Supplementary Figures for Soares et al.

Six Supplemental Figures and Legends

Supplementary Figure Legends

Figure S1, related to Figure 1. Distribution of H3K4me states in *wild type* and *jhd2Δ* cells. A Anchor plot of H3K4me states centered at the transcription start site (TSS) for RNApII transcripts in *JHD2* and *jhd2Δ*. ChIP-Seq SPMR values for nucleotide positions between -1500 and +1500 were averaged and plotted; red, H3K4me3; green, H3K4me2; dashed line, *JHD2*; full line *jhd2Δ*. **B** Kernel density estimation plot and histogram of H3K4me states maximum values in *JHD2* and *jhd2Δ*. H3K4me3 maximum values were calculated and plotted as described in **Figure 1C**; left panel, *JHD2*; right panel *jhd2Δ*. **C** Scatter plot of H3K4me3 maximum SPMR values *JHD2* versus *jhd2Δ*. **D** Heat map of H3K4me states in *JHD2* and *jhd2Δ.* Heat maps were created as in **Figure 1B**, right panels correspond to arithmetic difference between the matrixes on right and center panels (*jhd2Δ* - *JHD2*). Top panels H3K4me3; bottom panels H3K4me2. **E** Representative ChIP-Seq tracks. SPMR values for H3K4me3 and me2 for *JHD2* and *jhd2Δ* backgrounds are plotted from 200 bp upstream of the TSS to 200 bp downstream of the transcription termination site for *YCR091W*. Color code: red, *JHD2* H3K4me3; green, *JHD2* H3K4me2; blue, *jhd2Δ* H3K4me3; purple, *jhd2Δ* H3K4me2.

Figure S2, related to Figure 2. Effects of transcription levels and COMPASS activity on H3K4me distribution. A Boxplot representation of transcript sizes for all RNApII transcriptional units used in **Figure 2A** (green) compared to genes with "low H3K4me2 high H3K4me3" (purple, transcriptional units with maximum value of H3K4me3 SPMR above 40 and H3K4me2 below 20) and "low H3K4me3" (orange, transcriptional units with maximum value of H3K4me3 SPMR below 20 and H3K4me2 above 20) **B** Correlation of H3K4me3 and me2 peak properties with different estimates of transcription rates (TR) and RNA abundance (RA), in addition to the values presented on **Figure 1B** (RNA levels). Spearman correlations between maximum peak values or position (as described in **Figure 1B**) were calculated with different transcription rate estimates from Pelechano et al. (2010) and references within. Red, H3K4me3; green H3K4me2; dark maximum value; light, position of maximum value. **C** Values of maximum SPMR for H3K4me3 and H3K4me2 in *SPP1* and *spp1*Δ strains. Values for maximum

H3K4me3 (left panel) and H3K4me2 (right panel) were calculated as in **Figure 1C** for *SPP1* (red) and *spp1*Δ (green) and plotted as a gaussian kernel density plot.

Figure S3, related to Figure 3. A Individual heat map representations for H3K4me states in Rpb1 elongation rate mutants. Heat maps for *RPB1*, *rpb1-N488D,* and *rpb1-E1103G* as well as differences between wild type and corresponding mutants were plotted for H3K4me3 (left panels) and H3K4me2 (right panels). Color code as following, *RPB1* H3K4me3, red; *RPB1* H3K4me2 green; *rpb1* mutants H3K4me3, blue; *rpb1* mutants H3K4me2, purple. **B** Average ChIP-seq profiles of *RPB1* (red), *rpb1-N488D* (green), and *rpb1-E1103G* (blue) strains for H3, Rpb3, Rpb1-Ser5P, and Rpb1-Ser2P were generated using 500 bp windows around the transcription start site (TSS) and transcription termination site (tts), as well as middle (>250 from TSS and <250 from tts) regions, and scaling all genes to 100 data points. Genes shorter than 600 nt were excluded. Right panel shows the results for Rpb1-Ser5P considering only the top 10% genes in terms of value for this modification. **C** Heat map representation of H3K4me states for Rpb1 elongation rate mutants, normalized to Histone H3 levels. Heat maps for H3K4me3 (upper panels, red) and H3K4me2 (lower panes, green) for *RPB1*, *rpb1-N488D,* and *rpb1-E1103G* were normalized to H3 levels for the corresponding mutants.

