Supplemental Figure 1: Sgo1 protein is depleted during meiosis in *pCLB2-SGO1* cells.

The diploid *pCLB2-3HA-SGO1* (AM4236) strain was sporulated. (A) The percentage of binucleate plus tetranucleate cells (Meiosis I completed) and of tetranucleate cells (Meiosis II completed) is shown. (B) 3HA-Sgo1 levels were examined by western blot analysis of samples taken from the sporulating culture at the indicated timepoints. A sample taken from a cycling culture of the same strain is shown for comparison. Pgk1 is shown as a loading control.

Supplemental Figure 2: Deletion of *RTS1* suppresses the metaphase I arrest of Cdc20-depleted cells.

Diploid *pCLB2-CDC20* (AM4041) and *pCLB2-CDC20 rts1*Δ (AM3868) strains were sporulated. The percentage of cells with metaphase I (closed squares) and anaphase I (open squares) spindles are shown for *pCLB2-CDC20* (top), *pCLB2-CDC20 rts1*Δ (bottom) strains.

Supplemental Figure 3: The spindle elongation in cells depleted of Sgo1 does not require cohesin cleavage.

Diploid wild-type (A15086), *pCLB2-CDC20* (A6144) and *pCLB2-CDC20 pCLB2-SGO1* (A15269) strains each carrying *REC8-3HA* fusions and deleted for *UBR1* were sporulated.

(A) The percentage of cells with prophase I (closed diamonds), metaphase I (closed squares), anaphase I (closed triangles) spindles and sporulated cells (open squares) are shown for wild-type (left), *pCLB2-CDC20* (middle) and *pCLB2-CDC20 pCLB2-SGO1* (right) strains.

(B) Rec8 protein levels were examined by Western blot analysis. Extracts were run on 6% gels (top) and 10% gels (bottom). Positions of full length Rec8 and the C-terminal Rec8 cleavage fragment are indicated. The percentage of bi- and tetranucleate cells is shown below.

(C) Diploid wild type, *pCLB2-SGO1*, *pCLB2-CDC20* and *pCLB2-CDC20 pCLB2-SGO1* cells homozygous for either the wild type *REC8* gene (open symbols) or the non-cleavable *REC8-N* allele (closed symbols) were sporulated. The percentages of cells with metaphase I (circles) and anaphase I (squares) spindles were scored. Strains

used were AM4510 (wild type *REC8)*, AM3952 (*pCLB2-SGO1 REC8*), AM4514 (*pCLB2-CDC20 REC8*), AM4511 (*pCLB2-CDC20 pCLB2-SGO1 REC8*), AM3908 (*REC8-N*), AM3909 (*pCLB2-SGO1 REC8-N*), AM4512 (*pCLB2-CDC20 REC8-N*) and AM4513 (*pCLB2-CDC20 pCLB2-SGO1 REC8-N*).

Supplemental Figure 4: Cohesins are loaded and maintained at wild-type levels in Sgo1-depleted cells.

(A-C) Wild-type (A4758) and *pCLB2-SGO1* (A14910) cells carrying a *REC8-3HA* fusion were sporulated along with a wild-type strain lacking the fusion protein (No Tag, A4962).

(A) The percentage of mononucleate (closed diamonds), binucleate (closed squares), tetranucleated (closed triangles) as well as the sum of binucleate and tetranucleated (open squares) was determined at the indicated time points for *NoTag* (top), *REC8-3HA* (middle), and *pCLB2-SGO1 REC8-3HA* (bottom) strains.

(B) The locations of primer sets used for PCR after ChIP are shown on a schematic diagram of chromosome III. c130 represents a cohesin-positive pericentric region, c191.5 represents a cohesin-positive arm region, and c281 represents a negative control for cohesin association.

(C) PCR data after ChIP for NoTag (top), *REC8-3HA* (middle) and *pCLB2-SGO1 REC8-3HA* (bottom) strains. 2 μl of purified DNA after ChIP with anti-HA antibody or mock treatment was amplified along with 2 μl of 1:250 diluted input DNA.

