Supplementary Data

for

Subtelomeres constitute a safeguard for gene expression and chromosome homeostasis

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C
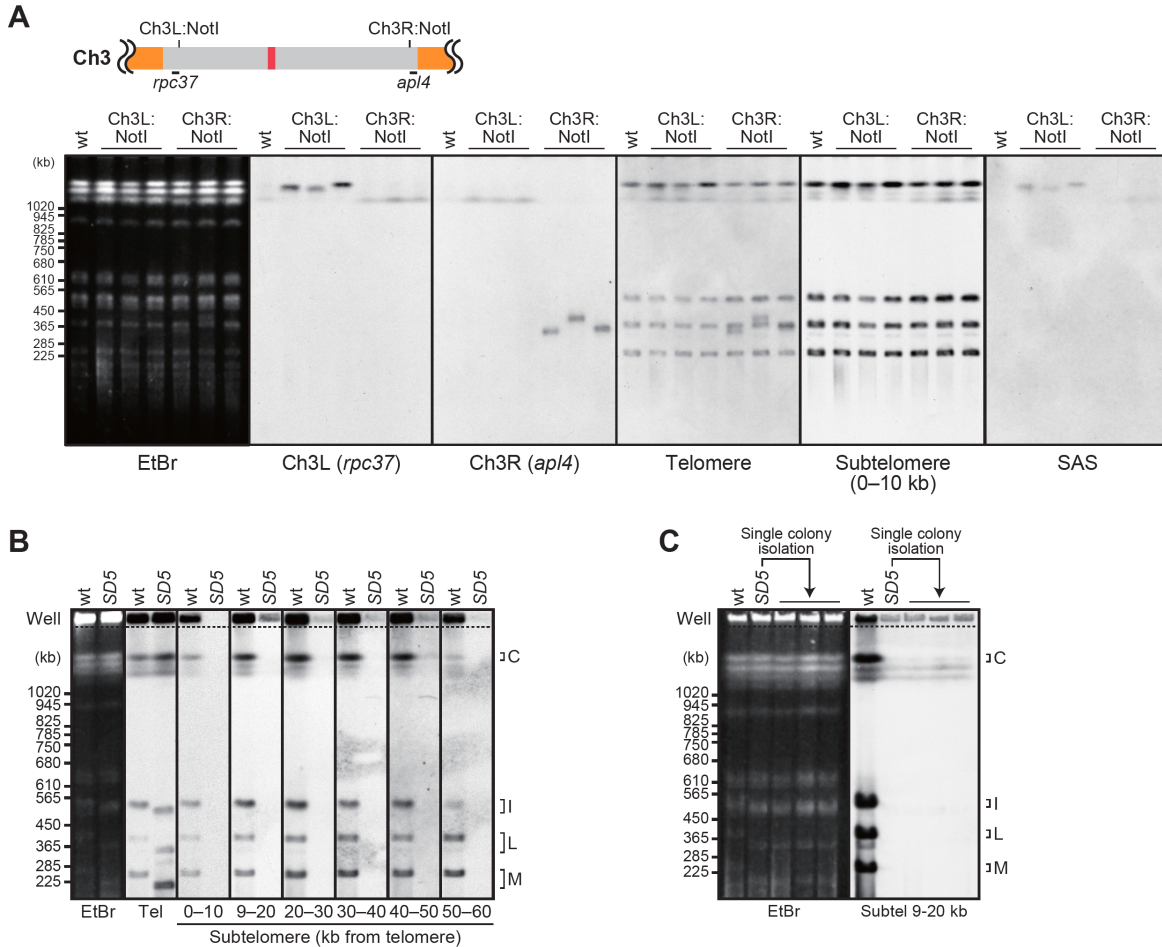
Figure S1. Construction of the *SD5* strain

(A) Determination of the location of the *SH* regions in chromosome 3 of *S. pombe*. Sequences recognized by the NotI enzyme were introduced into the *rpl2402* or and *mug170* loci of the left and right arms of chromosome 3, respectively (Ch3L:NotI and Ch3R:NotI, top panel), to enable the telomere-containing fragments of chromosome 3 to migrate different distances into gels during PFGE (note that the original chromosome 3 does not contain a NotI recognition site). Three independent clones of each insertion mutant were examined along with the parental wild-type strain. Genomic DNA was digested with NotI and analyzed by PFGE followed by Southern blotting. When the Southern blot membrane

was hybridized with probes specific for each arm, the signals from the left and right arms of chromosome 3 were detected at positions above the 1,020 kb marker and at approximately 400 kb, respectively (*rpc37* and *apl4*). When the membrane was hybridized with a probe for the SAS sequence, signals were detected only at the position of the left arm of chromosome 3, although the subtelomere (0–10 kb) signals were masked by those of the right arm of chromosome 2 (C fragments). Note that the differences in band size among the clones are probably due to copy number variation of the rDNA repeats.

(B) PFGE-Southern analyses of *SD5* using subtelomere DNA fragments covering all *SH* regions as probes. Genomic DNA was digested with NotI. Note that each *SH* region has a maximum size of 60 kb (Figure 1A). The remaining signals observed in *SD5* at the positions around the wells indicate the existence of *SH*-homologous regions at non-*SH* loci. Note that the sequence of the 17.5–19.5 kb region, *SH2R*, is 87% identical to that of chromosome 3 position 275342–277405, within the *mae2* gene locus in the *S. pombe* genome database (http://www.pombase.org).

(C) Confirmation of complete isolation of the *SD5* mutant. The original *SD5* mutant and its three descendants after single colony isolation were analyzed for the 9-20 kb region of the subtelomere by PFGE-Southern. Genomic DNA was digested with NotI. The similar patterns of Southern signals were detected in all of the *SD5* strains, demonstrating that the *SD5* mutant used in this study is not contaminated with the wild-type strain.
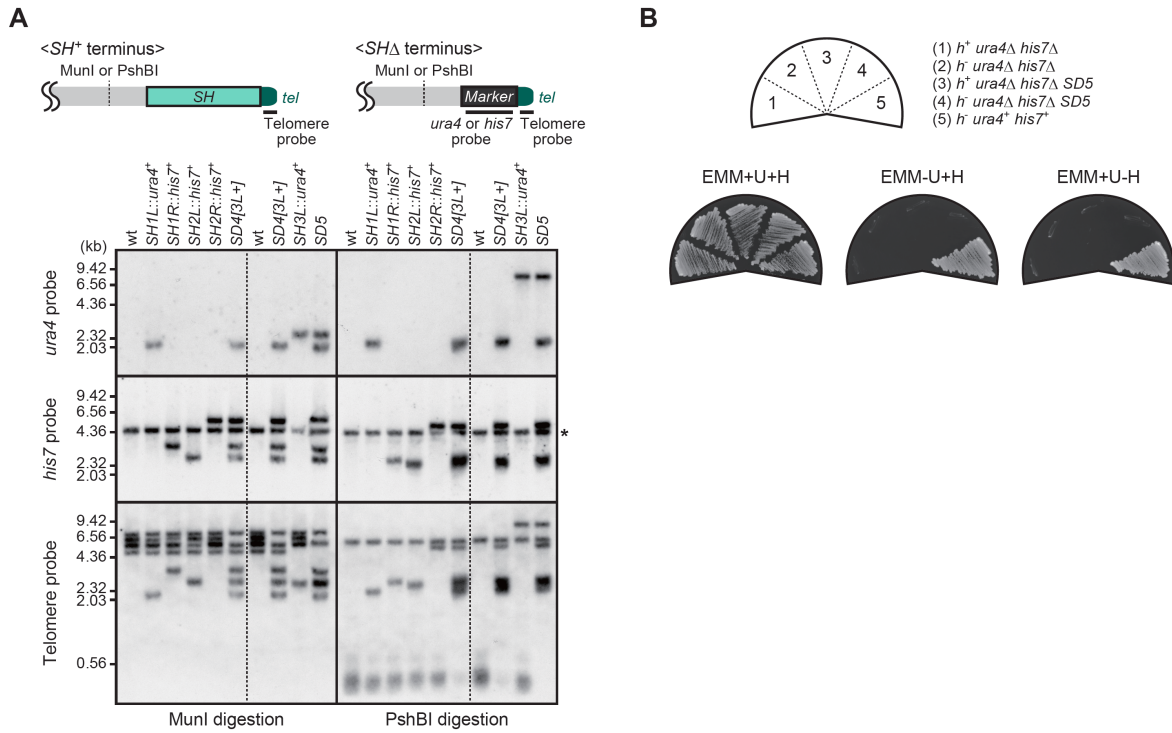
Figure S2. Status of the marker genes in the *SD* mutants

