Supplemental tables and figures

Table 1. *S.cerevisiae* strains used in this study.

Strain	Genotype/Phenotype	Ref
mcm5-461[*#]	*mcm5-461 ura3-52 leu2-3,112 ade2 lys2-801 MATα*	(Dziak *et al.*, 2003)
MCM5[*]	*mcm5-461::MCM5::LEU2 ura3-52 leu2-3,112 ade2 lys2-801 MATα*	(Dziak *et al.*, 2003)
W303[^]	*ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	
orc2-1[^]	*orc2-1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	(Ehrenhofer-Murray *et al.*, 1995)
orc5-1	*orc5-1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	(Ehrenhofer-Murray *et al.*, 1995)
cdc45-1[^]	*cdc45-1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	(Pasero *et al.*, 1999)
cdc6-1[^]	*cdc6-1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	(Liang and Stillman, 1997)
cdc7-1[^]	*cdc7-1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MAT***a** *ts at 37°C*	(Pasero *et al.*, 1999)
Δsir2	*sir2::TRP1 ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa*	(Rusche *et al.*, 2002)
LPY1030[^]	*ade2-1 his3-11,15 leu2-3, 112 trp1-1 ura3-1 can1-100 MATα with telomeric adh4::URA3-UAS$_{GAL}$-(C$_{1-3}$A)$_n$*	(Jacobson and Pillus, 2004)
LPY1029[^]	*LPY1030, except lacking the telomeric UAS$_{GAL}$ tethering site*	(Jacobson and Pillus, 2004)
GF100[^]	*ade2-1 trp1-1 can1-100 leu2-3,112 his3-11,15 ura3-1 MATa with telomeric adh4::URA3-UAS$_{GAL}$-TRP1-STAR-(C$_{1-3}$A)$_n$*	(Fourel *et al.*, 2002b)
BY4742	*Δhat1 his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 MATα*	ATCC #4040004
Δhat1[**]	*Δhat1 his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 MATα*	ATCC#4012827
Δgcn5[**]	*Δgcn5 his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 MATα*	ATCC#4017285
Δsas2[**]	*Δsas2 his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 MATα*	ATCC#4016568
Δsas3[**]	*Δsas3 his3Δ1 leu2Δ0 lys2Δ0 ura3Δ0 MATα*	ATCC#4013078

[*] These strains are derivatives of 8534-8C (Maine *et al.*, 1984; Hennessy *et al.*, 1991)
[#] This strain is identical to *cdc46-1* in (Dalton and Hopwood, 1997)
[^]These strains are derivatives of *W303*
[**]These strains are derivatives of *BY4742*

Table 2. FOA^R cells in ARS1-URA3-tel, ARS1(ACS$^-$)-URA3-tel, ARS1(B1$^-$)-URA3-tel, URA3-ARS1-tel, URA3-ARS1(B1$^-$)-tel.

Strains	*ARS1-URA3-tel*	*ARS1(ACS$^-$)-URA3-tel*	*ARS1*(B1$^-$)-*URA3-tel*	*URA3-ARS1-tel*	*URA3-ARS1*(B1$^-$)- *tel*
MCM5	56.7 ±7.0 (n=8)	45.5 ±7.8 (n=5)	89.0 ±7.8 (n=5)	56.1 ±7.9 (n=4)	80.0 ±5.1 (n=4)
W303	56.7 ±7.9 (n=8)	38.4 ±6.7 (n=7)	96.0 ±6.7 (n=5)	33.2 ±6.3 (n=9)	70.0 ±7.3 (n=4)
mcm5-461	80.0 ±6.1 (n=8)	36.5 ±3.2 (n=4)	77.0 ±3.2 (n=4)	57.0 ±5.3 (n=3)	81.0 ±6.6 (n=3)
orc2-1	77.0 ±6.2 (n=6)	0.2 ±0.2 (n=3)	83.0 ±0.2 (n=3)	91.3 ±4.3 (n=4)	88.0 ±5.2 (n=4)
orc5-1	83.0 ±4.0 (n=7)	0.1 ±0.1 (n=4)	83.0 ±0.1 (n=4)	94.9 ±3.9 (n=4)	99.0 ±5.4 (n=4)
cdc45-1	81.0 ±9.0 (n=6)	28.4 ±5.7 (n=4)	64.0 ±5.7 (n=4)	85.1 ±5.1 (n=4)	52.0 ±5.9 (n=5)
Δsas2	42.7 ±9.3 (n=3)	13.6 ±5.7 (n=3)	n/a	n/a	n/a
cdc7-1	63.0 ±12.0 (n=6)	32.0 ±6.9 (n=3)	86.0 ±6.4 (n=4)	n/a	n/a
cdc6-1	30.3 ±7.1 (n=4)	67.7 ±6.4 (n=4)	86.0 ±6.4 (n=4)	55.3 ±9.6 (n=4)	78.0 ±9.5 (n=4)
Δsir2	0.01 ±0.01 (n=3)	0.02 ±0.01 (n=3)	0.02 ±0.01 (n=3)	0.02 ±0.01(n=3)	0.01 ±0.01(n=3)

