Figure 3 and S7 changes in downstream promoter sequence alter polii pausing

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Contents

Description

This set of experiments is aimed at testing whether reporter-ChIP-nexus can detect changes in Pol II pausing after manipulating promoter sequences. To do this, we focused on downstream promoter sequences, as accumulating evidence suggests that downstream DNA influences Pol II pausing. We took two TATA promoters *Act5C* and *pepck*, and changed its downstream sequence to that of a pausing promoter *pk* or *dve*. Changes in paused Pol II stability were probed by performing Pol II ChIP-nexus at control and Triptolide (TRI) treated conditions.

Enviroment setup

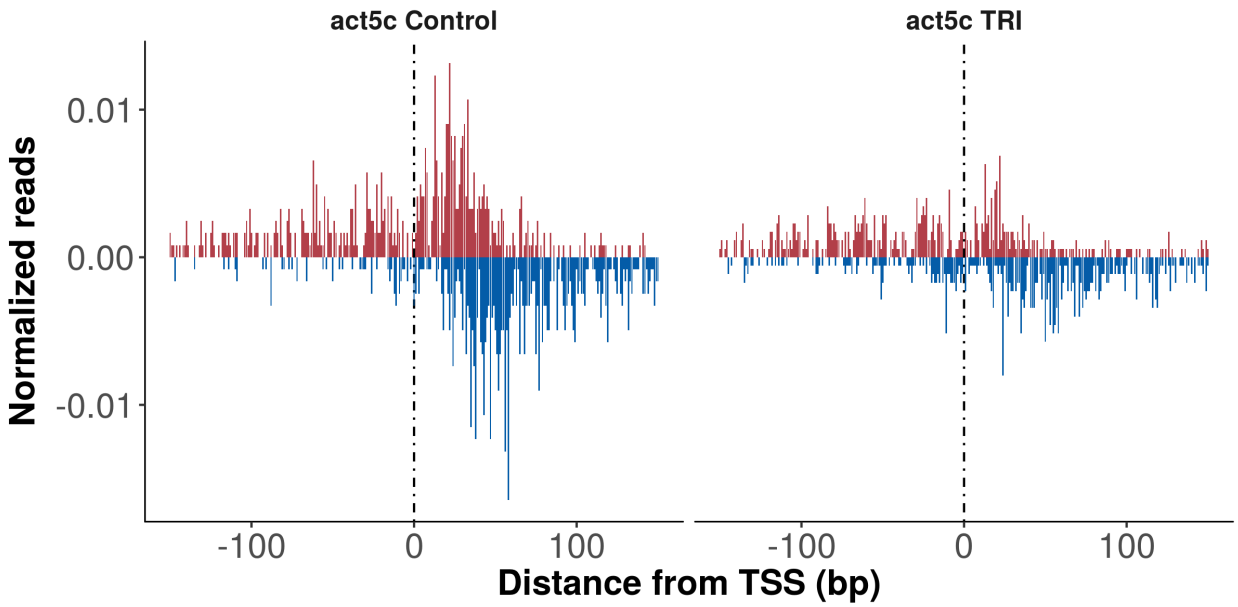
```
library(GenomicRanges, warn.conflicts=F)
library(magrittr)
library(Rmisc)

setwd("/data/analysis_code")
options(knitr.figure_dir =
          "Figure3_S7_changes_in_downstream_promoter_sequence_alter_polii_pausing")

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")
```

