Table S1. CGH on spotted microarrays accurately identifies S phase replication origins.

	Mean distance
Raghuraman et al. (2001)	6.5 kb
Wyrick et al. (2001)	3.9 kb
Yabuki et al. (2002)	3.5 kb
This study, four hybrizations	3.2 kb
This study, single hybridization	6.1 kb

Our analysis of the replication of a wild type yeast in the S288c background identified 212 replication origins throughout the genome, which is roughly comparable to the numbers obtained by Rhaguraman *et al.* (Raghuraman *et al.*, 2001) (332) and Yabuki *et al.* (Yabuki *et al.*, 2002) (260). Origins on chromosome III (Greenfeder and Newlon, 1992; Poloumienko *et al.*, 2001), VI (Yamashita *et al.*, 1997), V (Tanaka *et al.*, 1996) and X (Wyrick *et al.*, 2001) have been systematically mapped by 2-D gel electrophoresis and and/or ARS plasmid assay, and annotated in the Saccharomyces Genome Database (SGD) (Balakrishnan). For each origin that was identified on chromosome III, V, VI, and X, the distance to the closest annotated origin in SGD was determined and the mean of these distances was calculated (This study, four hybridizations). A similar comparison was performed for the other origins identified by three previously published genome-wide analyses of budding yeast origins (Raghuraman *et al.*, 2001; Yabuki *et al.*, 2002) or potential origins (Wyrick *et al.*, 2001). We note that for screening purposes, our assay can be streamlined even further by using replication profiles from a single microarray (This study, single hybridization.)