Garcia, J., Cochetel, N., Balic, J., Barros, S., Figueroa-Balderas, R., Castro, A., & Cantù, D. (2026). Genome-wide characterization of extant clonal diversity in Chilean Carménère. *OENO One, 60*(3).
https://doi.org/10.20870/oeno-one.2026.60.3.10011

SUPPLEMENTARY DATA

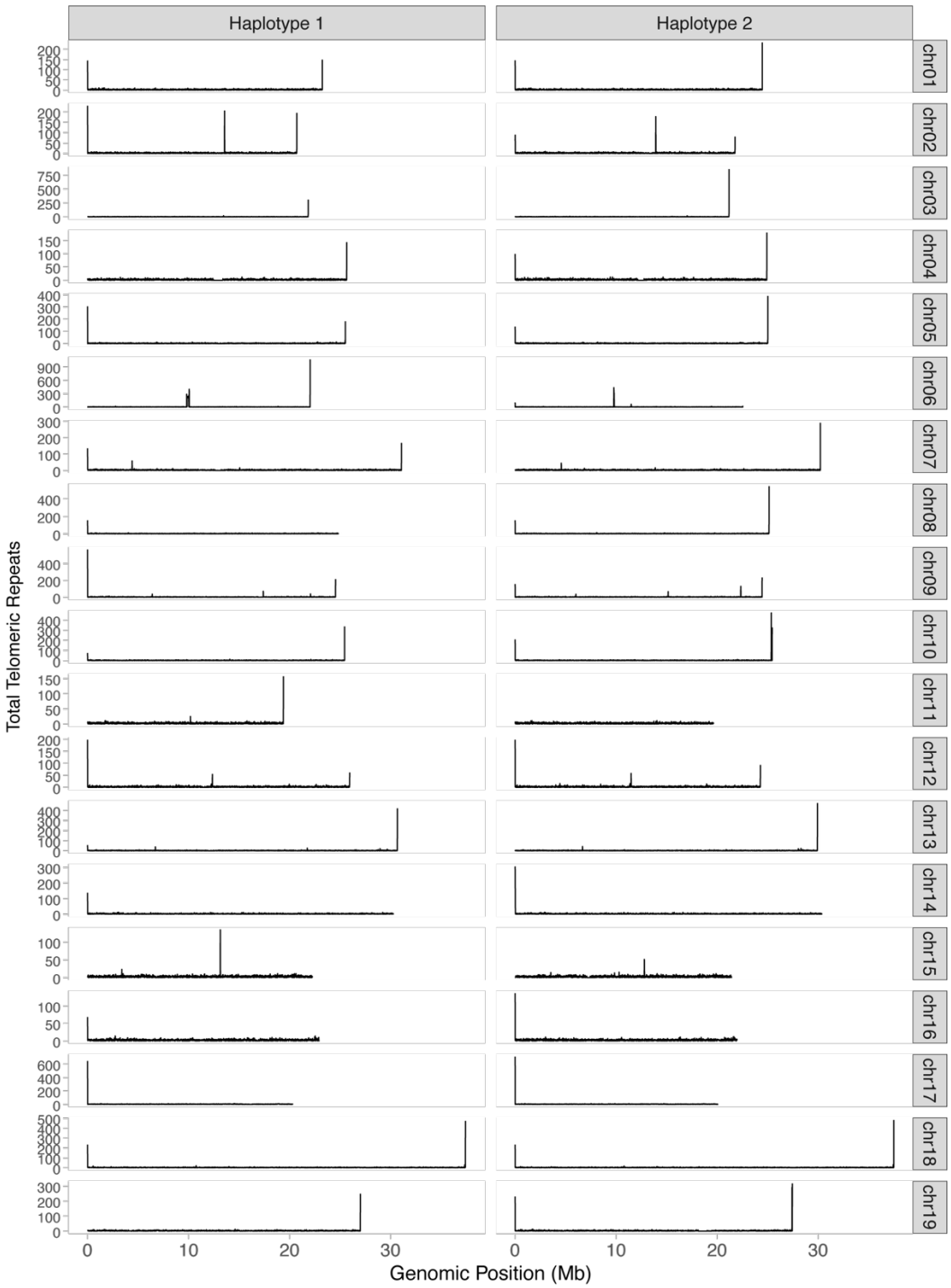

Figure S1. Distribution of telomeric repeat counts across pseudomolecules of the Carménère FPS 02 phased assembly.

The grapevine telomeric repeat unit (TTTAGGG) was quantified in non-overlapping 10 kbp windows along each pseudomolecule. Counts are displayed separately for Haplotype 1 and Haplotype 2 to allow direct comparison of telomeric repeat distribution between haplotypes. Peaks at chromosomal extremities are indicative of telomeric regions.

