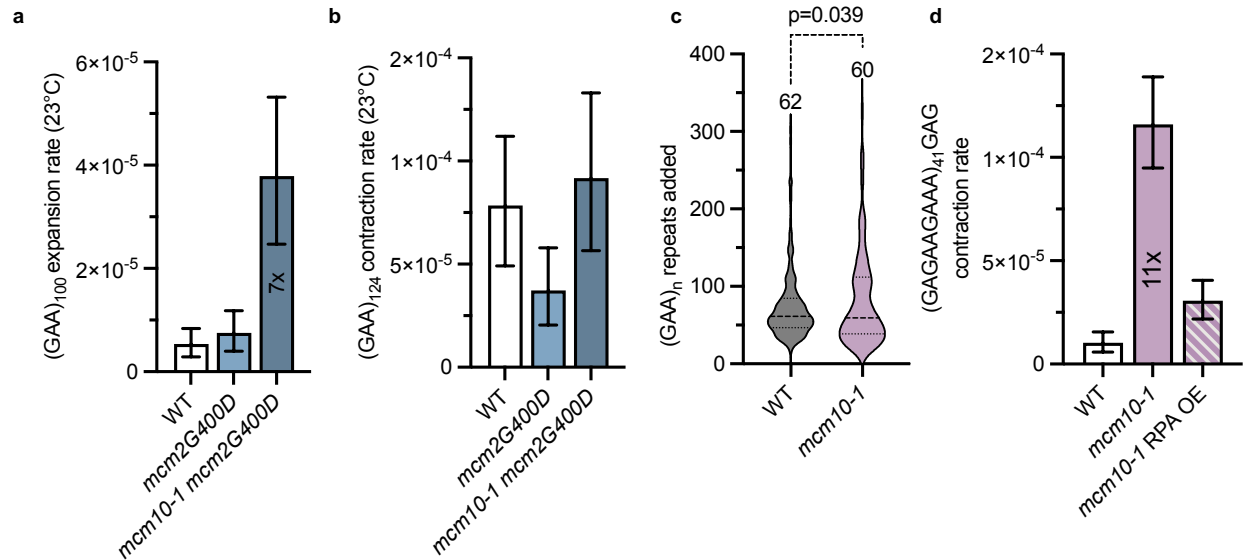
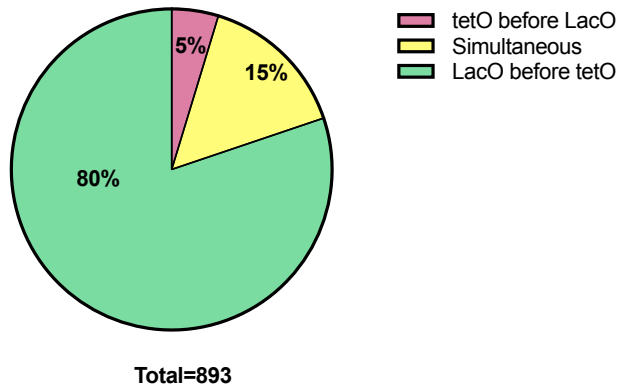


Supplementary Figures

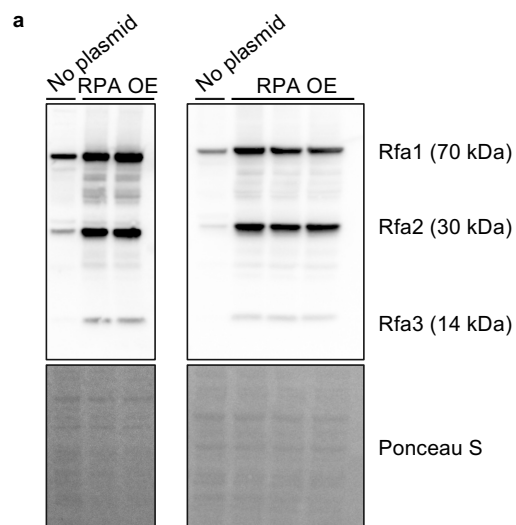


Supplementary Figure 1: Additional phenotypes related to the *mcm10-1* and *mcm2-G400D* mutant. **(a)** Expansion rates of the *mcm2-G400D* mutants at the permissive temperature (23°C). **(b)** Contraction rates of the *mcm2-G400D* mutants at the permissive temperature (23°C). **(c)** Distribution of the number of added repeats units for expansion events in the WT (n=154) and *mcm10-1* (n=178) for the fluctuation assay experiments in Fig. 1d. Dashed lines represent the median number of repeats added and quartiles, numbers above bars are the median. Pairwise comparisons of distributions were conducted using the nonparametric goodness-of-fit Kolmogorov-Smirnov test. p=0.039. **(d)** Contraction rates of (GAGAAGAAA)₄₁GAG repeat in the *mcm10-1* and *mcm10-1* RPA overexpression conditions at the semi-permissive temperature of 27°C.

