Supplementary data.

Legends to figures:

Figure S1.

Comparison of mapping data from partial MNase digestion (blue arrows), parallel sequencing (1) (orange arrows) and tiled micro-array determinations (2) (brown arrows). For the positions determined by parallel sequencing the coordinates shown are the average of the data from both DNA strands; for the positions determined by tiled microarray analysis the coordinates shown are taken from the HMM computed data. The precision of the determined positions varies depending on whether individual nucleosomes are well positioned or 'fuzzy'. Low resolution periodicity profiles (51 bp window) are shown for DNA sequences in selected loci. The genes shown are ADH2 (3), ADY2 (this work), BAR1 (4), CHA1 (5), GAL1_10 (6), HMLα (7), PHO5 (8), recombination enhancer (9), SUC2 (10), and RVS167/SAC7 (1,2). In some genes, e.g. ADH2, there is reasonable agreement between all three methods of determining positions. In others, e.g. CHA1, PHO5, recombination enhancer and RVS17/SAC7 there are regions where determinations by different methods differ substantially. For ADY2 and ADH2 the principal H2A-Z containing nucleosomes (blue dots) are indicated.

Figure S2. *In vivo* mapping of *ADY2* nucleosomes

(A) Nystatin permeabilised spheroplasts from *S. cerevisiae* cells (strain CY26, ref. 11) were treated with MNase (0.2, 0.4 and 0.8 units/0.25 ml), purified and digested with *Eco*RI restriction endonuclease (map position +792 from ATG). After electrophoresis on 1.5% agarose gel and Southern blotting, the samples were hybridised with probe E (arrow) obtained by PCR amplification of genomic DNA with the following oligonucleotides: 5'-GTACCATGAAATCCACTGTTATG-3' (forward, starting position +610 from ATG) and 5'-CTGCATATGCGTTGTACCAA-3' (reverse, starting positions +775). M, molecular weight marker; N, purified genomic DNA treated *in vitro* with MNase.

Nucleosome positions from the ATG are as follows: -2 (from -438 to -308); -1 (from -178 to -18); +1 (from -18 to +172); +2 (from +282 to +447).

(B) As in (A) but MNase doses were 0.3 and 0.6 units/0.25 mL, restriction endonuclease digestion was with *Sal*I (map position +1647 from ATG), hybridisation was with probe S (arrow), obtained with the following oligonucleotides: 5'-GAAGCCAGAAGAAAGCTG-3' (forward, starting position +1558 from ATG) and 5'-ATCACACTGTGACCAGCT-3' (reverse, starting position +1635 from ATG).
Nucleosome positions from the ATG are as follows: +2 (from +282 to +447); +3 (from +447 to +647); +4 (from +647 to +847); +5 (from +847 to +1017); +6 (from +1017 to +1207); +7 (from +1207 to +1347).

Figure S3.

Averaged periodicity profiles of DNA from promoter nucleosomes (black line), non-promoter nucleosomes (red line), chicken erythrocyte nucleosomes (blue line) and yeast *in vitro* selected nucleosomes (green line). Profiles calculated using a 51 bp window. The length of the DNA sequences from promoter and non-promoter nucleosomes is 151 bp, that from chicken erythrocyte and yeast *in vitro* selected nucleosomes is 145 bp. All sequences are aligned on their midpoints, indicated by an arrow. The difference in form between promoter and non-promoter yeast nucleosomal DNA is similar to that shown in Figure 4a calculated with a 21 bp window. The calculated periodicity values are higher for the 51 bp window because of the larger window size. The range of periodicity values for promoter DNA (0.92-1.28) is greater than that for the chicken erythrocyte set (0.95-1.08).

Figure S4

DNA stacking energy and periodicity profiles for S4.1) the ADH2/UBP15 and ADY2 genes and S4.2) the central regions of CHA1/VAC17 and GAL10/GAL1 genes. The stacking energy/base step was calculated using a running 50 bp window. Mapped nucleosome midpoints are shown as in Figure S1. Numbering of nucleosomes is directly related to the gene so, for example, for GAL10/GAL1 the -1 nucleosome of each gene is shown. The nucleosomes in the immediate vicinity of the UAS in this selection have average central stacking energies between -0.88 and -1.10 kcals/mole/base step. The midpoint of the sequences is indicated by an arrow.

Figure S5.

5.1 Comparison of A/T content and TpA distribution in the set of 'promoter' (black line) and 'non-promoter' (red line) yeast nucleosomal DNA sequences.
5.2 Comparison of the distributions of ApA/TpT and TpA base-steps in the chicken erythrocyte nucleosomal DNA sequences (black line) (12) and the yeast nucleosomal DNA sequences mapped by partial micrococcal nuclease digestion (red line).
In both figures the plots were calculated as a running 3-bond average as described in ref. 12. The midpoint of the sequences is indicated by an arrow.

References:

1. Mavrich, T.N., Ioshikhes, I.P., Venters, B.J., Jiang, C., Tomsho, L.P., Qi, J., Schuster, S.C., Albert, I. & Pugh, B.F. (2008). A barrier nucleosome model for statistical positioning of nucleosomes throughout the yeast genome. *Genome Res.* 18, 1073-1083.
2. Lee, W., Tillo, D., Bray, N., Morse, R.H., Davis, R.W., Hughes, T.R. & Nislow, C. (2007). A high-resolution atlas of nucleosome occupancy in yeast. *Nat. Genet.* 39, 1235-1244.
3. Verdone, L., Camilloni, G., Di Mauro, E. & Caserta, M. (1996). Chromatin remodeling during *Saccharomyces cerevisiae ADH2* gene activation. *Mol. Cell Biol* 16, 1978-1988.
4. Shimizu, M., Roth, S.Y., Szent-Gyorgyi, C. & Simpson, R.T. (1991). Nucleosomes are positioned with base pair precision adjacent to the α2 operator in *Saccharomyces cerevisiae*. *EMBO J.* 10, 3033-3041
5. Moreira, J.M. & Holmberg, S. (1998). Nucleosome structure of the yeast CHA1 promoter: analysis of activation-dependent chromatin remodeling of an RNA-polymerase-II-transcribed gene in TBP and RNA pol II mutants defective in vivo in response to acidic activators. *EMBO J.* 17, 6028-6038.
6. Li, B. & Reese, J.C. (2001). Ssn6-Tup1 regulates RNR3 by positioning nucleosomes and affecting the chromatin structure at the upstream repression sequence. *J. Biol. Chem.* 276, 33788-33797.
7. Weiss, K. & Simpson, R. T. (1998) High-resolution structural analysis of chromatin at specific loci: *Saccharomyces cerevisiae* silent mating type locus HMLα. *Mol. Cell. Biol.* 18, 5392-5403.

8. Almer, A., Rudolph, H., Hinnen, A. & Hörz, W. (1986). Removal of positioned nucleosomes from the yeast PHO5 promoter upon PHO5 induction releases additional upstream activating DNA elements. *EMBO J.* 5, 2689-2696.

9. Weiss, K. & Simpson, R.T. (1997). Cell type-specific chromatin organization of the region that governs directionality of yeast mating type switching. *EMBO J.* 16, 4352-4360

10. Gavin, I.M. & Simpson, R.T. (1997). Interplay of yeast global transcriptional regulators Ssn6p-Tup1p and Swi-Snf and their effect on chromatin structure. *EMBO J.* 16, 6263-6271.

11. Agricola, E., Verdone, L., Xella, B., Di Mauro, E. & Caserta, M. (2004). Common chromatin architecture, common chromatin remodeling, and common transcription kinetics of Adr1-dependent genes in *Saccharomyces cerevisiae*. *Biochemistry* 43, 8878-8884.

12. Satchwell, S.C., Drew, H.R. & Travers, A.A. (1986). Sequence periodicities in chicken nucleosome core DNA. *J. Mol. Biol.* 191, 659-675.