Per cent FOA^R cells in the constructs indicated above each column was measured in each of the cell strains indicated on the left. The average numbers for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown.

Table 3. FOA^R cells in GF6, GF6(ACS$^-$), GF6(B1$^-$), GF44, GF44(ACS$^-$) GF44(B1$^-$).

Strains	*GF6*	*GF6(ACS$^-$)*	*GF6(B1$^-$)*
MCM5	48.6 ±8.5 (n=5)	42.0 ±2.6 (n=3)	48.0 ±7.9 (n=3)
W303	63.5 ±9.3 (n=3)	58.0 ±7.8 (n=7)	64.4 ±6.5 (n=7)
mcm5-461	9.0 ±1.3 (n=6)	35.7 ±2.4 (n=4)	89.7 ±3.3 (n=4)
orc2-1	1.9 ±0.9 (n=5)	45.5 ±7.6 (n=4)	89.2 ±3.5 (n=4)
orc5-1	29.2 ±8.7 (n=2)	50.2 ±9.8 (n=6)	90.5 ±3.3 (n=6)
cdc45-1	5.3 ±3.1 (n=2)	28.4 ±5.5 (n=4)	31.3 ±6.9 (n=4)
Δsas2	50.9 ±9.9 (n=3)	4.8 ±3.0 (n=3)	n/a
cdc7-1	34.7 ±8.9 (n=3)	60.0 ±6.0 (n=4)	35.6 ±6.0 (n=4)
cdc6-1	61.2 ±7.2 (n=5)	49.5 ±5.2 (n=5)	72.2 ±3.9 (n=5)
Δsir2	0.03 ±0.001 (n=2)	0.02 ±0.001 (n=3)	0.03 ±0.001(n=3)
	GF44	*GF44(ACS$^-$)*	*GF44(B1$^-$)*
MCM	75.5 ±9.5 (n=5)	40.3 ±6.5 (n=6)	57.9 ±5.1 (n=6)
W303	68.5 ±9.7 (n=3)	41.1 ±7.9 (n=9)	51.8 ±6.0 (n=9)
mcm5-461	9.1 ±3.7 (n=6)	35.7 ±6.3 (n=5)	75.0 ±5.2 (n=5)
orc2-1	31.8 ±1.1 (n=3)	47.6 ±5.6 (n=5)	61.3 ±7.2 (n=5)
orc5-1	19.6 ±7.1 (n=2)	37.3 ±4.2 (n=8)	63.4 ±7.3 (n=8)
cdc45-1	7.5 ±4.0 (n=2)	56.1 ±6.8 (n=4)	62.8 ±5.7 (n=4)
Δsas2	53.1 ±8.9 (n=3)	8.5 ±4.3 (n=3)	n/a
cdc7-1	36.6 ±9.1 (n=2)	62.0 ±2.6 (n=4)	55.9 ±9.2 (n=6)
cdc6-1	27.9 ±9.4 (n=5)	55.1 ±5.6 (n=4)	41.5 ±5.6 (n=4)
Δsir2	0.02 ±0.001 (n=3)	0.02 ±0.001 (n=3)	0.02 ±0.01 (n=3)

Per cent FOA^R cells in the constructs indicated above each column was measured in each of the cell strains indicated on the left. The average numbers for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown.

Table 4. FOA^R cells in GF6(ACS$^-$ΔSTAR) and GF6*(B1$^-$*ΔSTAR).

