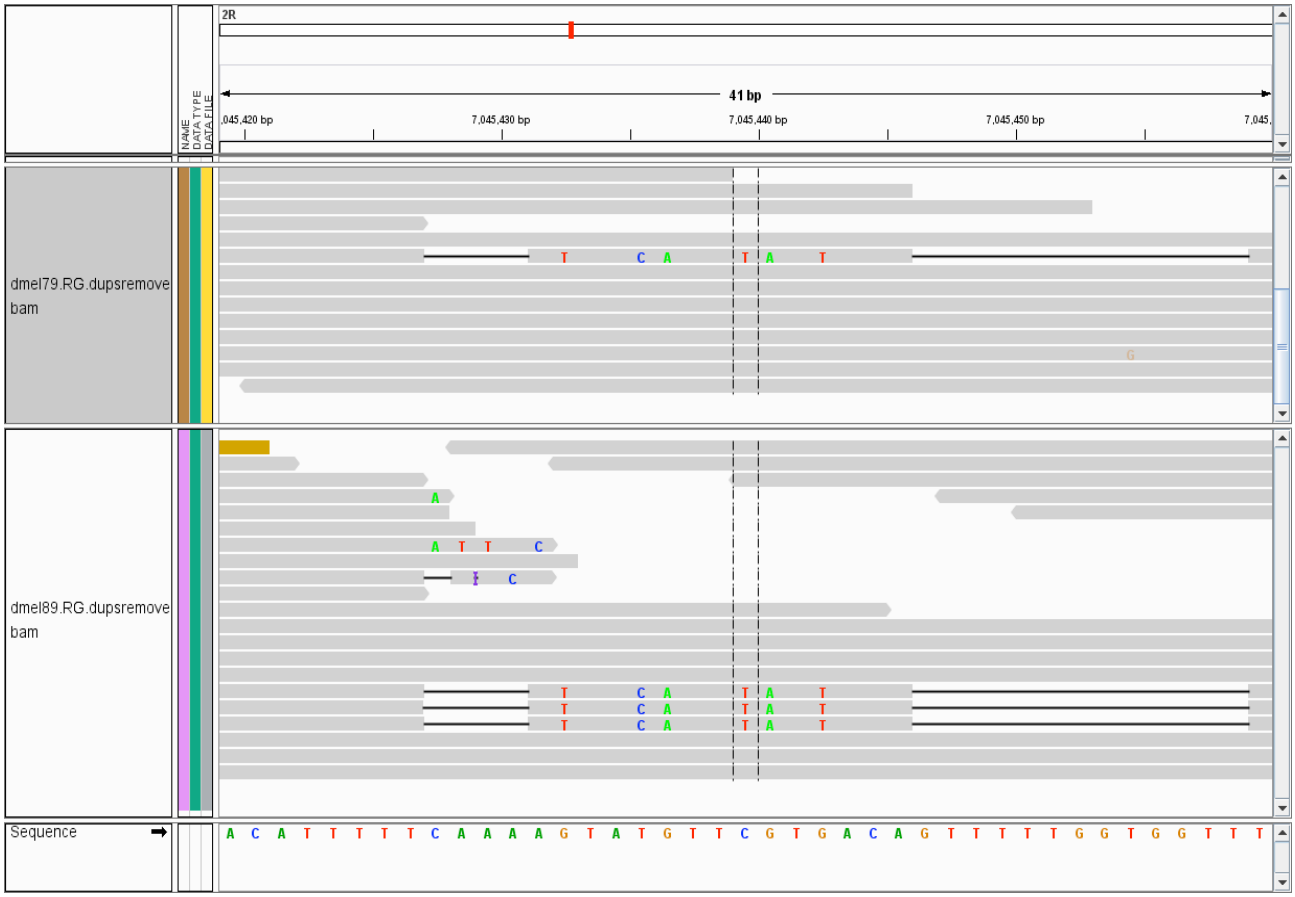


**Figure S1** Screenshot from the IGV showing a typical example of a read mapping error. The reference sequence is shown at the bottom, indicated by "Sequence →". Reads are indicated as horizontal grey bars, and only bases that differ from the reference are shown. Two individuals separated by a double horizontal line have a candidate C→T mutation at the focal site delimited by the vertical dotted lines. However, each of the reads containing the non-reference base (T) also has five SNPs and two deletions (shown as solid horizontal lines) in perfect association, i.e., none of these variants are present in the reads containing the reference base (C) at the focal site.