Figure S1.1

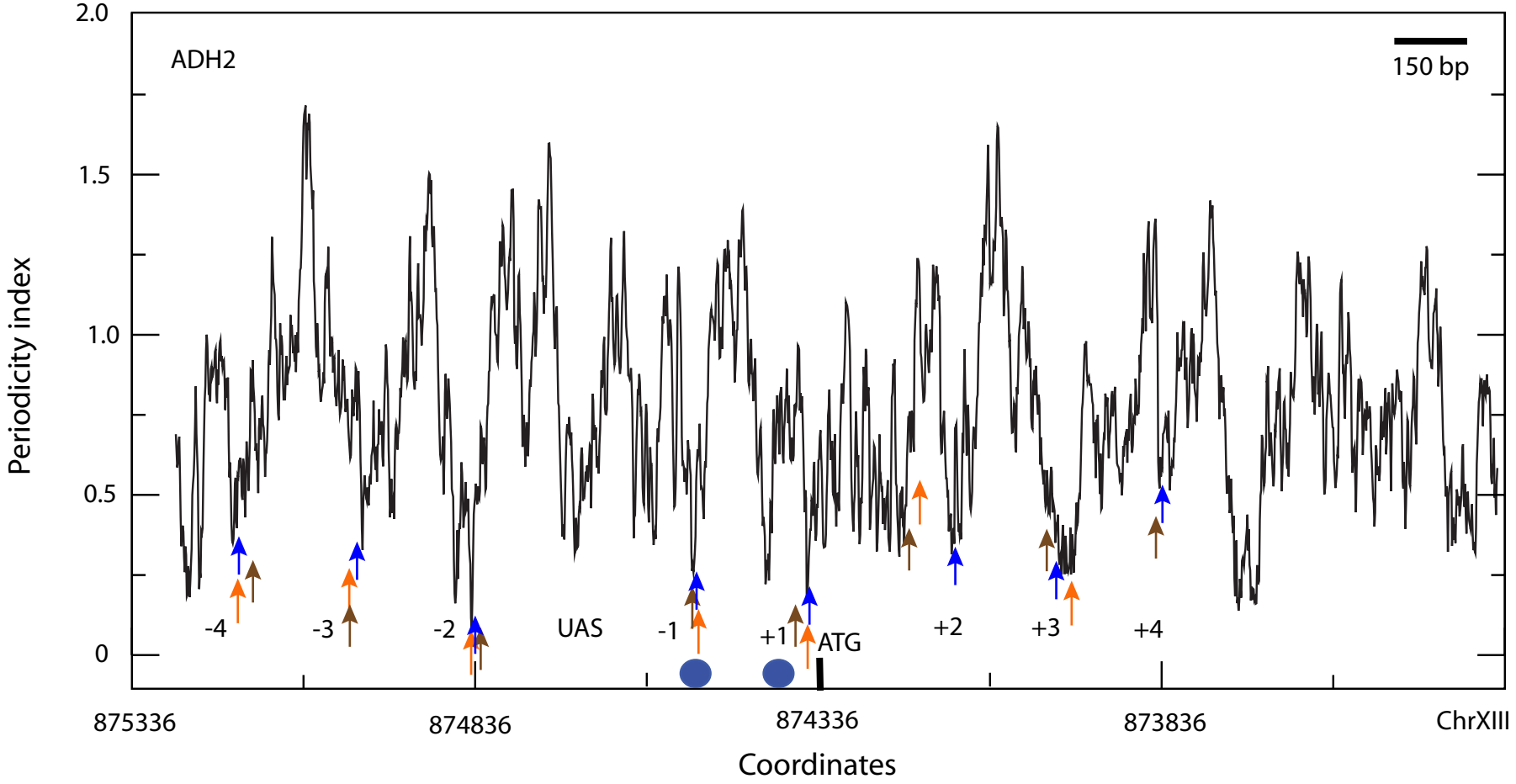

ADH2
150 bp
2.0
1.5
1.0
0.5
0
Periodicity index
-4
-3
-2
UAS
-1
+1
ATG
+2
+3
+4
875336
874836
874336
873836
ChrXIII
Coordinates

Figure S1.2

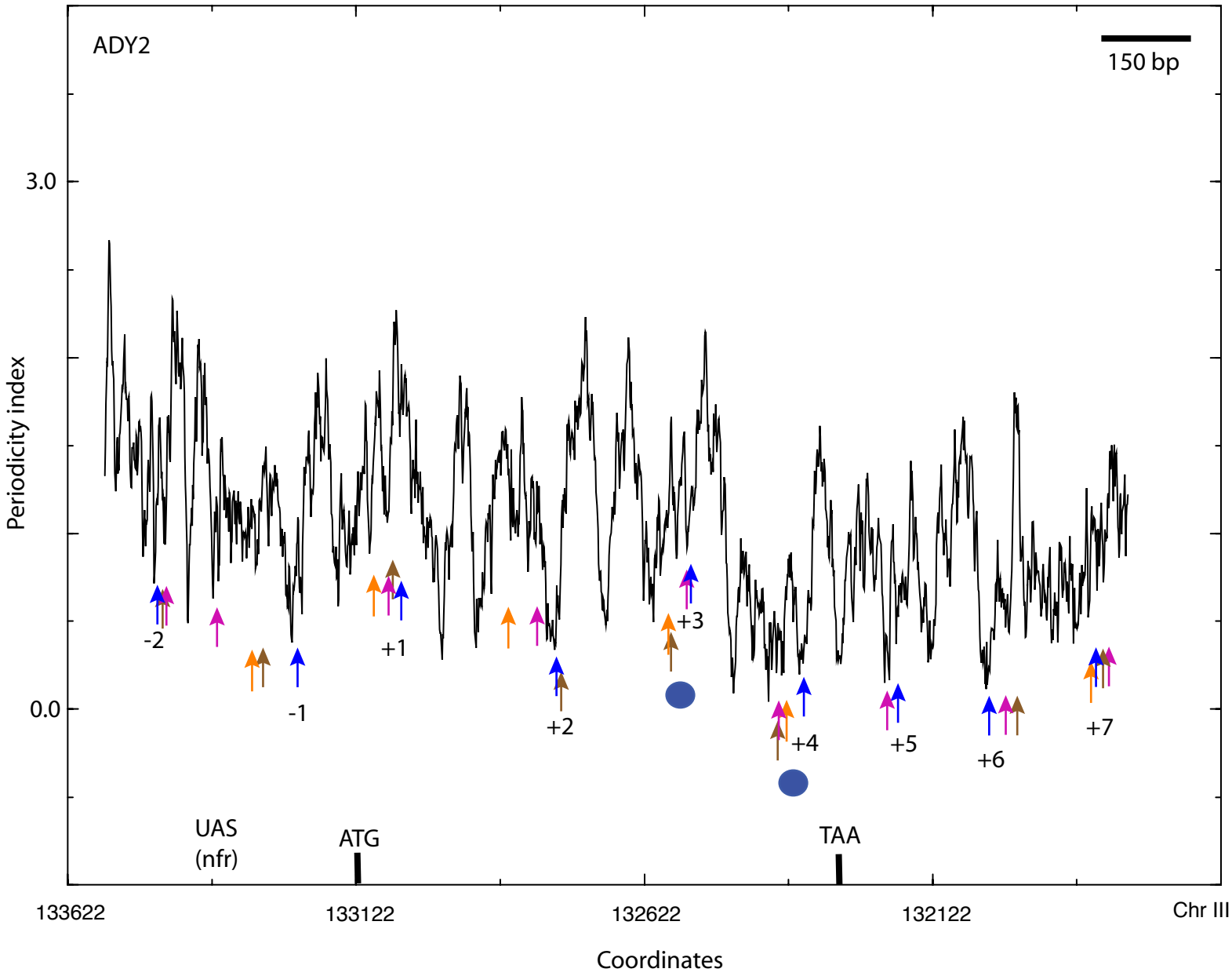

ADY2
150 bp
3.0
0.0
Periodicity index
-2
-1
+1
+2
+3
+4
+5
+6
+7
UAS
(nfr)
ATG
TAA
133622
133122
132622
132122
Chr III
Coordinates