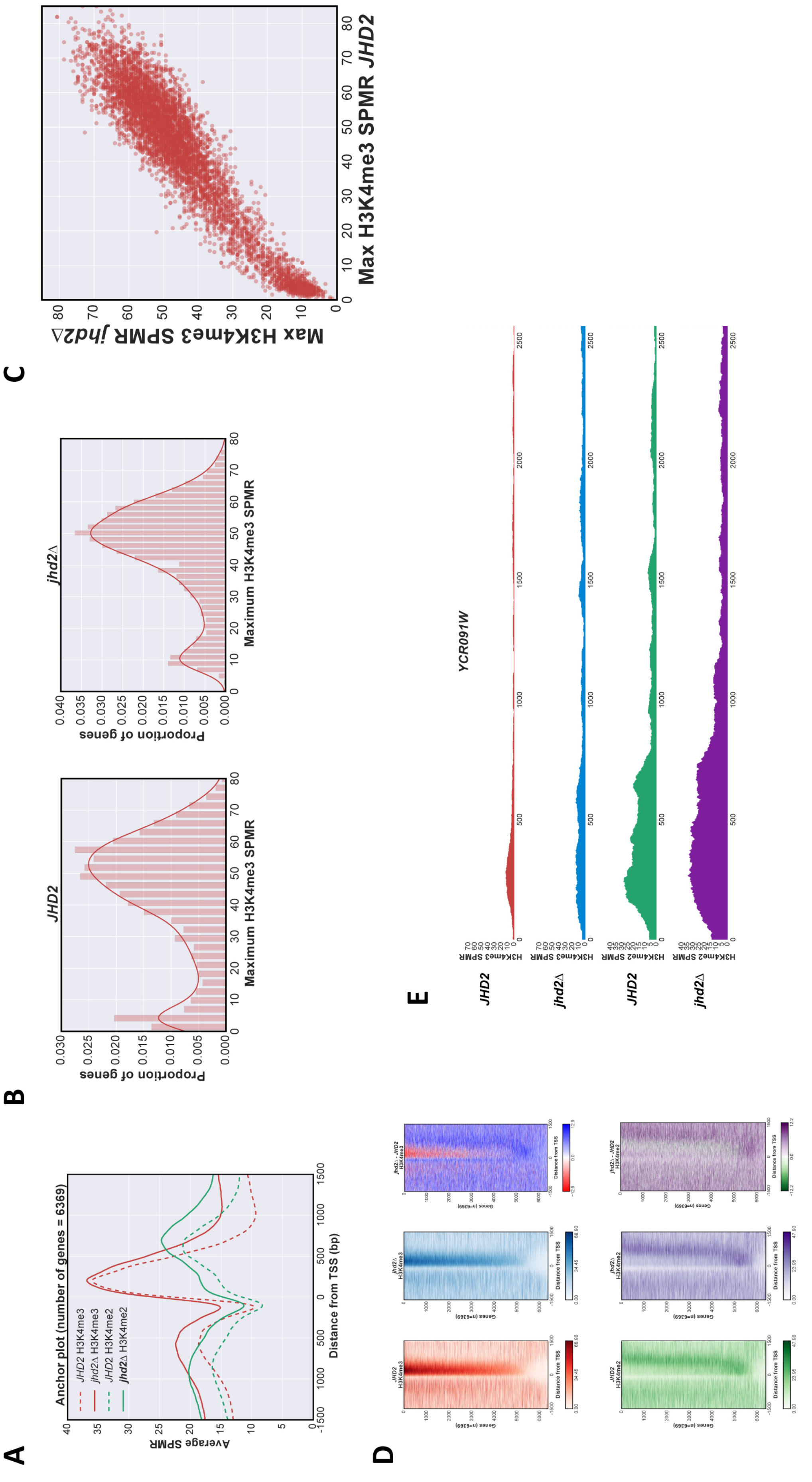
Figure S4, related to Figure 4. Effects of Set1 N-terminal truncation on H3K4me. A Anchor plot of H3K4me3 and me2 in *SET1* and *set1*Δ700 cells, averaged and plotted as in **Figure 4A**. Left panel H3K4me3; right panel, H3K4me2. Color code, red and green *SET1*; blue and purple *set1*Δ700. **B** Boxplot distribution of H3K4me3 ratios between *SET1* and *set1*Δ700. Ratio of maximum H3K4me3 SPMR values between *SET1* and *set1Δ700* were plotted for transcriptional units divided according to SAGA- and TFIID-dominated categories defined in Huisinga and Pugh (2004). **C** Distances between H3K4me3 and H3K4me2 maximum value peaks in *SET1* and *set1Δ700* cells. Position of maximum values of H3K4me3 and H3K4me2 SPMR were calculated as described in **Figure 1E** for *SET1*, left panel and *set1Δ700* cells, right panel. Differences between H3K4me3 and H3K4me2 position values were plotted as histogram and gaussian kernel density estimate plot.

