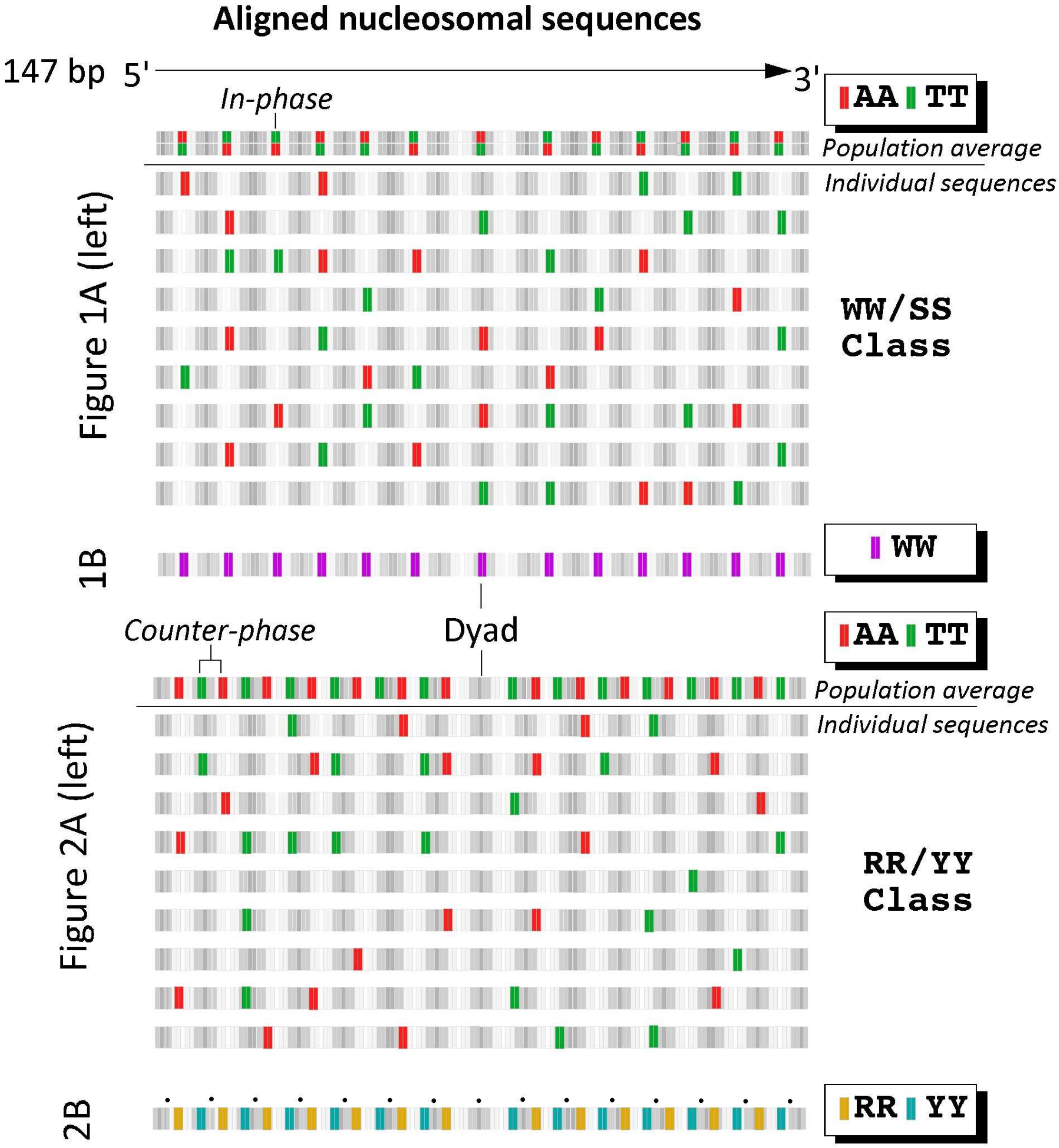
Supplementary Materials

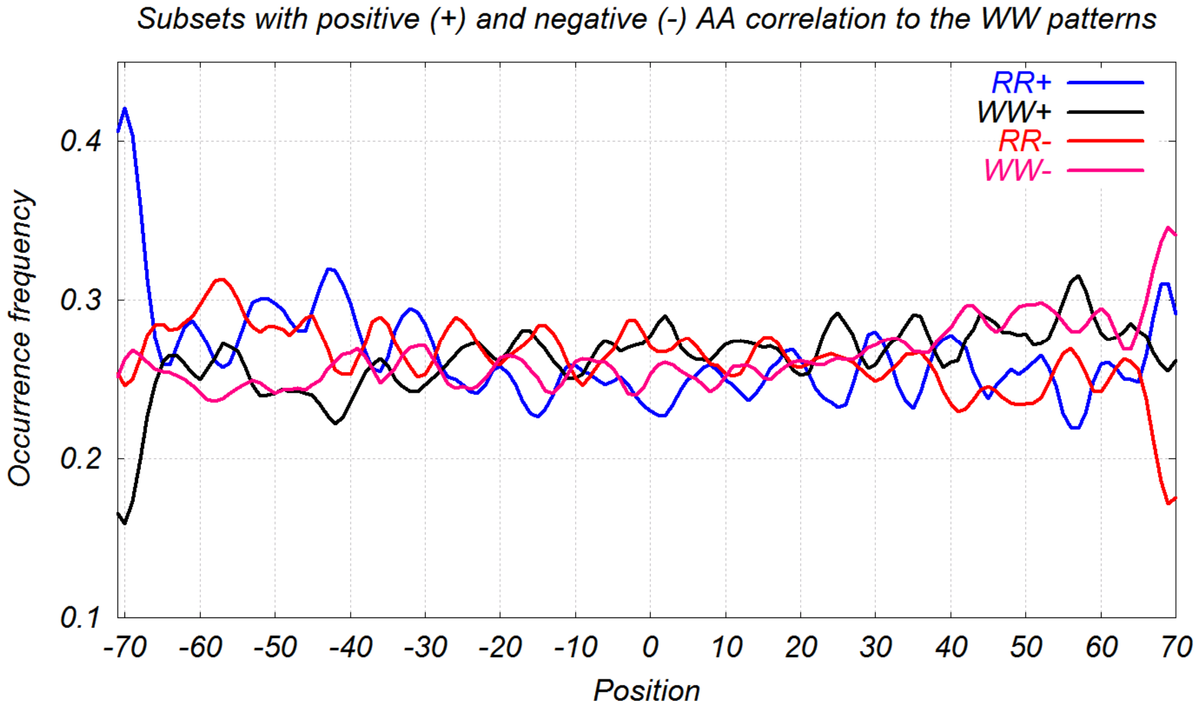
Supplementary Data

Yeast genes with highest correlation to the AA/TT component of the anti-RR/YY pattern (highest correlation of 0.8 or more in any given point of scanning of the genomic sequence (ORF + 1000bp up- and downstream) by the anti-AA/TT pattern: YBL105C, YBR179C, YDR319C, YER019W, YER119C, YGL045W, YGL046W, YGR111W, YGR125W, YHR072W, YJL005W, YJL025W, YJL131C, YJL155C, YJR062C, YJR063W, YJR064W, YKL189W, YLR028C, YLR187W, YLR412W, YML041C, YML113W, YML114C, YMR016C, YMR043W, YNL067W, YNL087W, YOL036W, YOR030W, YOR063W, YPL093W. Repressor proteins binding the aforementioned genes: ROX1, YFL052w, RDR1, NRG1, MGA1, RCS1.