Figure S1.3

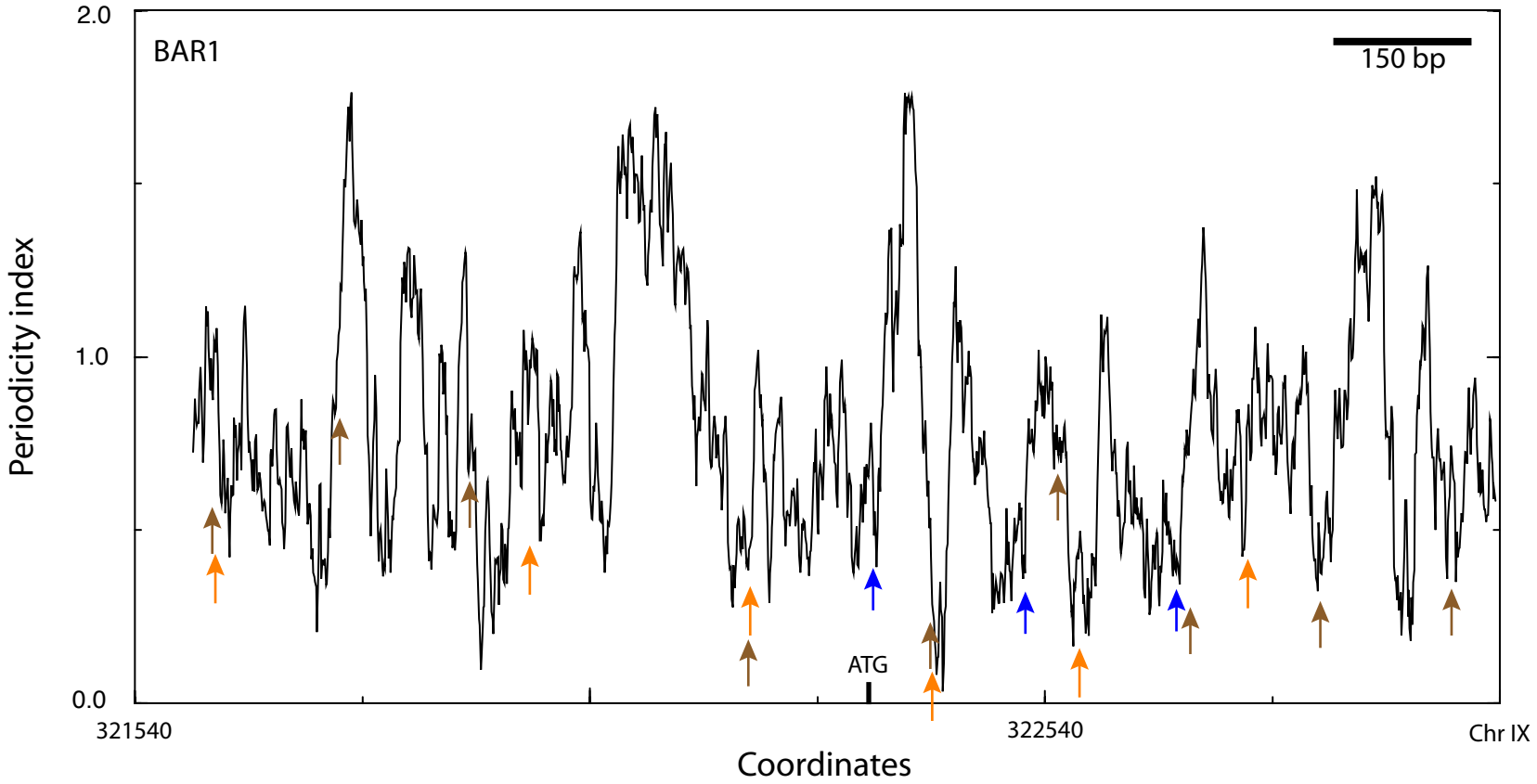

BAR1
150 bp
2.0
1.0
0.0
Periodicity index
ATG
321540
322540
Chr IX
Coordinates

Figure S1.4

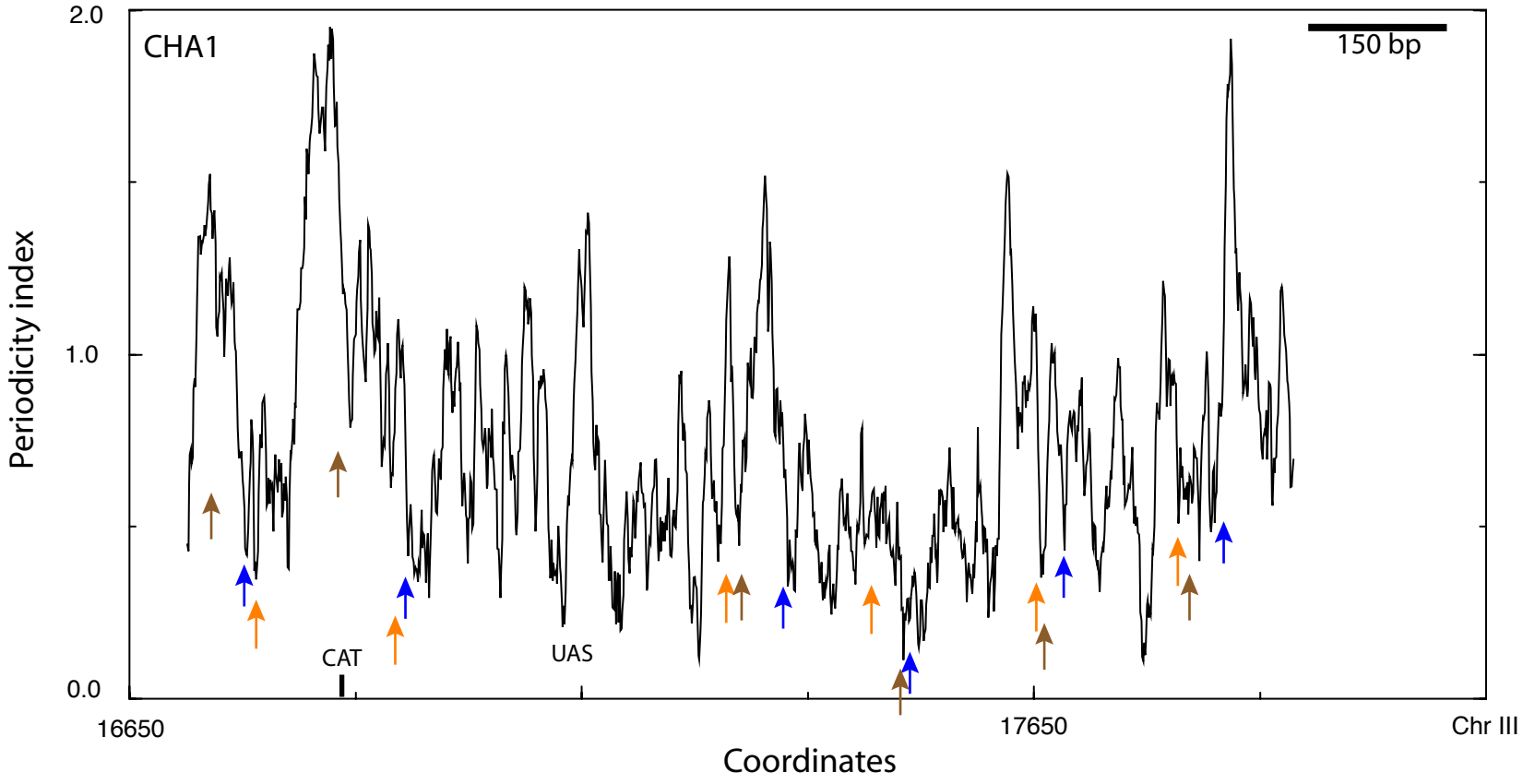

CHA1
150 bp
2.0
1.0
0.0
Periodicity index
CAT
UAS
16650
17650
Chr III
Coordinates

Figure S1.5

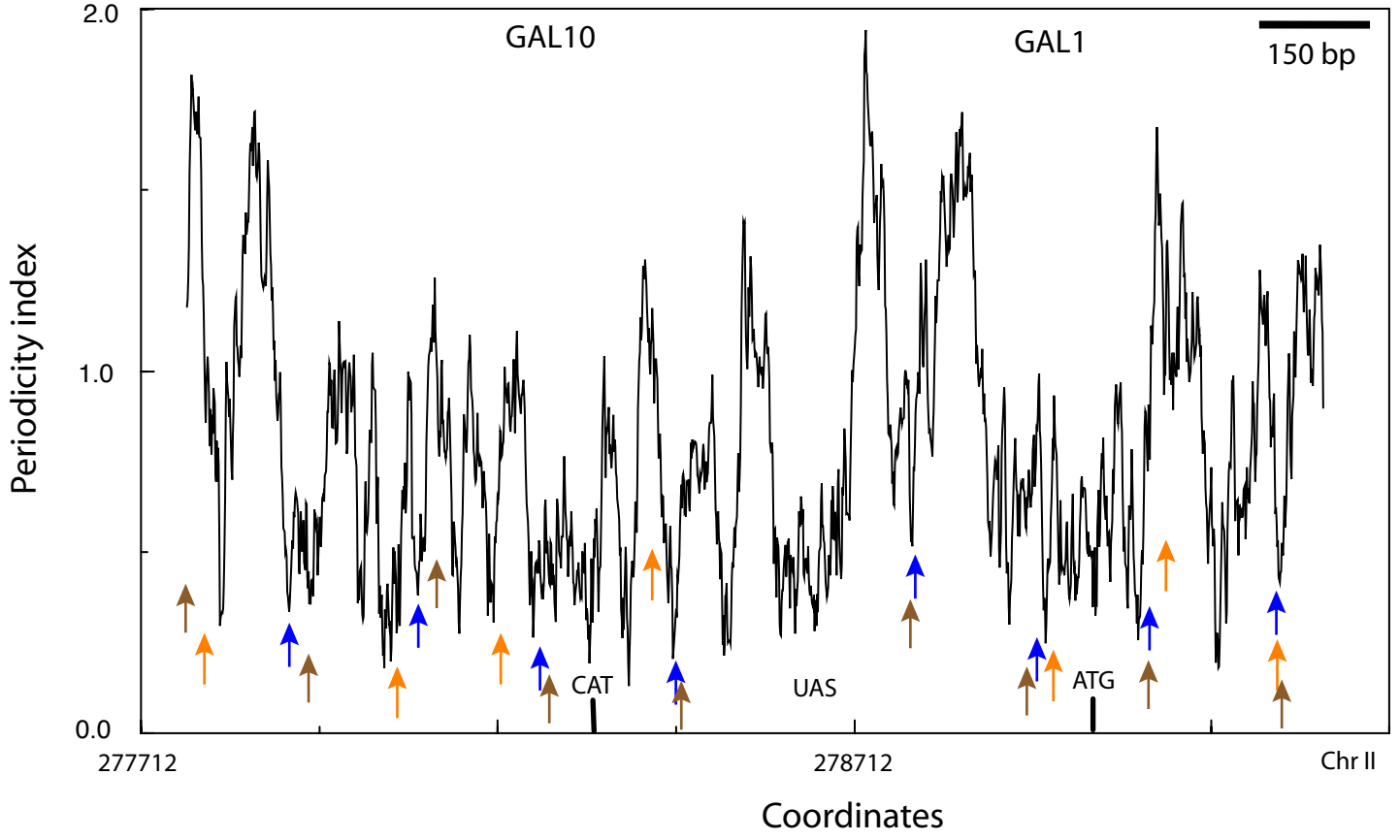

2.0
1.0
0.0
Periodicity index
GAL10
GAL1
150 bp
CAT
UAS
ATG
277712
278712
Chr II
Coordinates

