Supporting Information

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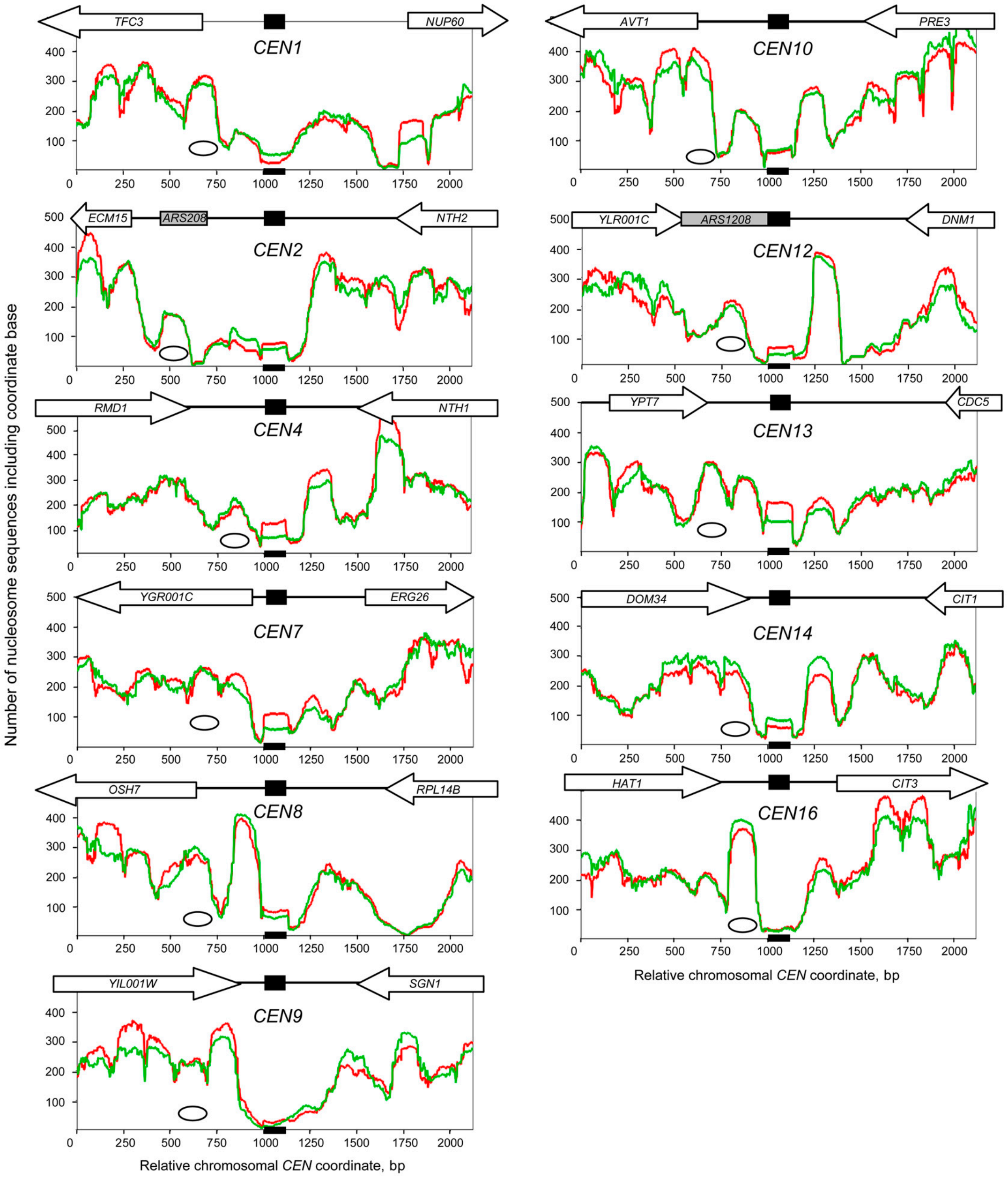

Fig. S1. Nucleosome occupancy profiles for all yeast centromeres not included in Fig. 2. The scale has been set arbitrarily such that the first nucleotide in CDEI in the *CEN* sequence as defined by the *Saccharomyces* Genome Database (black box) is at coordinate 1,001. Red trace: control cells; green trace: 3AT-treated cells. All nucleosome sequences were included. Raw data are shown. The data for 3AT-treated cells were multiplied by 1.27 to adjust for the different total numbers of nucleosomes sequenced for the two samples.

