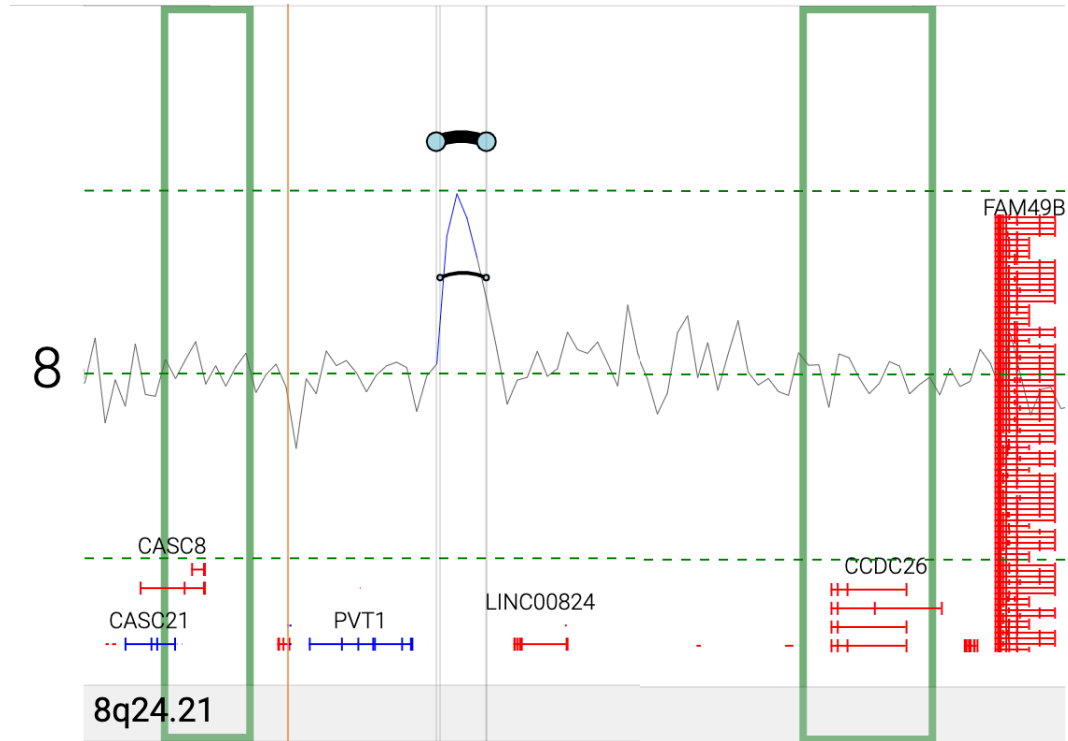
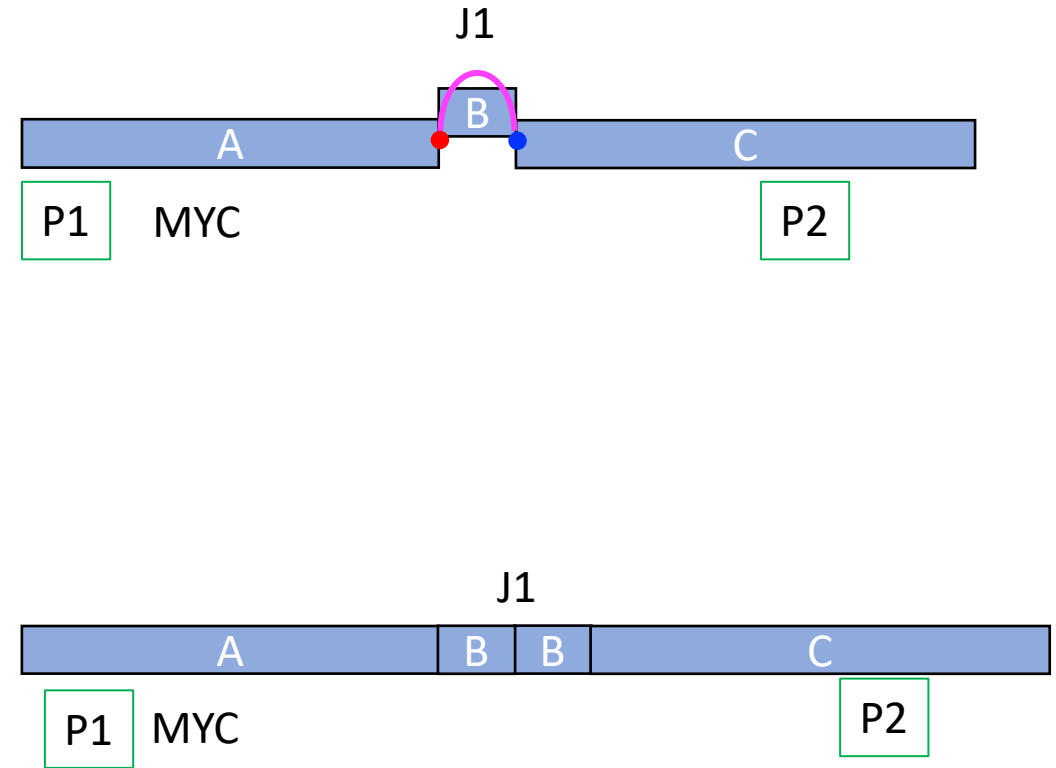