Figure S1.6

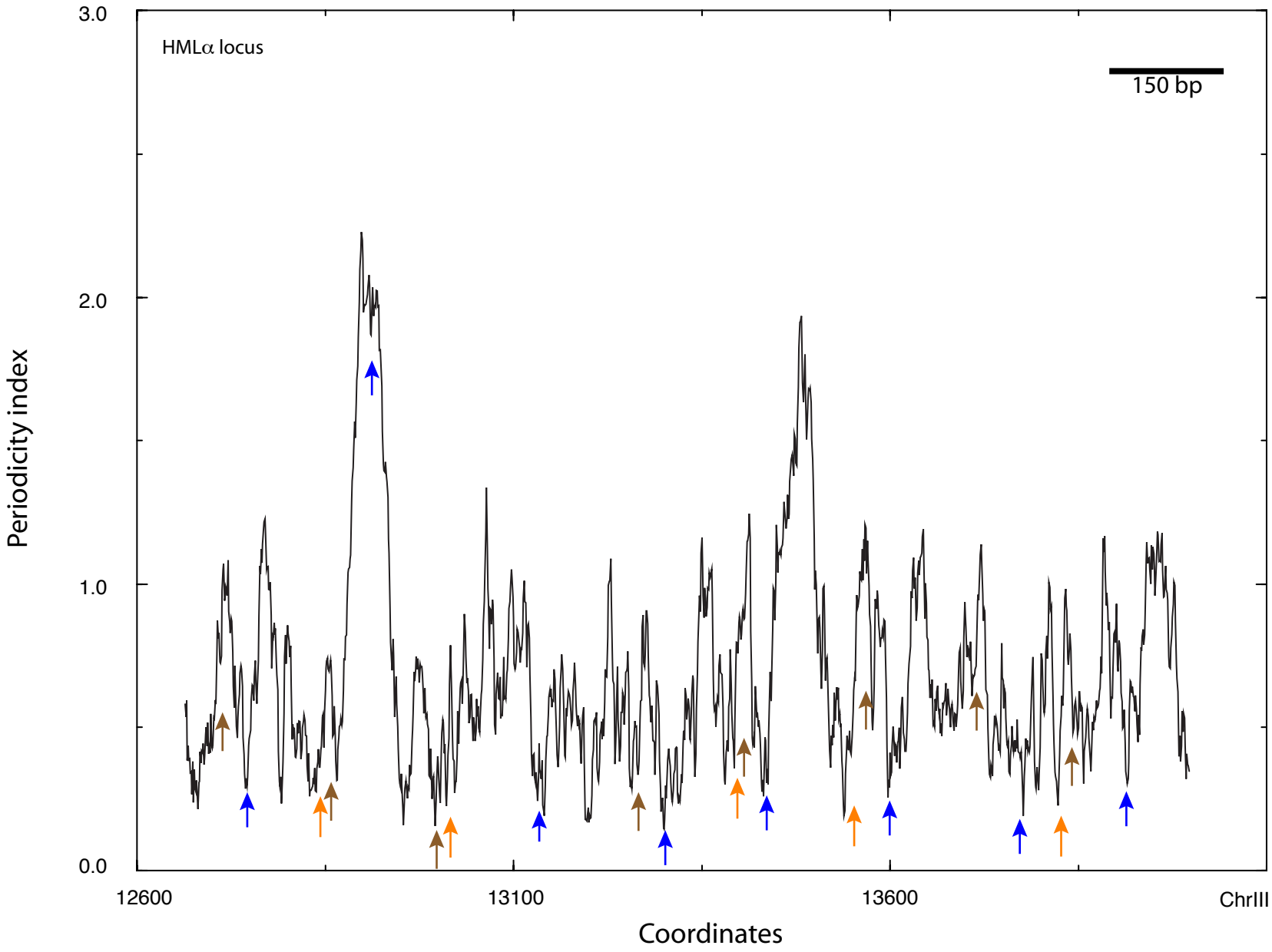

HMLα locus
150 bp
Periodicity index
3.0
2.0
1.0
0.0
12600
13100
13600
ChrIII
Coordinates

Figure S1.7

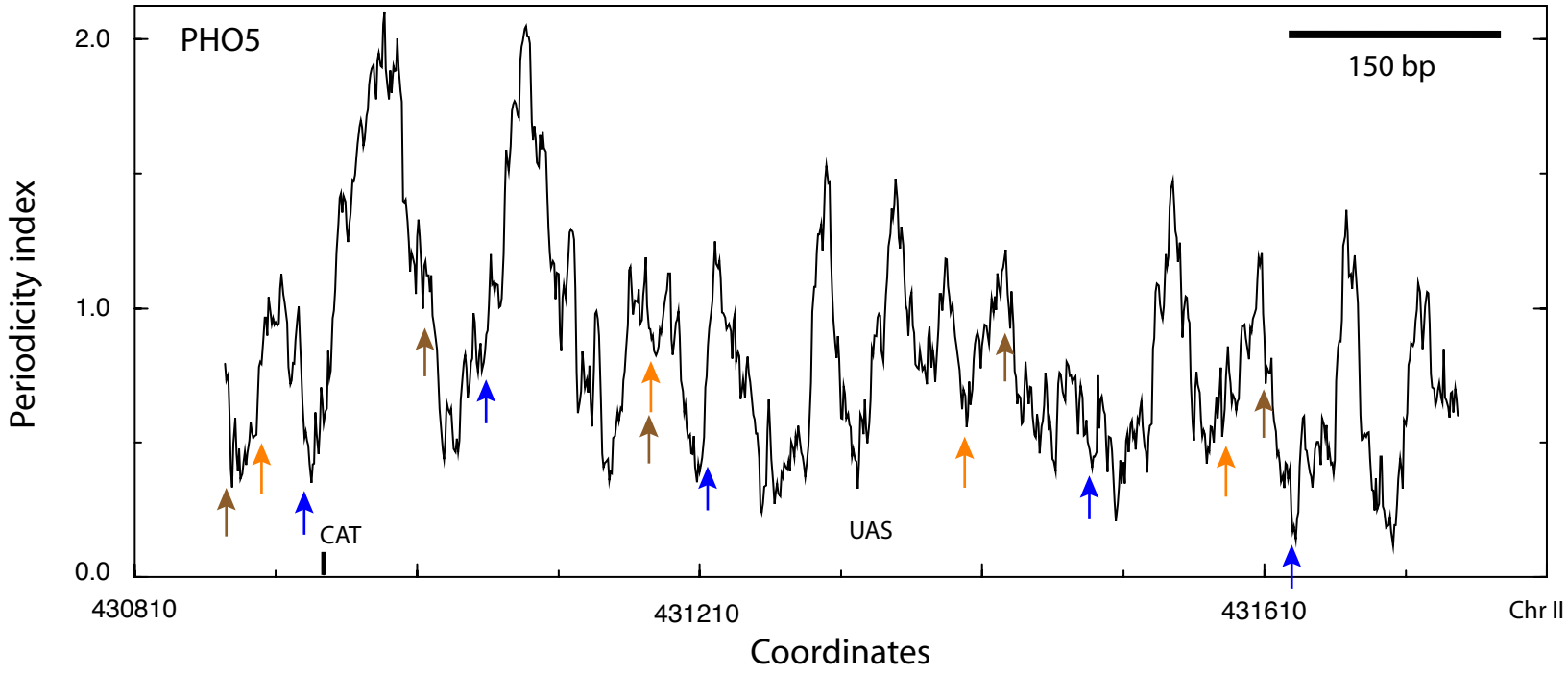

PHO5
150 bp
2.0
1.0
0.0
Periodicity index
CAT
UAS
430810
431210
431610
Chr II
Coordinates

Figure S1.8

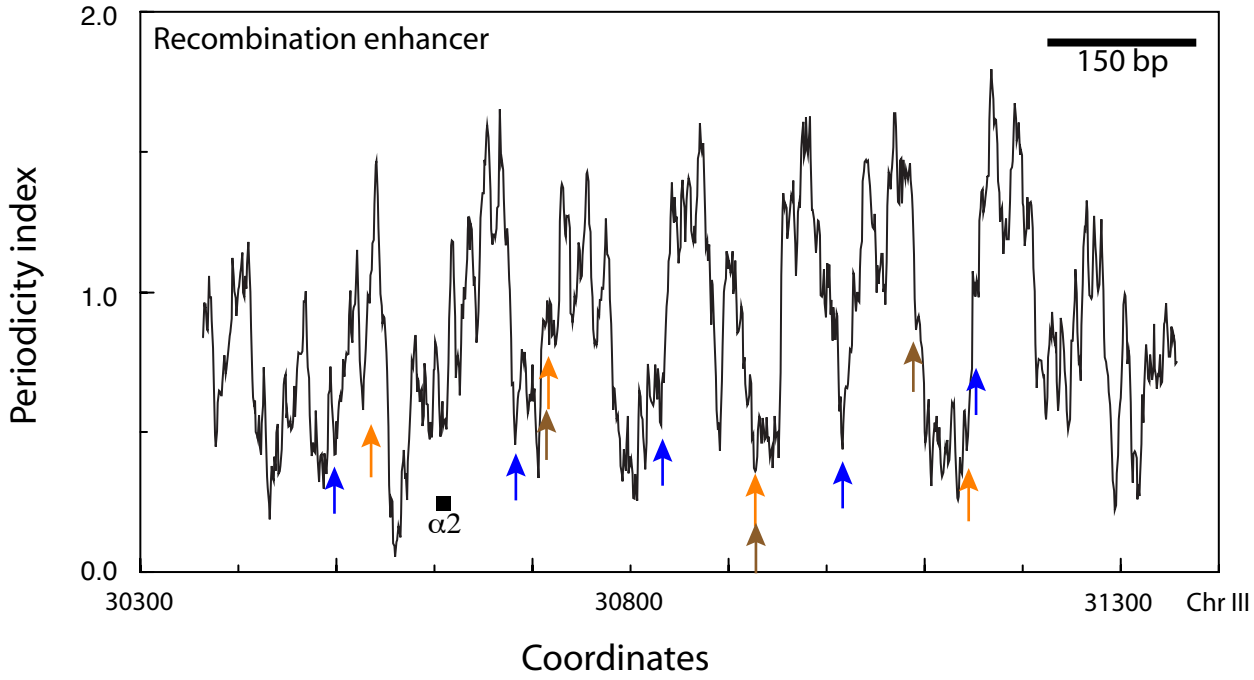

Recombination enhancer
150 bp
2.0
1.0
0.0
Periodicity index
α2
30300
30800
31300
Chr III
Coordinates