Strains	*GF6(ACS$^-$ΔSTAR)*	*GF6(B1$^-$ΔSTAR)*
MCM5	64.5 ±8.6 (n=3)	70.2 ±6.4 (n=3)
W303	52.2 ±9.8 (n=3)	55.1 ±8.3 (n=3)
mcm5-461	58.3 ±8.3 (n=3)	76.8 ±7.1 (n=3)
orc2-1	20.1 ±3.0 (n=6)	30.8 ±7.2 (n=6)
orc5-1	35.5 ±7.4 (n=6)	41.0 ±7.0 (n=6)
cdc45-1	40.1 ±7.9 (n=5)	53.2 ±7.2 (n=5)

Per cent FOA^R cells in the constructs indicated above each column was measured in each of the cell strains indicated on the left. The average numbers for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown.

Table 5A. FOA^R in W303/URA-UAS$_{GAL}$-tel, LPY1029 and LPY1030 cells expressing GBD-fusion proteins.

URA3-UAS$_{GAL4}$-tel	**%FOA^R Cells**
GBD	22.0 ±4.9 (n=3)
GBD-ORC1	23.1 ±7.8 (n=3)
GBD-ORC2	39.3 ±9.8 (n=3)
GBD-MCM10	86.5 ±8.3 (n=3)
GBD-mcm10-1	57.2 ±6.5 (n=3)
GBD-SIR1	75.7 ±6.3 (n=3)
GBD-MCM5	5.5 ±2.0 (n=3)
GBD-mcm5-1	8.8 ±2.8 (n=3)
GBD-mcm5-461	10.6 ±3.2 (n=3)
GBD-mcm5(bob1-1)	28.8 ±13.4 (n=6)
GBD-MCM3	56.3 ±7.9 (n=3)
URA3-tel(LPY1029)	
GAL4DBD-Orc1p	23.4 ±11 (n=6)
GAL4DBD-Mcm5-461p	58.9 ±7 (n=6)
GAL4DBD-Mcm5-1p	40.9 ±14 (n=6)
GAL4DBD-Mcm5p	19.3 ±4 (n=6)
GAL4DBDp	59.0 ±10 (n=6)
URA3- UAS$_{GAL4}$-tel(LPY1030)	
GAL4DBD-Orc1p	58.60 ±12 (n=6)
GAL4DBD-Mcm5-461p	1.94 ±0.4 (n=6)
GAL4DBD-Mcm5-1p	0.80 ±0.1 (n=6)
GAL4DBD-Mcm5p	0.61 ±0.1 (n=6)
GAL4DBDp	36.39 ±10 (n=6)

Per cent FOA^R cells transformed with vectors expressing the recombinant proteins presented on the left. The average numbers for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown. W303/ URA-UAS$_{GAL}$-tel contains four UAS$_{GAL}$ sites, while LPY1030 contains one UAS$_{GAL}$ site.

Table 5B. FOA^R in HAT deletion mutants harboring URA-UAS$_{GAL}$-tel and expressing GBD or GBD-Mcm5p.

Strains	**Protein**	**%FOA^R cells**
Δhat1	GBD	95.1 ±3.1(n=3)
	GBD-Mcm5p	93.2 ±3.4(n=3)
Δgcn5	GBD	84.7 ±7.1(n=3)
	GBD-Mcm5p	85.6 ±5.6(n=3)
Δsas2	GBD	94.3 ±3.1(n=3)
	GBD-Mcm5p	53.7 ±7.4(n=3)
Δsas3	GBD	95.6 ±2.8(n=3)
	GBD-Mcm5p	36.9 ±7.2(n=3)
wt	GBD	75.8 ±8.7(n=3)
	GBD-Mcm5p	13.7 ±6.2(n=3)

The average %FOA^R for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown.

Table 6. FOA^R , TRP+ and FOA^R&TRP+ cells in *GF100* and *GF100 Δrif1* .