Figure S5, related to Figures 5 and 6. Analysis of Set1 fusion to RNApII. A Schematic representation of constructs used. **B** Copy number amplification of Rpb4-Set1Δ500 fusion construct. SPMR tracks for *RPB4* (upper panels) and *SET1* (lower panels) loci in the input DNA are shown for WT strain YSB2723+pRS414-SET1(1-1080) and YSB2829 (YSB2824+pRS314-Rpb4-SET1Δ500).

C ChIP-Seq SPMR tracks for H3K4me3 and H3K4me2 on representative gene *YAL038W* (+/- 200bp from transcribed region) in *SET1* (upper panels), *set1Δ500* (middle panels), and *rpb4-set1Δ500* (lower panels). Left panels H3K4me3, right panels H3K4me2.

Figure S6, related to Figures 5 and 6. Fusing Set1 to RNApII does not overcome H2bub requirement for H3K4me methylation. A H3K4me levels in relevant strains. Protein extracts from the indicated cells were separated by SDS-PAGE and immunoblotted with the antibodies indicated on the right. Total histone H3 and TBP were used as loading controls. Lane 1, YSB2723+pRS314; lane 2, YSB2723+pRS414-SET1(1-1080); lane 3, YSB2723+pRS414-SET1Δ500; lane 4, YSB2824+pRS314; lane 5, YSB3347 = YSB2824+pRS314-Rpb4-SET1Δ500; lane 6, YSB3318 = YSB2723+pRS414-SET1(1-1080) + bre1Δ::URA3MX; lane 7, YSB3319 = YSB2723+pRS314-Rpb4-SET1Δ500+ bre1Δ::URA3MX+rpb4Δ::NatMX. pFL indicates that the full-length SET1 gene was carried on a plasmid.

Fig S1



A
Anchor plot (number of genes = 6369)
JHD2 H3K4me3
jhd2∆ H3K4me3
JHD2 H3K4me2
jhd2∆ H3K4me2
Average SPMR
Distance from TSS (bp)
B
JHD2
jhd2∆
Proportion of genes
Maximum H3K4me3 SPMR
C
Max H3K4me3 SPMR JHD2
Max H3K4me3 SPMR jhd2∆
D
JHD2 H3K4me3
jhd2∆ H3K4me3
jhd2∆ - JHD2 H3K4me3
JHD2 H3K4me2
jhd2∆ H3K4me2
jhd2∆ - JHD2 H3K4me2
Genes (n=6369)
Distance from TSS
E
YCR091W
JHD2
jhd2∆
JHD2
jhd2∆
H3K4me3 SPMR
H3K4me3 SPMR
H3K4me2 SPMR
H3K4me2 SPMR

