Supplementary information

for

Complete sequences of *Schizosaccharomyces pombe* subtelomeres reveal multiple patterns of genome variation

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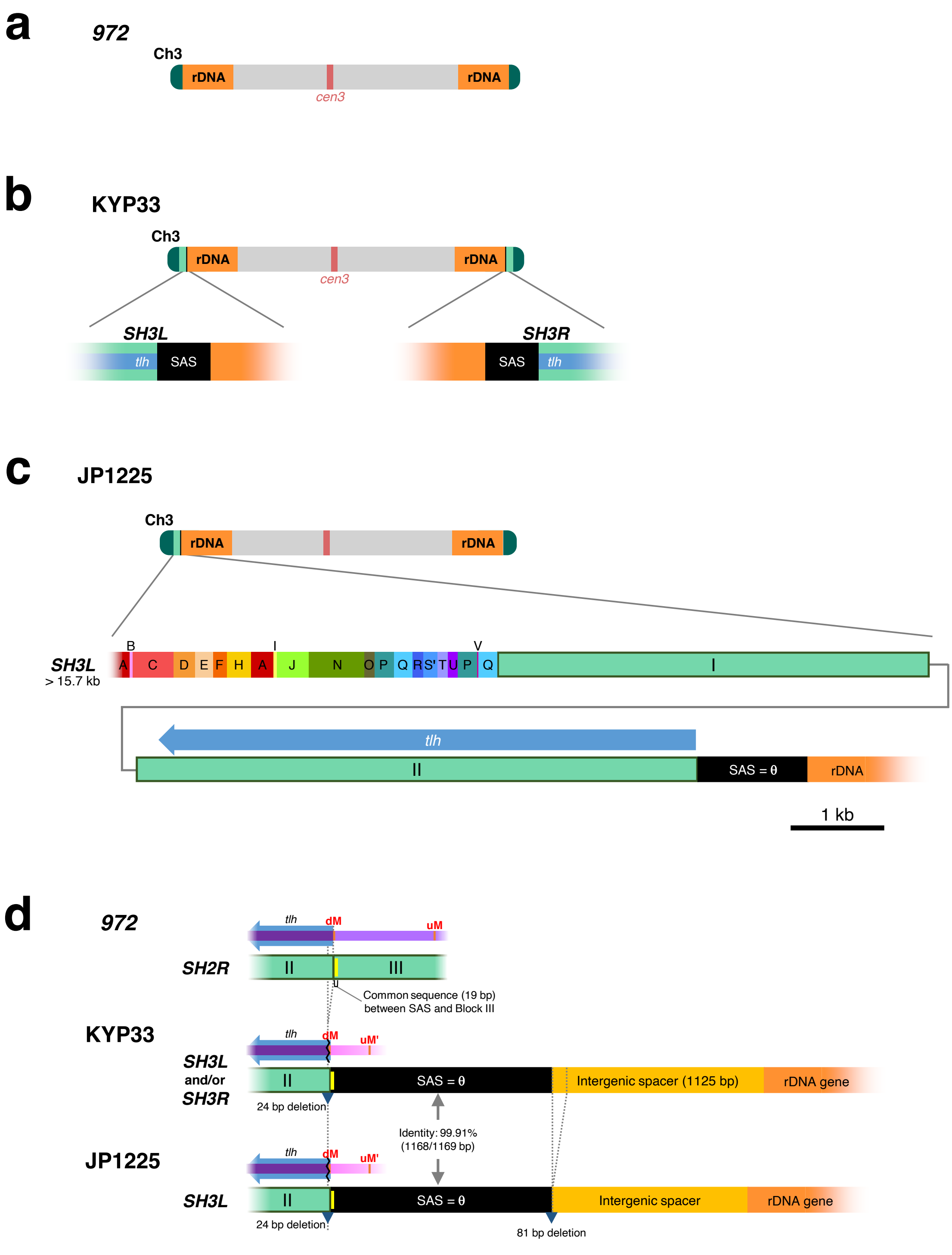


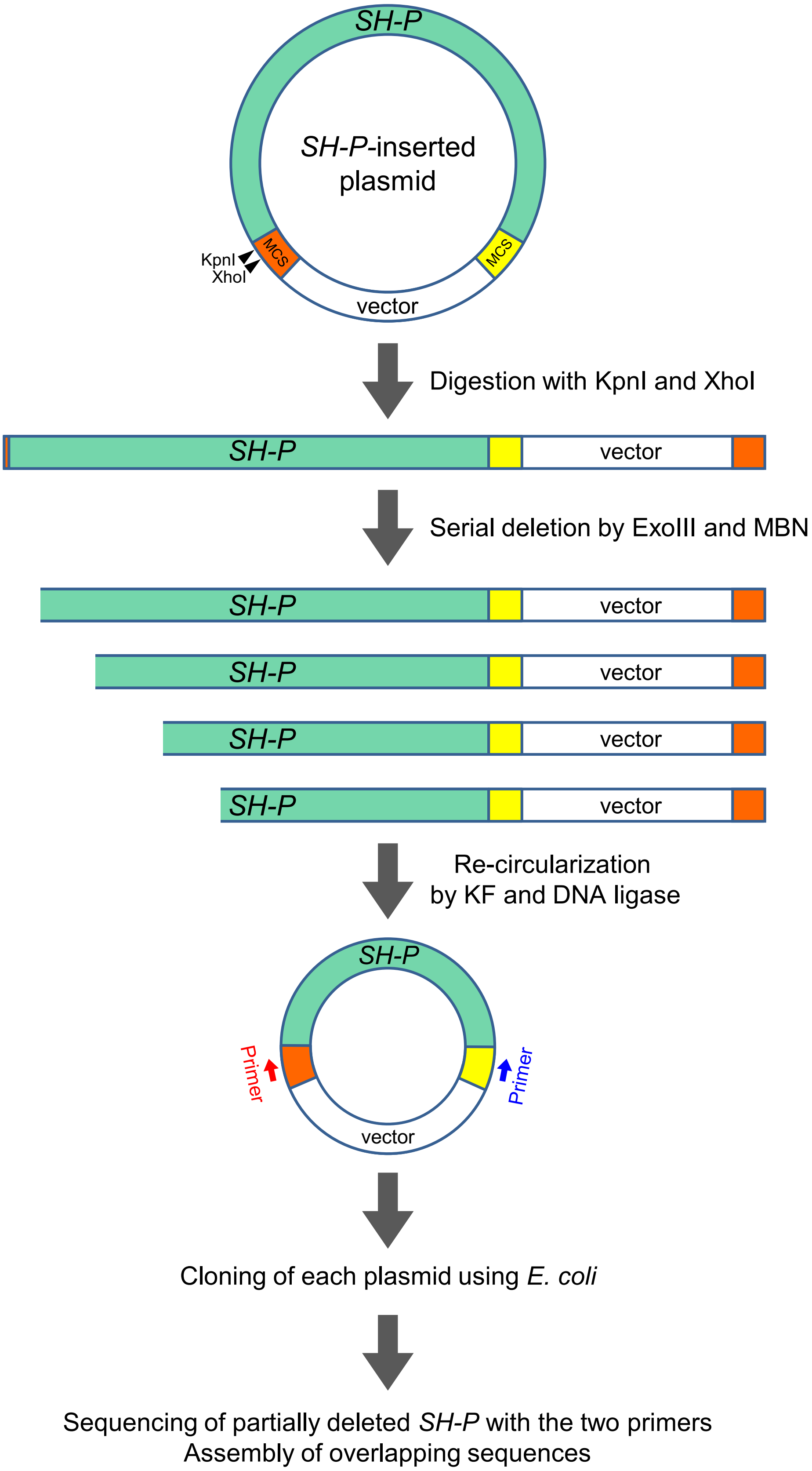
Supplementary Fig. 1 Structures of chromosome ends of Ch3 in descendent strains of *972*.

(a) Strain *972* has no subtelomere sequence in Ch3.

(b) Strain KYP33 (*h⁻ leu1-32 ura4-D18*) has subtelomeres including *SH* and SAS (subtelomere-associated sequence) sequences at both ends of Ch3[1].

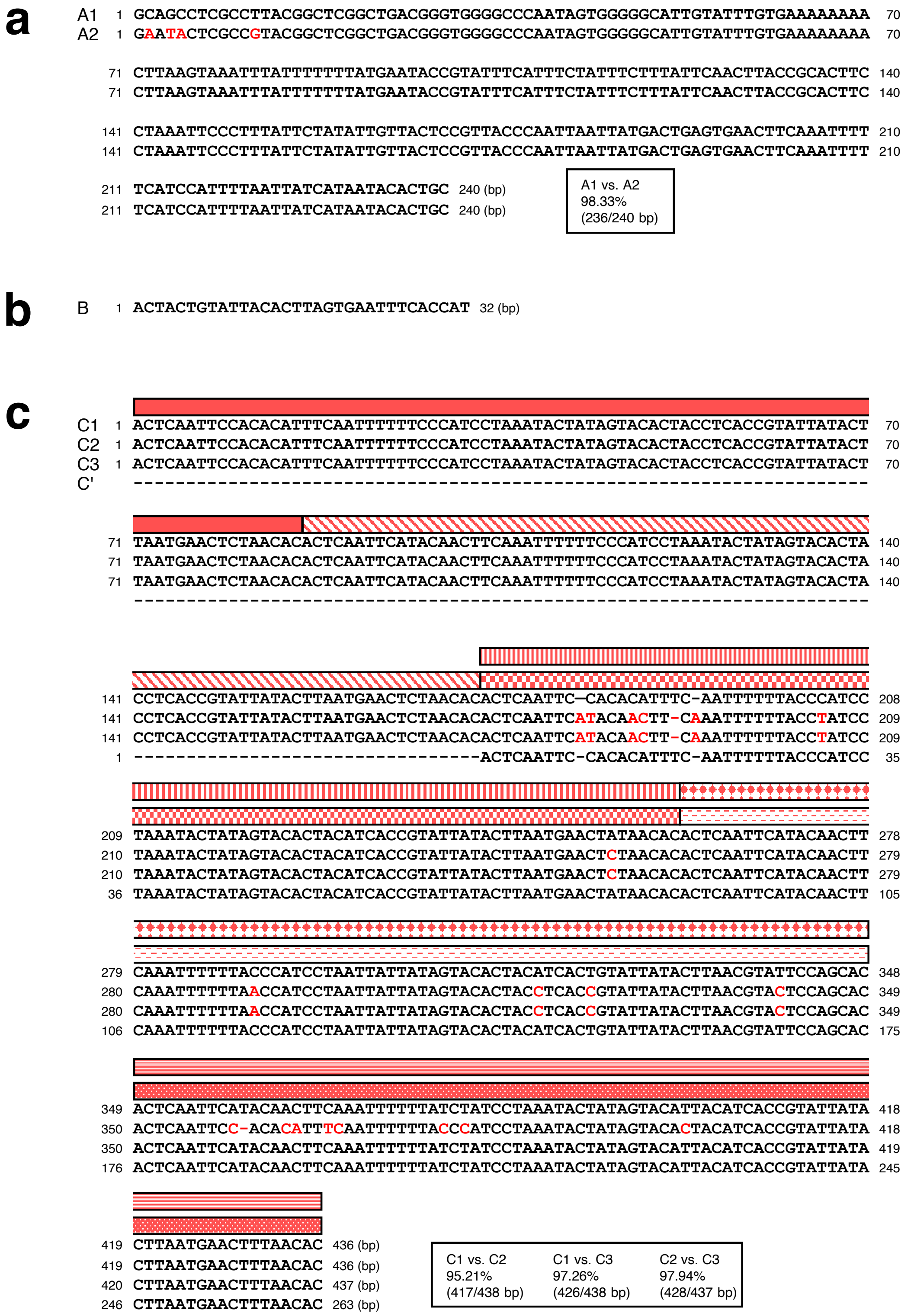
(c) Strain JP1225 (*h⁻ ade6-M216 leu1-32 ura4-D18 his7-366*) has a subtelomere including *SH-P* (homologous with pNSU71, see Fig. 3a), blocks I and II, and SAS at the left arm of Ch3[2].

(d) Detailed information for the Ch3 ends in the three strains. The sequence of SAS which has not been found in PomBase-*972*, is the same as that of box θ (see Fig. 6). Yellow box, common sequence (19 bp) between SAS and block III; blue arrow with a purple line, homologous region with the *tlh2* ORF defined in PomBase; pale purple line, predicted extension of the coding region of the *tlh2* gene as described in Fig. 8b; pink line, predicted in-frame extension of the coding region in the same reading frame; blue arrowhead, nucleotide deletion; dM (downstream M), the original first methionine codon of the *tlh2* ORF in PomBase-*972* or its corresponding first methionine codon in KYP33 and JP1225; uM (upstream M) and uM′, putative first methionine codons upstream of dM (also see the main text and Fig. 8b). Note that the 24 bp-deletions just downstream of dM codon in KYP33 and JP1225 do not cause frame shifts or premature nonsense mutation.


SH-P
SH-P-inserted plasmid
KpnI
XhoI
MCS
MCS
vector
Digestion with KpnI and XhoI
SH-P
vector
Serial deletion by ExoIII and MBN
SH-P
vector
SH-P
vector
SH-P
vector
SH-P
vector
Re-circularization by KF and DNA ligase
SH-P
Primer
Primer
vector
Cloning of each plasmid using E. coli
Sequencing of partially deleted SH-P with the two primers
Assembly of overlapping sequences

Supplementary Fig. 2 Sequencing of *SH-P* regions by the serial deletion method.

