

# HDAC inhibitor screen analysis

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## Overview

This vignette is used to analyze a CRISPR screen performed by treating SW480 cells using 3  $\mu$ M vorinostat in 0.1 % DMSO and 0.1 % DMSO as a control sample. It was screened in duplicates per treatment. Raw counts per sgRNA are the basis of the analysis.

All plots were used as given for the main figure panels. The compiled vignette pdf serves as an overview.

## Data input

```
treat1<-read_delim(file = "../raw_data_counts/counts_vorinostat_screen/Vorinostat1_S3_L001_R1_001.txt",
treat2<-read_delim(file = "../raw_data_counts/counts_vorinostat_screen/Vorinostat2_S4_L001_R1_001.txt",

dms01<-read_delim(file = "../raw_data_counts/counts_vorinostat_screen/DMS01_S1_L001_R1_001.txt",delim =
dms02<-read_delim(file = "../raw_data_counts/counts_vorinostat_screen/DMS02_S2_L001_R1_001.txt",delim =

mydata<-treat1 %>%
  left_join(treat2) %>%
  left_join(dms01) %>%
  left_join(dms02) %>%
  extract(sgRNA,c("sgRNA","gene_id"),"((\\w+)_.*)") %>%
  gather(treatment,count,-sgRNA,-gene_id) %>%
  extract(treatment,c("treatment","replicate"),"((\\w+)_ (\\d))")

anno<-read_delim("../meta_data/gene_names.txt",delim="\t")
```

## Lets normalize the data

```
mydata %<>%
  mutate(count=if_else(count>10,count,NA_real_)) %>%      #filter low read counts
  group_by(treatment,replicate) %>% #group by treatment and replicate
  mutate(normval=asinh(count/median(count,na.rm = T)))
```

## Lets do some data QC

### sgRNA-level replicate correlations

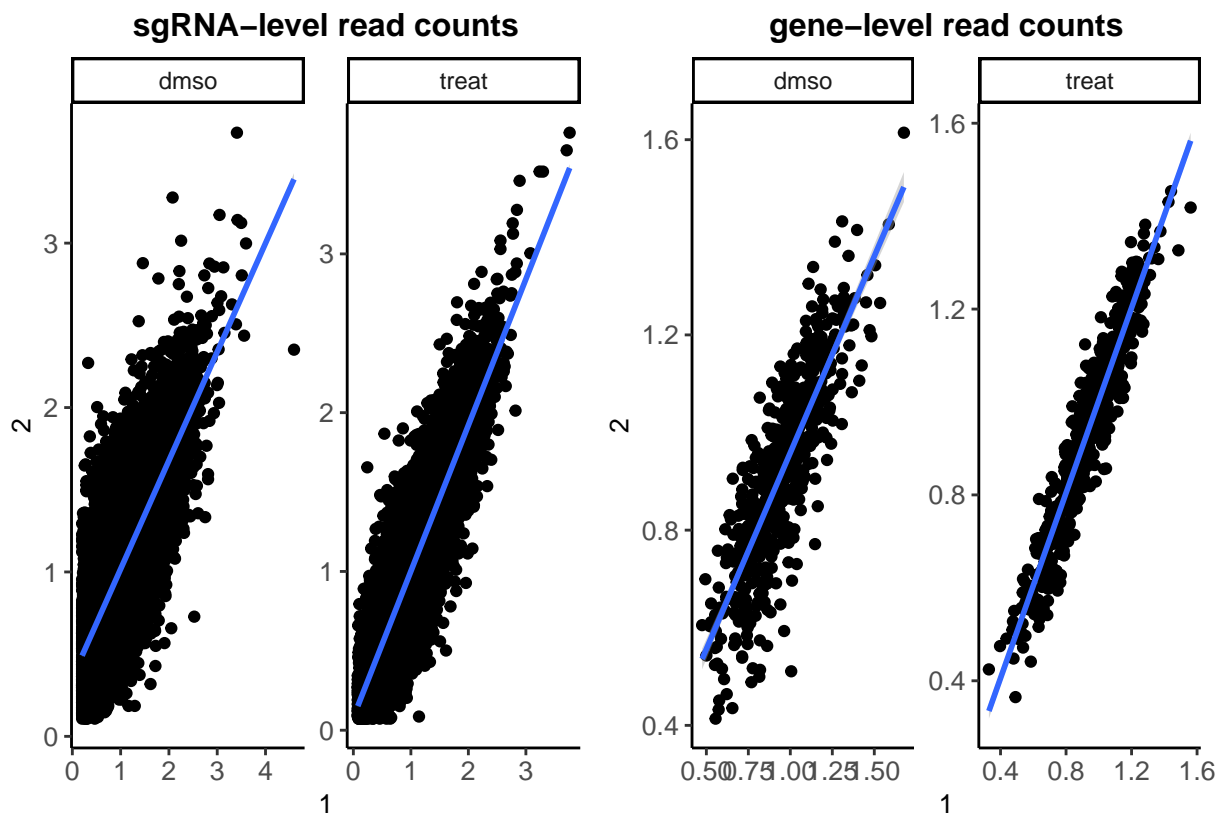
```
## $dms0
```

```
##   rowname  X1 X2
## 1      1
## 2      2 .78
##
## $treat
##   rowname  X1 X2
## 1      1
## 2      2 .89
```