Fig S2

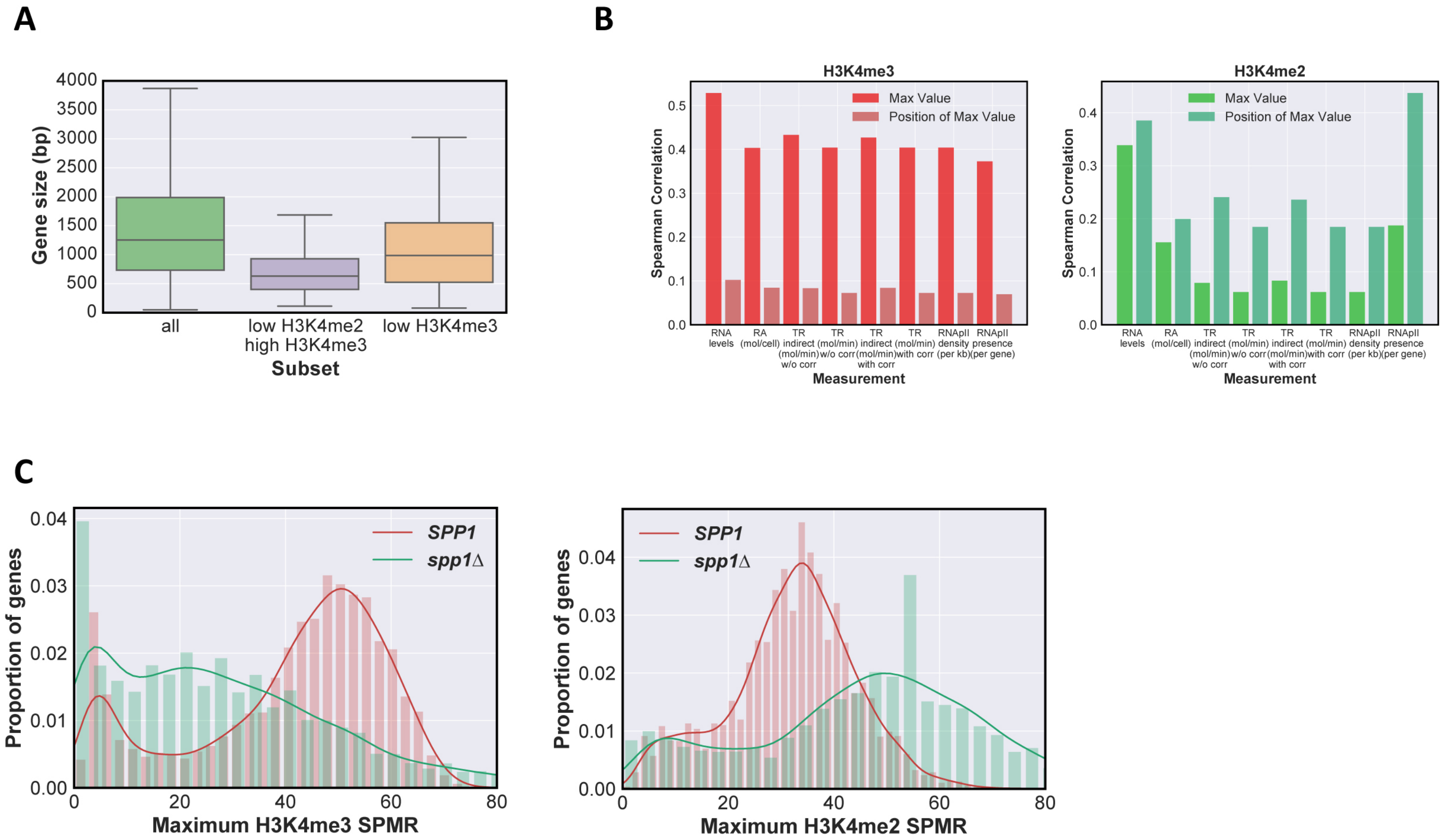

A
Gene size (bp)
4000
3500
3000
2500
2000
1500
1000
500
0
all
low H3K4me2
high H3K4me3
low H3K4me3
Subset
B
H3K4me3
Max Value
Position of Max Value
Spearman Correlation
0.0
0.1
0.2
0.3
0.4
0.5
RNA levels
RA (mol/cell)
TR indirect (mol/min) w/o corr
TR (mol/min) w/o corr
TR indirect (mol/min) with corr
TR (mol/min) with corr
RNApII density (per kb)
RNApII presence (per gene)
Measurement
H3K4me2
Max Value
Position of Max Value
Spearman Correlation
0.0
0.1
0.2
0.3
0.4
RNA levels
RA (mol/cell)
TR indirect (mol/min) w/o corr
TR (mol/min) w/o corr
TR indirect (mol/min) with corr
TR (mol/min) with corr
RNApII density (per kb)
RNApII presence (per gene)
Measurement
C
Proportion of genes
0.00
0.01
0.02
0.03
0.04
SPP1
spp1Δ
0
20
40
60
80
Maximum H3K4me3 SPMR
Proportion of genes
0.00
0.01
0.02
0.03
0.04
SPP1
spp1Δ
0
20
40
60
80
Maximum H3K4me2 SPMR