The *SH-P* region with various common segments (~5 kb) was amplified by PCR from a *972SD4* strain, and inserted into a vector. The resultant plasmid was digested with restriction enzymes, KpnI and XhoI, at the multi-cloning sites (MCSs) of the vector. The linearized plasmid was serially deleted from the 5′-overhang at XhoI site by treating with exonuclease III (ExoIII) and mung bean nuclease (MBN) for fixed times. After deletion of the *SH-P* DNA, both ends of the plasmid were blunted by klenow fragment (KF) and ligated by DNA ligase, and then re-circularized plasmids were cloned using *Escherichia coli* (*E. coli*). The partially deleted *SH-P* DNAs were sequenced using primers that anneal to MCSs of the vector. The sequence reads were assembled using overlapping sequences.



```
A1   1 GCAGCCTCGCCTTACGGCTCGGCTGACGGGTGGGGCCCAATAGTGGGGGCATTGTATTTGTGAAAAAAAA  70
A2   1 GAATACTCGCCGTACGGCTCGGCTGACGGGTGGGGCCCAATAGTGGGGGCATTGTATTTGTGAAAAAAAA  70

    71 CTTAAGTAAATTTATTTTTTTATGAATACCGTATTTCATTTCTATTTCTTTATTCAACTTACCGCACTTC 140
    71 CTTAAGTAAATTTATTTTTTTATGAATACCGTATTTCATTTCTATTTCTTTATTCAACTTACCGCACTTC 140

   141 CTAAATTCCCTTTATTCTATATTGTTACTCCGTTACCCAATTAATTATGACTGAGTGAACTTCAAATTTT 210
   141 CTAAATTCCCTTTATTCTATATTGTTACTCCGTTACCCAATTAATTATGACTGAGTGAACTTCAAATTTT 210

   211 TCATCCATTTTAATTATCATAATACACTGC 240 (bp)
   211 TCATCCATTTTAATTATCATAATACACTGC 240 (bp)
```

A1 vs. A2
98.33%
(236/240 bp)

```
B    1 ACTACTGTATTACACTTAGTGAATTTCACCAT 32 (bp)
```

```
C1   1 ACTCAATTCCACACATTTCAATTTTTTCCCATCCTAAATACTATAGTACACTACCTCACCGTATTATACT  70
C2   1 ACTCAATTCCACACATTTCAATTTTTTCCCATCCTAAATACTATAGTACACTACCTCACCGTATTATACT  70
C3   1 ACTCAATTCCACACATTTCAATTTTTTCCCATCCTAAATACTATAGTACACTACCTCACCGTATTATACT  70
C'     ----------------------------------------------------------------------

    71 TAATGAACTCTAACACACTCAATTCATACAACTTCAAATTTTTTCCCATCCTAAATACTATAGTACACTA 140
    71 TAATGAACTCTAACACACTCAATTCATACAACTTCAAATTTTTTCCCATCCTAAATACTATAGTACACTA 140
    71 TAATGAACTCTAACACACTCAATTCATACAACTTCAAATTTTTTCCCATCCTAAATACTATAGTACACTA 140
       ----------------------------------------------------------------------

   141 CCTCACCGTATTATACTTAATGAACTCTAACACACTCAATTC—CACACATTTC-AATTTTTTACCCATCC 208
   141 CCTCACCGTATTATACTTAATGAACTCTAACACACTCAATTCATACAACTT-CAAATTTTTTACCTATCC 209
   141 CCTCACCGTATTATACTTAATGAACTCTAACACACTCAATTCATACAACTT-CAAATTTTTTACCTATCC 209
     1 --------------------------------ACTCAATTC-CACACATTTC-AATTTTTTACCCATCC  35

   209 TAAATACTATAGTACACTACATCACCGTATTATACTTAATGAACTATAACACACTCAATTCATACAACTT 278
   210 TAAATACTATAGTACACTACATCACCGTATTATACTTAATGAACTCTAACACACTCAATTCATACAACTT 279
   210 TAAATACTATAGTACACTACATCACCGTATTATACTTAATGAACTCTAACACACTCAATTCATACAACTT 279
    36 TAAATACTATAGTACACTACATCACCGTATTATACTTAATGAACTATAACACACTCAATTCATACAACTT 105

   279 CAAATTTTTTACCCATCCTAATTATTATAGTACACTACATCACTGTATTATACTTAACGTATTCCAGCAC 348
   280 CAAATTTTTTAACCATCCTAATTATTATAGTACACTACCTCACCGTATTATACTTAACGTACTCCAGCAC 349
   280 CAAATTTTTTAACCATCCTAATTATTATAGTACACTACCTCACCGTATTATACTTAACGTACTCCAGCAC 349
   106 CAAATTTTTTACCCATCCTAATTATTATAGTACACTACATCACTGTATTATACTTAACGTATTCCAGCAC 175

   349 ACTCAATTCATACAACTTCAAATTTTTTATCTATCCTAAATACTATAGTACATTACATCACCGTATTATA 418
   350 ACTCAATTCC-ACACATTTCAATTTTTTACCCATCCTAAATACTATAGTACACTACATCACCGTATTATA 418
   350 ACTCAATTCATACAACTTCAAATTTTTTATCTATCCTAAATACTATAGTACATTACATCACCGTATTATA 419
   176 ACTCAATTCATACAACTTCAAATTTTTTATCTATCCTAAATACTATAGTACATTACATCACCGTATTATA 245

   419 CTTAATGAACTTTAACAC 436 (bp)
   419 CTTAATGAACTTTAACAC 436 (bp)
   420 CTTAATGAACTTTAACAC 437 (bp)
   246 CTTAATGAACTTTAACAC 263 (bp)
```

C1 vs. C2	C1 vs. C3	C2 vs. C3
95.21%	97.26%	97.94%
(417/438 bp)	(426/438 bp)	(428/437 bp)

c*

```
c1   1 ACTCAATTCC-ACACATTTCAA-TTTTTT-CCCATCCTAAATACTATAGTACACTACCTCACCGTATTAT  67
c2   1 ACTCAATTCATACAACTT-CAAATTTTTT-CCCATCCTAAATACTATAGTACACTACCTCACCGTATTAT  68
c3   1 ACTCAATTCC-ACACATTTCAA-TTTTTTACCCATCCTAAATACTATAGTACACTACATCACCGTATTAT  68
c4   1 ACTCAATTCATACAACTT-CAAATTTTTTACCCATCCTAATTATTATAGTACACTACATCACTGTATTAT  69
c5   1 ACTCAATTCATACAACTT-CAAATTTTTTATCTATCCTAAATACTATAGTACATTACATCACCGTATTAT  69
c6   1 ACTCAATTCATACAACTT-CAAATTTTTTACCTATCCTAAATACTATAGTACACTACATCACCGTATTAT  69
c7   1 ACTCAATTCATACAACTT-CAAATTTTTTAACCATCCTAATTATTATAGTACACTACCTCACCGTATTAT  69
c8   1 ACTCAATTCC-ACACATTTCAA-TTTTTTACCCATCCTAAATACTATAGTACACTACATCACCGTATTAT  68

    68 ACTTAATGAACTCTAACAC  86 (bp)
    69 ACTTAATGAACTCTAACAC  87 (bp)
    69 ACTTAATGAACTATAACAC  87 (bp)
    70 ACTTAACGTATTCCAGCAC  88 (bp)
    70 ACTTAATGAACTTTAACAC  88 (bp)
    70 ACTTAATGAACTCTAACAC  88 (bp)
    70 ACTTAACGTACTCCAGCAC  88 (bp)
    69 ACTTAATGAACTTTAACAC  87 (bp)
```

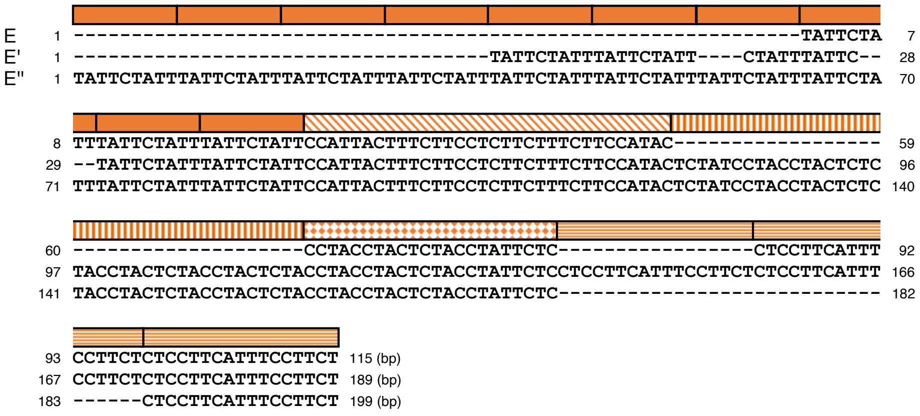
	c2		c3		c4		c5		c6		c7		c8	
	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)	Match /Total(bp)	Identity(%)
c1	82/88	93.18	84/87	96.55	73/89	82.02	77/89	86.52	80/89	89.89	75/89	84.27	84/87	96.55
c2			80/89	89.89	78/88	88.64	82/88	93.18	85/88	96.59	80/88	90.91	80/89	89.89
c3					74/89	83.15	79/89	88.76	81/89	91.01	74/89	83.15	86/87	98.85
c4							76/88	86.36	79/88	89.77	84/88	95.45	74/89	83.15
c5									85/88	96.59	77/88	87.50	80/89	89.89
c6											79/88	89.77	81/89	91.01
c7													74/89	83.15

d

```
D1   1 ACTCAGTTCAAATCAACTTCAAATTTTTCATCCGTTTTATTCACCCATGCACACTACACCACCGTATTAC  70
D2   1 ACTCAGTTCAAATCAACTTCAAATTTTTCATCCGTTTTATTCACCCATACACACTACACCACCTTATTAC  70
D3   1 ACTCAGTTCAAATCAACTTCAAATTTTTCATCCGTTTTATTCACCCATACACACTACACCACCTTATTAC  70

    71 AATTAGTGAATTCCAACATAGTCTAATTCCATGAACTTCAACTTTTTGTCCATCTTCACTATTGCACTAC 140
    71 AATTAGTGAATTCCAACATAGTCTAATTCCATGAACTTCAACTTTTTGTCCATCTTCACTATTGCACTAC 140
    71 AATTAGTGAATTCCAACATAGTCTAATTCCATGAACTTCAACTTTTTGTCCATCTTCACTATTGCACTAC 140

   141 CCTACATCCTCGTATTCTACTTAATCTACTCCAACACCTTTTAATCCATTCATCTTCTTTTCTTTTACTC 210
   141 CCTACATCCTCGTATTCTACTTAATCTACTCCAACACCTTTTAATCCATTCATCTTCTTTTCTTTTACTC 210
   141 CCTACATCCTCGTATTCTACTTAATCTACTCCAACACCTTTTAATCCATTCATCTTCTTTTCTTTTACTC 210

   211 TTTTATTTTATTTATTTTATT  231 (bp)
   211 TTTTATTTTATTTATTCTATT  231 (bp)
   211 TTTTATTTTATTTATTTTATT  231 (bp)
```

D1 vs. D2	D1 vs. D3	D2 vs. D3
98.70%	99.13%	99.57%
(228/231 bp)	(229/231 bp)	(230/231 bp)

e



```
E    1 ---------------------------------------------------------------TATTCTA   7
E'   1 ------------------------------------TATTCTATTTATTCTATT----CTATTTATTC--  28
E''  1 TATTCTATTTATTCTATTTATTCTATTTATTCTATTTATTCTATTTATTCTATTTATTCTATTTATTCTA  70

     8 TTTATTCTATTTATTCTATTCCATTACTTTCTTCCTCTTCTTTCTTCCATAC------------------  59
    29 --TATTCTATTTATTCTATTCCATTACTTTCTTCCTCTTCTTTCTTCCATACTCTATCCTACCTACTCTC  96
    71 TTTATTCTATTTATTCTATTCCATTACTTTCTTCCTCTTCTTTCTTCCATACTCTATCCTACCTACTCTC 140

    60 --------------------CCTACCTACTCTACCTATTCTC-----------------CTCCTTCATTT  92
    97 TACCTACTCTACCTACTCTACCTACCTACTCTACCTATTCTCCTCCTTCATTTCCTTCTCTCCTTCATTT 166
   141 TACCTACTCTACCTACTCTACCTACCTACTCTACCTATTCTC---------------------------- 182

    93 CCTTCTCTCCTTCATTTCCTTCT  115 (bp)
   167 CCTTCTCTCCTTCATTTCCTTCT  189 (bp)
   183 ------CTCCTTCATTTCCTTCT  199 (bp)
```

f

```
F1    1 CTCTCTCTAAAAACGTTTAACGAATACTCGCCTTACGGCTCGGCTGACGGGTGGGGG-CCAATAGTGGGG  69
F2    1 CTCTCTCTAAAAACGTTTAACGAATACTCGCCTTACGGCTCGGCTGACGGGTGGGGC-CCAATAGTGGGG  69
F3    1 CTCTCTCTAAAAACGTTTAACGAATACTCGCCTTACGGCTCGGCTGACGGGTGGGGGTCCAGTAGTGGGG  70

     70 GCATTTTATATATGTGAAAAAAACTTAAGTAAATTTAAATTTTTATAAATAACGCAACTTAATTATCTTT 139
     70 GCA--TTGTATATGTGAAAAAAACTTAAGTAAATTTAAATTTTTATAAATAACGCAGCTTAATTATCTTT 137
     71 GCA--TTGTATATGTGAAAAAAACTTAAGTAAATTTAAATTTTTATAAATAACGCAGCTTAATTATCTTT 138

    140 CTTTATCT  147 (bp)
    138 CTTTATCT  145 (bp)
    139 CTTTATCT  146 (bp)
```

F1 vs. F2	F1 vs. F3	F2 vs. F3
96.60%	95.95%	97.95%
(142/147 bp)	(142/148 bp)	(143/146 bp)

g

```
G     1 ATATTACCGTACGTTCTAATTGCTCCTTATTCTACATTGTTACTTTGTAACCCAATTAATTATGACTGAG  70
     71 TGAACTTCAAATTTTTCATCCATTACCATTACCATATTACGCTGCACTACAGTATTACACTTAGTGAATT 140
    141 TCAACAT  147 (bp)
```

h

```
H1    1 TCATTATCATACTACGCTGCACAACTGTAATCTACTTAATCTACTCCAATATAGTCCTCTGCTTTTATCT  70
H2    1 TCATTATCATACTACGCTGCACAACTATAATCTACTTAATGTACTCCAATATAGTCCTCTGCTTTTATCT  70

     71 TCTTTCCTCTTACTTTACTTATTTCTTTTACTCTCTTACTTTATTTATTTACTCTCCTTACTCTGTTTCT 140
     71 TCTTTCCTCTTACTTTACTTATTTCTTTTACTCTCTTACTTTATTTATTTACTCTCCTTACTCTGTTTCT 140

    141 TCTATTCTATTCATCTTACTTCTTCCTCATTTCTTCTCTCTTCTCTTCTATATCTTCTACTCTTTCATAC 210
    141 TCTATTCTATTCATCTTACTTCTTCCTCATTTCTTCTCTCTTCTCTTCTATATCTTCTACTCTTTCATAC 210

    211 CTCTCTTACCTCCATCCATTATCCATTCTCTCTCTCCAAAATCGTTTAAC  260 (bp)
    211 CTCTCTTACCTCCATCCATTATCCATTCTCTCTCTCCAAAATCGTTTAAC  260 (bp)
```

