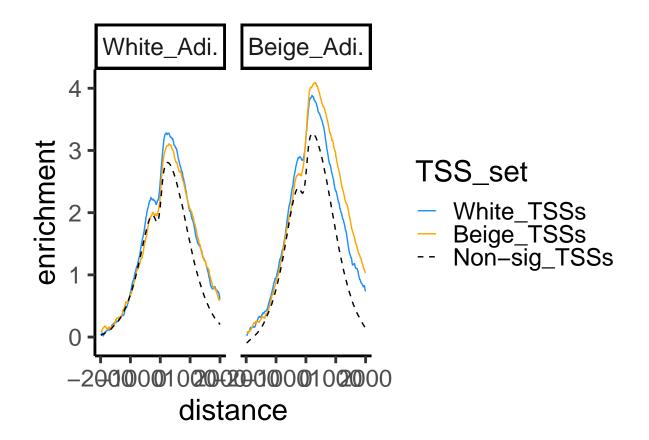
histone_profiles

2024-01-25

```
library(ggplot2)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
library(tidyr)
library(here); i_am("R/Figure3/Fig3B_histone_profiles.Rmd")
## here() starts at /projects/imb-pkbphil/sp/rnaseq/six_donor_trans/splicing_paper
## here() starts at /projects/imb-pkbphil/sp/rnaseq/six_donor_trans/splicing_paper
k4 = read.delim(here("31_leafcutter/histone_profile", "H3K4me3", "H3K4me3_white_beige-10.profile.tab"),
to_bins = function(colname){
  return (as.double(gsub("X","", colname)))
k4= pivot_longer(k4, 3:ncol(k4), names_to = "bin", names_transform = to_bins, values_to = "enrichment"
tail(k4)
## # A tibble: 6 x 4
##
                Х
                               bin enrichment
    bins
               <chr>
##
     <chr>
                          <dbl>
                                        <dbl>
## 1 Beige_Adi. Non-sig_TSSs
                              795
                                           NA
## 2 Beige_Adi. Non-sig_TSSs
                              796
                                           NA
## 3 Beige_Adi. Non-sig_TSSs
                               797
                                           NA
## 4 Beige_Adi. Non-sig_TSSs
                              798
                                           NA
## 5 Beige_Adi. Non-sig_TSSs
                              799
                                           NA
## 6 Beige_Adi. Non-sig_TSSs
                              800
                                           NA
```

```
k4=filter(k4, !is.na(enrichment))
colnames(k4) = c("Context", "TSS_set", "bin", "enrichment")
k4 = mutate(k4, distance = bin*10-2000)
head(k4)
## # A tibble: 6 x 5
##
    Context
              TSS\_set
                            bin enrichment distance
##
     <chr>
               <chr>
                          <dbl>
                                     <dbl>
                                              <dbl>
                                    0.0904
## 1 White_Adi. Beige_TSSs
                                              -1990
                             1
## 2 White_Adi. Beige_TSSs
                             2
                                   0.0892
                                              -1980
## 3 White_Adi. Beige_TSSs
                              3
                                    0.0875
                                              -1970
## 4 White_Adi. Beige_TSSs
                              4
                                    0.104
                                              -1960
## 5 White_Adi. Beige_TSSs
                              5
                                              -1950
                                    0.109
## 6 White_Adi. Beige_TSSs
                              6
                                    0.120
                                              -1940
k4$Context = factor(k4$Context, levels=c("White_Adi.", "Beige_Adi."))
k4$TSS_set = factor(k4$TSS_set, levels = c("White_TSSs", "Beige_TSSs", "Non-sig_TSSs"))
ggplot(k4) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set), s
  facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue","orange
  scale_linetype_manual(values=c("solid", "solid", "dashed"))
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
```

generated.



```
ggsave(here("31_leafcutter/histone_profile", "H3K4me3","H3K4me3_white_beige-10.profile.R.pdf"), width=1
#+
# geom_vline(aes(xintercept=-1000), linetype="dashed") + geom_vline(aes(xintercept=2000), linetype="dashed")
```

H3K27ac

head(k27)

k27=filter(k27, !is.na(enrichment))

k27 = mutate(k27, distance = bin*10-2000)