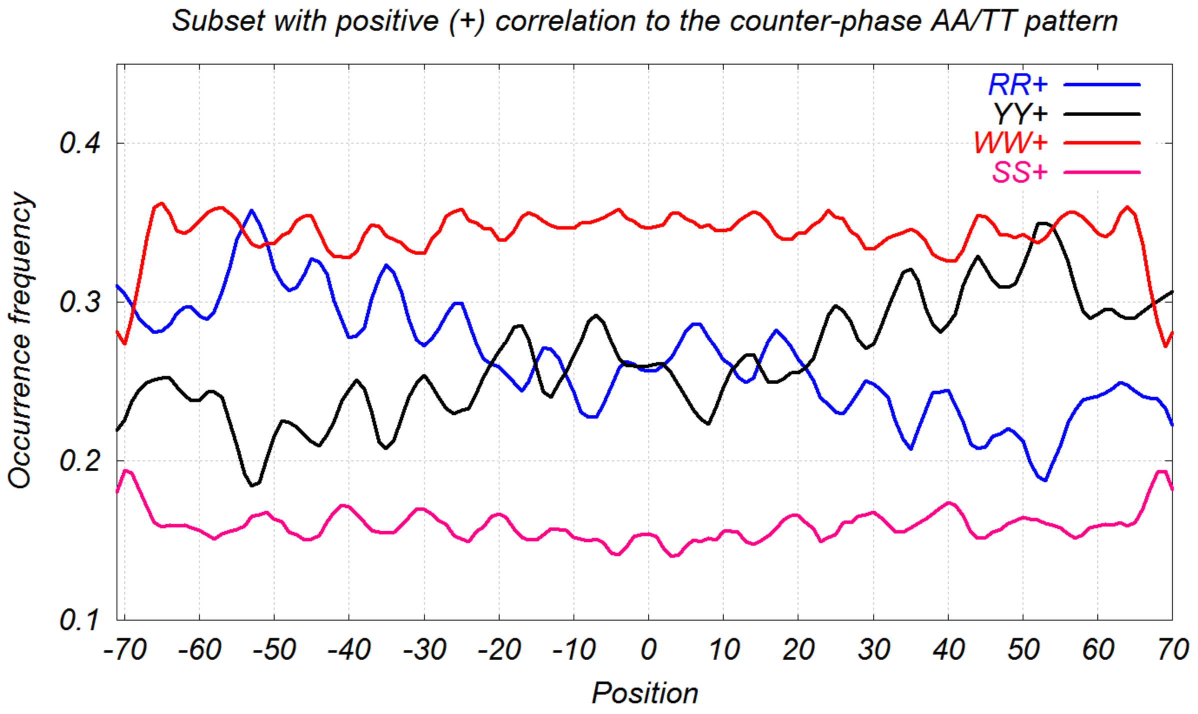
Supplementary Figures



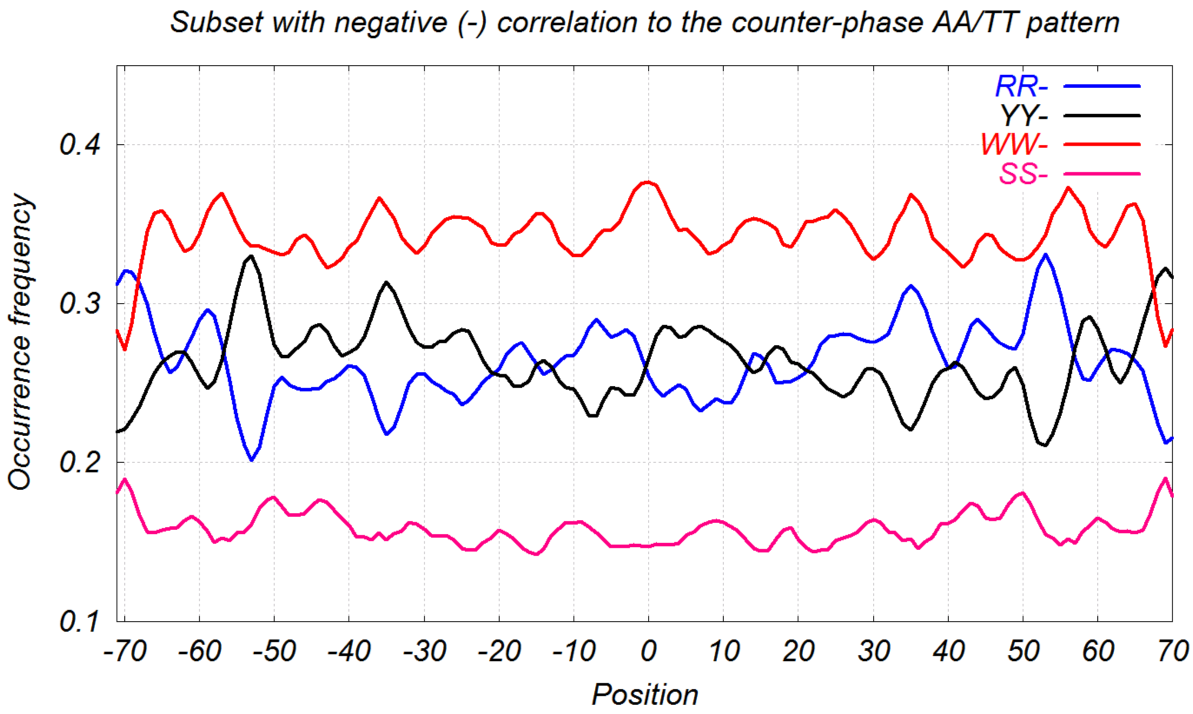
Supplementary Figure 1. Schematic of dinucleotide distributions in nucleosomal DNA sequences as it relates to main text Figures 1 and 2. Gray reflects where the major groove faces inward.