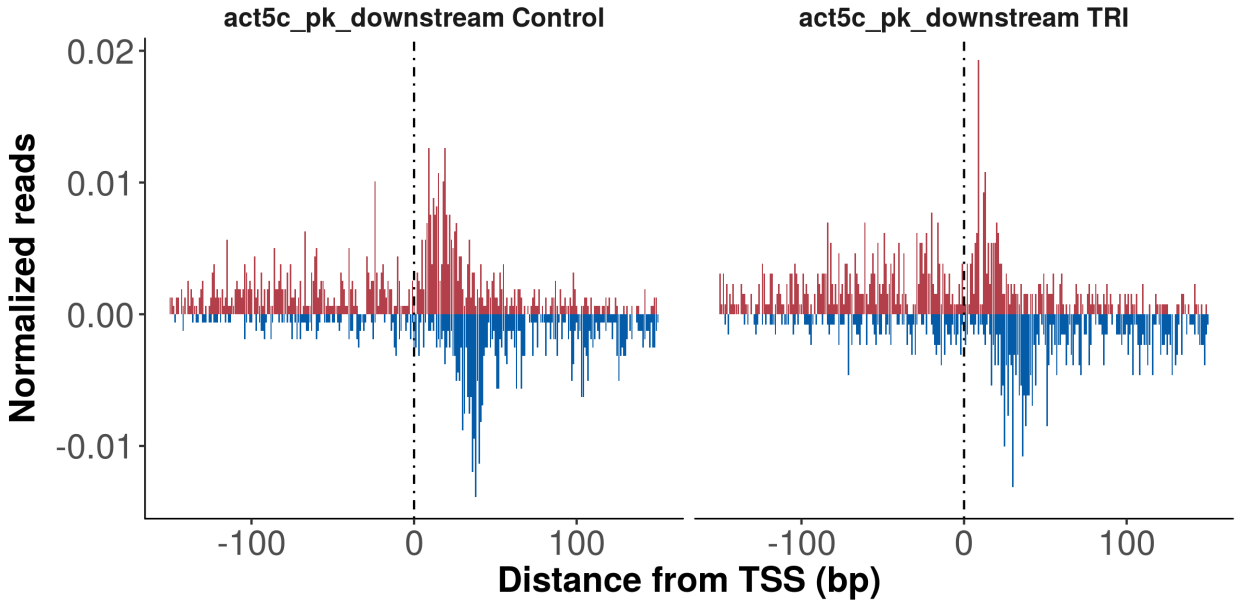
Analysis

Pol II ChIP-nexus profile after TRI treatment

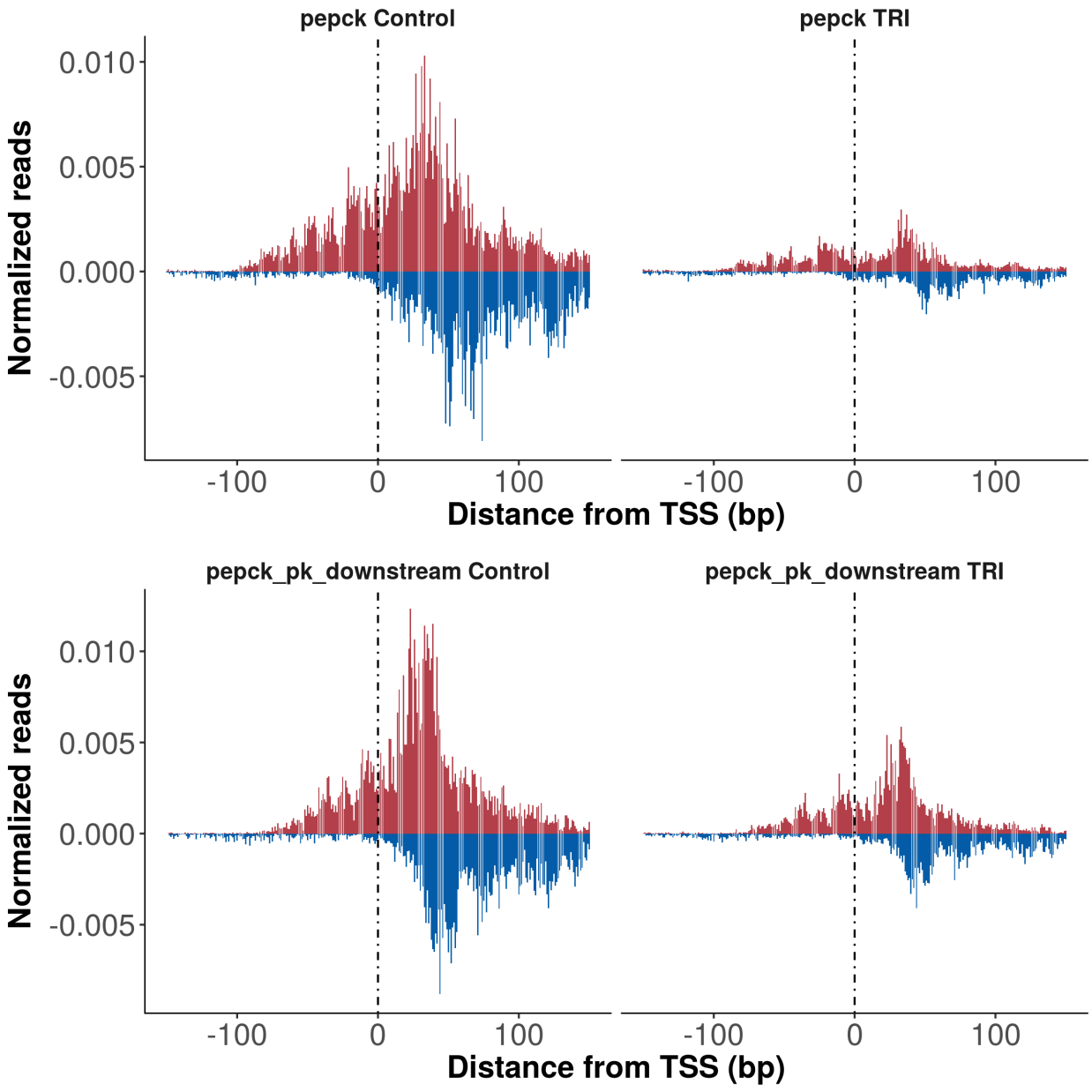
```
plasmid_annotations <- import("./plasmid_annotation.bed")

get_exo_metapeak <- function(sample, upstream=100, downstream=101,
                             smooth=NA, endogeneous = F, dps_sample_path=NULL){

  gene <- as.character(subset(sample_list, sample_name == sample)$gene)
    chromosome <- as.character(subset(sample_list, sample_name == sample )$chromosome)

    if(endogeneous ==F){

        sample_path <- load_bigwig(sample)
        region <- plasmid_annotations[seqnames(plasmid_annotations) == chromosome &
                                      plasmid_annotations$name == gene] %>%
                  resize(., 1, "start")
        seqlevels(region) <- chromosome
      metapeak <- exo_metapeak(region, sample_path,
                               upstream=upstream, downstream=downstream,
                               sample_name=gene, smooth=smooth)
      metapeak$sample <- paste(metapeak$sample_name, metapeak$strand)
      metapeak

    }else{

      region <- genome_annotations[grep(gene, genome_annotations$name, ignore.case = T)]
      seqlevels(region) <- as.character(seqnames(region))
      metapeak <- exo_metapeak(region, dps_sample_path,
                               upstream=upstream, downstream=downstream,
                               sample_name=gene, smooth=smooth)
      metapeak$sample <- paste(metapeak$sample_name, metapeak$strand)
      metapeak

    }
}

compare_dmso_and_tri <- function(dmso, tri, name,  plotting = T){

  plasmid_dmso <- get_exo_metapeak(dmso, upstream=150, downstream = 151)
  plasmid_tri <- get_exo_metapeak(tri, upstream=150, downstream = 151)

  plasmid_tri$reads <- plasmid_tri$reads / sum(abs(plasmid_dmso$reads))
  plasmid_dmso$reads <- plasmid_dmso$reads / sum(abs(plasmid_dmso$reads))


  plasmid_dmso$sample_name <- paste(name, "Control")
  plasmid_tri$sample_name <- paste(name, "TRI")

  if(plotting){
    metapeak <- rbind(plasmid_dmso, plasmid_tri)
    metapeak.p <- subset(metapeak, strand == "+")
```

