

HDAC inhibitor screen analysis

F. Heigwer

8/17/2018

Overview

This vignette is used to analyze a CRISPR screen performed by treating SW480 cells using 3 μ 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

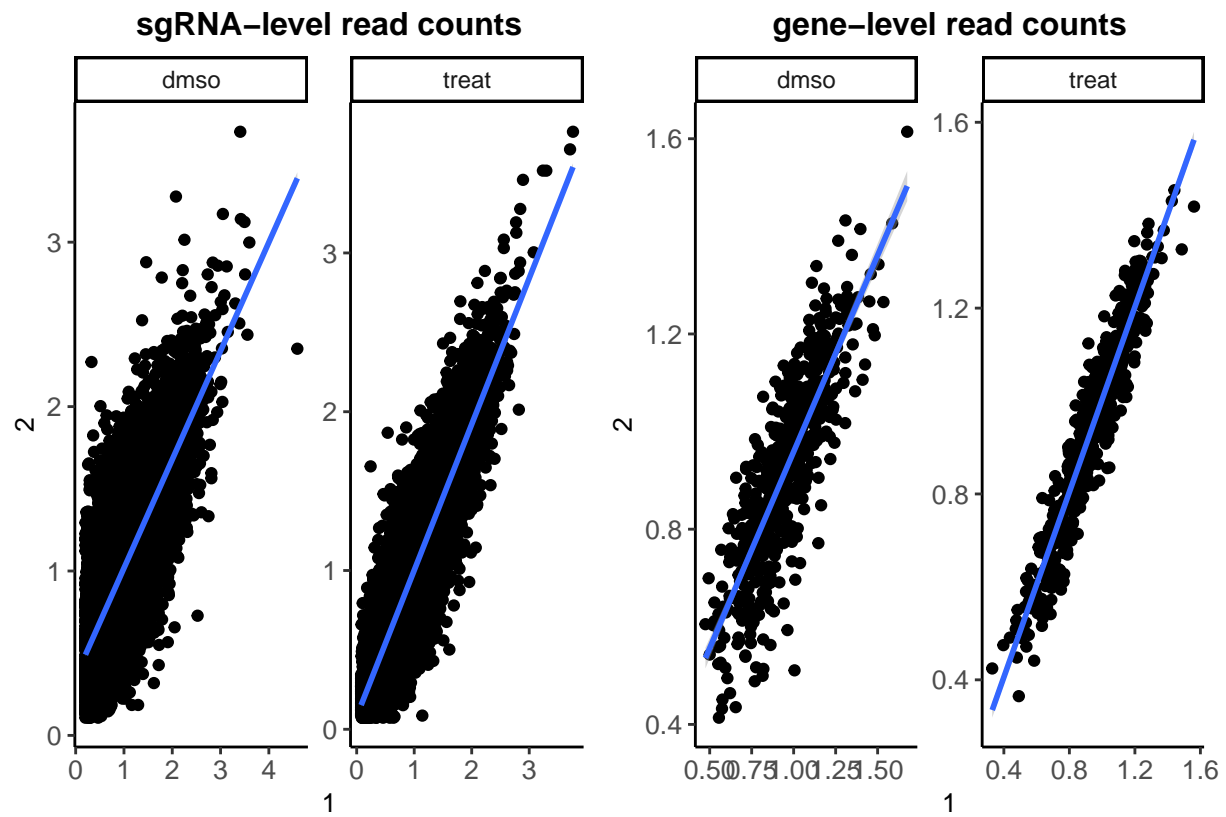
```
## $dms0
##   term    X1 X2
## 1      1
## 2      2  .78
##
```

```
## $treat
##   term   X1 X2
## 1     1
## 2     2 .89
```

