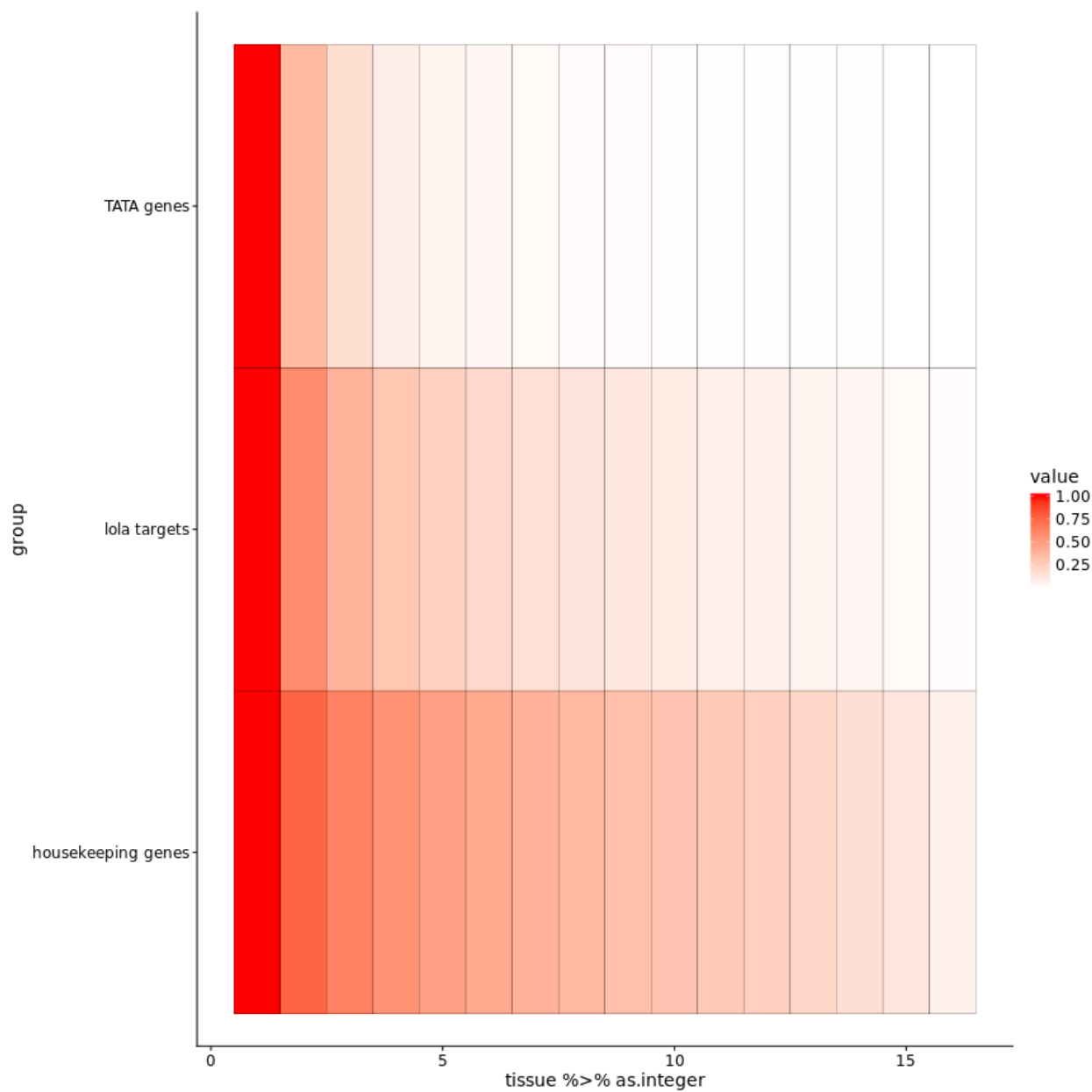**Project:** Promoter Opening

Author: Vivek

Generated: Sun Feb 28 2021, 08:42 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] grid       stats4    parallel  stats     graphics  grDevices utils
 [8] datasets   methods    base

other attached packages:
 [1] pander_0.6.3
 [2] cowplot_1.0.0
 [3] ggplot2_3.2.1
 [4] tidyr_1.0.0
 [5] Gviz_1.28.1
 [6] dplyr_0.8.3
 [7] magrittr_1.5
 [8] BSgenome.Dmelanogaster.UCSC.dm6_1.4.1
 [9] BSgenome_1.52.0
[10] rtracklayer_1.44.4
[11] Biostrings_2.52.0
[12] XVector_0.24.0
[13] TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.6
[14] GenomicFeatures_1.36.4
[15] AnnotationDbi_1.46.1
[16] Biobase_2.44.0
[17] GenomicRanges_1.36.1
[18] GenomeInfoDb_1.20.0
[19] IRanges_2.18.2
[20] S4Vectors_0.22.1
[21] BiocGenerics_0.30.0

loaded via a namespace (and not attached):
 [1] ProtGenerics_1.16.0      bitops_1.0-6
 [3] matrixStats_0.55.0       bit64_0.9-7
 [5] RColorBrewer_1.1-2       progress_1.2.2
 [7] httr_1.4.1               tools_3.6.1
 [9] backports_1.1.4          R6_2.4.0
[11] rpart_4.1-15             Hmisc_4.2-0
[13] DBI_1.0.0                lazyeval_0.2.2
[15] colorspace_1.4-1         nnet_7.3-12
[17] withr_2.1.2              tidyselect_0.2.5
[19] gridExtra_2.3            prettyunits_1.0.2
[21] curl_4.0                 bit_1.1-14
[23] compiler_3.6.1           htmlTable_1.13.1
[25] DelayedArray_0.10.0      labeling_0.3
[27] scales_1.0.0             checkmate_1.9.4
```

```
[29] stringr_1.4.0                   digest_0.6.20
[31] Rsamtools_2.0.0                 foreign_0.8-72
[33] rmarkdown_2.7                   base64enc_0.1-3
[35] dichromat_2.0-0                 pkgconfig_2.0.2
[37] htmltools_0.3.6                 ensembldb_2.8.0
[39] htmlwidgets_1.3                 rlang_0.4.0
[41] rstudioapi_0.10                 RSQLite_2.1.2
[43] BiocParallel_1.18.1            acepack_1.4.1
[45] VariantAnnotation_1.30.1       RCurl_1.95-4.12
[47] GenomeInfoDbData_1.2.1         Formula_1.2-3
[49] Matrix_1.2-17                  Rcpp_1.0.5
[51] munsell_0.5.0                  lifecycle_0.1.0
[53] stringi_1.4.3                  yaml_2.2.0
[55] SummarizedExperiment_1.14.1 zlibbioc_1.30.0
[57] blob_1.2.0                     crayon_1.3.4
[59] lattice_0.20-38                splines_3.6.1
[61] hms_0.5.1                      zeallot_0.1.0
[63] knitr_1.24                     pillar_1.4.2
[65] biomaRt_2.40.4                 XML_3.98-1.20
[67] glue_1.3.1                     evaluate_0.14
[69] biovizBase_1.32.0              latticeExtra_0.6-28
[71] data.table_1.12.2             vctrs_0.2.0
[73] gtable_0.3.0                   purrr_0.3.2
[75] assertthat_0.2.1              xfun_0.21
[77] AnnotationFilter_1.8.0        survival_2.44-1.1
[79] tibble_2.1.3                   GenomicAlignments_1.20.1
[81] memoise_1.1.0                  cluster_2.1.0
[83] ellipsis_0.2.0.1
```