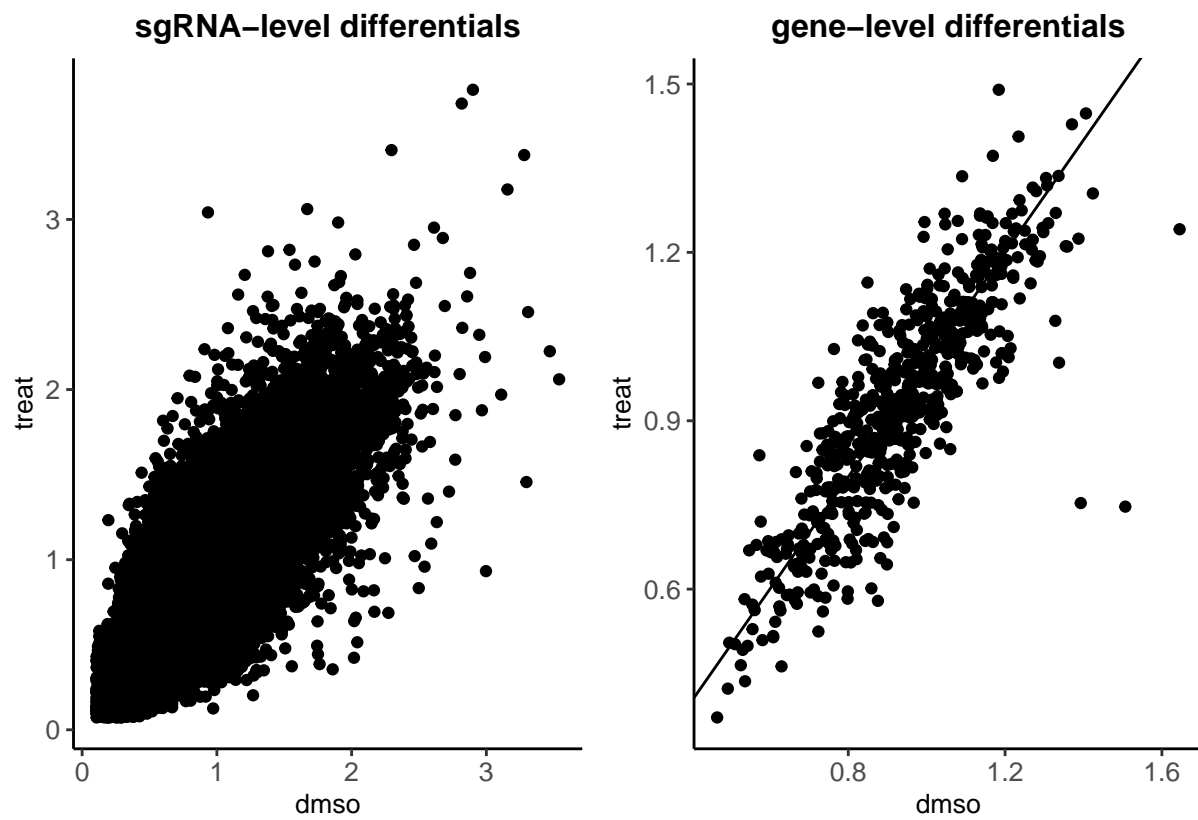
## gene-level replicate correlations

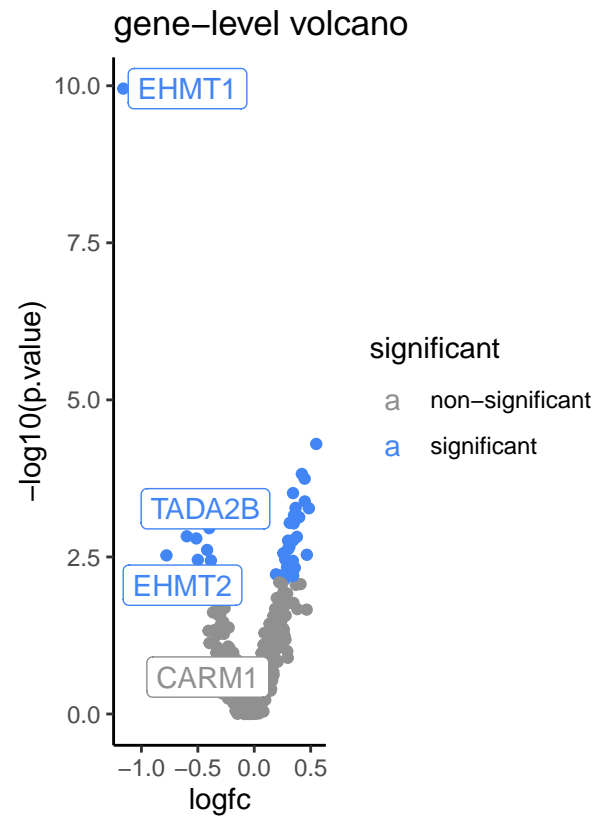
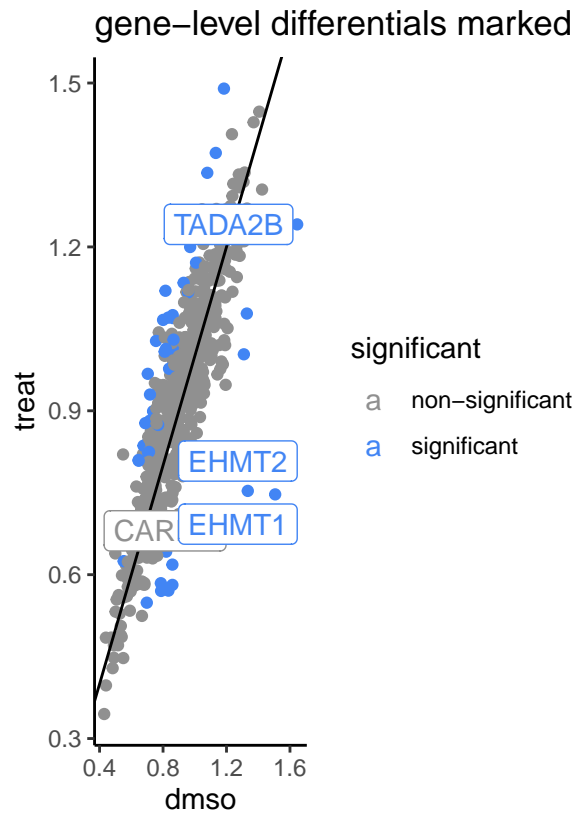
```
## $dms0
##   rowname  X1 X2
## 1      1
## 2      2 .84
##
## $treat
##   rowname  X1 X2
## 1      1
## 2      2 .95
```