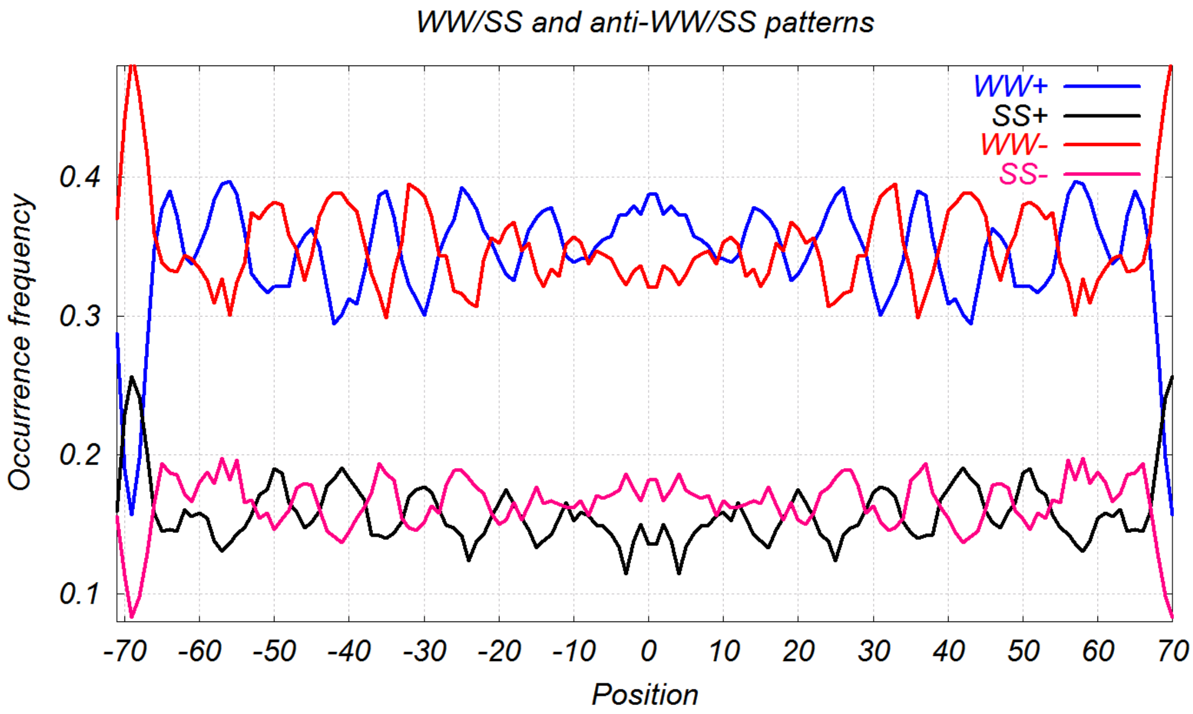
(A) Occurrence frequencies for combined dinucleotides along nucleosomal DNA sequence corresponding to Fig. 5 in the main text. Subsets with AAs positively correlating with the major WW pattern from (Albert et al. 2007) (+) and with AAs negatively correlating with the major WW (-) are shown. Position 0 coincides with the dyad symmetry of nucleosome.



(B) Dinucleotide occurrence frequencies along nucleosomal DNA sequence corresponding to Fig. 6A in the main text. Subset with positive correlation to the counter-phase AA/TT pattern from (Ioshikhes et al. 1996).

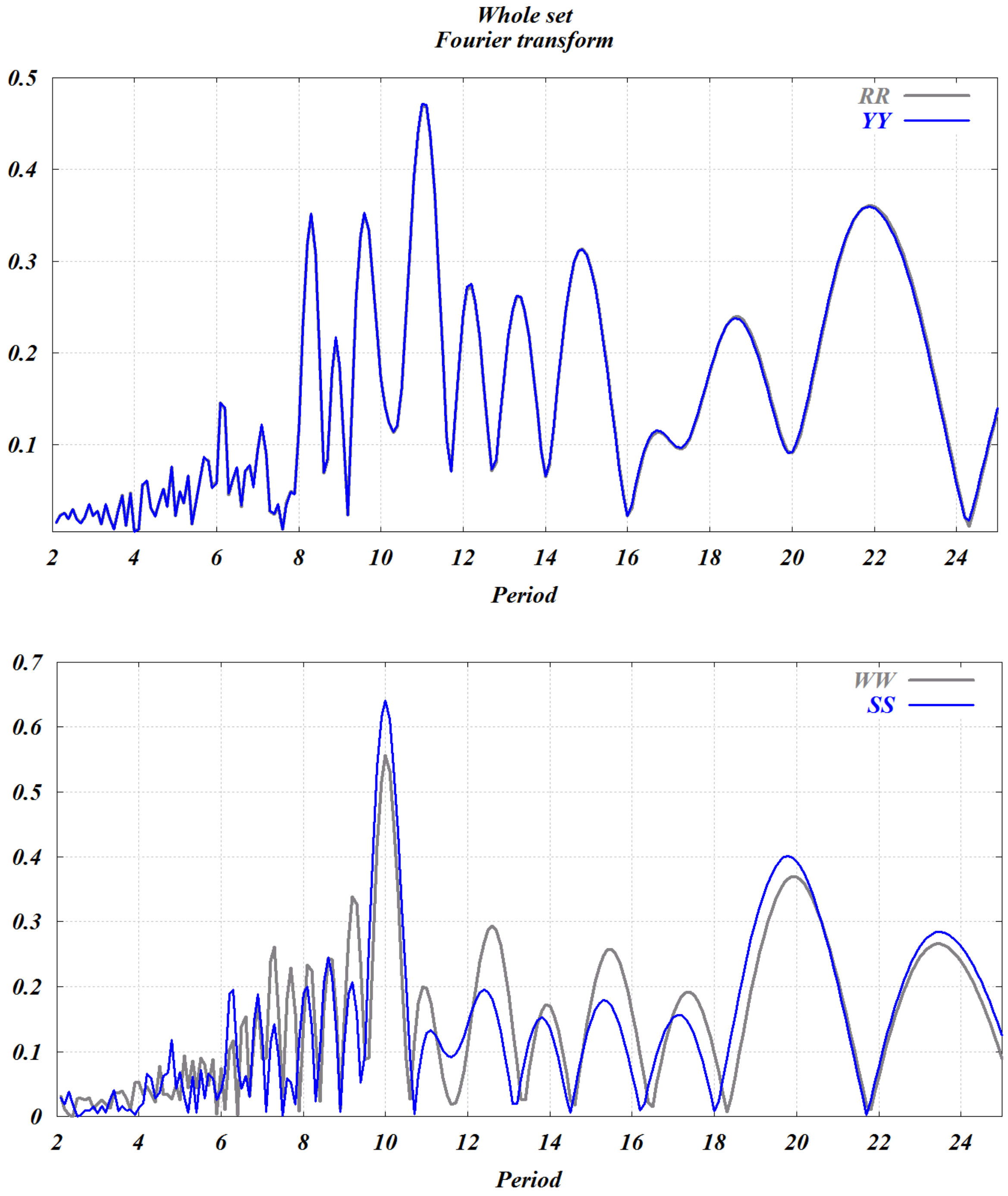


(C) Dinucleotide occurrence frequencies along nucleosomal DNA sequence corresponding to Fig. 6b in the main text. Subsets with negative correlation to the counter-phase AA/TT pattern from (Ioshikhes et al. 1996).