Figure S1.9

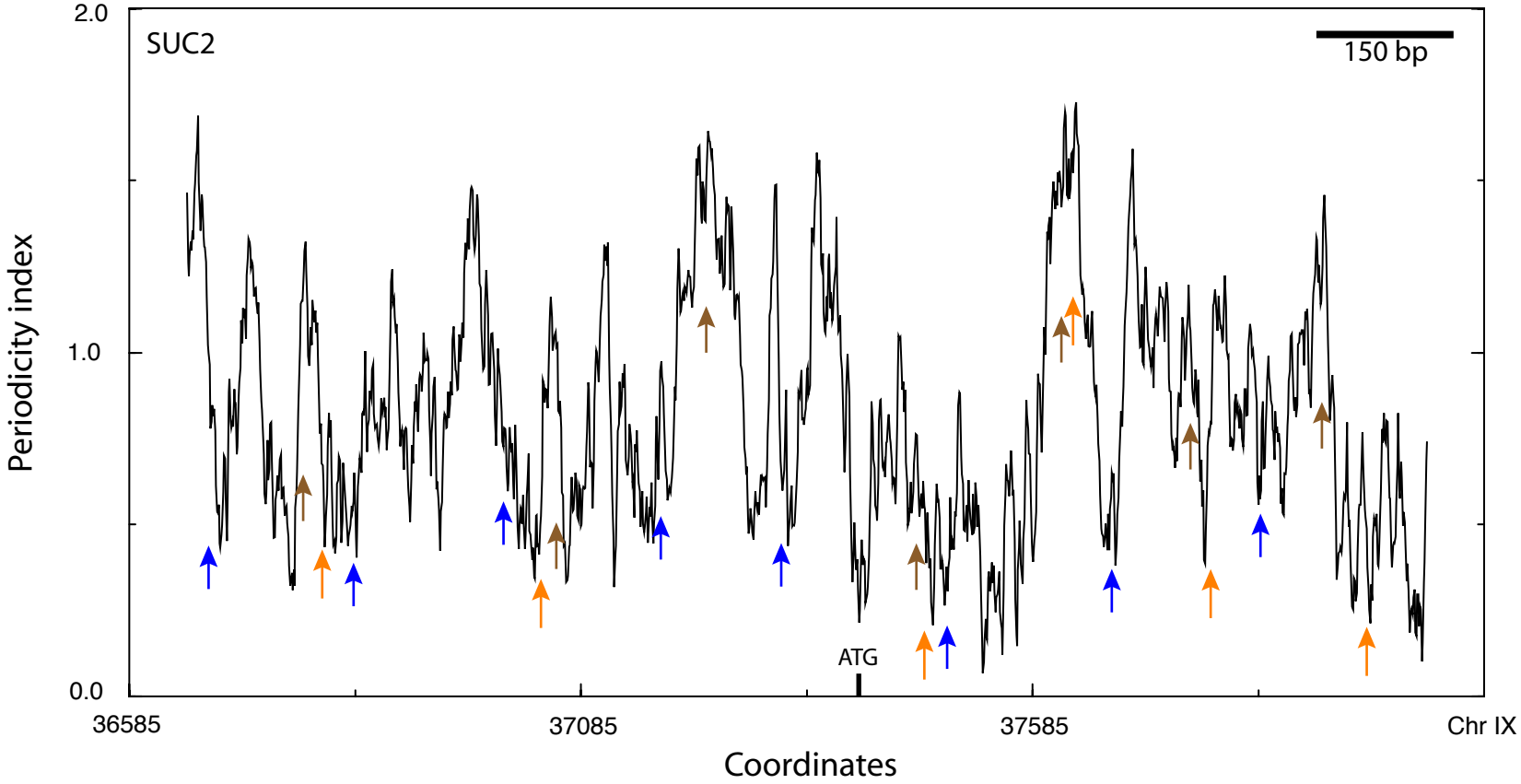

SUC2
150 bp
2.0
1.0
0.0
Periodicity index
ATG
36585
37085
37585
Chr IX
Coordinates

Figure S1.10

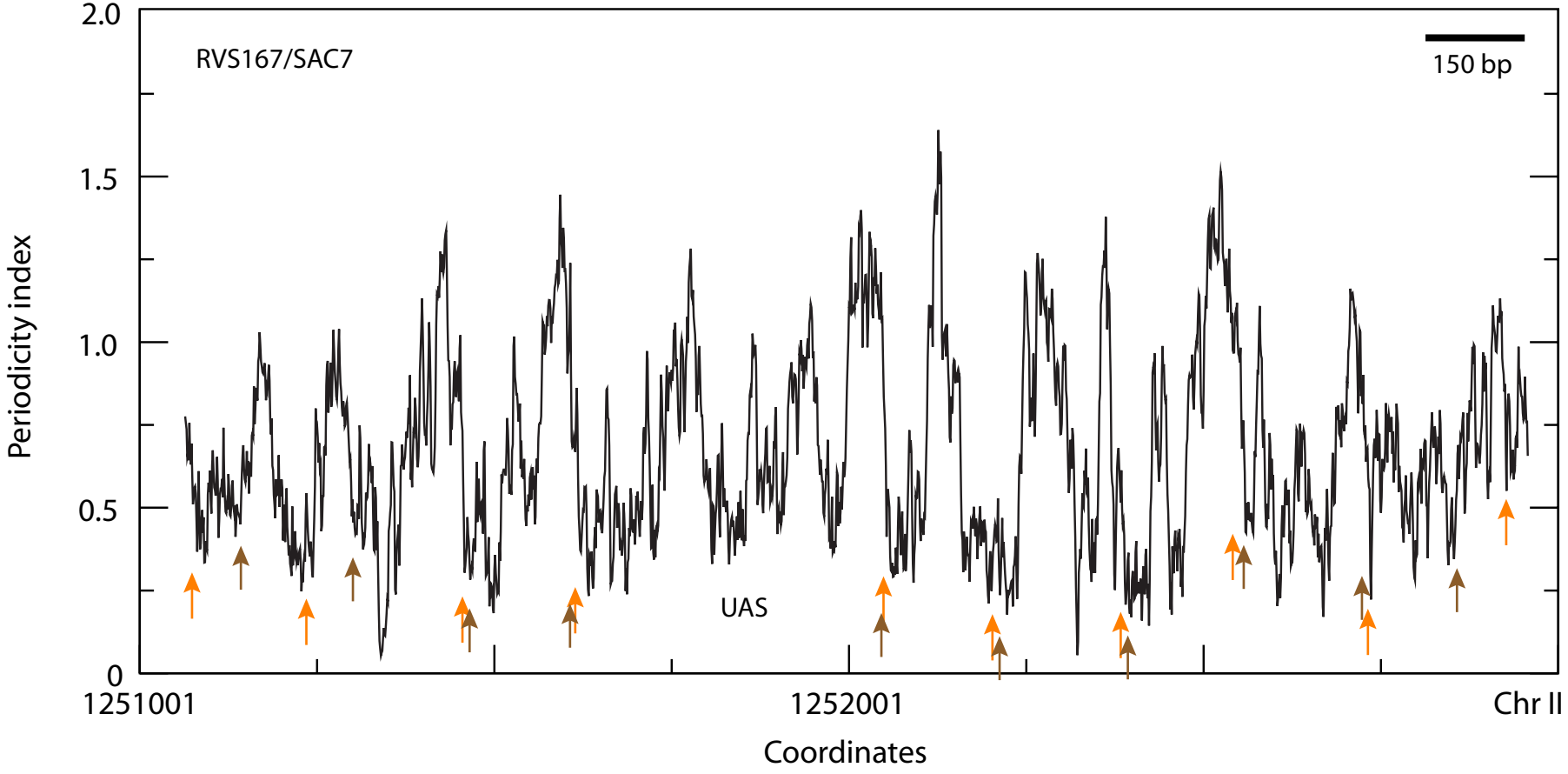

RVS167/SAC7
150 bp
UAS
Periodicity index
2.0
1.5
1.0
0.5
0
1251001
1252001
Chr II
Coordinates