H1 vs. H2
99.23%
(258/260 bp)

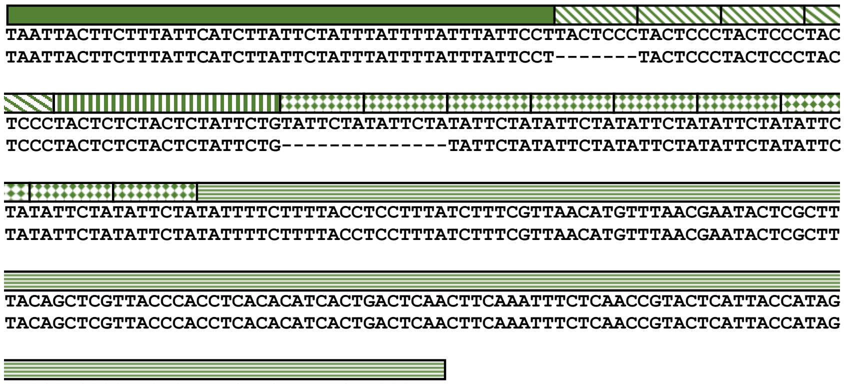
i

```
I     1 GCCCCTTTATTCTACTTACTGCACCCTAACGC  32 (bp)
```

j

```
J     1 ACTCAAGCCCACACATTTCAACTTTTTATTCACCATATCTCATTATATCTCCTAATCATACATAATGAAT  70
     71 CCTACCACGCTCAATTCAACCCAACTTCATTTTCTTCATTCATTTTCATTACCATAGTACGCTCCACAAC 140
    141 TGTAATCTACTTAATGTACTCCAACATACTCAACTTCCACACATTTCAAAATTTTTTTTACCCATTTTAT 210
    211 TTACCCCTATTATACTTACCGTACTCCAACACACTCAATACATACCAACTTCAAATTTTTTATGCATCTG 280
    281 ACTTTCCAATATACACTATGTATCCATCCTTATTTACTTTACTTTCTAATACTCTCTTACTT  342 (bp)
```

k



```
K     1 TAATTACTTCTTTATTCATCTTATTCTATTTATTTTATTTATTCCTTACTCCCTACTCCCTACTCCCTAC  70
K'    1 TAATTACTTCTTTATTCATCTTATTCTATTTATTTTATTTATTCCT-------TACTCCCTACTCCCTAC  63

     71 TCCCTACTCTCTACTCTATTCTGTATTCTATATTCTATATTCTATATTCTATATTCTATATTCTATATTC 140
     64 TCCCTACTCTCTACTCTATTCTG--------------TATTCTATATTCTATATTCTATATTCTATATTC 119

    141 TATATTCTATATTCTATATTTTCTTTTACCTCCTTTATCTTTCGTTAACATGTTTAACGAATACTCGCTT 210
    120 TATATTCTATATTCTATATTTTCTTTTACCTCCTTTATCTTTCGTTAACATGTTTAACGAATACTCGCTT 189

    211 TACAGCTCGTTACCCACCTCACACATCACTGACTCAACTTCAAATTTCTCAACCGTACTCATTACCATAG 280
    190 TACAGCTCGTTACCCACCTCACACATCACTGACTCAACTTCAAATTTCTCAACCGTACTCATTACCATAG 259

    281 TACGCTGCGCAACTGTAATCTACTTAATGAACCCTAA  317 (bp)
    260 TACGCTGCGCAACTGTAATCTACTTAATGAACCCTAA  296 (bp)
```

l

```
L1   1 CACACTCAATTCAAATCAACTTCAAATTTTTCATTCGTTTTATTCACCCATG 52 (bp)
L2   1 CACACTCAATTCAAATCAACTTCAAATTTTTCATCCGTTTTATTCACTCATG 52 (bp)
```

L1 vs. L2
96.15%
(50/52 bp)

m

```
M     1 TACACTATACTACCTTATTACCCTTAGTGAACCATAACACACTCACTTCAACCCAACTTCAAATTTTTCA  70
     71 TCCGTTTTATTCCACTCATGTACACTACACCACCTTATTCCTACACATTTTTATTCATTTTACTTTCTTA 140
    141 TTCTCCTACTCTTCTTATTCCATTATTTTCTTCCTCTTCTTTCTTCCATACTCTACTCTATCTGTTCTAC 210
    211 CTATTCTCCTCCTTCCTTCTCTCCTTTATTCTGCCCCTTCATTTTCTCCTTCATTTCCTTATACTTCTCT 280
    281 AACTACG 287 (bp)
```

n

```
N     1 TGATTACTTCTTCATTCTCCTACTTTATTTATTTTATTCATTTTATTTTATTTTATTTTATTTATTCGTT  70
     71 TTTAAATATTTAATTTACTCTCCTTACTTTATTTTTTTGATTTCTACTCTCTTCTATATATCCTACTCTT 140
    141 ATATTCTCTCCTTCATTTCCTTATTCCATATTGTTACTTCGTTATCCAGCTCACCATGACTGAGTCAACT 210
    211 TCAAATTTTTCATCCCCTTCAATTACCAAAGTCCACTACAATTCTCTATTTATATTCCTGCATCCCAACA 280
    281 CATTATTTCAACCACTTGTCTATCATAATTACTATAGTTCATTACTCATCCCTATTCTACTTAATGCACT 350
    351 CCAATATAGTCCCCTGCTTTTATCTTCTTTCCTCTTACTTTAATTGCTTCTTTATTCTCCTACCTTATTT 420
    421 ATTTTATTTATTTTATTTATTTTATTTTATTTTATTTATTTTATTTTACTCTCCTTACTCTATTTCTTCT 490
    491 ATATATTCTACTTATATATCCTGCTCCTTCATCCTACTCTCTTCTCTCTATATTTTACTCTTAAATTCTA 560
    561 TCTGTTACATTCTTGTCTTTCGTTAACAACA 591 (bp)
```

o

```
O1   1 TTTAACGATTACTCGCCTTACGGCTCGTTACTTGCTTCACACCTGACTAAGTGAACTTTGAATTTTTTTT  70
O2   1 TTTAACGATTACTCGCCTTACGTCTCGTTGCTCGCTTCACACCTGACTAAGTGAACTTTGAATTTTTTTT  70

    71 CCTTTATTAAAATGACCATCCTCAAAATTTCCCATCCTC 109 (bp)
    71 CCTTTATTAAAATGACCATCCTCAAAATTTCCCATCCTC 109 (bp)
```

O1 vs. O2
97.25%
(106/109 bp)

p

```
P1   1 CCCGACGACATATCACTCAACAAACGTTTTCAATAATTTTTTTTTCTTTTATCAATCATTTTATAATTTA  70
P2   1 CCCGACGACATATCACTCAACAAACTTTTTCAATAATTTTTTTTTCTTTTATTAATCATTTTATAATTTA  70
P3   1 CCCGACGACATATCACTCAACAAACTTTTTCAATAATTTTTTTTTCTTTTATTAATCATTTTATAATTTA  70
P4   1 CCCGACGACATATCACTCAACAAACGTTTTCAATAATTTTTTTTTCTTTTATCAATCATTTTATGATTTA  70

    71 TTTTCAATTTTCAACTGCCTGCTGTTTGTCGTTCATTGGCAAATAAATATTTTTCATTATTTTCTATCAT 140
    71 TTTTCAATTTTCAACTGCCTGCTGTTTGTCATTCATTGGCAAATAAATATTTTTCATTATTTTCTATCAT 140
    71 TTTTCAATTTTCAACTGCCTGCTGTTTGTCGTTCATTGGCAAATAAATATTTTTCATTATTTTCTATCAT 140
    71 TTTTCAATTTTCAACTGCCTGCTGTTTGTCGTTCATTGGCAAATAATTATTTTTCATTATTTTCTATCAT 140

   141 TATTTAATATTGTCTTTATTTGTGTTCCAATATTTGTATTTATATTTTTTATTTCATTTTATTTTG 206 (bp)
   141 TATTTAATATTGTCTTTATTTGTGTTCCAATATTTGTATTTATATTTTTTATTTCATTTTATTTTG 206 (bp)
   141 TATTTAATATTGTCTTTATTTGTGTTCCAATATTTGTATTTATATTTTTTATTTCATTTTATTTTG 206 (bp)
   141 TATTTAATATTGTCTTTATTTGTGTTCCAATATTTGTATTTATATTTTTTATTTCATTTTATTTTG 206 (bp)
```

	P2		P3		P4	
	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
P1	203/206	98.54	204/206	99.03	204/206	99.03
P2			205/206	99.51	201/206	97.57
P3					202/206	98.06

q

```
Q1    1 TTAATTTTATTTATTTCTGTATATTTATTCGTTTTTAAATATTTTATTTTATTTTATTTCATTTCATTTC  70
Q2    1 TTAATTTTATTTATTTCTATATATTTATTCGTTTTTAAATATTTTATTTTATTTTATTTCATTTCATTTC  70
Q3    1 TTAATTTTATTTATTTCTATATATTTATTCGTTTTTAAATATTTTATTTTATTTT-----ATTTCATTTC  65
Q4    1 TTAATTTTATTTATTTCTGTATATTTATTCGTTTTTAAATATTTTATTTTATTTTATTTTATTTCATTTC  70
Q5    1 TTAATTTTATTTATTTCTATATATTTATTCGTTTTTAAATATTTTATTTTATTTTATTTCATTTCATTTC  70

     71 ATTTTATTTTTTTATTTATTTTACACAATCATATTATTTGTTTAACATGACTAACATAAGCTCAATTTTC 140
     71 ATTTTATTTTTTTATTTATTTTACACAATCATATTATTTGTTTAACATGACTAACATAAGCTCAATTTTC 140
     66 ATTTTATTTTTTTATTTATTTTACGCAATCATATTATTTATTTAACATATCTAACATAAGCTCAATTTTC 135
     71 ATTTTATTTTTTTATTTATTTTACACAATCATATTATTTGTTTAACATGACTAACATAAGCTCAATTTTC 140
     71 ATTTTATTTTTTTATTTATTTTACGCAATCATATTATTTATTTAACATATCTAACATAAGCTCAATTTTC 140

    141 AAACACTTCATTTATCAAAGTACACCGCATGTTCCTATTATACTTACTGCACTCCAACATA 201 (bp)
    141 AAACACTTCATTTATCAAAGTACACCGCATGTTCCTATTATACTTACTGCACTCCAACATA 201 (bp)
    136 AAACACTTCATTTATCAAAGTACACCGCATGTTCCTATTATACTTACTGCACTCCAACATA 196 (bp)
    141 AAACACTTCATTTATCAAAGTACACCGCATGTTCCTATTATACTTACTGCACTCCAACATA 201 (bp)
    141 AAACACTTCATTTATCAAAGTACACCGCATGTTCCTATTATACTTACTGCACTCCAACATA 201 (bp)
```

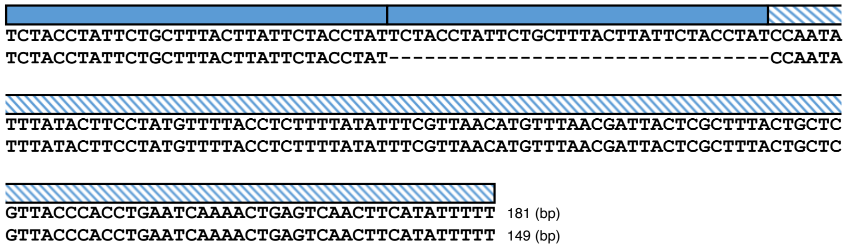
	Q2		Q3		Q4		Q5	
	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
Q1	200/201	99.50	191/201	95.02	200/201	99.50	196/201	97.51
Q2			192/201	95.52	199/201	99.00	197/201	98.01
Q3					191/201	95.02	196/201	97.51
Q4							195/201	97.01

r

```
R1    1 GTCCCCTTCATTGTATCTTCTTTTTTCTTACTTTACTTACTTCTTTGTTCTCCCATTTTTTATTATTATT  70
R2    1 GTCCCCTTCATTGTATCTTCTTTTTTCTTACTTTACTTACTTCTTTGTTCTCCCATTTTTTATTATTATT  70

     71 TCTTATTCCATTACTTTCTTCCTCTTCTTTCTTCCATATTCTAC 114 (bp)
     71 TCTTATTCCATTACTTTCTTCCTCTTCTTTCTTCCATACTCTAC 114 (bp)
```

R1 vs. R2
99.12%
(113/114 bp)

s



```
S     1 TCTACCTATTCTGCTTTACTTATTCTACCTATTCTACCTATTCTGCTTTACTTATTCTACCTATCCAATA  70
S'    1 TCTACCTATTCTGCTTTACTTATTCTACCTAT--------------------------------CCAATA  38

     71 TTTATACTTCCTATGTTTTACCTCTTTTATATTTCGTTAACATGTTTAACGATTACTCGCTTTACTGCTC 140
     39 TTTATACTTCCTATGTTTTACCTCTTTTATATTTCGTTAACATGTTTAACGATTACTCGCTTTACTGCTC 108

    141 GTTACCCACCTGAATCAAAACTGAGTCAACTTCATATTTTT 181 (bp)
    109 GTTACCCACCTGAATCAAAACTGAGTCAACTTCATATTTTT 149 (bp)
```

t

```
T     1 CATCCATCTTGATTATCATAATACACTGCGTATCTTTATTCAACTTACTGCATTACAACACAGCCTTATT  70
     71 CTATAAACTTCAAGTTTTCATTCATCTATCCTCATTCGCCATAT 114 (bp)
```

u

```
U1    1 TGCACTACATCCCCTTATTATACTTACTGCATCCCAACACACTCACTTCCACTCATTTCAGTGTTTTGTC  70
U2    1 CACACTACATCCCCTTATTATACTTACTGCATCCCAACACACTCACTTCCACTCATTTCAGTGTTTTGTC  70
U3    1 TGCACTACATCCCCTTATTATACTTACTGCATCCCAACACACTCACTTCCACTCATTTCAGTGTTTTATC  70

     71 CATCTTCACTACCACACTACACTACTCATTCTT 103 (bp)
     71 CATCTTCACTACCACACTACACTACTCATTCTT 103 (bp)
     71 CATCTTCACTACCACACTACACTACTCATTCTT 103 (bp)
```

