**Fig S1**

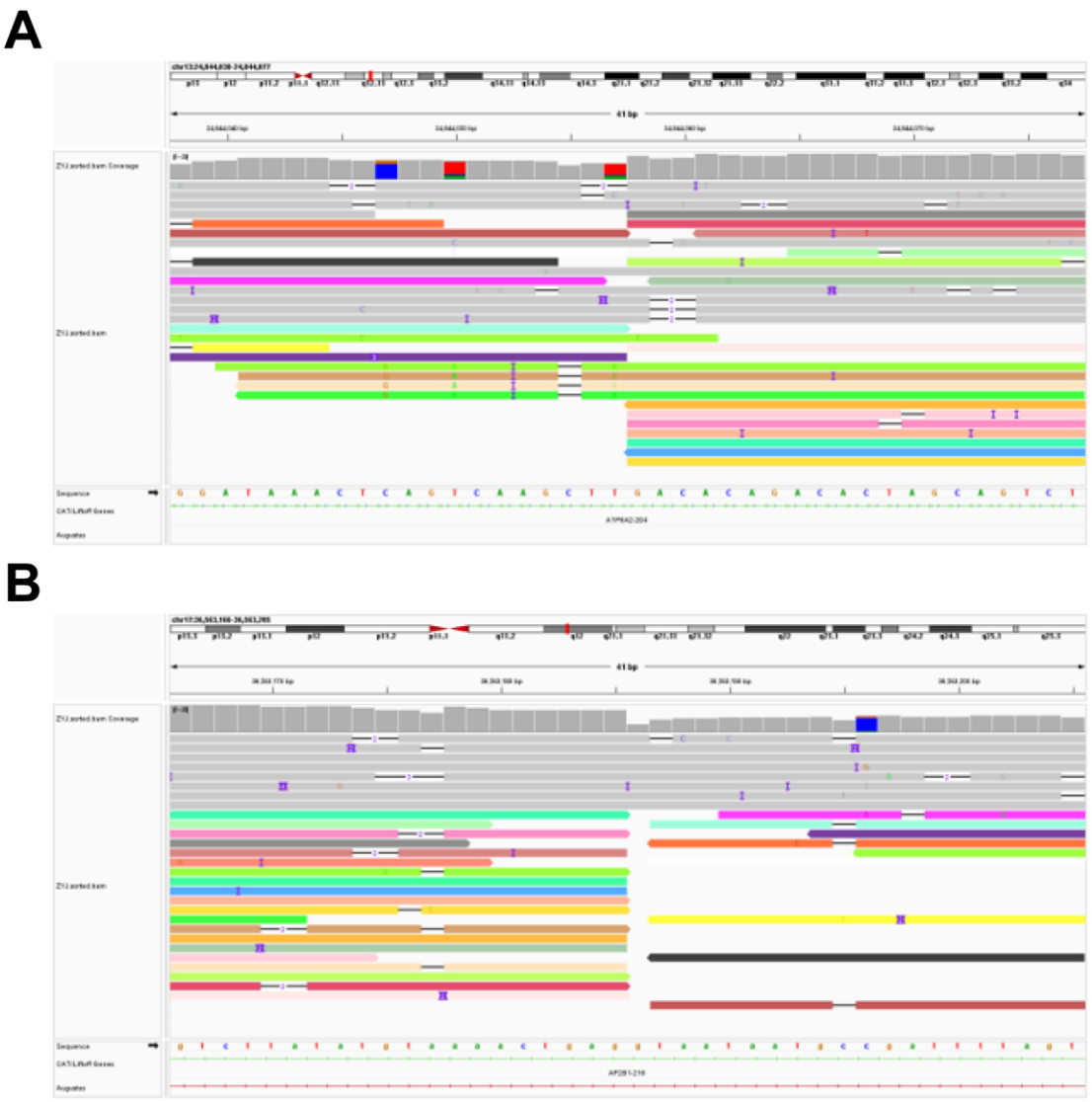


**Fig. S1** The IGV graphs revealed the breakpoints of ZYJ on chromosomes 13 and 17, as determined by the T2T-CHM13 reference genome. Colored reads indicated support for the translocation, while gray reads indicated support for the normal haplotype. Additionally, the sequencing depth of each locus was represented by the gray vertical bar. **A** The position of the breakpoint of translocation on chromosome 13 was 24,844,058 based on the T2T-CHM13 reference genome. The colored reads were linked with the pathogenic translocation. **B** The position of another breakpoint on chromosome 17 was 36,563,186 using the T2T-CHM13 reference genome.