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Research

(continued)

Methods

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Cover Complex genomic repeats (CGRs) are characterized by multiple genomic breaks and rearrangements that have the potential to affect multiple genes by creating gene fusions and interruptions. These are especially prevalent in cancer genomes. Whole-genome sequencing of human cancer genomes has facilitated the discovery and characterization of these CGRs. In this issue, a novel method (CouGaR) utilizing both depth of coverage and read mapping information is described. Additionally, to further help display and understand the structure of CGRs, CouGaR-viz, a generic stand-alone tool to visualize the copy count of regions, breakpoints, and relevant gene, is also described. The illustration shows one such occurrence of a CGR with genomic segments contributed by three different chromosomes to result in a circular contig. (Cover illustration by Jammie Mountz. [For details, see Dzamba et al., pp. 107–117.])