U1 vs. U2	U1 vs. U3	U2 vs. U3
98.06%	99.03%	97.09%
(101/103 bp)	(102/103 bp)	(100/103 bp)

v

V 1 **TTAATTTTATTTCA** 14 (bp)

w

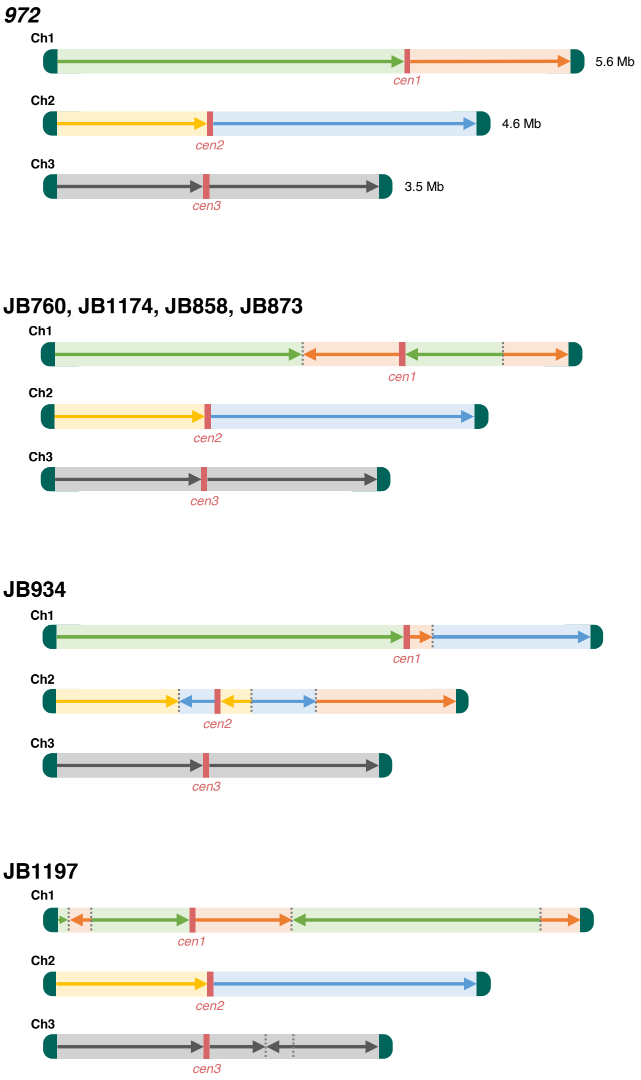
W 1 **TCTACTTATTCTACCTATACCTATTCTAC** 29 (bp)

x

X 1 **TAACCATCCTAATTATTATAGTACACTACTTGTCCCTATCACCTTTAACGTACTCCAG** 58 (bp)

Supplementary Fig. 3 Sequences of common segments in *SH-P* regions.

(a–x) Sequence alignments of variants and subtypes of segments A–X in Fig. 3. Nucleotide changes among variants are shown in red. Percentages of sequence identities among variants are indicated. Positions of common sequence motifs in segments C, E, K, and S are indicated by boxes according to Fig. 3b. Panel c* shows the sequence alignment of the common sequence motifs of segment C, c1–8. Nucleotide changes are indicated in red. The table below shows percentages of sequence identities between them.



Supplementary Fig. 4 Chromosome configurations of *972* and JB strains.

Schematic illustrations of chromosome structures in comparison with *972*. Arrows indicate sequence directions, left to right arms, in *972*. Note that positions of *subtel1R* and *subtel2R* in JB934 are swapped compared with those in *972* (also see Fig. 4e).

α

JB873-*SH1L* (216 bp)

TATTTACTCTCTTTATTCTATTTACTCTCTTTACTCTCTTCTCTGTATATCCTACTCTT
ATATTCTATCTGTTGCCTTCTTGTCTTTCGTTAACTACGTTTAGCGAATACTCGCCTT
ACGTCTCGTTAACTGCCCAATTCACACATCGCCGACTCAACTTTGAATTTTTCGCCC
ACCTTGTTTACCAAATTAACTATCCTCTACATTTTTCATCCT

β

JB873-*SH1L* (574 bp)

TGTTAATTTTATCTTTTTTTTTCTATTTATCTTTCTATATTTATTCGTTTTTAATTCTTT
TTTTTTTTTTTTTTTTATTTTATTCAACACTACCACATTATTTGTCCAACATGACTAAC
TCAACTTCATTCAAATCTTTCATCCATTCCATTGATCATACACTATTTATCCTTATTA
TACTTACTGACTTCTAACATAATACAACTAATTCAGCTTCAATCTTCAAATAATGAA
TCTTATTGATCGCCTTATTGTTACTTTATGTATTCTAACACACTTTACCCTCTCAACT
AATTATCTTCATTCAATTCCTCCTCCTCTTATTCTCTTCTTCATCTTACCTTCTACTTT
TTCATCTTCATCTTATTTTCTTCTTTTTCTTTCTTTACTCTCTTCTCTCTTCTCTCTTCT
CTTCTCTTCTATACCTACTCTACCTATATATTCTATATATTCTATCTCTCCTACCTCTT
CTACTATCATATCTTCATTCCACTTTATTCCCTTATCCTTCCTTAACAGCACTTAACG
AATACTTGCCCTACAGCTCGTTACTCTCTTCACACACGTCTCAGTC

γ

JB873-*SH1L* (242 bp)

TATTCTATTTTATTCTATTTATTTTATTCTATTTATTTTATTCTATTTATTTTATTCTAT
TTATTTTATTTACTCTCCTTACTCTATTCCTCATCTTCTTTTCTCTTTTACTTCAATATT
CCTCTTCATCCTACTCTGTTACTTTCTTATTCTATTTATTTACTTTATTTTTTTTTATTT
TTTTTACTTTATTATTTATTTCCGTACTCTCTTATTTTATTTACTCTATTCTATATTCT
ATA

δ

JB873-*SH1L* (68 bp)

CATTTTTTCGTCCACTTTATTCCCTCGTGTACACTACATATCTTTATTCACATTACTG
CGCTCCAACA

θ

JB760-contig 1 (1169 bp)

GGCAGTAGAAATGTGAAAACAACAAAATGAAGGGATAAATAATGTATCAACAAAT
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GAAATGACAGAAATGACAGCCATGTCAAAGAGCATCCAAGTATAAAAAGATTGAA
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CCCCTTTACATACTACCTTTGACCTAGTTTTCCTCGATTTTGTAGAAAGTGGTGCTAC
TTTGTGAATTTCATCCATATCGGTGCTTCTAGGGTAGGGTTTGACATTTGTCGAACG
CAATACGCAGTACTACAGAAAAATCCACTTCCCACCAAAGGGTTTTGCCTCACCCT
TCCTATTACTTTGAATACCAAAAGATAATCCATTTCTCTCTAAAATCTTTATGTATA
GCGAATTTGATAAAATTAAAATGATTTCTTTTCTTTTCTTTTCTTCTTTTTATTCAAC
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TTTTATATTTATTTAAACAATTTCATTGAATAAACAATTTTTTATTCATTTTAATTTA
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GAGATGGCATTGACATGGCATGGCATTGCATTGAAACGATGACTCTGGTCTGTTCT
CGTTCCATTTCATTCCCTCTCGTTACTCATCGTTGATTCTCATCGAAATACGTTCTCT
ATCCCTAACTCTCCCTATTCATAACTGAGATAGGACATGCCAAAACAACCGAGATA
GACTCGTTCTCTCTCGTTAAATTCCAATTCTTACGTCATTTCCCCATCTCACAAACCA
TCCAATCCTACCCATCTCCACCTCTA

ι

JB1174-*SH1L* (1840 bp)

AAAGTATTCCCATCCATTCCTCTCTATTTCCCTTTTATTTCATTCACTCACCGTATTT
CTCTCCAATCTCCCTTCACCCATCACTCACTCACCAACTTATCCAATCTCTCTTCACC
TAATCGCCTACTCTTCACCCACTCCTTTCCATTCACTTGATTCACTTGTTTTACCATT
CTTTTTTCACTTCCTCGTATTCAATTGATTTTCTTTAGCCATGTCGCTCCTTTTCATAA
ACTGTATGGTTTTGACTTTATAATTCAAACATTCTTGTAATTAGTATGGTGTTCATTT
GGTTAACGATTGAATGATAGTCATTTATACATTTCTTTCTTTTACAACAACAGCTAT

TATAATTTACTGTTTATTTCAACCAATTTATTTTTTTTTTAAAAATCTAACATATATG
AAACAAATTCCTTATTGTATTCACAACAAGCTTGCATTTTATTGCAAAATGTAAAGA
AATATTTTTATTTATTATTTATTATTTATTATTTATTATTTATTATTTATTATTTATTA
TTTATTATTTATTATTTATCTTATTTTTATTTTATTTTTTTTTTTTTTATCGATCTTAGT
GTACATGTCCCTTTTATAAAAAAAAAAAATAAAATAAAATAAAATTCTCTTCAAAA
AAAAAAAATATCATCAAACCACAACATATTGTCGAATACACTTTTTATAATATATTT
TCAATACTACGTGTAAAGTATTTTACCAACCATTTTTCGTTTTGTCTTAGTATTCAAT
TTAGTTCGTAATGTCGATTACCAAATTCCATCTTCTTTTGCCGTATTTTGTAACCACA
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ATAAACGGTGATACTTTCTATCAATTCCTTAATATGGAATATCATGCAAACAACATT
TGAAAAATGTTGCCACAAATAAACATCCTTCCATTAATTTACATCGTTAATTAGCAA
TTGCTTGAAGGTATTTTTTTTTTTTTGAAACTTTTGACAGCATTTGGTCAGTTGGGAT
GGATGGTAATTTGACAAGGCACATGTCTTATACGCAACGGAAAAACATTGCAAATG
TTGCAATTGTCCCGTTTAATCATCCACTGAGTGGGAAACCATTTTTTTCTTGTTTCTG
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GAACTTTCAAGTTACACCTTTTCCATTAACATGTTCGTTGATTGTGTGGGTGTCGAT
CATAAGAATGTTGAACGAACTGTCTAATGGGGTAACAAAACAAATTAAACAGTCTT
TCTCATGAACTTGAAAAACTTTGAACTTTTTTTAGTTGGTTCATAATTCTTGCACGCT
GTAGTACC

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JB1174-*SH1L* (1193 bp)

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CATAATATAATATCTCAATGCCACAATAGAAAGAGAAACGGGTAAAATCGAGCAA
TGGGCTTTTCAGCAAAAAAACTTGTTGCGCGTTTTATCGTAGTGACTAAAAATCATC

AATCTTCCCAAGTAAACAAACAATTGCCTTACCGAGTCTTTAGAGTTTTGAAATGTC
CAGTACGATTGTTCTTGAGACCTAGCTGGCTGTCCTGCCGATATTGTGATTAAAAGG
TATAGTAACTCATTGAATTGGGACGCGAGTTGTCTGTATTGATTCAAAGCTGGCAC
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TTGCTGAATATTGGCTTGAGTCACTGTGGGAAGGTACTTTGTCCGTAGTTCGCCATT
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TTTGTAATTTGGAAAACATTGATTGATATAGCCTTTTCAAATCATCAAGACTAAACT
TGTACAAACCATTCACATGATCGCTAACATGTGGGTATGCAGAGTTCACTGGTTTG
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TCGGTCATTGTCGATAAATTTACTTTTCCTTCTTTTATCAAATTTTGAAATTCGTAAA
TGCCACACAGTCTCAGTGAAAACAACAAACGAGAAATTAACGGTAATAATTCATAA
GCATATCGCGATCATCCATCTTCATAAATCGACGCACAAGCTAGAAATCTATTGCA
AGGCATATCCACAAGTTCTTCATTGTACTCATATCGTTTGAAAAAGGCCAGTTTAAG
AACATTGTGAACTTTTTCCAGTACCTTGTCATATTCCTTTAAAGTAAGTTGCGTACA
AACT

λ

JB1174-*SH1L* (1015 bp)

TCCTCTACATTCTCCCTTAGCACACTTCCTTCGTTTCCTTCCAAAGTGCGTAACAAA
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TTTGGTAAAAAATATCCATATTTCTTAGGTACTCCTGTAGGTTTTTTTTGTTGTATT
ATCCGTCCTGAATACTTTTTGCGACGACAAATGTGTGGGTAAAGTGTAGGGTAGGG
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TATTGTCATTTTATTGAACATGAAACATAATTTGAAAGCTACTCTAGTATTCATTTTT
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AACTCCATTTCATCTACTTTACCCCCAGATTCCGCATCATATCTACAACATGATCGT
AAAGCTTGAAATACCATTTACCTGTACTTTGGCAGTTATG

μ
JB1174-*SH1R* (551 bp)
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GCTATGTTAAAAAATATATATATATATATATATATATATATATGTAAACCTAAATACAA
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TGTCGGCTATTGCTTGTTTGTAATCCGTTATATTCCATGCATGTAGTACGAATGGTA
TCAAAGTCCCGCGTGACCAAGTAGTACATAGACGAGGAAACGCTCCGTACGCTCCA
TTATGCTCCTCATGATTAAGACAACAAAACAAACAAATATCTTGGTATGTAATGTC
ATGCGGGCAACACTTGTAAGAGTGTTGTTGAAAACAATAA

ν
JB1174-*SH1R* (573 bp)
AAGTTTTTTGTTTTAACAAAGTCGACCGAGTTTTTAAATCATCTTTGAATTGCCTCTT
TGATGGGATAAATGTATGTGGGCTTTTAGTGTTATTAGTGCTATTAGTGACAGCAGT
ACTACTACTATCAGTAGTAGAAGTGGCAATACTAGTACAACTAGTTGTATTTGTAA
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ACTGTTACCTCCATTTCCTTTGTCCGTATGAAAAGCTCCTTCCGCTGCCAGAACCTC
CTCTGCCTCACCATCCTCGTTGTTCTATATGATTGAGTGGCGAACACGGTAACAAAG
TCGATATTCAAAGTTGTAGAATTCAATTCGATTCCAAATTCACAAAGACTTGTGCAT
GGTAAACATCTTGAGCACTTGAGTGCATTTGGTAAAAGATCACACGATACAAACGT
ATTATTCATCCCTAATCCTATAAACGCTCGAGCACACTGTTCTTTGTCGTTTATAAA

