

Population sequencing reveals clonal diversity and ancestral inbreeding in the grapevine cultivar Chardonnay



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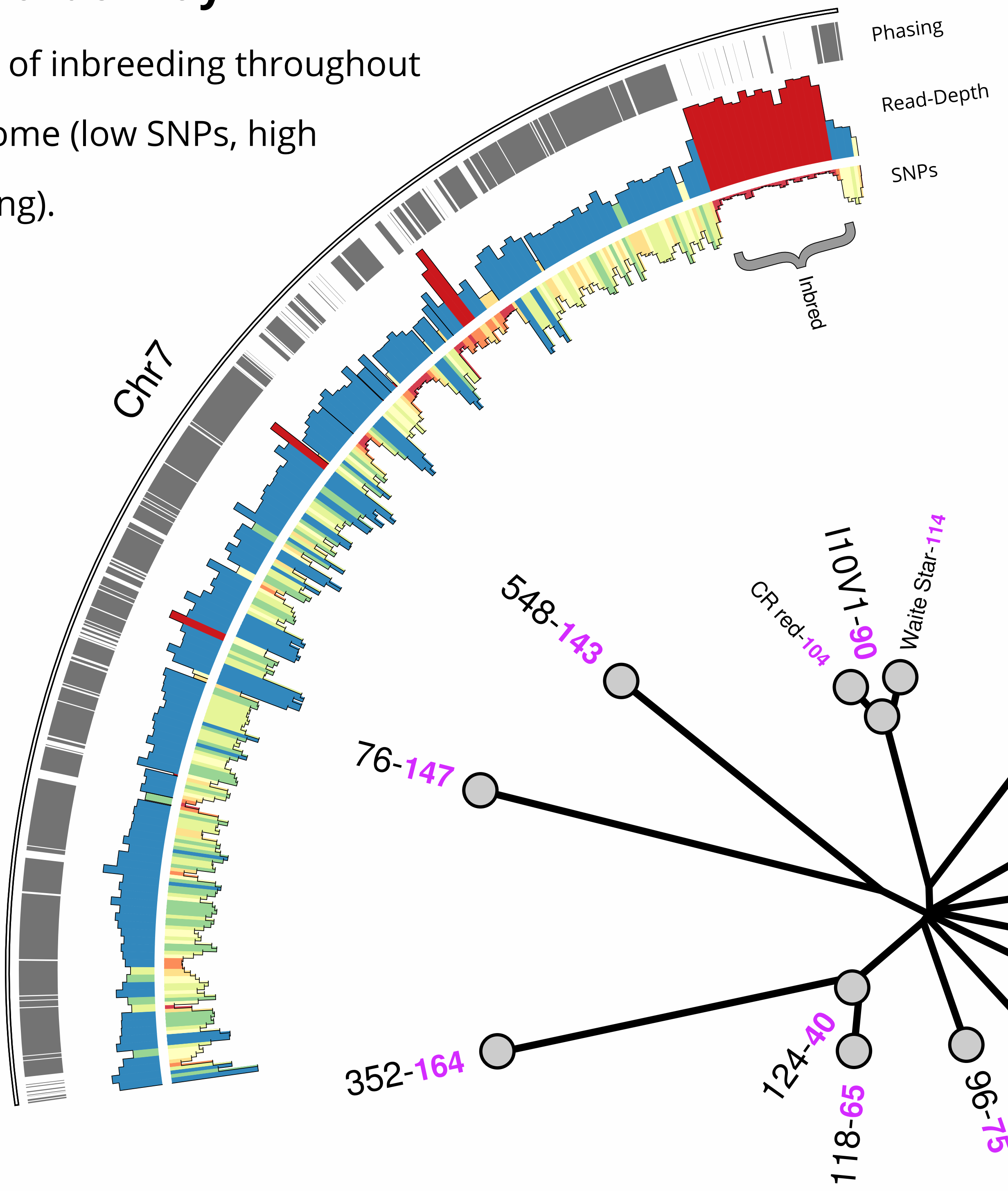
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Chardonnay genome assembly, clonal mutations, and insights into Chardonnay's heritage

The Chardonnay genome was assembled using the latest long-read sequencing technology, allowing far greater insight than was previously possible. There are many clones for Chardonnay due to genetic mutations accumulating during propagation. Fifteen clones were sequenced and 1,620 mutations were identified that distinguish them. Chardonnay was compared to sequencing of its parents—Pinot Noir and Gouais Blanc. There is evidence of inbreeding from a genetic backcross between Pinot Noir and a progenitor of Gouais Blanc, making Pinot Noir both Chardonnay's parent and probably its great-grandparent.

