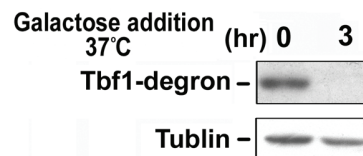


## Legends to Supp. Figures

## Supplemental figures

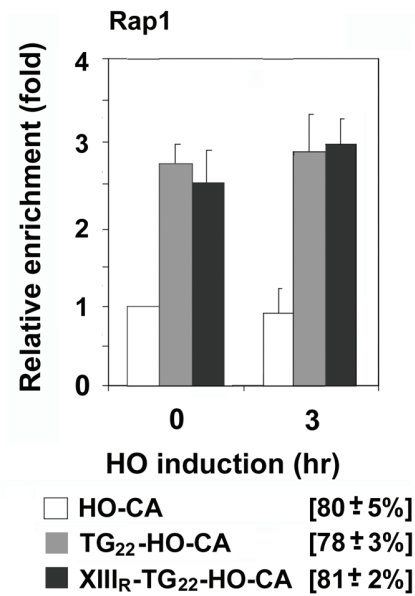
## Fig. S1

**Supp. Fig. 1. *UBR1*-induced Tbf1 protein degradation in nocodazole arrested cells.**

*tbf1* degron mutant (*tbf1-d*) (KSC2853) cells were grown in sucrose at 30°C and synchronized at G2/M with nocodazole. After synchronization, the culture was incubated with galactose and concomitantly shifted to 37°C. Aliquots of cells were collected at the indicated times after incubation with galactose at 37°C and subjected to immunoblotting analysis with anti-myc antibodies.

## Supplemental figures

### Fig. S2

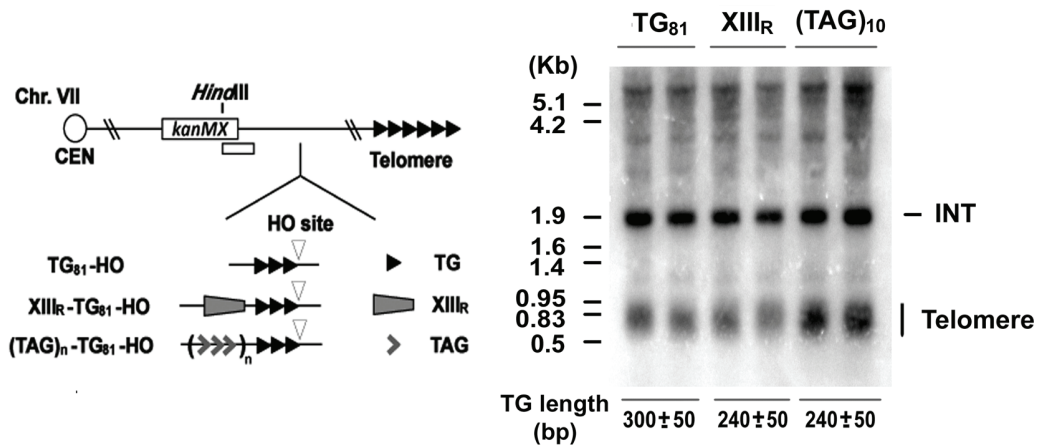


#### Supp. Fig. 2. Rap1 binding at the TG<sub>22</sub> sequence.

TG<sub>22</sub>-HO-CA (KSC2883), XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA (KSC2884) or HO-CA (KSC2893) cells expressing HA-tagged Rap1 protein were transformed with the GAL-HO plasmid. Transformants were analyzed for Rap1 binding as in Fig. 1B.

## Supplemental figures

### Fig. S3



**Supp. Fig. 3. Telomere addition at  $TG_{81}$  ends with the subtelomeric  $XIII_R$  or 10XTTAGGG sequence.**  $TG_{81}$ -HO (KSC2214),  $XIII_R$ - $TG_{81}$ -HO (KSC2760) or  $TAG_{10}$ - $TG_{81}$ -HO (KSC2568) cells carrying the GAL-HO plasmid were grown in galactose for seven days after multiple dilutions. Genomic DNA was digested with *HindIII* and then analyzed by Southern blot using the  $^{32}P$ -labeled DNA fragment probe (white bar) (Hirano *et al.*, 2009). The band marked INT is derived from the *SMC2* locus and serves as a loading control.

