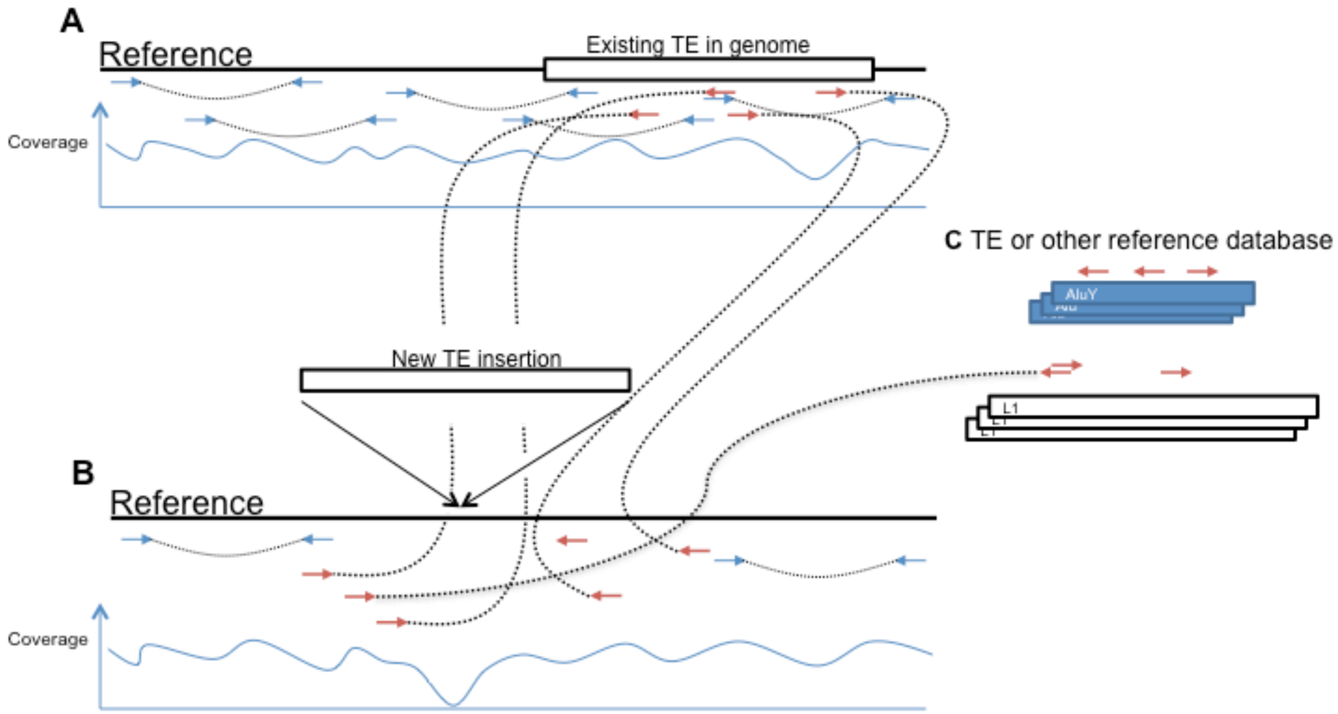
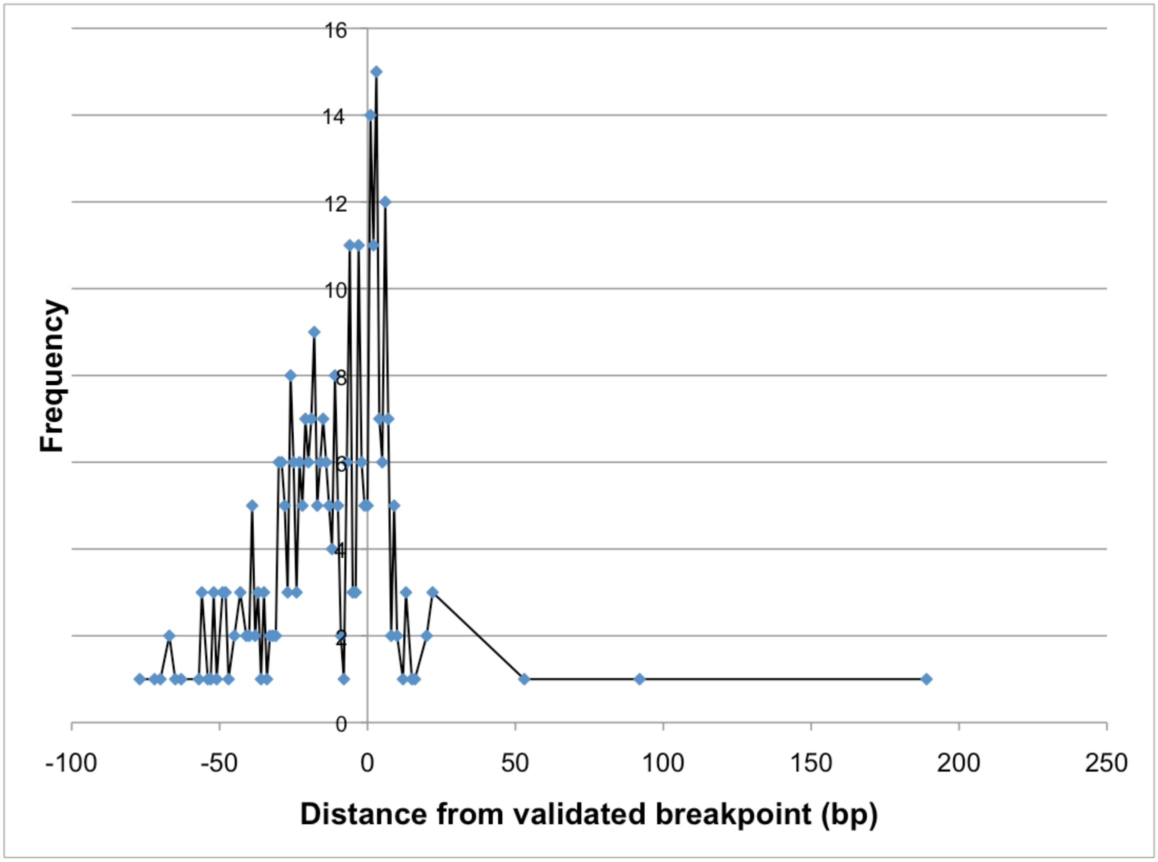
