

Figure S3 Paused Pol II stability at eight *Drosophila pseudoobscura* promoters

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Description

To test the stability of paused Pol II in *Drosophila pseudoobscura* ML83-63 cells, we performed Pol II ChIP-nexus under control and Triptolide (TRI) teated conditions. TRI blocks transcription initiation and results in the loss of Pol II signal at the pausing position. The degree of Pol II signal loss is propotional to the stability of paused Pol II.

Enviroment setup

```
library(GenomicRanges, warn.conflicts=F)
library(magrittr)

setwd("/data/analysis_code")
options(knitr.figure_dir =
  "FigureS3_paused_polii_stability_at_eight_drosophila_pseudoobscura_promoters"
)

source("shared_code/knitr_common.r")
source("shared_code/ggplot_common.r")
source("shared_code/granges_common.r")
source("shared_code/metapeak_common.r")
source("shared_code/sample_common.r")
```

Analysis

Paused Pol II stability

```
plasmid_annotations <- import("./plasmid_annotation.bed")
genome_annotations <- import("./dps_genome_annotation.bed")
```

```

dps_dmso_path <- load_bigwig("genome_dps_dmso_1h_rpb3_chipnexus")
dps_tri_path <- load_bigwig("genome_dps_triptolide_1h_rpb3_chipnexus")

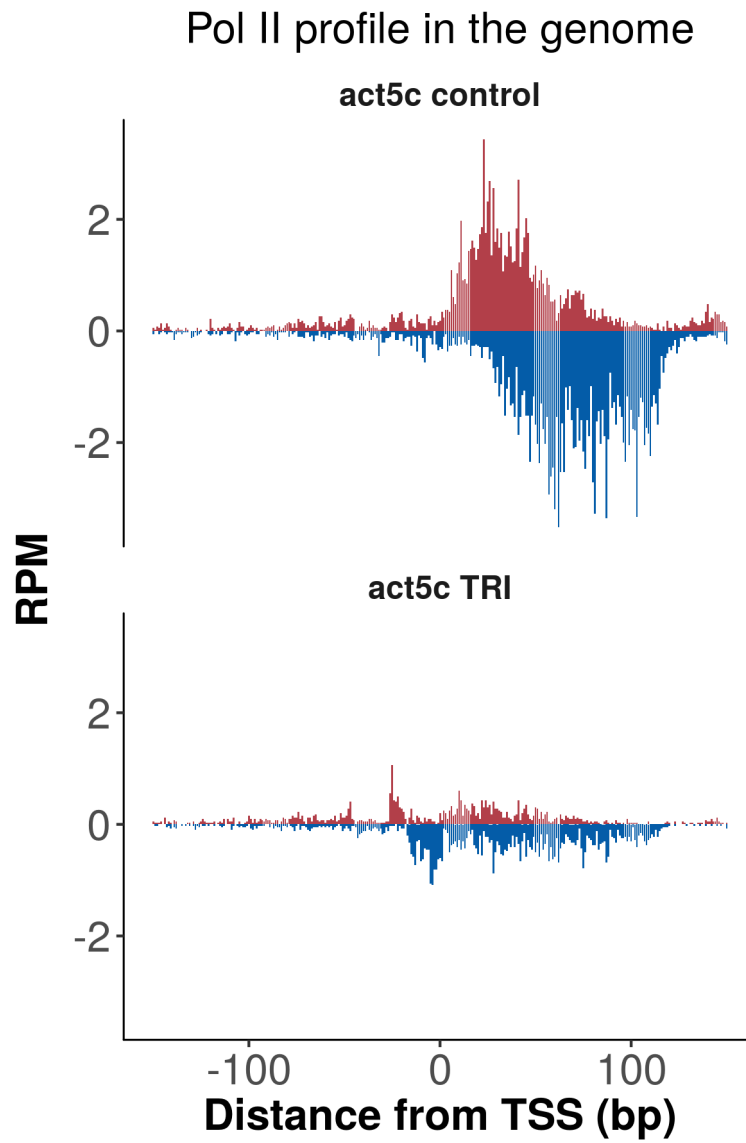
