Supplemental Table 1. *Saccharomyces cerevisiae* strains used in this study.

Strain	Relevant genotype	Figure
AMy1105	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA*	1a, c, 2a, b, c, d, 3a, Extended Data Fig. 1b, 3, 4a, 5b, 6a, 10a
AMy1145	*MATa SCC1-6HA*	Extended Data Fig. 9d, e
AMy2508	*MATa, cdc20::URA3::pMET-CDC20*	2a, b, e, 3d, 4e, Extended Data Fig. 6a, b, 7, 8a, b, c, 10e
AMy3950	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA chl4Δ::KanMX6*	1b, c, 2c, d, Extended Data Fig. 1b
AMy6389	*MATa cdc20::URA3::pMET-CDC20 SGO1-6HA::TRP1*	Extended Data Fig. 4a, b, c, d, e, f
AMy6471	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT his3::PURA3::tetR-GFP::HIS3 ~1kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy6884	*MATa cdc20::URA3::pMET-CDC20 sgo1(Y47A;Q50A;S52A)::hphMX4*	Extended Data Fig. 8a, b
AMy7217	*MATa cdc20::URA3::pMET-CDC20 sgo1Δ::KanMX6*	Extended Data Fig. 8a, b
AMy8955	*MATa cdc20::URA3::pMET-CDC20 BRN1-6HA::TRP1*	Extended Data Fig. 4a, b, c, d
AMy14126	*MATa, cdc20::URA3::pMET-CDC20 his3::PURA3::tetR-GFP::HIS3 SCC1-6HA::TRP1 SCC2-6HIS-3xFLAG::KAN ~1kbR_CEN3::tetOx224::URA3*	Extended Data Fig. 9a
AMy16144	*MATa cdc20::URA3::pMET-CDC20 CEN3Δ::LEU2 CEN6-URA3::CHRIII ~260kb SCC1-6HA*	Extended Data Fig. 3

Strain	Relevant genotype	Figure
AMy16541	*MATa SCC1-6HA PTC1-pURA3-URA3-MED2*	Extended Data Fig. 9d, e
AMy16721	*MATa SCC1-6HA MED2-pURA3-URA3-PTC1*	Extended Data Fig. 9d, e
AMy22078	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA pMAF1-MAF1::loxp (reversed orientation) pPTC1-PTC1::loxp (reversed orientation) pRPT2-RPT2::loxp (reversed orientation) pSOK1-SOK1-loxp-KANMX-loxp (reversed orientation)*	3a, Extended Data Fig. 10a
AMy22900	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~7kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy22936	*MATa cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~3kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy23081	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~3kbR_CEN1::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy23082	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~1kbR_CEN1::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy23125	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2~7kbR_CEN1::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy23185	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~18kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy25236	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~23kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy25297	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~8kbR_CEN1::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy25298	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA pMAF1-MAF1::loxp (reversed orientation) pPTC1-PTC1::loxp (reversed orientation) pRPT2-RPT2::loxp (reversed orientation) pSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) SGO1-6HIS-3FLAG::URA3*	Extended Data Fig. 10a

Strain	**Relevant genotype**	**Figure**
AMy25299	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA pMAF1-MAF1::loxp (reversed orientation) pPTC1-PTC1::loxp (reversed orientation) pRPT2-RPT2::loxp (reversed orientation) pSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) BRN1-6HIS-3FLAG::NATMX6*	Extended Data Fig. 10a
AMy25379	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA BRN1-6HIS-3FLAG::NATMX6*	Extended Data Fig. 10a
AMy25409	*MATa cdc20::URA3::pMET-CDC20 SCC1-6HA SGO1-6HIS-3FLAG::URA3*	Extended Data Fig. 10a
AMy25764	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~21kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy26822	*MATa, cdc20::URA3::pMET-CDC20 chl4Δ::KanMX6*	2c, d, e, Extended Data Fig. 6a, 7 , 8c
AMy26964	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~12kbR_CEN1::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy26965	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~12kbR_CEN3::tetOx224::URA3*	1d, Extended Data Fig. 5c
AMy26966	*MATa, cdc20::URA3::pMET-CDC20 SCC1-6HA rad61Δ::TRP1*	Extended Data Fig. 1a
AMy27213	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~4kbR_CEN4::tetOx224::URA3*	3b, 4a, 4b, Extended Data Fig. 10b, c
AMy27214	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 ~11.5kbR_CEN4::tetOx224::URA3*	3b, 5a, Extended Data Fig. 10b, c
AMy27215	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 pMAF1-MAF1::loxp (reversed orientation) pPTC1-PTC1::loxp (reversed orientation) pRPT2-RPT2::loxp (reversed orientation) pSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) ~13.5kbR_CEN4::tetOx224::URA3*	3b, 5a, Extended Data Fig. 10b, c
AMy27216	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::tetR-GFP::LEU2 pMAF1-MAF1::loxp (reversed orientation) pPTC1-PTC1::loxp*	3b, 4a, 4b, Extended