(A) The marker genes (*ura4+* and *his7+*) used for the deletion of *SH*s are stably maintained. Genomic DNA of each strain was digested with Mun1 or PshB1 (the upper schematic diagram shows their target sites) and analyzed by Southern blots using *ura4*, *his7*, and telomere probes. The asterisk indicates the endogenous *his7* gene with a point mutation (*his7-366*).

(B) The marker genes used for the *SH* deletion are silenced. Cells were incubated on EMM+U+H (selective medium supplemented with uracil and histidine), EMM-U+H (lacking uracil), and EMM+U-H (lacking histidine) to examine auxotrophy for uracil and histidine. All of the media were supplemented with adenine, leucine, and lysine. In this assay, the endogenous *his7-366* gene was deleted because this mutant form tends to convert to the wild-type (*his7+*) form.
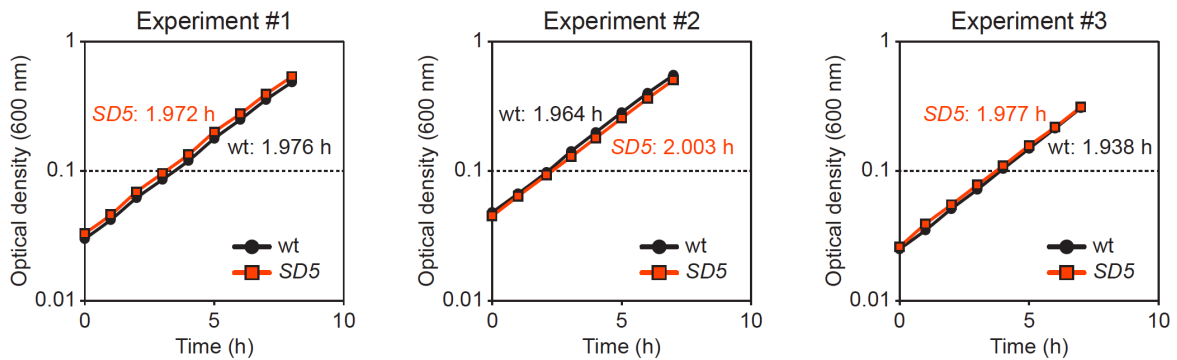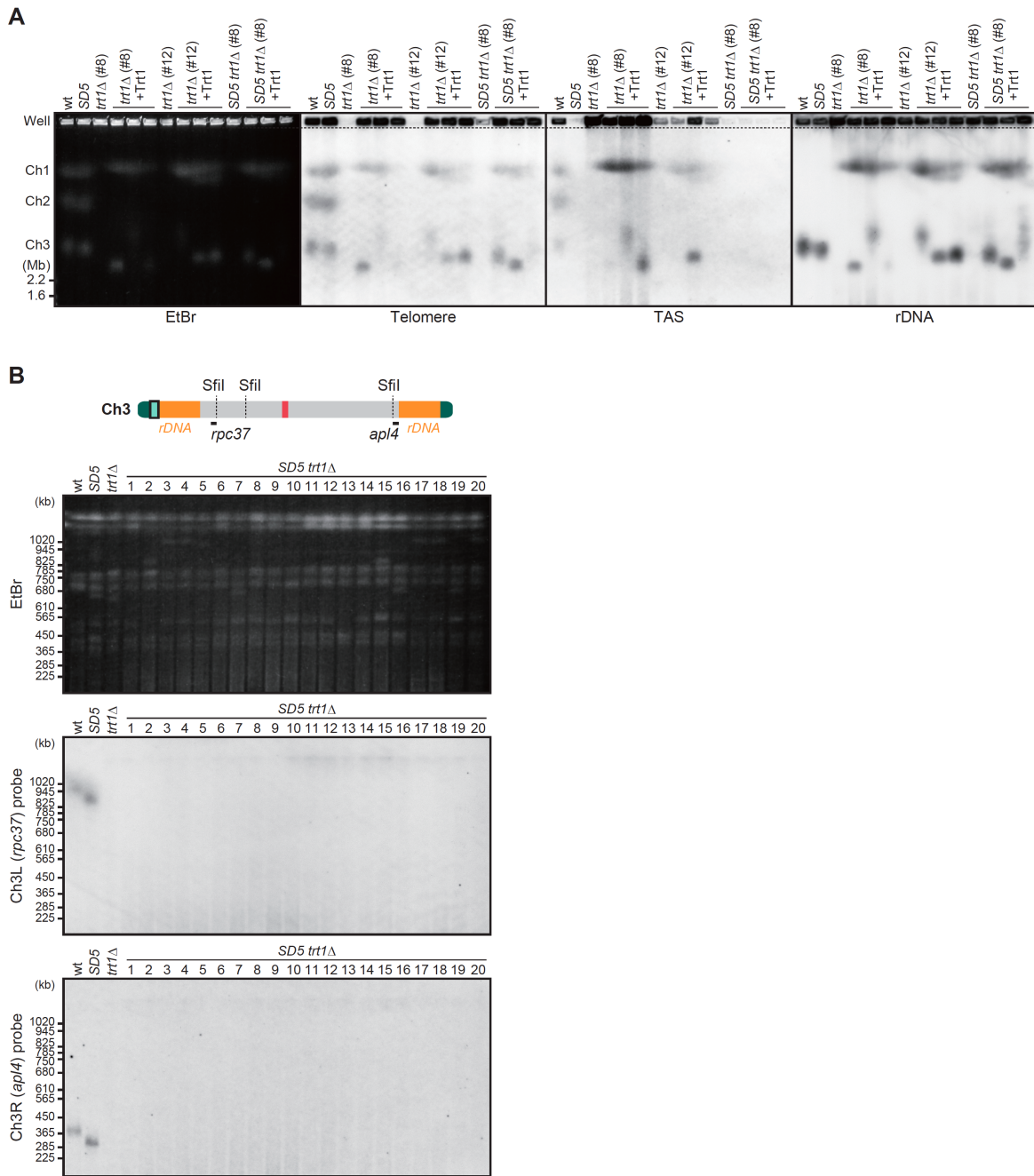
Figure S3. *SD5* **mutant cells proliferate at a rate similar to that of the wild-type strain**
Growth curves for wild-type (wt) and *SD5* strains. Cells were grown exponentially in YES liquid medium at 32°C, and the optical densities of cultures at 600 nm were measured every hour. Data from the three independent experiments are shown separately. Doubling times, estimated by the least-squares method, are indicated on each graph.
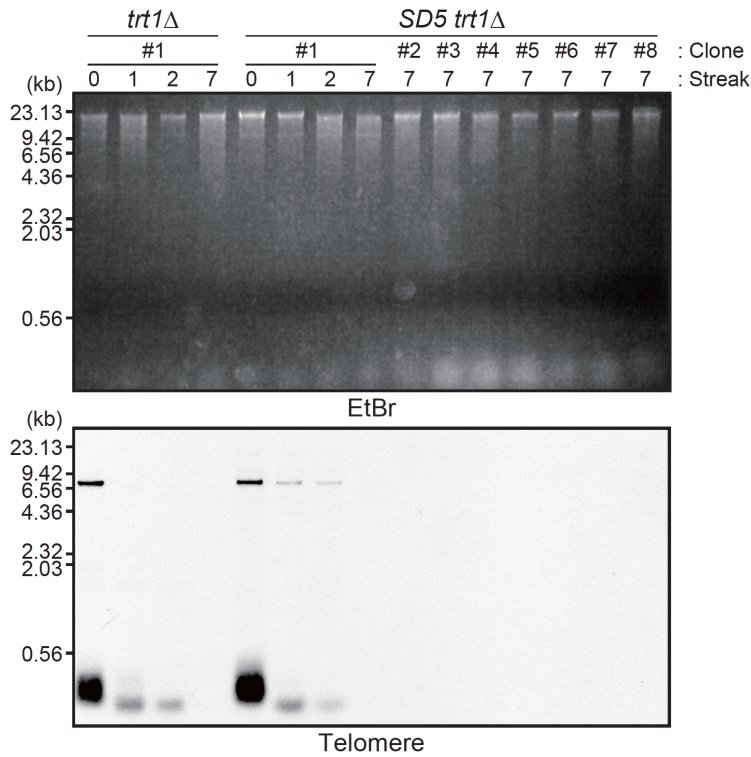
**Figure S4. Absence of telomere DNA in *SD5 trt1*Δ survivors**