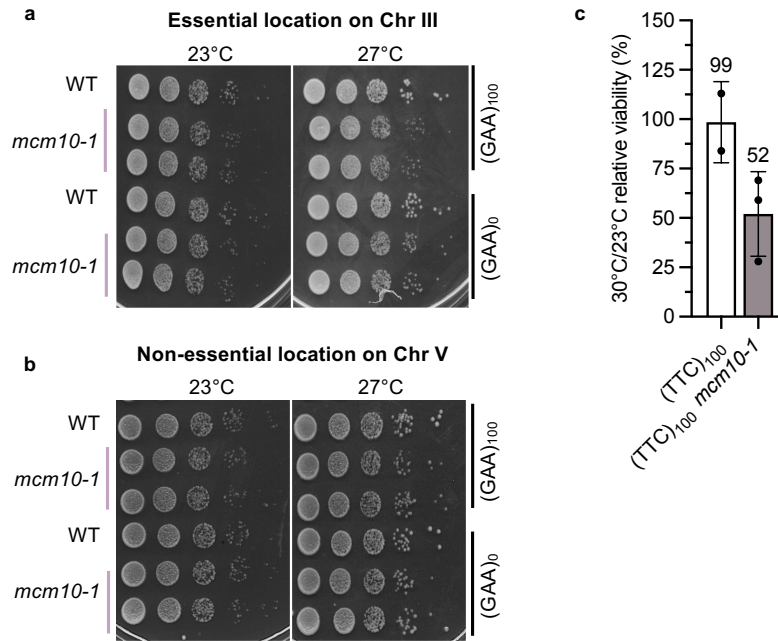
a Replication fork directionality for WT GAA100 cassette (CM454)



Supplementary Figure 2: Replication fork directionalities. (a) Replication fork directionality chart for the wild-type live-cell microscopy strain containing the expansion cassette with the (GAA)₁₀₀ repeat (strain CM454). Cells (n=893) were counted as “lacO before tetO” (left-to-right fork) if the Δ time between the doubling in intensity of the lacO and tetO was $\geq +5$ min, as “simultaneous” if the Δ time was between -5 and +5 min and as “tetO before lacO” (right-to-left fork) if the Δ time was ≤ -5 min. Data is represented in % of cells in each category. Raw data is provided in the Source Data file. Refers to data in Fig. 3.

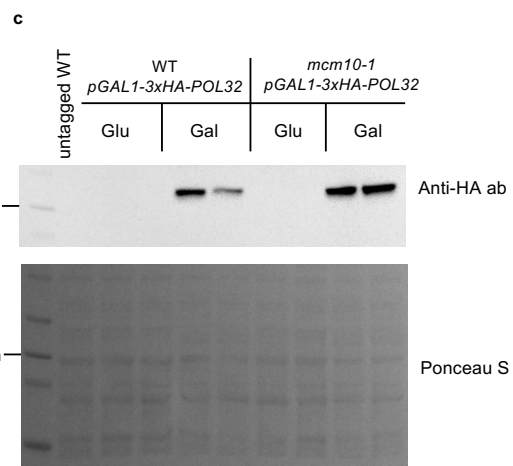
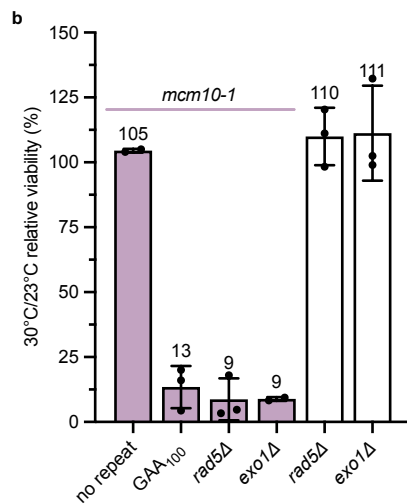
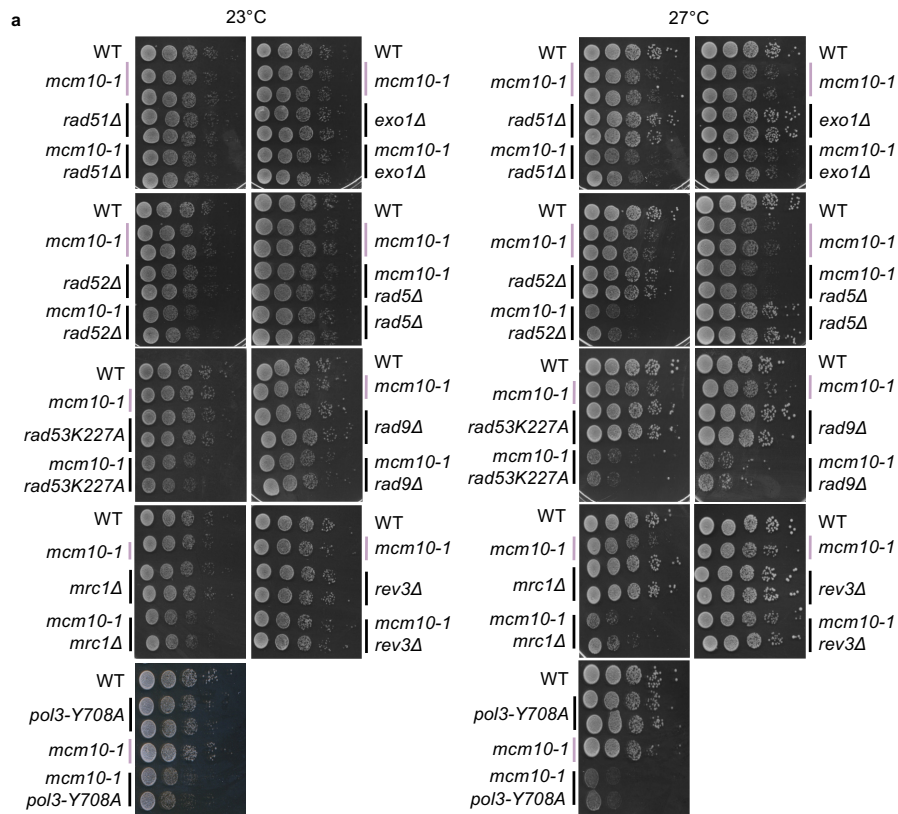


