

# Redhai publication 2023 selected plots

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Last modified:

```
print(date())
```

```
## [1] "Tue Dec 19 13:23:05 2023"
```

The following code is used to produce selected plots for the publication: **Rab35 restrains regional Wnt activation by regulating a Cdc42-JNK signalling relay in the intestine**

## Import

```
library(tidyverse)
library(plotrix)
library(cowplot)
library(viridis)
library(readxl)
library(ggrepel)
library(padr)
library(gmodels)
library(rstatix)
theme_set(theme_cowplot())
```

## Figure 1b

### Prepare data

```
screen_result_apc <- read_excel("FINAL modifier screen apc .xlsx", range = "A3:T126")

screen_result_apc_long <- screen_result_apc %>%
  rename("gene_name" = "...1") %>%
  mutate(GENE = str_replace_all(gene_name, c("rnai" = "RNAi", "1DN" = "1-DN", "wt" = "WT", "-WT" = " WT", "GDI" = "GDI"))) %>%
  select(!"gene_name") %>%
  group_by(GENE) %>%
  mutate(duplicate_line = dplyr::row_number()) %>%
  mutate(GENE = ifelse(duplicate_line > 1, paste(GENE, "line", duplicate_line, sep = " "), GENE)) %>%
```

```

ungroup() %>%
select(!"duplicate_line") %>%
pivot_longer(!"GENE", names_to = "column_name", values_to = "score") %>%
filter(!is.na(score)) %>%
select(!"column_name")

screen_result_apc_long <- screen_result_apc_long %>%
  left_join(screen_result_apc_long %>%
    group_by(GENE) %>%
    summarise(mean_score = mean(score), sd_score = sd(score), sem_score = std.error(score)))

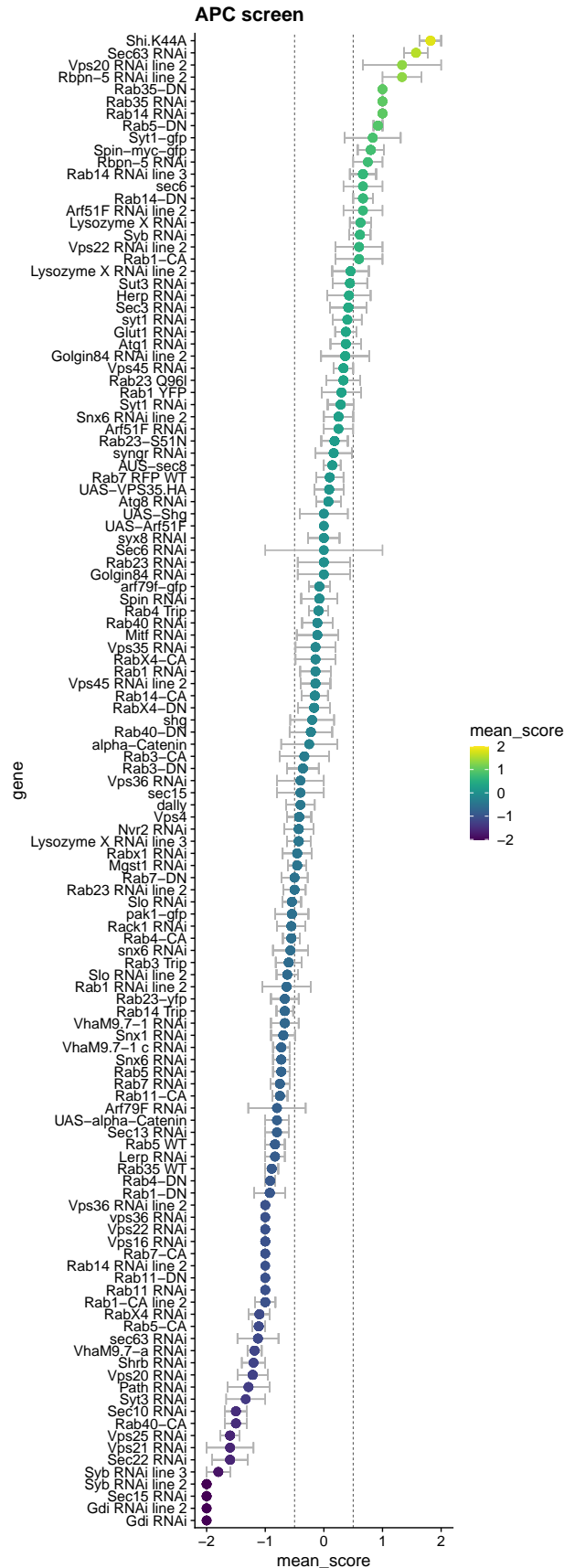
```

