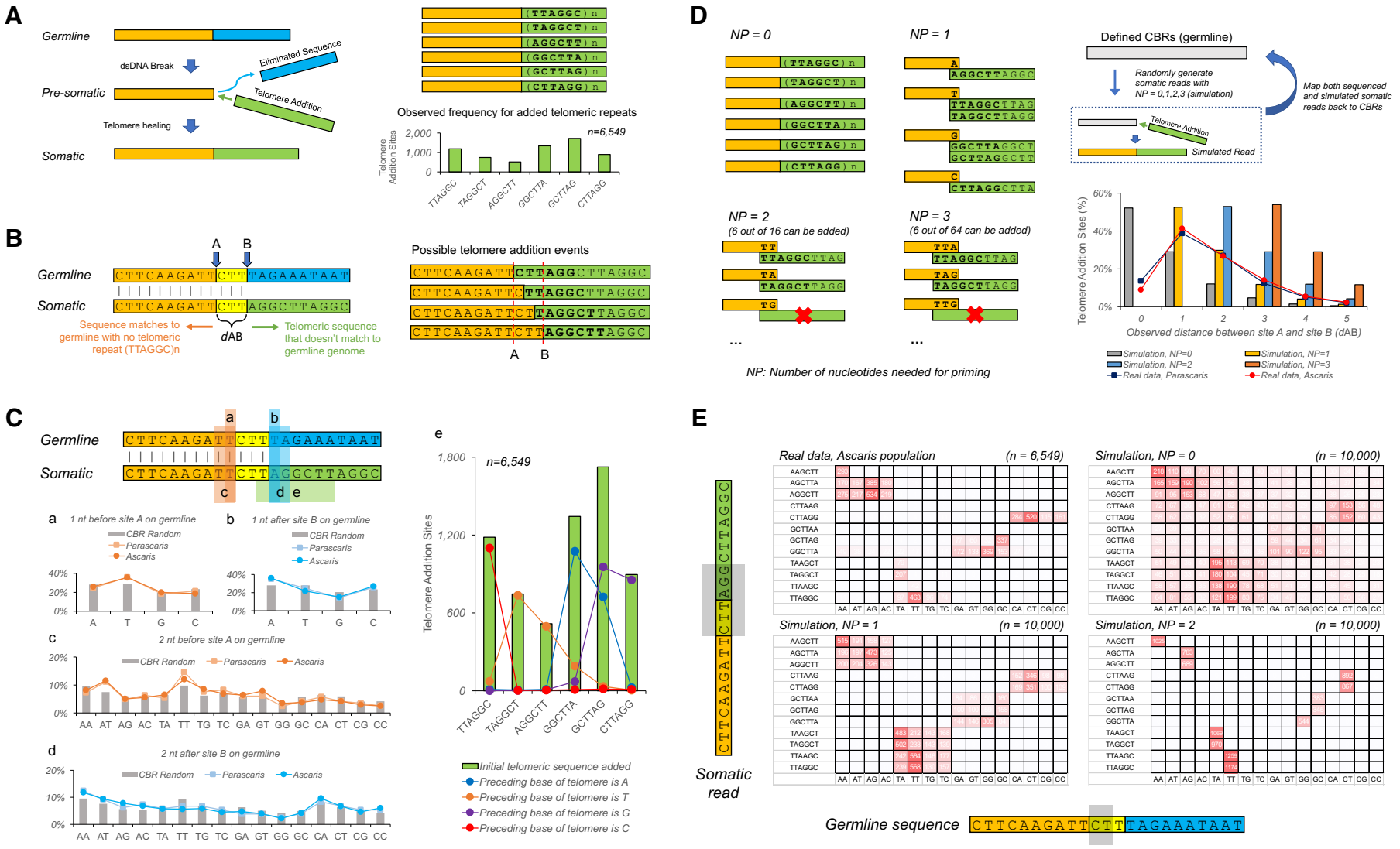

Figure S11. Sequence analysis of telomere addition sites. A. Telomere healing in *Ascaris* DNA elimination. After a dsDNA break, telomeric repeats are added to the ends of the DNA break. We do not know whether healing occurs directly at the break ends, if there is resection before telomere addition, or if internal priming occurs within the DNA for the addition of the telomere. Six possible repeat units that can be added are illustrated with their observed frequencies in *Ascaris* (right). **B.** An example of observed telomere healing sites. Sequence upstream of site A can be mapped only to the germline genome; sequence downstream of site B can be mapped to only telomeric repeats; and sequence between A and B sites (yellow) can be mapped to both the germline and the telomeric sequences. Possible telomere addition events for this example are illustrated (right). **C**. Nucleotide frequencies observed for the indicated positions (top, a through e in the shaded area) of all telomere healing sites. For sites a to d, the "CBR random" (gray) is the frequency for the single or dinucleotides derived from all known *Ascaris* CBR regions. Note the consistency between the observed frequencies and the CBR random frequency for sites a to d. We also compared the frequency of the added telomeric repeats (site e) and the frequency for the one base pair preceding the telomere repeats (P site, red). Note in most cases, the preceding nucleotide (P) is also matching to the telomeric repeat unit. **D.** Models for telomere healing where no telomere priming occurs (NP = 0), 1 nucleotide of the telomere is used (NP = 1), or where 2-3 telomeric nucleotides are used for telomere addition priming (NP = 2 and NP = 3). Sequences from the CBR regions were used to simulate the four different telomere healing models. After simulation, the four datasets and the real sequencing reads with telomere additions were mapped back to the CBR sequences using the same approach. Shown in the plot are the frequencies in % (y-axis) for the distance between site A and B in different healing models and in the real data. Note that the observed frequencies match best to NP = 1, priming with a single telomere template nucleotide for both *Ascaris* and *Parascaris.* **E.** Relationship between the last two nucleotides (x-axis) in germline and the added telomeric sequence (y-axis) in the somatic cells. Simulated and observed data for the frequency of the indicated area (shaded gray area) around the telomere addition sites is illustrated in a 16 x 12 matrix for each dataset. Note that the observed data match mostly the NP = 1, single nucleotide priming. However, for a group of dinucleotides (AA and TA), it also matched to the NP = 2, two nucleotide priming.