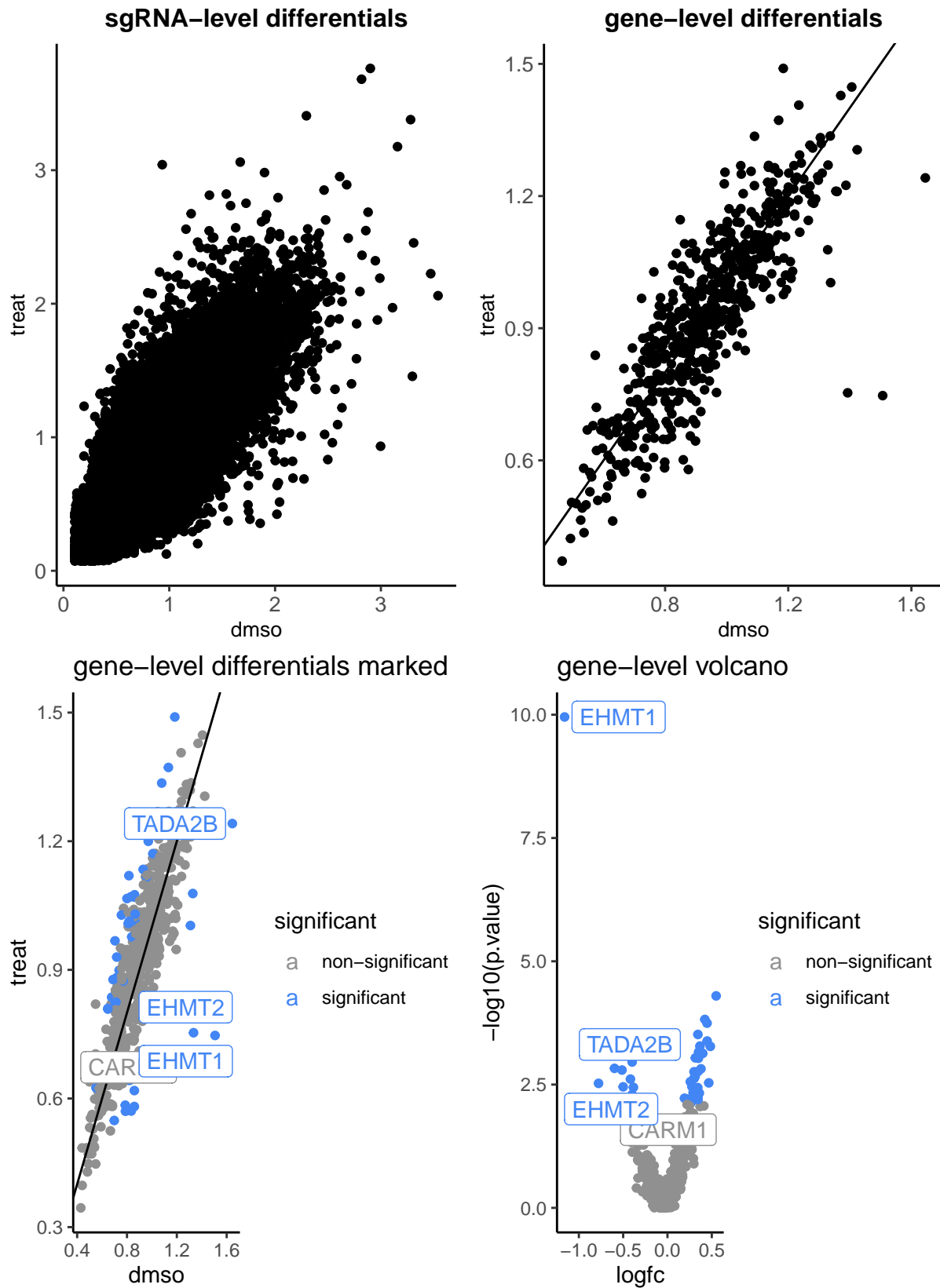
gene-level replicate correlations

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

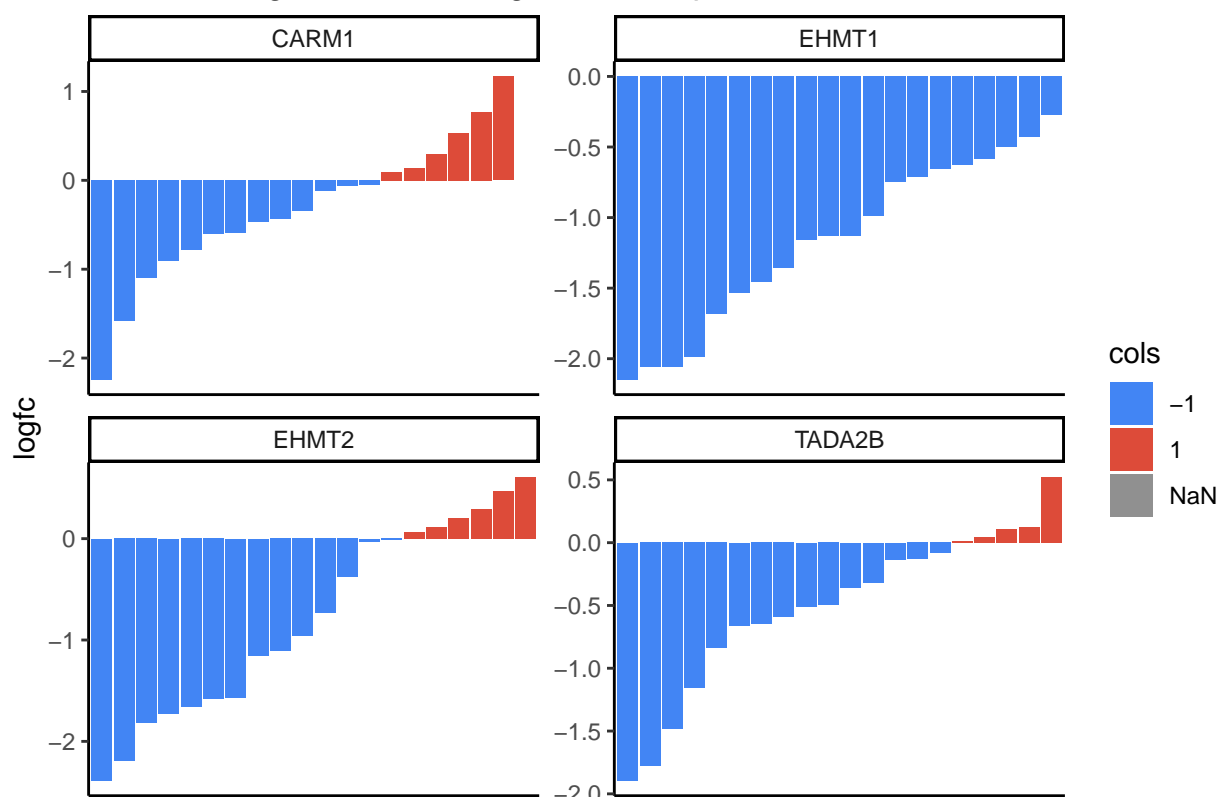