A. Telomeric Tandem Duplication (TTD)

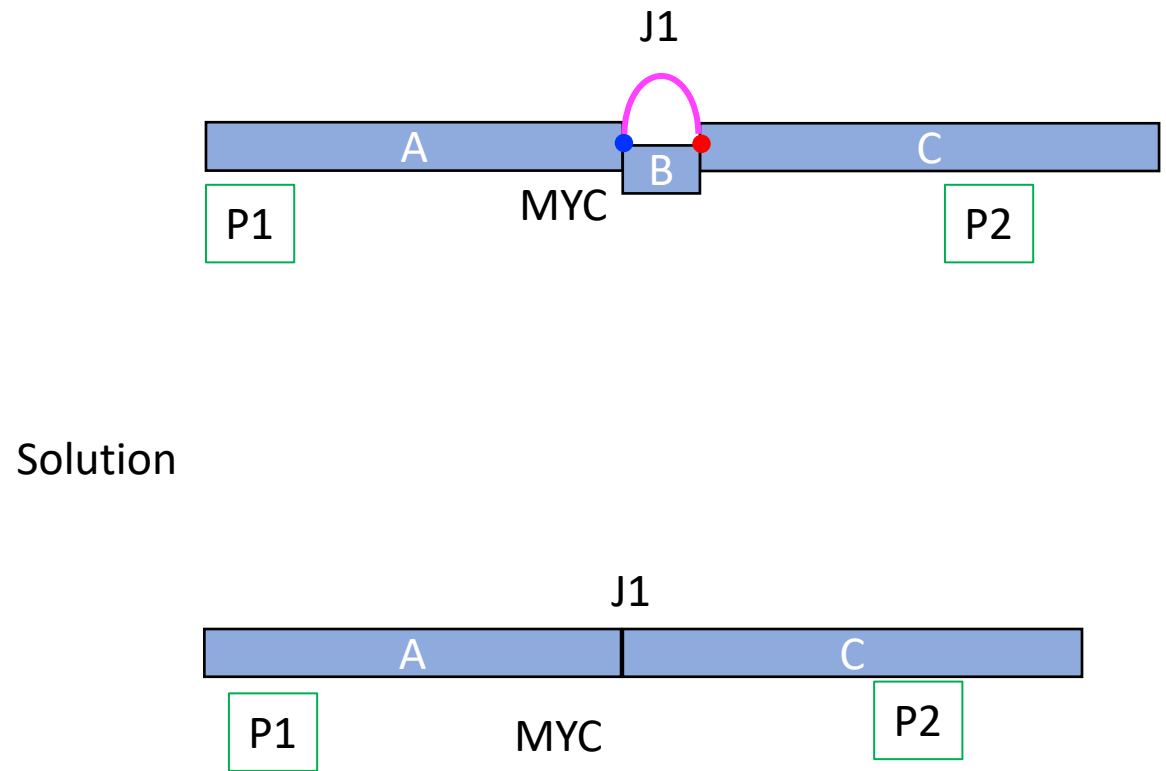
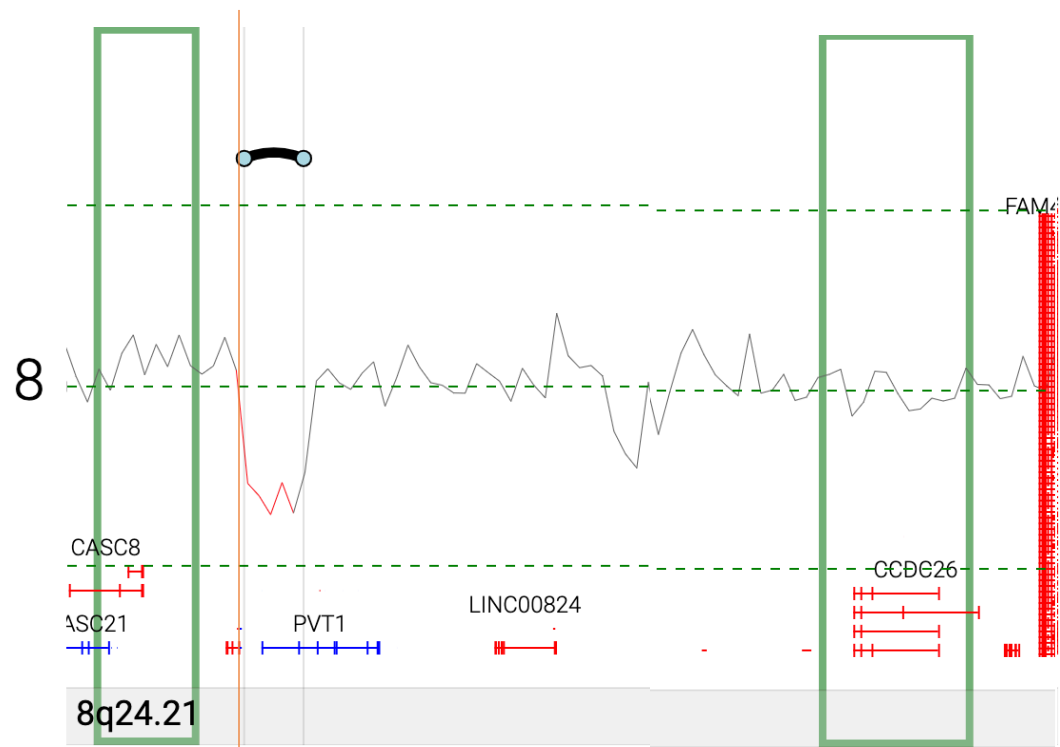
Supplemental Figure 1



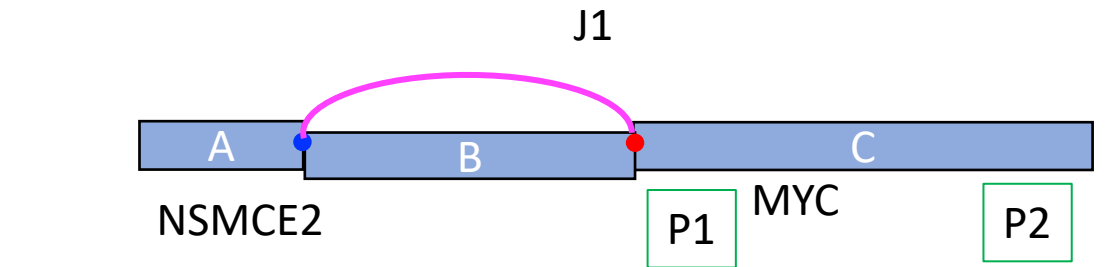
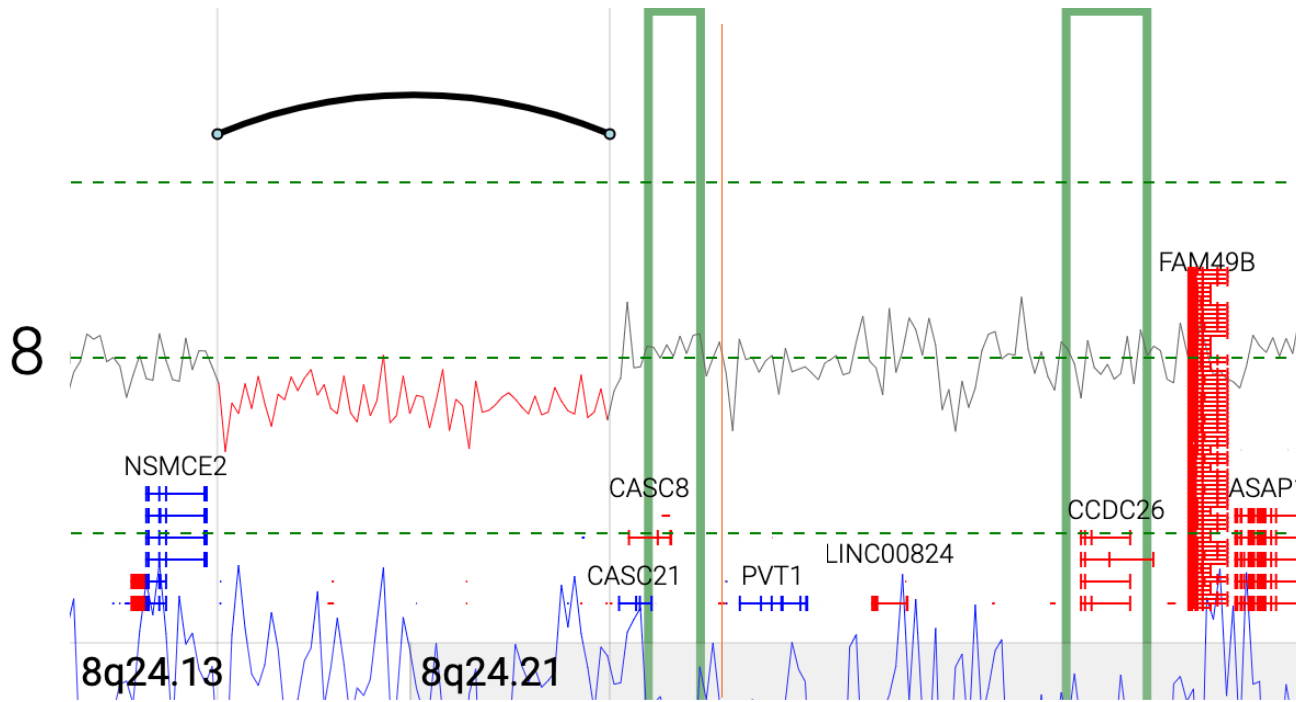
Solution