GF100	% FOA^R		%TRP+		TRP+/ FOA^R	
GAL4DBD-GCN5	0.31	±0.10 (n=6)	80.01	±5.1 (n=6)	0.04	±0.02 (n=6)
GAL4DBD-ORC1	8.17	±0.59 (n=6)	36.23	±3.3 (n=6)	0.01	±0.01 (n=6)
GAL4DBD-mcm5-461	0.22	±0.17 (n=6)	94.1	±8.8 (n=6)	0.02	±0.01 (n=3)
GAL4DBD-mcm5-1	0.38	±0.15 (n=6)	84.5	±18.7 (n=6)	0.04	±0.01 (n=3)
GAL4DBD-MCM5	0.71	±0.37 (n=6)	91.4	±1.2 (n=6)	0.03	±0.004 (n=4)
GAL4DBD	3.42	±0.26 (n=6)	68.5	±4.0 (n=6)	0.01	±0.01(n=6)

GF100Δrif1	% FOA^R		%TRP+		TRP+/ FOA^R	
GAL4DBD-GCN5	23.02	±2.02 (n=6)	48.4	±6.2(n=6)	0.8	±0.1 (n=6)
GAL4DBD-ORC1	74.9	±3.18 (n=6)	5.01	±1.9 (n=6)	0.4	±0.05 (n=6)
GAL4DBD-mcm5-461	57.6	±6.41 (n=6)	19.6	±3.1 (n=6)	0.4	±0.1 (n=6)
GAL4DBD-mcm5-1	51.4	±3.86 (n=6)	29.2	±1.9 (n=6)	1.4	±0.2 (n=6)
GAL4DBD-MCM5	23.7	±2.12 (n=6)	45.6	±6.2 (n=6)	1.0	±0.1 (n=6)
GAL4DBD	70.8	±3.41 (n=6)	5.8	±1.2 (n=6)	1.7	±0.2 (n=6)

Cells transformed with vectors expressing the recombinant proteins presented on the left are shown. The average numbers for *n* triplicate measurements (shown in parenthesis) and the standard errors are shown.

Supplemental Figure # 1:

A) The sequence of *MCM5(CDC46)* is shown. The positions of the mutations in *mcm5-461* (G549) and *mcm5-1* (G1981) are shown in rectangles and bold script.

B) The amino acid sequence of Mcm5p is shown. The Zn-finger domain (amino acid residues 183-235) and the conserved heptad K/R repeat (amino acid residues 651-664) are highlighted in grey. The ATPase motif (MCM box) is underlined. The positions of the amino acid substitutions in Mcm5-461p (C183Y) and Mcm5-1p (E661K) are in rectangles and bold script.

Comments to Supplemental Figure 1: The mutation in *mcm5-461* (C183Y) is identical to the previously reported *cdc46-1* mutation (Dalton and Hopwood, 1997) and locates to the Zn-finger domain. It affects the interaction of Mcm5p with Mcm7p and the assembly of the MCM hexamer (Dalton and Hopwood, 1997). By homology with the archeal Mcm protein, this mutation is also expected to interfere with the association of the MCM hexamer with DNA (Fletcher *et al.*, 2003). The E661K mutation in *mcm5-1* locates in the conserved heptad K/R repeat. It has been postulated that this repeat provides a surface for interaction with other proteins, including other Mcm proteins (Kubota *et al.*, 1997).

A)