Figure S2

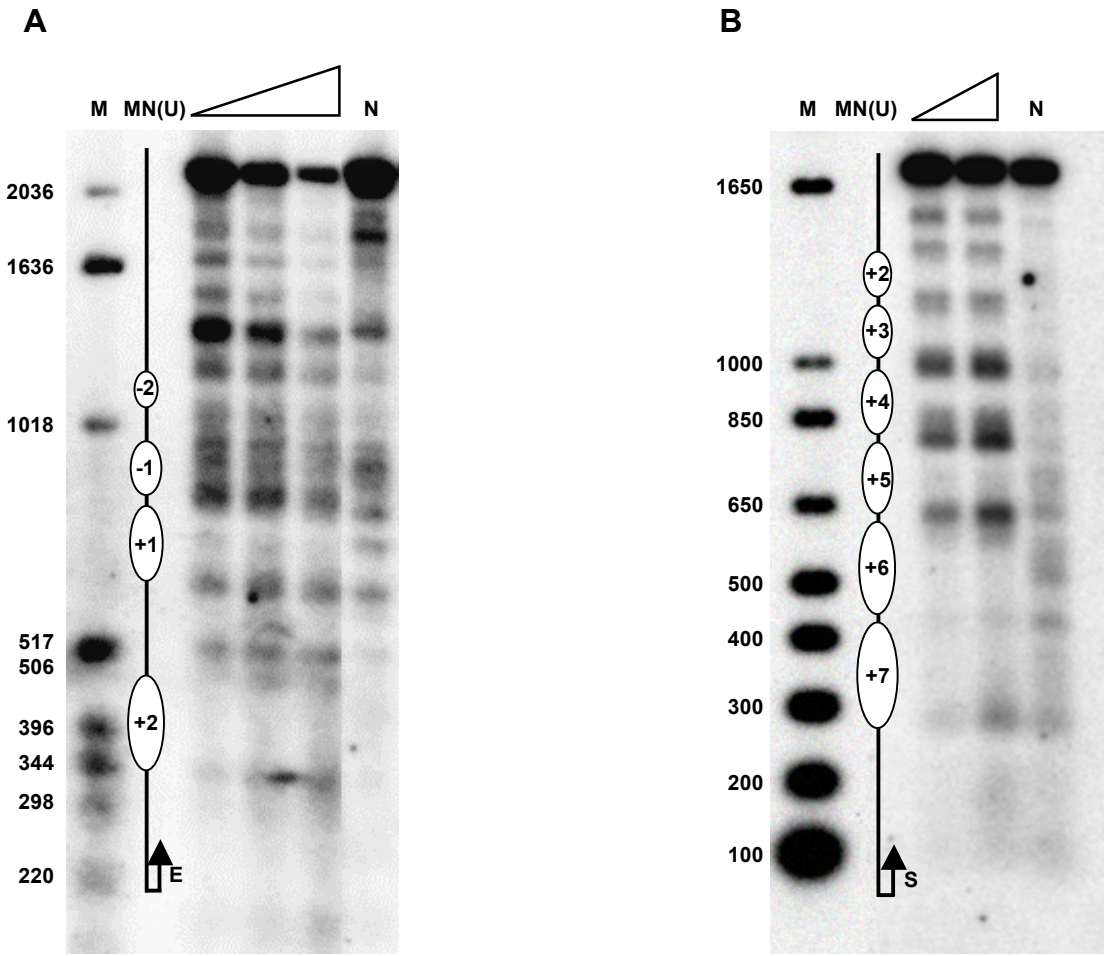

A
M
MN(U)
N
2036
1636
1018
517
506
396
344
298
220
-2
-1
+1
+2
E
B
M
MN(U)
N
1650
1000
850
650
500
400
300
200
100
+2
+3
+4
+5
+6
+7
S

Figure S3

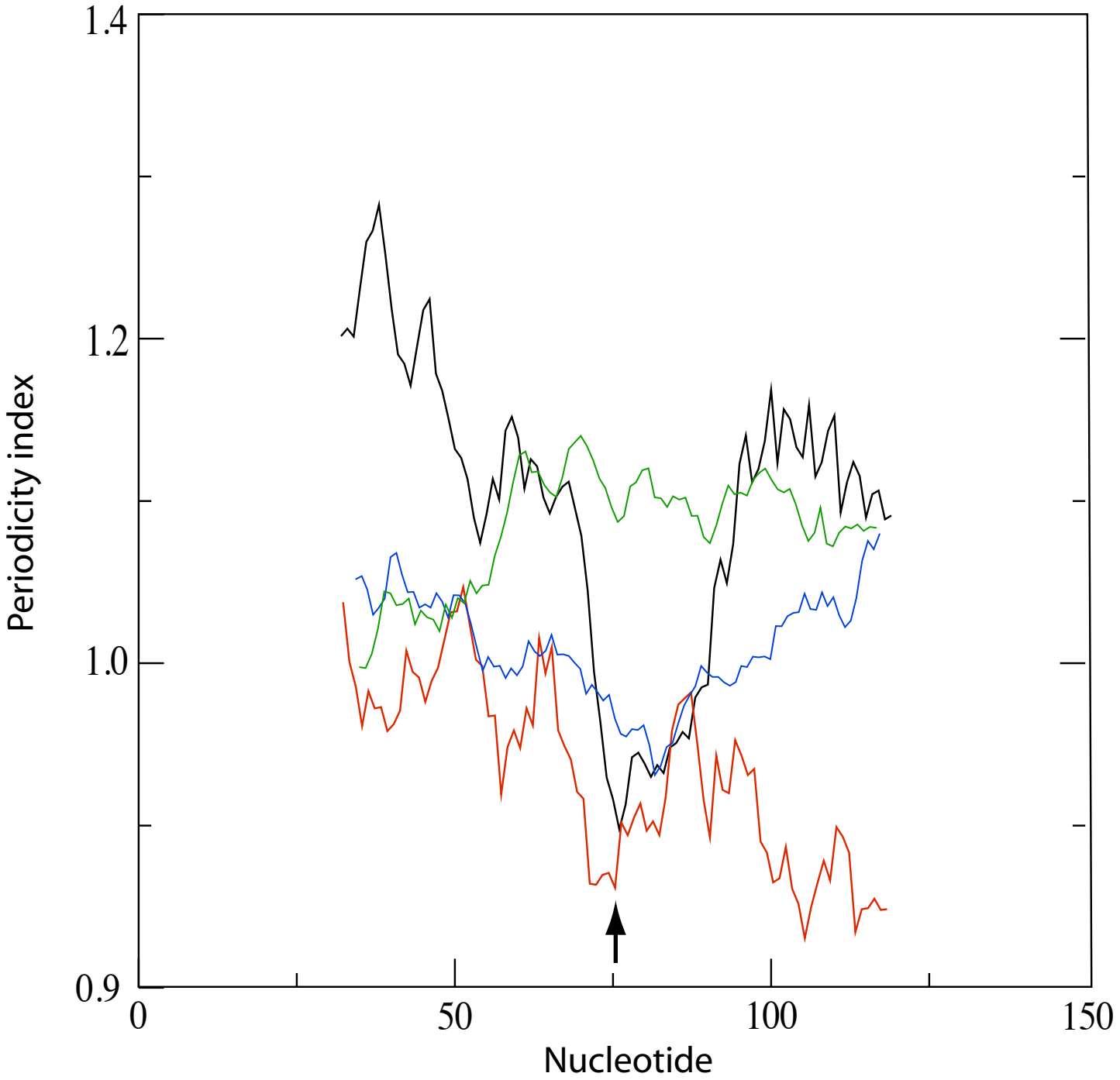
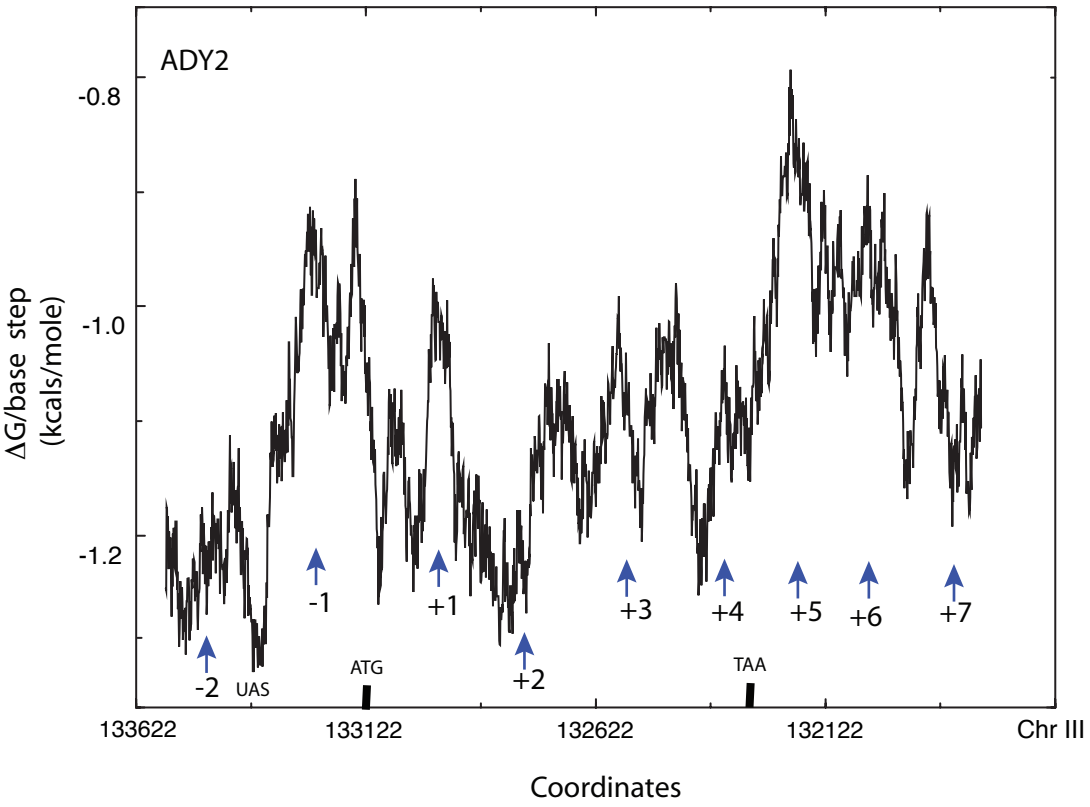