**Table 1. Strains used in this study**

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KSC2214	<i>MATa-inc</i>	<i>VII-L::KanMX-TG<sub>8I</sub>-HO</i>
KSC2849	<i>MATa-inc</i>	<i>VII-L::KanMX-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2760	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-TG<sub>8I</sub>-HO</i>
KSC2850	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2851	<i>MATa-inc</i>	<i>VII-L::KanMX-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2852	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2853	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-TG<sub>8I</sub>-HO <i>tbfl</i>-degron::ura3 <i>GAL-UBR1::HIS3</i></i>
KSC2854	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-TG<sub>8I</sub>-HO MRE11-3HA::HphMX <i>tbfl</i>-degron::ura3 <i>GAL-UBR1::HIS3</i></i>
KSC2855	<i>MATa-inc</i>	<i>VII-L::KanMX-XIII<sub>R</sub>-TG<sub>8I</sub>-HO TEL1-2HA::TRP1 <i>tbfl</i>-degron::ura3 <i>GAL-UBR1::HIS3</i></i>
KSC2856	<i>MATa-inc</i>	<i>VII-L::KanMX-(TAG)<sub>2</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2857	<i>MATa-inc</i>	<i>VII-L::KanMX-(TAG)<sub>4</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2568	<i>MATa-inc</i>	<i>VII-L::KanMX-(TAG)<sub>10</sub>-TG<sub>8I</sub>-HO</i>
KSC2858	<i>MATa-inc</i>	<i>VII-L::KanMX-(TAG)<sub>10</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2859	<i>MATa-inc</i>	<i>VII-L::KanMX-(TAG)<sub>10</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1 <i>rif1Δ::ura3 rif2Δ::HphMX</i></i>
KSC2860	<i>MATa-inc</i>	<i>VII-L::KanMX-(CTA)<sub>10</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2861	<i>MATa-inc</i>	<i>VII-L::KanMX-lacO<sub>8</sub>-TG<sub>8I</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2862	<i>MATa-inc</i>	<i>VII-L::KanMX-lacO<sub>8</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1</i>
KSC2863	<i>MATa-inc</i>	<i>VII-L::KanMX-lacO<sub>8</sub>-tetO<sub>4</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1 <i>sir2Δ::LEU2</i></i>
KSC2864	<i>MATa-inc</i>	<i>VII-L::KanMX-lacO<sub>8</sub>-tetO<sub>4</sub>-HO MRE11-9myc::TRP1 TEL1-2HA::TRP1 <i>rif1Δ::ura3 rif2Δ::HphMX sir2Δ::LEU2</i></i>
KSC2505	<i>MATa/MATa</i>	<i>TBF1/tbflΔ:: HphMX</i>
KSC1602	<i>MATa</i>	<i>GAL-UBR1::HIS3</i>
KSC2756	<i>MATa</i>	<i>tbfl</i> -degron::KanMX <i>GAL-UBR1::HIS3</i>

KSC2867 **MATa** *tbfl-degtron::KanMX GAL-UBR1::HIS3 est1A::ura3 [YCpU-EST1]*  
 KSC2865 **MATa-inc** *VII -L::KanMX-lacO<sub>8</sub>-TG<sub>81</sub>-HO tbfl-degtron::ura3 GAL-UBR1::HIS3 MRE11-3HA::HphMX*  
 KSC2866 **MATa-inc** *VII -L::KanMX-lacO<sub>8</sub>-TG<sub>81</sub>-HO tbfl-degtron::ura3 GAL-UBR1::HIS3 TEL1-2HA::TRP1*  
 KSC2891 **MATa** *tbfl-degtron::KanMX GAL-UBR1::HIS3 stn1-13::URA3*  
 KSC2230 **MATa-inc** *VII -L::KanMX-TG<sub>22</sub>-HO-CA*  
 KSC2901 **MATa-inc** *VII -L::KanMX-TG<sub>22</sub>-HO-CA MRE11-9myc::TRP1*  
 KSC2895 **MATa-inc** *VII -L::KanMX-TG<sub>22</sub>-HO-CA TEL1-2HA::TRP1*  
 KSC2898 **MATa-inc** *VII -L::KanMX-TG<sub>22</sub>-HO-CA MEC1-2HA::LEU2*  
 KSC2834 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA*  
 KSC2892 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA MRE11-9myc::TRP1*  
 KSC2896 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA TEL1-2HA::TRP1*  
 KSC2899 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA MEC1-2HA::LEU2*  
 KSC2836 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA tbfl-degtron::URA3 GAL-UBR1::HIS3*  
 KSC2839 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA GAL-UBR1::HIS3*  
 KSC2894 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-HO-CA*  
 KSC2905 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-HO-CA MRE11-9myc::TRP1*  
 KSC2897 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-HO-CA TEL1-2HA::TRP1*  
 KSC2900 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-HO-CA MEC1-2HA::LEU2*  
 KSC2883 **MATa-inc** *VII -L::KanMX-TG<sub>22</sub>-HO-CA RAP1-6HA::TRP1*  
 KSC2884 **MATa-inc** *VII -L::KanMX-XIII<sub>R</sub>-TG<sub>22</sub>-HO-CA RAP1-6HA::TRP1*  
 KSC2893 **MATa-inc** *VII -L::KanMX-HO-CA RAP1-6HA::TRP1*

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All the strains are isogenic and derived from KSC006 (**MATa** *ade1 his2 leu2 trp1 ura3*)(Wakayama *et al.*, 2001). **MATa-inc** is a mutation of the HO cleavage site (Sweetser *et al.*, 1994).

