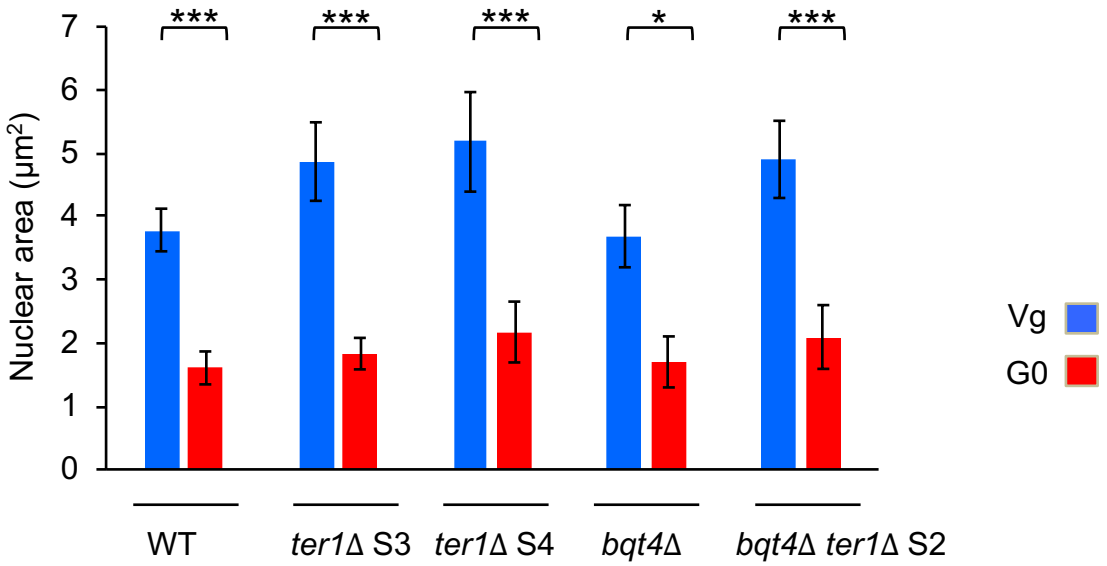

***
***
***
*
***
Nuclear area (μm²)
0
1
2
3
4
5
6
7
WT
ter1Δ S3
ter1Δ S4
bqt4Δ
bqt4Δ ter1Δ S2
Vg
G0

Figure S1

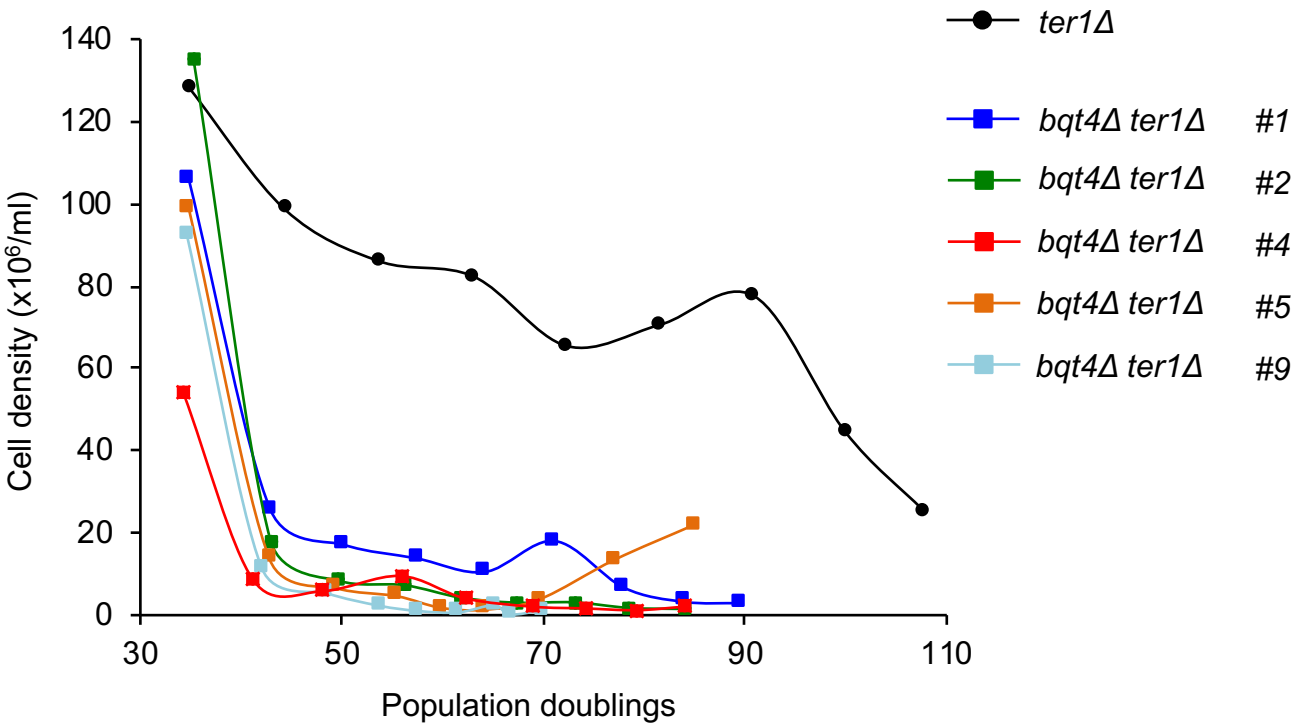

ter1Δ
bqt4Δ ter1Δ #1
bqt4Δ ter1Δ #2