Supplementary Figure 3: RPA overexpression validation by Western Blot. (a) Western blot analysis of various strains either containing the 2 μ multicopy plasmid containing all three RPA genes (*RFA1*, *RFA2* and *RFA3*), or without plasmid. The RPA antibody (AS07-214) detects all three RPA subunits: Rfa1p (70 kDa), Rfa2p (30 kDa) and Rfa3p (14 kDa). Ponceau S staining was used as a control for total protein loading.

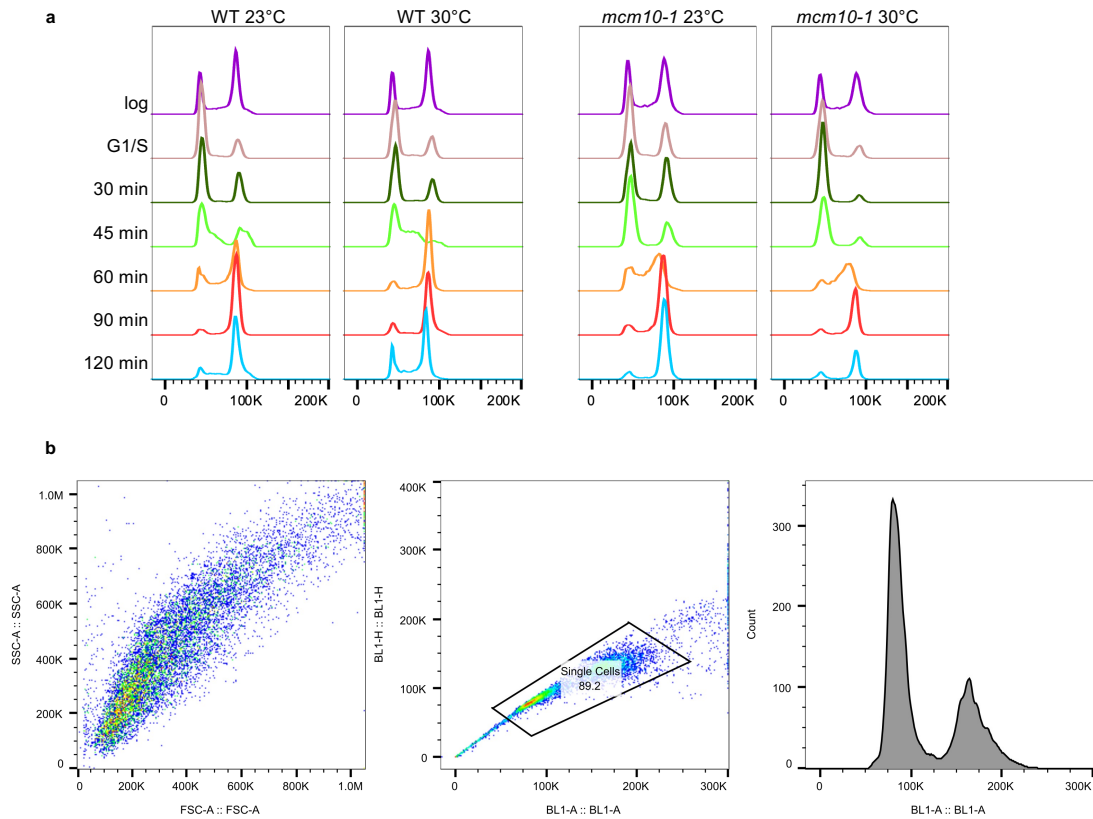


Supplementary Figure 4: Spot tests of *mcm10-1* strains at different temperatures and repeat-orientation dependent viability defects.