Fig S3

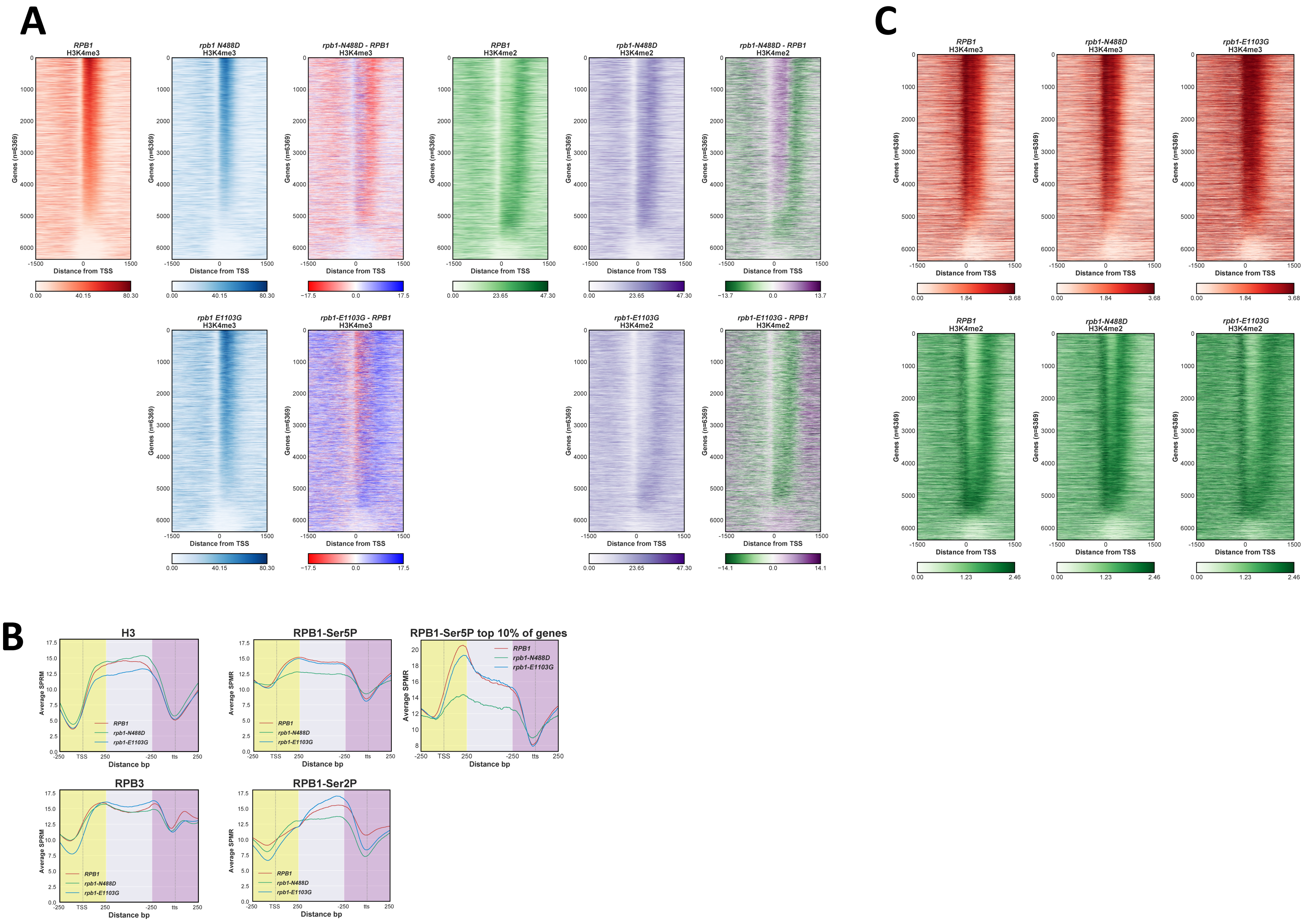
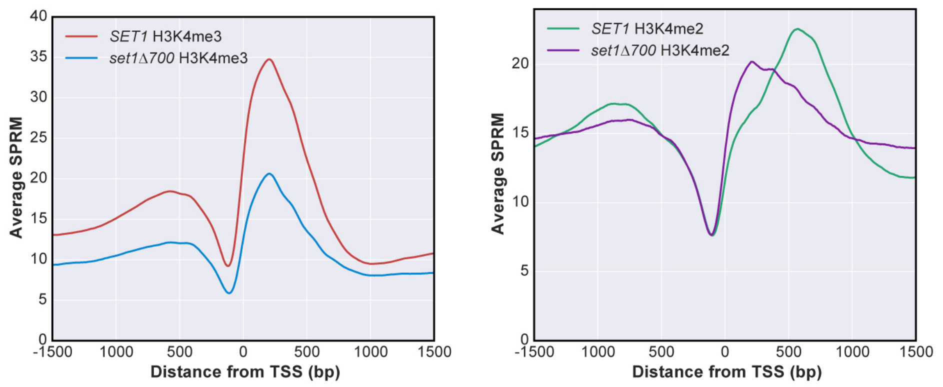