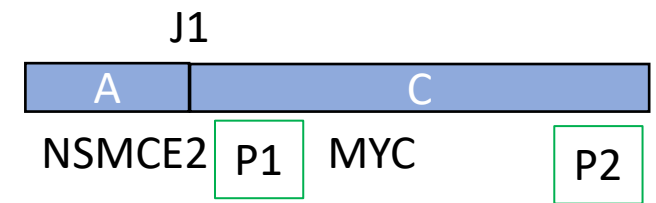
B. Terminal deletion



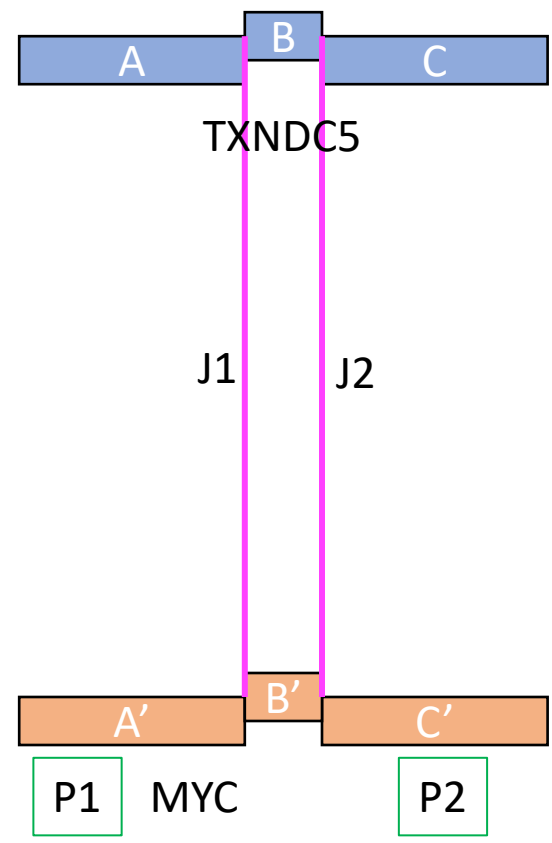
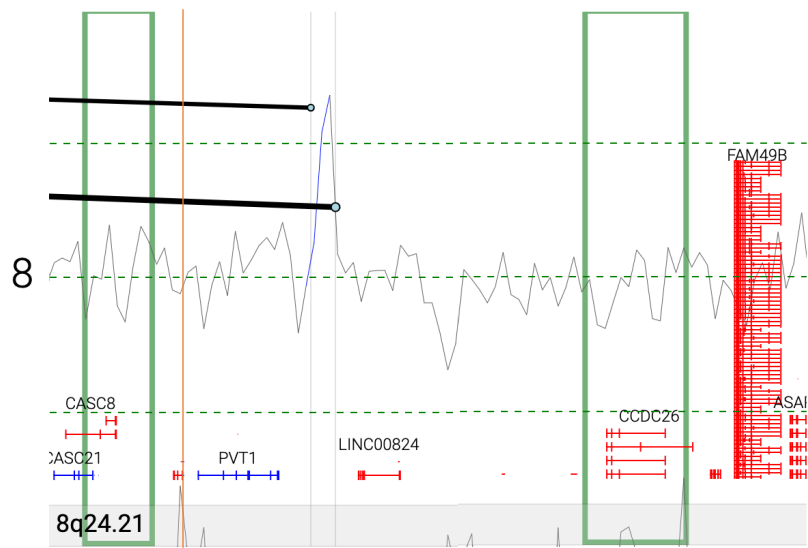
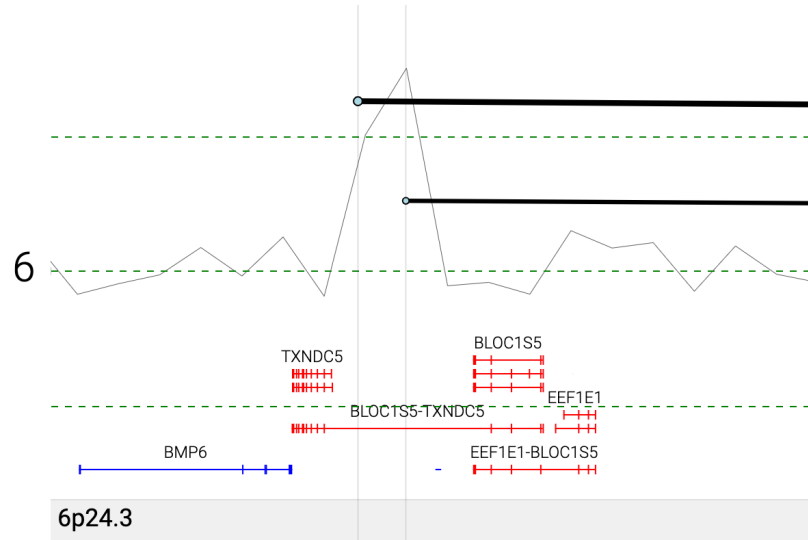
C. Proximal deletion