Inbreeding in Chardonnay

There are indications of inbreeding throughout the Chardonnay genome (low SNPs, high read-depth, no phasing).

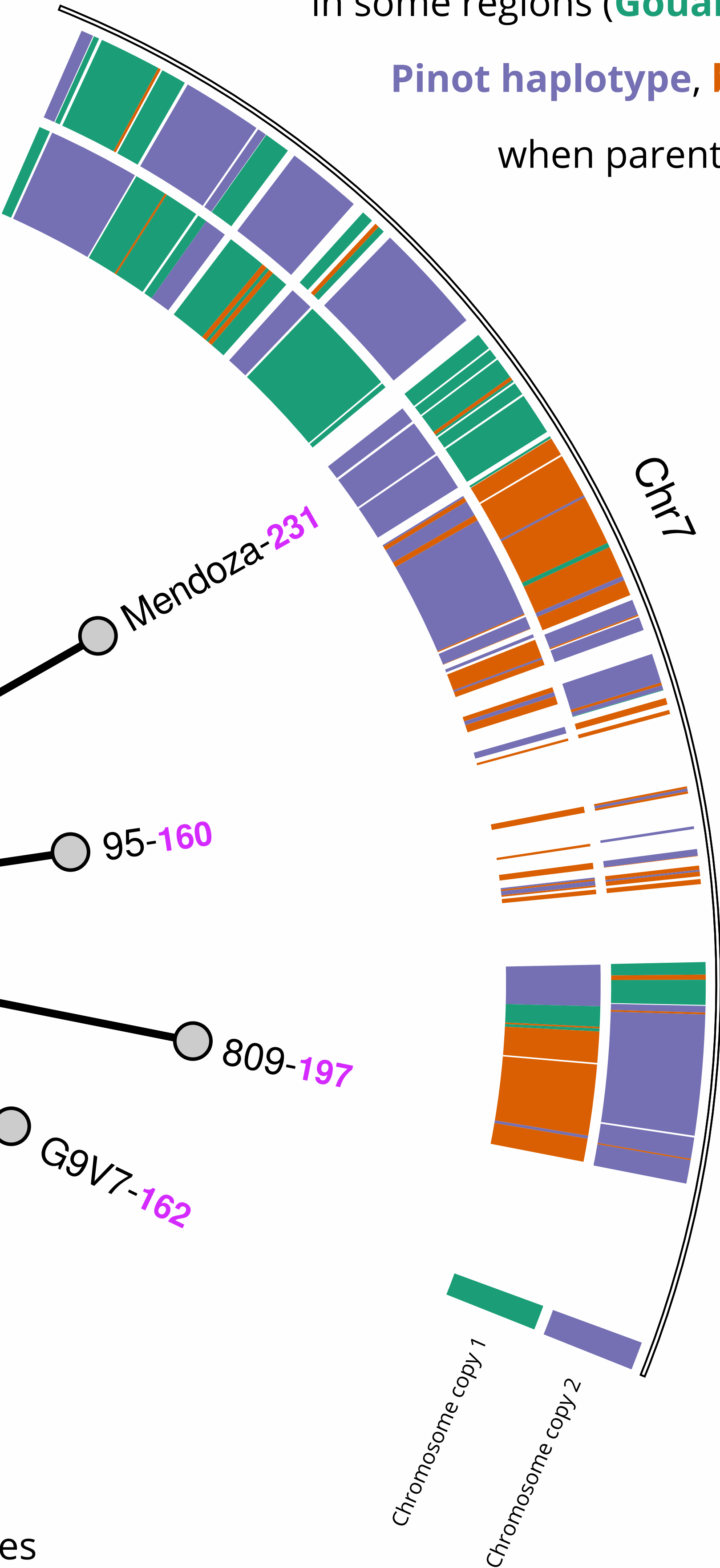


Chardonnay clones

Phylogenetic analysis of clonal mutations reveals diversity among Chardonnay clones (Clone ID-number of markers).

Pinot Noir DNA in Gouais Blanc's genome

Chardonnay sequence matched both parents in some regions (Gouais haplotype, Pinot haplotype, both). Occurs when parents are related.



Utility of clonal mutations

Clonal mutations are useful genetic 'markers'. Markers enable authenticity testing of unknown clones. Genic mutations can confer unique traits (like Muscat character).

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