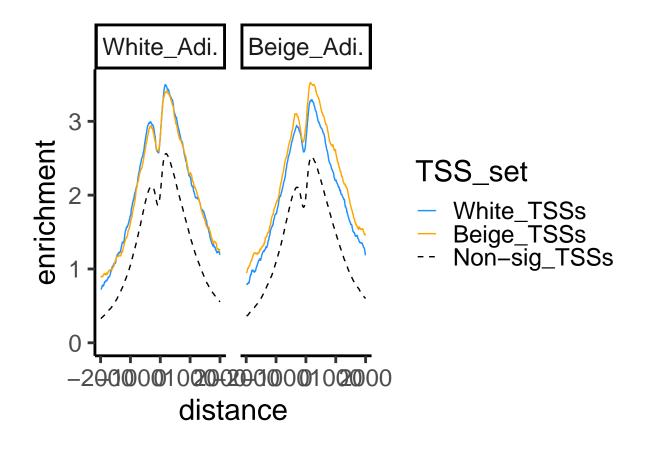
colnames(k27) = c("Context", "TSS_set", "bin", "enrichment")

```
k27 = read.delim(here("31_leafcutter/histone_profile", "H3K27ac", "H3K27ac_white_beige-10.profile.tab"),
k27= pivot_longer(k27, 3:ncol(k27), names_to = "bin", names_transform = to_bins, values_to = "enrichmen
tail(k27)
## # A tibble: 6 x 4
##
    bins
                               bin enrichment
                <chr>
                             <dbl>
                                         <dbl>
## 1 Beige_Adi. Non-sig_TSSs
                               795
                                            NA
## 2 Beige_Adi. Non-sig_TSSs
                               796
                                            NA
## 3 Beige_Adi. Non-sig_TSSs
                               797
                                            NA
## 4 Beige_Adi. Non-sig_TSSs
                               798
                                            NA
## 5 Beige_Adi. Non-sig_TSSs
                               799
                                            NA
## 6 Beige_Adi. Non-sig_TSSs
```

```
Context
                TSS_set
                              bin enrichment distance
##
                <chr>>
                            <dbl>
                                       <dbl>
                                                <dbl>
## 1 White_Adi. Beige_TSSs
                                       0.907
                                                -1990
                                1
## 2 White_Adi. Beige_TSSs
                                2
                                       0.896
                                                -1980
## 3 White_Adi. Beige_TSSs
                                3
                                       0.895
                                                -1970
## 4 White_Adi. Beige_TSSs
                                       0.893
                                                -1960
## 5 White_Adi. Beige_TSSs
                                5
                                       0.899
                                                 -1950
## 6 White_Adi. Beige_TSSs
                                       0.902
                                                -1940
k27$Context = factor(k27$Context, levels=c("White_Adi.", "Beige_Adi."))
k27$TSS_set = factor(k27$TSS_set, levels = c("White_TSSs", "Beige_TSSs", "Non-sig_TSSs"))
ggplot(k27) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set),
  facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue","orange
  scale_linetype_manual(values=c("solid", "solid", "dashed")) + coord_cartesian(y=c(0, max(k27\$enrichment)
```

A tibble: 6 x 5

##

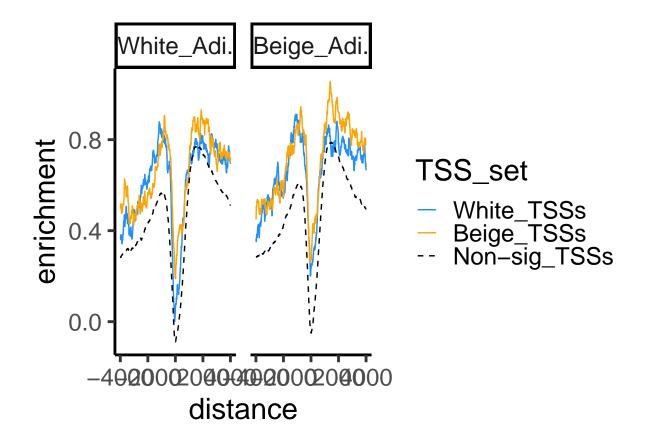


```
ggsave(here("31_leafcutter/histone_profile", "H3K27ac", "H3K27ac_white_beige-10.profile.R.pdf"), width=1
# + geom_hline(aes(yintercept=1)) +
\# geom\_vline(aes(xintercept=1000)) + geom\_vline(aes(xintercept=-1000))
```

