SUPPLEMENTARY INFORMATION FOR MCCUNE ET AL.

Supplementary Table 1. Repetitive ORFs excluded from analysis of microarray data.

Supplementary Figure 1. Comparison of chromosome XV replication profiles: A representative replication profile for the pooled S phase sample from wild type cells overlaid on published replication profiles (RAGHURAMAN *et al*. 2001; YABUKI *et al*. 2002).

Supplementary Figure 2. Replication profiles for *CLB5 CLB6* and *clb5Δ CLB6*: Single value decomposition was used to integrate the four wild-type and four *clb5Δ* replication profiles and produce "gold standard" profiles for each strain. The bar below each pair of profiles indicates the Z score from wild-type to *clb5Δ* percent replication comparisons at each coordinate. CDRs with the least significant difference between wild-type and *clb5Δ* are yellow, those with more variation between the strains are orange, and those with the greatest difference are red. Non-CDR coordinates are blue and inconclusive coordinates (those where the same-strain comparisons gave significant Z scores) are gray.

Supplementary Figure 3. Rescue of CDR delayed replication: Replication profiles of all 16 chromosomes in wild type (*CLB5 CLB6[-HA]*; red), *clb5Δ* mutant (*clb5Δ CLB6[-HA]*, blue) and a *clb5Δ* mutant with the stabilized version of Clb6p (*clb5Δ clb6[Δ100-HA]*, green) were generated by density transfer microarray analysis on samples collected at 40 and 60 minutes during transit of cells through S phase; each plot is the average of two array hybridizations. To facilitate visual comparison of the profiles, the plots have been offset to maximize overlap without stretching or compressing them on the Y-axis.

Supplementary Figure 4. Replication profiles for KK14-3a: Replication profiles of all 16 chromosomes in a *CLB5 CLB6 cdc7-1* strain. See Figure 6 legend for details.

Supplementary Data 1. Wild-type and *clb5* percent replication values: Wild-type ("WT") and *clb5Δ* mutant percent replication values are given for all coordinates. Raw data values are derived from either the first (1) or second (2) hybridization of data series A or series B. The "gold standard" ("std.") values were obtained using single value decomposition to combine the raw percent replication values for each strain.

Supplementary Data 2. Z scores and *CLB5*-dependence: *Z* scores were derived from the average absolute difference for same-strain comparisons ("same_strain") or for wild-type versus *clb5* comparisons ("WT_v_*clb5*"). All coordinates for which the same-strain comparisons give $Z \geq 4.886$ are designated "inconclusive." Of the remaining coordinates, those where the wild-type to *clb5* comparisons yield $Z \geq 4.886$ are designated "CDR" for *CLB5*-**D**ependent **R**egion; those where $Z < 4.886$ are "non-CDR."

Supplementary Data 3. Rescue of CDR delayed replication—percent replication values: Percent replication values for *CLB5 CLB6^{-HA}*, *clb5Δ CLB6^{-HA}*, and *clb5Δ clb6$^{Δ100-HA}$* are given for all coordinates. Each value reflects the mean of two hybridizations.

Supplementary Data 4. Kinetics of replication in *CLB5 CLB6 cdc7-1*: Percent replication values for KK14-3a (*CLB5 CLB6 cdc7-1*) are given for all coordinates. A and B, reciprocal (Cy3 vs. Cy5) hybridizations.

Supplementary Data 5. Time of first detectable activation of the 200 most prominent origins: Origins marked with asterisks are members of a group of 64 well-separated origins,

used to estimate origin firing activity (see text and Figure 7). Annotation of origins as "Confirmed" or "Likely" is based on OriDB (NIEDUSZYNSKI *et al*. 2007); http://www.oridb.org. "Unchecked" indicates origins that fire in *RAD53* cells during brief exposure to hydroxyurea (FENG *et al*. 2006).

LITERATURE CITED (SUPPLEMENTARY MATERIAL)

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RAGHURAMAN, M. K., E. A. WINZELER, D. COLLINGWOOD, S. HUNT, L. WODICKA *et al*., 2001 Replication dynamics of the yeast genome. Science **294:** 115-121.

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