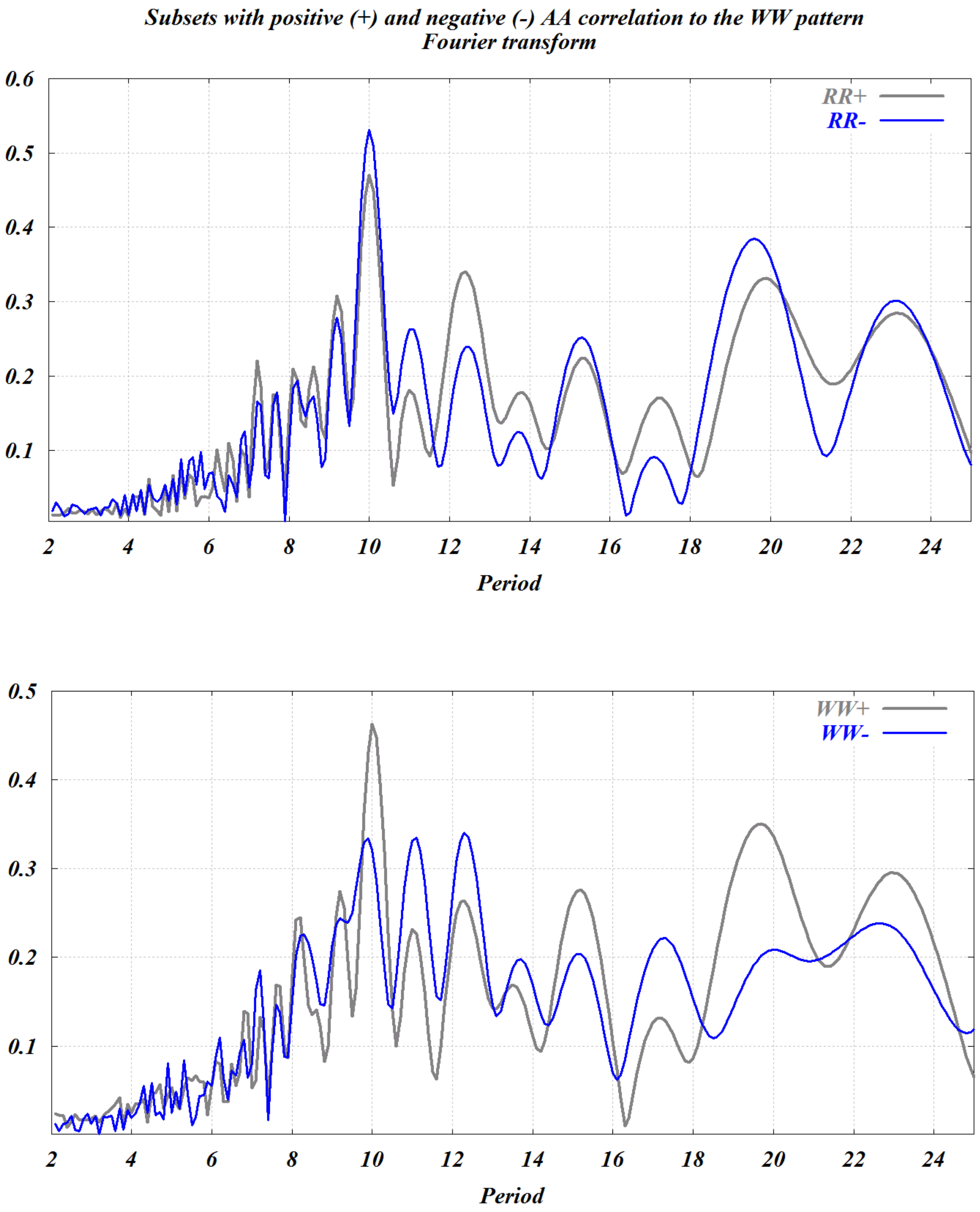


(D) Dinucleotide occurrence frequencies along nucleosomal DNA sequence corresponding to Fig. 7 in the main text. Subsets with positive (+) and negative (-) WW/SS correlation to the major WW/SS pattern (Albert et al. 2007).

Supplementary Figure 2. Combined dinucleotide occurrence frequency distributions along nucleosomal DNA sequence. Subsets with positive (+) and negative (-) correlation to the different patterns (panels A-D correspond respectively to Figs. 5, 6A, 6B, and 7 in the main text).



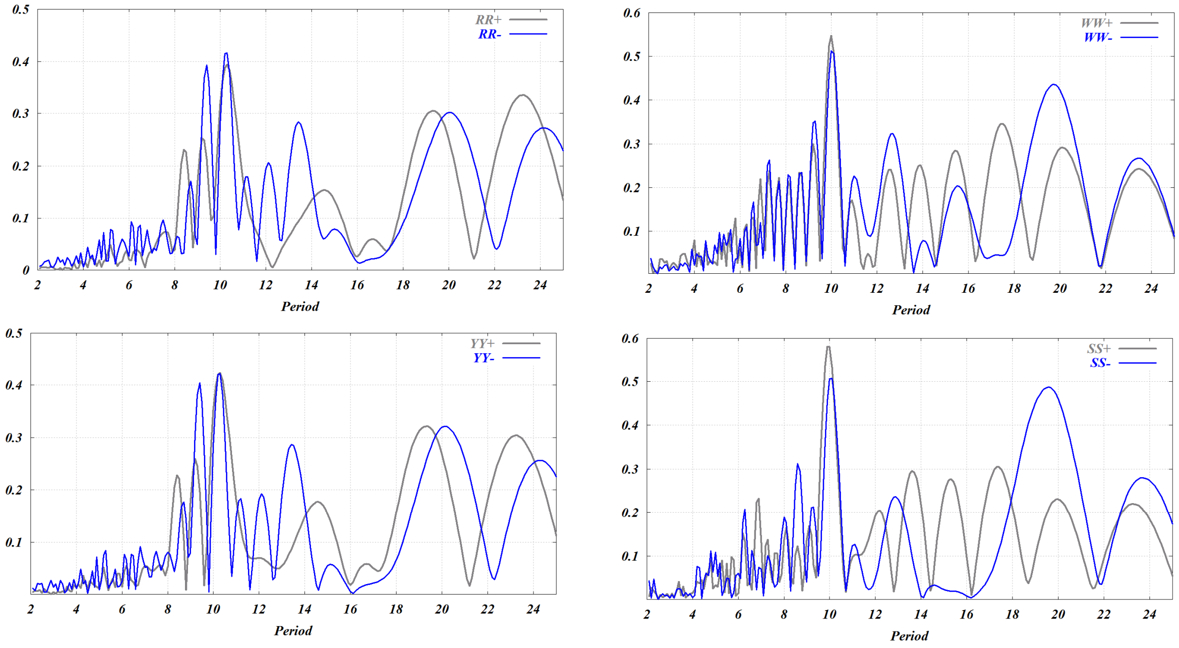
(A) Fourier transform of dinucleotide distributions along nucleosomal DNA sequence for well phased H2A.Z nucleosomes used as a training set (according to Albert et al. 2007) (corresponds to Fig. 3 in the main text.) The spectra coincide for RR and YY (top panel).