## Plot

```

screen_result_apc_long %>%
  ggplot(aes(y=reorder(GENE, mean_score), x=mean_score, color = mean_score)) +
  geom_vline(xintercept = c(0.5, -0.5), size = 0.25, colour = 'gray30', linetype = "dashed") +
  geom_errorbar(aes(xmin = mean_score - sem_score, xmax = mean_score + sem_score), color = "gray70") +
  geom_point(size = 3) +
  scale_color_viridis(limits=c(-2, 2)) +
  theme_cowplot() +
  ylab("gene") +
  xlim(-2, 2) +
  ggtitle("APC screen")

```



## Figure 2b

### Prepare data

```
expression_data <- read_excel("APC_data.xlsx", col_names = FALSE)
expression_data <- expression_data %>%
  select(where(~!all(is.na(.x)))) %>%
  filter(!row_number() %in% c(1,2,3)) %>%
  split.default(rep(c("Control", "APC RNAi", "APC RNAi + Rab35 CA", "APC RNAi + Rab35 DN"), each = 6)) %>%
  bind_rows(.id = "genotype")
# Rename:
new_names <- paste(rep(c("position", "expression"), 3), rep(seq(1,3), each = 2), sep = "_")
old_names <- colnames(expression_data)[2:7]
expression_data.wide <- expression_data %>% rename_at(vars(old_names), function(x) new_names)
expression_data.long <- expression_data.wide %>%
  pivot_longer(cols = !genotype, cols_vary = "slowest", names_to = c(".value", "line"), names_pattern =
  mutate(position = as.numeric(position), expression = as.numeric(expression)) %>%
  filter(!is.na(position))
```

### Plot

```
line_colors <- c("#A5A5A5", "#A41629", "#008C00", "#061276")

expression_data.long.scaled <- expression_data.long %>%
  group_by(genotype) %>%
  mutate(max_position = max(position)) %>%
  mutate(scaled_position = position/max_position) %>%
  ungroup()

expression_data.long.scaled %>%
  ggplot(aes(x=scaled_position, y=expression, color=genotype)) +
  geom_point(aes(shape = line), size = 1, alpha = 0.5) +
  geom_smooth() +
  labs(x = "scaled position") +
  scale_color_manual(values = rev(line_colors)) +
  theme(legend.position = "bottom")
```