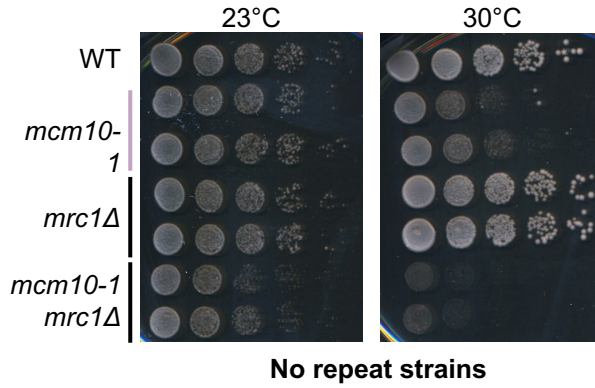
(a) Spot tests of strains containing either the no repeat or the (GAA)₁₀₀ repeat cassette at the chromosome III location in wild-type and *mcm10-1* backgrounds at the permissive (23°C) and semi-permissive (30°C) temperatures. Cells were grown to an OD₆₀₀=1 in YPDUA medium at the permissive temperature and then spotted as a 1:10 serial dilution on YPDUA plates and grown for 3 days. **(b)** Spot test as described in **a** but for the same cassettes at the non-essential chromosome V location. **(c)** Viability assay of a strain containing the expansion cassette represented in Fig. 1b with an inverted repeat, in which (TTC)₁₀₀ is the lagging-strand template. Each datapoint represents the percent relative survival as determined by colony forming unit (CFU) counts. The mean is plotted, and the bars indicate standard deviation. Each assay was conducted using at least two biological replicates.



Supplementary Figure 5: Spot tests of *mcm10-1* double mutants at different temperatures and additional instability rates. **(a)** Spot tests of strains containing the (GAA)₁₀₀ cassette for various *mcm10-1* double mutants at the permissive temperature (23°C) and at the semi-permissive temperature (27°C). Cells were grown to an OD₆₀₀=1 in YPDUA medium at the permissive temperature and then spotted as a 1:10 serial dilution on YPDUA plates and grown for 2-3 days at each temperature. **(b)** Viability assays for additional *mcm10-1* double mutants, conducted as described in Fig. 5b. **(c)** Western blot of the *pGAL1-3xHA-POL32* strains used in Fig. 5d to detect Pol32 protein levels under repressive (glucose) and inducing (galactose) conditions at 23°C. *pGAL1-3xHA-POL32* was detected using Anti-HA Tag antibody 05-904 (Sigma Aldrich, 1 µg/ml dilution in 5% skim milk in TBS-T).



Supplementary Figure 6: Flow Cytometry of DNA content for WT and *mcm10-1* at 23°C versus 30°C and gating strategy. (a) Cell cycle analysis of WT and *mcm10-1* cells as described for Fig. 6f, conducted at both the permissive temperature of 23°C and the semi-permissive temperature of 30°C. **(b)** Representation of the gating strategy used for the flow cytometry data. 10,000 events were acquired and then singlets were gated (labeled Single cells), data was represented as fluorescent signal area (BL1-A) x count to create the represented histogram plots.



Supplementary Figure 7: Spot tests of strains containing the no repeat control cassette for the *mcm10-1 mrc1Δ* double mutant at the permissive temperature (23°C) and at the semi-permissive temperature (30°C). Cells were grown to an OD₆₀₀=1 in YPDUA medium at the permissive temperature and then spotted as a 1:10 serial dilution on YPDUA plates and grown for 2-3 days at each temperature.

Supplementary Table 1: List of strains used in this study.

Strain Name	Genotype	Comments
CM25	CM77 <i>mcm10-1</i> (P269L)	<i>ts</i> , This study
CM26	CM77 <i>mcm10-1</i> (P269L)	<i>ts</i> , This study
CM77	MATa <i>leu2-Δ1</i> , <i>trp1-Δ63</i> , <i>ura3-52</i> , <i>his3-200</i> (CH1585), <i>ade2::KanMX</i> , MIP1-wt, HAP1-wt, ChrIII(75594-75641):: PGAL-UR-(GAA)128-A3-TRP1	PMID: 2944739 6
JAH112	MATa <i>leu2-Δ1</i> <i>trp1-Δ63</i> <i>ura3-52</i> <i>his3-200</i> (CH1585) <i>bar1Δ::HIS3</i> ChrIII(75423-75715)::pUR-URA3-Int-GAA100d-TRP1	PMID: 2314266 7
CM71	MATa <i>leu2-Δ1</i> <i>trp1-Δ63</i> <i>ura3-52</i> <i>his3-200</i> (CH1585) <i>bar1Δ::HIS3</i> ChrIII(75423-75715)::pUR-URA3-Int-GAA100d-TRP1	PMID: 2314266 7
CM72	CM71 <i>mcm10-1</i> (P269L)	<i>ts</i> , This study
CM73	CM71 <i>mcm10-1</i> (P269L)	<i>ts</i> , This study
CM85	CM71 <i>mcm2G400D</i>	This study
CM86	CM71 <i>mcm2G400D</i>	This study
CM88	CM72 <i>mcm2G400D</i>	This study
CM89	CM72 <i>mcm2G400D</i>	This study