Strain	Relevant genotype	Figure
	(reversed orientation) pRPT2-RPT2::loxp (reversed orientation) pSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) ~4kbR_CEN4::tetOx224::URA3	Data Fig. 10b, c
AMy27936	*MATa, cdc20::URA3::pMET-CDC20 PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation)*	3d, Extended Data Fig. 10d, e
AMy28477	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~23kb to right of CEN4)*	Extended Data Fig. 10c
AMy28478	*MATa, cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~23kb to right of CEN4) MCD1-6HA PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation)*	Extended Data Fig. 10c
AMy28726	*MATa cdc20::URA3::pMET-CDC20 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~0.5kb to right of CEN3. INSIDE the boundary) MCD1-6HA PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation)*	4b
AMy28787	*MATa ipl1-321 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4)*	4c, 4d
AMy28788	*MATa Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4)*	4c, 4d
AMy28790	*MATa ipl1-321 MCD1-6HA Spc42-tdTomato::NAT PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4)*	4c, 4d
AMy28791	*MATa MCD1-6HA Spc42-tdTomato::NAT PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp*	4c, 4d

Strain	Relevant genotype	Figure
	(reversed orientation) leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4)	
AMy28792	*MET-CDC20::URA3 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4) pURA3::ABIx2-V5::TRP1 (between RAD57 and MAF1 at chr IV RIGHT border, transcribed away from CEN4) pURA3::PYLx2-3FLAG::HisMX6 (between PTC1 and MED2 at chr IV LEFT border, transcribed away from CEN4)*	3c
AMy28793	*MET-CDC20::URA3 Spc42-tdTomato::NAT leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~11.5kb to right of CEN4) pURA3::ABIx2-V5::TRP1 (between RAD57 and MAF1 at chr IV RIGHT border, transcribed away from CEN4) pURA3::PYLx2-3FLAG::HisMX6 (between PTC1 and MED2 at chr IV LEFT border, transcribed away from CEN4)*	3c
AMy28794	*MCD1-6HA MET-CDC20::URA3 Spc42-tdTomato::NAT PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~4kb to right of CEN4) pURA3::ABIx2-V5::TRP1 (between RAD57 and MAF1 at chr IV RIGHT border, transcribed away from CEN4) pURA3::PYLx2-3FLAG::HisMX6 (between PTC1 and MED2 at chr IV LEFT border, transcribed away from CEN4)*	3c
AMy28878	*MCD1-6HA MET-CDC20::URA3 Spc42-tdTomato::NAT PMAF1-MAF1::loxp (in opposite orientation) PPTC1-PTC1::loxp (reversed orientation) PRPT2-RPT2::loxp (reversed orientation) PSOK1-SOK1-loxp-KANMX-loxp (reversed orientation) leu2::PURA3::tetR-GFP::LEU2 tetOx224-URA3 (tetOs ~13.5kb to right of CEN4) pURA3::ABIx2-V5::TRP1 (between RAD57 and MAF1 at chr IV RIGHT border, transcribed away from CEN4) pURA3::PYLx2-3FLAG::HisMX6 (between PTC1 and MED2 at chr IV LEFT border, transcribed away from CEN4)*	3c

Supplemental Table 2. Plasmids generated in this study.

Plasmid	Characteristics
AMp1298	*pMAF1-MAF2 LoxP-KanMX6-LoxP*
AMp1302	*pPTC1-PTC1 LoxP-KanMX6-LoxP*
AMp1332	*pRPT2-RPT2 LoxP-KanMX6-LoxP*
AMp1360	*pSOK1-SOK1 LoxP-kanMX6-LoxP*
AMp1411	*pRS306(tetOx224) + 502bp genomic sequence (2901bp right of centromere 3) to integrate tetOs ~3kb to right of CEN3*
AMp1412	*pRS306(tetOx224) + 635bp genomic sequence (6453bp right of centromere 3) to integrate tetOs ~7kb to right of CEN3*
AMp1413	*pRS306(tetOx224) + 514bp genomic sequence (17546bp right of centromere 3) to integrate tetOs ~18kb to right of CEN3*
AMp1433	*pRS306(tetOx224) + 676bp genomic sequence (674bp right of centromere 1) to integrate tetOs ~1kb to right of CEN1*
AMp1436	*pRS306(tetOx224) + 443bp genomic sequence (7123bp right of centromere 1) to integrate tetOs ~7kb to right of CEN1*
AMp1437	*pRS306(tetOx224) + 377bp genomic sequence (3456bp right of centromere 1) to integrate tetOs ~3kb to right of CEN1*
AMp1538	*pRS306(tetOx224) + 442bp genomic sequence (8105bp right of centromere 1) to integrate tetOs ~8kb to right of CEN1*
AMp1539	*pRS306(tetOx224) + 632bp genomic sequence (23137bp right of centromere 3) to integrate tetOs ~18kb to right of CEN3*
AMp1562	*pRS306(tetOx224) + 611bp genomic sequence (20810bp right of centromere 3) to integrate tetOs ~21kb to right of CEN3*
AMp1669	*pRS306(tetOx224) + 505bp genomic sequence (12611bp right of centromere 1) to integrate tetOs ~12kb to right of CEN1*
AMp1670	*pRS306(tetOx224) + 375bp genomic sequence (11156bp right of centromere 3) to integrate tetOs ~12kb to right of CEN3*

