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Clonal improvement-associated somatic mutations identified from diploid genome assembly in Tempranillo grapevine cultivar

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Tempranillo is the third most widely grown red wine cultivar worldwide and the most relevant in the Iberian Peninsula. Here we produced a diploid genome assembly of Tempranillo to study the origin of clonal improvement in this cultivar. After PacBio and Oxford Nanopore sequencing, a trio binning approach produced chromosome-arm level and complete assemblies for the two haplo-phases. Based on the *de novo* assembly, we searched for genetic variation in ten re-sequenced Tempranillo clones selected for variation in agronomically relevant traits including fruit colour, low fruit sugar accumulation adaptable to warmer climates or loose bunches that are less prone to fungal diseases. Thousands of somatic mutations were detected in the ten clones, which, combined with gene annotations based on PacBio Iso-seq, identified candidate dominant missense variants related with selected phenotypes. We could also phase inter-chromosomal structural variation (SV) in the origin of white gape and loose cluster phenotypes. Our results provide a quality genome assembly for inter- and intra-cultivar comparisons and release candidate missense and SV mutations that could be responsible for clonal diversification and improvement.

Keywords: somatic variation, clonal improvement, genome assembly, variant calling, structural variation, candidate mutations