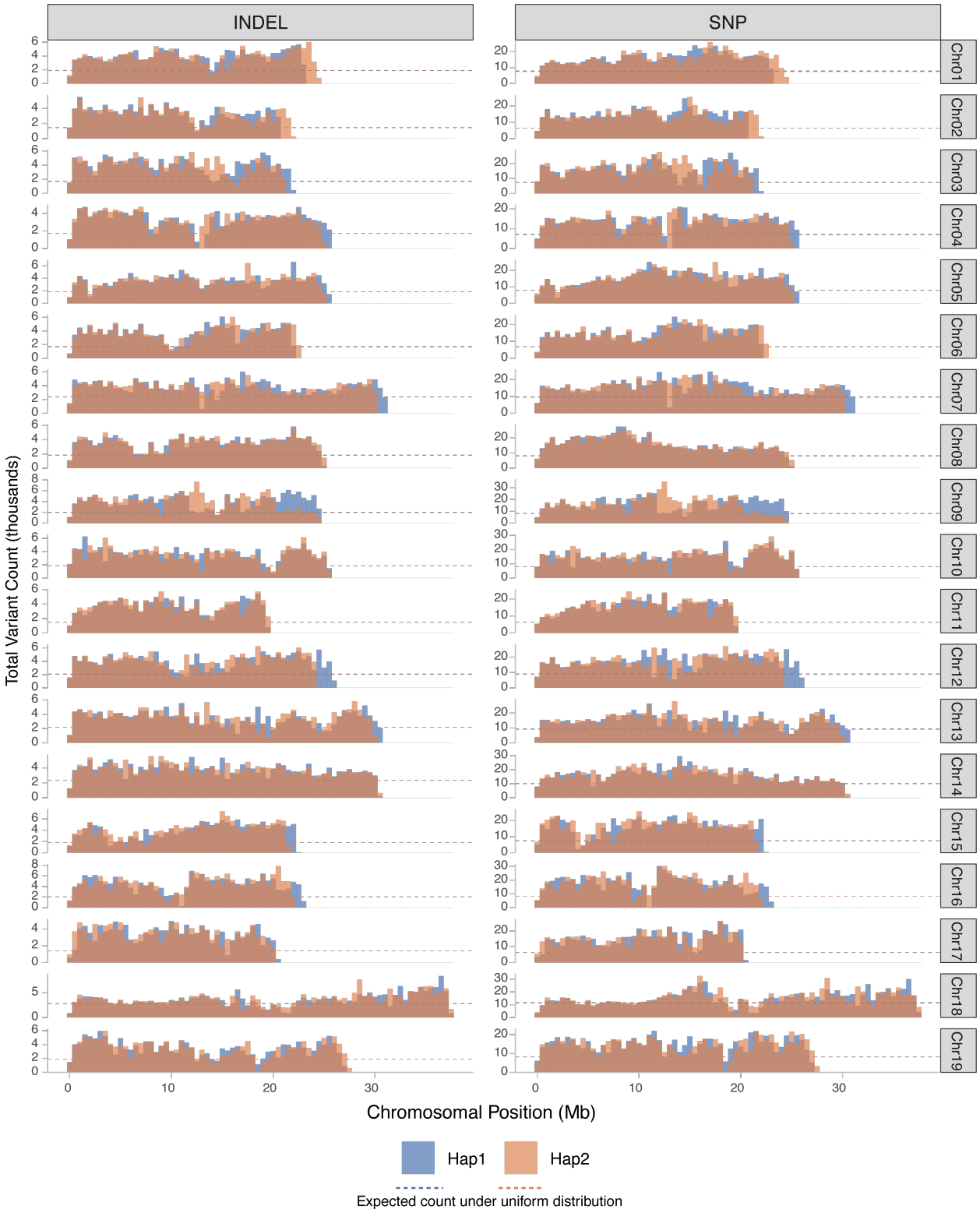

Figure S2. Variant density across pseudomolecules of the Carménère FPS 02 phased assembly.

Single nucleotide variants (SNVs) and insertions/deletions (INDELs) were counted in non-overlapping 10 kbp windows and summarized as a histogram with 0.5 Mbp bins. Each panel corresponds to a pair of equivalent pseudomolecules from Haplotype 1 and Haplotype 2, overlaid for direct comparison. The dashed horizontal line indicates the expected variant count per bin under a uniform distribution across the pseudomolecule.