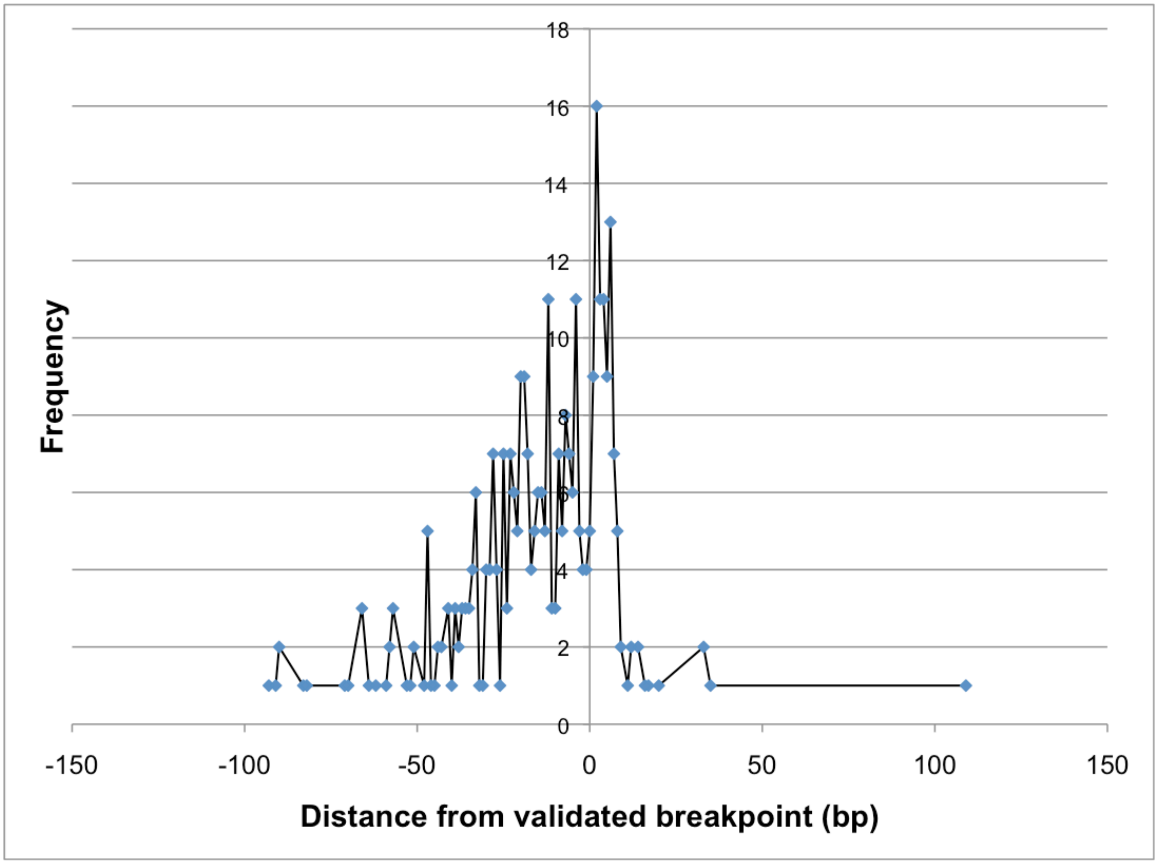