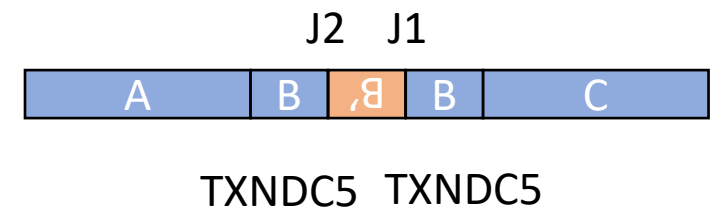
Solution



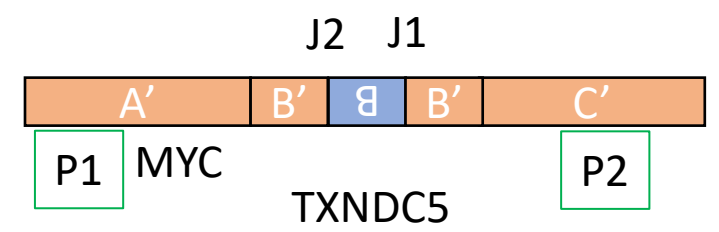
D. Non-Ig insertion



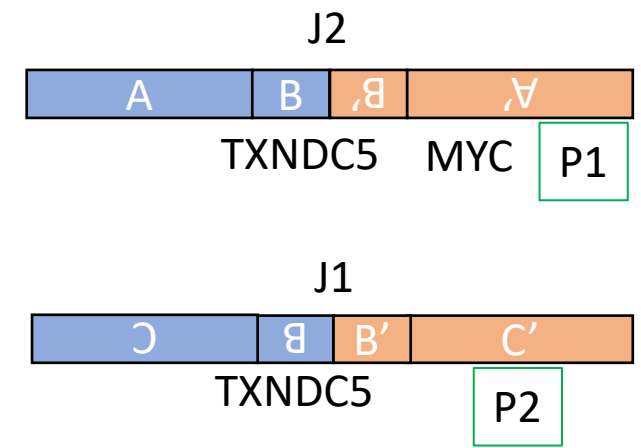
Solution 1



