Figure EV1.
Figure EV1. Contact maps and 3D genome representations of the five cell cycle synchronization states.

A, B Contact maps generated from synchronized cell populations described in this study, with each vector (or bin) corresponding to 5 kb. x- and y-axis represent the 16 chromosomes of the yeast genome, displayed atop the maps. Brown to yellow color scales reflect high to low contact frequencies, respectively (log10). Magnification panels in (B) show variations of the contact frequencies between synchronized populations. Yellow and pink arrowheads point at centromeres and rDNA positions, respectively.

C 3D average representations of the Hi-C contact maps of synchronized cell populations of panel (A). The color code represents the chromosomal arm length, and centromeres, telomeres, and rDNA flanking regions are highlighted.

Figure EV2. Contact maps and 3D genome representations during replication.

A, B Contact maps recovered from cell populations undergoing replication after G1 release. For each contact map, the FACS profile is displayed. x- and y-axis represent the 16 chromosomes of the yeast genome. The same color code as in Fig EV1. Magnification panels in (B) highlight changes of the contact frequencies during S-phase progression. Yellow and pink arrowheads point at centromeres and rDNA positions, respectively.

C 3D average representations of the Hi-C contact maps of synchronized cell populations of panel (A). The color code represents the chromosomal arm length, and centromeres, telomeres, and rDNA flanking regions are highlighted.
Figure EV2.
Figure EV3. Contact maps and 3D genome representations during M phase.

A, B Contact maps of cell populations synchronized in metaphase (cdc20) and anaphase (cdc15) and released into mitosis from cdc15 block (+20 min, +40 min, and +60 min). The corresponding FACS profiles and representative DAPI-stained cells are displayed on the left on the maps. X- and y-axis represent the 16 chromosomes of the yeast genome. The same color code as in Fig EV1. Magnification panels in (B) display variations of the contact frequencies during mitotic progression. Yellow and pink arrowheads point at centromeres and rDNA positions, respectively.

C 3D average representations of the Hi-C contact maps of panel (A). The color code represents the chromosomal arm length, and centromeres, telomeres, and rDNA flanking regions are highlighted.
Figure EV3.
Figure EV4. Nocodazole affects chromosome 12 conformation.

A, B Contact maps of G1 synchronized cell populations released either in the presence of nocodazole (G2/M noc) or at cdc15 non-permissive temperature followed by a nocodazole treatment (cdc15 noc). The corresponding FACS profiles and representative DAPI-stained cells are displayed on the left on the maps. x- and y-axis represent the 16 chromosomes of the yeast genome. The same color code as in Fig EV1. Magnification panels in (B) display variations of the contact frequencies. Yellow and pink arrowheads point at centromeres and rDNA positions, respectively.

C 3D average representations of the Hi-C contact maps of panel (A). The color code represents the chromosomal arm length, and centromeres, telomeres, and rDNA flanking regions are highlighted.
Figure EV5. Condensin and decatenation influence on chromatin structure during mitosis.

A, B Contact maps of cell populations arrested in anaphase, either defective with condensation (cdc14 or smc2-aid cdc15 +IAA) or depleted of topoisomerase 2 (top2-aid cdc15 +IAA). The corresponding FACS profiles and representative DAPI-stained cells are displayed on the left on the maps. x- and y-axis represent the 16 chromosomes of the yeast genome. The same color code as in Fig EV2. Magnification panels in (B) display variations of the contact frequencies. Yellow and pink arrowheads point at centromeres and rDNA positions, respectively.

C 3D average representations of the Hi-C contact maps of panel (A). The color code represents the chromosomal arm length, and centromeres, telomeres, and rDNA flanking regions are highlighted.