graphics



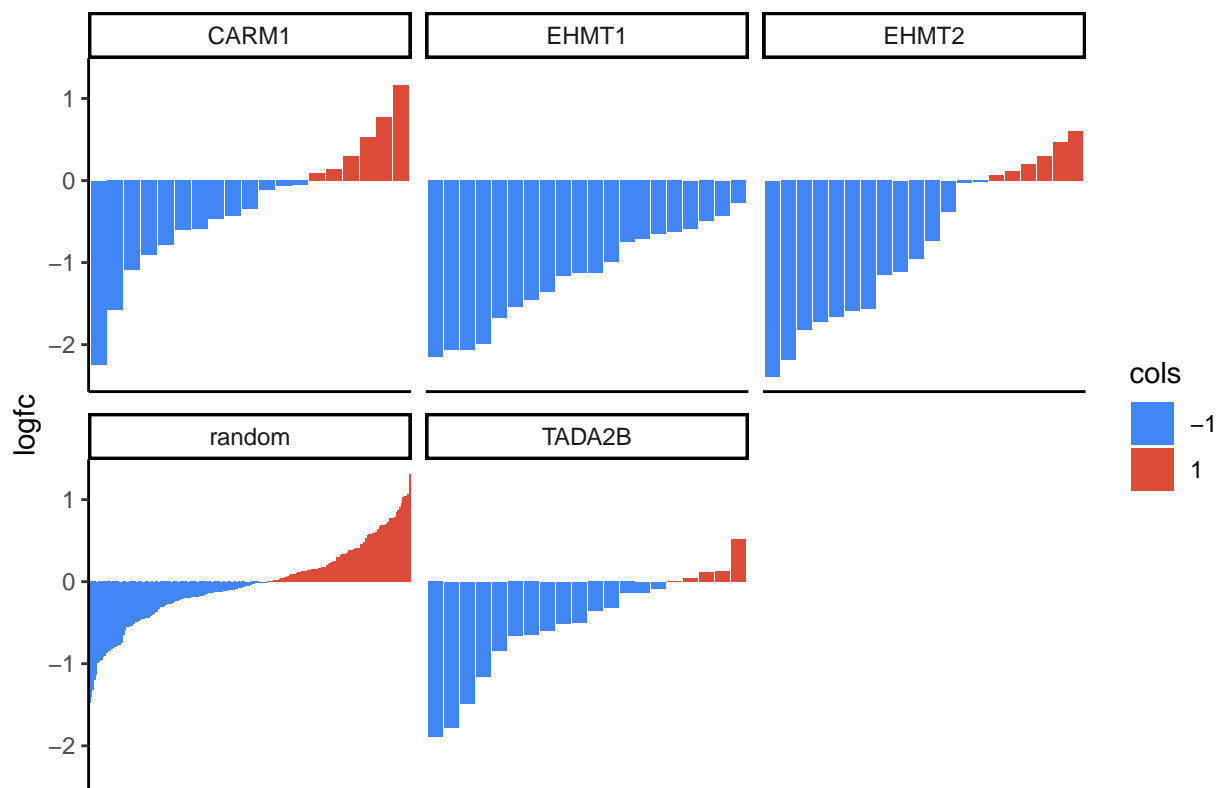
QC looks very nice and good so lets call some fold changes and hits thereof



