

Supplementary Figure 1. Eroded telomeres are rearranged in quiescence.

a) Genomic DNA from quiescent *ter1+* and *ter1D* cells was digested by *EcoRI* and analyzed by Southern blot with Telo/STE1 and chromosomal probes. 1, 4, 6, and 8 correspond to the number of days in G0 before harvesting. For *ter1Δ* cells, S1, S3, S5 and S7 indicate the number of days in senescence before cells were starved from nitrogen. STEEx are shown by asterisks

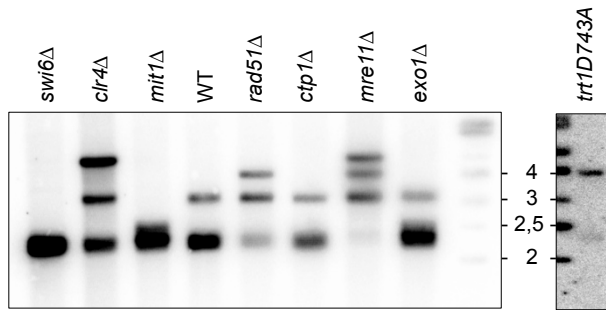
b) A senescence kinetics was performed from a strain expressing a catalytically dead version of the telomerase (*trt1^{D743A}*) after the loss of a plasmid bearing *trt1+*. At days 1, 3 and 5 of senescence, *trt1^{D743A}* cells were starved from nitrogen and kept for 8 days in quiescence. Cells were collected at different time points of the senescence kinetics (S1-S5) and for S1, S3, and S5 cells were starved from nitrogen and collected after 1, 4, and 8 days in quiescence. A *ter1D* strain was used as control. Genomic DNA was extracted, digested with *EcoRI* and analyzed by Southern blot with the STE1/Telo probe. STEEx was detected in the *trt1^{D743A}* strain according to its *NsiI* pattern (Supplementary Figure 3) and are shown by asterisks