(D-E) *pCLB2-CDC20* (A6144) and *pCLB2-CDC20 pCLB2-SGO1* (A15269) cells each carrying a *REC8-3HA* fusion were sporulated.

(D) The percentage of mononucleate (closed diamonds), binucleate (closed squares), tetranucleated (closed triangles) as well as the sum of binucleate and tetranucleated (open squares) was determined at the indicated time points for *pCLB2-CDC20* (top) and *pCLB2-CDC20 pCLB2-SGO1* (bottom) strains.

(E) PCR data after ChIP for *pCLB2-CDC20* (top) and *pCLB2-CDC20 pCLB2-SGO1* (bottom) strains. 2 μl of purified DNA after ChIP with anti-HA antibody or mock treatment was amplified along with 2 μl of 1:250 diluted input DNA. Samples were taken at 0, 4, and 8 hours after induction of meiosis and anti-HA immunoprecipitations were performed in duplicate.

Supplemental Figure 5: Metaphase I-arrested *mam1Δ* cells achieve similar levels of sister kinetochore bi-orientation in the presence and absence of Sgo1.

pCLB2-CDC20 (A7118), *pCLB2-CDC20 mam1Δ* (A7316), *pCLB2-CDC20 mam1Δ spo11Δ* (A8127), *pCLB2-CDC20 pCLB2-SGO1* (A17838) and *pCLB2-CDC20 pCLB2-SGO1 mam1Δ* (A18705) cells with heterozygous CENV GFP dots were sporulated.

(A) The percentage of metaphase I spindles is shown for *pCLB2-CDC20* (open circles), *pCLB2-CDC20 mam1Δ* (open squares), *pCLB2-CDC20 mam1Δ spo11Δ* (open triangles), *pCLB2-CDC20 pCLB2-SGO1* (closed circles) and *pCLB2-CDC20 pCLB2-SGO1 mam1Δ* (closed squares) cells.

(B) The percentage of cells with 2 visible GFP dots is shown for *pCLB2-CDC20* (open circles), *pCLB2-CDC20 mam1Δ* (open squares), *pCLB2-CDC20 mam1Δ spo11Δ* (open triangles), *pCLB2-CDC20 pCLB2-SGO1* (closed circles) and *pCLB2-CDC20 pCLB2-SGO1 mam1Δ* (closed squares) cells.

Supplemental Figure 6: Sgo1 depletion does not alter Ipl1 protein levels or localization.

(A, B) Diploid *pCLB2-CDC20* (A18102) and *pCLB2-CDC20 pCLB2-SGO1* (A18089) strains each carrying *IPL1-13MYC* and *NDC10-6HA* alleles were sporulated.

(A) The percentage of *pCLB2-CDC20* cells (closed squares) and *pCLB2-CDC20 pCLB2-SGO1* cells (closed diamonds) with metaphase I spindles as well as *pCLB2-CDC20* cells (open squares) and *pCLB2-CDC20 pCLB2-SGO1* cells (open diamonds) with anaphase I spindles were analyzed at the indicated time points.

(B) Western blot showing levels of Ipl1 and Pgk1 throughout the meiotic time course.