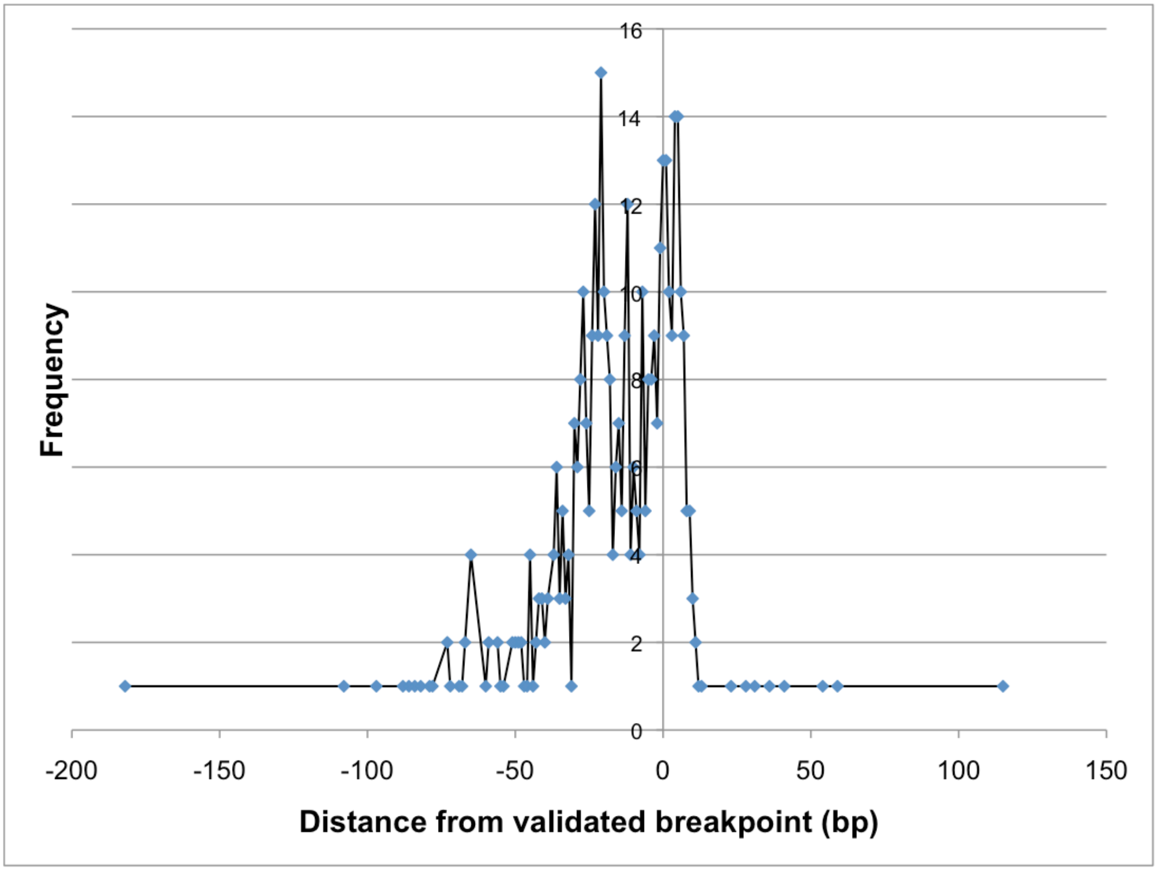
Supplementary Figure 1: Schematic of the TE discovery and calling procedure implemented in RetroSeq.