Southern blot analysis of ApaI-digested genomic DNA from wild-type and *SD5* strains after Trt1 deletion. Genomic DNA was prepared from cells streaked 0, 1, 2, or 7 times on YES medium plates after deletion of Trt1. EtBr, ethidium bromide staining of the gel (upper). Telomere, Southern blot using telomere DNA as a probe (lower). Clone numbers correspond to those in Figures 3 and 4.

Figure S5. HAATI-type mode of chromosomes in the survivors

(A) Type C strains exhibit a HAATI-type survival mode. PFGE-Southern analyses of whole chromosomes without restriction enzyme treatment. Re-introduction of Trt1 enabled

chromosomes to migrate into the gel, and amplified *SH* and/or rDNA were detected in the multiple chromosomes in three independent clones. TAS, a probe for TAS1-3 in *SH* (see Figure 1D).

(B) Ends of chromosome 3 of the survivors (types A, B, and C) exhibit a HAATI-type mode. PFGE-Southern analyses of SfiI restriction fragments of genomic DNA *trt1Δ* (#1) and *SD5 trt1Δ* (#1-20). DNA sequences of the *rpc37* and *apl4* genes were used to detect rDNA-containing SfiI fragments of *3L* and *3R*, respectively. The ends of chromosome 3 of these survivors did not migrate into the gel.
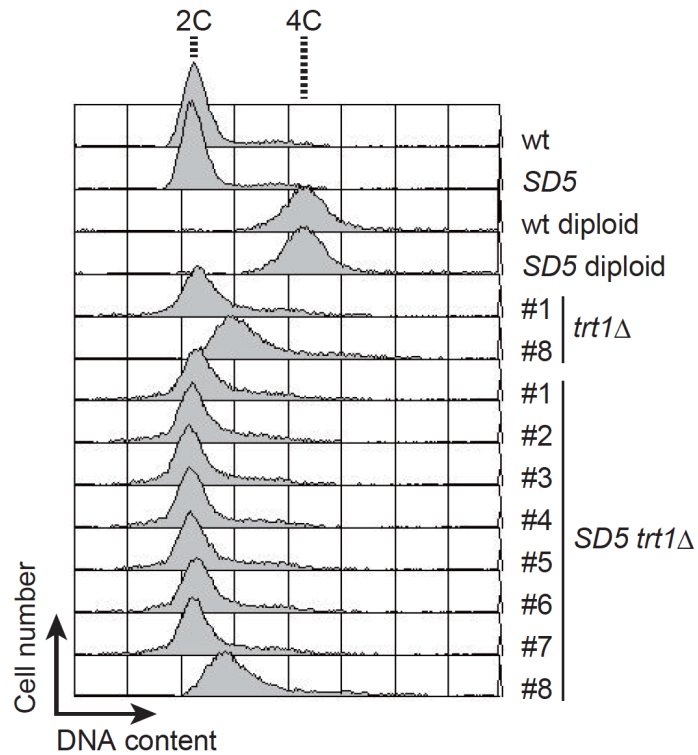
Figure S6. *SD5 trt1Δ* **survivors maintain a haploid state**

FACS (fluorescence activated cell sorting) analyses of exponentially growing cells of *trt1Δ* (#1 and 8) and *SD5 trt1Δ* (#1-8). Majority of *S. pombe* haploid cells are in G_2 phase, exhibiting a 2C DNA content, whereas wild-type diploid cells exhibit a 4C DNA content. Type C survivors (*trt1Δ#8* and *SD5 trt1Δ#8*) showed a moderate increase of the DNA content most likely due to the amplification of *SH* and/or rDNA (see Figure S5A).

Clone #	Sequences at fusion sites	Genomic loci at fusion sites
1	*1L-110.8 kb* *1R-101.3 kb* ACCTCGTTCC`TCAG`TTTAGTTATT	LTR
	2L-118.6 kb *2R-61.0 kb* CCTCAGTTCA`GTTAT...(60 b)...CTACT`CATCAACCTG	LTR
2	*1L-69.4 kb* *2L-84.1 kb* ATGAACCGAG`CAAAGTAACACTACGTGCTTTTTGCAAAA`AACTAACAAG	**L-asparaginase** (SPAC977.12, SPBPB8B6.05c)
	1R-147.5 kb *2R-72.2 kb* CTTTATTACA`AAACATGG`CGTTCGAGTT	**Phosphoprotein phosphatase** (SPAC1039.02, SPBPB2B2.06c)
3	*1L-110.5 kb* *2R-104.9 kb* GTAGCAACTA`AGTATAGGTATTGTATTAACT`AGGTTATAAT	LTR
	1R-61.4 kb *2L-107.2 kb* ACGAAGTGGG`ACTTGTTAAAATTAAAT`CTGGATAATG	**L-asparaginase** (SPAC186.03, SPBPB21E7.09)
4	*1L-110.5 kb* *2R-104.9 kb* GTAGCAACTA`AGTATAGGTATTGTATTAACT`AGGTTATAAT	LTR
	1R-62.2 kb *2L-107.0 kb* AACCGCGATG`TTTTT...(557 b)...TTCCT`GCTTATTTCC	**L-asparaginase** (SPAC186.03, SPBPB21E7.09)
5	*1L-110.5 kb* *2R-105.0 kb* ATATAGCTCA`TAACTGAACTGAGGAACGAGGTTCAG`CAATAGCTCT	LTR
	1R-61.6 kb *2L-107.1 kb* TCAAAACATT`ACTGATATATTCAG`TCTTGAGTAT	**L-asparaginase** (SPAC186.03, SPBPB21E7.09)
6	*1L-110.5 kb* *1R-101.4 kb* TCCTCAGTTC`AGTTAT`TCACTATATC	LTR
	2L-118.6 kb *2R-61.0 kb* AGAGCTACTG`CTGAACCTCGTTCCTCAGTTC`GGTTATGAGC	LTR
7	*1L-110.8 kb* *1L-110.6 kb* *2L-118.5 kb* GTTCCTCAGC`TCAGTTAT`GAGCT...(105 b)...CACCC`CAGTTCTACG`TATCCTTAAA	LTR
	2L-106.4 kb *1R-62.5 kb* AAATATCGCA`GTTTC...(258 b)...AAAAT`CGTAACATTG	**L-asparaginase** (SPBPB21E7.09, SPAC186.03)
	2L-118.5 kb *2R-61.1 kb* CGTATCCTTA`AATCAGATACCAAACTGCGTAG`CTTACAATAG	LTR

Figure S7. DNA sequences of the intra- and inter-chromosomal end fusion sites in *SD5 trt1Δ* survivors (#1–7)

Letters in black and enclosed by a box indicate common sequences shared by two chromosome arms that were fused, and letters in blue, red, or orange indicate sequences specific to each arm. Distance from a fusion site to the nearest telomere is also indicated. The right column shows genomic loci at the fusion sites. LTR, long terminal repeat.