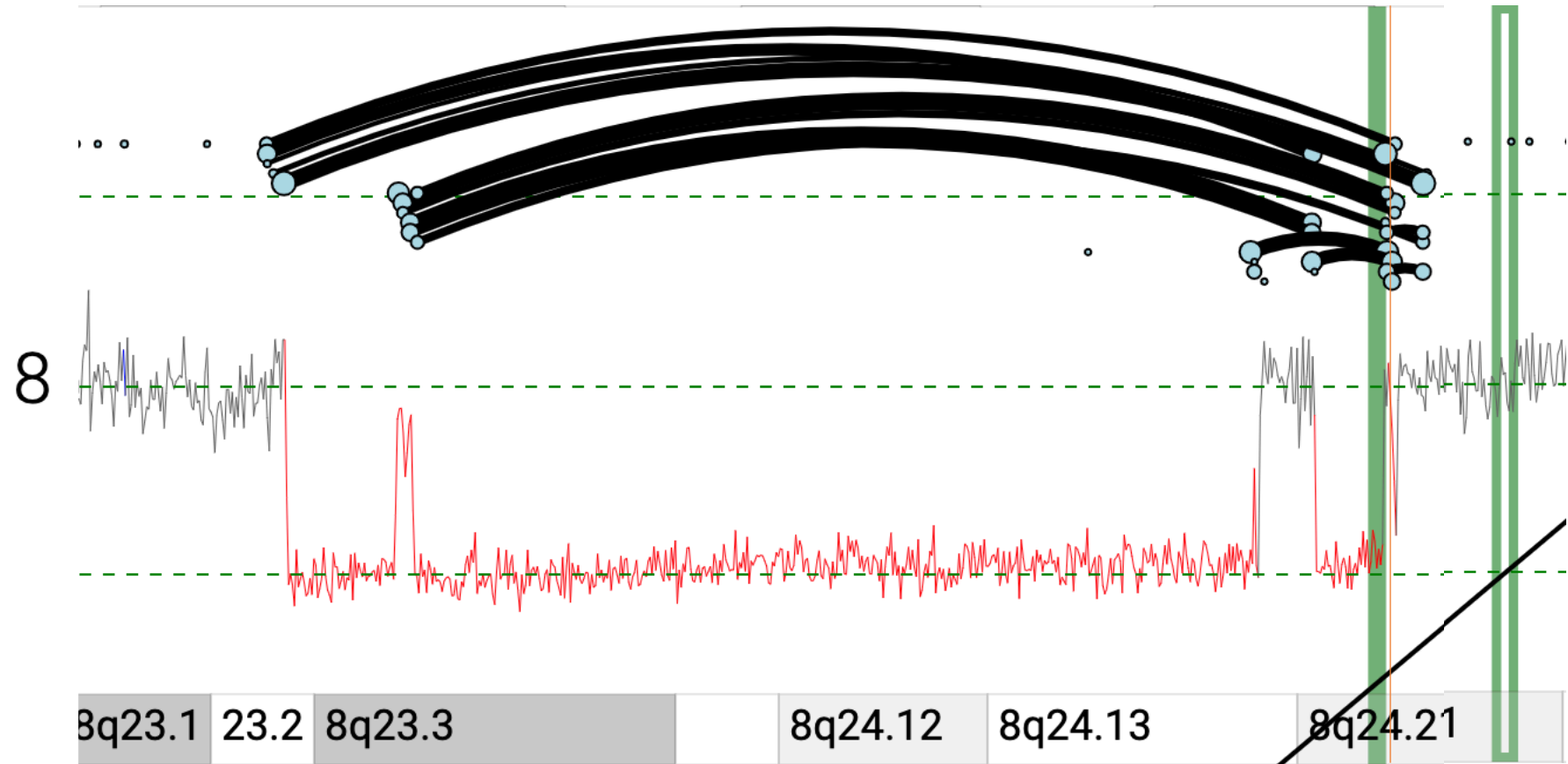
Solution 2



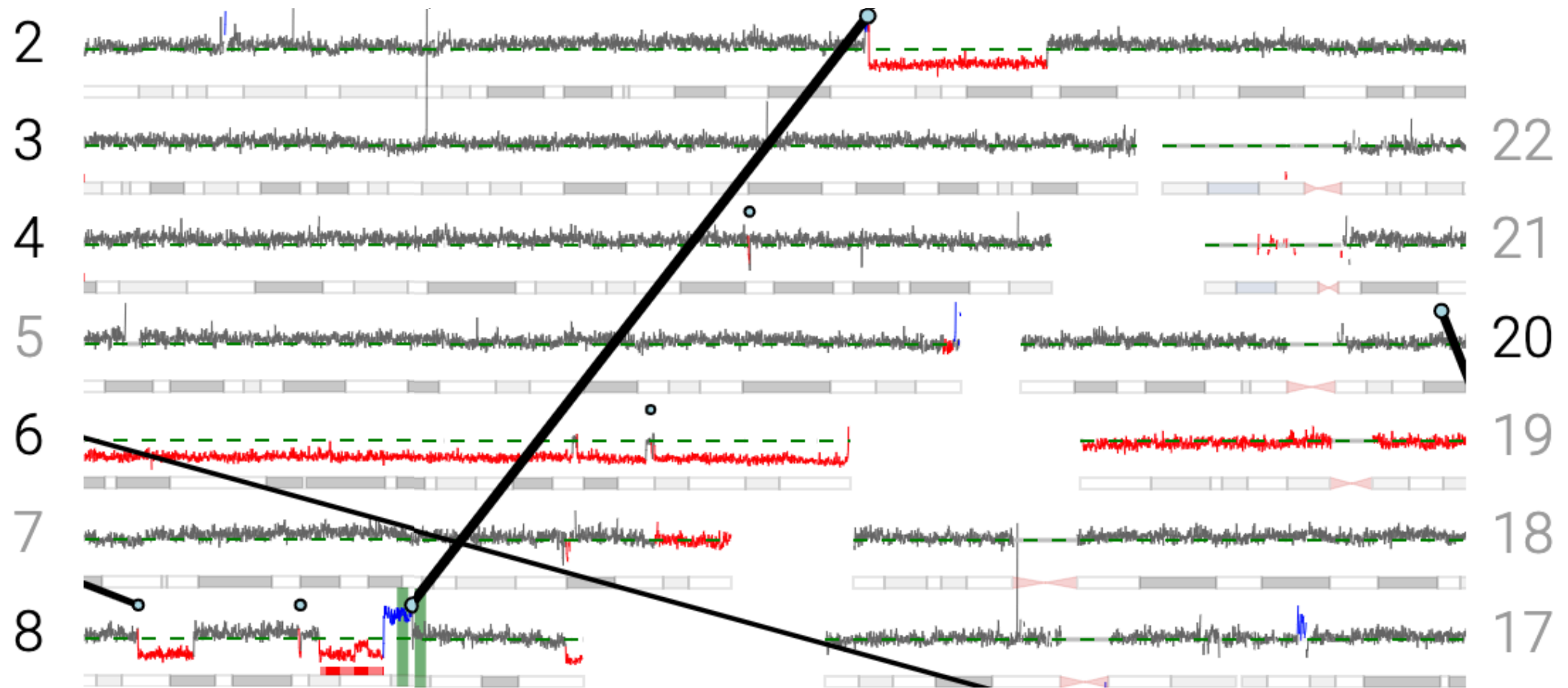
Solution 3



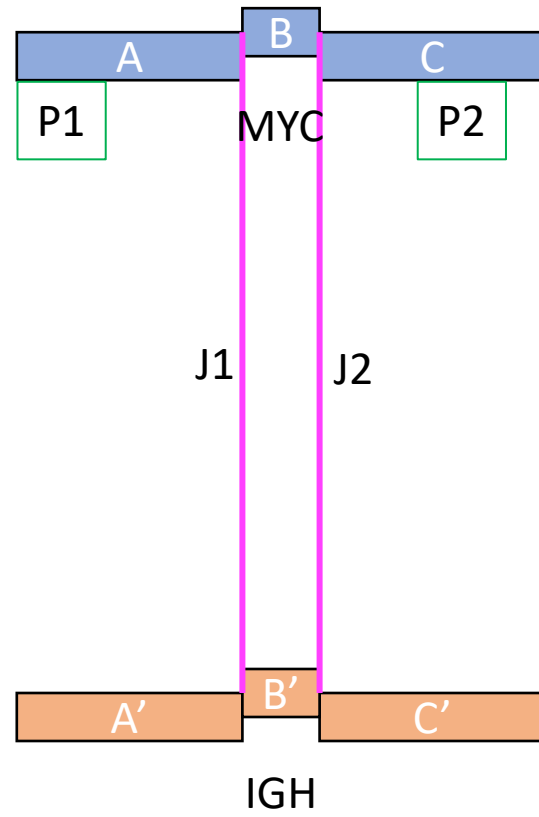
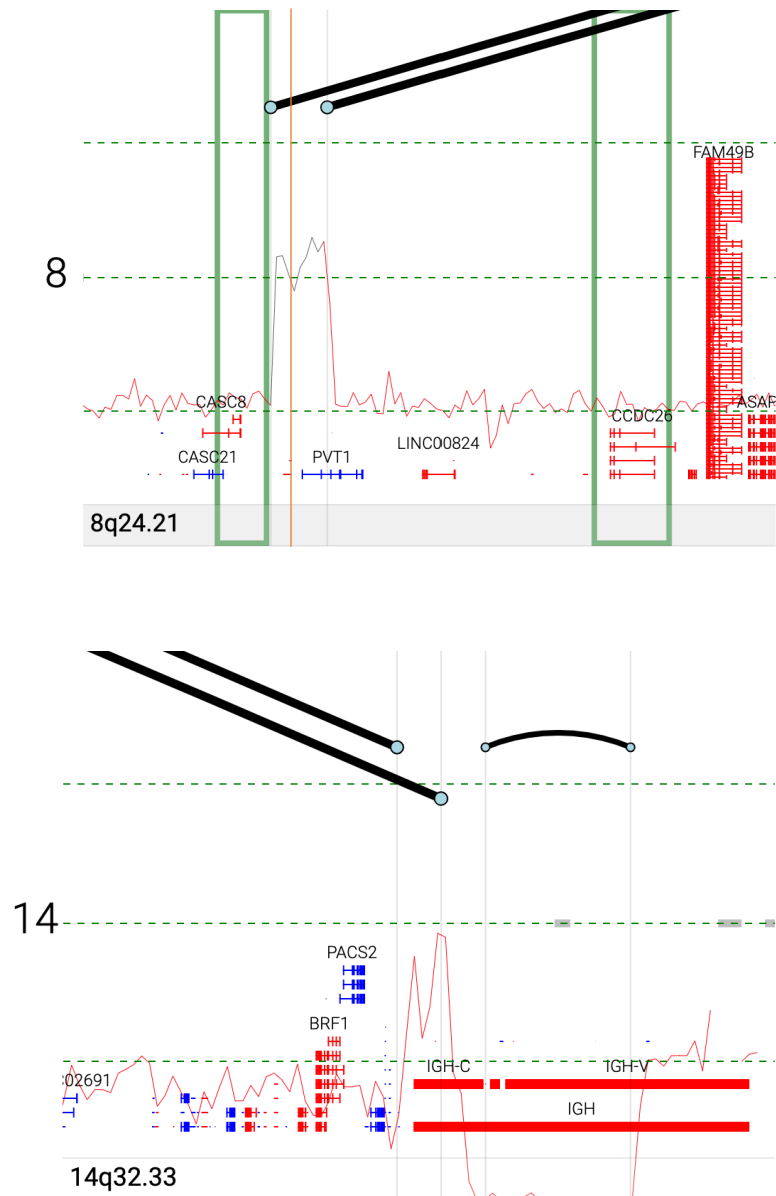
E. Complex Del



