filename = "../03_output/elt2_regulated_TFs_GFP_reporter_plot.pdf", width = 7, height = 7)
```

```
t.test(x = analysis_df %>% filter(gene == "ELT2", RNAi == "L4440") %>% pull(AU),
       y = analysis_df %>% filter(gene == "ELT2", RNAi == "ELT2") %>% pull(AU))$p.value
```

```
## [1] 1.210741e-18
```

```
t.test(x = analysis_df %>% filter(gene == "CEBP1", RNAi == "L4440") %>% pull(AU),
       y = analysis_df %>% filter(gene == "CEBP1", RNAi == "ELT2") %>% pull(AU))$p.value
```

```
## [1] 3.319637e-06
```

```
t.test(x = analysis_df %>% filter(gene == "ETS4", RNAi == "L4440") %>% pull(AU),
       y = analysis_df %>% filter(gene == "ETS4", RNAi == "ELT2") %>% pull(AU))$p.value
```

```
## [1] 1.331861e-08
```

```
t.test(x = analysis_df %>% filter(gene == "PQM1", RNAi == "L4440") %>% pull(AU),
       y = analysis_df %>% filter(gene == "PQM1", RNAi == "ELT2") %>% pull(AU))$p.value
```

```
## [1] 1.455525e-08
```

Number of worms in each sample/treatment pair

```
analysis_df %>% group_by(gene, RNAi) %>% summarise(n())
```

```
## `summarise()` has grouped output by 'gene'. You can override using the
## `.groups` argument.
```

```
## # A tibble: 8 x 3
## # Groups:   gene [4]
##   gene RNAi `n()`
##   <fct> <fct> <int>
## 1 ELT2 L4440    37
## 2 ELT2 ELT2     38
## 3 CEBP1 L4440    50
## 4 CEBP1 ELT2     43
```

```
## 5 ETS4 L4440 55
## 6 ETS4 ELT2 51
## 7 PQM1 L4440 47
## 8 PQM1 ELT2 56

analysis_df %>% group_by(gene, RNAi) %>% summarise(mean(AU))

## `summarise()` has grouped output by 'gene'. You can override using the
## `.groups` argument.

## # A tibble: 8 x 3
## # Groups:   gene [4]
##   gene RNAi `mean(AU)`
##   <fct> <fct>      <dbl>
## 1 ELT2 L4440      430.
## 2 ELT2 ELT2      208.
## 3 CEBP1 L4440     308.
## 4 CEBP1 ELT2     416.
## 5 ETS4 L4440     245.
## 6 ETS4 ELT2     420.
## 7 PQM1 L4440     562.
## 8 PQM1 ELT2     396.
```

## Session info

```
sessionInfo()

## R version 4.1.0 (2021-05-18)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.1/Resources/lib/libRlapack.dylib
##
## 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] forcats_0.5.1  stringr_1.4.0  dplyr_1.0.8    purrr_0.3.4
## [5] readr_2.1.2    tidyr_1.2.0    tibble_3.1.6   ggplot2_3.3.5
## [9] tidyverse_1.3.1
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.1.2 xfun_0.30      haven_2.4.3    colorspace_2.0-3
## [5] vctrs_0.4.0      generics_0.1.2 htmltools_0.5.2 yaml_2.3.5
## [9] utf8_1.2.2       rlang_1.0.2    pillar_1.7.0   glue_1.6.2
## [13] withr_2.5.0      DBI_1.1.2      bit64_4.0.5    dbplyr_2.1.1
## [17] modelr_0.1.8     readxl_1.4.0   lifecycle_1.0.1 munsell_0.5.0
## [21] gtable_0.3.0     cellranger_1.1.0 rvest_1.0.2    evaluate_0.15
## [25] knitr_1.38       tzdb_0.3.0     fastmap_1.1.0  parallel_4.1.0
```

## [29]	fansi_1.0.3	highr_0.9	broom_0.8.0	backports_1.4.1
## [33]	scales_1.2.0	vroom_1.5.7	jsonlite_1.8.0	farver_2.1.0
## [37]	bit_4.0.4	fs_1.5.2	hms_1.1.1	digest_0.6.29
## [41]	stringi_1.7.6	grid_4.1.0	cli_3.2.0	tools_4.1.0
## [45]	magrittr_2.0.3	crayon_1.5.1	pkgconfig_2.0.3	ellipsis_0.3.2
## [49]	xml2_1.3.3	reprex_2.0.1	lubridate_1.8.0	assertthat_0.2.1
## [53]	rmarkdown_2.13	httr_1.4.2	rstudioapi_0.13	R6_2.5.1
## [57]	compiler_4.1.0			