CM59	CM77 <i>mcm2G400D</i>	This study
CM60	CM77 <i>mcm2G400D</i>	This study
CM67	CM25 <i>mcm2G400D</i>	This study
CM68	CM25 <i>mcm2G400D</i>	This study
CM195	CM25 <i>rad53K227A</i>	This study
CM197	CM25 <i>rad53K227A</i>	This study
CM200	CM72 <i>rad53K227A</i>	This study
CM201	CM72 <i>rad53K227A</i>	This study
CM221	CM71 <i>rad5::HygB</i>	This study
CM222	CM71 <i>rad5::HygB</i>	This study
CM218	CM72 <i>rad5::HygB</i>	This study
CM219	CM72 <i>rad5::HygB</i>	This study
CM227	CM71 <i>ctf4Δ</i>	This study
CM229	CM71 <i>ctf4Δ</i>	This study
SMYU170	CM77 <i>ctf4::HygB</i>	This study
CM148	CM77 <i>ctf4Δ</i>	This study
CM299	CM25 (pSK_UC57_2u_HIS3_RFA1_RFA2_RFA3)	This study
CM300	CM25 (pSK_UC57_2u_HIS3_RFA1_RFA2_RFA3)	This study
CM304	SMY706 (<i>leu2Δ1</i> , <i>trp1Δ63</i> , <i>ura3Δ52</i> , <i>his3Δ200</i> , MIP1, HAP1, MATa) <i>ura3Δ bar1Δ</i> + ChrIII(75423-75715)::pUR-UR-TTC100-A3-TRP1	This study
CM305	SMY706 (<i>leu2Δ1</i> , <i>trp1Δ63</i> , <i>ura3Δ52</i> , <i>his3Δ200</i> , MIP1, HAP1, MATa) <i>ura3Δ bar1Δ</i> + ChrIII(75423-75715)::pUR-UR-TTC100-A3-TRP1	This study
CM388	CM72 with CMP72 (pSK_UC57_2u_LEU2_RFA1_RFA2_RFA3)	This study
CM389	CM72 with CMP72 (pSK_UC57_2u_LEU2_RFA1_RFA2_RFA3)	This study
CM345	CM71 <i>rad51Δ</i>	This study
CM346	CM71 <i>rad51Δ</i>	This study
CM348	CM72 <i>rad51Δ</i>	This study
CM349	CM72 <i>rad51Δ</i>	This study
CM361	CM71 <i>rad52Δ</i>	This study
CM362	CM71 <i>rad52Δ</i>	This study
CM363	CM72 <i>rad52Δ</i>	This study
CM365	CM72 <i>rad52Δ</i>	This study
CM355	CM71 <i>exo1Δ</i>	This study
CM357	CM71 <i>exo1Δ</i>	This study
CM358	CM72 <i>exo1Δ</i>	This study
CM359	CM72 <i>exo1Δ</i>	This study

CM415	YEG150 <i>mcm10-1</i>	This study
CM416	YEG150 <i>mcm10-1</i>	This study
CM438	YEG200 <i>mcm10-1</i>	This study
CM439	YEG200 <i>mcm10-1</i>	This study
CM440	YEG200 <i>mcm10-1</i>	This study
CM315	CM304 <i>mcm10-1</i>	This study
CM316	CM305 <i>mcm10-1</i>	This study
YEG236/1	CM71 <i>rad53K227A</i>	PMID: 34849883
YEG236/2	CM71 <i>rad53K227A</i>	PMID: 34849883
YEG200/1	CM71 <i>mrc1::natMX</i>	PMID: 34849883
YEG200/3	CM71 <i>mrc1::natMX</i>	PMID: 34849883
YEG150/1	CM71 <i>rad9Δ</i>	PMID: 34849883
YEG150/2	CM71 <i>rad9Δ</i>	PMID: 34849883
CM153	CM72 GAA40	This study
CM154	CM72 GAA40	This study
CM155	CM71 GAA40	This study
CM156	CM71 GAA40	This study
SMYUD24	MATa, leu2-Δ1, trp1-Δ63, ura3-52, his3-200, ade2Δ::KanMX4, HAP1-wt, ChrIII(75594- 75641)::PGal1-UR-(GAGAAGAAA)41GAG-A3-TRP1	PMID: 3191146 8
SMYUD25	MATa, leu2-Δ1, trp1-Δ63, ura3-52, his3-200, ade2Δ::KanMX4, HAP1-wt, ChrIII(75594- 75641)::PGal1-UR-(GAGAAGAAA)41GAG-A3-TRP1	PMID: 3191146 8
CM281	SMYUD24 <i>mcm10-1</i>	This study
CM282	SMYUD24 <i>mcm10-1</i>	This study
JAH281	MATa leu2-Δ1, trp1-Δ63, ura3-52, his3-200 (CH1585), ade2::KanMX, MIP1-wt, HAP1-wt, ChrIII(75594-75641)::pUR-UR-no repeat control-A3-TRP1	This study
CM409	JAH281 <i>mcm10-1</i>	This study
CM410	JAH281 <i>mcm10-1</i>	This study
JAH293	MATa, leu2-1, trp1-63, his3-200, ura3Δ, bar1Δ, Chr. V arm loss centromere-facing no repeat control	This study