combine_dmso_and_tri <- function(gr, sample_dmso_path, sample_tri_path){
  dmso_metapeak <- exo_metapeak(gr, sample_dmso_path,
                                upstream = 150, downstream = 151,
                                sample_name = paste(gr$name, "control"))
  tri_metapeak <- exo_metapeak(gr, sample_tri_path,
                                upstream = 150, downstream = 151,
                                sample_name = paste(gr$name, "TRI"))

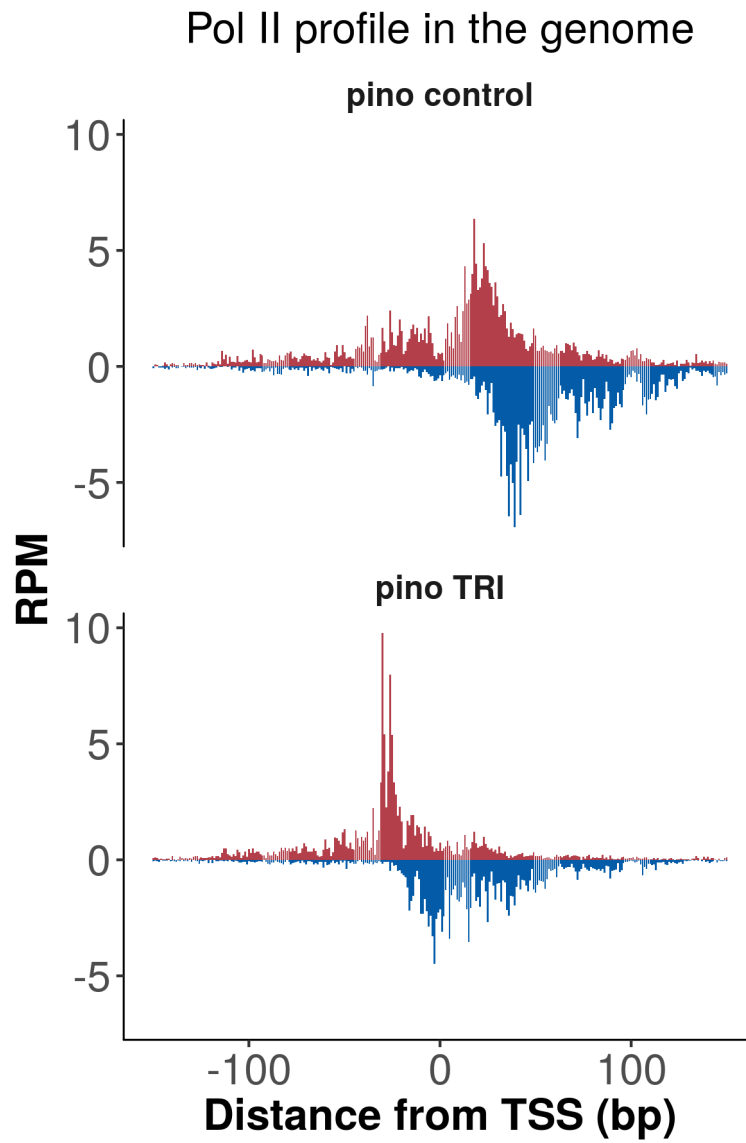
  metapeak <- rbind(dmso_metapeak, tri_metapeak)
  x <- ggplot(subset(metapeak, strand == "+"),
              aes(x = tss_distance, y = reads,