Plasmid	**Characteristics**
AMp1676	*pRS306(tetOx224) + 535bp genomic sequence (3765bp right of centromere 4) to integrate tetOs ~4kb to right of CEN4*
AMp1677	*pRS306(tetOx224) + 594bp genomic sequence (11426bp right of centromere 4) to integrate tetOs ~11kb to right of CEN4*
AMp1678	*pRS306(tetOx224) + 560bp genomic sequence (13745bp right of centromere 4) to integrate tetOs ~14kb to right of CEN4 in MAF1-SOK1 reversed orientation strain*
AMp1776	*pRS306(tetOx224) + 505bp genomic sequence (20660bp right of centromere 4) to integrate tetOs ~21kb to right of CEN4*
AMp1781	*pURA3::ABIx2-V5::TRP1*
AMp1792	*pRS306(tetOx224) + 585bp genomic sequence (576bp right of centromere 3) to integrate tetOs ~0,5kb to right of CEN3*
AMp1796	*pURA3::PYLx2-FLAG::HISMX6*

Supplemental Table 3. SacCer3 genome coordinates used to generate plots showing ChIP-Seq averages.

Chr.	Left arm peak	Left border	CEN	Right border	Right arm peak
I	134298	147806	151523	160211	166415
II	212364	235228	238265	244311	284156
III	92933	101301	114443	114443	139263
IV	401066	440767	448766	456742	477402
V	138610	145845	152046	166000	189212
VI	137306	143961	148569	154425	172326
VII	469180	489446	496979	504623	531467
VIII	76328	100445	105645	109984	119742
IX	318507	350183	355687	365766	377053
X	409512	431178	436366	440892	453193
XI	411713	432938	440188	446723	458573
XII	128912	134084	150888	161639	168074
XIII	251386	256267	268090	279763	294742
XIV	609784	616470	628817	644043	648792
XV	309510	321621	326643	334818	367254
XVI	533727	550434	556015	560618	577268

Supplemental Table 4. qPCR primer sequences used in this study.

Primer pair	Sequence (5'-3')			
	Forward primer	**Ref.**	**Reverse primer**	**Ref.**
p1	AGATGAAACTCAGGCTACCA	782	TGCAACATCGTTAGTTCTTG	783
p2	ACAAAGGATGATTTGTCAGG	910	CTCTCTCCTTGGCTTGTTTA	911
p3	TACAGCAAATGTTGGTGATT	4877	ACCTGCTTGTTCAACTCTCT	4978
p4	TTTAATCCTAGCGTGTGATG	5657	TCCAAAGCATATCTAACCAA	5658
p5	TCTCTCACATGACGAATGAG	1321	GACTTGTAAACCGTGTTGTG	1322
p6	ACAACAACAGCAGTGAGAAG	4881	TATTGTTATTGTCGTTCCCA	4882
p7	TTTCCAATCCTGGAGATAAC	5561	GAGGTCTAATTCGCCATTAT	5562
p8	GGAGCAATACCAGAACAATG	5909	ATCATCATTTCTGCTCCAAC	5910
p9	AAGTTGGAGCAGAAATGATG	5911	TTTGCTGAGATTGACTGAAA	5912
p10	TTTAGTTGTGCATCGCATAC	5917	CGTTACAAGCGGGTAATATC	5918
p11	ATAAGGAACGTGCTGCTACT	5549	CACACAAGTTTGTTTGCTTT	5550
p12	TGCGGGTGTATACAGAATAG	5547	GCCTCTAGGTTCCTTTGTTA	5548
p13	GGTTTAGATGACAAGGGAGA	5545	GCAAATAGTCCTCTTCCAAC	5546
p14	CCGAGGCTTTCATAGCTTA	794	ACCGGAAGGAAGAATAAGAA	795
p15	AGAAACCACCCATAATTGAG	4885	ACGATAGTCAAATTTCCGTT	4886
p16	TCAAATGAATACGAAGGAGA	4891	AGGGATTCTTCTTGATCTGA	4892
p17	CGATAGTATTGATTGTGGGA	1337	CCAGGAAATGCTTCTAACTT	1338

Supplemental Table 5. Hi-C libraries generated in this study.

Sample	Total unique reads (R1/R2)	Valid unique Hi-C pairs
WT - Tension	36 299 576 / 43 078 602	17 937 575
WT – No tension	34 921 366 / 42 352 447	17 779 189
chl4Δ - Tension	38 653 664 / 44 991 486	19 530 920
sgo1Δ – No tension	37 702 242 / 43 924 423	20 318 535
sgo1-3A – No tension	45 109 744 / 53 348 344	21 068 633
chl4Δ – No tension	64 306 395 / 70 848 109	62 060 500
Reoriented - Tension	70 760 639 / 76 584 915	76 278 472