Figure S4.1


ADY2
-0.8
-1.0
-1.2
ΔG/base step (kcals/mole)
-2
UAS
-1
ATG
+1
+2
+3
+4
TAA
+5
+6
+7
133622
133122
132622
132122
Chr III
Coordinates

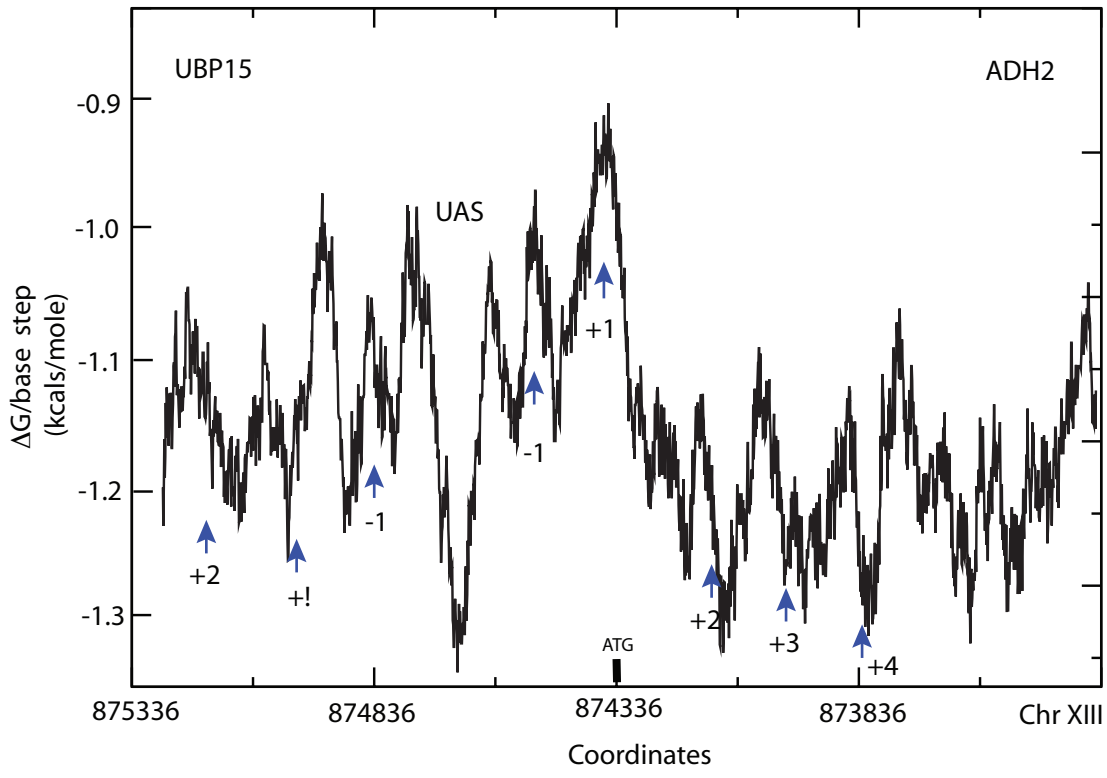
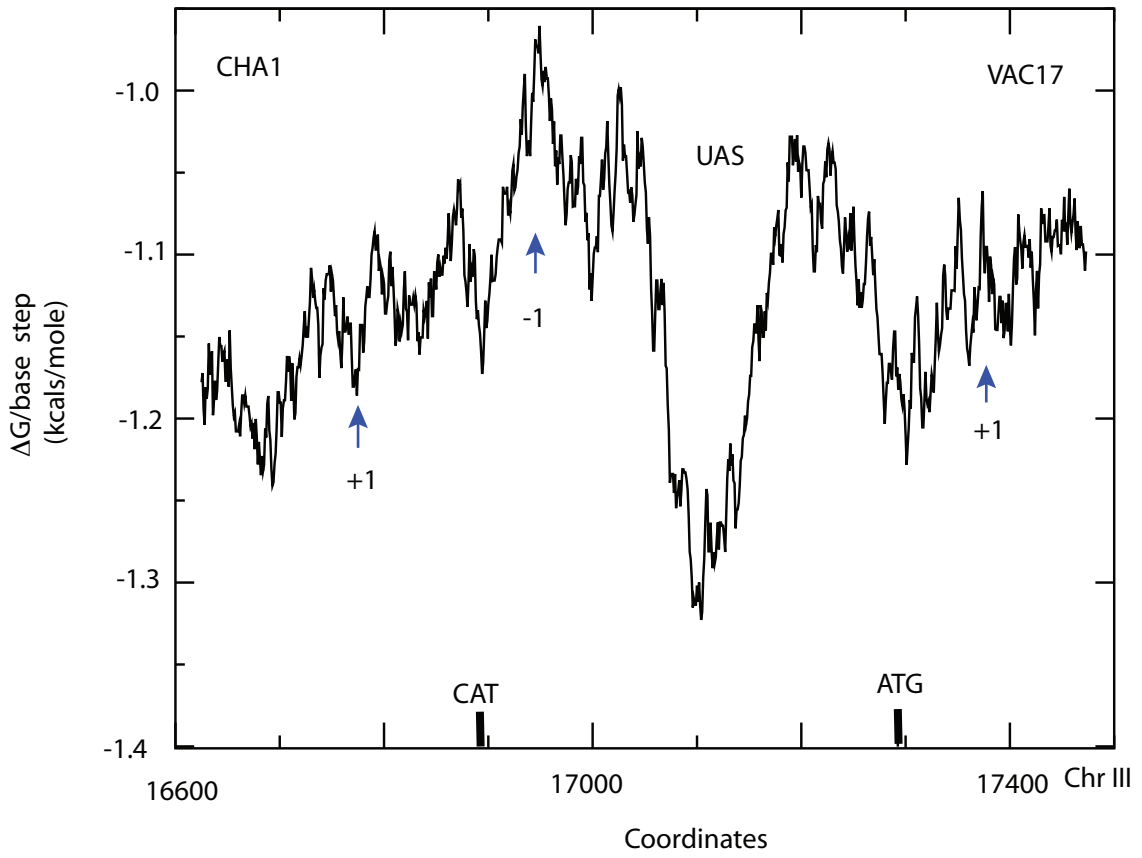

UBP15
ADH2
-0.9
-1.0
-1.1
-1.2
-1.3
ΔG/base step (kcals/mole)
UAS
+2
+!
-1
-1
+1
ATG
+2
+3
+4
875336
874836
874336
873836
Chr XIII
Coordinates

Figure S4.2


CHA1
VAC17
UAS
-1.0
-1.1
-1.2
-1.3
-1.4
ΔG/base step
(kcals/mole)
+1
-1
+1
CAT
ATG
16600
17000
17400
Chr III
Coordinates