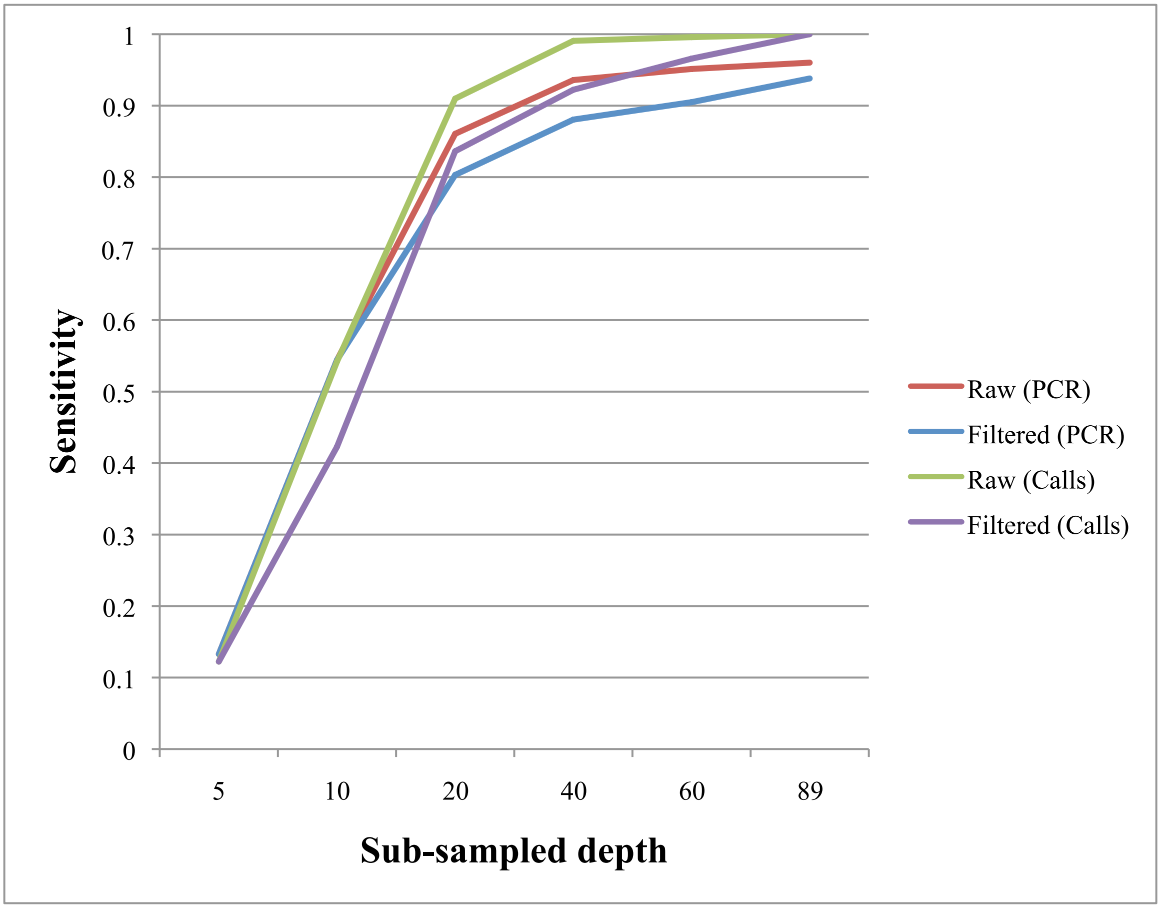
Supplementary Figure 2: Frequency distributions showing the difference between the locations of the breakpoints predicted by RetroSeq and the breakpoints determined by PCR and sequencing for NA12891



Supplementary Figure 3: Frequency distributions showing the difference between the locations of the breakpoints predicted by RetroSeq and the breakpoints determined by PCR and sequencing for NA12892



Supplementary Figure 4: Frequency distributions showing the difference between the locations of the breakpoints predicted by RetroSeq and the breakpoints determined by PCR and sequencing for NA12878



Supplementary Figure 5: Recovery rates for NA12878 at various sequencing depths relative to PCR validated calls ('PCR') and 1000 genomes computational calls ('Calls') from Stewart *et al.* (2011). Raw refers to the total calls output by RetroSeq and filtered refers to the final calls.

Type	**RetroSeq**	**Tangram**	**Tea**
Alu	5.1	12.2	13.3
L1	35	12.0	22.0
Total	**7.7**	**12.1**	**14.3**

Supplementary Table 1: False discovery rates (%) for the child (NA12878) for each of the callers based on the number of calls private to the child and not found in either of the parents. The rates are presented by type of element and an overall rate considering all of the calls.