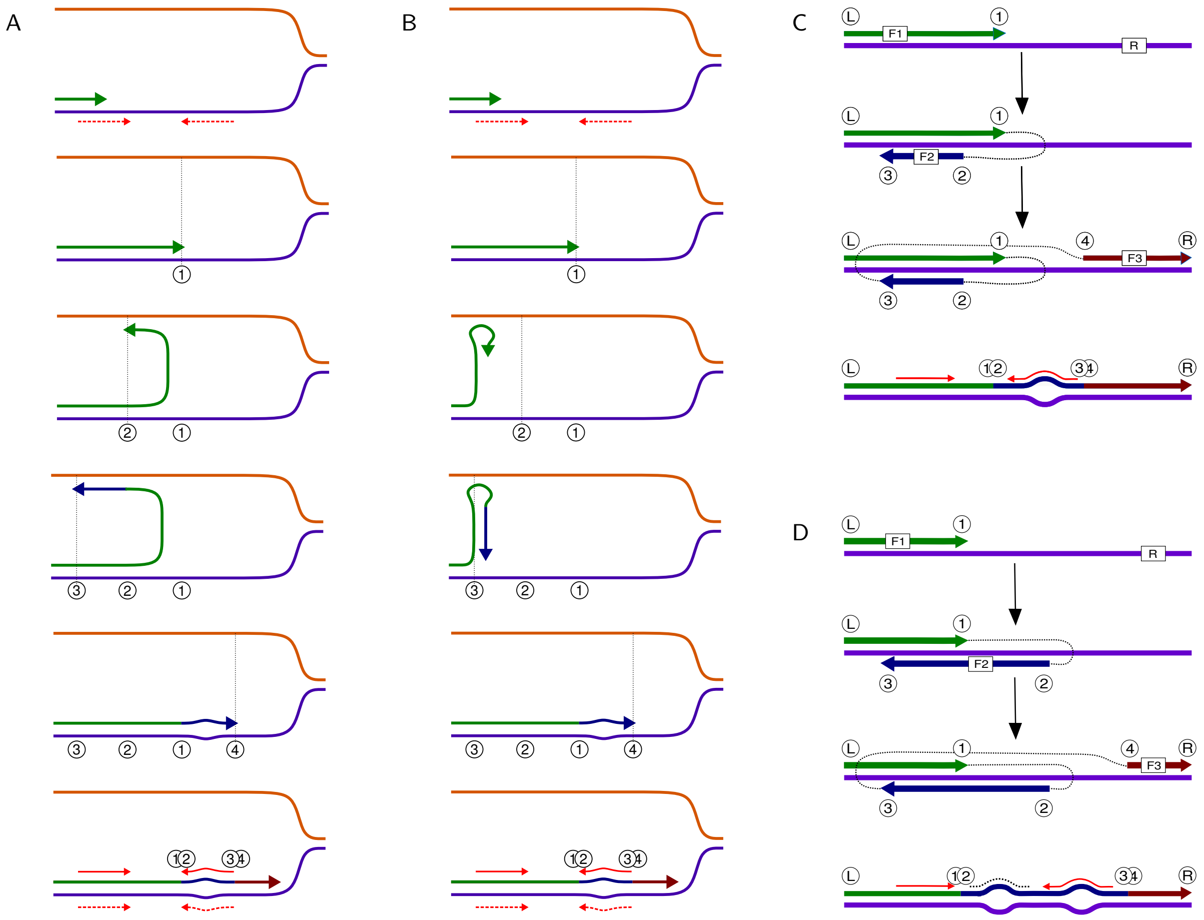

Fig S1. Classic vs. four-point model of template switching. (**A**, **B**) In the classic model of Ripley (1982), the replication (green arrow) switches the template and starts to go backward either along the opposite strand (**A**) or along the newly synthesized strand (**B**). After a synthesis of a short fragment (blue arrow), the replication switches back to the original strand and continues normally (dark red arrow). As a result, the near-perfect inverted repeat (red dashed arrows) has been converted into a perfect inverted repeat (red arrows), causing mismatches between the sequences (bulge). (**C**) The four-point model of Löytynoja and Goldman (2017) is a computationally tractable representation of the switch process and relaxes some of the assumptions underlying the Ripley model. The model assumes four points, ① - ④, where the replication process changes from one template to another and copying of the fragment ②→③ in a reverse complement manner. The outcome of the switch process depends on the relative positions of points ①-④, and the type 3-2-1-4 (read from left to right) shown here is consistent with the process shown in (A) & (B) and can take place either intra- or inter-strand. (**D**) The outcome of the template switch process depends on the relative positions of points ① - ④, and certain combinations, such as 3-1-2-4 shown here, can occur only interstrand, some may produce multiple repeats, and others only an inversion. See Löytynoja and Goldman (2017) for enumeration and outcomes of all possible switch point combinations. In this study, candidate template switch events were required to explain at least two sequence changes (indicated with bulges in the schematic figures) of which at least one is a base change, and have ②→③ region, inferred to be copied from the other template, of at least 8 bases long. It is possible that some of inferred template switch events were in fact created by multiple independent base changes, insertions or deletions.