TGATTGCATATCAGTATCAATATGCAGTTTTTTGCAAGTTTTGAAACTCCTTATACA
ACAAC

ξ

JB934-*SH2L* (1457 bp)

ATTCATAACAGACTTTGTCCCATTCGAACCACAATTGGCAAAGAATCTACCAACGT
ATTACTACTGCTTCCTCCATTGTTTTATTTATATAACTGGCTTTGTCATTAATAAACG
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TTGTCCAAGATTCGCTTCACTTCCTTTTTCGTCCTACAACATATAATAGCTCGATTGT
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GGTTTTGACGACAATTTGGTTGAAAGATTCGTATTCAGACTAGTTGTTGTTTGCATG
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AAATATTCAAAGCTGTTGACCTCGTATGACCAGCCTGTAAATCAAATGTAGAGTTC
CCTTCCTCCTGTTTTTCCAAATTGTATTCTTTAAAAAAATGAGCAATGTGTCTATAGT
TACGAAAACCTAAAGATTTCCTATAACAAACAATTGCCTTATCGAGTTTTTAGAGTT
TGAAATGTTCAGTATGATTGTTCTTGCGATGTTGCTGGCTG

o

JB1174-*SH2L* (4838 bp)

TCAATTTTCATTATCACATTTATTGAAATCAACTTATGAACAACTTGCTTTATGACA
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ATTACTCGATTTGTTGGTTTTCCATATTTTCATAGAAGGAGTTACAAGTTTTATACA
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TTGATTTACAAGCGCTTGATGTCAGAAATGTTGCGTTTATTCAGCTTATGCTTTAGG
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CGCAAACGAGGGCACTCACCAATGTAACTATGATACACACAGTATCTACAGCTTAA
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TGATCGAATATTTAATTCGCTTAGAATTTGGTTTAGACTACTATGCTTTATAAGCAA
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TTATATTATTTTAACAAAAGATAAGTGGTAAGAAATATTCATTCCTCGGATAAAAA
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AACGGAAATGCCAATTGAGATGGTAGATGGACCTAAATGAAGAGTGAATGTCCAA
CCCCACTTACGAACAGCATTTCGACTCCATTTGGGGTCAACAAGTACTAGGTACTTG
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TAACTATGAGCTGCACAATTATCAGTCCTTAAAAGGATTCATAATCTATGTCATTAG
TCCCATGCTTGCTCAGATCACCAAATCGTGTAAATTTCTGCTTGACAATGTAATTGT
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AATCAACAAGTGCTAATTTAAAATATAAATATAAATATAAATATAAATATAAATAT
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AGTGTAACTATTACATTACTATAATGTTGTAATAACGTAGCAAAAATGTTAAAATTT
AGAATTCGAAATATTTGAGCAAAATTATTTTGAACAAGACAAAAAAAAAAATCATAC
TAAACATAAGGCTTTTTTTACTGCCTATCTCTCTTATACGGTTTCCACACATAATCG
AATATTAATTTTAGGAATAAATTAAATG

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JB1174-*SH2L* (570 bp)
CGGTAGTTTTAACGTAGTGCAAGGTAAATGTGCATGTTGGACTTGATGTATTGGGG
TAATCTCAATATATGTATGTACCAATTGTTTTTTAAATCGTATGAACGTTTTACAAC
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CGA

ρ
JB934-*SH1R′* (6406 bp)
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TAACACCAAAAATATAGACACATTTTAAGTCGGTAAATACACGTTGCCAAATGATT
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CTTTTTAG

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JB858-*SH2L* (450 bp)
TGGGGGGAGCAGGTAGTTGTCGCTCATTAGAAGTATCGCAAGCCTCACTGTTTGCC
TCAACAATGTTTGCTTTATCCTTTATCTCATCCTGAATGAACTTGTCTGTTTCATAGA
CGACAAGATCATCGTCTTCATATCATCTGCTTAATTATTTTTCTTTATTATATAATTG
ATGGTTGGAAGTGAGTATCGACATTCCTTGAAATGTTCAACGATTCTTTGTACGTTA
ACAAAATGCTTACATACAAACAAGCAACTGACAGACACCCACTTTGTAAAAAATAT
CCGTATTTCTTATGTACTCTAATCCCTTCCAATAAAATCGGGTGAAAGCAGCAACAA
CGAGTGTAGAGTCGGCGGCTTGATGAATTTGAGCTCATACTGCACCGCTAGTTATT
GCCATCGAAAGTATTCGTTCACCAGACTTCGCCCATGCATACTATTCTTACG

τ

JB858-*SH2R* (1280 bp)

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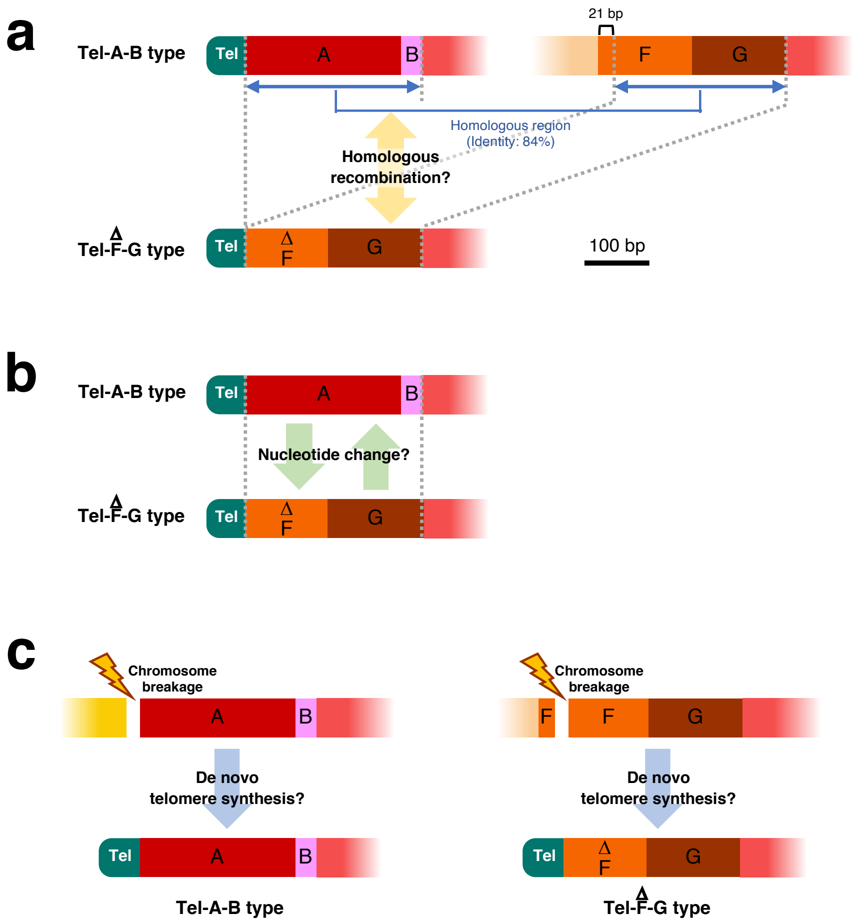
GCCTTTATATTTTTCTTTTTTGCATTAAACGAAAATTTATGGCATATGTTTTCGCTAC
CATTAACATTTTCTCTCTATGAAATTAAAAATAATGC

Supplementary Fig. 5 Homologous box sequences shared by the subtelomeres in JB strains (except for JB22) but not in *972*.

Representative sequences of black boxes (α–δ and θ–τ) are shown.



Supplementary Fig. 6 Hypothetical models for the two types of chromosome ends.

(a) Homologous recombination occurred between the homologous sequences, A-B and ΔF-G, in the same or different subtelomeres, which resulted in formation of the two types of chromosome ends, Tel-A-B and Tel-ΔF-G.

(b) Mutations were introduced into either A-B or ΔF-G sequences, which produced the two types of sequences at chromosome ends.

(c) G-rich sequences at the ends of segments A and ΔF induced chromosome breakage and *de novo* telomere synthesis.

a

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ΨSH1L-L          1 ATTGATTGCTTTAATTTCAAACATGTCCCCTTTAATAGTTGGGACTTTAATAATTATCCTATTGTCAGGA  70
ΨSH1L-R, ΨSH1R   1 ATTGATTGCTTTAATTTCAAACATGTCCCCTTTAATAGTTGGGACTTTAATAATTATCCTATTGTCAGGA  70
ΨSH2L, ΨSH2R     1 ATTGATTGCTTTAATTTCAAACATGTCCCCTTTAATAGTTGGGACTTTAATAATTATCCTATTGTCAGGA  70

                71 CTCGCAACTGCTTTTTATGTTACGTGGCAAGGCAGACTCATTTGTGCTGGTGTAGGGCTCATACTTGAAC 140
                71 CTCGCAACTGCTTTTTATGTTACGTGGCAAGGCAGACTCATTTGTGCTGGTGTAGGGCTCATACTTGAAC 140
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               281 GGACCTAGATTGGTTAACACATTAGGTGGT---------TCTTCGCCTACTACAAAACGG-GTAATCTAT 340

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               481 GGTGTACATATGACATTGAATGGAACAGATATGATTCATTATTATAATAAAACTTATGTAATTAATTATT 550 (bp)
               481 GGTGTACATATGACATTGAATGGAACAGATATGATTCATTATTATAATAAAACTTACGTAATTAATTATT 550 (bp)
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b

	ΨSH1L-R, ΨSH1R		*ΨSH2L, ΨSH2R*	
	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
ΨSH1L-L	546/560	97.50	545/560	97.32
ΨSH1L-R, ΨSH1R			549/550	99.82

c

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ΩSH1L-L               1 GTTGTAAGGATTACGAGATGCCAACATCATAATGCTTTTCCTAAATAAATGAGACACCTCAGAACGTAAA  70
ΩSH1L-R               1 GTTGTAAGGATTACGAGATGCCAACATCATAATGCTTTTCCTAAATAAATGAGACACCTCAGAACGTAAA  70
ΩSH1R                 1 GTTGTAAGGATTACGAGATGCCAACATCATAATGCTTTTCCTAAATAAATGAGACACCTCAGAACGTAAA  70
ΩSH2L-L, ΩSH2R-L      1 GTTGTAAGGATTACGAGATGCCAACATCATAATGCTTTTCCTAAATAAATGAGACACCTCAGAACGTAAA  70
ΩSH2L-R, ΩSH2R-R      1 GTTGTAAGGATTACGAGATGCCAACATCATAATGCTTTTCCTAAATAAATGAGACACCTCAGAACGTAAA  70

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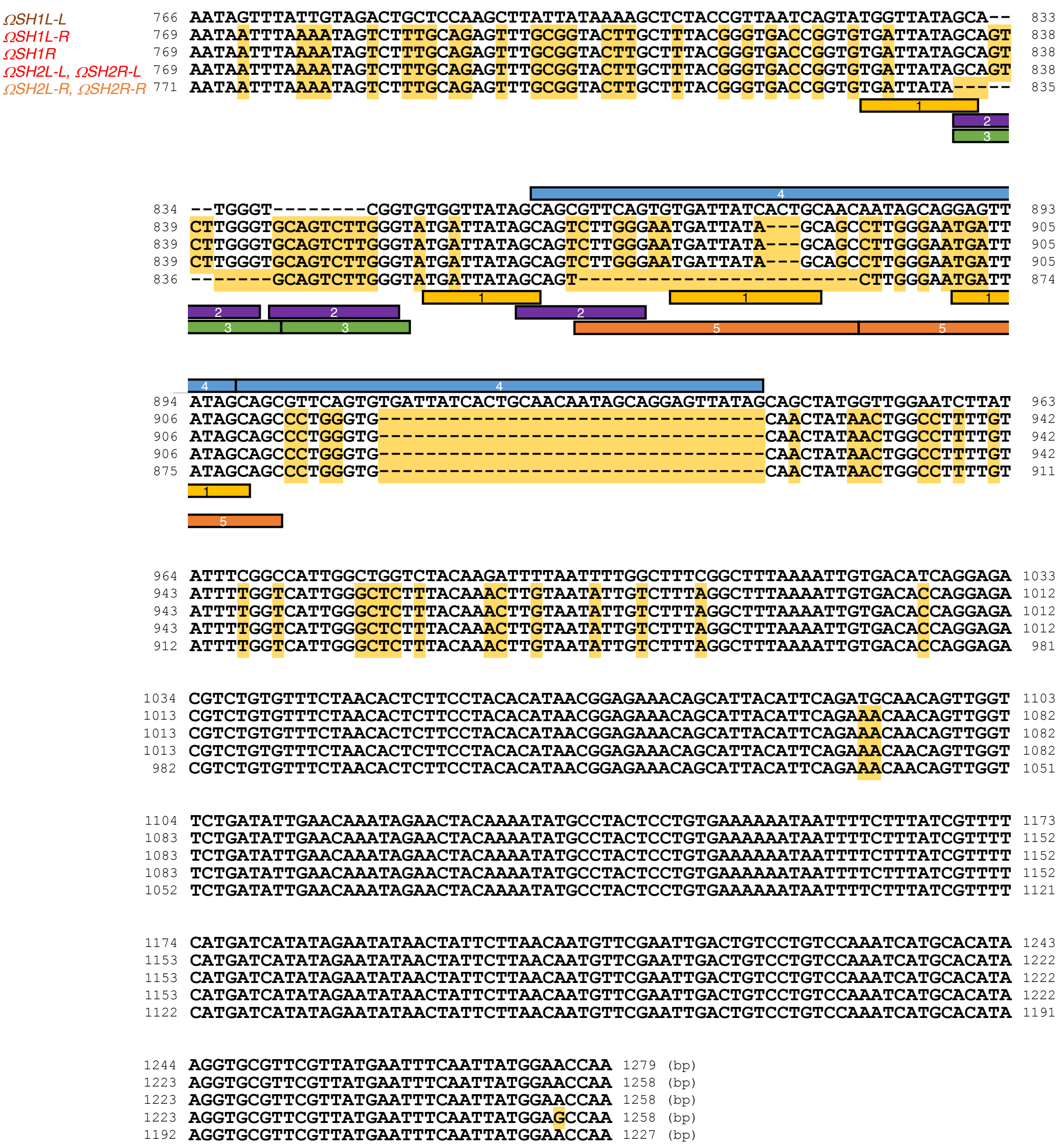

