

# De novo assembly of separate haplotypes solves the high-heterozygosity inconvenience of grapevine genomes

## A completely-phased diploid genome assembly for 'Malbec' cultivar (*Vitis vinifera* L.)

### 1- INTRODUCTION

- Grapevine cultivars originate from outcrossing two pre-existing cultivars and are clonally propagated. They have diploid and highly heterozygous genomes, challenging to assemble.
- Malbec is the main cultivar for Argentina wine industry, and its parental cultivars are Prunelard and Magdeleine Noire des Charentes.

### 2- METHODS

Malbec genome *de novo* assembly  
mother-father-offspring trio approach

Prunelard  
short-reads

Malbec  
long-reads

Magdeleine  
short-reads

Canu-Trio-Binning  
software

Malbec reads were separately assemble  
into two haplotypes (haplomes)

Haplome  
Prunelard

Haplome  
Magdeleine

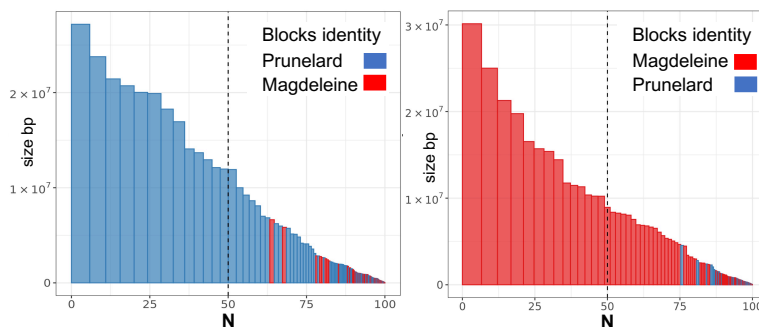
Post-processed for assembly corrections

### 3- RESULTS

Table 1. Malbec haplomes assembly statistics

Haplome	Size (Mb)	N50 (Mb)	# BUSCO genes (Cost_v3)
Magdeleine	479	6.6	41,866
Prunelard	480.4	7.8	41,884

Figure 1. Haplomes blocks composition (Mercury)



### 4- DISCUSSION

- We obtained two contiguous, complete and truly phased assemblies (haplomes) for Malbec, with the expected size for grapevines' haploid genomes (Table 1).
- Haplomes were composed by genomic data of the corresponding parental cultivar, with a very small percentage (<0.13%) of miss-assigned blocks (Figure 1).
- Canu-TB proved to be a valid approach to overcome the high heterozygosity that hampers grapevines' genomes *de novo* assembly.

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