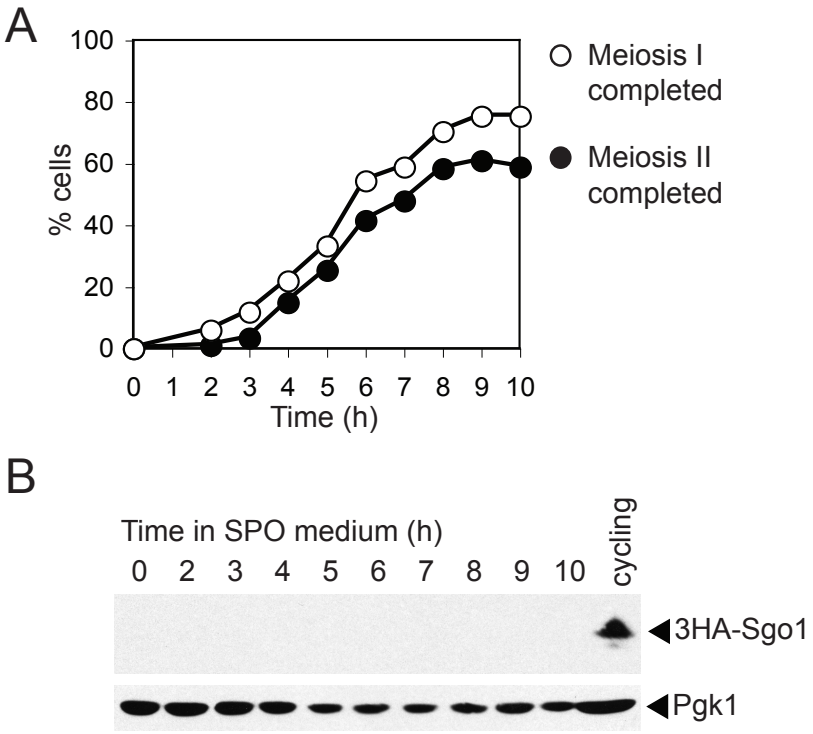
(C-D) Diploid wild type (AM3907), *pCLB2-SGO1* (AM4614), *pCLB2-CDC20* (AM4470) and *pCLB2-CDC20 pCLB2-SGO1* (AM4469) strains each carrying *IPL1-6HA* and *IML3-9MYC* were sporulated.

(C) Representative images of Ipl1 localization on spread meiotic chromosomes. Ipl1 staining is shown in red, Iml3, a kinetochore marker, is shown in green and the chromosomes are shown in blue.

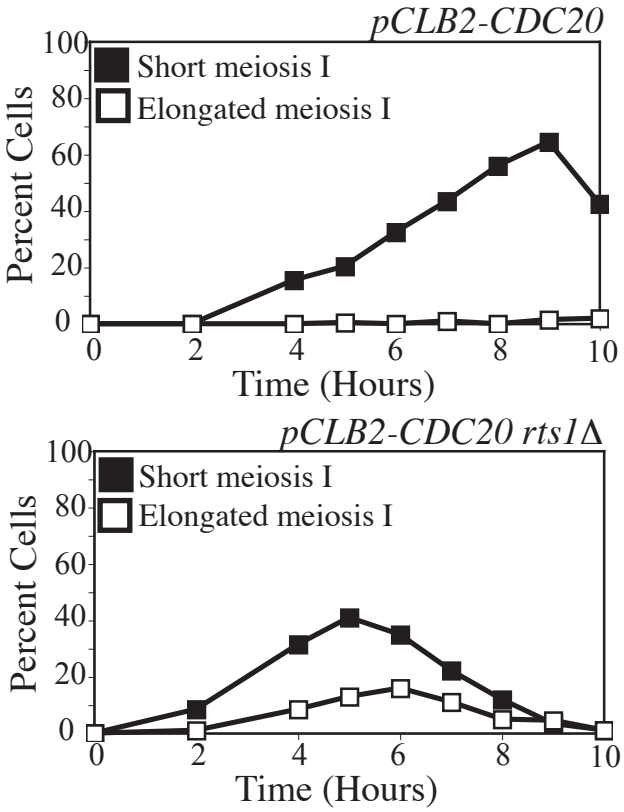
(D) Quantification of Ipl1 localization to kinetochores on chromosome spreads. Cells in which Ipl1 colocalized with the kinetochore protein, Iml3, were scored as

“localized”. Cells in which less than 50% of the kinetochore foci (Iml3) lacked Ipl1 staining were scored as “part-localized”. Approximately 100 cells were scored each class, except tetranucleate cells, in which case 50 cells were scored.

