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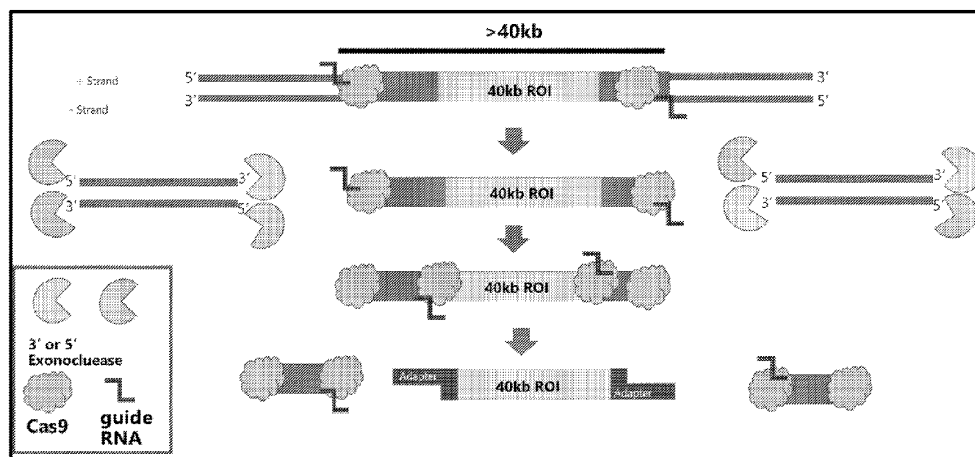


FIG. 17

(57) Abstract: Provided herein are improved methods of analyzing (e.g., sequencing, genotyping, structural analysis) complex genomic regions. In some cases, the methods involve the use of a CRISPR-associated endonuclease and an outer pair of guide RNAs and an inner pair of guide RNAs to excise a genomic region of interest from genomic DNA. The methods further involve the use of long-read sequencing to sequence the genetic region of interest. In some cases, the methods are amplification-free.

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