

Supplementary data

A high-density integrated map for grapevine based on three mapping populations genotyped by the *Vitis*18K SNP chip

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Figure S1: Decay of LD estimated for each of the 19 grapevine chromosomes. A regression line for the average r^2 value estimated in sequential bins of 20 Kb against the physical distances between SNP is shown for each of the three populations. Decay in CSxC ('Cabernet Sauvignon' x 'Corvina', 142 plants) is shown in blue, in DRxG1 ('Deckrot' x G1-7720, 137 plants) in red and in RRxCS ('Rhine Riesling' x 'Cabernet Sauvignon', 139 plants) in green, respectively. The LD decay for the population built including individuals from each of the three populations (418 plants) is shown in yellow. Abbreviations: chr = chromosome.

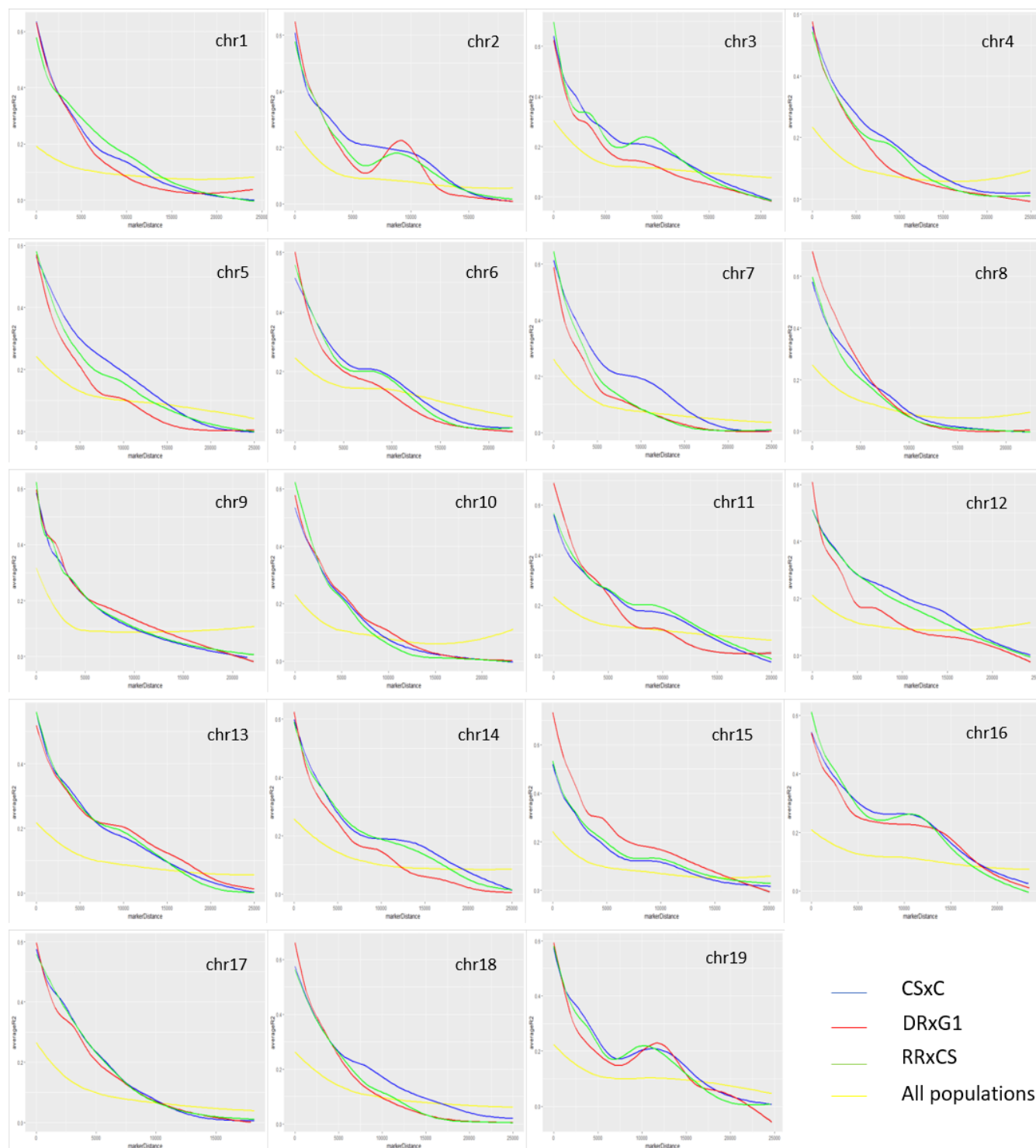


Figure S2: Detailed grapevine integrated map based on three mapping populations (CSxC: ‘Cabernet Sauvignon’ x ‘Corvina’, DRxG1: ‘Deckrot’ x G1-7720 and RRxCs: ‘Rhine Riesling’ x ‘Cabernet Sauvignon’) indicating the names of all non-collinear (with the ‘PN40024 12X.v2’ assembly and between populations) markers and markers mapped in all three populations (bold). Markers that are in non-collinear positions with the ‘PN40024 12X.v2’ genome assembly order are indicated in blue (dark blue if supported by more than one population map, shared conflicts introduced by conflict solving are not highlighted). The population map involved in the conflict is indicated with suffix –A (CSxC), –B (DRxG1) or –C (RRxCs). Markers that are in non-collinear positions between population maps are indicated in red with the suffixes –AB (CSxC vs DRxG1), –AC (CSxC vs RRxCs) or –BC (DRxG1 vs RRxCs) to indicate conflictual populations. Priority is given to red labeling. The suffixes (1) (2) (3) indicate the number of population maps in which the markers were mapped. Markers that are collinear with the ‘PN40024 12X.v2’ assembly and between population maps and are not mapped in all three populations are only indicated with a line.

