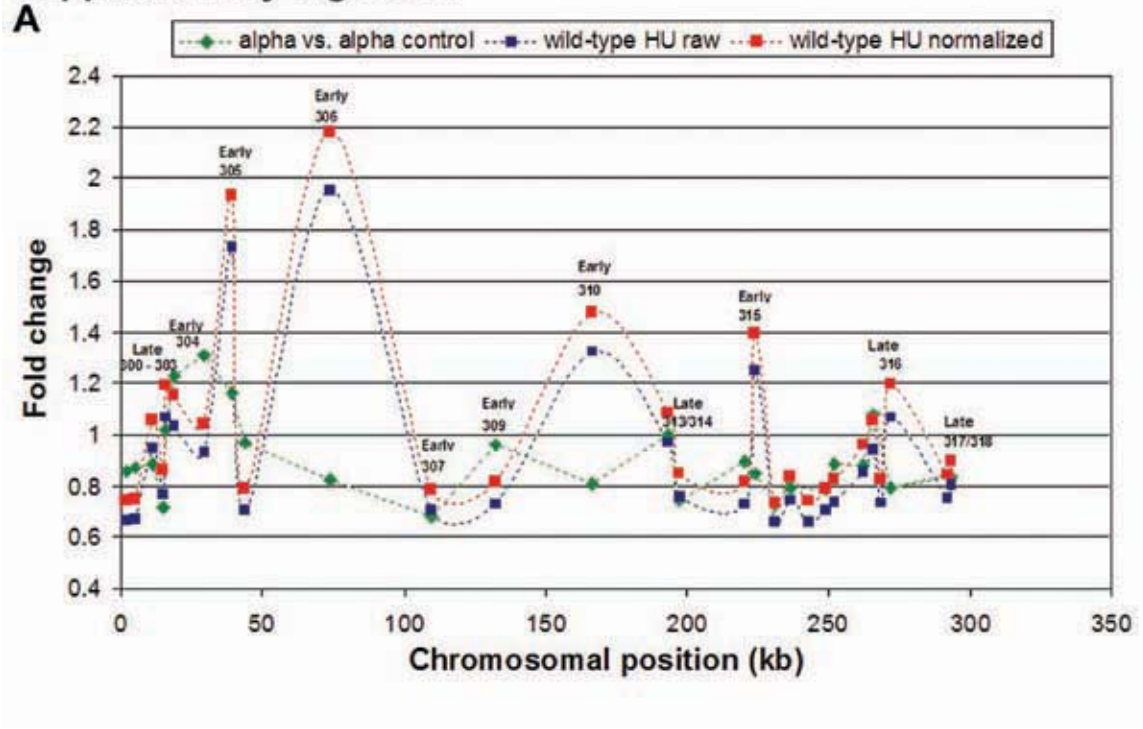
Supplementary Figure S1. (A) Comparison of normalized and raw data for wild-type chromosome III. Raw Cy5/Cy3 ratios were normalized using 36 negative controls (described in Experimental Procedures), which are origin flanking sequences located at least 20 kb away from an origin. For each hybridization experiment, an "alpha vs. alpha" control was used to estimate background variation. **(B) Replication origin activation profile for chromosome XIII in wild-type cells after 120 min in 0.2 M HU.** Activation of replication origins in the presence of 0.2 M HU (arrested for 120 min) was determined by monitoring copy number changes on a replication origin array. Chromosome XIII is shown as a cartoon at the top of the figure above the replication profile. The distribution of replication origins on the chromosome is indicated by black bars. The letter E indicates early-firing origins (Raghuraman *et al*, 2001). Each point on the graph represents the average of three independent experiments. The significance level used is one standard deviation above background variation (corresponding to approximately 20% of total signal). All scored origins had a p-value < 0.05. The replication profile for wild-type chromosome XIII based on an earlier high-density microarray analysis (Yabuki *et al*, 2002) is also shown. The significance level that was used by Yabuki and coworkers is 10% of total signal. Activated origins are indicated by their respective numbers.

Supplementary Figure S1

A



Supplementary Figure S1

B