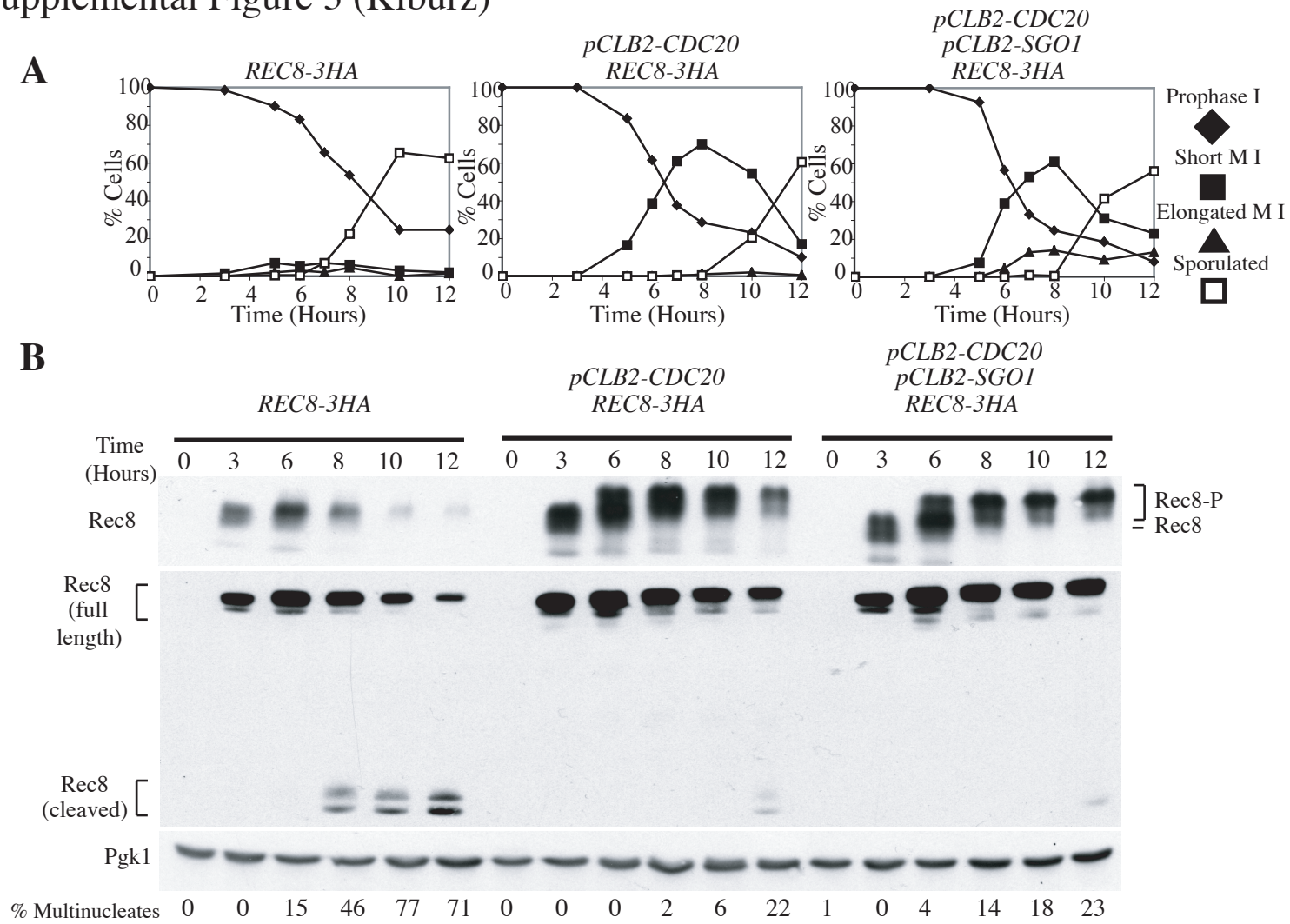
Supplemental Figure 1 (Kiburz)