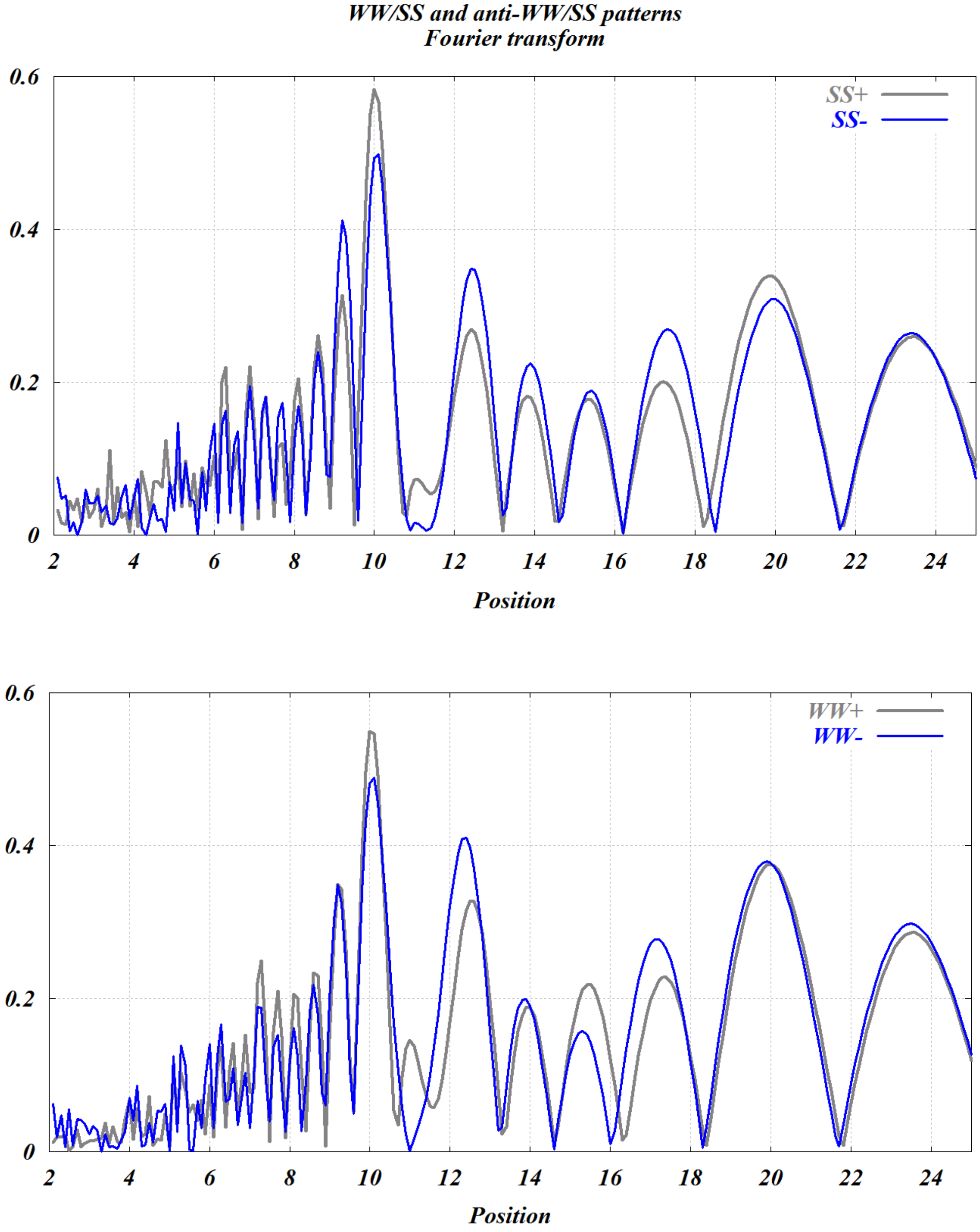
Subsets with positive (+) and negative (-) AA correlation to the WW pattern
Fourier transform

(B) Fourier transform of dinucleotide distributions along nucleosomal DNA sequence for subsets with AAs positively correlating with the major WW pattern from (Albert et al. 2007) (+) and with AAs negatively correlating with the major WW pattern (-) (corresponds to Fig. 5 in the main text).

Subsets with positive (+) and negative (-) correlation to the counter-phase AA/TT pattern
Fourier transform