## graphics

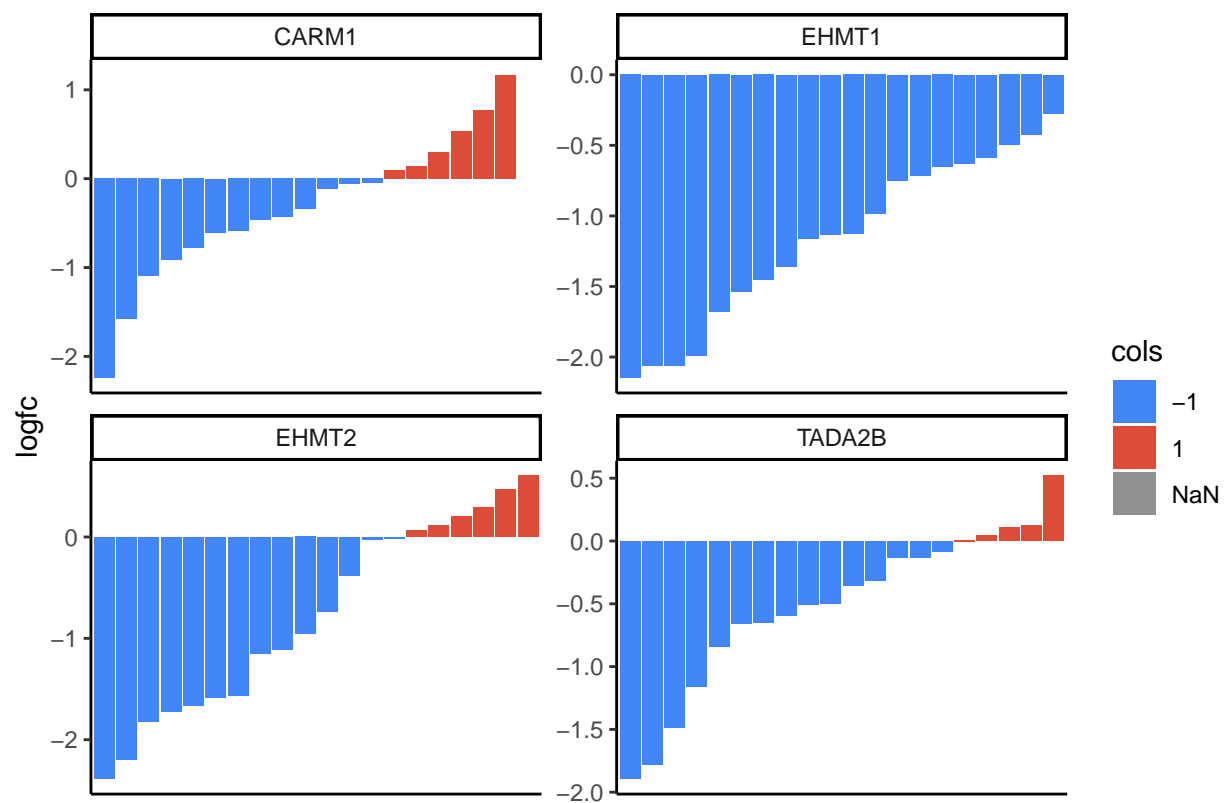


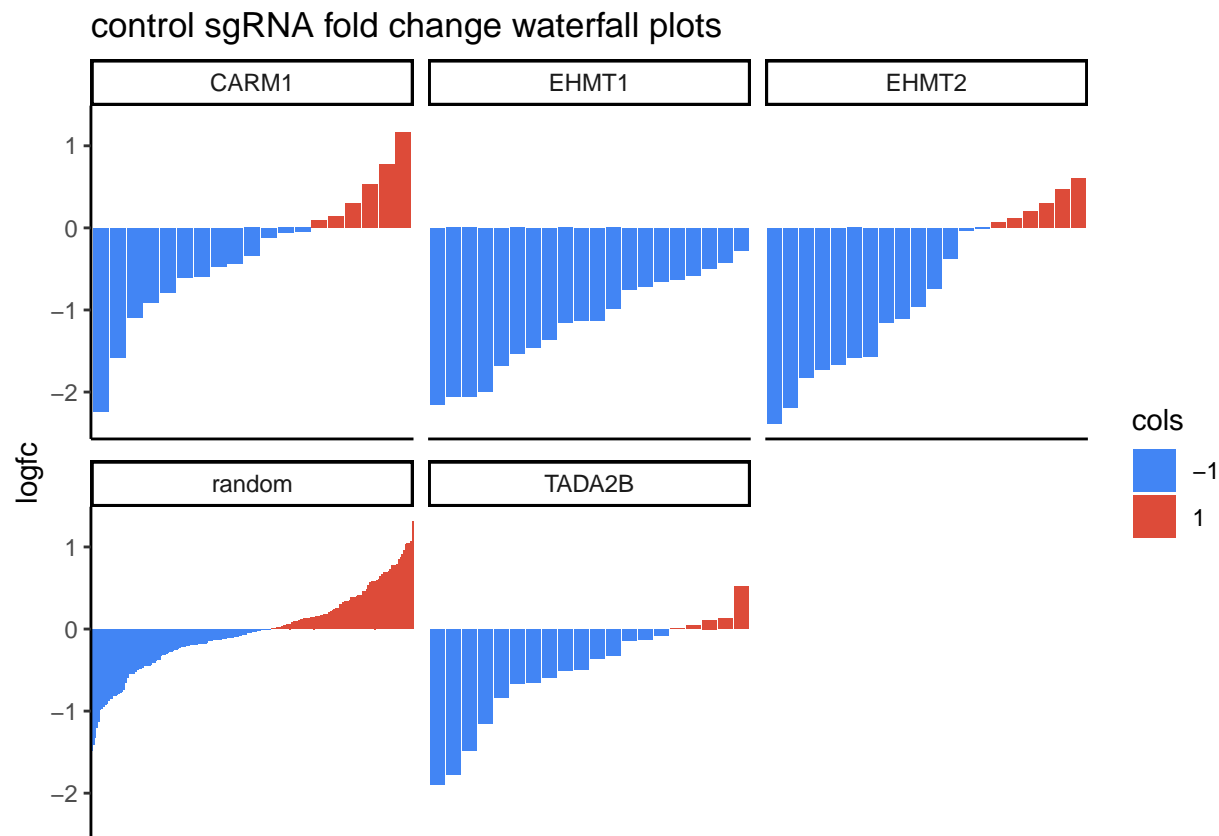
QC looks very nice and good so lets call some fold changes and hits thereof