A

B
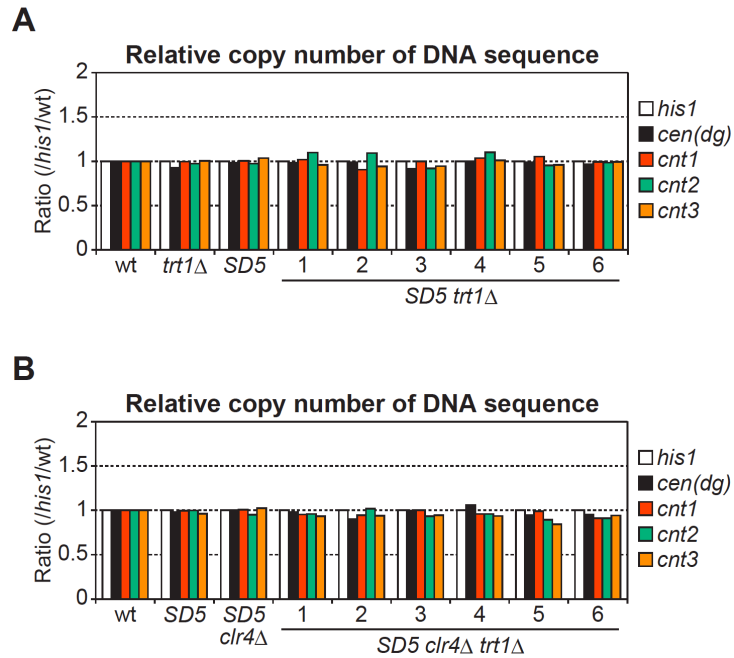
Figure S8. Centromere DNA is normally present in *SD5 trt1Δ* and *SD5 trt1Δ clr4Δ* survivors

(A) Relative copy numbers of genomic DNA sequences at each centromere region were analyzed by quantitative PCR. Values were normalized to that of the *his1* locus, and then compared with those of the wild-type strain. The strains presented in Figure 6A were analyzed.

(B) The strains presented in Figure 6D were analyzed.
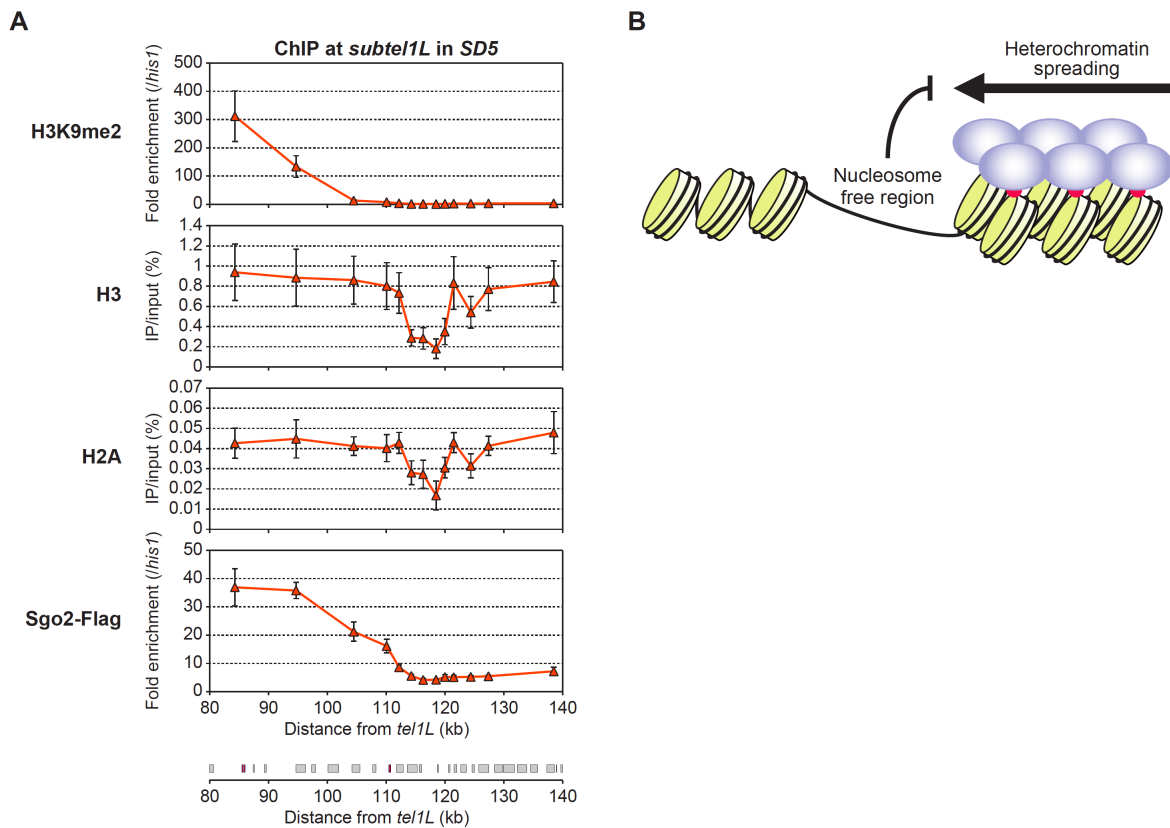
Figure S9. Nucleosome-free configuration at the border of *subtel1L*

(A) ChIP analyses of the distributions of H3K9me2, total H3, total H2A, and Sgo2-Flag at 80–139 kb from *tel1L*. In the graphs of H3K9me2 and Sgo2-Flag, fold enrichment relative to the *his1* locus is shown. In the graphs for H3 and H2A, recovery of immunoprecipitated DNA relative to total input DNA is shown. Boxes below the graph indicate the ORFs of genes located in this region. *LTR*s are shown in magenta. Errors bars indicate the s. d. (n = 3).

(B) Model of subtelomeric chromatin boundary. Step-by-step heterochromatin spread may be blocked by the nucleosome-free configuration at the border of subtelomeres.
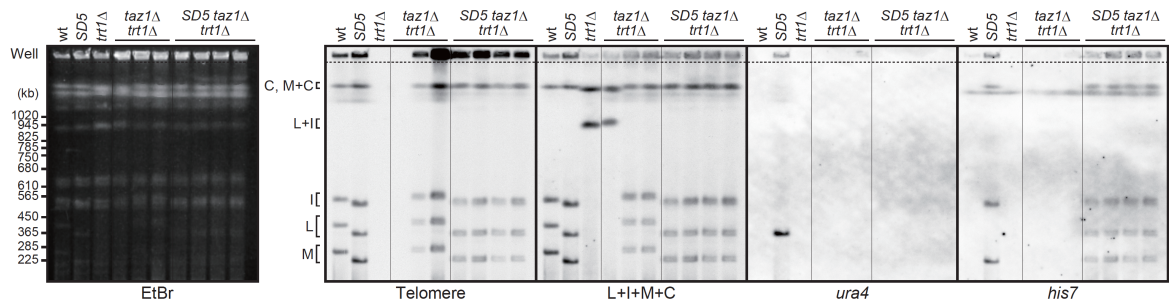
Figure S10. *SH* is not required for cell survival by homologous recombination after the telomerase loss

