Supporting Information

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(a) type O

(b) type S_0^0

(c) type S_1^0

(d) type S_0^1

(e) type S_1^1

(f) type C

Fig. S1. Possible states of the telomere–protein complex. Types O, S_0^0, S_0^1, S_1^0, and S_1^1 represent the open state U. A superscript one indicates the presence of a TRF2 dimer at the end of the telomere; a subscript one indicates a TRF2 dimer at an internal site within distance *d* of the end of the telomere. Type C is the t loop or the closed state.

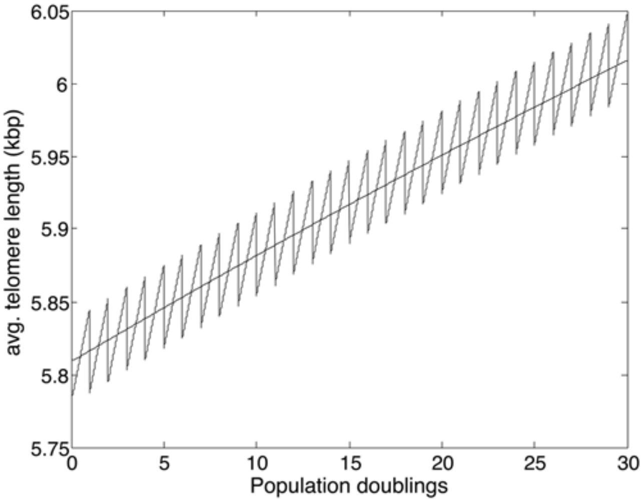

Fig. S2. Trajectories of the deterministic and reduced models. In the time scale of cell generations, the reduced model (smooth line) is a good approximation to the deterministic model (jagged line). See the main text for discussion.

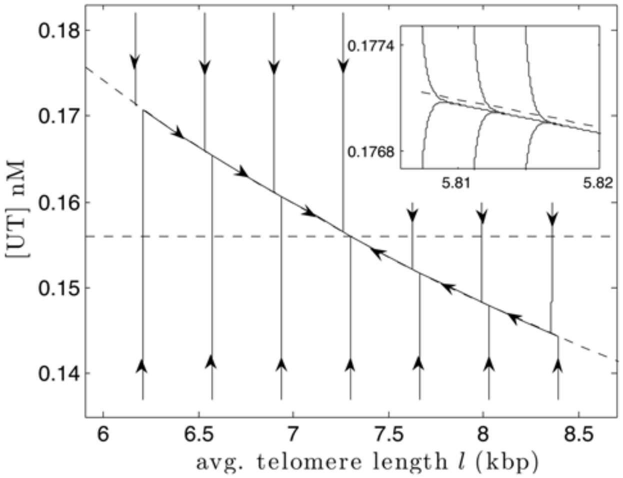

Fig. S3. Phase plane of the reduced model. The trajectories are plotted in solid lines, and the arrows track the direction of movement. The nullclines are plotted with dashed lines (the *l* nullcline is parallel to the *l* axis). In the *Inset* we plot a section of the phase plane at a scale that allows us to distinguish between the trajectories and the [UT] nullcline. A trajectory that starts at an arbitrary point $([\mathrm{UT}]_0, l_0)$ approaches rapidly the point in the [UT] nullcline corresponding to l_0 and then, at a much slower pace, follows a path very close to this nullcline toward the equilibrium point, which means that the path of the trajectory depends only very weakly on the initial value $[\mathrm{UT}]_0$. This feature is significant, given that the replication fork may knock out any telomerase molecules bound to the telomere and we have no way of estimating the initial value of [UT].

Table S1. Statistics on telomere length for different distributions of the 3′ overhang length

Distribution of the 3′ overhang length μ	mean l (kbp)	standard Deviation σ (kbp)	skewness Estimator G_1
Delta	6.63	0.955	0.126
Gaussian	6.59	0.994	0.099
Weibull	6.57	1.037	0.110

For the Weibull distribution we use the maximum likelihood estimator method to fit the data from BJ fibroblasts (human foreskin) in Huffman et al. (1). All three distributions have the same mean θ, and the variance of the normal distribution equals $\theta/3$. For the Delta distribution we fix $\mu = \theta$. All statistics were generated by using 100 independent samples. μ is the length of 3′ overhang, *l* is the average length of the telomeres in a cell, and σ is the standard deviation.

1. Huffman, KE, Levene, SD, Tesmer, VM, Shay, JW, Wright, WE, (2000) Telomere shortening is proportional to the size of the g-rich telomeric 3′-overhang, *J Biol Chem* 275:19719–19722.