If we use the 1 enrichment threshold on the highest peak then a full +2000/-2000 is a good window

H3K4me1

```
me1 = read.delim(here("31_leafcutter/histone_profile", "H3K4me1/H3K4me1_white_beige-10.profile.tab"), si
me1= pivot_longer(me1, 3:ncol(me1), names_to = "bin", names_transform = to_bins, values_to = "enrichmen
tail(me1)
## # A tibble: 6 x 4
    bins
               Х
                               bin enrichment
     <chr>
                <chr>
                                        <dbl>
##
                             <dbl>
## 1 Beige_Adi. Non-sig_TSSs
                              1595
                                           NΑ
## 2 Beige_Adi. Non-sig_TSSs
                              1596
                                           NA
## 3 Beige_Adi. Non-sig_TSSs
                              1597
                                           NA
## 4 Beige_Adi. Non-sig_TSSs
                              1598
                                           NA
## 5 Beige_Adi. Non-sig_TSSs
                              1599
                                           NA
## 6 Beige_Adi. Non-sig_TSSs
                                           NA
me1=filter(me1, !is.na(enrichment))
colnames(me1) = c("Context", "TSS_set", "bin", "enrichment")
me1 = mutate(me1, distance = bin*10-4000)
head(me1)
## # A tibble: 6 x 5
    Context
             TSS set
                             bin enrichment distance
##
     <chr>
                <chr>
                           <dbl>
                                      <dbl>
                                               <dbl>
## 1 White_Adi. Beige_TSSs
                               1
                                      0.496
                                                -3990
## 2 White_Adi. Beige_TSSs
                                               -3980
                               2
                                      0.503
## 3 White_Adi. Beige_TSSs
                               3
                                      0.519
                                               -3970
## 4 White_Adi. Beige_TSSs
                               4
                                               -3960
                                      0.513
## 5 White_Adi. Beige_TSSs
                               5
                                      0.512
                                               -3950
## 6 White_Adi. Beige_TSSs
                               6
                                      0.505
                                               -3940
me1$Context = factor(me1$Context, levels=c("White_Adi.","Beige_Adi."))
me1$TSS_set = factor(me1$TSS_set, levels = c("White_TSSs", "Beige_TSSs", "Non-sig_TSSs"))
ggplot(me1) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set),
  facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue", "orange
  scale_linetype_manual(values=c("solid", "solid", "dashed"))
```



```
ggsave(here("31_leafcutter/histone_profile", "H3K4me1","H3K4me1_white_beige-10.profile.R.pdf"), width=1
#+ geom_hline(aes(yintercept=0.25)) + geom_vline(aes(xintercept=-250)) +
# geom_vline(aes(xintercept=500)) + geom_vline(aes(xintercept=-2000))
```

Should probably do the upstream and downstream windows... I wouldn't do stats on depletion levels, cos that depends on the noise/input and stuff. But the most obvious one is +500 to 4000... or is it? upstream is the promoter, makes more sense