PFGE-Southern analyses of the Not1 fragments of chromosomes in survivors of *taz1Δ trt1Δ* or *SD5 taz1Δ trt1Δ*. The *trt1Δ* strain was used for a control of a survivor with circular chromosomes. Spores from diploid cells (*taz1+/- trt1+/-* with or without *SD5/SD5*) were dissected, and survivors after more than seven streaks were analyzed by PFGE-Southern using telomere, L+I+M+C (see Figure 1D), *ura4*, and *his7* as probes. Two of the three survivors of *taz1Δ trt1Δ* and all the four survivors of *SD5 taz1Δ trt1Δ* contained linear chromosomes 1 and 2, exhibiting L, I, M, and C fragments, whereas one *taz1Δ trt1Δ* survivor showed chromosome circularization, exhibiting L+I fragment. The asterisk indicates the endogenous *his7* gene with a point mutation (*his7-366*). Note that the *his7*[+] marker gene, which was used for the deletion of three *SH* regions (*SH1R*, *SH2L*, and *SH2R*), was detected with the *1L* fragment (L) as well as with the other fragments (I, M, and C), suggesting the possibility that the multiple *his7*[+] genes next to the telomeres were involved in the expansion of telomere DNA by homologous recombination. Interestingly, the *ura4*[+] marker gene used for the deletion of *SH1L* and *SH3L* was completely absent from the *SD5 taz1Δ trt1Δ* survivors, suggesting that dynamic rearrangements have occurred at the chromosome ends in these survivors.

Supplementary Tables

Table S1. Internal genes with significant changes of expression in *SD5*

Gene name	Systematic ID	Gene product	Ratio (*SD5*/wt, log2)
Chromosome 1			
pdc202	SPAC13A11.06	pyruvate decarboxylase	-0.3
urg2	SPAC1002.17c	uracil phosphoribosyltransferase	-0.2
urg1	SPAC1002.19	GTP cyclohydrolase II	-0.3
	SPAC3H1.06c	transmembrane transporter	-0.3
	SPAC2E1P3.05c	fungal cellulose binding domain protein	-0.2
fip1	SPAC1F7.07c	iron permease	1
fio1	SPAC1F7.08	iron transport multicopper oxidase	0.8
	SPAC27D7.09c	But2 family protein	0.2
Chromosome 2			
urh1	SPBC1683.06c	uridine ribohydrolase	-0.3
	SPBC660.05	WW domain containing conserved fungal protein	-0.4
fet4	SPBP26C9.03c	iron/zinc ion transmembrane transporter	-0.2
	SPBC31A8.02		0.8
isp4	SPBC29B5.02c	OPT oligopeptide transmembrane transporter family	-0.2
	SPBC27.05		0.3
	SPBC1711.15c	*Schizosaccharomyces pombe* specific protein	0.3
	SPBC17G9.12c	hydrolase	0.5
str1	SPBC4F6.09	siderophore-iron transmembrane transporter	0.5
spo6	SPBC1778.04	Spo4-Spo6 kinase complex regulatory subunit	0.7
htd2	SPBC1105.15c	3-hydroxyacyl-ACP dehydratase	-0.4
rpr2	SPBC1105.16c	RNase P subunit	0.3
met6	SPBC56F2.11	homoserine O-acetyltransferase	-0.2
Chromosome 3			
nic1	SPCC1884.02	NiCoT heavy metal ion transmembrane transporter	-0.3
	SPCC18B5.02c		0.3
ctr4	SPCC1393.10	copper transporter complex subunit	-0.4
	SPCC338.18		0.4
inv1	SPCC191.11	external invertase, beta-fructofuranosidase	-0.4
amt1	SPCPB1C11.01	ammonium transmembrane transporter	-0.3

Genes indicated by blue shades are related to metal transport.

Table S2. Fission yeast strains used in this study

Figure 1D

JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST3579	h^- *ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$*
ST3580	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7$^+$*
ST3582	h^- *ade6-M210 leu1-32 ura4-D18 his7-366 SH2L::his7$^+$*
ST3583	h^- *ade6-M210 leu1-32 ura4-D18 his7-366 SH2R::his7$^+$*
ST3593	h^- *ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$*

Figure 1F

JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST3593	h^- *ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$*
ST3585	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH3L::ura4$^+$*
ST3479	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*

Figures 2A and 2B

JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*

Figures 2C and 2D

JP1224	h^+ *ade6-M210 leu1-32 ura4-D18 his7-366*
JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST3524	h^+ *ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*
ST3479	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*

Figure 2E

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺
JP3189	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 rad3::kanʳ*
ST2776	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 clr4::hygʳ*
JP3204	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 taz1::hygʳ rap1::ura4⁺*

Figure 2F

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3579	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺*
ST3580	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7⁺*
ST3582	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH2L::his7⁺*
ST3583	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH2R::his7⁺*
ST3585	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH3L::ura4⁺*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺

Figure 2G

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
YN2373	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 taz1::hygʳ*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺
ST3482	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ taz1::hygʳ

Figure 3

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺
JP3689-3696	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#1-8)
JP3799-3810	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#9-20)

Figure 4

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ (#1)*
JP3697-3704	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ (#1-8)*
JP3811-3822	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ (#9-20)*

Figure 5B

JP3697-3702	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ (#1-6)*

Figures 5C and 5D

JP3703	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ (#7)*

Figures 6A and 6B

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ (#1)*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3697-3702	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ (#1-6)*

Figure 6C

ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
ST3499	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hygʳ*
JP3697-3699	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*

SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kan^r (#1-3)

ST4381-4396	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hyg^r trt1::kan^r (#1-16)

Figure 6D

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺
ST3499	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hyg^r
ST4381-4386	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hyg^r trt1::kan^r (#1-6)

Figure 7A

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3587	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1R::his7⁺ SH2L::his7⁺*
	SH2R::his7⁺ SH3L::ura4⁺
ST3589	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH2L::his7⁺*
	SH2R::his7⁺ SH3L::ura4⁺
ST3590	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2R::his7⁺SH3L::ura4⁺
ST3591	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH3L::ura4⁺
ST3593	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺

Figures 7B and 7C

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺

Figure 8B

ST3591	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH3L::ura4⁺*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
ST4213	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ subtel2R(52.3-74.8kb)::natʳ*

Figure 8C

ST3591	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH3L::ura4⁺*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
ST4213	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ subtel2R(52.3-74.8kb)::natʳ*
ST4839	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH3L::ura4⁺ sgo2-3flag-kanʳ*
ST4841	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ sgo2-3flag-kanʳ*
ST4843	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ subtel2R(52.3-74.8kb)::natʳ sgo2-3flag-kanʳ*

Figures 9A and 9B

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*

Figures 10A and 10B

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST2776	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 clr4::hygʳ*

ST3479	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*
ST3499	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$ clr4::hyg^r*

Figure 10C

JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST2776	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 clr4::hyg^r*
ST3479	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$*
ST3499	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4$^+$ SH1R::his7$^+$* *SH2L::his7$^+$ SH2R::his7$^+$ SH3L::ura4$^+$ clr4::hyg^r*
ST3183	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 nhe1::kan^r*
JP3560	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 spc1::kan^r*

