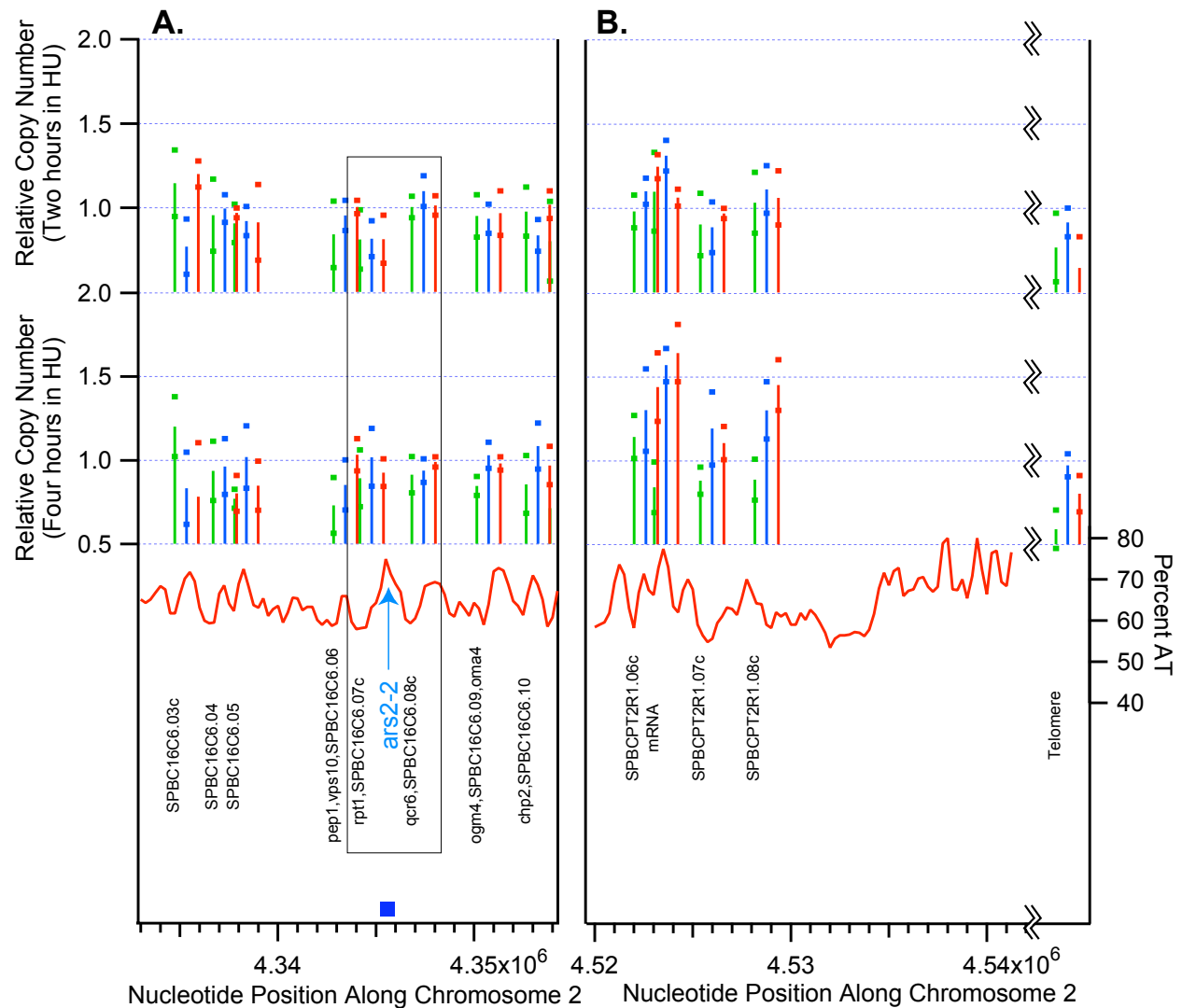




Explanatory text:

The two late-replicating origins that were previously characterized by 2D gel electrophoresis, *ars2-2* and telomeric origins [1], produced signals that were below the threshold for origin function both in our microarray assays (Additional files 10 and 12) and also in the microarray studies of Feng *et al.* [2] and Heichinger *et al.* [3]. However, Hayashi *et al.* [4] detected a pre-RC at the chromosomal position of *ars2-2*. They found that this pre-RC was inactive in wild-type cells but somewhat more active in *cds1Δ* cells [4]. In addition *ars2-2* and the telomeres did not satisfy the criteria for AT islands [5]. By 2D gel electrophoresis, these regions generated weak bubble arcs only in late S phase, only after HU was removed from HU-blocked cells [1]. The 2D gel results indicated that these regions were replicated only slightly if at all in cells blocked in hydroxyurea for 3 hours, consistent with the under-replication (most values of relative copy number less than 1.0) of the probes flanking *ars2-2* (box in panel A) and of the telomere-associated-sequence probe (rightmost probe in panel B), even after 4 hours. However, both regions showed slightly greater replication in checkpoint-mutant than in wild-type cells at four hours after release.

Legend:

The diagrams are explained in the legend to Figure 2 (main text). (A) The box contains the signals from the probes flanking *ars2-2*. The position of *ars2-2* is indicated with blue text and a blue arrow. (B) The right end of chromosome 2, showing the last 4 probes in the sequenced portion of the chromosome plus the telomere-associated sequence (TAS) probe, which detects sequences within 1 kb of the simple-sequence repeats at the telomere. The zig-zag lines indicate a gap in the known nucleotide sequence at the indicated position.

References

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