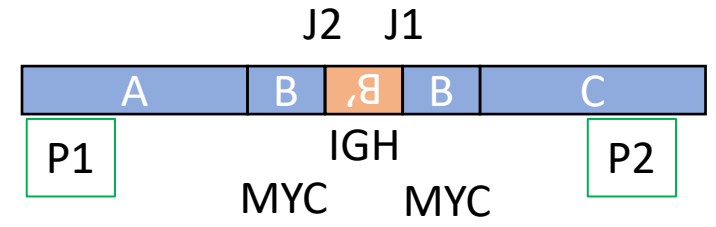
F. Complex gain



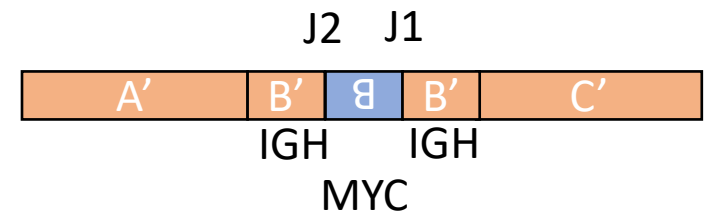
G. Ig-Insertion



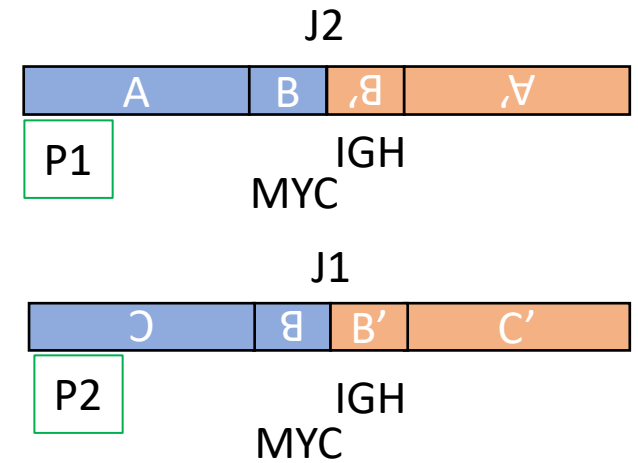
Solution 1



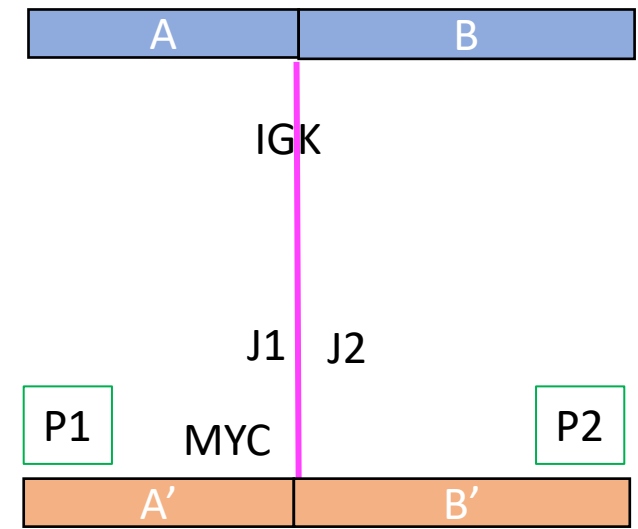
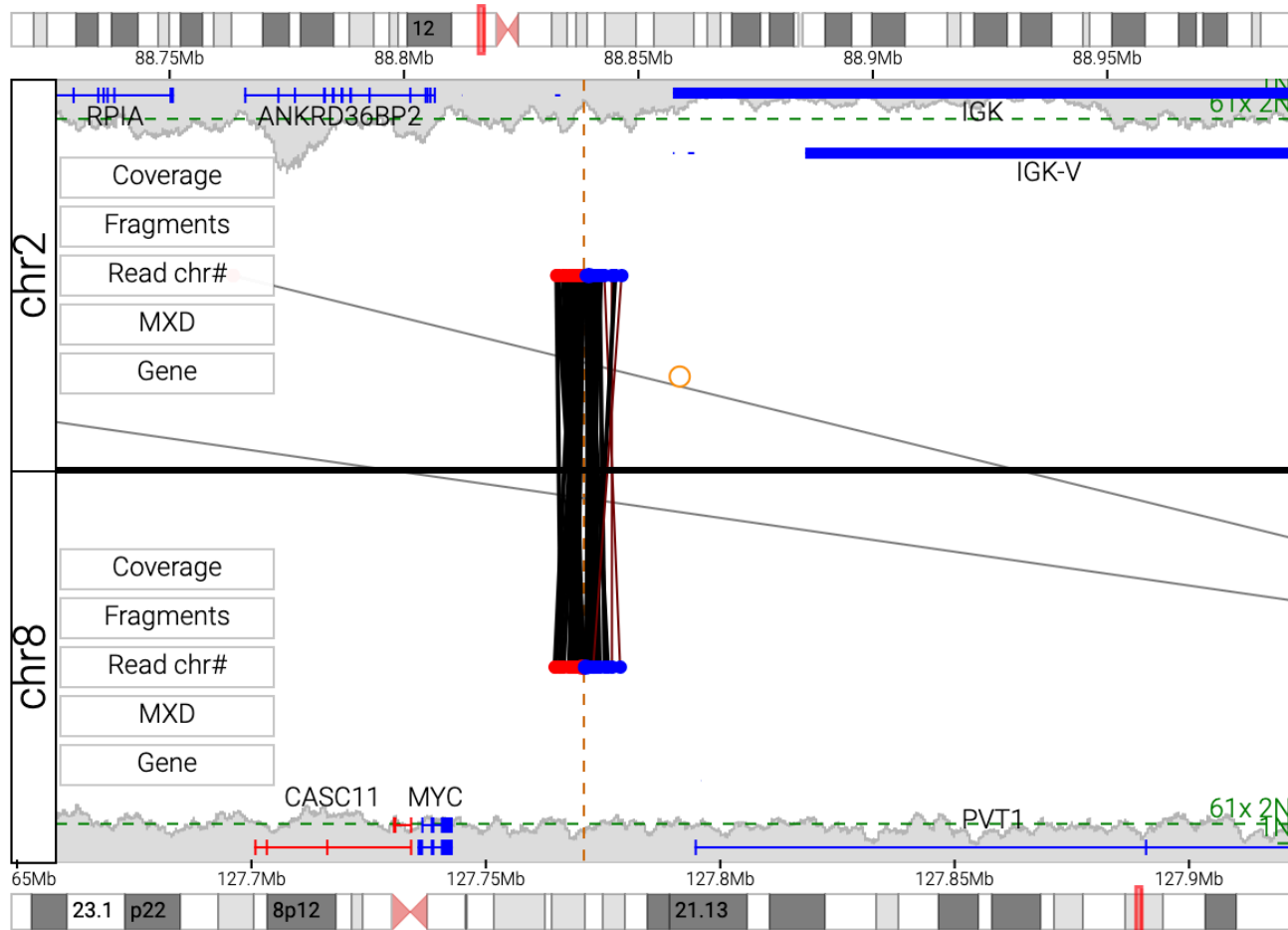
Solution 2



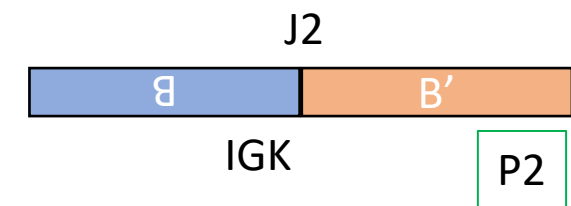
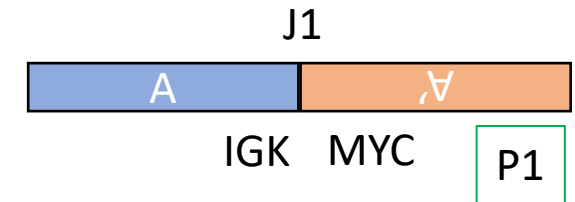
Solution 3



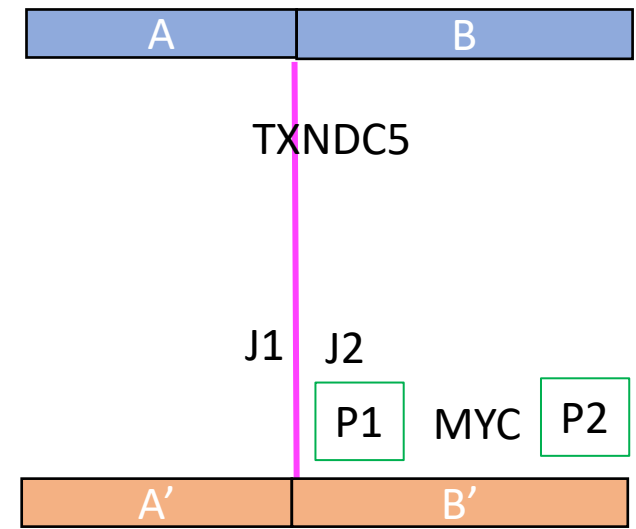
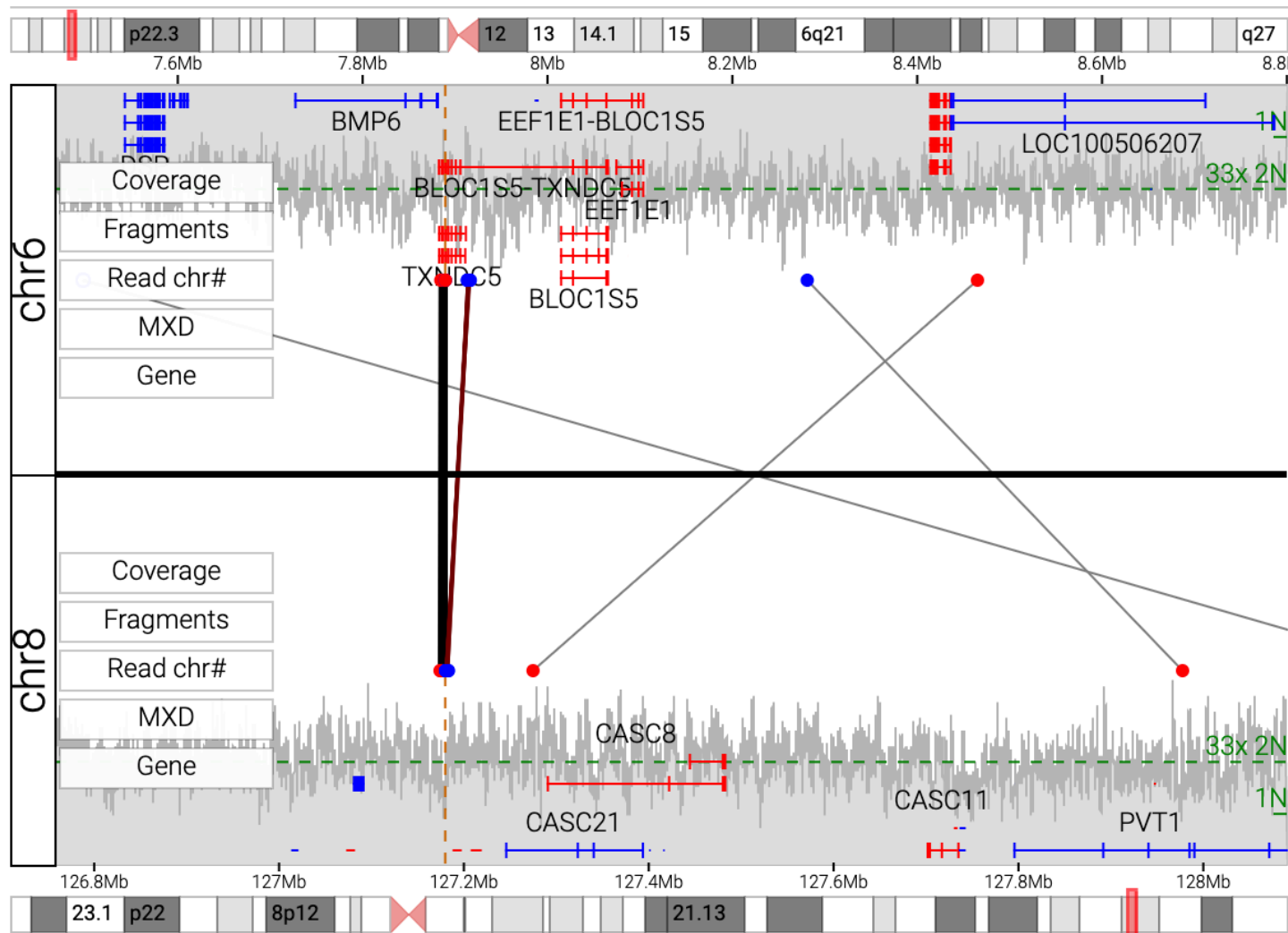
H. Ig-translocation