Table 2. List of oligonucleotides used in this study

Name	Sequence
KSX006	5'-AATTAACCCTCACTAAAGGGAAC-3'
KSX007	5'-TAATACGACTCACTATAGGGCGA-3'
KS1255	5'-GTTAAGCTTGCCTCGTCCCCGC-3'
KS1311	5'-GCAACCAGTATAATTGAGGCTGC-3'
KS1312	5'-GCTGTGATTGATACTAACGCC-3'
KS1679	5'-GAGAGTAGAGGTAGATGTGCAATTGTGTGT-3'
KS1744	5'-GTTGTTTCTGAAACATGGCAAAGG-3'
KS1745	5'-CAACCAAACCGTTATTCATTCGTG-3'
KS1746	5'-AAAGAATTCAAATGTGAGCGGATAACAATTAATGTGAGCGAGTA ACAACCGGCAGTGAGCGCAACGCAATTAATTGTGAGCGCTCACA ATTCAATTGTCTCTCACATCTACCTCTACTC-3'
KS1747	5'-AAAGAGCTCAAATCACCGCGGGGCAACCTTTCTCTTCTTCTT TGG-3'
KS1756	5'-AAAGTCGACATGGTGAATATGTAACGTTATACG-3'
KS2037	5'-AAAGACTGAGCTGAATGAAGTCTC-3'
KS2038	5'-CGTCTGAGAATCTTGAACAACAAC-3'
KS2091	5'-AAACCGCGGATGGATTCGCAAGTGCC-3'
KS2092	5'-AAAGAGCTCACCAGA AATGAACGTGACG-3'
KS2110	5'-AAAGGATCCTCAGTTATTAGAAGCCCCAAAAGAGC-3'
KS2324	5'-AAAGAATTCCCTAACCCCTAACCCCTAACCCCTAACTCTCACATCTAC CTCTACTC-3'
KS2325	5'-AAAGAATTCCCTAACCCCTAACTCTCACATCTACCTCTACTC-3'
KS2327	5'-AAAGAATTCTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGG GTTAGGGTTAGGGTTAGGGTTAGGG CTCTCACATCTACCTCTAC TC-3'

KS2330 5'-GCCAAGCTTGCATGCCTGCAGGTCGACGGTAAGGGCTCCAGC  
C-3'

KS2331 5'-GAATTCGAGCTCGGTACCCGGGGATCCGTGAAAGGGAGCGTG  
GA-3'

KS2335 5'-CATCATCACCATCACCACGATTAT-3'

KS2336 5'-ATCTTTATAATCGTGGTGATGGTGATGATGATCCATGACAAATGG  
GGA AAG-3'

KS2337 5'-ATTACGCGTATCCTTATGACGTACCAGATTATGCGGATTCGCAA  
GTGCCCAA-3'

KS2338 5'-GATACGCGTAATCTGGAACATCGTATGGATAATCCATGACAAATG  
GGGAAAG-3'

KS2438 5'-ATCGGATCCTCTAGATAGGGTAGGGTTAGGGTAGGGTTAGGGTAG  
TGTTAGGGTGGAATTCGAA-3'

KS2439 5'-TTCGAATTCCACCCTAACACTACCCTAACCTACCCTAACCTAC  
CCTATCTAGAGGATCCGAT-3'

KS2446 5'-GGAGTTGGGAAACCATAAAC-3'

KS2492 5'-GTGGCGCCTGGTTTATGGTTTCCCAACTCCGCTTACATTGCCGGC  
TTGAAA-3'

KS2497 5'-GGAAAGTTTGCGAAATCGGCGGCTATCCTATATCTTGAT-3'

KS2498 5'-TAGGATAGCCGCCGATTTGCGAAACTTTCCGCTTTGTTTC-3'

KS2503 5'-TATCTTGATGCGAAAACAGCGGCTTACATTGCCGGCTTG-3'

KS2504 5'-AATGTAAGCCGCTGTTTTCGCATCAAGATATAGGATAGC-3'

KS2577 5'-ATAGAATTCCCCCTGACCCACACCCACACCCACACACTCTTCC  
ACCCTAACACTAC-3'