                  fill = strand))+
    geom_bar(fill="#B23F49", stat="identity") +
    geom_bar(data=subset(metapeak, strand == "-"),
              aes(x=tss_distance, y=reads),
              fill="#045CA8", stat="identity")+
    ggtitle("Pol II profile in the genome") +
    xlab("Distance from TSS (bp)") +
    ylab("RPM") +
    facet_wrap(facets = "sample_name", ncol =1 )

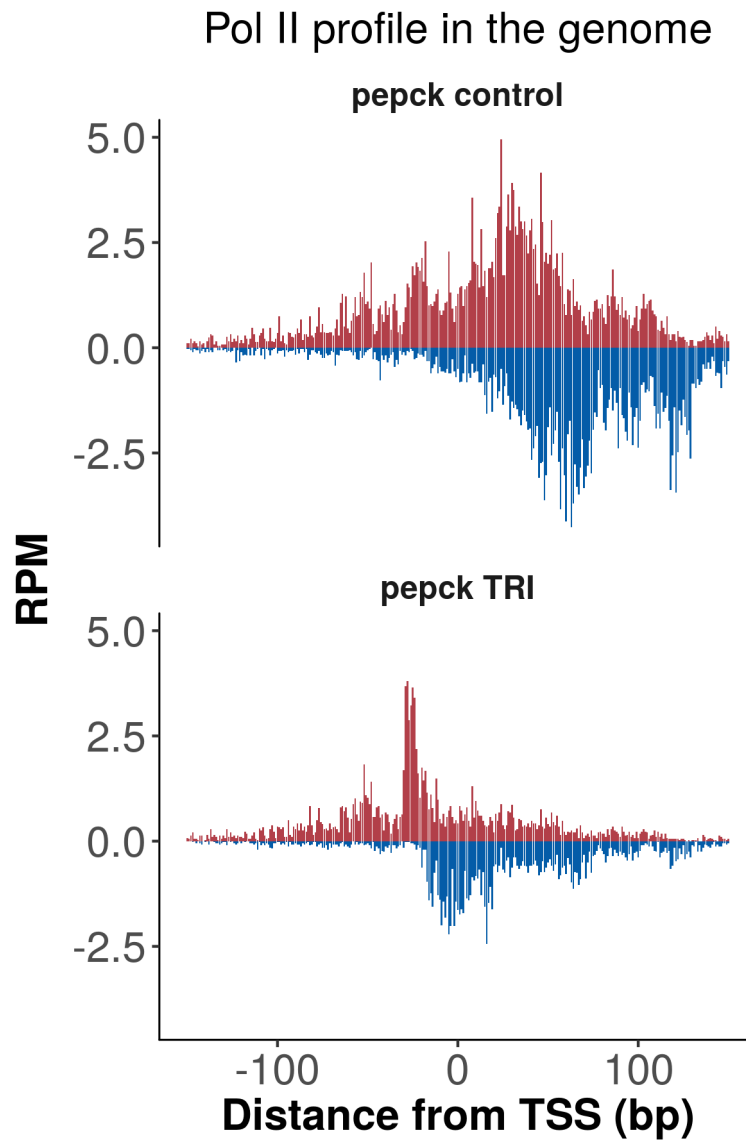
  print(x)
}

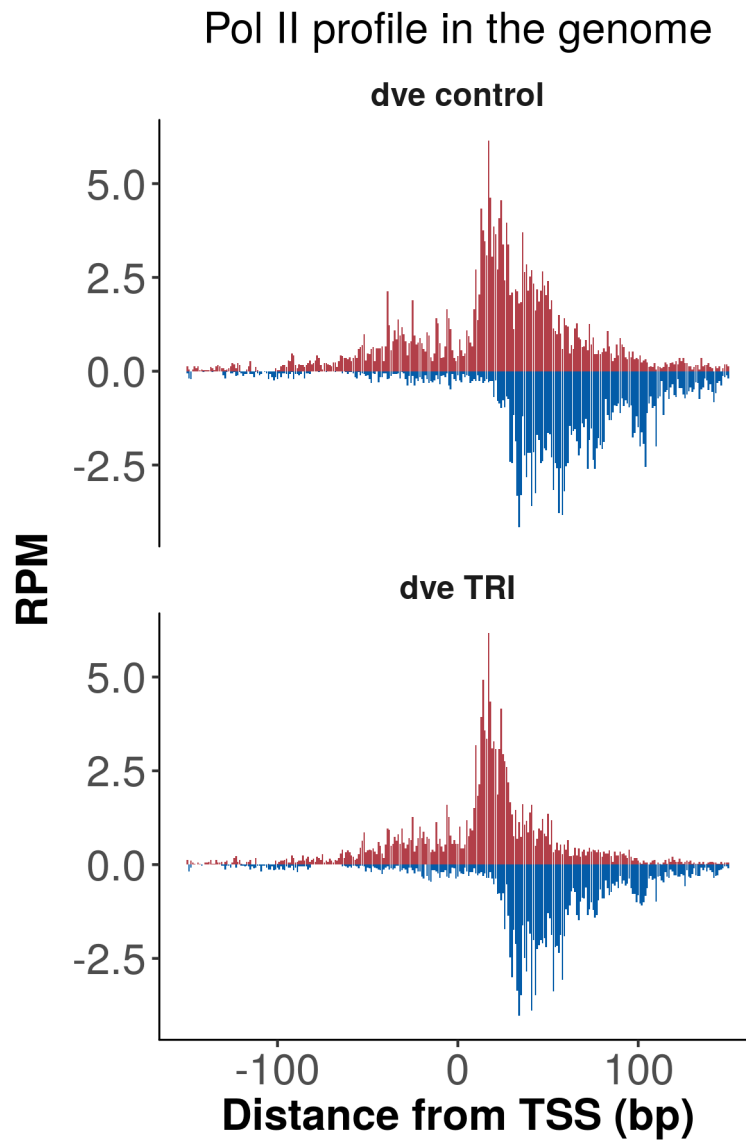
nothing <- lapply(genome_annotations, function(x){
  combine_dmso_and_tri(x, dps_dmso_path, dps_tri_path)
})

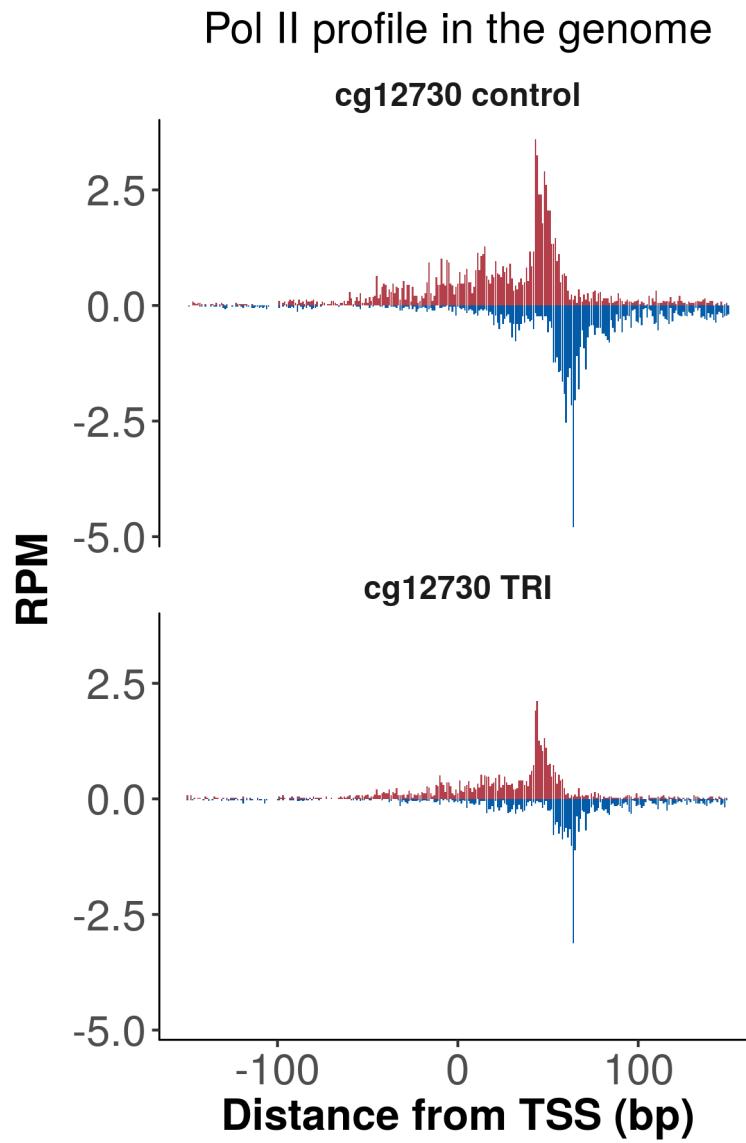
```