bqt4Δ ter1Δ #4
bqt4Δ ter1Δ #5
bqt4Δ ter1Δ #9
Cell density (x10^6/ml)
140
120
100
80
60
40
20
0
30
50
70
90
110
Population doublings

Figure S2

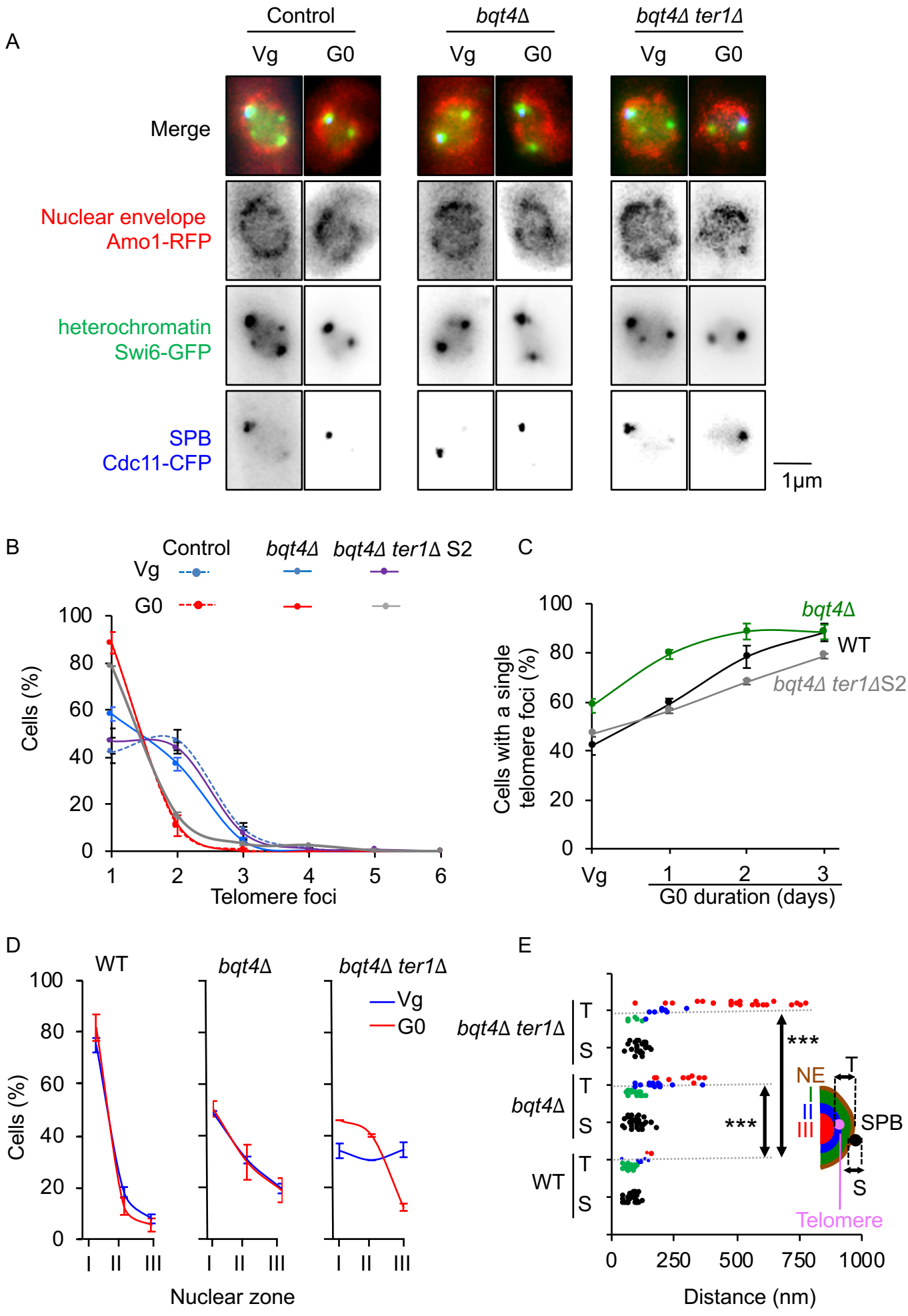
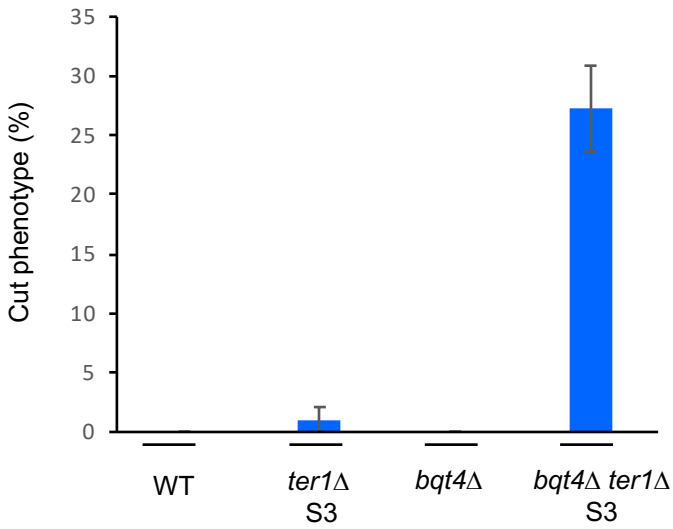

