

## HIGH-DENSITY CONSENSUS LINKAGE MAP BASED ON THREE MAPPING POPULATIONS USING THE VITIS18K SNP CHIP FOR GRAPEVINE BREEDING

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The improvement of grapevine through biotechnology requires the understanding and identification of molecular bases of traits of interest. These determinants can be identified through studying the association between molecular markers, such as SNPs, and target traits. The Vitis18K SNP chip provides an inexpensive genotyping tool that allows for genome-wide scale marker analysis across populations. The majority of linkage maps are based on a single mapping population, but a consensus map obtained from multiple mapping populations can increase marker density and provide insight into marker order conservation.

Here we present a consensus map based on three mapping populations. The genetic parents consist of well-known wine cultivars such as 'Cabernet Sauvignon', 'Corvina' and 'Riesling' often used for constructing linkage maps, but also include lesser known varieties like 'Deckrot' and a table grape selection, G1-7720.

We have first developed three high-density population maps with an average inter-locus gap ranging between 0.74 and 0.99 cM. These maps show high correlation (0.9797 – 0.9997) with the 'PN40024 12X.2' reference assembly, whilst still allowing to report on approximately 100 markers with large order discrepancies, of which a third is consistent across multiple populations. Furthermore, our genetic data provide information useful to further refine the grapevine genome assembly, by anchoring yet unanchored sequences. Finally, we present a consensus map including 6 895 molecular markers and with an inter-locus gap distance of 0.53 cM. Importantly the consensus map shows even higher collinearity to the reference assembly compared to the single population maps. All together this study provides a promising tool for the identification of molecular determinants associated with traits of interest, releases information useful for researchers using the Vitis18K SNP chip and allows to increase our current understanding of the grapevine genome.