Table 1

ST4658,4659	h^+/h^- *ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18* *his7-366/his7-366 SH1L::ura4$^+$/SH1L::ura4$^+$ SH1R::his7$^+$/SH1R::his7$^+$* *SH2L::his7$^+$/SH2L::his7$^+$ SH2R::his7$^+$/SH2R::his7$^+$ SH3L::ura4$^+$/SH3L::ura4$^+$* *trt1$^{+/}$trt1::kan^r rad51$^+$/rad51::hyg^r (#1,2)*
ST4661,4662	h^+/h^- *ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18* *his7-366/his7-366 SH1L::ura4$^+$/SH1L::ura4$^+$ SH1R::his7$^+$/SH1R::his7$^+$* *SH2L::his7$^+$/SH2L::his7$^+$ SH2R::his7$^+$/SH2R::his7$^+$ SH3L::ura4$^+$/SH3L::ura4$^+$* *trt1$^{+/}$trt1::kan^r rad52$^+$/rad52::hyg^r (#1,2)*

Figure S1A

JP1225	h^- *ade6-M216 leu1-32 ura4-D18 his7-366*
ST3654	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 rpc37-kan^r-NotI-rpl2402 (#1)*
ST3655	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 rpc37- kan^r-NotI-rpl2402 (#2)*
ST3656	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 rpc37- kan^r-NotI-rpl2402 (#3)*
ST3657	h^- *ade6-M216 leu1-32 ura4-D18 his7-366 ppk38- kan^r-NotI-mug170 (#1)*

| ST3658 | *h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 ppk38- kanʳ-NotI-mug170 (#2)* |
| ST3659 | *h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 ppk38- kanʳ-NotI-mug170 (#3)* |

Figures S1B and S1C

| JP1225 | *h⁻ ade6-M216 leu1-32 ura4-D18 his7-366* |
| ST3479 | *h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺* |

Figure S2A

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3579	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺*
ST3580	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7⁺*
ST3582	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH2L::his7⁺*
ST3583	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH2R::his7⁺*
ST3593	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺*
JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3593	*h⁻ ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺*
ST3585	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH3L::ura4⁺*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*

Figure S2B

ST5171	*h⁺ ade6-M210 leu1-32 ura4-D18 his7::BSD*
ST5173	*h⁻ ade6-M216 leu1-32 ura4-D18 his7::BSD*
ST5175	*h⁺ ade6-M210 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ his7::BSD*
ST5177	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ his7::BSD*
JK107	*h⁻*

Figure S3

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*

Figure S4

JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#1)
JP3697-3704	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ* (#1-8)

Figure S5A

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3696	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#8)
ST5125-5127	*h⁻ ade6-M216 ura4-D18 his7-366 trt1::kanʳ leu1::trt1⁺-hygʳ* (#8-1, 2, 3)
JP3802	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#12)
ST5128-5130	*h⁻ ade6-M216 ura4-D18 his7-366 trt1::kanʳ leu1::trt1⁺-hygʳ* (#12-1, 2, 3)
JP3704	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ* (#8)
ST5131-5133	*h⁻ ade6-M216 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ leu1::trt1⁺-hygʳ* (#8-1, 2, 3)

Figure S5B

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ* (#1)
JP3697-3704	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kanʳ* (#1-8)
JP3811-3822	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺*

SH2R::his7^r SH3L::ura4⁺ trt1::kan^r (#9-20)

Figure S6

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
ST3526	*h⁺/h⁻ ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18 his7-366/his7-366*
ST3527	*h⁺/h⁻ ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18 his7-366/his7⁺ SH1L::ura4⁺/SH1L::ura4⁺ SH1R::his7⁺/SH1R::his7⁺ SH2L::his7⁺/SH2L::his7⁺ SH2R::his7⁺/SH2R::his7⁺ SH3L::ura4⁺/SH3L::ura4⁺*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kan^r* (#1)
JP3696	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kan^r* (#8)
JP3697-3704	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kan^r* (#1-8)

Figure S7

JP3697-3703	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kan^r* (#1-7)

Figure S8A

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kan^r* (#1)
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3697-3702	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ trt1::kan^r* (#1-6)

Figure S8B

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*

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| | *SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺* |

ST3499	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hygʳ
ST4381-4386	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ clr4::hygʳ trt1::kanʳ (#1-6)

Figure S9A

ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺
ST4841	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4⁺ SH1R::his7⁺*
	SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ sgo2-3flag-kanʳ

Figure S10

JP1225	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*
ST3479	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*
JP3689	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 trt1::kanʳ (#1)*
ST5180-5182	*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366 taz1::hygʳ trt1::kanʳ (#2-4)*
ST5183-5186	*h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺ taz1::hygʳ trt1::kanʳ (#1-4)*
ST5134	*h⁺/h⁻ ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18 his7-366/his7-366 taz1⁺/taz1::hygʳ trt1⁺/trt1::kanʳ*
ST5138	*h⁺/h⁻ ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18 his7-366/his7⁺ SH1L::ura4⁺/SH1L::ura4⁺ SH1R::his7⁺/SH1R::his7⁺ SH2L::his7⁺/SH2L::his7⁺ SH2R::his7⁺/SH2R::his7⁺ SH3L::ura4⁺/SH3L::ura4⁺ taz1⁺/taz1::hygʳ trt1⁺/trt1::kanʳ*

Table S1

| JP1225 | *h⁻ ade6-M216 leu1-32 ura4-D18 his7-366* |

ST3479   *h⁻ ade6-M216 leu1-32 ura4-D18 SH1L::ura4⁺ SH1R::his7⁺ SH2L::his7⁺ SH2R::his7⁺ SH3L::ura4⁺*

Table S3. Primers used for strain construction

rad3 **deletion** (PCR-based)

cs125   5′-AGCTGGGTCACTCGATCTTTC-3′

cs126   5′-GGGGATCCGTCGACCTGCAGCGTACGAAAGTCCACGCTGTAAAGAGAG-3′

cs127   5′-GTTTAAACGAGCTCGAATTCATCGATTGTTGAATCTTTCCCAGAACC-3′

cs128   5′-AGCCCAACCAATGTACATTTC-3′

clr4 **deletion** (PCR-based)

jk1467   5′-AGTAATATCCTAACATATGACATATAG-3′

jk1468   5′-GGGGATCCGTCGACCTGCAGCGTACGACGCAAAACTAATAACCTCTTGTTTG-3′

jk1469   5′-GTTTAAACGAGCTCGAATTCATCGATCCACTCCTGTTCACCTAATATAGC-3′

jk1470   5′-CTTCACATGTGCGCAGCAGATG-3′

taz1 **deletion** (PCR-based)

jk969   5′-TTGTTTCAGTTTGACGTTCTTGTTG-3′

jk970   5′-GGGGATCCGTCGACCTGCAGCGTACGATCTGTACTTTGCACGCTTATCATC-3′

jk967   5′-GTTTAAACGAGCTCGAATTCATCGATGTCTCCGGATAGAGTTTGTTCATG-3′

jk968   5′-TTGTGCTTCACTCATTTACGATTCC-3′

rap1 **deletion** (PCR-based)

if1   5′-TTCATAACAATGATGAATTCTGAA-3′

if2   5′-TTAATTAACCCGGGGATCCGAGTTCATACTTTTATTCTTTTTTTGC-3′

jk1209   5′-GTTTAAACGAGCTCGAATTCATCGATCCGAGCATCTCTGCCCAAATTC-3′

jk1210   5′-ATGAAGAATCTGGAGTTGACGTAG-3′

nhe1 **deletion** (PCR-based)

st55   5′-TATTGAGATAAAATGCCTTAATCCAATCAG-3′

st56   5′-GGGGATCCGTCGACCTGCAGCGTACGAAGTAATTAGGCAATATCCACAAGAG-3′

st57   5′-GTTTAAACGAGCTCGAATTCATCGATTAGGAAAGCTCTTTTAATGTCAATTC-3′

st58   5′-TCCGTTTTCTTAGTTTCTTACATAAAATAG-3′

spc1 **deletion** (PCR-based)