A
RPB1 H3K4me3
rpb1 N488D H3K4me3
rpb1-N488D - RPB1 H3K4me3
RPB1 H3K4me2
rpb1-N488D H3K4me2
rpb1-N488D - RPB1 H3K4me2
rpb1 E1103G H3K4me3
rpb1-E1103G - RPB1 H3K4me3
rpb1-E1103G H3K4me2
rpb1-E1103G - RPB1 H3K4me2
Genes (n=6369)
0
1000
2000
3000
4000
5000
6000
Distance from TSS
-1500
0
1500
0.00
40.15
80.30
−17.5
0.0
17.5
23.65
47.30
−13.7
13.7
−14.1
14.1
B
H3
RPB1-Ser5P
RPB1-Ser5P top 10% of genes
RPB3
RPB1-Ser2P
Average SPRM
Average SPMR
Distance bp
-250
TSS
250
tts
RPB1
rpb1-N488D
rpb1-E1103G
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
8
10
12
14
16
18
20
C
RPB1 H3K4me3
rpb1-N488D H3K4me3
rpb1-E1103G H3K4me3
RPB1 H3K4me2
rpb1-N488D H3K4me2
rpb1-E1103G H3K4me2
1.84
3.68
1.23
2.46

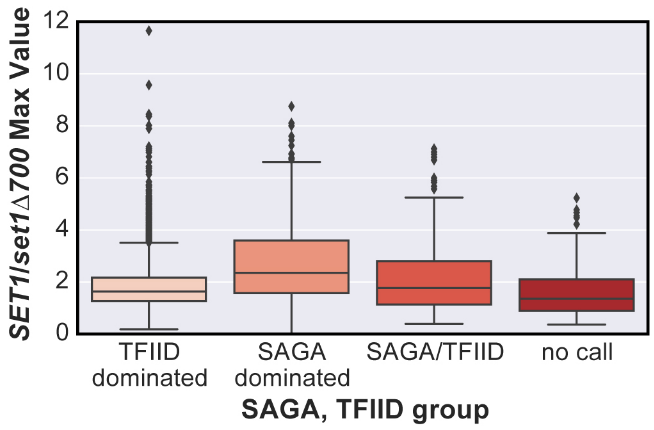
Fig S4

A



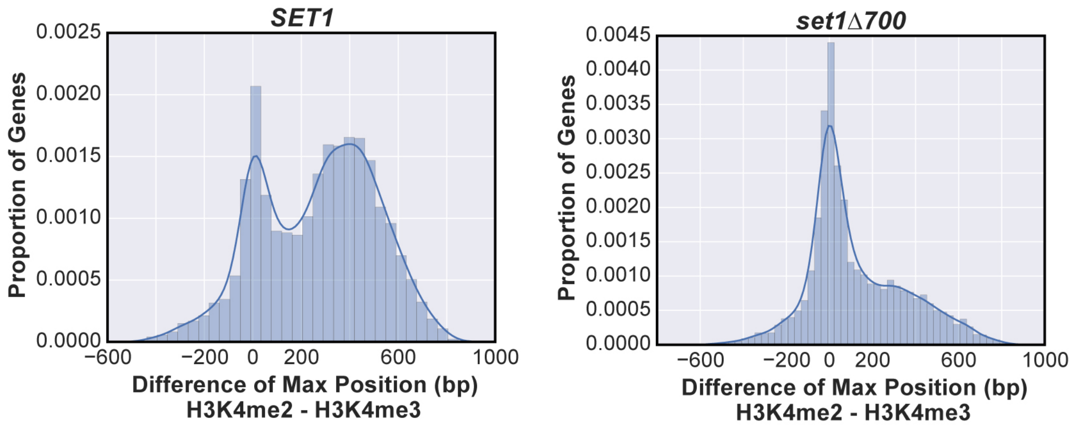
SET1 H3K4me3
set1Δ700 H3K4me3
Average SPRM
40
35
30
25
20
15
10
5
0
-1500
1000
500
0
500
1000
1500
Distance from TSS (bp)
SET1 H3K4me2
set1Δ700 H3K4me2
Average SPRM
20
15
10
5
0
-1500
1000
500
0
500
1000
1500
Distance from TSS (bp)