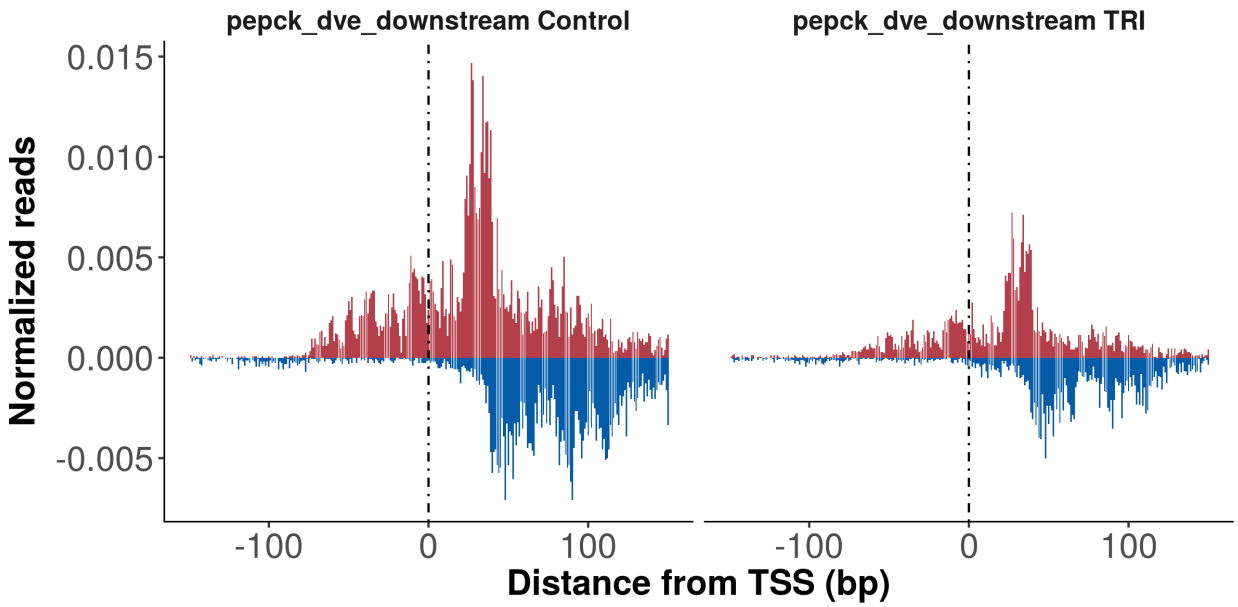
```
    metapeak.n <- subset(metapeak, strand == "-")

  plot <- ggplot(metapeak.p, aes(x = tss_distance, y = reads, fill = strand))+
          geom_bar(fill="#B23F49", stat="identity") +
          geom_vline(xintercept =0, linetype = "dotdash")+
          geom_bar(data=metapeak.n, aes(x=tss_distance, y=reads),
                   fill="#045CA8", stat="identity")+
          xlab("Distance from TSS (bp)")+ ylab("Normalized reads")+
          facet_wrap(facets = "sample_name", ncol =2 )
  print(plot)
  }

  dmso_sig <- subset(plasmid_dmso, tss_distance >0 & tss_distance <= 80)$reads %>%
              abs() %>% sum()
  tri_sig <-  subset(plasmid_tri, tss_distance >0 & tss_distance <= 80)$reads%>%
              abs() %>% sum()

  sig_df <- data.frame(condition = c("dmso", "tri"),
                       paused_polii = c(dmso_sig, tri_sig),
                       name = name)
  sig_df$paused_pol_norm <- sig_df$paused_polii / sig_df$paused_polii[1]
  sig_df
}



name_list <-c("act5c", "act5c_pk_downstream")

act5c_pol_sig_rep1 <- mapply(compare_dmso_and_tri,
       paste0("reporter_dmso_5m_dps_", name_list, "_rpb3_chipnexus_rep1"),
       paste0("reporter_triptolide_5m_dps_", name_list, "_rpb3_chipnexus_rep1"),
       name_list, SIMPLIFY = F, USE.NAMES =F)  %>% do.call(rbind, .)
```






```
act5c_pol_sig_rep2 <- mapply(compare_dmso_and_tri,
       paste0("reporter_dmso_5m_dps_", name_list, "_rpb3_chipnexus_rep2"),
       paste0("reporter_triptolide_5m_dps_", name_list, "_rpb3_chipnexus_rep2"),
       name_list, list(F), SIMPLIFY = F, USE.NAMES =F)  %>% do.call(rbind, .)

name_list2 <-c("pepck", "pepck_pk_downstream", "pepck_dve_downstream")

pepck_pol_sig_rep1 <- mapply(compare_dmso_and_tri,
       paste0("reporter_dmso_5m_dps_", name_list2, "_rpb3_chipnexus_rep1"),
       paste0("reporter_triptolide_5m_dps_", name_list2, "_rpb3_chipnexus_rep1"),
       name_list2, SIMPLIFY = F, USE.NAMES =F)  %>% do.call(rbind, .)
```


