SUPPLEMENTAL FIGURE LEGENDS

<u>Supplemental Fig. 1</u> Characterization of an additional RPA1-like predicted protein in *T. thermophila*. *A*, Comparison of *T. thermophila* Rpa1 and the RPA1-like protein Rlp1. Amino acid identity (ID) and additional similarity (SIM) determinations within the predicted OB-fold domains were performed using ClustalW. The GenBank accession number for the confirmed mRNA of *RLP1* is GU384877. *B*, *RLP1* knockout (KO) strains. A Southern blot of digested genomic DNA from four clonally isolated cell lines disrupted for *RLP1* is shown. The wild-type gene restriction fragment (WT) is entirely replaced by the restriction fragment from gene disruption with the selectable marker cassette (neo2). The fragment labeled "bg" is from background non-specific hybridization.

Supplemental Fig. 2. Product dissociation profiles for Teb1^{FL} and Teb1^C holoenzymes.

The intensities of products ending in TT-3' or TTG-3' from each repeat synthesis were quantified separately, normalized for content of radiolabeled dGTP, and then summed to represent the total product. Relative molar amount of product is plotted on a log scale. Number of G-tracts includes primer sequence. *A*, Quantification of product profiles for reactions from Fig. 5A, using the two 40 minute reaction time points. Reactions contained final concentrations of 0.3 μ M dGTP, 200 nM (GT₂G₃)₃, and 200 nM of the indicated form of Teb1.

B, Quantification of product profiles for reactions from Fig. 5B, comparing the $(GT_2G_3)_3$ and NT6 $(T_2G_4)_3$ primers with sequences shown in Fig. 5C. Reactions contained final concentrations of 0.3 μ M dGTP, 200 nM primer, and 1 μ M Teb1^C. The higher concentration of Teb1^C compared to assays in (*A*) reduced the amount of low-RAP enzyme. Note the minor peak of product dissociation after synthesis of nine repeats, likely resulting from folding of a second G-quadruplex involving repeats five through nine.



Supplemental Figure 2



В



Α