B



SET1/set1Δ700 Max Value
12
10
8
6
4
2
0
TFIID dominated
SAGA dominated
SAGA/TFIID
no call
SAGA, TFIID group

C



SET1
Proportion of Genes
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
−600
−200
0
200
600
1000
Difference of Max Position (bp)
H3K4me2 - H3K4me3
set1Δ700
Proportion of Genes
0.0045
0.0040
0.0035
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
−600
−200
0
200
600
1000
Difference of Max Position (bp)
H3K4me2 - H3K4me3

Fig S5

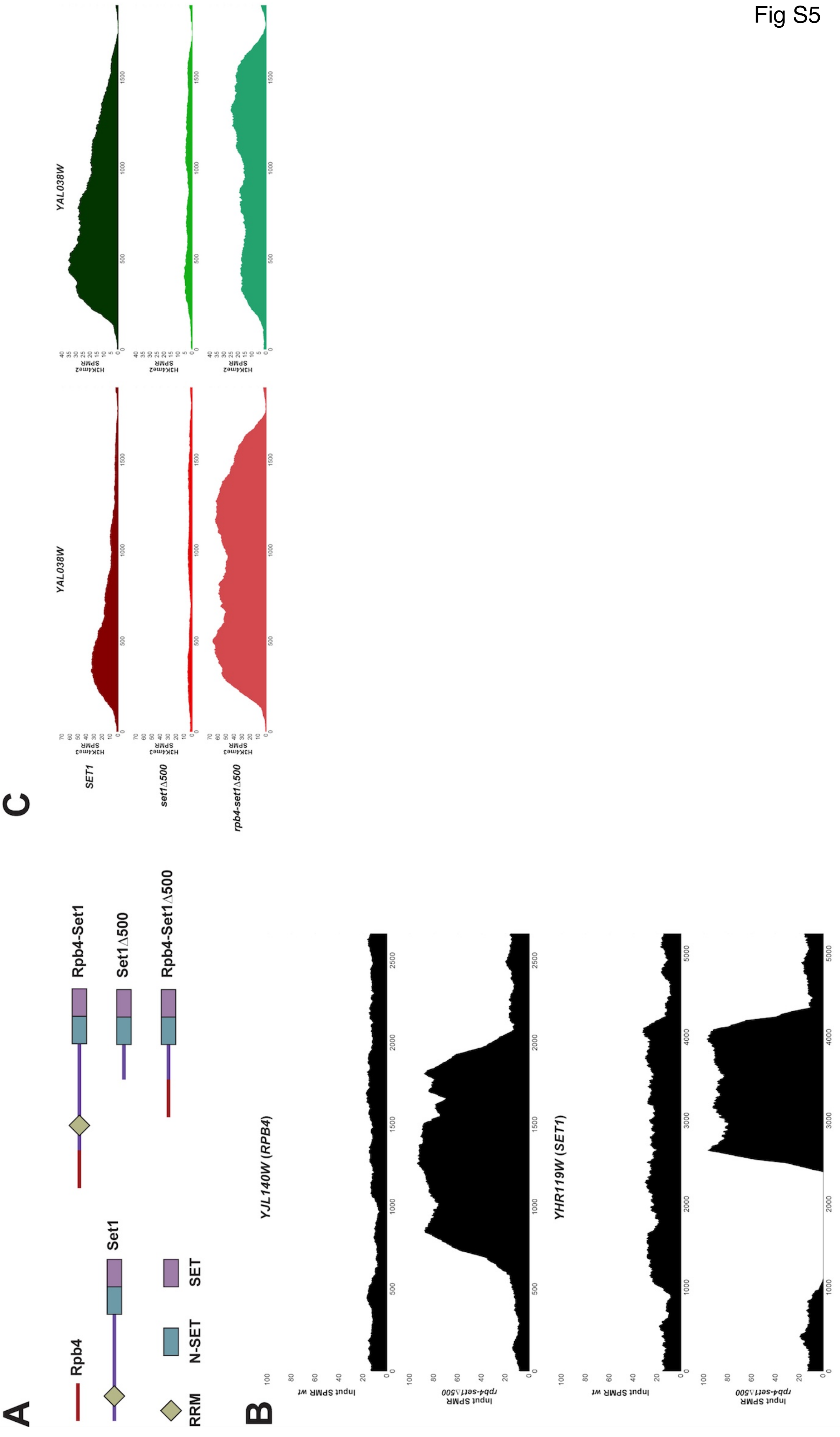