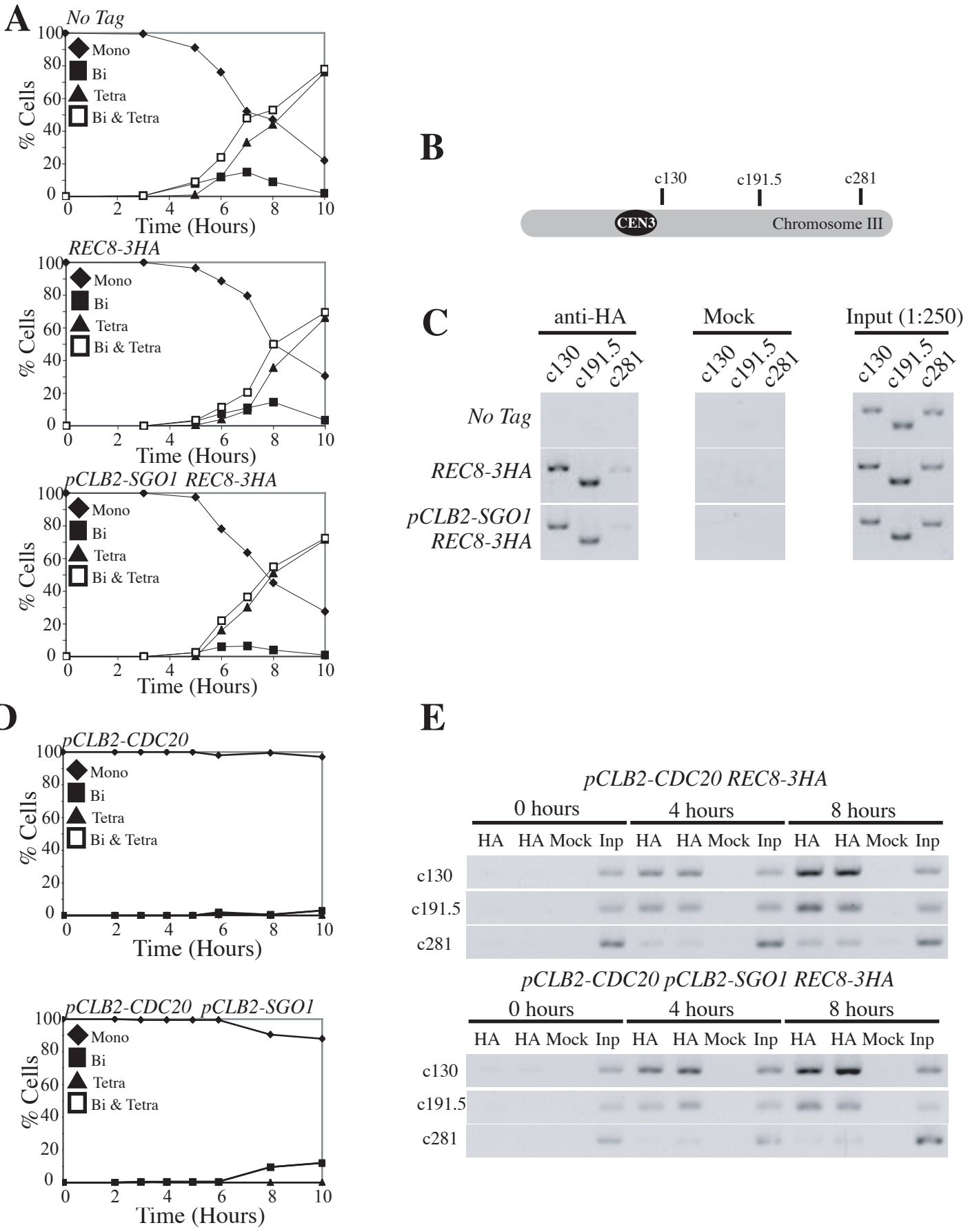
Supplemental Figure 2 (Kiburz)