pepck Control
pepck TRI
pepck_pk_downstream Control
pepck_pk_downstream TRI
Normalized reads
0.010
0.005
0.000
-0.005
-100
0
100
Distance from TSS (bp)

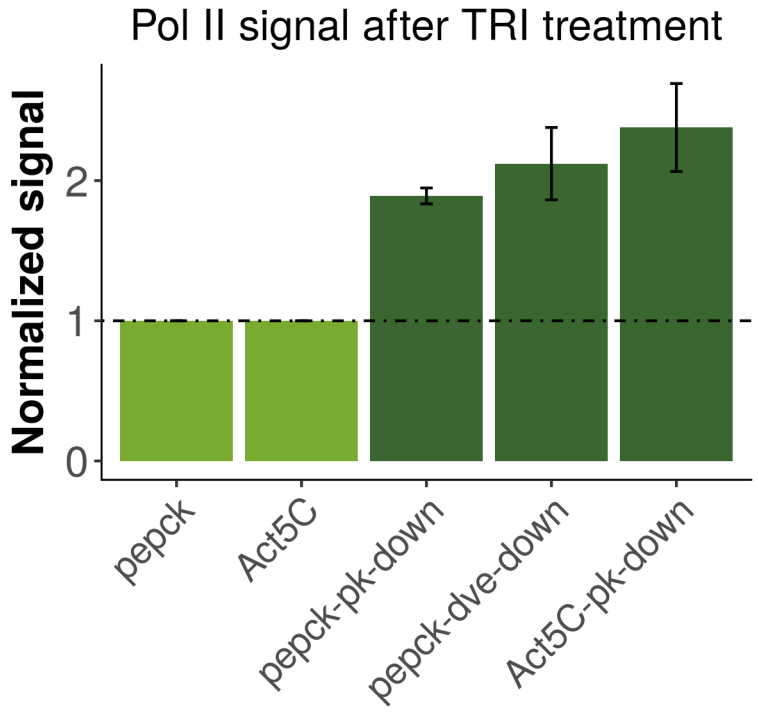



```
pepck_pol_sig_rep2 <- mapply(compare_dmso_and_tri,
       paste0("reporter_dmso_5m_dps_", name_list2, "_rpb3_chipnexus_rep2"),
       paste0("reporter_triptolide_5m_dps_", name_list2, "_rpb3_chipnexus_rep2"),
       name_list2,  list(F), SIMPLIFY = F, USE.NAMES =F)  %>% do.call(rbind, .)
```

Quantify Pol II changes

```
process_pol_sig <- function(df, control_n = 1){
  df_sub <- subset(df, condition == "tri")
  df_sub$paused_pol_norm <- df_sub$paused_pol_norm /  df_sub$paused_pol_norm[control_n]
  df_sub
}

sig_df_list <- list(act5c_pol_sig_rep1, act5c_pol_sig_rep2,
                    pepck_pol_sig_rep1, pepck_pol_sig_rep2)

sig_df <- lapply(sig_df_list, process_pol_sig) %>% do.call(rbind, .)

summary_df <- summarySE(sig_df, measurevar="paused_pol_norm",
                        groupvars=c("name", "condition"))

summary_df$name <- factor(summary_df$name,
                          levels = c( "pepck", "act5c",
                                      "pepck_pk_downstream",
                                      "pepck_dve_downstream",
                                      "act5c_pk_downstream"))

ggplot(summary_df, aes(x=name, y=paused_pol_norm)) +
  geom_bar(stat= "identity", position = "dodge",
           fill = c(rep("#79AB30", 2), rep("#3A672F", 3))) +
  geom_errorbar(aes(ymin=paused_pol_norm-se, ymax=paused_pol_norm+se),
                width=.1, position=position_dodge(.9)) +
```

```
  ggtitle("Pol II signal after TRI treatment")+
  ylab("Normalized signal")+
  xlab("")+
  scale_x_discrete(labels=c("pepck", "Act5C", "pepck-pk-down",
                            "pepck-dve-down", "Act5C-pk-down")) +
  geom_hline(yintercept = 1, lty = 4) +
  theme(axis.text.x = element_text(size=14, angle = 45, hjust = 1))
```



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] reshape2_1.4.3       rtracklayer_1.38.3   ggplot2_2.2.1
##  [4] pander_0.6.1         Rmisc_1.5            plyr_1.8.4
##  [7] lattice_0.20-35      magrittr_1.5         GenomicRanges_1.30.3
## [10] GenomeInfoDb_1.14.0  IRanges_2.12.0       S4Vectors_0.16.0
## [13] 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               XVector_0.18.0
##  [5] bitops_1.0-6               tools_3.4.4
##  [7] zlibbioc_1.24.0            digest_0.6.15
##  [9] evaluate_0.10.1            tibble_1.4.2
## [11] gtable_0.2.0               rlang_0.2.1
## [13] Matrix_1.2-14              DelayedArray_0.4.1
## [15] yaml_2.1.19                GenomeInfoDbData_1.0.0
## [17] stringr_1.3.1              knitr_1.20
## [19] Biostrings_2.46.0          rprojroot_1.3-2
## [21] grid_3.4.4                 Biobase_2.38.0
## [23] XML_3.98-1.11              BiocParallel_1.12.0
## [25] rmarkdown_1.10             matrixStats_0.53.1
## [27] GenomicAlignments_1.14.2   backports_1.1.2
## [29] scales_0.5.0               Rsamtools_1.30.0
## [31] htmltools_0.3.6            SummarizedExperiment_1.8.1
## [33] colorspace_1.3-2           labeling_0.3
## [35] stringi_1.2.3              RCurl_1.95-4.10
## [37] lazyeval_0.2.1             munsell_0.5.0
```