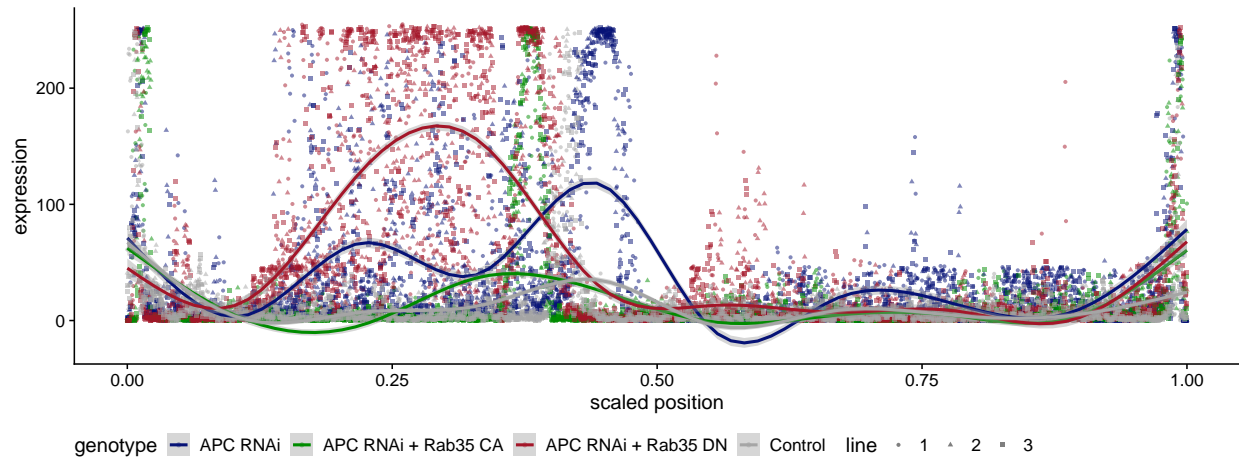


Figure 3h

## Prepare data

```
pla_negative_gfp <- read_excel("PLA quantifications.xlsx", range = "C6:AD35") %>% select(matches("Distance"))
pla_negative_gfp.wide <- pla_negative_gfp %>%
  split.default(rep(paste0("gut", seq(1, ncol(pla_negative_gfp)/6)), each = 6)) %>%
  bind_rows(.id = "gut")

new_names <- paste(rep(c("distance", "expression"), 3), rep(seq(1,3), each = 2), sep = "_")
old_names <- colnames(pla_negative_gfp.wide[2:ncol(pla_negative_gfp.wide)])

pla_negative_gfp.long <- pla_negative_gfp.wide %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
  mutate(genotype = "GFP") %>%
  relocate(genotype)

pla_negative_rfp <- read_excel("PLA quantifications.xlsx", range = "C39:AD68") %>% select(matches("Distance"))
pla_negative_rfp.wide <- pla_negative_rfp %>%
  split.default(rep(paste0("gut", seq(1, ncol(pla_negative_rfp)/6)), each = 6)) %>%
  bind_rows(.id = "gut")

old_names <- colnames(pla_negative_rfp.wide[2:ncol(pla_negative_rfp.wide)])

pla_negative_rfp.long <- pla_negative_rfp.wide %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
  mutate(genotype = "RFP") %>%
  relocate(genotype)

pla_negative.long <- bind_rows(pla_negative_gfp.long, pla_negative_rfp.long) %>%
  filter(!is.na(distance))
```

```

pla_positive_gfp <- read_excel("PLA quantifications.xlsx", range = "C75:AD104") %>% select(matches("Dis

pla_positive_gfp.wide <- pla_positive_gfp %>%
  split.default(rep(paste0("gut", seq(1,ncol(pla_positive_gfp)/6)), each = 6)) %>%
  bind_rows(.id = "gut")

old_names <- colnames(pla_positive_gfp.wide[2:ncol(pla_positive_gfp.wide)])

pla_positive_gfp.long <- pla_positive_gfp.wide %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
  mutate(genotype = "GFP") %>%
  relocate(genotype)

pla_positive_rfp <- read_excel("PLA quantifications.xlsx", range = "C107:AD136") %>% select(matches("Dis

pla_positive_rfp.wide <- pla_positive_rfp %>%
  split.default(rep(paste0("gut", seq(1,ncol(pla_positive_rfp)/6)), each = 6)) %>%
  bind_rows(.id = "gut")

old_names <- colnames(pla_positive_rfp.wide[2:ncol(pla_positive_rfp.wide)])

pla_positive_rfp.long <- pla_positive_rfp.wide %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
  mutate(genotype = "RFP") %>%
  relocate(genotype)

pla_positive.long <- bind_rows(pla_positive_gfp.long, pla_positive_rfp.long) %>%
  filter(!is.na(distance))

```

## Plot

```

pla_positive.long %>%
  mutate(title = "PLA positive") %>%
  bind_rows(pla_negative.long %>% mutate(title = "PLA negative")) %>%
  ggplot(aes(x=distance, y=expression, color=genotype)) +
  geom_point(alpha=0.5) +
  geom_smooth() +
  scale_color_manual(values = line_colors[c(1,3,2)]) +
  theme(legend.position = "bottom") +
  facet_grid(cols = vars(title))