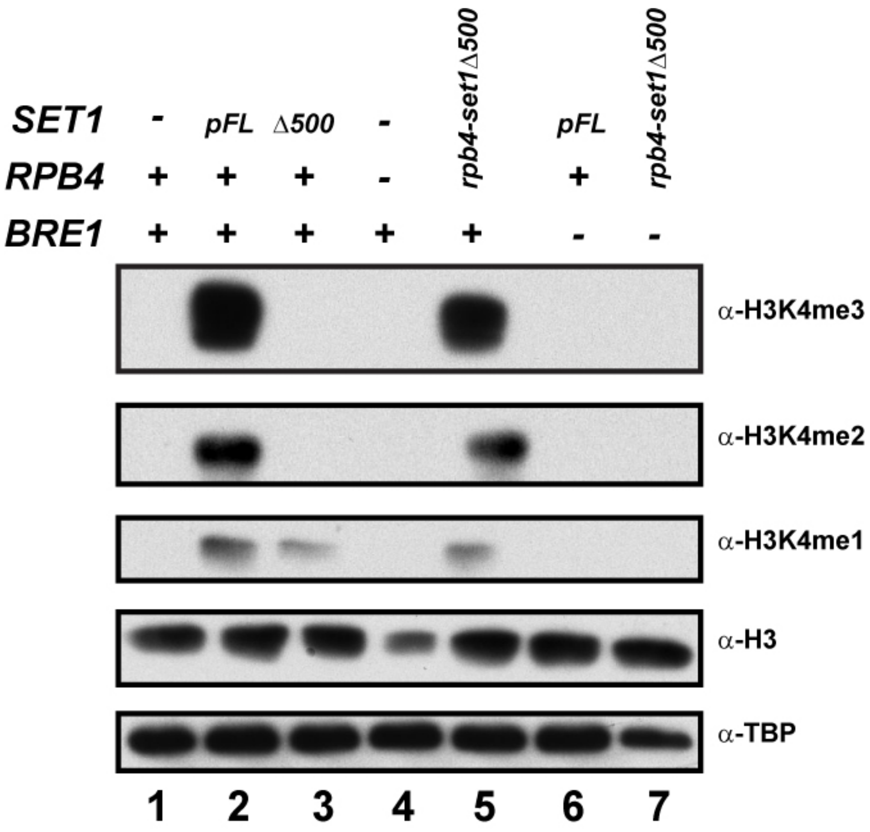

A
Rpb4
Set1
Rpb4-Set1
Set1Δ500
Rpb4-Set1Δ500
RRM
N-SET
SET
B
YJL140W (RPB4)
Input SPMR wt
Input SPMR rpb4-set1Δ500
YHR119W (SET1)
0
20
40
60
80
100
0
500
1000
1500
2000
2500
3000
4000
5000
C
YAL038W
SET1
set1Δ500
rpb4-set1Δ500
H3K4me3 SPMR
H3K4me2 SPMR
0
10
20
30
40
50
60
70
5
15
25
35

Fig S6


SET1
RPB4
BRE1
-
pFL
Δ500
-
rpb4-set1Δ500
pFL
rpb4-set1Δ500
+ + + - + -
+ + + + + - -
α-H3K4me3
α-H3K4me2
α-H3K4me1
α-H3
α-TBP
1 2 3 4 5 6 7