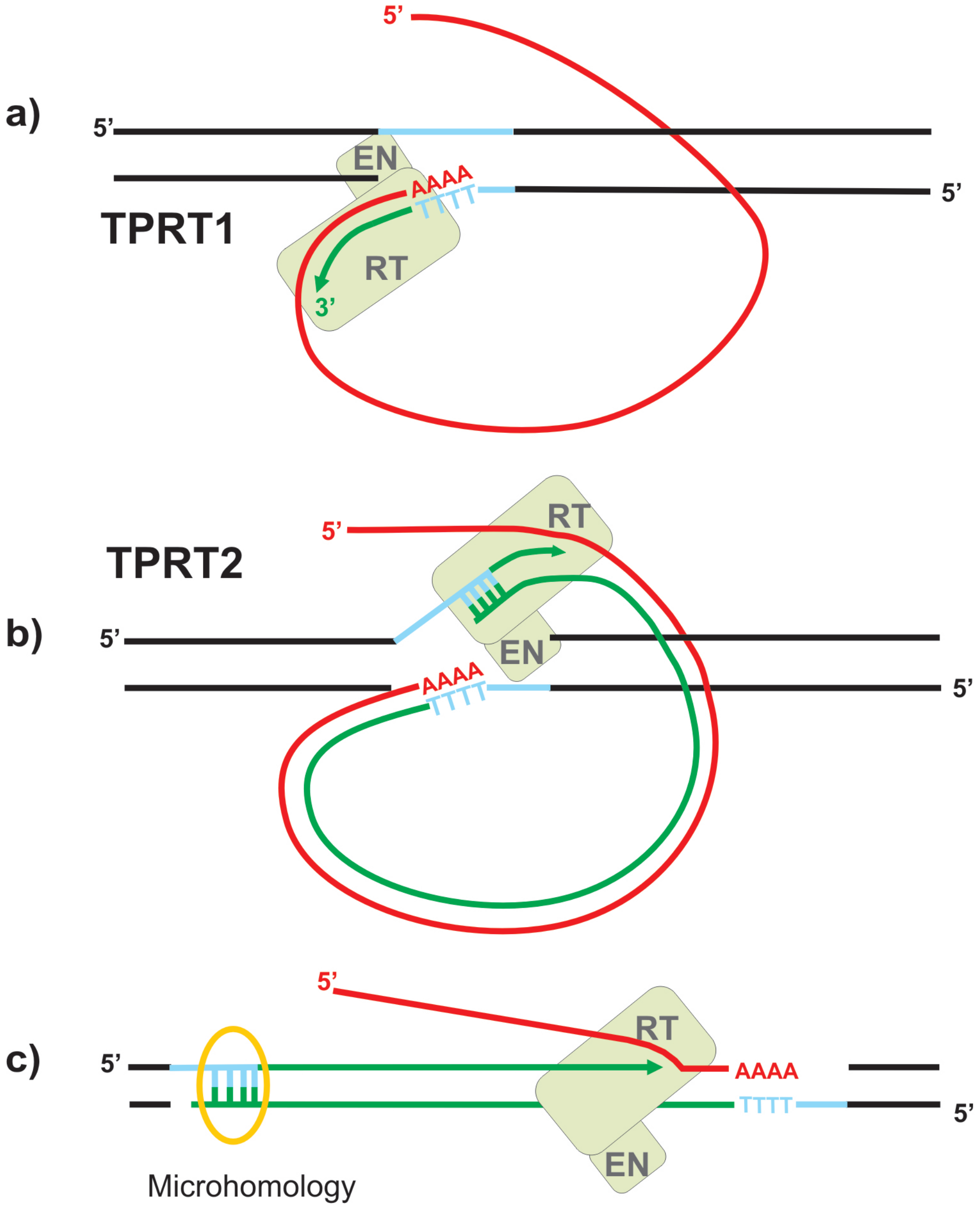

Supplementary Figure 1: Double-TPRT model. The described model is based on the TPRT model developed for R2Bm (Luan et al., 1993) and L1 (Cost et al., 2002). (a) The L1 EN domain creates the first nick within the consensus target sequence 3'-AA↑TTTT-5', generating a free 3'-OH. T-rich sequences at the cleaved target site anneal with the poly(A) tail of the L1 transcript (red) and the free 3'-OH of the cleaved target DNA then acts as a primer for cDNA synthesis (green) performed by L1 RT. (b) Nicking of the target top strand is carried out by L1 EN, generating a 3' overhang. Base pairing of this 3' overhang with the L1 cDNA primes L1 second-strand synthesis (green) which is carried out by L1 RT. (c) The L1 RNA could be displaced during continued polymerization by the L1 RT activity, or could be degraded by host RNAse H; Fill-in of the gaps by host-encoded DNA polymerase and subsequent ligation yields a direct repeat of the original sequence.