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1    ATGTCATTTG ATAGACCGGA AATATACAGT GCTCCTGTTT TACAAGGAGA
51   ATCTCCTAAC GACGATGATA ATACTGAAAT CATAAAGTCC TTTAAGAATT
101  TCATTTTGGA GTTCAGACTT GACTCGCAAT TTATTTACAG AGATCAGTTA
151  AGGAACAACA TCCTTGTGAA GAATTATTCT TTAACGGTTA ACATGGAGCA
201  TTTGATCGGA TATAACGAAG ACATATATAA GAAACTATCA GACGAACCTT
251  CAGATATCAT TCCATTATTC GAAACCGCGA TCACACAAGT GGCTAAAAGG
301  ATAAGTATTC TAAGCAGAGC TCAATCTGCT AATAACAATG ACAAAGATCC
351  AGAAAATACT AGTATGGATA CTGATTCTCT CTTATTGAAC TCTTTACCAA
401  CATTTCAATT AATTTTAAAC TCCAATGCAA ATCAGATTCC ATTGAGAGAT
451  TTGGATTCTG AACACGTCTC CAAGATTGTC CGTTTATCAG GTATTATAAT
501  ATCCACGTCA GTTTTATCTT CCCGTGCCAC GTACCTTTCT ATAATGTGCA
551  GAAATTGCAG ACACACAACA TCAATAACAA TCAACAATTT CAATTCTATC
601  ACAGGCAATA CCGTCAGTTT ACCACGTTCT TGCTTATCTA CGATTGAGAG
651  TGAATCTTCT ATGGCAAACG AGTCGAATAT TGGTGATGAA TCGACCAAGA
701  AAAATTGTGG ACCTGATCCA TATATTATTA TCCATGAGTC TTCAAAGTTT
751  ATTGATCAAC AGTTTTTAAA ATTACAGGAA ATCCCAGAAC TGGTTCCAGT
801  AGGTGAGATG CCTAGAAACT TAACAATGAC TTGTGACCGA TACCTAACAA
851  ACAAAGTTAT TCCTGGTACG AGAGTCACTA TAGTAGGTAT TTATTCCATC
901  TATAATTCTA AAAATGGTGC CGGATCCGGA AGGAGCGGGG GTGGAAATGG
951  AGGAAGTGGT GTTGCTATTA GAACACCTTA TATCAAAATA TTAGGTATTC
1001 AGTCCGATGT AGAAACCTCC TCTATTTGGA ATTCAGTAAC TATGTTTACT
1051 GAGGAGGAAG AAGAGGAATT TCTACAGCTA AGTAGAAACC CGAAGCTTTA
1101 TGAAATTTTG ACCAACTCTA TTGCCCCCTC TATTTTTGGT AATGAAGATA
1151 TAAAAAAAGC CATTGTATGT TTATTGATGG GTGGTTCCAA GAAGATATTA
1201 CCCGATGGTA TGAGGTTAAG AGGTGATATC AATGTACTAT TATTAGGTGA
1251 TCCAGGTACC GCCAAATCTC AACTATTGAA ATTTGTGGAG AAAGTGTCAC
1301 CTATTGCGGT ATATACATCT GGTAAGGGAT CTTCTGCAGC TGGGTTAACT
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1351 GCCAGTGTAC AAAGAGATCC GATGACAAGA GAATTTTATT TGGAAGGTGG
1401 TGCTATGGTG CTTGCCGATG GTGGTGTTGT ATGCATCGAT GAATTCGATA
1451 AAATGAGAGA TGAAGATAGA GTGGCCATTC ATGAAGCTAT GGAGCAGCAA
1501 ACAATCTCCA TCGCAAAAGC TGGTATCACT ACAGTGCTAA ATTCTAGAAC
1551 TAGTGTTTTA GCGGCTGCTA ATCCGATATA CGGCCGGTAT GATGATTTGA
1601 AGTCTCCTGG TGACAACATT GATTTCCAAA CTACTATTTT ATCCCGTTTT
1651 GATATGATTT TTATTGTTAA GGATGACCAT AATGAAGAAC GTGATATTTC
1701 AATAGCTAAC CACGTTATTA ATATTCATAC AGGAAATGCT AATGCTATGC
1751 AAAACCAACA AGAGGAAAAT GGCAGTGAAA TTAGTATTGA AAAGATGAAA
1801 CGTTACATTA CGTATTGTAG ATTGAAATGT GCACCAAGAC TTTCACCGCA
1851 GGCCGCTGAA AAACT*GTCAT* CGAACTTCGT CACCATTAGG AAGCAATTAT
1901 TAATCAACGA ATTAGAGTCA ACGGAAAGGT CGTCTATTCC AATTACCATT
1951 CGTCAATTAG AAGCTATTAT TAGAATAACA **G**AATCATTAG CCAAGTTAGA
2001 ATTAAGTCCT ATTGCACAGG AGAGACATGT TGACGAAGCT ATTAGATTGT
2051 TTCAAGCTTC CACAATGGAC GCAGCGTCTC AGGATCCAAT TGGCGGCTTA
2101 AATCAAGCAA GCGGAACATC TTTGTCAGAA ATCCGTCGTT TTGAACAAGA
2151 ACTAAAAAGA AGATTACCTA TAGGCTGGTC TACTTCTTAT CAAACTTTGA
2201 GGAGAGAATT TGTAGATACA CATAGATTTT CTCAATTAGC ACTGGATAAG
2251 GCCTTATATG CCCTAGAGAA GCATGAAACA ATTCAATTGA GACACCAGGG
2301 ACAGAATATT TACAGAAGTG GTGTATGA