candidate sgRNA fold change waterfall plots





## Session info

```
## R version 4.0.0 (2020-04-24)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19041)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=German_Germany.1252 LC_CTYPE=German_Germany.1252
## [3] LC_MONETARY=German_Germany.1252 LC_NUMERIC=C
## [5] LC_TIME=German_Germany.1252
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] patchwork_1.0.0 broom_0.5.6      ggrepel_0.8.2    ggrastr_0.2.3
## [5] corr_0.4.2      FitAR_1.94      bestglm_0.37.3   ltsa_1.4.6
## [9] leaps_3.1       lattice_0.20-41 readxl_1.3.1     forcats_0.5.0
## [13] stringr_1.4.0   dplyr_0.8.5     purrr_0.3.4      readr_1.3.1
## [17] tidyr_1.0.3     tibble_3.0.1    ggplot2_3.3.0    tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
```

```

## [1] httr_1.4.2      jsonlite_1.7.2  splines_4.0.0   foreach_1.5.1
## [5] modelr_0.1.7    assertthat_0.2.1 vipor_0.4.5     cellranger_1.1.0
## [9] yaml_2.2.1      pillar_1.4.4    backports_1.1.6 glue_1.4.1
## [13] digest_0.6.25   rvest_0.3.5     colorspace_1.4-1 htmltools_0.4.0
## [17] Matrix_1.2-18   pkgconfig_2.0.3 haven_2.2.0     scales_1.1.1
## [21] grpreg_3.3.0    mgcv_1.8-31     generics_0.1.0 farver_2.0.3
## [25] ellipsis_0.3.1  withr_2.4.1     cli_2.0.2       survival_3.1-12
## [29] magrittr_1.5     crayon_1.3.4    evaluate_0.14   fs_1.4.1
## [33] fansi_0.4.1     nlme_3.1-147    xml2_1.3.2      beeswarm_0.3.1
## [37] registry_0.5-1  tools_4.0.0     hms_0.5.3       lifecycle_1.0.0
## [41] munsell_0.5.0   reprex_0.3.0    glmnet_4.1-1    pls_2.7-3
## [45] compiler_4.0.0  rlang_0.4.10    grid_4.0.0      iterators_1.0.13
## [49] rstudioapi_0.11 labeling_0.3      rmarkdown_2.1   gtable_0.3.0
## [53] codetools_0.2-16 DBI_1.1.0        TSP_1.1-10      R6_2.4.1
## [57] seriation_1.2-9 lubridate_1.7.8 knitr_1.28       shape_1.4.5
## [61] stringi_1.4.6   ggbeeswarm_0.6.0 Rcpp_1.0.4.6     vctrs_0.3.0
## [65] dbplyr_1.4.3    tidysselect_1.1.0 xfun_0.13

```