A
Control
bqt4Δ
bqt4Δ ter1Δ
Vg
G0
Merge
Nuclear envelope
Amo1-RFP
heterochromatin
Swi6-GFP
SPB
Cdc11-CFP
1μm
B
Control
bqt4Δ
bqt4Δ ter1Δ S2
Vg
G0
Cells (%)
Telomere foci
C
bqt4Δ
WT
bqt4Δ ter1ΔS2
Cells with a single telomere foci (%)
G0 duration (days)
D
WT
bqt4Δ
bqt4Δ ter1Δ
Vg
G0
Cells (%)
Nuclear zone
E
bqt4Δ ter1Δ
bqt4Δ
WT
T
S
***
NE
SPB
Telomere
Distance (nm)

Figure S3

A


Cut phenotype (%)
35
30
25
20
15
10
5
0
WT
ter1Δ
S3
bqt4Δ
bqt4Δ ter1Δ
S3

B

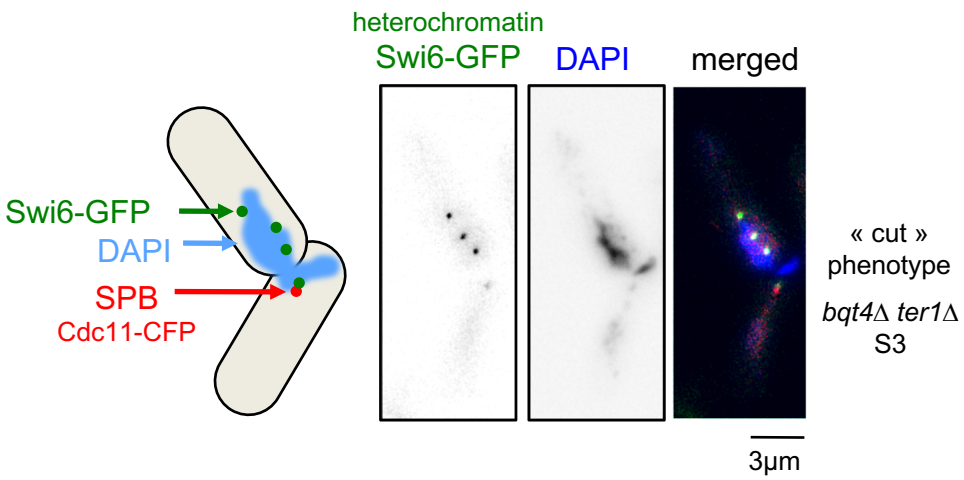

heterochromatin
Swi6-GFP
DAPI
merged
Swi6-GFP
DAPI
SPB
Cdc11-CFP
« cut »
phenotype
bqt4Δ ter1Δ
S3
3µm