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ΩSH1R                  769 AATAATTTAAAATAGTCTTTGCAGAGTTTGCGGTACTTGCTTTACGGGTGACCGGTGTGATTATAGCAGT   838
ΩSH2L-L, ΩSH2R-L       769 AATAATTTAAAATAGTCTTTGCAGAGTTTGCGGTACTTGCTTTACGGGTGACCGGTGTGATTATAGCAGT   838
ΩSH2L-R, ΩSH2R-R       771 AATAATTTAAAATAGTCTTTGCAGAGTTTGCGGTACTTGCTTTACGGGTGACCGGTGTGATTATA-----   835

                       834 --TGGGT--------CGGTGTGGTTATAGCAGCGTTCAGTGTGATTATCACTGCAACAATAGCAGGAGTT   893
                       839 CTTGGGTGCAGTCTTGGGTATGATTATAGCAGTCTTGGGAATGATTATA---GCAGCCTTGGGAATGATT   905
                       839 CTTGGGTGCAGTCTTGGGTATGATTATAGCAGTCTTGGGAATGATTATA---GCAGCCTTGGGAATGATT   905
                       839 CTTGGGTGCAGTCTTGGGTATGATTATAGCAGTCTTGGGAATGATTATA---GCAGCCTTGGGAATGATT   905
                       836 -------GCAGTCTTGGGTATGATTATAGCAGT------------------------CTTGGGAATGATT   874

                       894 ATAGCAGCGTTCAGTGTGATTATCACTGCAACAATAGCAGGAGTTATAGCAGCTATGGTTGGAATCTTAT   963
                       906 ATAGCAGCCCTGGGTG---------------------------------CAACTATAACTGGCCTTTTGT   942
                       906 ATAGCAGCCCTGGGTG---------------------------------CAACTATAACTGGCCTTTTGT   942
                       906 ATAGCAGCCCTGGGTG---------------------------------CAACTATAACTGGCCTTTTGT   942
                       875 ATAGCAGCCCTGGGTG---------------------------------CAACTATAACTGGCCTTTTGT   911

                       964 ATTTCGGCCATTGGCTGGTCTACAAGATTTTAATTTTGGCTTTCGGCTTTAAAATTGTGACATCAGGAGA 1033
                       943 ATTTTGGTCATTGGGCTCTTTACAAACTTGTAATATTGTCTTTAGGCTTTAAAATTGTGACACCAGGAGA 1012
                       943 ATTTTGGTCATTGGGCTCTTTACAAACTTGTAATATTGTCTTTAGGCTTTAAAATTGTGACACCAGGAGA 1012
                       943 ATTTTGGTCATTGGGCTCTTTACAAACTTGTAATATTGTCTTTAGGCTTTAAAATTGTGACACCAGGAGA 1012
                       912 ATTTTGGTCATTGGGCTCTTTACAAACTTGTAATATTGTCTTTAGGCTTTAAAATTGTGACACCAGGAGA  981

                      1034 CGTCTGTGTTTCTAACACTCTTCCTACACATAACGGAGAAACAGCATTACATTCAGATGCAACAGTTGGT 1103
                      1013 CGTCTGTGTTTCTAACACTCTTCCTACACATAACGGAGAAACAGCATTACATTCAGAAACAACAGTTGGT 1082
                      1013 CGTCTGTGTTTCTAACACTCTTCCTACACATAACGGAGAAACAGCATTACATTCAGAAACAACAGTTGGT 1082
                      1013 CGTCTGTGTTTCTAACACTCTTCCTACACATAACGGAGAAACAGCATTACATTCAGAAACAACAGTTGGT 1082
                       982 CGTCTGTGTTTCTAACACTCTTCCTACACATAACGGAGAAACAGCATTACATTCAGAAACAACAGTTGGT 1051

                      1104 TCTGATATTGAACAAATAGAACTACAAAATATGCCTACTCCTGTGAAAAAATAATTTTCTTTATCGTTTT 1173
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                      1174 CATGATCATATAGAATATAACTATTCTTAACAATGTTCGAATTGACTGTCCTGTCCAAATCATGCACATA 1243
                      1153 CATGATCATATAGAATATAACTATTCTTAACAATGTTCGAATTGACTGTCCTGTCCAAATCATGCACATA 1222
                      1153 CATGATCATATAGAATATAACTATTCTTAACAATGTTCGAATTGACTGTCCTGTCCAAATCATGCACATA 1222
                      1153 CATGATCATATAGAATATAACTATTCTTAACAATGTTCGAATTGACTGTCCTGTCCAAATCATGCACATA 1222
                      1122 CATGATCATATAGAATATAACTATTCTTAACAATGTTCGAATTGACTGTCCTGTCCAAATCATGCACATA 1191

                      1244 AGGTGCGTTCGTTATGAATTTCAATTATGGAACCAA 1279 (bp)
                      1223 AGGTGCGTTCGTTATGAATTTCAATTATGGAACCAA 1258 (bp)
                      1223 AGGTGCGTTCGTTATGAATTTCAATTATGGAACCAA 1258 (bp)
                      1223 AGGTGCGTTCGTTATGGAGCCAA 1258 (bp)
                      1192 AGGTGCGTTCGTTATGAATTTCAATTATGGAACCAA 1227 (bp)
```

d

	ΩSH1L-R		*ΩSH1R*		*ΩSH2L-L, ΩSH2R-L*		*ΩSH2L-R, ΩSH2R-R*	
	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
ΩSH1L-L	1099/1294	84.93	1097/1294	84.78	1098/1294	84.85	1077/1292	83.36
ΩSH1L-R			1256/1258	99.84	1255/1258	99.76	1225/1260	97.22
ΩSH1R					1253/1258	99.60	1223/1260	97.06
ΩSH2L-L, ΩSH2R-L							1222/1260	96.98

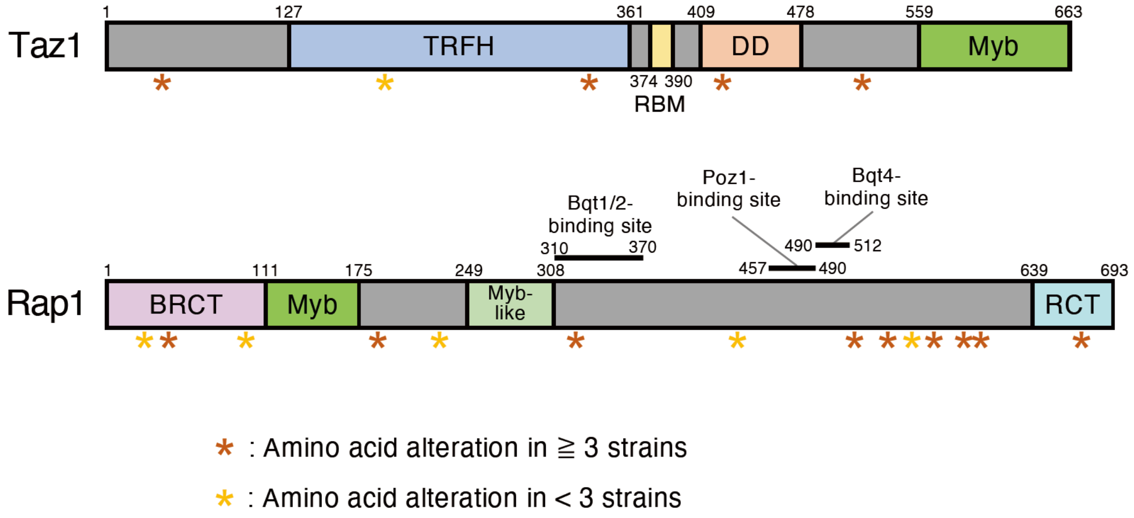
Supplementary Fig. 7 Homologous sequences at the ends of changes in *SH-D* regions.

(a) Homologous *Ψ* sequences located at the ends of the 3.7 kb-change (purple and pink boxes in Fig. 5a–b). *ΨSH1L-L* (purple) and *ΨSH1L-R* (pink) are *Ψ* sequences on the left side and the right side of the 3.7 kb-insertion in *SH1L* in Fig. 5a–b, respectively; *ΨSH1R*, *ΨSH2L*, and *ΨSH2R* (pink) are *Ψ* sequences in *SH1R*, *SH2L*, and *SH2R*, respectively. Differences in sequences between *ΨSH1L-L* and the others are highlighted in yellow. Note that sequences of the pairs, *ΨSH1L-R* and *ΨSH1R*, and *ΨSH2L* and *ΨSH2R* are 100% identical.

(b) Sequence identities between *Ψ* sequences in (a).

(c) Homologous *Ω* sequences at the ends of the 7.1 kb-change (brown, red, and orange boxes in Fig. 5a–b). *ΩSH1L-L* (brown) and *ΩSH1L-R* (red) are sequences on the left side and the right side of the 7.1 kb-insertion, respectively, in *SH1L* in Fig. 5a–b; *ΩSH1R* (red), that in *SH1R*; *ΩSH2L-L* (red) and *ΩSH2L-R* (orange) are on the left side and the right side of the insertion in *SH2L*, respectively; *ΩSH2R-L* (red) and *ΩSH2R-R* (orange) are on the left side and the right side of the insertion in *SH2R*, respectively. Note that the region containing multiple repeat units (boxes 1–5) shows high sequence variation. Differences in sequences between *ΩSH1L-L* and the others are highlighted in yellow. Note that sequences of the pairs, *ΩSH2L-L* and *ΩSH2R-L*, and *ΩSH2L-R* and *ΩSH2R-R* are 100% identical.

(d) Sequence identities between *Ω* sequences in (c).



Supplementary Fig. 8 Variation of amino acid sequences of Taz1 and Rap1 in JB strains.

Amino acid alterations of Taz1 and Rap1 in JB strains compared with those in PomBase-*972*. Orange asterisk, amino acid alteration found in no less than three JB strains; yellow asterisk, that in less than three JB strains. TRFH, TRF-homology domain, RBM, Rap1-binding motif; DD, dimerization domain; Myb, Myb domain[3,4]. BRCT, BRCA1 C-terminal domain; Myb, Myb domain; Myb-like, Myb-like domain; RCT, Rap1 C-terminal domain; black bars, regions for interactions with Bqt1/2, Poz1 or Bqt4 proteins[3,5-8].

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                     4525719                                                                4525788
PomBase-tlh2         TATTCGTGATGAGAATCAACGTTGCAATTTTGTTTGTAGAAAATTGCCCTTCGAAAATTCGAAAATTTGG
tlh1 (972SD4[1L+])   TATTCGTGATGAGAATCAACGTTGCAATTTTGTTTGTAGAAAATTGCCCTTCGAAAATTCGAAAATTTGG
tlh3 (972SD4[1R+])   TATTCGTGATGAGAATCAACGTTGCAATTTTGTTTGTAGAAAATTGCCCTTCGAAAATTCGAAAATTTGG
tlh4 (972SD4[2L+])   TATTCGTGATGAGAATCAACGTTGCAATTTTGTTTGTAGAAAATTGCCCTTCGAAAATTCGAAAATTTGG
tlh2 (972SD4[2R+])   TATTCGTGATGAGAATCAACGTTGCAATTTTGTTTGTAGAAAATTGCCCTTCGAAAATTCGAAAATTTGG

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                     ATTATATTCATTCTTCATTTTCTCTCTTGGCCATTATTTTTTTTTTTTTTTT--AATACCTCTGTGTCTC
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4529816                                                               4529885
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4530096                                                                4530165
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4531006                                                                4531075
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4531216                                                                4531285
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   GCAAATGGGAAGACACGAATCATGATCGCTACCAAGGCATTCGGACTCGGTATCAACTATATGGGAGTGC

4531356                                                              4531425
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4531426                                                              4531495
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4531496                                                              4531565
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   GATTCGATGAAAAACTTTCTTAATGATAATACGATGTGTGTTCGATCGTTTCTCGCAAGTGAAATGGATG
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4531636                                                              4531705
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   TGAAGAATCAACTGTGTCTACGATGTATGGAGTGAAACCGACATTGCCAGAAACACCGAAACCAGCCATT
   TGAAGAATCAACTGTGTCTACGATGTATGGAGTGAAACCGACATTGCCAGAAACACCGAAACCAGCCATT

4531706                                                              4531775
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   GCAACACATTCGCGTTATAATGCATCGTTTTCGTCTTCCCCCCACCACAGCCAGGGAATAGCAGTGGTA
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   GCAACACATTCGCGTTATAATGCATCGTTTTCGTCTTCCCCCTACCACAGCCAGGGAGTAGCAGTGGTA

4531776                                                              4531845
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   TGAGTGCTATGAACACTAACACTACTAGTACTACGCCAGTGTCTTTGTCGGAATTATCGGAAATCACTTT
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4531916                                                              4531985
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    AACAGGGCGTCAACCATGACATGAATCGTGTTCATGGTAGTGTTGGAGGTATGAGTGGTATTGTTGGTAT

4532056                                                             4532119
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    TGGTATTGGTATTGGTGATGGTGATGGTGATGG------TGATGTTGATTCTCGTACCATTCATTTCGCC
    TGGTATTGGTATTGGTGATGGTGATGGTGATGGTGATGGTGATGTTGATTCTCGTACCATTCATTTCGCC
    TGGTATTGGTATTGGTGATGGTGATGGTGATGT------TGATGTTGATTCTCGTACCATTCATTTCGCC
    TGGTATTGGTATTGGTGATGGTGATGGTGATGT------TGATGTTGATTCTCGTACCATTCATTTCGCC

4532120                                                             4532189
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    GAGTATAAAAGTCGTGTGCAAGCCGTCAAAAAACAATGGGTAGACTCAACTGACATTTCAGCACAACTCG
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4532190                                                             4532259
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    AGCGATTCTTTCGAGTGTATAAAGATGAATGTCTAAGTTGCACTCTTGGTAACCCAGACACAGAAATTCG
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4532260                                                             4532329
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4532330                                                             4532399
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4532400                                                             4532469
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4532470                                                             4532539
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    AGTTTACTATGCTTGGAACAATGTACAATACCGAAGGACTATTGCAGATAAATTCTTACAAGGTGATGTA

4532540                                                             4532609
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4532610                                                             4532679
                                     T
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    ATTACTTGTTGTCTGATGTTTTGCAAATCATGTAATTTTTTACTGATGCAAGACAACGTTTCATATCGTG
    ATTACTTGTTGTCTGATGTTTTGCAAATCATGTAATTTTTTACTGATGCAAGACAACGTTTCATATCGTG
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4532750                                                                 4532819
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4532820                                                                 4532889
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4532890                                                                 4532959
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4532960                                                                 4533029
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   AATCAACTATTTACAAAGACAAGTTTTTATAACTTTTCGAAAATCAAAAGTATTCAAAATTTTGTTTGCT
   AATCAACTATTTACAAAGACAAGTTTTTATAACTTTTCGAAAATCAAAAGTATTCAAAATTTTGTTTGCT
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4533030                                                                 4533099
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4533100                                      4533144
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   CTTGTATGTTGTTTTCATATCGGAACATTCATGAAGGAGAAGGCA
```
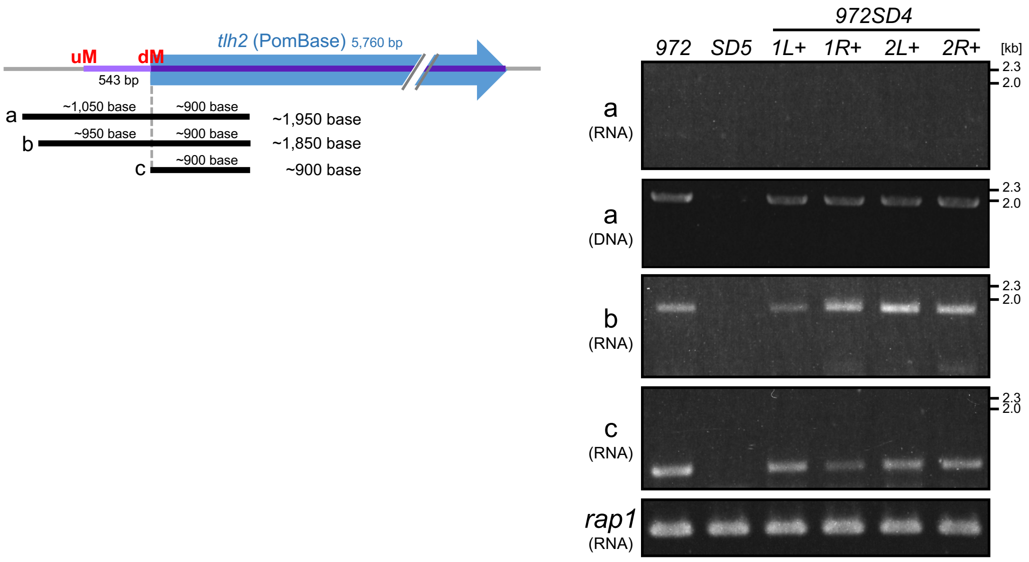
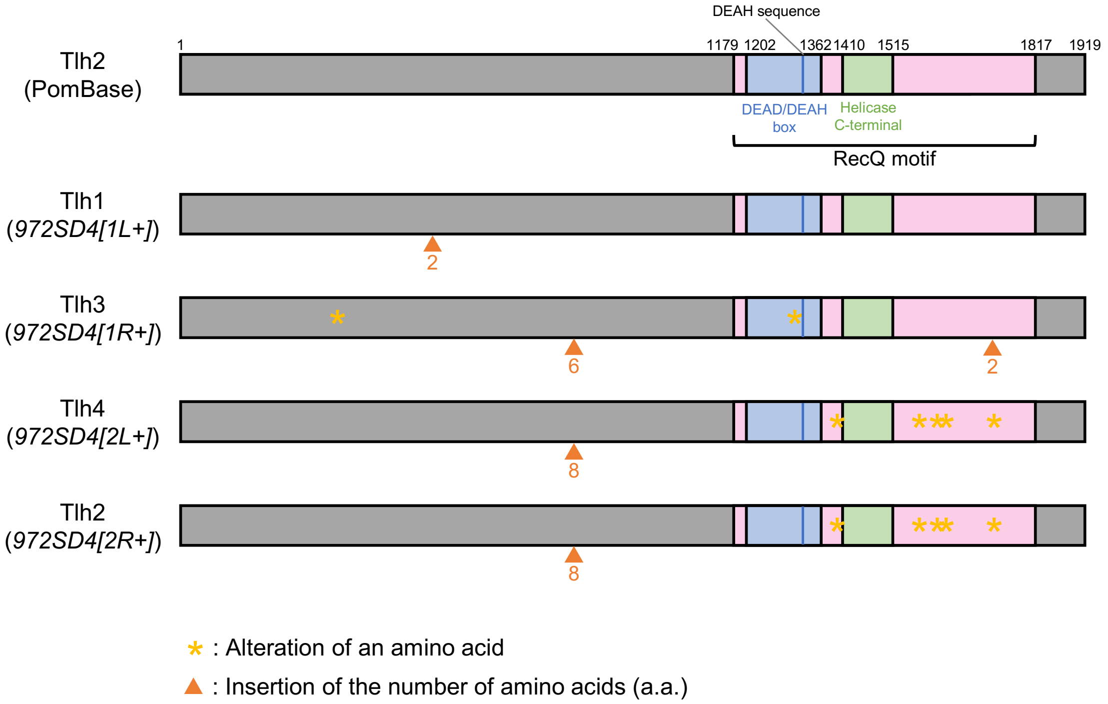

