

ABSTRACT

Compositions and methods for detecting rare sequence variants

In some aspects, the present disclosure provides methods for identifying sequence variants in a nucleic acid sample. In some embodiments, a method comprises identifying sequence differences between sequencing reads and a reference sequence, and calling a sequence difference that occurs in at least two different circular polynucleotides, such as two circular polynucleotides having different junctions, as the sequence variant. In some aspects, the present disclosure provides compositions and systems useful in the described methods.

Fig. 7