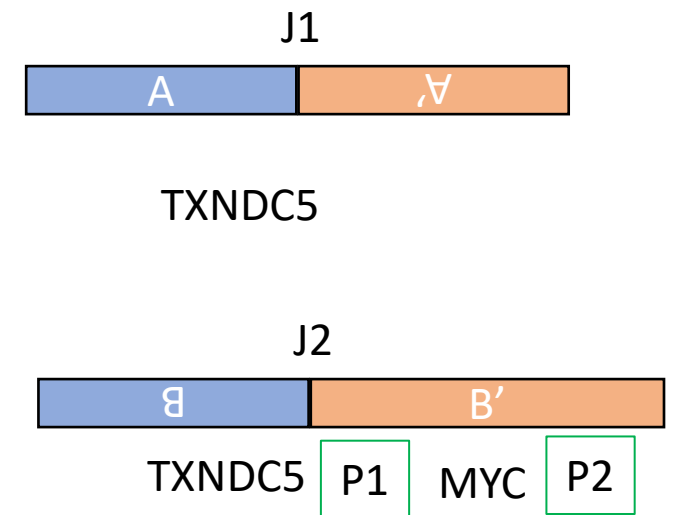
Solution



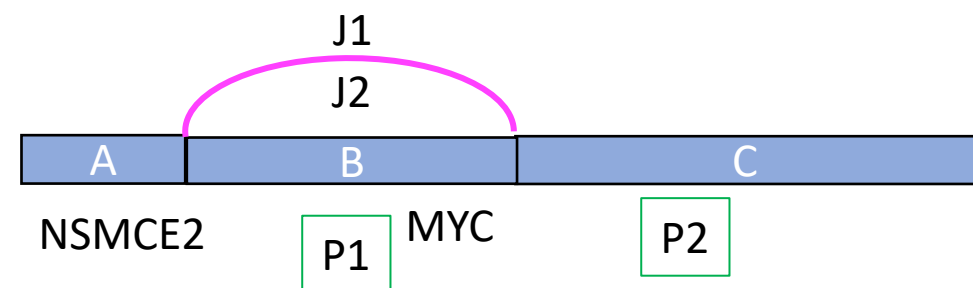
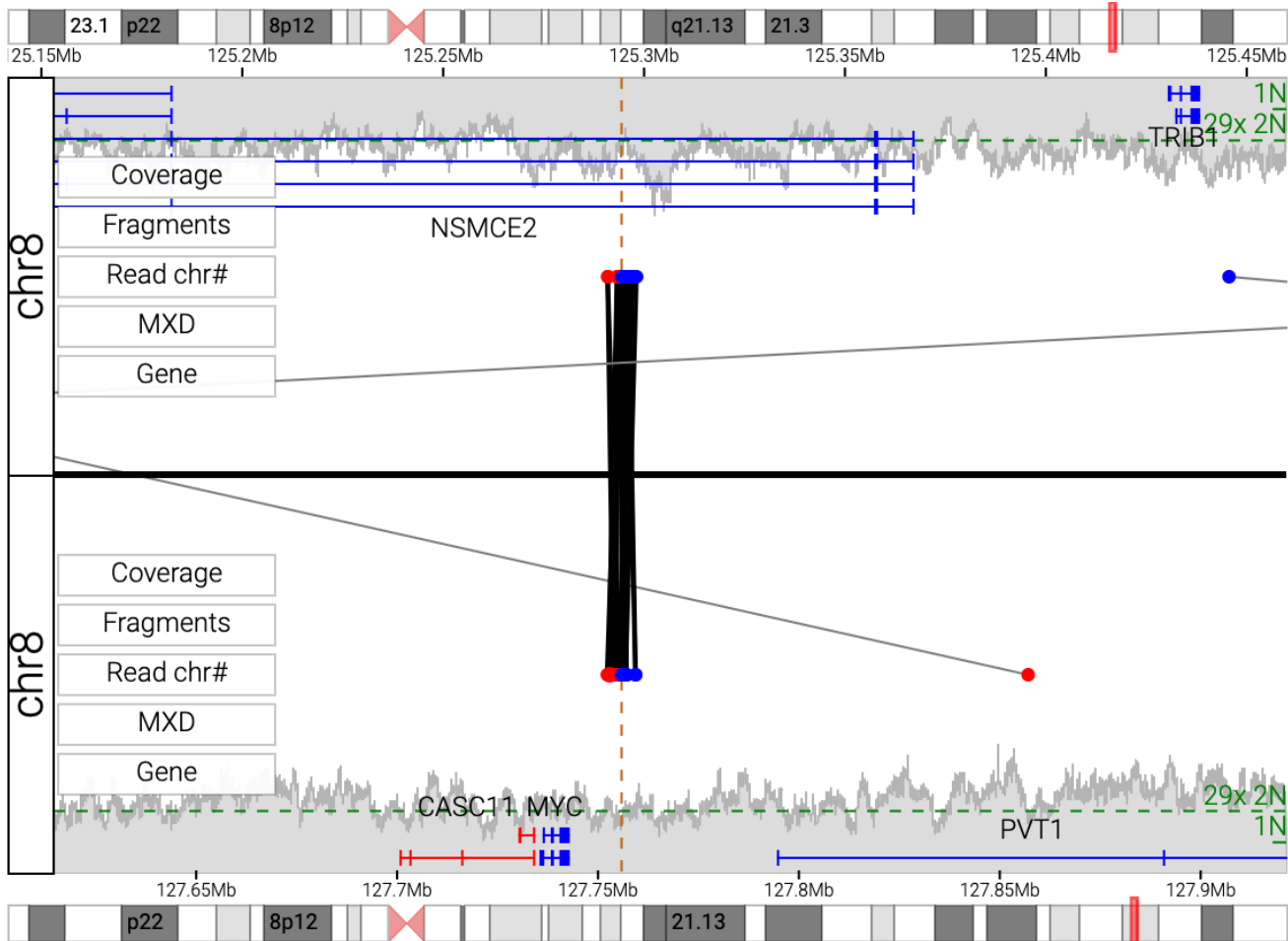
I. Non-Ig translocation



