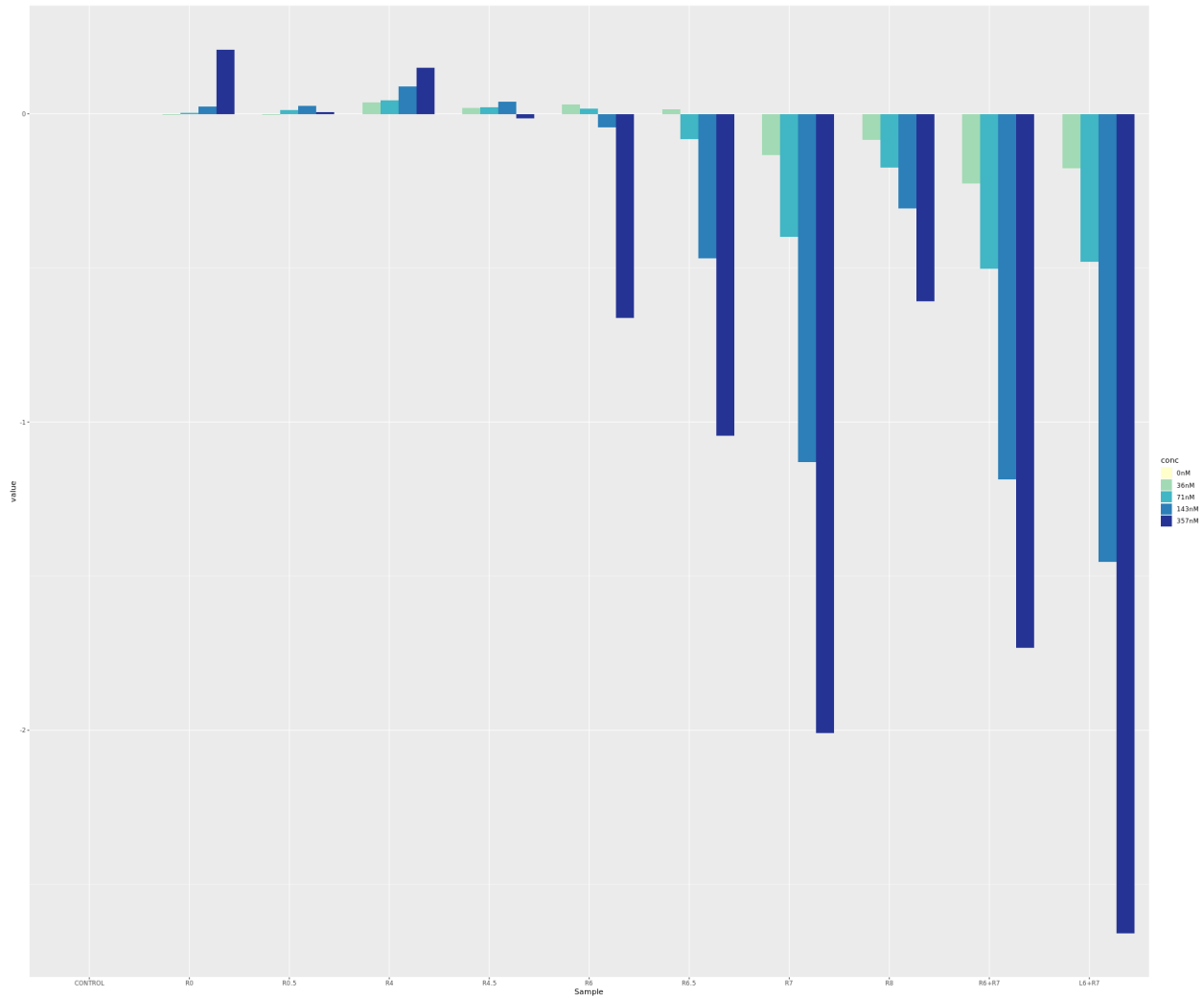


Annotate the clusters based on MCC correlation and manual identification with markers and replot TSNE projection

Project: Promoter Opening

Author: Vivek

Generated: Sun Feb 28 2021, 08:32 PM



Session information

For reproducibility, this analysis was performed with the following R/Bioconductor session:

R version 3.6.1 (2019-07-05)

Platform: x86_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 18.04.2 LTS

Matrix products: default

BLAS: /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.7.1

LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.7.1

```

locale:
[1] LC_CTYPE=C.UTF-8      LC_NUMERIC=C          LC_TIME=C.UTF-8
[4] LC_COLLATE=C.UTF-8    LC_MONETARY=C.UTF-8   LC_MESSAGES=C.UTF-8
[7] LC_PAPER=C.UTF-8      LC_NAME=C             LC_ADDRESS=C
[10] LC_TELEPHONE=C        LC_MEASUREMENT=C.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods    base

other attached packages:
[1] ggplot2_3.2.1      RColorBrewer_1.1-2  magrittr_1.5        dplyr_0.8.3
[5] tidyr_1.0.0        cowplot_1.0.0       pander_0.6.3

loaded via a namespace (and not attached):
[1] Rcpp_1.0.5          pillar_1.4.2        compiler_3.6.1      tools_3.6.1
[5] zeallot_0.1.0       digest_0.6.20       evaluate_0.14       tibble_2.1.3
[9] lifecycle_0.1.0     gtable_0.3.0        pkgconfig_2.0.2     rlang_0.4.0
[13] yaml_2.2.0          xfun_0.21           withr_2.1.2         stringr_1.4.0
[17] knitr_1.24          vctrs_0.2.0         grid_3.6.1          tidyselect_0.2.5
[21] glue_1.3.1          R6_2.4.0            rmarkdown_2.7       purrr_0.3.2
[25] ellipsis_0.2.0.1    scales_1.0.0        backports_1.1.4     htmltools_0.3.6
[29] assertthat_0.2.1    colorspace_1.4-1    labeling_0.3         stringi_1.4.3
[33] lazyeval_0.2.2      munsell_0.5.0       crayon_1.3.4        Cairo_1.5-10

```