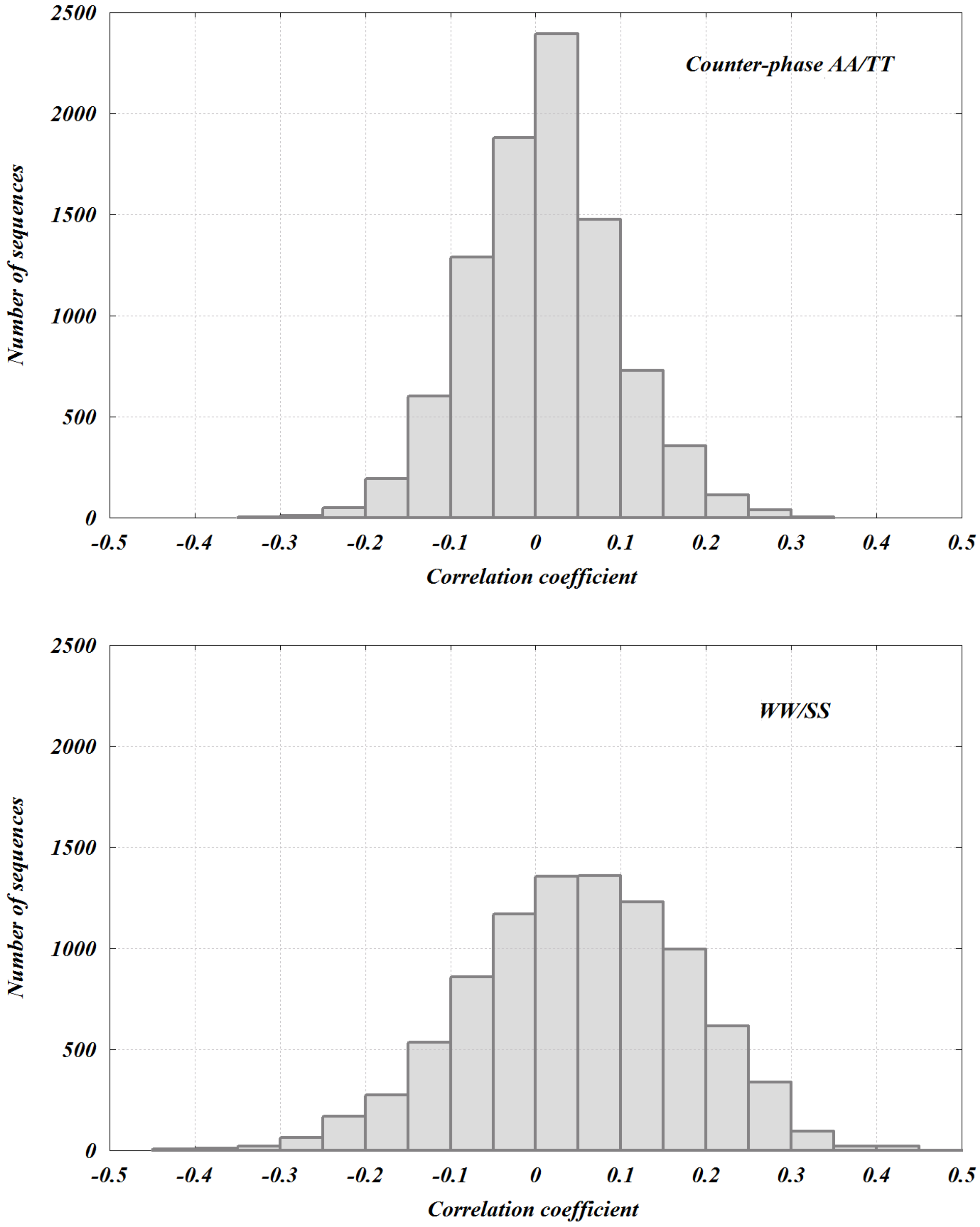


(C) Fourier transform of dinucleotide distributions along nucleosomal DNA sequence for subsets with positive (+) and negative (-) correlation to the counter-phase AA/TT pattern (Ioshikhes et al. 1996) (corresponds to Figs. 6A and B in the main text).

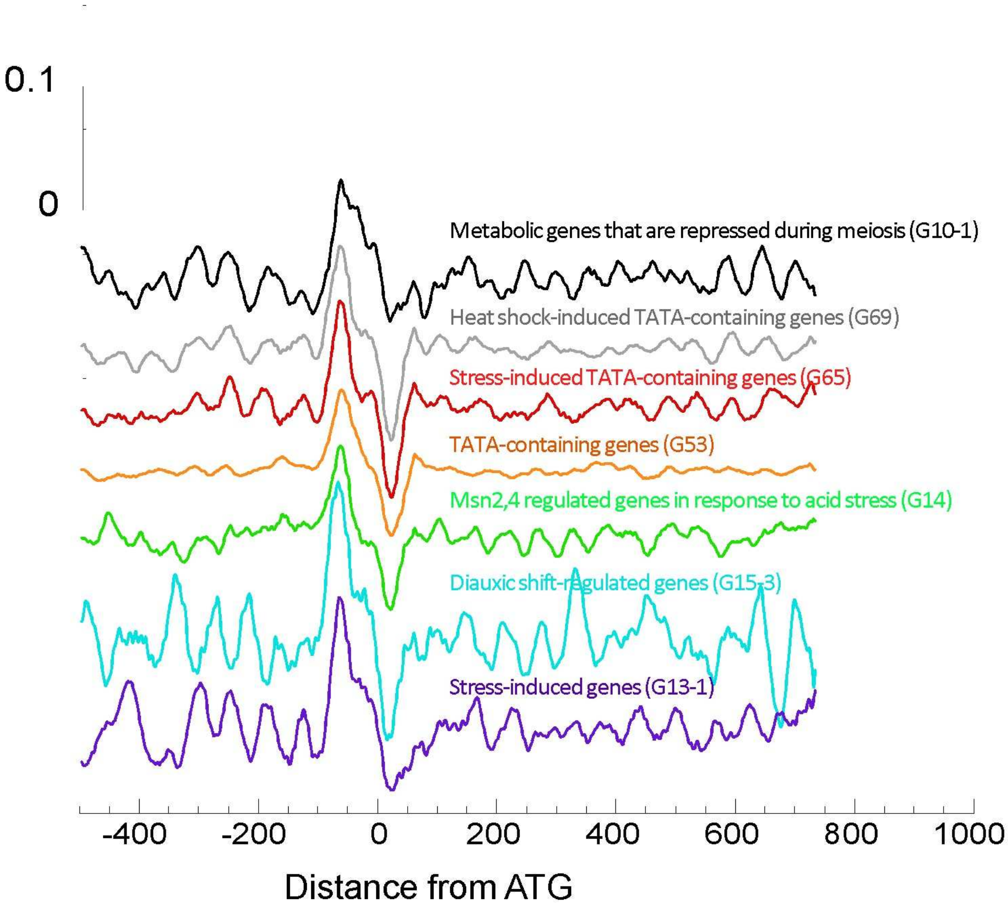


(D) Fourier transform of dinucleotide distributions along nucleosomal DNA sequence for subsets with positive (+) and negative (-) WW/SS correlation to the major WW/SS pattern (Albert et al. 2007) (corresponds to Fig. 7 in the main text).