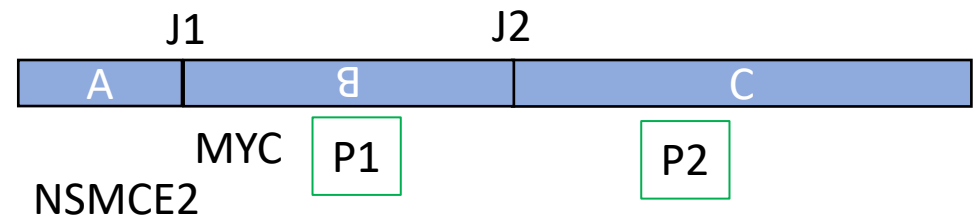
Solution



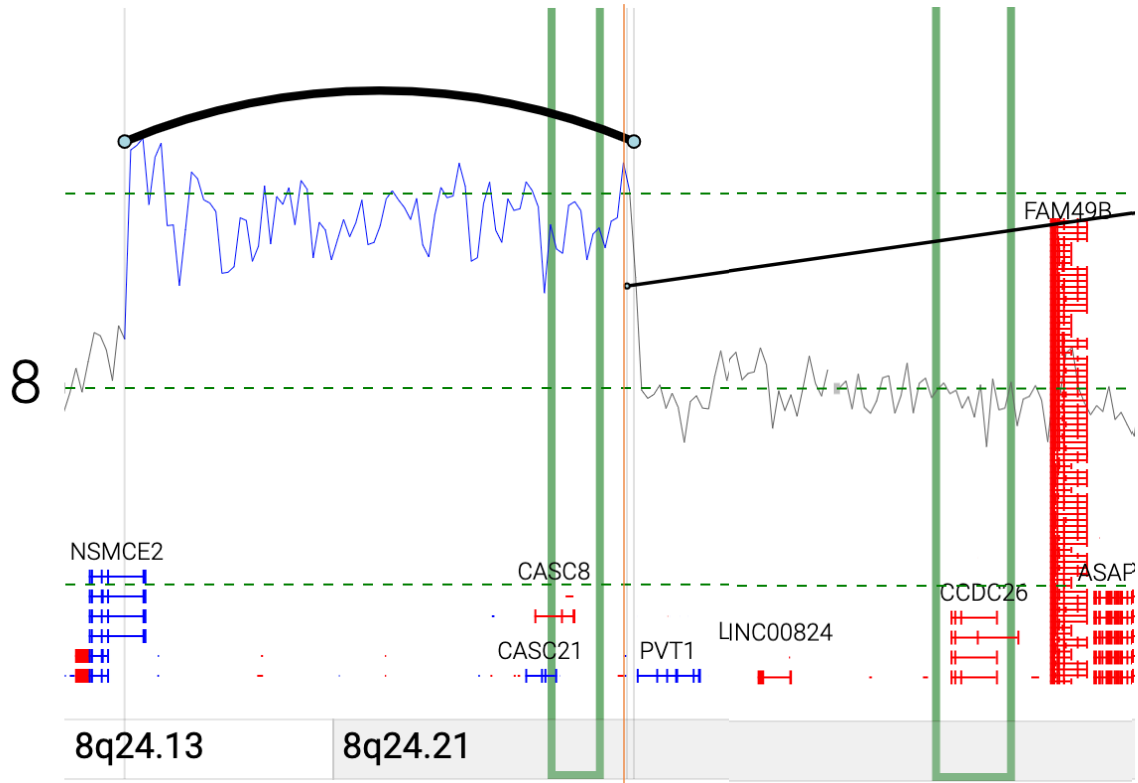
J. Inversion



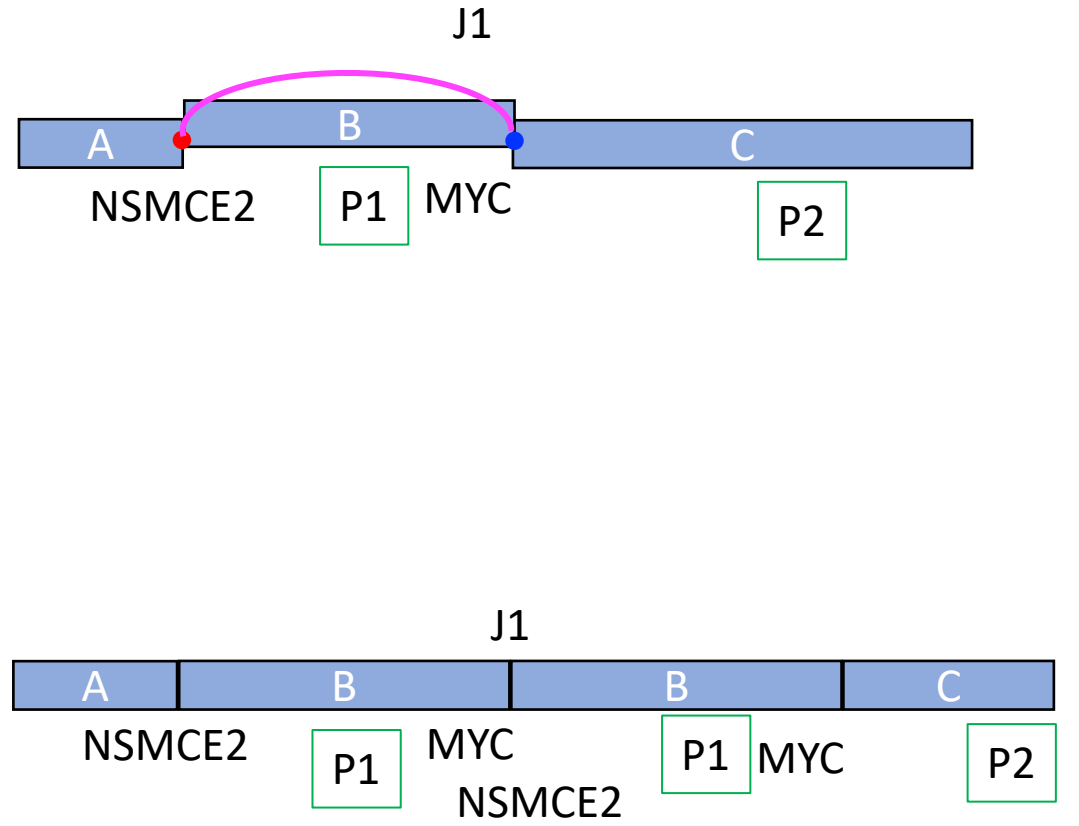
Solution



K. Simple gain



Solution



Supplemental Figure 1: Schematic diagrams of *MYC* SV and genomic architecture predicted from WGS data. A-K, example cases showing either whole genome views or focused plots of different *MYC* SVs. Green boxes show location of the 5' and 3' *MYC* BAP probes and orange line indicates location of the *MYC* gene. Schematic structures of each genomic event are indicated. In some cases the exact genomic event is not possible to be resolved using WGS and multiple solutions are presented. The single case of an inversion was included in the proximal del category due to the proximity of the breakpoint near the *NSMCE2* gene common in the proximal del groups.