



# Book of Abstracts

Oral & Poster Abstracts



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### The construction of a high-density consensus map based on three mapping populations using the Vitis18K SNP chip and a reference genome sequence

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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. Data analysis in linkage map construction for large datasets can be time consuming or requires extensive coding skills. Different algorithms can allow for faster analyses, but quite often at the cost of number of markers mapped, or accuracy. In this study, we used a workflow which combines the genetic data of a mapping population with a reference genome sequence to construct three high-density population maps with an average inter-locus gap distance 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. Finally, we present a consensus map containing 6 895 molecular markers with an inter-locus gap distance of 0.53 cM, which shows even higher collinearity to the reference assembly compared to the single population maps. The presented workflow helps to construct linkage maps faster and more accurately, whilst the consensus map provides a promising tool for the identification of molecular determinants associated with traits of interest. This information is useful for researchers who want to use the Vitis18K SNP chip, but also showcase the integration of data which allows us to further our understanding of the grapevine genome.

**Keywords:** Vitis18K SNP chip, high-density consensus map, collinearity, reference assembly, data integration