jk1623   5′-GTTGATCTAATAAAGCTGGCTTAAC-3′

jk1624   5′-GGGGATCCGTCGACCTGCAGCGTACGATTTATTCAAACTGGTTACAAAAAGGAC-3′

jk1625   5′-GTTTAAACGAGCTCGAATTCATCGATACAAGTTGTAGATAAAGCCTTAAAAG-3′

jk1626   5′-TTATAAAACCCGTAACTACATTAACG-3′

trt1 deletion (PCR-based)

jk1631   5′-GGTATCATCCAACGTTTGCCTTG-3′

jk1632   5′-GGGGATCCGTCGACCTGCAGCGTACGAGCAAGTTACAAGTAACCATTAAGCA-3′

jk1633   5′-GTTTAAACGAGCTCGAATTCATCGATGTCATTTTCAATTTATTATATACATCC-3′

jk1634   5′-GTTTCTTTTCGTCTCAGTAGCAAG-3′

rad51 deletion (PCR-based)

jk1318   5′-GAATAAGACGACTACACGCTATGG-3′

jk1319   5′-GGGGATCCGTCGACCTGCAGCGTACGATAACTTGTTAAGCACGAAATTATCAC-3′

jk1320   5′-GTTTAAACGAGCTCGAATTCATCGATTTGCAAATTCTATGGGATGAGTTTG-3′

jk1321   5′-CAAGAATTTAGCATTTTGCGTGCG-3′

rad52 deletion (PCR-based)

st381   5′-CATTAGAAGGTTCGAAGAAGTATGG-3′

st382   5′-GGGGATCCGTCGACCTGCAGCGTACGACCCTTCTAGCTTATATGAAGCAGT-3′

st383   5′-GTTTAAACGAGCTCGAATTCATCGATTAAAAGTAATGAGGCAAAATGTGA-3′

st384   5′-AAACGACTTCCGCGATAAAG-3′

NotI insertion in Ch3L (PCR-based)

st179   5′-CAATTTGATGGTCGGTCTAATTC-3′

st180   5′-GGGGATCCGTCGACCTGCAGCGTACGACATCTGTAAGTAAATACGACTTACTCTTG-3′

st181   5′-GTTTAAACGAGCTCGAATTCATCGATGCGGCCGCCTAACATGATGACTGAAAATATTGACG-3′

st182   5′-GTTTGTCATGGACTGTCCTTTAC-3′

NotI insertion in Ch3R (PCR-based)

st183   5′-CCTGTAAACTTAAAATCTGTGGAAAAC-3′

st184   5′-GGGGATCCGTCGACCTGCAGCGTACGAAAACGGTAACTTAGTTGGTAAAAAAAC-3′

st185   5′-GTTTAAACGAGCTCGAATTCATCGATGCGGCCGCTGTTTTGGAATGTTTACCATCGAG-3′

st186   5′-CTTTATCCAAACACCGGTTTCC-3′

subtel2R(52.3–74.8kb) deletion (PCR-based)

km33   5′-GACGACGGACTTTGTGAAGGA-3′

st73   5′-GGGGATCCGTCGACCTGCAGCGTACGAGATTAACGAAATAGATTAGAATTGC-3′

st22   5′-GTTTAAACGAGCTCGAATTCATCGATTCCCGCTGATAAACATCGATTCAC-3′

jk700   5′-TCCGCAAATTTTGTTAGCCAT-3′

Table S4. Primer sets used for quantitative PCR

his1

  jk1335   5′-CGAAGACGTGCTTCAGCGA-3′

  jk1336   5′-TGTCCACCTCGGAATCACTG-3′

ade6

  st15   5′-GAAAGATGCTGCCGTCATTTTAG-3′

  st16   5′-GCTGCGGTACGAGCATAAGTAAC-3′

cen(dg)

  st17   5′-AATTGTGGTGGTGTGGTAATAC-3′

  st18   5′-GGGTTCATCGTTTCCATTCAG-3′

cnt1

  st334   5′-CCTTCTGGAGTTCTTTGGACCTACT-3′

  st335   5′-CAAACGGAGGACGATGAACTAAT-3′

cnt2

  st323   5′-ACTAATAACGGAATAGATCAAACAAGCTC-3′

  st324   5′-TATTTAACCAGCAAATTCATAGATTTGAC-3′

cnt3

  st325   5′-AGCATTCGATAATTTGAGCTTTAATG-3′

  st326   5′-AAAATGTGAATGTAAGGCCGTTCT-3′

tlh

  jk457   5′-CACTCATTTCTTTGCTGATCACTTACT-3′

  jk458   5′-TCGATAGAGATACGTTCATCTCATAGTGT-3′

rDNA

  TB19   5′-GGGAACCAGGACTTTTACCTTGA-3′

  TB20   5′-AACTTGCCTGCTTTGAACACTCTA-3′

subtel-2.8 kb

  jk614   5′-GTCTCGTTGCTCGCTTCACA-3′

  jk615   5′-GGAGGATGGGAAATTTTGAGGAT-3′

subtel-9.0 kb

jk620   5′-TTCTTAATCATTATCAAGTATTCATTGCAA-3′

jk621   5′-ACAGTAAACTATGATCGCTTTTGAAGAC-3′

subtel-14.7 kb

jk1607   5′-GCTTGGTCAACATCATCTTGTCG-3′

jk1608   5′-GGGAGCAGCAAGACAAAGGTG-3′

subtel-20.0 kb

jk455   5′-AACGAGTTGTGCAATGTTAGTAAGGT-3′

jk456   5′-GACCGCTACGCAACCATAAAG-3′

subtel-27.2 kb

jk554   5′-GCTGCATGTTTATATCCTTGGCT-3′

jk555   5′-GACCCCAATGGCCGAGAT-3′

subtel-30.0 kb

jk388   5′-GGCACAATTTCATTTCGTTTAGTTTAC-3′

jk389   5′-TGTTACTCATACTTGAAATACAATTTGAATG-3′

subtel-33.7 kb

jk686   5′-GCATTCCAGCAGAACCAGGT-3′

jk687   5′-GCAAACACCCACCCTGAAGTA-3′

subtel-37.9 kb

jk690   5′-TGAAACGGGTTCTTACTGCGT-3′

jk691   5′-GCTCCATCCATTGTCATTGGT-3′

subtel-41.6 kb

jk692   5′-CGCGCACTTTTCGGACATA-3′

jk693   5′-TGCAAGTCGCCGAAACTACC-3′

subtel-45.7 kb

jk696   5′-TTGAATCCCTCATCCAAAGGA-3′

jk697   5′-TTGGTGTCAGCCCATTGAACT-3′

subtel1L-65.0 kb (nhe1)