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CEN2            TAAATCATGTGACTTATTTATTTAATTATTATTAAGTAAAAAAGATTTTCTATTTAAATTTATT A ATTAATTTTTTTTCTTAAATAATTATTTTATGTTTTTGTTTTCCGAAAAAGAAAAATATTTCAACA
CEN3     TAGTACAAATAAGTCACATGATGATATTTGATTTTATTATATATTTTTAAAAAAAGTAAAAAAATAAAAAGTAG T TTATTTTTAAAAAATAAAATTTAAAATATTAGTGTATTTGATTTCCGAAAGTTAAAAAAGAAATAGT
CEN4        TTGCAAAAGGTCACATGCTTATAATCAACTTTTTTAAAAAATTTAAAATACTTTTTTATTTTTTATTTT   TAAACATAAATGAAATAATTTATTTATTGTTTATGATTACCGAAACATAAAACCTGCTCAAGAAAAAGA
CEN5  AACATCAAATTAATCACGTGCTTTTTAAAAAATATAAATTTAATTTCATTTTCTATTTCAATATTTATTAAATA A AAAATTTGAAAAATATATAAAAATTGTAGCAGTATTAGATTTCCGAAAAGAAAAAAAGGTTTCAAGAA
CEN6     TTCTTTTCATCACGTGCTATAAAAATAATTATAATTTAAATTTTTTAATATAAATATATAAATTAAAAATA G AAAGTAAAAAAAGAAATTAAAGAAAAAATAGTTTTTGTTTTCCGAAGATGTAAAATAGGTTGAAAGTT
CEN7         ATATATCACGTGTTATATTTACTATATAAAAATTCAATAAATAAAAAGTTAGAAGATAAAAATTATA T TATACATATTTTTATTTTTATTATAATTTTTGTTTTTGCCTTCCGAAAAGAAAATAGTTTTTTGTA
CEN8  TAGGATGGTAATCACATGACTAATAATTCTTTTAATTTTAATTAATTTAATAAAATTAAAATAATATATATACT A AATTGTTTATTAAAAATGATTAAACATTGGGTTTTGTGTTCCGAACTTAGAAAATTGGTTAAGACA
CEN10       CTTAATCACGTGTTAAATAATTAATTTACTTTAAAATTTATTTTTTAATATAAAATATTTATTCTTTT   TATTTAAAAATAAAAAACACAAAAAAACAATGTTTATGATTTCCGAACCTAAATATACACTTTACGAG
CEN11         ATAAGTCACATGATAAAAACATATTTAAAATTTTAAAAAAATTAATTTTCAAAATAAATTTATTAT A TTTTTTTAATTACATAATCATAAAAATAAATGTTCATGATTTCCGAACGTATAAAATAAGAATGTTACGA
CEN12        TTAAATCACGTGTAATAAATATTATTAAAAAGTTTATTAAAATAAAATAATAATTTAAATTACTATT T TTAAATAAGTTTTATTTTTTAATAACACTATTGTATTTGTTATCCGAACAATAAAAACATTTTATTAGCT
CEN13  GTGACAAAAAATCACATGACTACCTAACAAAATATTTATTTTTCTTTTTTAATATTTGAAAATACTAAAATAT   TTTTGTTGTTTTTTGAAAAAAGGATTTTTAATGTGTATGCGTTCCGAACTTTAAATATAACGTCAGCGTA
CEN14          GTTAGTCACGTGCAGCTTTTTAAAAATATTTTAAAACATTTTAAAAAATATACATTTTTTTATTA T TTTTTTATATATTAATGTTAAAATTTATTTATGTATTTGTCTTCCGAAAAGTAAAATAACGTTCAAATTTGG
CEN15         TAATATCACGTGAACTTATTTTGCATTTAAAAAAAAGTAAAAACTATTTGCTAAAATATATTTTTT T AATTTTTAAAAATAATGTTTTAATTATTTAATGTATATGACTTCCGAAAAATATATATTTGATAACA
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Fig. S2. Alignment of the *CEN* nucleosome kernels according to their dyad axes (i.e., the centers of the kernel sequences). Nucleotides within the *CEN* sequence are indicated in red, those outside *CEN* but within the kernel are in black and those that are outside the kernel are in gray. Nucleotides underlined in CDEI and CDEIII represent the specific binding sites of Cbf1 and CBF3 (Cep3), respectively. Fig. S2 is an expanded version of Fig. 4*A*, showing the entire *CEN* sequences.