

A DNA Sequence Element that Advances Replication Origin Activation Time in *Saccharomyces cerevisiae*

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Comparative Hybridization

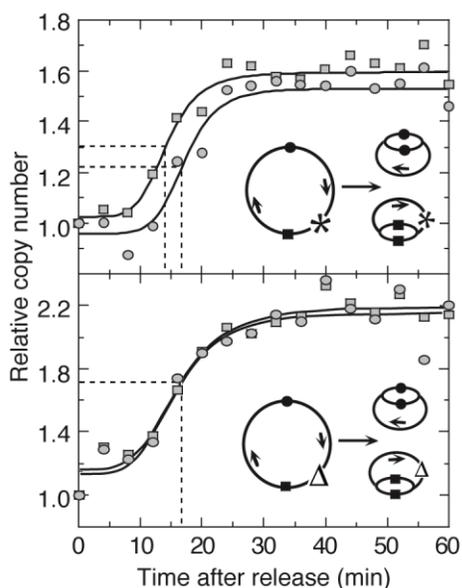


Figure S1 *ARS1*^S activation time analyzed by plasmid pop-out assay. The two plasmid copies of *ARS1* were separated from each other in vivo. Upper panel: separation from plasmid pN&Sdir. Lower panel: separation from plasmid pN&SΔ9dir derived from pN&Sdir by deleting the NsiI-NcoI fragment. Replication kinetics determined by the comparative hybridization method (FRIEDMAN et al. 1995) are plotted for each separated, single-ARS plasmid: plasmid pS' or pS'Δ (squares) and plasmid pN' (circles). Recombinase target sites are indicated by arrows on the cartoons and (Δ) indicates the NsiI-SmaI deletion of the bias element (*). The Trep value for each plasmid is shown as a dotted line intersecting the X-axis.

References cited

Friedman, K. L., M. K. Raghuraman, W. L. Fangman and B. J. Brewer, 1995 Analysis of the temporal program of replication initiation in yeast chromosomes. *J Cell Sci Suppl* 19: 51-58.

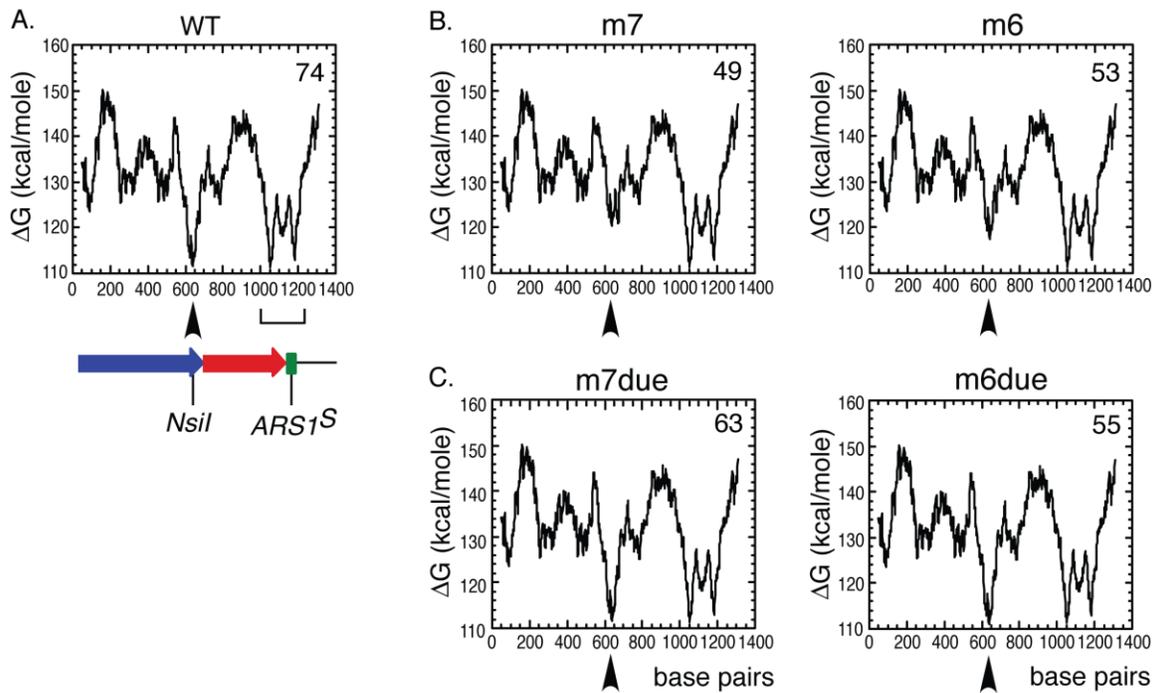


Figure S2 Examining the importance of a DUE at the bias determinant. Helical stability plots depicting the energy of unwinding (ΔG) of duplex DNA for the region containing the bias determinant (black arrow head). The percent of *ARS1^S* usage is depicted in the upper right corner. The cartoon depicts the sequence that was analyzed: the 3' end of *URA3* (blue arrow), the 3' end of *TRP1* (red arrow) and *ARS1^S* (green box). (A) Helical stability for the WT bias determinant and its surrounding region. The bracket indicates the *ARS1* DUE. (B) Helical stability for bias determinant mutants m6 and m7. (C) Helical stability for bias determinant mutants (see Materials and Methods) that maintain the presence of DUE but lack *ARS1^S* bias.