>pNSU70

TCAGATGCATAAAAAATTTGAAGTTGGTATGTATTGAGTGTGTTGGAGTACGGTAAGTATAATAGGGCTAAATAA
NsiI
AATGGGTAAAAAAATTTTGAATGTGTGGAACTTGAGTATGTTGGAGTACATTAAGTAGATTACAGTTGTGGAG
pNsiI Fw
CGTACTATGGTAATGAAAATGAATGAAGAAAATGAAGTTGGGTGAATTGAGCGTGGTAGGATTCATTATGTATG
ATTAGGAGATATAATGAGATATGGTGAATAAAAAAGTTGAAATGGTGGGCTTGAGTGCCTTAGGGTGCCTAGTAAGT
pNsiI Rev
AGAATAAAGGGGCGCAGTGTATTATGATAATTAAAAATGGATGAAAAATTTGAAGTTCAGTCACTCAGTCATAATTAATT
pApaI Fw
GGGTAACGGAGTAACAATATAGAATAAAGGGAATTTAGGAAGTCCGGTAAGTTGAATAAAGAAAATAGAAATGAAA
HRS
TACGGTATTCATAAAAAATAAATTTACTTAAAGTTTTTTTTTCACAAATACAATGCCCCACATATTGGGCCCCACC
ApaI
CGTCAGCCGAGCCGTACGGCGAGTATTCGTTAAACGATTTTGGAGAGAGAGAATGGATAATGGATGGAGGTAAGA
pApaI Rev
GAGGTATGAAAGAGTAGAAGATATAGAAGAGAAGAGAGAAGAAAATGAGGAAGAAGTAAGATGAATAGAATAGAAG
AAACAGACTAAGGAGAGTAAATAAATAAAGTAAGAGAGTAAAAGAAAATAAGTAACTAAGAGGAAAGAAGATAAA
AGCAGAGGACTATATTGGAGTAGATTAAGTAGATTACAGTTGTGCAGCGTAGTATGATAATGAAGATAAAGAAA
pSwaI Fw
ATAATTAAGCTGCGTTATTTATAAAAAATTTAAATTTACTTAAAGTTTTTTTTCACATATAACAATGCCCCACTACTG
SwaI
GACCCCAACCGTCAGCCGAGCCGTAAGCGGAGTATTCGTTAAACGTTTTTAGAGAGAGAGAAGGAAATGAAGGA
pSwaI Rev
GAGAAGGAAAATGAAGGAGAGAAGGAAAATGAAGGAGGAGAATAGGTAGAGTAGGTAGGTAGAGTAGGTAGAGTAGG
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TCATGGAATTAGACTATGTTGGAATTCACATAATTGTAATAAGGTGGTGTAGTGTGTATGGGTGAATAAAACGGAT
EcoRI
GAAAAATTTGAAGTTGATTGAACTGAGTGTGTTAAAGTTCATTAAGTATAATACGGTGATGTAGTGTACTATAG
TATTTAGGATGGGTAAAAAATTTGAAATGTGTGGAATTTGAGTGTGCTGGAGTACGTTAAGTATAATACGGTGAGGT
AGTGTACTATAAATAATTAGGATGGTTAAAAAATTTGAAGTTGTATGAATTTGAGTGTGTTAGAGTTCATTAAGTAT
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TGTGTGGAATTTAGTATGTTGAAATTCACATAAGTGTAAATACAGTAGTGAGTGTATTATGATAATTAAAAATGGAT
pApaI Fw
GAAAAATTTGAAGTTCAGTCACTCAGTCATAATTAATTTGGGTAACGGAGTAACAATATAGAATAAAGGGAATTTAGGAA
TERRA TSS **HRS**
GTGCGGTAAGTTGAATAAAGAAAATAGAAATGAAATACGGTATTCATAAAAAATAAATTTACTTAAAGTTTTTTTT
CACAAATACAATGCCCCACATATTGGGCCCCACCCGTCAGCCGAGCCGTAAGGCGAGGCTGCGGGTTACAAGGTT
ApaI *pApaI Rev*
ACGTGTTACACGGTTACAGGTTACAGGGGGTTACGGTTACAGGGGTTACAGGGGTTACAGGGGTTACGGTTACAG
GGTTACAGGTTACACGGTTACAGTTTACGGTTACAGGGTTACAGGGTTACAGGGTTACAGGGGTTACGGTTACAC
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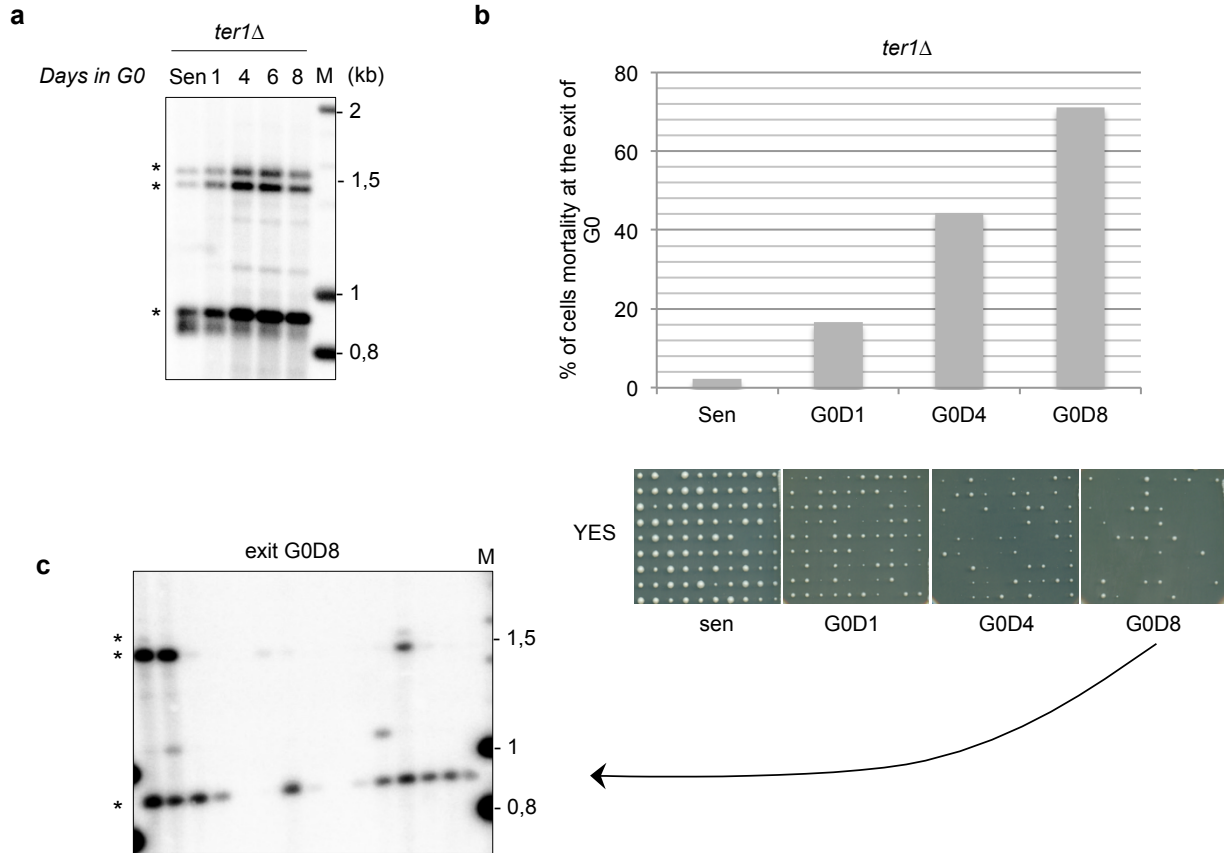
Supplementary Figure 2. Subtelomeric region sequences of pNSU70 and pNSU64.

The homologous repeated sequence (HRS, grey box), colored oligonucleotides used for RT-qPCR, and restriction sites are annotated in subtelomeric sequences of pNSU64 and pNSU70.



Supplementary Figure 3. Subtelomeric patterns of strains used in this study.

Genomic DNA of the indicated strains was digested by *Nsi*I and analyzed by Southern blot with a STE1 probe.



Supplementary Figure 4. Cell viability at G0 exit.

a) *EcoRI*-digested genomic DNAs from senescent and nitrogen-starved *ter1D* cells were analyzed by Southern blot.

b) Senescent (Sen) and quiescent *ter1D* cells after 1, 4, or 8 days in G0 were micromanipulated and plated onto YES plate. The percentage of cells that were not able to form a colony was plotted. Pictures of agar plates are shown

c) Fifteen clones that were able to exit G0 after 8 days of quiescence were grown for approximately 32 pds. Their genomic DNA was then extracted, digested by *EcoRI* and analyzed by Southern blot with a Telo/STE1 probe. STEEx are shown by asterisks.