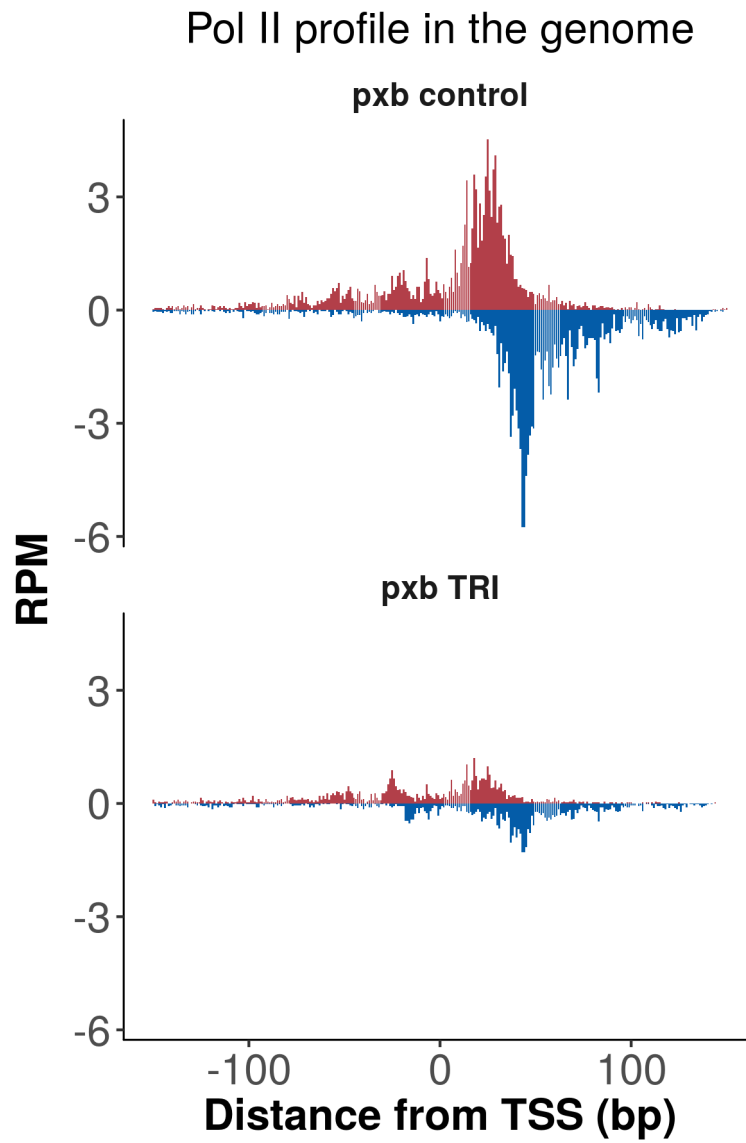


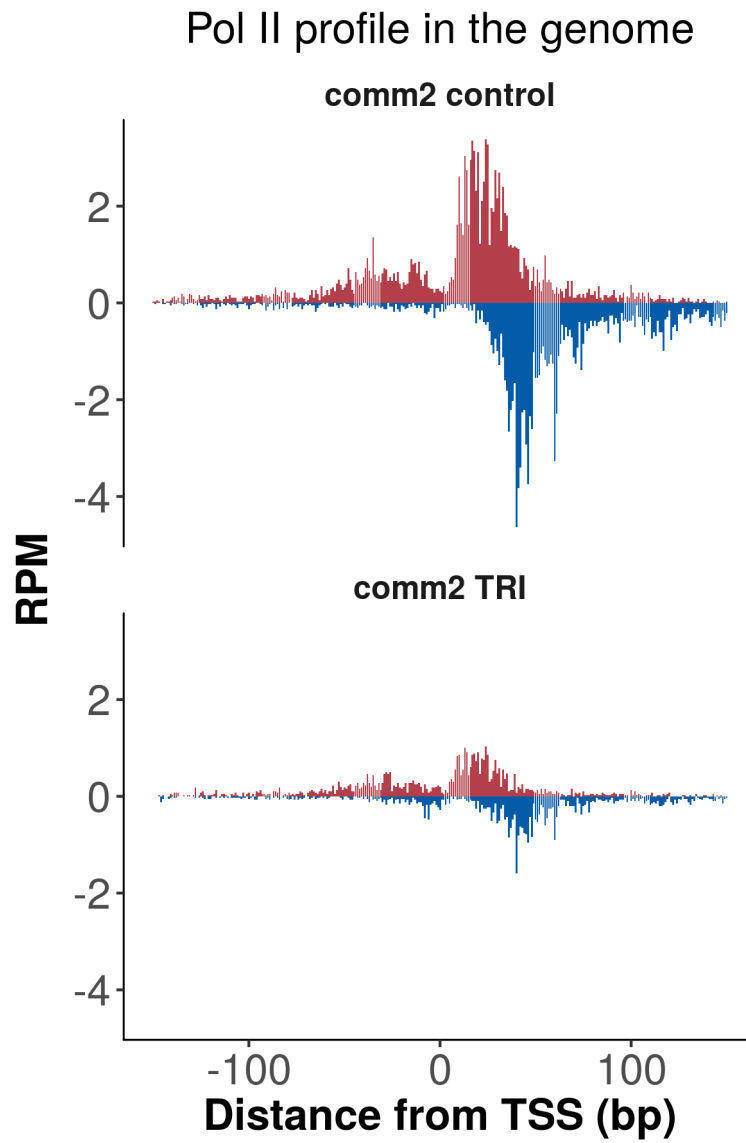


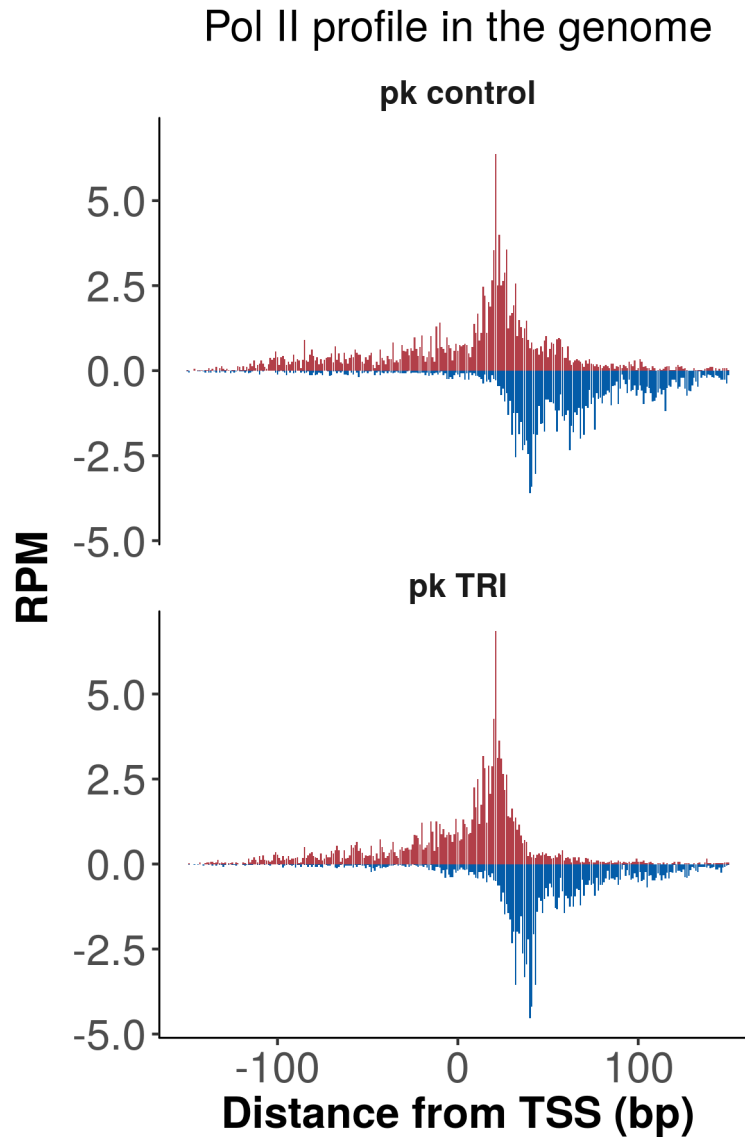












Session Info

This analysis was performed with the following R/Bioconductor session:

```
sessionInfo()
```

```
## R version 3.4.4 (2018-03-15)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
```

```

## [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=en_US.UTF-8     LC_NAME=C
## [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4      stats      graphics  grDevices  utils      datasets
## [8] methods    base
##
## other attached packages:
## [1] lattice_0.20-35      reshape2_1.4.3      rtracklayer_1.38.3
## [4] ggplot2_2.2.1        pander_0.6.1        magrittr_1.5
## [7] GenomicRanges_1.30.3 GenomeInfoDb_1.14.0 IRanges_2.12.0
## [10] S4Vectors_0.16.0     BiocGenerics_0.24.0
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.17          compiler_3.4.4
## [3] pillar_1.2.3          plyr_1.8.4
## [5] XVector_0.18.0        bitops_1.0-6
## [7] tools_3.4.4           zlibbioc_1.24.0
## [9] digest_0.6.15         evaluate_0.10.1
## [11] tibble_1.4.2          gtable_0.2.0
## [13] rlang_0.2.1           Matrix_1.2-14
## [15] DelayedArray_0.4.1    yaml_2.1.19
## [17] GenomeInfoDbData_1.0.0 stringr_1.3.1
## [19] knitr_1.20            Biostrings_2.46.0
## [21] rprojroot_1.3-2       grid_3.4.4
## [23] Biobase_2.38.0        XML_3.98-1.11
## [25] BiocParallel_1.12.0   rmarkdown_1.10
## [27] matrixStats_0.53.1    backports_1.1.2
## [29] scales_0.5.0          Rsamtools_1.30.0
## [31] htmltools_0.3.6       GenomicAlignments_1.14.2
## [33] SummarizedExperiment_1.8.1 colorspace_1.3-2
## [35] labeling_0.3          stringi_1.2.3
## [37] RCurl_1.95-4.10       lazyeval_0.2.1
## [39] munsell_0.5.0

```