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De novo phasing resolves haplotype sequences in complex plant genomes

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摘要	Genome phasing is a recently developed assembly method that separates heterozygous eukaryotic genomic regions and builds haplotype-resolved assemblies. Because differences between haplotypes are ignored in most published de novo genomes, assemblies are available as consensus genomes consisting of haplotype mixtures, thus increasing the need for genome phasing. Here, we review the operating principles and characteristics of several freely available and widely used phasing tools (TrioCanu, FALCON-Phase, and ALLHiC). An examination of downstream analyses using haplotype-resolved genome assemblies in plants indicated significant differences among haplotypes regarding chromosomal rearrangements, sequence insertions, and expression of specific alleles that contribute to acquisition of the biological characteristics of plant species. Finally, we suggest directions to solve addressing limitations of current genome-phasing methods. This review provides insights into the current progress, limitations, and future directions of de novo genome phasing, which will enable researchers to easily access and utilize genome-phasing in studies involving highly heterozygous complex plant genomes.
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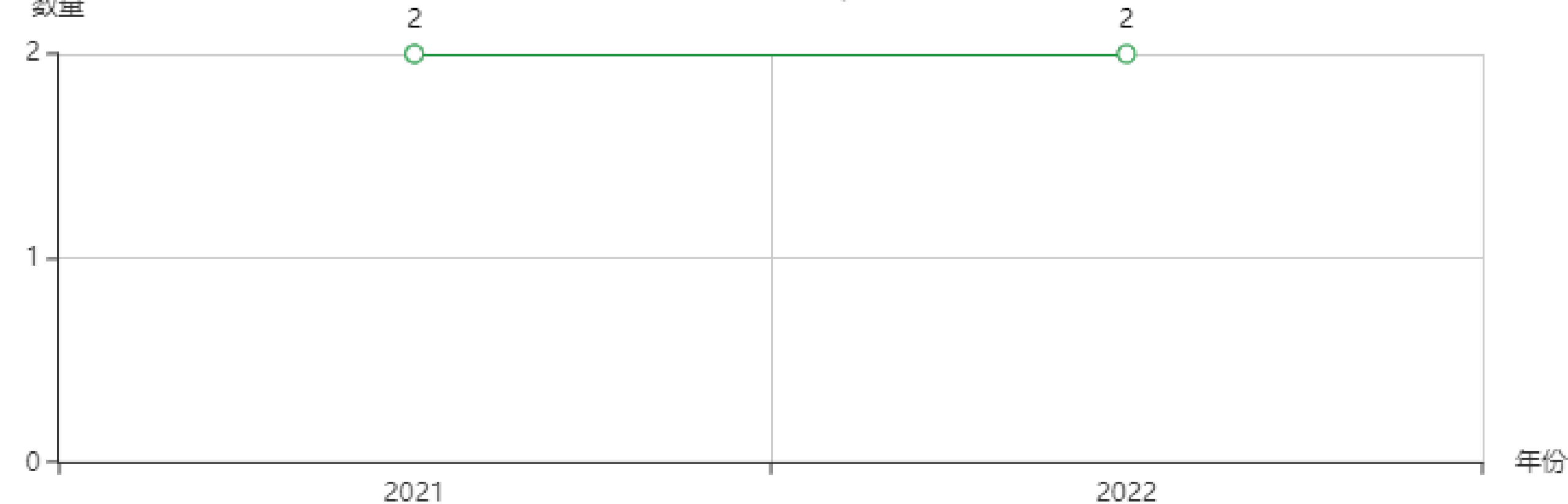
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