```

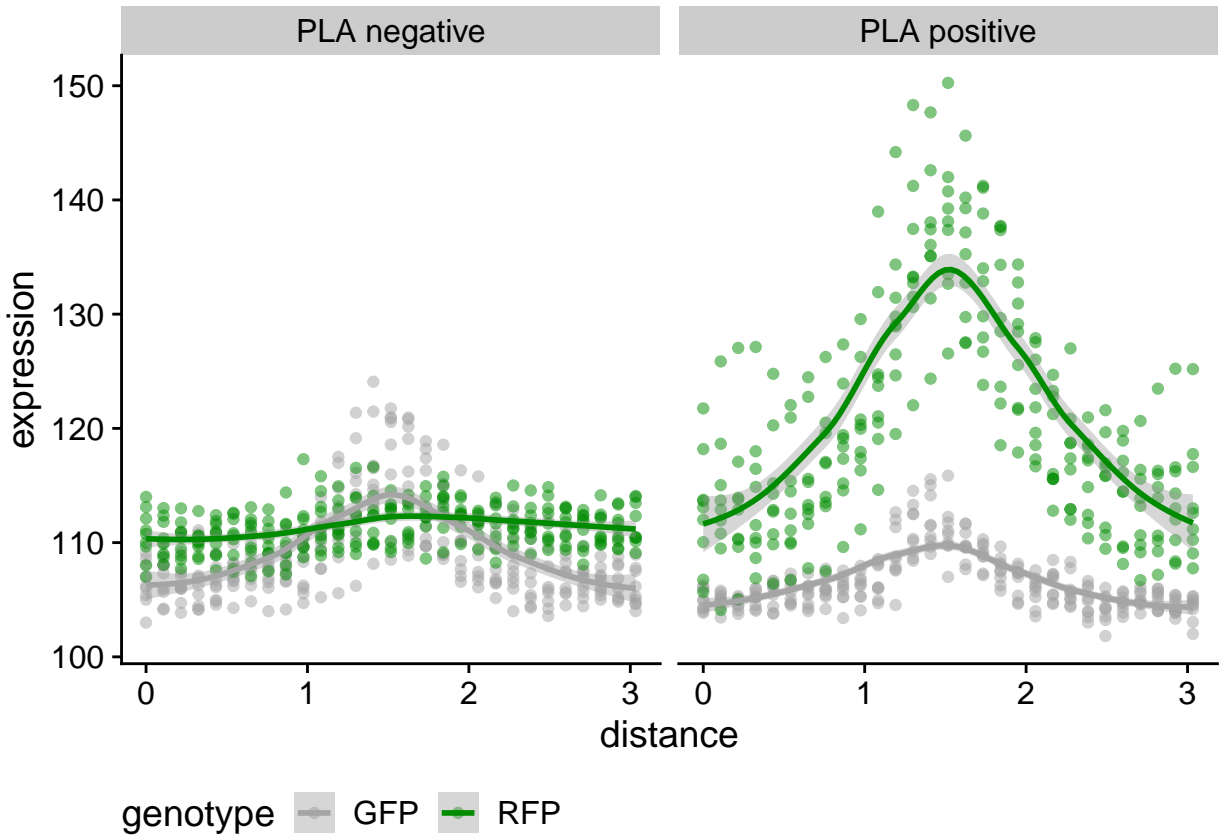


Figure 4b

Prepare data

```
fz3_intestine_control <- read_excel("Fz3 quantification along intestine myots.xlsx", range = "G10:L6139")

old_names <- colnames(fz3_intestine_control)

fz3_intestine_control.long <- fz3_intestine_control %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  mutate(gut = 1) %>%
  pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
  mutate(genotype = "control") %>%
  relocate(genotype)

fz3_intestine_dcr_apc <- read_excel("Fz3 quantification along intestine myots.xlsx", range = "O10:T6102")

old_names <- colnames(fz3_intestine_dcr_apc)

fz3_intestine_dcr_apc.long <- fz3_intestine_dcr_apc %>%
  rename_at(vars(old_names), function(x) new_names) %>%
  mutate(gut = 1) %>%
```

```

pivot_longer(cols = !gut, cols_vary = "slowest", names_to = c(".value", "cell"), names_pattern = "(.*)")
mutate(genotype = "dcr, APC RNAi") %>%
relocate(genotype)

fz3_intestine.long <- bind_rows(fz3_intestine_control.long , fz3_intestine_dcr_apc.long) %>%
  filter(!is.na(distance))