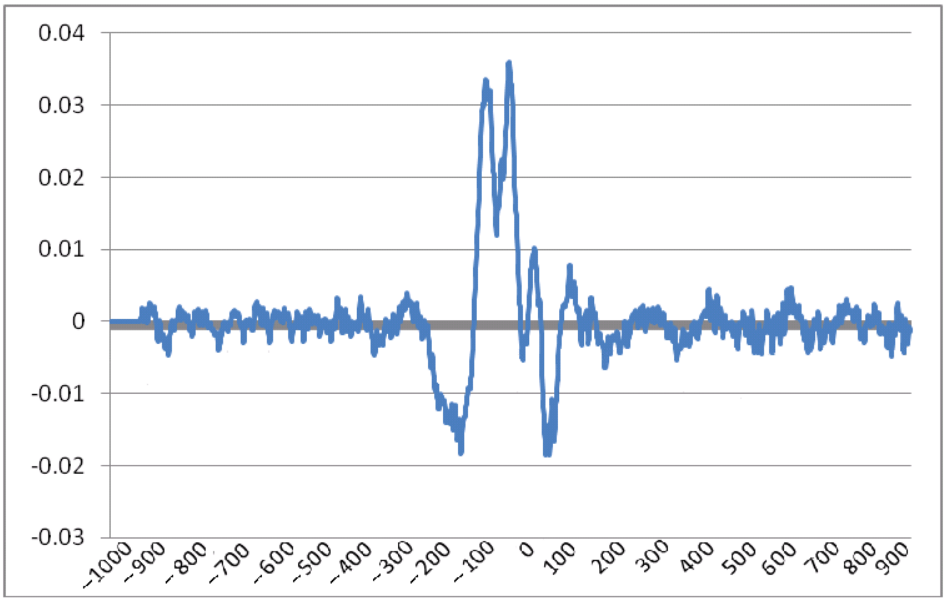
Supplementary Figure 3. Fourier transform of dinucleotide distributions along DNA sequence for sets with positive (+) and negative (-) correlation to the different patterns (panels A-D correspond respectively to Figs. 3, 5, 6a,b and 7 in the main text). Period with length ~10 bp is clearly observed in each graph.



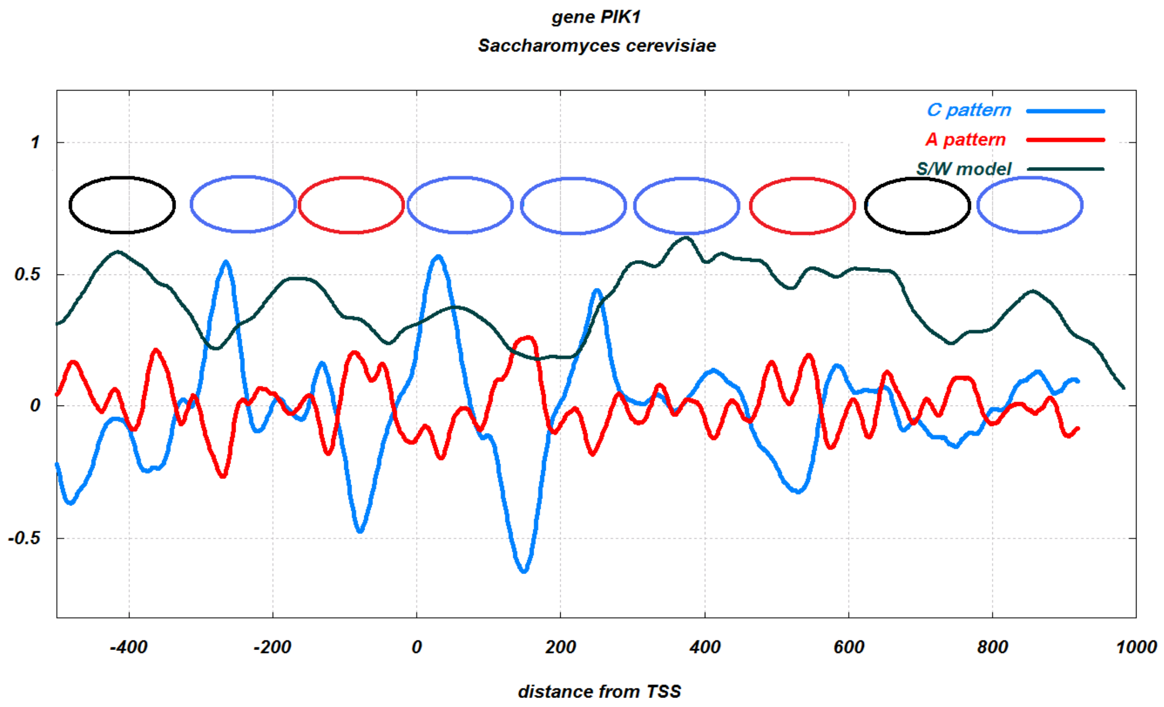
Supplementary Figure 4. Distributions of number of nucleosomal sequences with different correlation to anti counter-phase AA/TT pattern from (Ioshikhes et al. 1996) (top) and WW/SS pattern from (Albert et al. 2007) (bottom).