B)

1 **M** S F D R P E I Y S A P V L Q G E S P N D D D N T E I I K S F K N F I L E F R L **40**
41 D S Q F I Y R D Q L R N N I L V K N Y S L T V N **M** E H L I G Y N E D I Y K K L **79**
80 S D E P S D I I P L F E T A I T Q V A K R I S I L S R A Q S A N N N D K D P E N T S **121**
122 **M** D T D S L L L N S L P T F Q L I L N S N A N Q I P L R D L D S E H V S K I V R **161**
162 L S G I I I S T S V L S S R A T Y L S I **M** **C** R N C R H T T S I T I N N F N S I T G 201
202 N T V S L P R S C L S T I E S E S S Met A N E S N I G D E S T K K N C G P D P Y I **241**
242 I I H E S S K F I D Q Q F L K L Q E I P E L V P V G E **M** P R N L T **M** T C D R Y **280**
281 L T N K V I P G T R V T I V G I Y S I Y N S K N G A G S G R S G G G N G G S G V **320**
321 A I R T P Y I K I L G I Q S D V E T S S I W N S V T **M** F T E E E E E E E F L Q L S **360**
361 R N P K L Y E I L T N S I A P S I F G N E D I K K A I V C L L **M** G G S K K I L P **400**
401 D G **M** R L R G D I N V L L L G D P G T A K S Q L L K F V E K V S P I A V Y T S **439**
440 G K G S S A A G L T A S V Q R D P **M** T R E F Y L E G G A **M** V L A D G G V V **476**
477 C I D E F D K **M** R D E D R V A I H E A **M** E Q Q T I S I A K A G I T T V L N S **514**
515 R T S V L A A A N P I Y G R Y D D L K S P G D N I D F Q T T I L S R F D **M** I F I **554**
555 V K D D H N E E R D I S I A N H V I N I H T G N A N A **M** Q N Q Q E E N G S E I **593**
594 S I E K **M** K R Y I T Y C R L K C A P R L S P Q A A E K L S S N F V T I R K Q L L **633**
634 I N E L E S T E R S S I P I T I R Q L E A I I R I T **E** S L A K L E L S P I A Q E R H V **676**
677 D E A I R L F Q A S T **M** D A A S Q D P I G G L N Q A S G T S L S E I R R F E Q E **716**
717 L K R R L P I G W S T S Y Q T L R R E F V D T H R F S Q L A L D K A L Y A L E K **756**
757 H E T I Q L R H Q G Q N I Y R S G V **Stop**
775

Supplemental Figure #2

Wild type *W303* or *cdc7-1* cells harboring URA3-UAS_{GAL}-tel (shown on the top) were transformed with plasmids carrying expression cassettes for the GBD-fusion proteins shown on the left. Per cent FOA^R for each recombinant protein was acquired and average value and error are shown on the right. The ratio $\%FOA^R_{GAL4\text{-}fusion}$ /$\%FOA^R_{GAL4DBD}$ was calculated and plotted in the graph. Values below 1 indicate that the tethered proteins have anti-silencing activity and values above 1 indicate silencing activity.

Comments to Supplemental Figure #2. On-going research in our lab has shown that *cdc7-1* cells are very slow in exiting from repressed or de-repressed state at the telomere (slow recovery from SC-ura or SC/FOA plates, respectively). For this reason the experiments in *cdc7-1* were performed after selection on either SC-ura and SC/FOA plates followed by growth in non-selective medium to maintain the expressing plasmids but allow variegation of *URA3*. After 40 generations the assessment of % FOA was performed. Mcm5p does not show any anti-repression activity in *cdc7-1* regardless of the initial selection. Under the same experimental conditions Orc1p still acts as a repressor after initial selection was on SC-ura. We therefore believe that the lack of silencing activity in *cdc7-1* is not a consequence of the slow recovery phenotype but reflects an independent deficiency of the *cdc7-1* cells.

Additional note: the silencing activity of Orc1p is not evident after selection on SC/FOA because of the already high level (75%) of repression.