**Detection of transmitted loci between scion and rootstock of graft plants**

First genome sequencing data of DVIT1380, DVIT2228, C3309, Chardonnay, Riparia Glorie and Cabernet Sauvignon, and RNA-Seq data of Riesling were used to infer genotypes at each genomic position of these accessions. The genome and RNA-Seq reads were mapped to the *V. vinifera* reference genome (12X; ([Jaillon, et al., 2007](#_ENREF_1))) using BWA allowing up to four edit distances ([Li and Durbin, 2009](#_ENREF_2)). Only uniquely mapped reads were kept. Potential PCR duplicates were removed based on the mapping results. Following alignment, the coverage of each genomic position by base A, G, C and T was calculated based on the mpileup file generated by SAMtools ([Li, et al., 2009](#_ENREF_3)). Only homozygous genomic loci and loci with different genotypes between the scion and the rootstock of a graft plant (we call them SNP loci) were used for downstream transmitted locus identification. For each homozygous locus, we required at least 7 reads supporting the dominant allele and that the reads supporting the minor allele were less than 10% of the reads from the dominant allele.

RNA-Seq reads from the rootstock and the scion of a graft plant were then aligned to the *V. vinifera* reference genome and the coverage of each genome locus by A, G, C and T was derived, using the same method describe above. A SNP locus was identified as a transmitted locus if (1) at least two reads from the receptor RNA-Seq library had same genotype with the donor genome at the locus (Figure 1a); or (2) a read from the receptor RNA-seq library had same genotype with the donor genome at the locus and at least one flanking SNP locus (Figure 1b); or (3) a read from the receptor RNA-seq library had same genotype with the donor genome at the locus, and at least one read from the receptor RNA-seq library had same genotype with the donor genome at additional loci from the same gene (Figure 1c). The identified genomic loci represented a high-confidence set of loci with transmitted transcripts between scion and rootstock of a graft plant.

**Transmission rate estimation**

After obtaining the high-confidence transmitted loci, we used a window-based approach to estimate the mRNA transmission rate between scion and rootstock. For each transmitted locus, a window centered at the locus was generated. The window was extended to the left and right by a size of read length, respectively. To estimate the transmission rate from donor to receptor, we counted the number of the donor and receptor RNA-seq reads, respectively, that perfectly matched the donor genome within the transmission window (Figure 2).

References

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