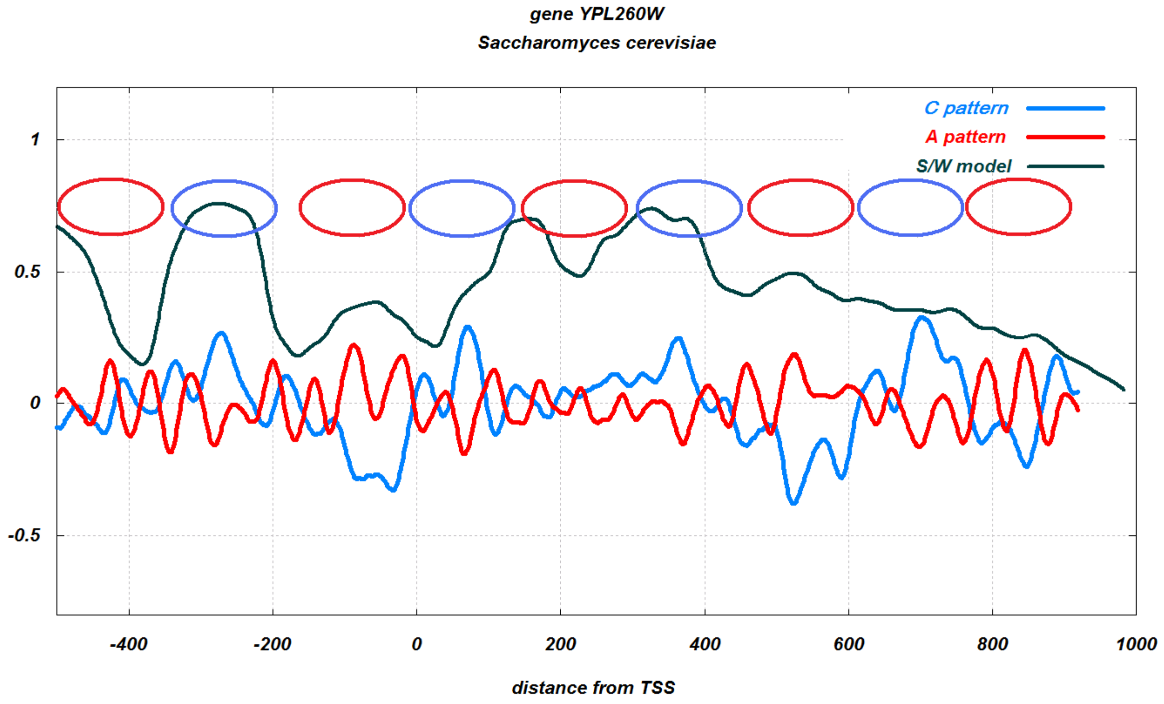


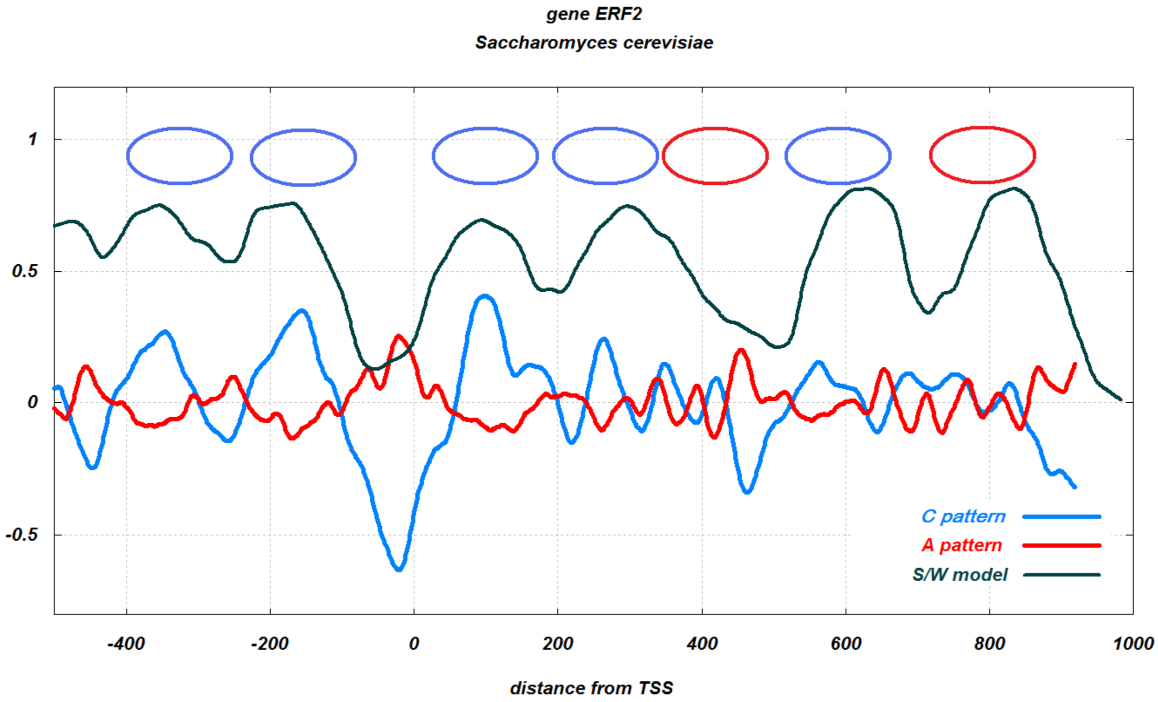
Supplementary Figure 5. Most prominent anti-NPS correlation distributions around first ATG codon for different promoter groups. The genes studied were those potentially repressible (genes that have low transcription frequency or turned down upon heat shock or are active only during sporulation or have TATA boxes). Center of tentative nucleosome window is shown at the X axis, with correlation magnitude at the Y. Anti- counter-phase AA/TT pattern was used for mapping. Position 0 coincides with the 1st ATG codon. Notice clear peaks in the area depleted of regular nucleosomes. Subsets of genes were from retrieved from other studies: Metabolic genes that become repressed during meiosis (Gasch et al. 2000). TATA-containing genes induced by heat shock (Basehoar et al. 2004; Zanton et al. 2004). TATA-containing genes up-regulated in response to environmental stress (Gasch et al. 2000; Basehoar et al. 2004). TATA box containing genes (Basehoar et al. 2004). Msn2,4-regulated genes in response to acid stress (Causton et al. 2001). Genes regulated in response to diauxic shift (Causton et al. 2001). Common environmental stress response genes up-regulated by stress (Causton et al. 2001).



Supplementary Figure 6. General average anti-NPS distribution around TSS (David et al. 2006).


gene PIK1
Saccharomyces cerevisiae
C pattern
A pattern
S/W model
1
0.5
0
-0.5
-400
-200
0
200
400
600
800
1000
distance from TSS


gene YPL260W
Saccharomyces cerevisiae
C pattern
A pattern
S/W model
1
0.5
0
-0.5
-400
-200
0
200
400
600
800
1000
distance from TSS



Supplementary Figure 7. Examples of the nucleosome mapping for particular promoters. NPS correlation profiles for various patterns are provided. Blue line (C) is related to the counter-phase AA/TT pattern published in (Mavrich at al. 2008a), red line (A) – to the counter-phase anti-NPS AA/TT pattern discussed here. Nucleosomes successfully mapped by either of the patterns are depicted by blue or red ovals respectively. Black ovals represent nucleosomes not mapped by either of the patterns. Mapping by an alternative model (Segal et al. 2006) is presented by black line (SW).

Supplementary references

Basehoar AD, Zanton SJ, Pugh BF. 2004. Identification and distinct regulation of yeast TATA box-containing genes. *Cell* **116:** 699-709.

Causton HC, Ren B, Koh SS, Harbison CT, Kanin E, Jennings EG, Lee TI, True HL, Lander ES, Young RA. 2001. Remodeling of yeast genome expression in response to environmental changes. *Mol Biol Cell* **12:** 323-337.

Gasch AP, Spellman PT, Kao CM, Carmel-Harel O, Eisen MB, Storz G, Botstein D, Brown PO. 2000. Genomic expression programs in the response of yeast cells to environmental changes. *Mol Biol Cell* **11:** 4241-4257.

Zanton SJ, Pugh BF. 2004. Changes in genome-wide occupancy of core transcriptional regulators during heat stress. *Proc Natl Acad Sci USA* **101:** 16843-16848.