

Haplotype-resolved genome assemblies of Chasselas and Ugni Blanc

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Haplotype-resolved genome assemblies were produced for Chasselas and Ugni Blanc, two heterozygous real-field genetic pool *Vitis vinifera* cultivars by combining high-fidelity long-read sequencing (HiFi) and high-throughput chromosome conformation capture (Hi-C). The telomere-to-telomere full coverage of the chromosomes allowed us to assemble separately the two haplotypes of both cultivars and revealed structural variations between the two haplotypes of a given cultivar. The deletions/insertions, inversions, translocations, and duplications provide insight into the evolutionary history and parental relationship among grape varieties. Integration of de novo single long-read sequencing of full-length transcript isoforms (Iso-Seq) yielded a highly improved genome annotation. Given its higher contiguity, and the robustness of the IsoSeq-based annotation, the Chasselas assembly meets the standard to become the annotated reference genome for *Vitis vinifera*.

Keywords: Genome assembly, Genome annotation, HiFi, Hi-C, Iso-Seq.