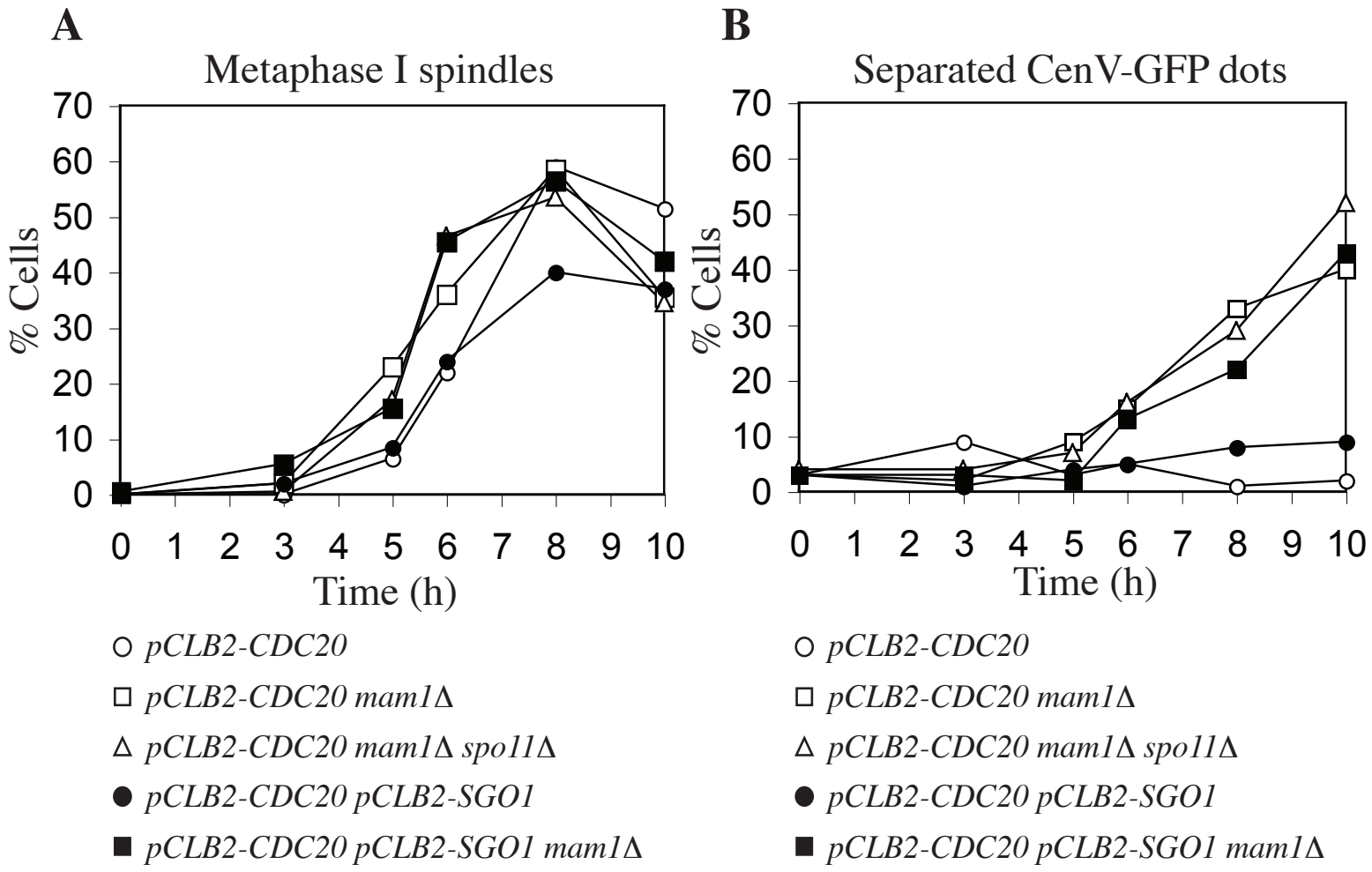
Supplemental Figure 3 (Kiburz)



Supplemental Figure 4 (Kiburz)



Supplemental Figure 5 (Kiburz)



Supplemental Figure 6 (Kiburz)