Figure S5.

A

WT

WT

tos4Δ hcm1Δ yox1Δ yhp1Δ

B

WT

tos4Δ hcm1Δ yox1Δ yhp1Δ

4Δ
Figure S5.

C

G1 genes (peak time 0-15%)  
G1/S genes (peak time 16-30%)

early S genes (peak time 31-45%)  
late S genes (peak time 46-60%)

G2/M genes (peak time 61-75%)  
M/G1 genes (peak time 76-100%)

D

CIN8 WT vs. CIN8 4P  
HTZ1 WT vs. HTZ1 4P

HST3 WT vs. HST3 4P  
CDC5 WT vs. CDC5 4P

KIN3 WT vs. KIN3 4P  
DBF2 WT vs. DBF2 4P
Figure S5. Analysis of cell cycle-regulated gene expression in 4P cells. (A) TF protein expression in wild type and 4P cells from Figure 3A. Protein levels were quantified with ImageJ, normalized to Cdk1 levels and plotted. (B) Analysis of cell cycle progression in cells lacking all four S-phase TFs. Wild type and tos4Δ hcm1Δ yhp1Δ yox1Δ strains were arrested in G1 with alpha-factor, released into the cell cycle, and samples were collected after the indicated number of minutes for FACS analysis. Cells lacking all 4 TFs delay in mitotic progression, as seen by comparing the 75 and 85 minute time points. (C) 930 cell cycle-regulated genes (as defined by (Pramila et al, 2006)), from expression microarrays were divided into 6 groups based on when the expression of those genes peaked, and the TFs known to regulate genes at each stage. G1 genes peak at 0-15% of the cell cycle (136 genes, many regulated by Ace2/Swi5), G1/S genes peak at 16-30% (166 genes, many regulated by SBF and MBF), early S genes peak at 31-45% (164 genes, many predicted Hcm1 targets), late S genes peak at 46-60% (170 genes, many predicted Hcm1 targets), G2/M genes peak at 61-75% (130 genes, many regulated by Fkh2/Ndd1), and M/G1 genes that peak at 76-100% (164 genes, many regulated by Yox1 and Yhp1). Expression of representative genes in each group across the cell cycle is shown. (D) Validation of microarray data by RT-qPCR for representative S-phase genes (HTZ1, CIN8), G2/M genes (HST3, CDC5), and M/G1 genes (KIN3, DBF2) are shown.