CM351	MATa, leu2-1, trp1-63, his3-200, ura3Δ, bar1Δ, ChrV(33,834-33,999)::UR-(GAA)100-A3 TRP1	This study
CM353	MATa, leu2-1, trp1-63, his3-200, ura3Δ, bar1Δ, ChrV(33,834-33,999)::UR-(GAA)100-A3 TRP1	This study
CM366	CM351 <i>mcm10-1</i>	This study
CM368	CM353 <i>mcm10-1</i>	This study
CM377	JAH293 <i>mcm10-1</i>	This study
CM378	JAH293 <i>mcm10-1</i>	This study
CM438	YEG200 <i>mcm10-1</i>	This study
CM439	YEG200 <i>mcm10-1</i>	This study
CM440	YEG200 <i>mcm10-1</i>	This study
CM441	CM71 <i>rev3::HygB</i>	This study
CM443	JAH112 <i>rev3::HygB</i>	This study
CM445	CM72 <i>rev3::HygB</i>	This study
CM447	CM73 <i>rev3::HygB</i>	This study
CM477	CM281 <i>mcm2G400D</i>	This study
CM478	CM282 <i>mcm2G400D</i>	This study
CM466	CM71 + pRS415	This study
CM467	CM71 + pRS415	This study
CM468	CM72 + pRS415	This study
CM469	CM72 + pRS415	This study
CM480	CM438 pRS415	This study
CM481	CM438 pRS415	This study
CM462	CM438 pAO139 (<i>mrc1AQ</i>)	This study
CM463	CM438 pAO139 (<i>mrc1AQ</i>)	This study
CM252	CM71 <i>Pol1-3xFLAG-KanMX</i>	This study
CM257	CM72 <i>Pol1-3xFLAG-KanMX</i>	This study
CM485	CM71 <i>pol3-Y708A</i>	This study
CM487	CM71 <i>pol3-Y708A</i>	This study
CM488	CM72 <i>pol3-y708A</i>	This study
CM490	CM72 <i>pol3-y708A</i>	This study
CM491	CM71 <i>kanMX-pGAL1-3xHA-POL32</i>	This study
CM492	CM71 <i>kanMX-pGAL1-3xHA-POL32</i>	This study
CM493	CM72 <i>kanMX-pGAL1-3xHA-POL32</i>	This study
CM494	CM72 <i>kanMX-pGAL1-3xHA-POL32</i>	This study
CM153	CM72 GAA40	This study

CM154	CM72 GAA45	This study
CM296	CM281 + <i>pSK_UC57_2u_HIS3_RFA1_RFA2_RFA3</i>	This study
CM297	CM281 + <i>pSK_UC57_2u_HIS3_RFA1_RFA2_RFA3</i>	This study
CM454	CM343 ChrIV(336,187)::URA3-Int-norpt-TRP1	This study
CM343	W1588, MATa, leu2-3,112, trp1-1, can1-100, ura3-1, ade2-1, chrIV(332,960)::LacOx128, chrIV(336,187)::NatMX, chrIV(352,560)::TetOx128, ade1Δ::LacI-Envy-KanMX-TetR-tdTomato	This study
CM425	CM343 ChrIV(336,187)::URA3-Int-GAA100d-TRP1	This study
CM471	CM454 <i>mcm10-1</i>	This study
CM436	CM425 <i>mcm10-1</i>	This study
CM371	CM71 + CMP72 (pSK_UC57_2u_LEU2_RFA1_RFA2_RFA3)	This study
CM372	CM71 + CMP73 (pSK_UC57_2u_LEU2_RFA1_RFA2_RFA3)	This study
CM373	CM71 + CMP74 (pSK_UC57_2u_LEU2_RFA1_RFA2_RFA3)	This study
CM315	CM304 <i>mcm10-1</i>	This study
CM316	CM305 <i>mcm10-1</i>	This study
CM317	CM305 <i>mcm10-1</i>	This study
CM497	JAH281 <i>mrc1::kanMX</i>	This study
CM498	JAH281 <i>mrc1::kanMX</i>	This study
CM499	CM77 <i>mrc1::his3</i>	This study
CM500	CM77 <i>mrc1::his3</i>	This study
CM501	CM409 <i>mrc1::his3</i>	This study
CM502	CM409 <i>mrc1::his3</i>	This study

