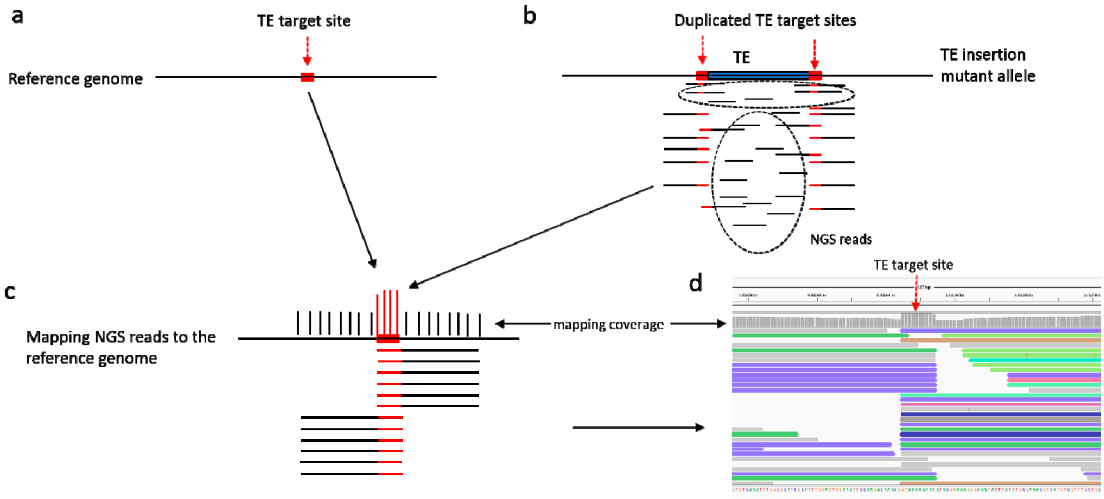

Figure S1. How to identify a TE insertion site using IGV. A short sequence in a genome (reference genome) may become a target sit for TE insertion (a). During TE insertion, the short target sequence is duplicated. The Next Generation Sequence (NGS) reads are generated from the TE insertion mutant allele (b). When the NGS reads are mapped to the reference genome, the reads that are marked within the two circles in (b) and contain mostly the TE sequences can not be mapped to the reference. The rest reads containing the target sequence are mapped. Due to the duplication of the target sequence, mapping coverage is higher at the target site than the adjacent sites (c). This high mapping coverage can be seen using IGV as an indication of TE insertion site.