candidate sgRNA fold change waterfall plots



control sgRNA fold change waterfall plots



Session info

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/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] patchwork_1.1.1 broom_0.7.6      ggrepel_0.9.1   ggrastr_0.2.3
## [5] corrr_0.4.3      FitAR_1.94       bestglm_0.37.3  ltsa_1.4.6
## [9] leaps_3.1        lattice_0.20-41 readxl_1.3.1     forcats_0.5.1
## [13] stringr_1.4.0    dplyr_1.0.5      purrr_0.3.4     readr_1.4.0
## [17] tidyr_1.1.3      tibble_3.1.0     ggplot2_3.3.3   tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.2          jsonlite_1.7.2     splines_4.0.3     foreach_1.5.1
## [5] modelr_0.1.8        assertthat_0.2.1   highr_0.8          vipor_0.4.5
## [9] cellranger_1.1.0    yaml_2.2.1         pillar_1.5.1       backports_1.2.1
## [13] glue_1.4.2          digest_0.6.27      rvest_1.0.0        colorspace_2.0-0
## [17] htmltools_0.5.1.1  Matrix_1.3-2       pkgconfig_2.0.3    haven_2.3.1
## [21] scales_1.1.1        grpreg_3.3.1       mgcv_1.8-34        generics_0.1.0
## [25] farver_2.1.0        ellipsis_0.3.1     withr_2.4.1        cli_2.4.0
## [29] survival_3.2-10     magrittr_2.0.1     crayon_1.4.1       evaluate_0.14
## [33] fs_1.5.0            fansi_0.4.2        nlme_3.1-152       xml2_1.3.2
## [37] beeswarm_0.3.1      registry_0.5-1     tools_4.0.3        hms_1.0.0
## [41] lifecycle_1.0.0     munsell_0.5.0      reprex_2.0.0        glmnet_4.1-1
## [45] pls_2.7-3           compiler_4.0.3     rlang_0.4.10       grid_4.0.3
## [49] iterators_1.0.13    rstudioapi_0.13    labeling_0.4.2     rmarkdown_2.7
## [53] gtable_0.3.0        codetools_0.2-18   DBI_1.1.1          TSP_1.1-10
## [57] R6_2.5.0            seriation_1.2-9    lubridate_1.7.10   knitr_1.31
## [61] utf8_1.2.1          shape_1.4.5        stringi_1.5.3      ggbeeswarm_0.6.0
## [65] Rcpp_1.0.6          vctrs_0.3.7        dbplyr_2.1.0       tidyselect_1.1.0
## [69] xfun_0.22
```