yn114   5′-TCCGGACATTAAGACATGGAAA-3′

yn115   5′-CAAACCCCTATTGGTCCGAAA-3′

subtel1L-74.8 kb

yn116	5′-TCCCTCCAATGTCTTTCAGCAT-3′
yn117	5′-GGCCCCTACGAACCGTAATT-3′

subtel1L-84.3 kb

yn118	5′-GCTGATGTTGCACCAGTTCAA-3′
yn119	5′-GAAACAACTATTCAGCCGATGCT-3′

subtel1L-94.7 kb

yn120	5′-TTTATCTCAATGTCCGGATGGTT-3′
yn121	5′-CCAAGATGCCGCTAATGGAA-3′

subtel1L-104.5 kb

yn122	5′-CGATTTTCTCAGCGGGAACT-3′
yn123	5′-TGGCGTCTTTGCTTCCAAA-3′

subtel1L-110.1 kb

st221	5′-ACGGCAGAGGTATACAAATAATCATAAG-3′
st222	5′-CCCGAACGTATATCATCGCAAT-3′

subtel1L-112.2 kb

st429	5′-AACATTCGTTTCTTCATCCACAAC-3′
st430	5′-TCTAATCCACGAACTCCATCACA-3′

subtel1L-114.3 kb

st94	5′-TGGCAAGAAGCTCCAAGAATTC-3′
st95	5′-AGCGTTTCCATCCCTGGTTA-3′

subtel1L-116.3 kb

st431	5′-TCATTATCTTTGGTGTGTGCAAGA-3′
st432	5′-CTCGGAGCTCATCTGTAAAGCTT-3′

subtel1L-118.5 kb

st433	5′-AATGGCTGATTGGCTACTGATTAAT-3′
st434	5′-CCCGTCTTCAAAGGAATCAATT-3′

subtel1L-120.0 kb

st457	5′-CATAGCATTGCACAATCTCTCGAT-3′
st458	5′-TCACAAGAAGGCCTATTCAATCC-3′

subtel1L-121.5 kb

| st447 | 5′-AAATGGTGTTAAGCGGTTATTCG-3′ |
| st448 | 5′-GATGGAATACCCCATGTGGAAA-3′ |

subtel1L-124.4 kb

| st96 | 5′-AACAATGGACACTTCGCAATTAAC-3′ |
| st97 | 5′-GGGAATCTCGATTTGACATAATGA-3′ |

subtel1L-127.4 kb

| st449 | 5′-TTCTGTAGCGATGGTTCCCAT-3′ |
| st450 | 5′-CTCCACGCACGAATGCTCT-3′ |

subtel1L-138.5 kb

| st455 | 5′-GGCCTCCCCAAAGGATTG-3′ |
| st456 | 5′-ATTGCTTCGTCAGAAATCCCA-3′ |

subtel1R-40.7 kb

| jk714 | 5′-AATTAATTCGGTGCATCGTGC-3′ |
| jk715 | 5′-GATGCAACGTTCATTTGCGT-3′ |

subtel1R-50.5 kb

| jk724 | 5′-TTCCGCTACAACCCGTTTAAA-3′ |
| jk725 | 5′-AAAGCGATAGCATAAGTGTATTCGAA-3′ |

subtel1R-60.6 kb

| jk734 | 5′-TCGTTTTGGTGCCGCTAAAT-3′ |
| jk735 | 5′-AATAATGGTCACTAGATGTGCGGTT-3′ |

subtel1R-72.5 kb

| jk746 | 5′-AAACAAAGCAGATTCCCACAGAA-3′ |
| jk747 | 5′-TCAAACCAAGTTTGCTCACCC-3′ |

subtel1R-82.3 kb

| jk752 | 5′-GTTTATGGGAACAGCTGATGCAT-3′ |
| jk753 | 5′-AAGGCATTTTTGCATATTTGTGC-3′ |

subtel1R-92.4 kb

| jk756 | 5′-TTTTACCACAGTACTTGATCACGAATTT-3′ |
| jk757 | 5′-TTATGCAAGAGTTCTGTGATTTGAAA-3′ |

subtel2L-63.1 kb

yn124	5′-CACCCCAAGTAACCAAATATGGA-3′
yn125	5′-CGACTGACAACAAAAGCGATTTT-3′

subtel2L-72.5 kb

yn126	5′-TGAACTTTCCGCTCGTGAAA-3′
yn127	5′-TTCTTGGCTGAATGAGAAAGTTGT-3′

subtel2L-83.1 kb

yn128	5′-ACTGGCTTGAGTAGAAGGTGCTTT-3′
yn129	5′-CCACACTCGGTTGTAAGATCATCA-3′

subtel2L-92.5 kb

yn130	5′-ATCTACCTATGGATTCGGTTTAGCA-3′
yn131	5′-CTACTTGACGACGACGAATCTGA-3′

subtel2L-102.8 kb

yn132	5′-TGCAATCAAAGGACCGAATAAA-3′
yn133	5′-TGCAAAAAATGCTGGCGTTA-3′

subtel2L-109.8 kb

st177	5′-AAAAAGGGATATTTGTTCAGCAGAAC-3′
st178	5′-ATGAAAATTCTGACGAAGAAGATGAG -3′

subtel2R-51.8 kb

jk700	5′-TCCGCAAATTTTGTTAGCCAT-3′
jk701	5′-AGCTTAATTCGTGATGCAAGTTTTTA-3′

subtel2R-61.7 kb

km20	5′-CACTTACGCCATAGTGGATTGC-3′
km21	5′-CGAAAGACTGACTAAGCGAATCG-3′

subtel2R-71.6 kb

km28	5′-CCCGACTCCCTCAACATGAA-3′
km29	5′-CAAAAGCACAAGGGTTGACCA-3′

subtel2R-79.8 kb

km36	5′-CGGTTACTAGTGCCACTGCATT-3′
km37	5′-CCATTTAAGTAGTTGCGGCGA-3′

subtel2R-89.8 kb

st110   5′-TGCGGACATCATAACATGCTAAA-3′

st111   5′-TTCAATATACACCGAGGTCCGAAT-3′

subtel2R-92.8 kb

st80   5′-CGTATGAAGTGCTACGATGAAACA-3′

st81   5′-GCATGGTTTTGGGATGATTTAGA-3′

subtel2R-93.8 kb

st84   5′-CCGTTCGTGTGAATGGTACCT-3′

st85   5′-CACAGCACTAGCATTGCAAAGAG-3′

subtel2R-94.9 kb

st86   5′-TCAAAGACATGGTTCTCGTAATCC-3′

st87   5′-GCGATTCCAACAGCATCGA-3′

subtel2R-95.9 kb

st82   5′-CATATCGAAGGTCAGCGTCTAAAA-3′

st83   5′-TCCCCAGACCAAGATATAATTGTTTAA-3′

subtel2R-98.9 kb

km38   5′-TTCAGGATTAAGGTAACGCGGT-3′

km39   5′-TTGCAGTTGTCCGCTAGTGC-3′

subtel2R-100.3 kb

st459   5′-GCGTGTGAATTCGGCAATATAC-3′

st460   5′-CGTGATCAGTCAAGGGCAGTT-3′

subtel2R-101.6 kb

st461   5′-GCTAAATGAGCTCAGGATTGAAGAA-3′

st462   5′-CTTTTATCACCCTCACTAATTGCATTAT-3′

subtel2R-103.5 kb

st104   5′-TTTATGCATCCAACCGTTCGA-3′

st105   5′-TTTCAATTGTCAGTTTGCCTATATATGG-3′

subtel2R-107.1 kb

st213   5′-GCGACAAATGTGAATCAGTGTCTAT-3′

st214   5′-GCTTTACTCCTTTCAGGCGTATG-3′

subtel2R-110.8 kb

km40   5′-CCTATGCCTACGCATTCAGCTC-3′

km41   5′-CGATCGTCCACTACTTCACGTTT-3′

subtel2R-122.8 kb

st106   5′-AATTTTACCGGCTTCGCATCT-3′

st107   5′-TGCGTTTTCTCCGTGAATGA-3′

subtel2R-135.1 kb

st215   5′- GCAGCTCTATTTGTCTCATAACGTTTAA-3′

st216   5′- CAGAACTTTGATTGCGGTAATTGA-3′

subtel2R-149.9 kb

st112   5′-TCTACTCTGCTATCCACTAATTCCGTAT-3′

st113   5′-TTTCAATCAAAACATCGCATCTTAC-3′

subtel3L-15.9 kb

st153   5′-CCAGTCAGCCATCGCTTATCA-3′

st154   5′-TTTCGTATGGCTGGTCTATTTCAC-3′

subtel3L-16.8 kb

st155   5′-CGTTGATTCTCATCGAAATACGTT-3′

st156   5′-GGTTGTTTTGGCATGTCCTATCT-3′