Supplementary Fig. 9 Sequence alignment of the *tlh1–4* genes in *972SD4* with the PomBase-*tlh2* gene.

These sequences cover the same region as shown in Fig. 8b. Differences in sequences between PomBase-*tlh2* and the others are highlighted in yellow. Putative first Met codons, uM, uM′, dM, and dM′, and termination codons, T, are indicated in red and blue, respectively (also see Fig. 8b).



Supplementary Fig. 10 RNA expression from the upstream region of the *tlh* genes.

Expression of RNA from various regions (a–c) of the *tlh* loci and the *rap1* locus (control) was analyzed by RT-PCR in strains *972*, *SD5*, and *972SD4*. The PCR products were analyzed by gel electrophoresis. Genomic DNA of region (a) was also analyzed as a control of PCR (the second row). Note that primers used in PCRs for the a–c regions recognize all of the *tlh1–4* genes. These data were reproduced twice.



Supplementary Fig. 11 Variation of amino acid sequences among Tlh1–4 in *972SD4*.

Comparison of amino acid sequences of Tlh1–4 proteins in *972SD4* with that of Tlh2 in PomBase. Yellow asterisk, alteration of an amino acid; orange triangle, insertion of the number of amino acids. Conserved domains in RecQ-type helicases are indicated[9].

Supplementary Table 1 Definitions of homologous block and box sequences in *SH-D* regions.

Length and position of each sequence corresponding to PomBase are shown.

		Position in PomBase	
Block or box	Length (bp)	Ch	bp
I	4,629	2	4,532,900 – 4,537,528
II (*tlh*)	6,015	2	4,526,885 – 4,532,899
III	6,471	2	4,520,414 – 4,526,884
ΨSH1L-L	560	1	12,136 – 12,695
IV	3,137	1	12,696 – 15,832
ΨSH2R	550	2	4,519,864 – 4,520,413
V	5,027	2	4,514,837 – 4,519,863
ΩSH1L-L	1,279	1	21,352 – 22,630
ΩSH2R-L	1,258	2	4,513,579 – 4,514,836
VI	5,868	2	4,507,711 – 4,513,578
ΩSH2R-R	1,227	2	4,506,484 – 4,507,710
VII	6,173	2	4,500,311 – 4,506,483
VIII	1,872	2	4,498,439 – 4,500,310
IX	1,347	2	4,497,092 – 4,498,438
X	4,962	2	4,492,130 – 4,497,091
XI	8,659	1	40,622 – 49,280
ε	11,504	1	49,281 – 60,784
ζ	12,489	1	5,545,205 – 5,557,693
η	507	2	29,493 – 29,999

Supplementary Table 2 Identities between genome sequences of *S. pombe* strains and those in PomBase.

				vs. PomBase					
		Positions in PomBase		*972SD4[2R+] #1*		*972SD4[2R+] #2*		JB22 (*972*)	
	Locus	Ch	bp	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
Subtelomere	*tlh2*	2	4,525,719 – 4,533,144	7,410/7,452	99.44	7,408/7,452	99.41	▨	▨
	SH-D		4,521,826 – 4,524,375	2,549/2,550	99.96	2,549/2,550	99.96	▨	▨
			4,510,792 – 4,512,641	1,850/1,850	100.00	1,850/1,850	100.00	▨	▨
			4,504,812 – 4,506,754	1,943/1,943	100.00	1,943/1,943	100.00	▨	▨
	SU		4,489,185 – 4,490,293	1,109/1,109	100.00	1,109/1,109	100.00	1,109/1,109	100.00
			4,484,916 – 4,486,915	2,000/2,000	100.00	2,000/2,000	100.00	2,000/2,000	100.00
			4,469,756 – 4,472,805	3,050/3,050	100.00	3,050/3,050	100.00	3,050/3,050	100.00
			4,454,962 – 4,458,161	3,200/3,200	100.00	3,200/3,200	100.00	3,200/3,200	100.00
	Boundary		4,439,149 – 4,443,731	4,583/4,583	100.00	4,583/4,583	100.00	4,583/4,583	100.00
	SA		4,431,856 – 4,435,505	3,650/3,650	100.00	3,650/3,650	100.00	3,650/3,650	100.00
Shelterin complex	*rap1*	2	3,098,366 – 3,100,576	2,211/2,211	100.00	2,211/2,211	100.00	2,211/2,211	100.00
	taz1	1	3,091,237 – 3,093,228	1,992/1,992	100.00	1,992/1,992	100.00	1,992/1,992	100.00
	pot1	1	4,129,529 – 4,131,314	1,786/1,786	100.00	1,786/1,786	100.00	1,786/1,786	100.00
Non-essential genes	*gcn5*	1	4,974,116 – 4,975,480	1,365/1,365	100.00	1,365/1,365	100.00	1,365/1,365	100.00
	clr4	2	456,575 – 458,047	1,473/1,473	100.00	1,473/1,473	100.00	1,473/1,473	100.00
	sty1	1	206,864 – 207,913	1,050/1,050	100.00	1,050/1,050	100.00	1,050/1,050	100.00
	zfs1	2	3,483,454 – 3,484,668	1,215/1,215	100.00	1,215/1,215	100.00	1,215/1,215	100.00
Essential genes	*cdc13*	2	421,123 – 422,571	1,449/1,449	100.00	1,449/1,449	100.00	1,449/1,449	100.00
	act1	2	1,476,149 – 1,477,276	1,128/1,128	100.00	1,128/1,128	100.00	1,128/1,128	100.00

				vs. PomBase					
		Positions in PomBase		JB760		JB1174		JB934	
	Locus	Ch	bp	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
Subtelomere	*tlh2*	2	4,525,719 – 4,533,144	▨	▨	▨	▨	▨	▨
	SH-D		4,521,826 – 4,524,375	▨	▨	▨	▨	▨	▨
			4,510,792 – 4,512,641	▨	▨	▨	▨	▨	▨
			4,504,812 – 4,506,754	▨	▨	▨	▨	▨	▨
	SU		4,489,185 – 4,490,293	1,109/1,109	100.00	1,109/1,109	100.00	Homologous sequences were not found	
			4,484,916 – 4,486,915	2,000/2,000	100.00	2,000/2,000	100.00		
			4,469,756 – 4,472,805	3,050/3,050	100.00	3,049/3,050	99.97	3,024/3,058	98.89
			4,454,962 – 4,458,161	3,200/3,200	100.00	3,200/3,200	100.00	3,154/3,209	98.29
	Boundary		4,439,149 – 4,443,731	4,583/4,583	100.00	4,582/4,583	99.98	4,533/4,599	98.56
	SA		4,431,856 – 4,435,505	3,650/3,650	100.00	3,650/3,650	100.00	3,630/3,655	99.32
Shelterin complex	*rap1*	2	3,098,366 – 3,100,576	2,209/2,212	99.86	2,209/2,212	99.86	2,191/2,211	99.10
	taz1	1	3,091,237 – 3,093,228	1,991/1,992	99.95	1,992/1,992	100.00	1,991/1,992	99.95
	pot1	1	4,129,529 – 4,131,314	1,785/1,786	99.94	1,786/1,786	100.00	1,786/1,786	100.00
Non-essential genes	*gcn5*	1	4,974,116 – 4,975,480	1,365/1,365	100.00	1,365/1,365	100.00	1,365/1,365	100.00
	clr4	2	456,575 – 458,047	1,473/1,473	100.00	1,473/1,473	100.00	1,472/1,473	99.93
	sty1	1	206,864 – 207,913	1,050/1,050	100.00	1,050/1,050	100.00	1,048/1,050	99.81
	zfs1	2	3,483,454 – 3,484,668	1,215/1,215	100.00	1,215/1,215	100.00	1,215/1,215	100.00
Essential genes	*cdc13*	2	421,123 – 422,571	1,449/1,449	100.00	1,449/1,449	100.00	1,448/1,449	99.93
	act1	2	1,476,149 – 1,477,276	1,127/1,128	99.91	1,128/1,128	100.00	1,128/1,128	100.00

				vs. PomBase					
		Positions in PomBase		JB858		JB873		JB1197	
	Locus	Ch	bp	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)	Match /Total (bp)	Identity (%)
Subtelomere	*tlh2*	2	4,525,719 – 4,533,144	▨	▨	▨	▨	▨	▨
	SH-D		4,521,826 – 4,524,375	▨	▨	▨	▨	▨	▨
			4,510,792 – 4,512,641	▨	▨	▨	▨	▨	▨
			4,504,812 – 4,506,754	▨	▨	▨	▨	▨	▨
	SU		4,489,185 – 4,490,293	1,098/1,109	99.01	1,098/1,109	99.01	1,098/1,109	99.01
			4,484,916 – 4,486,915	1,984/2,000	99.20	1,985/2,000	99.25	1,984/2,000	99.20
			4,469,756 – 4,472,805	3,021/3,058	98.79	3,023/3,058	98.86	3,022/3,057	98.86
			4,454,962 – 4,458,161	3,153/3,217	98.01	3,151/3,221	97.83	3,153/3,219	97.95
	Boundary		4,439,149 – 4,443,731	4,528/4,603	98.37	4,529/4,602	98.41	4,522/4,607	98.15
	SA		4,431,856 – 4,435,505	3,631/3,655	99.34	3,631/3,655	99.34	3,630/3,655	99.32
Shelterin complex	*rap1*	2	3,098,366 – 3,100,576	2,192/2,211	99.14	2,192/2,211	99.14	2,183/2,211	98.73
	taz1	1	3,091,237 – 3,093,228	1,982/1,992	99.50	1,982/1,992	99.50	1,983/1,992	99.55
	pot1	1	4,129,529 – 4,131,314	1,786/1,786	100.00	1,786/1,786	100.00	1,785/1,786	99.94
Non-essential genes	*gcn5*	1	4,974,116 – 4,975,480	1,364/1,365	99.93	1,365/1,365	100.00	1,362/1,365	99.78
	clr4	2	456,575 – 458,047	1,472/1,473	99.93	1,472/1,473	99.93	1,464/1,473	99.39
	sty1	1	206,864 – 207,913	1,049/1,050	99.90	1,048/1,050	99.81	1,049/1,050	99.90
	zfs1	2	3,483,454 – 3,484,668	1,215/1,215	100.00	1,215/1,215	100.00	1,213/1,215	99.84
Essential genes	*cdc13*	2	421,123 – 422,571	1,448/1,449	99.93	1,448/1,449	99.93	1,448/1,449	99.93
	act1	2	1,476,149 – 1,477,276	1,128/1,128	100.00	1,128/1,128	100.00	1,127/1,128	99.91

Supplementary Table 3 Fission yeast strains used in this study.

