A

CHROM	POS	REF	ALT
chr10	53250728	A	G
chr10	53250729	A	C
chr10	53250732	G	A
chr10	53250734	A	G
chr10	53250738	C	G
chr10	53250743	T	C
chr10	53250757	C	A
chr10	53250766	A	T
chr10	53250767	G	A
chr10	53250770	G	A
chr10	53250771	C	A
chr10	53250796	T	G
chr10	53250797	T	C
chr10	53250800	T	C
chr10	53250801	A	T
chr10	53250804	A	T
chr10	53250805	C	G
chr10	53250810	T	G
chr10	53250811	T	C

B

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                                                  **  * *   *    *             *        **  **                      **  **  **    **
ALT ACTTGAAATGGAAGAAAGGGTTTGGATAGgcAGaAgCACgCCAAcATGAAAAGTGAGGaCCTACATCtaTGaaATCATGGGACTCCTTCTAGGTGATgcCActGAtgTAGGgcCTCACTTTTCATGTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG
REF ACTTGAAATGGAAGAAAGGGTTTGGATAGAAAGGAACACCCCAATATGAAAAGTGAGGCCCTACATCAGTGGCATCATGGGACTCCTTCTAGGTGATTTCATAGAACTAGGTTCTCACTTTTCATGTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG

Switch process:

                    ①                                                                  ④                ⑤                                                                  ⑧
FW: ACTTGAAATGGAAGA                                                                    TGGGACTCCTTCTAGG                                                                  GTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG
RF: ACTTGAAATGGAAGAAAGGGTTTGGATAGAAAGGAACACCCCAATATGAAAAGTGAGGCCCTACATCAGTGGCATCATGGGACTCCTTCTAGGTGATTTCATAGAACTAGGTTCTCACTTTTCATGTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG
BW:                                                  TACTTTTCACTCCGGGATGTAGTCACCGTAGT                                  ACTAAAGTATCTACATCCAGGAGTGAAAAGTACAACCGCACGAAGACGGATAGGTTTGGGAA
                                                     ⑦                                ⑥                ③                          **    *                                                                  ②

Template-switch alignment:
                                                                                                   *     **
ALT ACTTGAAATGGAAGA|AAGGGTTTGGATAGGCAGAAGCACGCCAACATGAAAAGTGAGgACCTAcaTCTATGAAATCA|TGGGACTCCTTCTAGG|TGATGCCACTGATGTAGGGCCTCACTTTTCAT|GTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG
REF ACTTGAAATGGAAGA|AAGGGTTTGGATAGGCAGAAGCACGCCAACATGAAAAGTGAGAACCTAGTTCTATGAAATCA|TGGGACTCCTTCTAGG|TGATGCCACTGATGTAGGGCCTCACTTTTCAT|GTTGGCGTGCTTCTGCCTATCCAAACCCTTGAGATCCAGG
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Fig S13. Large gnomAD MNV explained by two TSMs. (**A**) A cluster of 19 base changes in gnomAD MNV data. (**B**) Of the 19 base differences (top), 16 can be explained with two TSM events (middle, bottom). DNA replication proceeds from left to right (green); at ①, the replication jumps to ② on the opposite strand and proceeds in a reverse-complement manner until ③ (blue); it then jumps to ④ in the original template and proceeds until ⑤ (magenta); the replication again changes the template (either to the opposite strand or to the newly synthesized strand), jumps to ⑥ and continues until in reverse-complement manner until ⑦ (orange); the replication makes a final jump to ⑧ in the original template and continues normally (red).