H3K27me3

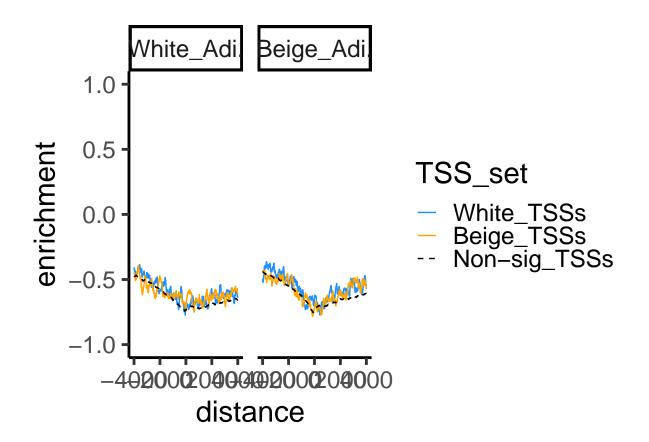
```
pc = read.delim(here("31_leafcutter/histone_profile", "H3K27me3/H3K27me3_white_beige-10.profile.tab"),
pc= pivot_longer(pc, 3:ncol(pc), names_to = "bin", names_transform = to_bins, values_to = "enrichment"
tail(pc)
```

```
## # A tibble: 6 x 4
##
     bins
                Х
                                 bin enrichment
##
     <chr>>
                 <chr>>
                                          <dbl>
                               <dbl>
## 1 Beige_Adi. Non-sig_TSSs
                               1595
                                             NA
## 2 Beige_Adi. Non-sig_TSSs
                               1596
                                             NA
## 3 Beige_Adi. Non-sig_TSSs
                               1597
                                             NA
## 4 Beige_Adi. Non-sig_TSSs
                               1598
                                             NA
## 5 Beige_Adi. Non-sig_TSSs
                               1599
                                             NA
## 6 Beige_Adi. Non-sig_TSSs
                               1600
                                             NA
```

```
colnames(pc) = c("Context", "TSS_set", "bin", "enrichment")
pc = mutate(pc, distance = bin*10-4000)
head(pc)
## # A tibble: 6 x 5
##
     Context
                TSS set
                              bin enrichment distance
     <chr>
##
                <chr>
                            <dbl>
                                        <dbl>
                                                 <dbl>
## 1 White_Adi. Beige_TSSs
                                       -0.459
                                                 -3990
                                1
                                       -0.451
## 2 White_Adi. Beige_TSSs
                                2
                                                 -3980
## 3 White_Adi. Beige_TSSs
                                3
                                       -0.453
                                                 -3970
## 4 White_Adi. Beige_TSSs
                                4
                                      -0.458
                                                 -3960
                                                 -3950
## 5 White_Adi. Beige_TSSs
                                5
                                       -0.468
## 6 White_Adi. Beige_TSSs
                                       -0.474
                                                 -3940
```

pc=filter(pc, !is.na(enrichment))

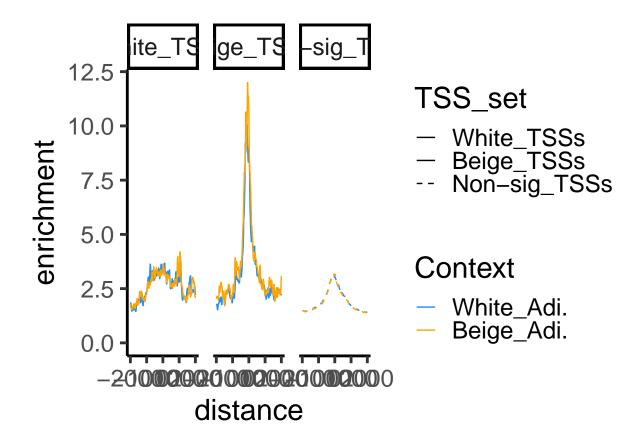
```
pc$Context = factor(pc$Context, levels=c("White_Adi.","Beige_Adi."))
pc$TSS_set = factor(pc$TSS_set, levels = c("White_TSSs","Beige_TSSs","Non-sig_TSSs"))
ggplot(pc) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set), s
facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue","orange
scale_linetype_manual(values=c("solid","solid","dashed"))+ coord_cartesian(y=c(-1,1))
```



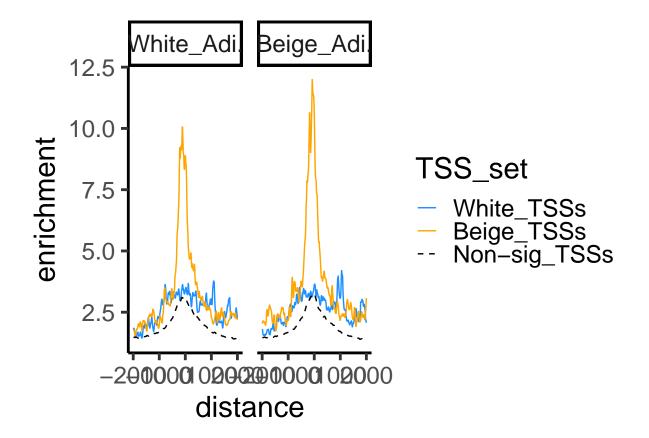
```
ggsave(here("31_leafcutter/histone_profile", "H3K27me3","H3K27me3_white_beige-10.profile.R.pdf"), width
#+ geom_hline(aes(yintercept=0))
```

