**Detect transmitting loci**

For both DNA and mRNA sequencing data, short reads (100-bp) were mapped to the grape reference genome using BWA. Only uniquely mapped reads were used in detecting transmitting loci. Potential PCR duplicates were removed based on the mapping results. At each genomic position covered by mapped read(s), we counted the read coverage of each nucleotide (figure 1a), which reflects the genotype composition of the sequenced material. For RNA-seq data, however, nucleotide at the start or end position of a read was excluded.

We then compiled a raw list of genomic positions with potential transcript transmissions between scion and rootstock based on their genomic and transcriptomic genotypes. Figure 1a shows a potential transmitting locus. A locus was added to the list if it met all of the following conditions: (1) homozygous genotypes in both rootstock and scion genomes. We required at least 7 reads supporting a dominant allele and that the reads supporting the minor allele are less than 10% of the reads from the dominant allele. (2) different genotypes between rootstock and scion DNA. (3) transmitting mRNA. Reads comprising scion (or rootstock) transcripts have two alleles – one transcribed from the scion DNA and the other transmitted from rootstock mRNA (figure 1a).

After obtaining the raw list of potential transmitting loci, we did further filtration to reduce false positives due to misalignment of short reads, sequencing errors, or reference genome assembly errors or incompleteness. A locus was kept if it met any one of the following conditions: (1) a flanking SNP from the same read. A read from scion RNA-seq library, which supports the potential transmitting locus, was perfectly matched with the rootstock DNA, but it exhibits one SNP at the locus and additional SNP(s) at the neighboring position(s) with respect to the scion DNA (figure 1b). If a read derived from rootstock RNA-seq library supports mRNA transmission from scion to rootstock, then this read is perfectly matched with the scion DNA but has two or more SNPs relative to the rootstock DNA. (2) two or more reads supporting the same locus. At least two reads from RNA-seq library support this potential locus (figure 1c). (3) additional transmitting locus from the same gene. There is another read supporting another transmitting locus from the same gene (figure 1d). The kept genomic positions represent a high-confidence set of loci with transmitting transcripts between scion and rootstock.

**Estimate transmission rate**

After obtaining the high-confidence transmitting loci, we used a window-based approach to estimate the mRNA transmission rate between scion and rootstock (figure 2). For each transmitting locus, a window centered at the locus position was generated. The window was extended to the left by a size of read length and also to the right by the read length. To estimate the transmission rate from rootstock to scion (figure 2), we counted the number of the rootstock RNA-seq reads that were perfectly matched with the rootstock DNA and mapped within the transmission window. We then counted all of the scion RNA-seq reads that were also perfectly matched with the rootstock DNA and mapped within the transmission window. Such reads in the scion RNA-seq library must be transmitted from the rootstock because there is an SNP between scion and rootstock at the locus. Similarly, transmission rate from scion to rootstock can also be estimated.