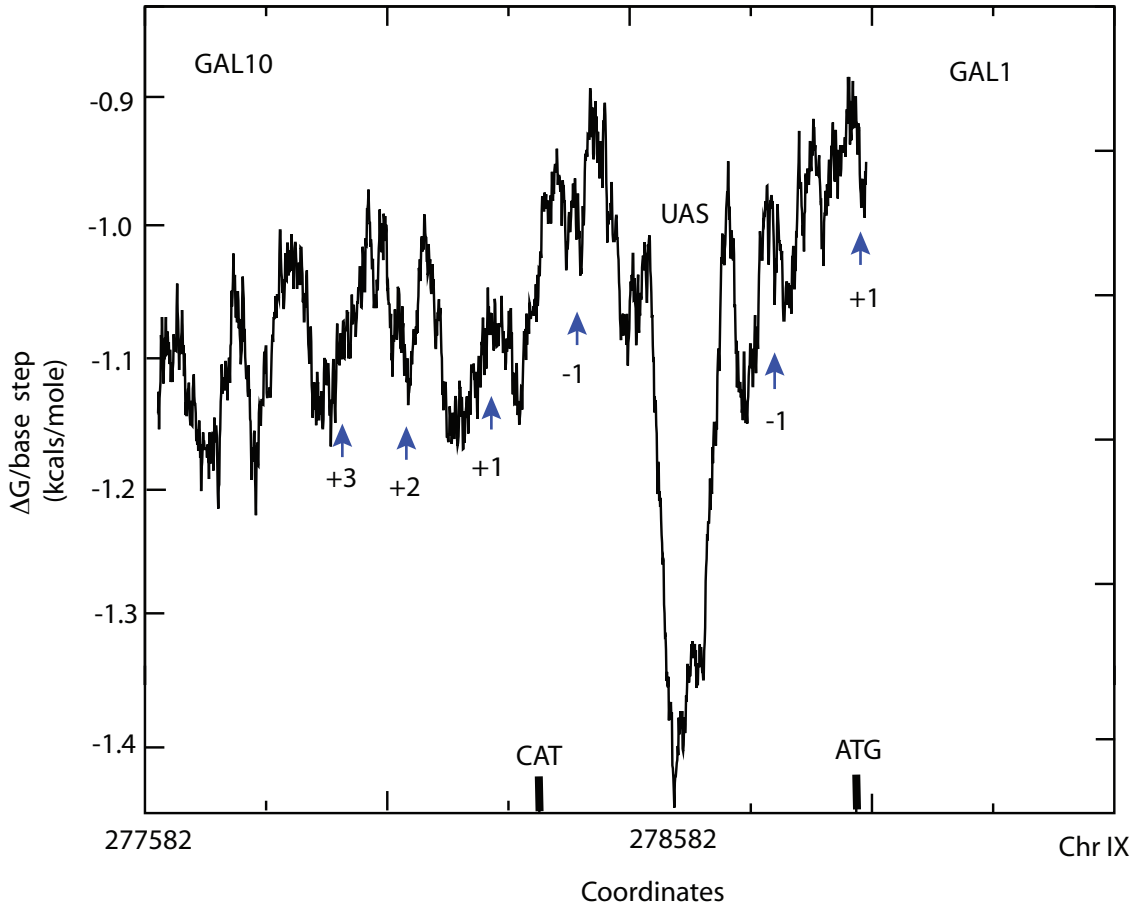
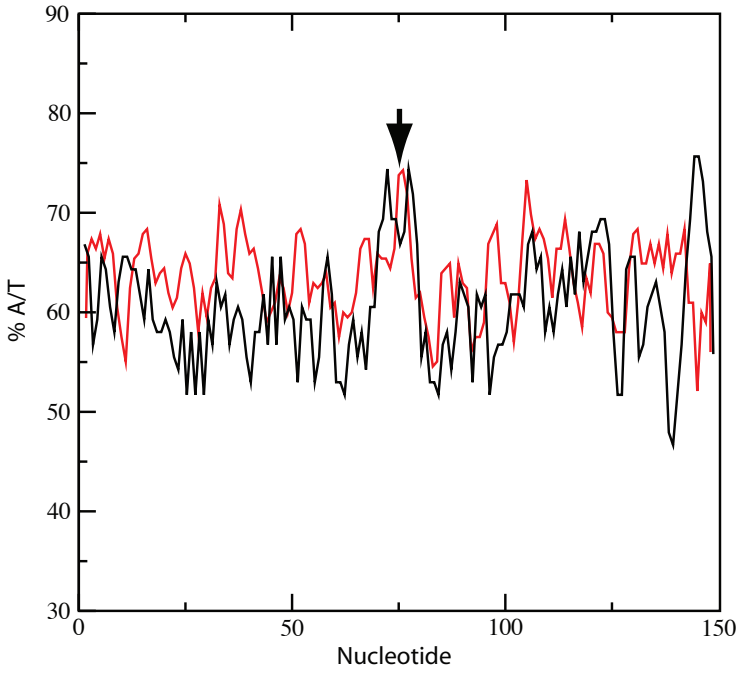

GAL10
GAL1
UAS
-0.9
-1.0
-1.1
-1.2
-1.3
-1.4
ΔG/base step
(kcals/mole)
+3
+2
+1
-1
-1
+1
CAT
ATG
277582
278582
Chr IX
Coordinates

Figure S5.1

a)



b)

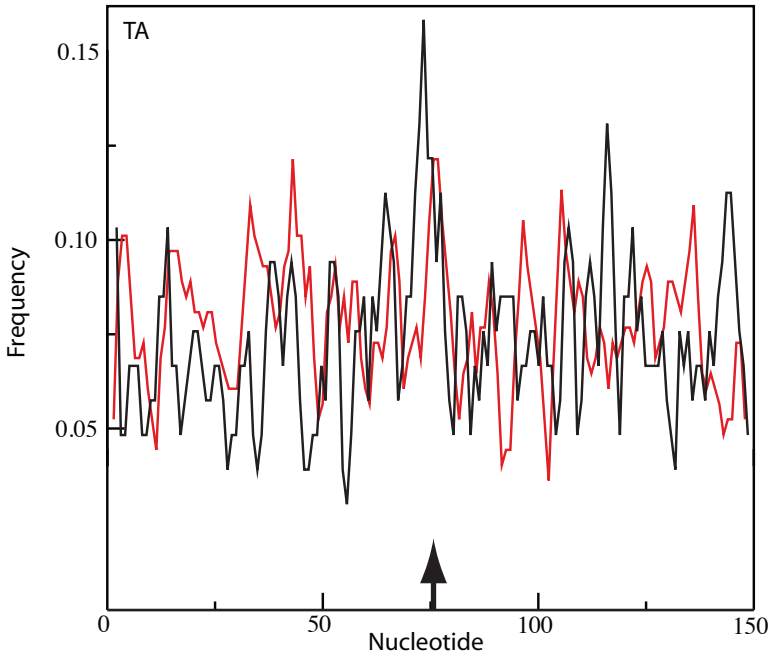
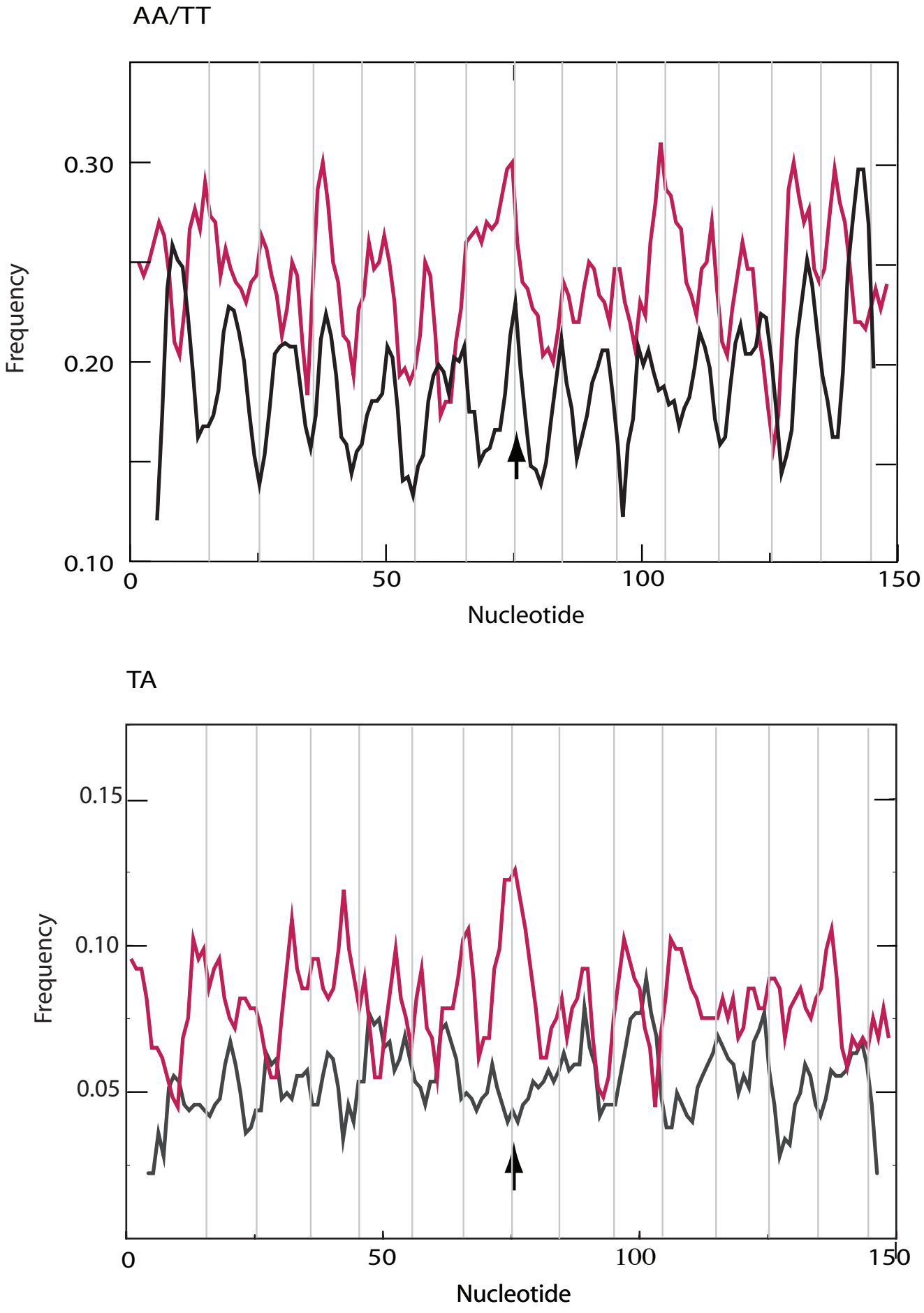


Figure S5.2


AA/TT
0.30
0.20
0.10
Frequency
0
50
100
150
Nucleotide
TA
0.15
0.10
0.05
Frequency
0
50
100
150
Nucleotide