PPARG

```
pparg = read.delim(here("31_leafcutter/histone_profile", "PPARG/PPARG_white_beige-10.profile.tab"), ski
pparg= pivot_longer(pparg, 3:ncol(pparg), names_to = "bin", names_transform = to_bins, values_to = "enr
tail(pparg)
## # A tibble: 6 x 4
     bins
##
                               bin enrichment
                X
##
     <chr>
                <chr>
                             <dbl>
                                         <dbl>
## 1 Beige_Adi. Non-sig_TSSs
                               795
                                            NA
## 2 Beige_Adi. Non-sig_TSSs
                               796
                                            NA
## 3 Beige_Adi. Non-sig_TSSs
                               797
                                            NA
## 4 Beige_Adi. Non-sig_TSSs
                               798
                                            NA
## 5 Beige_Adi. Non-sig_TSSs
                               799
                                            NA
## 6 Beige_Adi. Non-sig_TSSs
                               800
                                            NΑ
pparg=filter(pparg, !is.na(enrichment))
colnames(pparg) = c("Context", "TSS_set", "bin", "enrichment")
pparg = mutate(pparg, distance = bin*10-2000)
head(pparg)
## # A tibble: 6 x 5
##
     Context
                TSS_set
                             bin enrichment distance
##
     <chr>
                <chr>
                            <dbl>
                                       <dbl>
                                                <dbl>
## 1 White_Adi. Beige_TSSs
                                       1.80
                                                -1990
                               1
## 2 White_Adi. Beige_TSSs
                               2
                                       1.77
                                                -1980
## 3 White_Adi. Beige_TSSs
                               3
                                       1.75
                                                -1970
## 4 White_Adi. Beige_TSSs
                               4
                                        1.75
                                                -1960
## 5 White_Adi. Beige_TSSs
                               5
                                        1.68
                                                -1950
## 6 White_Adi. Beige_TSSs
                               6
                                       1.59
                                                -1940
pparg$Context = factor(pparg$Context, levels=c("White_Adi.", "Beige_Adi."))
pparg$TSS_set = factor(pparg$TSS_set, levels = c("White_TSSs", "Beige_TSSs", "Non-sig_TSSs"))
ggplot(pparg) + geom_line(aes(x=distance, y=enrichment, group=Context, color=Context, linetype=TSS_set)
  facet_wrap(~TSS_set) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue", "orange
  scale_linetype_manual(values=c("solid", "solid", "dashed"))+ coord_cartesian(y=c(0,12))
```



```
ggsave(here("31_leafcutter/histone_profile", "PPARG", "PPARG_white_beige-10.profile.R.pdf"), width=15, h
ggplot(pparg) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set)
facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue", "orange
scale_linetype_manual(values=c("solid", "solid", "dashed"))#+ coord_cartesian(y=c(-1,1))
```



```
#+ geom_hline(aes(yintercept=0))
```