972/JK107	*h*$^-$
JP1225	*h*$^-$ *ade6-M216 leu1-32 ura4-D18 his7-366* (CHP429 from C. Hoffman)
ST3524 (*SD5*)	*h*$^+$ *ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4*$^+$ *SH1R::his7*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST3479 (*SD5*)	*h*$^-$ *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4*$^+$ *SH1R::his7*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5057 (*972SD4[1L+]* #1)	*h*$^+$ *ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5058 (*972SD4[1L+]* #2)	*h*$^-$ *ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5345 (*972SD4[1L+]* #3)	*h*$^-$ *ade6-M210 leu1-32 ura4-D18 SH1R::his7*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5059 (*972SD4[1R+]* #1)	*h*$^-$ *ura4-D18 SH1L::ura4*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5346 (*972SD4[1R+]* #2)	*h*$^+$ *ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST5347 (*972SD4[1R+]* #3)	*h*$^+$ *ade6-M210 leu1-32 his7-366 SH1L::ura4*$^+$ *SH2L::his7*$^+$ *SH2R::his7*$^+$ *SH3L::ura4*$^+$
ST4932 (*972SD4[2L+]* #1)	*h*$^-$ *ura4-D18 SH1L::ura4*$^+$ *SH1R::his7*$^+$ *SH2R::his7*$^+$*SH3L::ura4*$^+$
ST5060 (*972SD4[2L+]* #2)	

h^{-} ade6-M210 ura4-D18 SH1L::ura4^{+} SH1R::his7^{+}
SH2R::his7^{+}SH3L::ura4^{+}

ST5348 (*972SD4[2L+]* #3)
h^{+} ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4^{+} SH1R::his7^{+}
SH2R::his7^{+}SH3L::ura4^{+}

ST5349 (*972SD4[2R+]* #1)
h^{-} ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4^{+} SH1R::his7^{+}
SH2L::his7^{+} SH3L::ura4^{+}

ST5350 (*972SD4[2R+]* #2)
h^{+} ade6-M210 leu1-32 ura4-D18 his7-366 SH1L::ura4^{+} SH1R::his7^{+}
SH2L::his7^{+} SH3L::ura4^{+}

ST5351 (*972SD4[2R+]* #3)
h^{-} ade6-M210 SH1L::ura4^{+} SH1R::his7^{+} SH2L::his7^{+} SH3L::ura4^{+}

For Fig. 8c

JP3827 (972 *clr4*Δ) *h^{-} clr4::kanMX6*
ST3499 (*SD5 clr4*Δ) *h^{-} ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4^{+} SH1R::his7^{+}*
SH2L::his7^{+} SH2R::his7^{+} SH3L::ura4^{+} clr4::hphMX6

JP5831 (*972SD4[1L+] clr4*Δ #1)
h^{+} ade6-M216 leu1-32 ura4-D18 his7-366 SH1R::his7^{+} SH2L::his7^{+}
SH2R::his7^{+} SH3L::ura4^{+} clr4::hphMX6

JP5833 (*972SD4[1R+] clr4*Δ #1)
h^{-} ura4-D18 SH1L::ura4^{+} SH2L::his7^{+} SH2R::his7^{+} SH3L::ura4^{+}
clr4::hphMX6

JP5835 (*972SD4[2L+] clr4*Δ #1)
h^{-} ura4-D18 SH1L::ura4^{+} SH1R::his7^{+} SH2R::his7^{+}SH3L::ura4^{+}
clr4::hphMX6

JP5837 (*972SD4[2R+] clr4*Δ #1)
h^{-} ade6-M216 leu1-32 ura4-D18 his7-366 SH1L::ura4^{+} SH1R::his7^{+}
SH2L::his7^{+} SH3L::ura4^{+} clr4::hphMX6

Supplementary Table 4 PCR primers used in this study.

For amplification of the *SPBCPT2R1.03* ORF

st498	5′- ATGAGTATTGAATTCGATGACAG-3′
st499	5′- ACCATTCAAATTGTATTTCAAGTATG-3′

For amplification of *SH-D* regions

subtel-5.2-7.9 kb

jk618	5′-GCCTACCGCTTGCAGTTGTT-3′
jk621	5′-ACAGTAAACTATGATCGCTTTTGAAGAC-3′

subtel-7.9-9.3 kb

jk620	5′-TTCTTAATCATTATCAAGTATTCATTGCAA-3′
jk452	5′-CAACTTGCGAGAATGTAAACTACGTATTC-3′

subtel-9.1-10.8 kb

jk451	5′-TGCCTTTCTAGCCCATGACCTA-3′
jk385	5′-CAGCATTAACCAACAGTGGTCTTC-3′

subtel-10.7-13.2 kb

jk384	5′-GCTCTCGACAAAGCCGTTCT-3′
jk387	5′-CATCAGCAACGTCGCCAACT-3′

subtel-13.0-15.1 kb

jk386	5′-TTCCAAGTATGCCAGCTTATCATC-3′
jk454	5′-TAAAGATTCATGGAACCATCATTTG-3′

subtel-14.9-17.2 kb

jk453	5′-AAAGAATTCGAATCACCCATACCA-3′
jk683	5′-GGGTCAAAACCTGCGCATAA-3′

subtel-17.1-19.0 kb

jk682	5′-AATTTCAGTTGCCAAGGGACA-3′
jk456	5′-GACCGCTACGCAACCATAAAG-3′

subtel-18.9-21.3 kb

jk455	5′-AACGAGTTGTGCAATGTTAGTAAGGT-3′
jk561	5′-TGACCACCCTCATAAGCCTGT-3′

subtel-21.3-23.3 kb

jk560	5′-TGTTACGTGGCAAGGCAGACT-3′
jk559	5′-AACTCGCTTGATGAATGGGTG-3′

subtel-23.3-26.2 kb

jk558	5′-GACAACCCGACCCATGGAT-3′
jk555	5′-GACCCCAATGGCCGAGAT-3′

subtel-26.2-27.7 kb

jk554	5′-GCTGCATGTTTATATCCTTGGCT-3′
jk689	5′-GAGCCCAATGACCAAAATACAAA-3′

subtel-27.7-29.0 kb

jk688	5′-CAGCCCTGGGTGCAACTATAA-3′
jk389	5′-TGTTACTCATACTTGAAATACAATTTGAATG-3′

subtel-34.9-36.9 kb

tk74	5′-ACATTCAGAAACAACAGTTGG-3′
jk691	5′-GCTCCATCCATTGTCATTGGT-3′

For detection of lengths of *SH-D* regions

subtel2R-4.2-11.1 kb **(i)**

tk121	5′-ATTCTTTTCACTTTCTTTTCCTCG-3′
tk66	5′-CCATGATGTCGTTACGGC-3′

subtel2R-9.3-15.7 kb **(ii)**

jk451	5′-TGCCTTTCTAGCCCATGACCTA-3′
tk79	5′-CATTCATTTTCTACACGCTCTATTATTTC-3′

subtel2R-14.8-20.7 kb **(iii)**

jk1611	5′-CATCCGGCGATATCTCTAGCAG-3′
tk44	5′-CAAAGTTGTATTCATGCTTGTTAC-3′

subtel2R-20.6-22.1 kb **(iv)**

tk114	5′-TCATTACCAAAGTTTAAAACGC-3′
tk113	5′-AGTCTGAATGTGCCAACTC-3′

subtel2R-22.1-26.7 kb **(v)**

tk122	5′-GAGTTGGCACATTCAGACT-3′
tk123	5′-GGTATCGGTCACCGATATAGC-3′

subtel2R-26.7-35.4 kb **(vi)**

tk102	5′-GCTATATCGGTGACCGATACC-3′
tk130	5′-GGGAGTCCAAATTGGTTCAA-3′

subtel2R-35.4-40.9 kb **(vii)**

tk76	5′-TTGAACCAATTTGGACTCCC-3′
tk144	5′-GGTGTTGCGGGATCTTCA-3′

subtel2R-40.7-44.1 kb **(viii)**

jk692	5′-CGCGCACTTTTCGGACATA-3′
tk115	5′-GTATGATTTTTCAAACTGTCCC-3′

subtel2R-44.1-47.5 kb **(ix)**

tk124	5′-GGGACAGTTTGAAAAATCATAC-3′
tk125	5′-CAACGACTAAGTCTATACATCGG-3′

rap1 **(control)**

jk900	5′-AATTGTAAAGCCTTACTCGGCCCAAAAGGATTATACACAAAG-3′
jk1219	5′-ATGAAGAATCTGGAGTTGACGTAG-3′

For *Ch2R* sequencing

subtel2R-17.1-19.8 kb

jk682	5′-AATTTCAGTTGCCAAGGGACA-3′
tk52	5′-GGAATTGATTATTCAACTCATTGGAC-3′

subtel2R-29.0-30.9 kb

jk388	5′-GGCACAATTTCATTTCGTTTAGTTTAC-3′
jk685	5′-TGCCGGTATTTAAGATGCACAT-3′

subtel2R-34.6-36.9 kb

jk688	5′-CAGCCCTGGGTGCAACTATAA-3′
jk691	5′-GCTCCATCCATTGTCATTGGT-3′

subtel2R-50.8-52.3 kb

jk700	5′-TCCGCAAATTTTGTTAGCCAT-3′
jk703	5′-ACGGGCGGTATGGATCAAT-3′

subtel2R-54.8-57.0 kb

jk704	5′-TTCCAATCCCAGAGTCGTGTC-3′
jk707	5′-AATAGACTTGGTCTGGATGAAGCAG-3′

subtel2R-69.0-72.2 kb

jk710	5′-GCTTTTATGCAATGTCTTGACGA-3′
tk131	5′-CCTTGATACATGGAACCTCG-3′

subtel2R-83.6-86.4 kb

tk133	5′-AGTCCTTGTCCGGCAGAATCT-3′
tk132	5′-AAGCTATCTGGGAAGCCG-3′

subtel2R-98.0-102.7 kb

km38	5′-TTCAGGATTAAGGTAACGCGGT-3′
st104	5′-TTTATGCATCCAACCGTTCGA-3′

2R-106.2-110.0 kb

st214	5′-GCTTTACTCCTTTCAGGCGTATG-3′
km41	5′-CGATCGTCCACTACTTCACGTTT-3′

For sequencing of control gene loci

rap1

jk926	5′-CACTCCACTTACTCATCCAGC-3′
jk1219	5′-ATGAAGAATCTGGAGTTGACGTAG-3′

taz1

jk1918	5′-TGGTATTCTTACATTGTTCTAAGGGATTATG-3′
jk1222	5′-TAACAAAACTATCCGAGTCTTGTC-3′

pot1

jk1916	5′-CTTTTACCAATTCCATTTAGGTTTCTGAG-3′
jk1917	5′-CTTTATAAAATTCTCCCAATATAGAGCTTTCC-3′

gcn5

jk1914	5′-TGCTCGTTTCATCTTGTATCGTTCTT-3′
jk1915	5′-TTTGGAAGGCACAAAAGATATTCGTG-3′

clr4

jk1908	5′-AAATTCGTTCAGGCATCATTTGG-3′
jk1909	5′-TGCTTAGAAAATGAATGACCTTTTTCAG-3′

sty1

jk1912	5′-AGTTACTTTTCGATATAGACGAAGGAC-3′
jk1913	5′-CTAAAATTCCATGGAACCGAGATGAT-3′

zfs1

jk1906	5′-TTCTTTGTTCGTTTATAACTAATC-3′
jk1907	5′-AAGGAGGATAGGAAAGTAAGCGTCATA-3′

cdc13

jk1904	5′-CTCTTTTTTATCATTTCTGTTACCTGAACC-3′
jk1905	5′-AACTAATACACATATAAAGAGCGCTTG-3′

act1

jk1910	5′-ACCTCAGCCAGCCGTGTTATAACTTA-3′
jk1911	5′-AAAGTTCCTCATGAGATGTTAAGAGC-3′

For detection of RNA and DNA from upstream of the *tlh* ORFs

jk567 (a)	5′-TTGCTGCTGCACAAAGCTTTTTG-3′
tk79 (b)	5′-CATTCATTTTCTACACGCTCTATTATTTC-3′
jk1612 (c)	5′-TGGTCGTCGCTTCAGAAATTG-3′
tk41	5′-ATGTTTTGTGCATCTTCTTTCTCC-3′

***rap1* (control)**

jk1300	5′-TATAAAGAATTCTCTAAATGAAGTTTCACGCAAGGT-3′
jk1206	5′-TATAAACCCGGGGTATCCTCAACATTCTCTTGAATC-3′

For detection of RNA from *dh*-homologous regions in the *tlh* genes

dh-homologous region

jk458	5′-TCGATAGAGATACGTTCATCTCATAGTGT-3′
jk457	5′-CACTCATTTCTTTGCTGATCACTTACT-3′

***his1* (control)**

jk1335	5′-CGAAGACGTGCTTCAGCGA-3′
jk1336	5′-TGTCCACCTCGGAATCACTG-3′

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