Figure S4

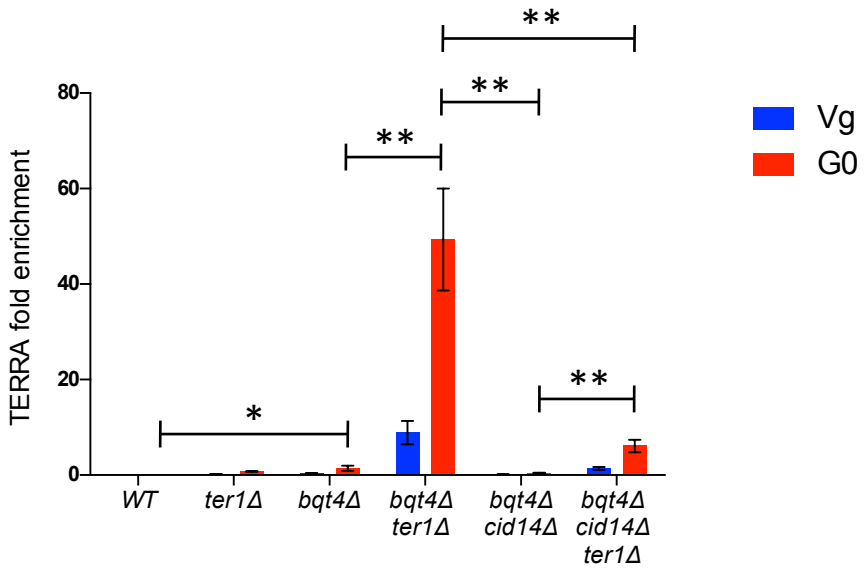

TERRA fold enrichment
80
60
40
20
0
*
**
**
**
**
Vg
G0
WT
ter1Δ
bqt4Δ
bqt4Δ ter1Δ
bqt4Δ cid14Δ
bqt4Δ cid14Δ ter1Δ

Figure S5

Supplemental figure legends

Figure S1: Measurement of the average nucleus radius of indicated strains in vegetative (Vg) and quiescent (G0) state. This experiment was repeated in triplicate. Error bars represent SEM. P-values are calculated from two-tailed *t*-test. test (***p< 0.0005 ; *p<0.05).

Figure S2: Senescence curves of *bqt4*Δ *ter1*Δ cells

Freshly deleted *ter1* colonies from WT and *bqt4*Δ strains were grown in liquid YES medium for several days by serial dilutions. Population doublings were monitored by cell counting. The *bqt4*Δ *ter1* #2 clone is presented in figure 5 and S3.

Figure S3: Telomere localization in *bqt4*Δ *ter1*Δ cells

WT and *bqt4*Δ telomerase positive (*ter1*+) and negative (*ter1*Δ) strains were starved from nitrogen. A) Visualization of telomeric foci, the nuclear envelope (NE) and the spindle pole body (SPB) by live microscopy in vegetative (Vg) and quiescent (G0) *ter1*Δ cells. Swi6-GFP (green), Amo1-RFP (red) and Cdc11-CFP (green) mark the telomeres and centromeres (heterochromatin), the NE and the SPBs, respectively. B) Percentage of cells that display one or several telomeric foci after 3 days in G0. For *ter1*Δ cells, imaging was processed from streak 2 (S2). C) Percentage of cells that display one telomeric focus with time in quiescence. D) Percentage of cells that display a unique telomeric hypercluster and its localization relative to the NE in the three equal concentric zones of the nucleus. E) Distance to NE of the telomeric foci in Vg and G0 cells. p-values are indicated. This experiment was repeated in triplicate and for each experiment >100 nuclei with a hyper-cluster were analyzed (***p< 0.0005). Error bars represent SEM.

Figure S4: *bqt4*Δ *ter1*Δ cells exhibit a high level of “cut” phenotype

A) “cut” phenotype were quantified in WT and *bqt4*Δ growing cells, in telomerase plus and *ter1*Δ background from streak 3 (S3). B) Example of “cut” phenotype observed by fluorescent microscopy. Swi6-GFP (green) and Cdc11-CFP (red) mark telomeres and centromeres (heterochromatin) and the SPBs, receptively. DAPI (blue) marks chromatin. In “cut” cells, the nucleus is divided in two parts by the septum.

Figure S5: TERRA level determination in vegetative (Vg) and in quiescent (G0) cells RNA was extracted in vegetative (Vg) and in quiescent (G0 after 48H) cells from the indicated strains. RNA levels were determined by RT-qPCR using a random hexanucleotide primer followed by qPCR with specific oligonucleotides for TERRA and control Fcp1. TERRA fold enrichment was determined as the ratio of TERRA over Fcp1 RNA levels (*p< 0.05; **p< 0.005). Error bars represent SEM.