

The figure displays genomic data across a 13,000 bp region, with the x-axis labeled 'Position in reference' ranging from 0 to 13,000. The y-axis on the left is labeled 'reads' and ranges from -5,000 to 5,000.

The top track shows read depth, with blue bars representing the reference and red bars representing the sample. The depth is generally high, with a significant peak around 11,000 bp.

The middle track shows variants, with black bars representing SNPs and red bars representing indels. A large red bar is visible around 11,000 bp, indicating a large deletion or insertion.

The bottom track shows structural variants, with blue lines representing the reference and red lines representing the sample. The structural variants are mostly small indels and deletions, with a large deletion around 11,000 bp.

Contig/Read coverage OK

Read depth

Contig/Read coverage OK