Supplementary Table 2: List of primers used in this study

Name	Sequence	Purpose
pRCC plasmid amplification oligos to introduce CRISPR/Cas9 guides		
Mcm10_pRCC_F	GGTCTCCATGGTAGTACTTCgttttagagctagaaatagcaagttaaataagg	<i>mcm10-1</i> (P269L) mutation
Mcm10_pRCC_R	GAAGTACTACCATGGAGACCcgatcatttatctttcactgcggag	
Mcm2_pRCC_F	GCTCCCGGAACCGTTCCTCCgttttagagctagaaatagcaagttaaataagg	<i>mcm2G400D</i> mutation
Mcm2_pRCC_R	GGAGGAACGGTTCGGGAGCcgatcatttatctttcactgcggag	
Rad53_pRCC_F	AACTACTGGGAAAACATTCGgttttagagctagaaatagcaagttaaataagg	<i>rad53K227A</i> mutation
Rad53_pRCC_R	CGAATGTTTTCCAGTAGTTtccgatcatttatctttcactgcggag	
CTF4_pRCC_F	AACAATAACGCGAACCGGGGgttttagagctagaaatagcaagttaaataagg	CTF4 deletion
CTF4_pRCC_R	CCCCGGTTCGCGTTATTGTTcgatcatttatctttcactgcggag	

rad51_pRCC_F	TCAGCGGTTTCGGATTAGACCggttttagagctagaaatagcaagttaaataagg	RAD51 deletion
rad51_pRCC_R	GGTCTAATCCGAACCGCTGAcgatcatttatctttcactgcggag	
rad52_pRCC_F	ACCAGGTTCTTCGTCGAGTCgttttagagctagaaatagcaagttaaataagg	RAD52 deletion
rad52_pRCC_R	GACTCGACGAAGAACCTGGTcgatcatttatctttcactgcggag	
Pol3_pRCC_F	TGGTTTTACAGGAGCGACGGgttttagagctagaaatagcaagttaaataagg	Pol3-Y708A
Pol3_pRCC_R	CCGTCGCTCCTGTAAAACCAcgatcatttatctttcactgcggag	mutation
CRISPR/Cas9 repair templates		
Mcm10- 1_rep_temp	TAGAAAGATATTATAATCTTCGCCTGGGTGATGTGATAGC AATATTAATCTTGAAGTACTACCATGGAGACCCTCAGGGC GAGGAAATTTTATCAAATC	mcm10-1 mutation
Mcm2- G400D_rep_temp	ATTATCAAAGGGTTACGCTCCAGGAAGCTCCCGGAACCGT TCCTCCAGACCGTCTACCAAGACATAGAGAAGTCATTTTGT TGGCGGATTTGGTAGATGT	mcm2-G400D mutation
Rad53_repairtem p_F	TTGCCACAGTAAAGAAAGCCATTGAAAGAATACTACTGGGAA AACATTCGCCGTGGCGATTATAAGTAAACGCAAAGTAATA GGCAATATGGATGGTGTGAC	Rad53-K227A mutation
Rad53_repairtem p_R	GTCACACCATCCATATTGCCTATTACTTTGCGTTTACTTAT AATCGCCACGGCGAATGTTTTCCCAGTAGTTCTTTCAATGG CTTTCTTACTGTGGCAA	
CTF4del_rep_tem p	AAATAATTGAGAAGGGCAAGAAGTGACGTAAATATACTA GACGTACTATTAAAAATGTAAAATATATATACGCAAGAGA CAATTATTTGATACCTGTTCA	CTF4 deletion
rad51_repairtemp _F	CGACAAAGAGCAGACGTAGTTATTTGTTAAAGGCCTACTA ATTTGTTATCGTCATGTATTTGGTCTCTTG	RAD51 deletion
rad51_repairtemp _R	AGAGGAGAATTGAAAGTAAACCTGTGTAAATAAATAGAG ACAAGAGACCAAATACATGACGATAACAAAT	
rad52_repairtemp _F	TTAGTCTGTTAAGAAAAGACGAAAAATATAGCGGCGGGCG GGTTACGCGACCGGTATCGAAACGCTTCCTGGCCG	RAD52 deletion
rad52_repairtemp _R	AGGATTTTGGAGTAATAAATAATGATGCAAATTTTTTATTT GTTTCGGCCAGGAAGCGTTTCGATACCGGTCGCG	
Exo1_repairtempl ate	ACCACATTAAATAAAAAGGAGCTCGAAAAAACTGAAAGG CGTAGAAAGGAAAGTTAAGTACTGCACGTTTCATATCGGA GGTATATTTTTCAAATGAAAA	EXO1 deletion
Pol3_Y708A_rep _temp	TTTTAAATGGTAGACAATTGGCTTTGAAGATTTTCAGCTAAC TCTGTCgcgGGTTTTACAGGAGCGACGGTtGGTAAATTGCCA TGTTTAGCCATTTCTT	Pol3-Y708A mutation