```

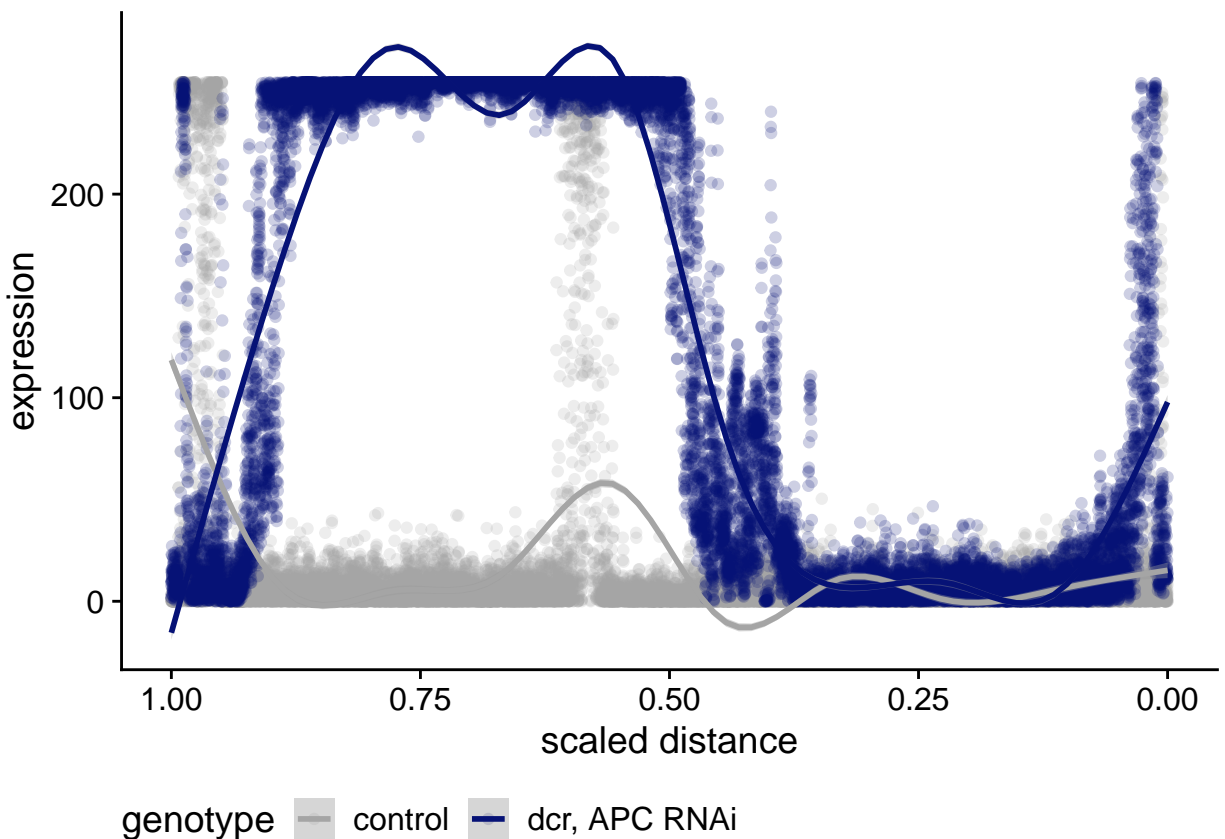
## Plot

```

fz3_intestine.long.scaled <- fz3_intestine.long %>%
  group_by(genotype, cell) %>%
  mutate(max_distance = max(distance)) %>%
  mutate(scaled_distance = distance/max_distance) %>%
  ungroup()

fz3_intestine.long.scaled %>%
  ggplot(aes(x=scaled_distance, y=expression, color=genotype)) +
  geom_point(alpha=0.2) +
  geom_smooth() +
  scale_color_manual(values = line_colors[c(1,4)]) +
  xlab("scaled distance") +
  theme(legend.position = "bottom") +
  scale_x_reverse()

```





## Session info

```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: aarch64-apple-darwin20 (64-bit)
## Running under: macOS 14.2
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2-arm64/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] rstatix_0.7.2      gmodels_2.18.1.1  padr_0.6.2        ggrepel_0.9.3
## [5] readxl_1.4.2       viridis_0.6.3     viridisLite_0.4.2 cowplot_1.1.1
## [9] plotrix_3.8-2      lubridate_1.9.2   forcats_1.0.0     stringr_1.5.0
## [13] dplyr_1.1.2        purrr_1.0.1       readr_2.1.4       tidyr_1.3.0
## [17] tibble_3.2.1       ggplot2_3.4.2     tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.10      lattice_0.21-8    gtools_3.9.4      digest_0.6.31
## [5] utf8_1.2.3       R6_2.5.1          cellranger_1.1.0  backports_1.4.1
## [9] evaluate_0.21    highr_0.10        pillar_1.9.0      rlang_1.1.1
## [13] rematch_1.0.1    rstudioapi_0.14   gdata_2.19.0      car_3.1-2
## [17] Matrix_1.5-4.1   rmarkdown_2.22    labeling_0.4.2     splines_4.2.2
## [21] munsell_0.5.0    broom_1.0.5        compiler_4.2.2     xfun_0.39
## [25] pkgconfig_2.0.3  mgcv_1.8-42       htmltools_0.5.5    tidyselect_1.2.0
## [29] gridExtra_2.3     codetools_0.2-19  fansi_1.0.4        tzdb_0.4.0
## [33] withr_2.5.0      MASS_7.3-60       grid_4.2.2         nlme_3.1-162
## [37] gtable_0.3.3     lifecycle_1.0.3   magrittr_2.0.3     scales_1.2.1
## [41] cli_3.6.1         stringi_1.7.12    carData_3.0-5      farver_2.1.1
## [45] generics_0.1.3    vctrs_0.6.2       tools_4.2.2        glue_1.6.2
## [49] hms_1.1.3         abind_1.4-5        fastmap_1.1.1      yaml_2.3.7
## [53] timechange_0.2.0  colorspace_2.1-0  knitr_1.43
```