

Erratum

Richard Egel (Ed.)
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Unfortunately, in Chapter 6 (on page 80) appears a wrong Figure 6.2.
Kindly see the correct image on the following page.

Please take our apologies for any inconvenience.

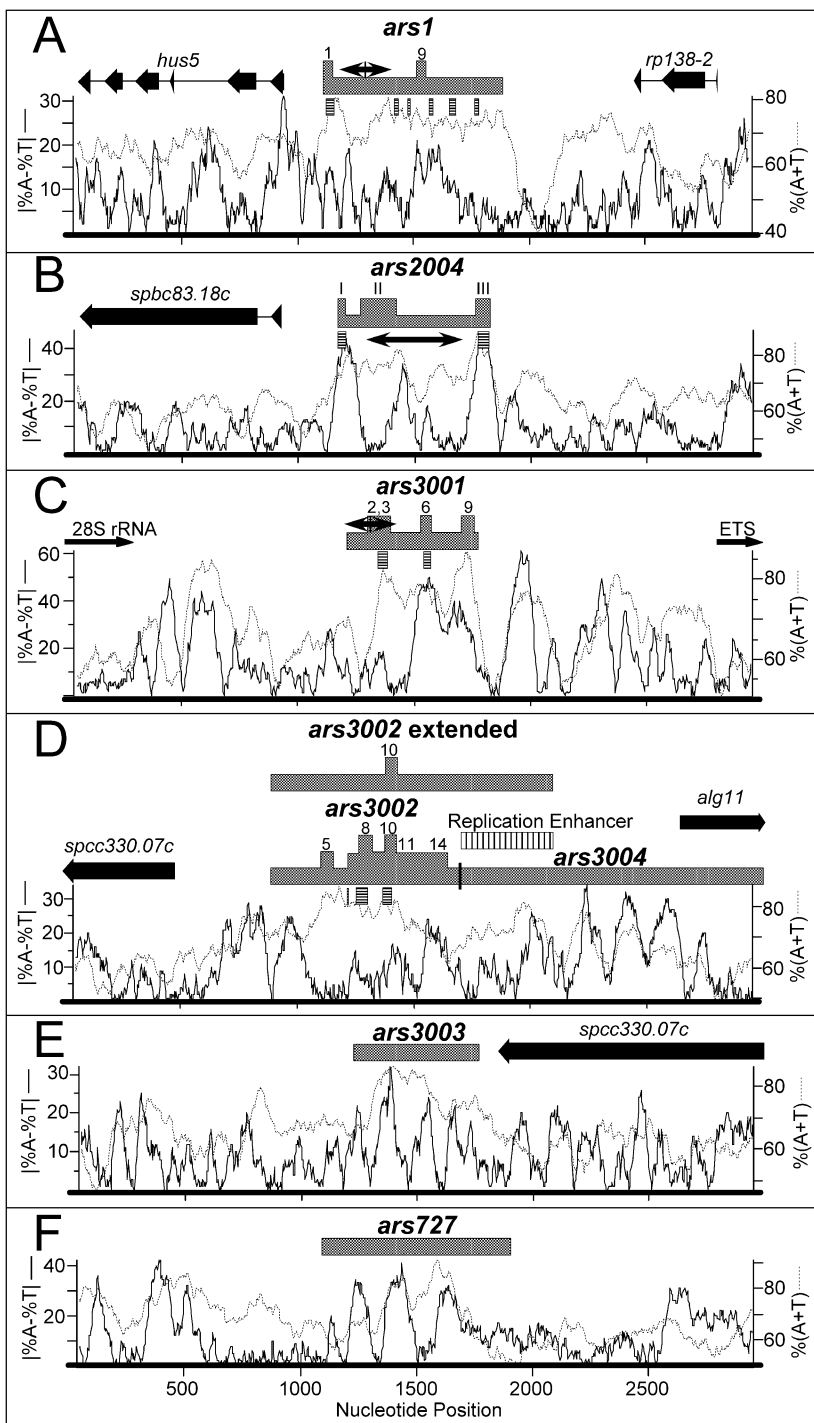




Fig. 6.2A–F. Sequence compositions of characterized fission yeast ARS elements. See the text for references to the studies on which these diagrams are based. In each panel, the *thin dotted line* indicates % (A+T), while the *thicker solid line* indicates $|\%A-\%T|$. In both cases, percentages were evaluated in windows of 100 bp centered on the indicated nucleotide. The *thick horizontal arrows* indicate exons, and the *thin lines* connecting them indicate introns. The *gray horizontal bars* indicate ARS elements, based on *external* deletion analyses. The *rectangular extensions above the gray bars* indicate regions that are especially important for ARS activity, based on *internal* deletion analyses. The *small boxes with horizontal stripes below the gray bars* are regions demonstrated to bind purified SpORC in vitro. The *double-headed arrows* in A–C indicate regions in which initiation sites have been mapped. The *horizontal arrows* in C indicate the external transcribed spacer (ETS) and 28S rRNA gene of the primary rRNA transcript. The *horizontal box with vertical stripes* in D represents a replication enhancer, a region that has no independent ARS activity but significantly stimulates the activity of nearby ARS elements. (Analyzed nucleotide regions in EMBL cosmids: A 2397–5396 of SPAC30D11; B 33533–36532 of SPBC83; C the central 2.3 kb are GenBank AF040270, the flanking regions are in 34500–38903 of SPCC569; D, E 18418–21418 and 15,554–18,553 of SPCC330; F 12,747–15,746 of SPBC3B8)

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