Gene replacement primers		
Rev3_pAG_F	ATGTCGAGGGAGTCGAACGACACAATACAGAGCGATACG GTTAGATCATCCGGATCCCCGGGTAAATTAA	Rev3 deletion, used with pAG32
Rev3_pAG_R	GCGAGACATATCTGTGTCTAGATTACCAATCATTTAGAGAT ATTAATGCTGCATAGGCCACTAGTGGATCTG	
Gene tagging primers		
Pol1-PL3FLAG- KanMX_F	CGATTGTGGACGTCGCTACGTTGATATGACTAGCATATTTG ATTCATGCTAAATaggaacaaaagctggag	Pol1-3xFLAG- KanMX tagging
Pol1-PL3FLAG- KanMX_R	TTTTCTTACTATATAGAATATTCATGAGATCACACAACACA TACAAAATACTTACctataggcgcaattgggt	
Pol32_F4	TTTTGAAAAGTACGCAGAAGTTCGTTACATCGCAATCAGA TCAGCTCGAAgaattcgagctcgtttaaac	KanMX-pGAL1- 3xHA-POL32 tagging
Pol32_R3	ACCTCAGTGAAGAGCTTCTCATTGATAAAATATGACGCCTT TTGATCCATgcactgagcagcgtaatctg	
Checking primers		
Mcm10_check_F	GCCTGAATACGCCAACTG	MCM10 amplification for sequencing
Mcm10_check_R	AATTCGAAGGTTGAAGGATTTG	
Mcm2_F	TTAGCGGAGTCCAAAGCCAT	MCM2 amplification for sequencing
Mcm2_R	TCACGTTCTTCTTCTTCAGTCCA	
CTF4_upstr_F	GCGACGCGTAATAAAAGTTTCC	CTF4 external check
CTF4_dnstr_R	AAAATTTCGCAAGGACGCTTC	
CTF4_F	GCCTGGAAAATCCAAGCGGAC	CTF4 ORF absence
CTF4_R	CACATCTTCCGCATTTCGCTTC	
RAD51_chk_F	CAATTCGCAAGAAACGCACT	RAD51 ORF absence
RAD51_chk_R	AAGTAGTCATCGGGAAGAAGAGTA	
RAD51_upstr_F	TTTCTGTCCTGGTTTGTTTACAGTA	RAD51 external check
RAD52_chk_in_F	GCCAAGAAATCTGCCGTTAC	RAD52 ORF absence
RAD52_chk_in_R	TGAGCTTTCGCTGATTTTCATCC	
Ex52_R	ACGTCGCTAAAGATGGTATGGTA	RAD52 external check
E52x-F	CTAGAGGATTTTGGAGTAATAAATAATGATG	
Exo1_F	CAGCGGGAGGGAAAACATGAT	EXO1 ORF absence
Exo1_R	CTCTGTTGGCTAGAGGTTGGTG	

exo1_KOchk_Fwd	GTATTACGTCCAAACTAAGTTCGCG	EXO1 external check
exo1_KOchk_rev	GACCGCTAGCGGCTTGATTAG	
Rad53_seq_F	TGGTGTAGGCGTGGAATCAG	RAD53
Rad53_seq_R	TTTGGCCAGACCAAAGTCGG	amplification for sequencing
REV3_upstr_F	CGAGTGCAGTGCCTCTAGAAATAGTGT	REV3 external primers
Rev3_down_R	GGCGTTATTAATGCATCTGGGTCC	
JK183_hygRleft_rev	ACAGTCACATCATGCCCCCTG	HYG internal primer for REV3 check
Repeat length primers		
A2	CTCGATGTGCAGAACCTGAAGCTTGATCT	Check repeat length of (GAA)100 strains
B2	GCTCGAGTGCAGACCTCAAATTCGATGA	
T1	GCCGCTCGAGTGAACCTGAAGCTTGATCT	Check repeat length of (TTC)100 strains
T2	AGCTGAGTGCAGACCTCAAATTCGATGA	
Live-cell microscopy strain construction		
cm343_int_F	CGCGTGATGTGAACATCAGCCCTTAGTTGAACTCTGTGGA CACAAGACTAACGTGCGGATCCGGAGATCTAGC	Inserting expansion cassettes in CM343 at the NAT locus
cm343_int_R	TAGCTCGTAGATAGATACTGACAGACTGATACTCTACGCT CATACGATACCCGGGCGATAAGCTAGCAGG	
cm343_norpt_int	TAGCTCGTAGATAGATACTGACAGACTGATACTCTACGCT CATACGATCCGGGCGATAAGCTAGGGCA	