MED1

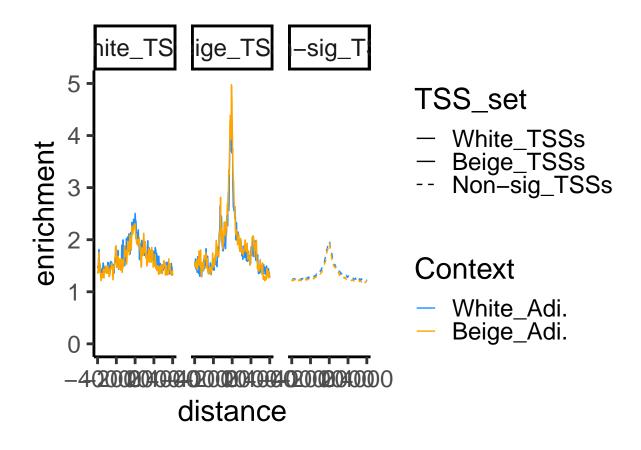
```
med1 = read.delim(here("31_leafcutter/histone_profile", "MED1/MED1_white_beige-10.profile.tab"), skip=1
med1= pivot_longer(med1, 3:ncol(med1), names_to = "bin", names_transform = to_bins, values_to = "enrichtail(med1)
```

```
## # A tibble: 6 x 4
##
     bins
                               bin enrichment
     <chr>>
                <chr>>
                              <dbl>
                                         <dbl>
## 1 Beige_Adi. Non-sig_TSSs 1595
                                            NA
## 2 Beige_Adi. Non-sig_TSSs
                              1596
## 3 Beige_Adi. Non-sig_TSSs
                              1597
                                            NA
## 4 Beige_Adi. Non-sig_TSSs
                              1598
## 5 Beige_Adi. Non-sig_TSSs
                                            NA
                              1599
## 6 Beige_Adi. Non-sig_TSSs
med1=filter(med1, !is.na(enrichment))
colnames(med1) = c("Context", "TSS_set", "bin", "enrichment")
med1 = mutate(med1, distance = bin*10-4000)
head(med1)
```

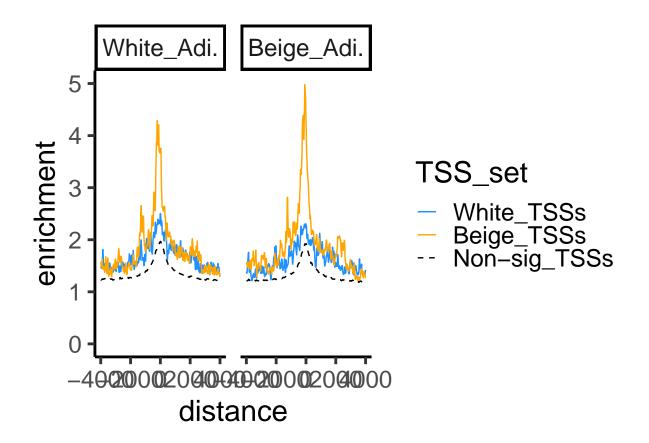
A tibble: 6 x 5

```
##
     Context
                 TSS_set
                               bin enrichment distance
##
     <chr>>
                 <chr>
                             <dbl>
                                         <dbl>
                                                  <dbl>
## 1 White_Adi. Beige_TSSs
                                                  -3990
                                         1.58
## 2 White_Adi. Beige_TSSs
                                 2
                                         1.54
                                                  -3980
## 3 White_Adi. Beige_TSSs
                                 3
                                         1.50
                                                  -3970
## 4 White_Adi. Beige_TSSs
                                 4
                                                  -3960
                                         1.49
## 5 White_Adi. Beige_TSSs
                                 5
                                                  -3950
                                         1.48
                                                  -3940
## 6 White_Adi. Beige_TSSs
                                         1.48
```

```
med1$Context = factor(med1$Context, levels=c("White_Adi.","Beige_Adi."))
med1$TSS_set = factor(med1$TSS_set, levels = c("White_TSSs","Beige_TSSs","Non-sig_TSSs"))
ggplot(med1) + geom_line(aes(x=distance, y=enrichment, group=Context, color=Context, linetype=TSS_set),
   facet_wrap(~TSS_set) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue","orange
   scale_linetype_manual(values=c("solid","solid","dashed"))+ coord_cartesian(y=c(0,5))
```



```
ggsave(here("31_leafcutter/histone_profile", "MED1", "MED1_white_beige-10.profile.R.pdf"), width=15, hei
ggplot(med1) + geom_line(aes(x=distance, y=enrichment, group=TSS_set, color=TSS_set, linetype=TSS_set),
  facet_wrap(~Context) + theme_classic(base_size=22) +scale_color_manual(values= c("dodgerblue", "orange
  scale_linetype_manual(values=c("solid", "solid", "dashed"))+ coord_cartesian(y=c(0,5))
```



#+ geom_hline(aes(yintercept=0))