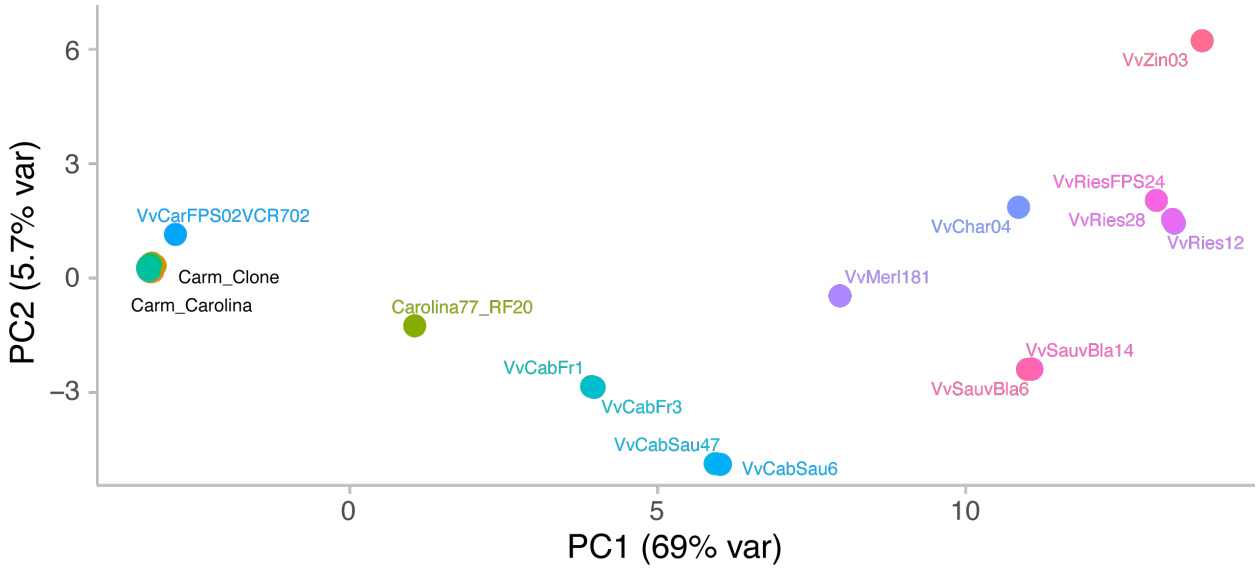

Figure S3. Principal component analysis of kinship-based genetic distances among Carménère clones and reference cultivars.

Principal component analysis (PCA) of the pairwise distance matrix derived from kinship estimation across Carménère clones and outgroup cultivars. Each point represents one sample, coloured by sample. Abbreviations: Carm_Carolina, Carménère accessions named Carolina in the present study; Carm_Clone, Carménère accessions named Clone in the present study; VvCar, Carménère accession from a previously published dataset; VvCabFr, Cabernet Franc clones; VvCabSau, Cabernet-Sauvignon clones; VvMerl, Merlot clone; VvSauvBla, Sauvignon blanc clones; VvChar, Chardonnay clone; VvRies, Riesling clones; VvZin, Zinfandel clone.

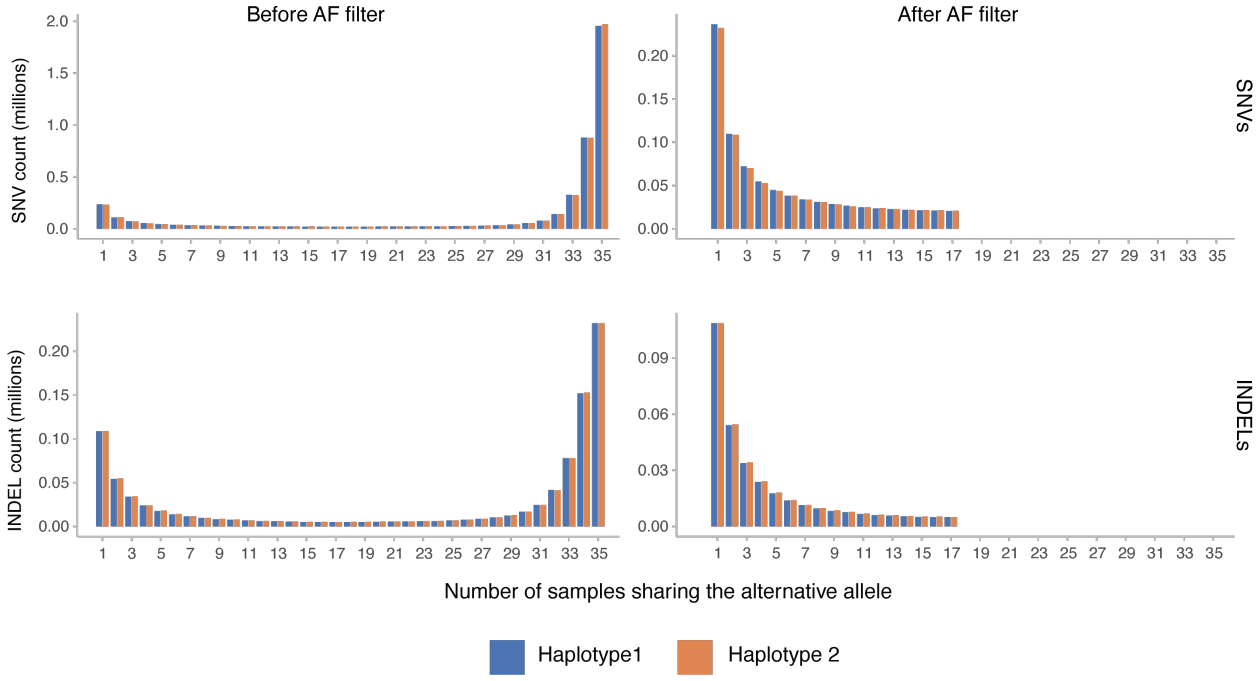

Figure S4. Distribution of variants by the number of samples sharing each variant, before and after alternative allele frequency filtering.

Each bar represents the total number of variants (SNVs or INDELs) observed in exactly k samples, where k ranges from 1 to 35 samples. Distributions are shown before and after applying the alternative allele frequency filter (alternative allele frequency < 0.25).

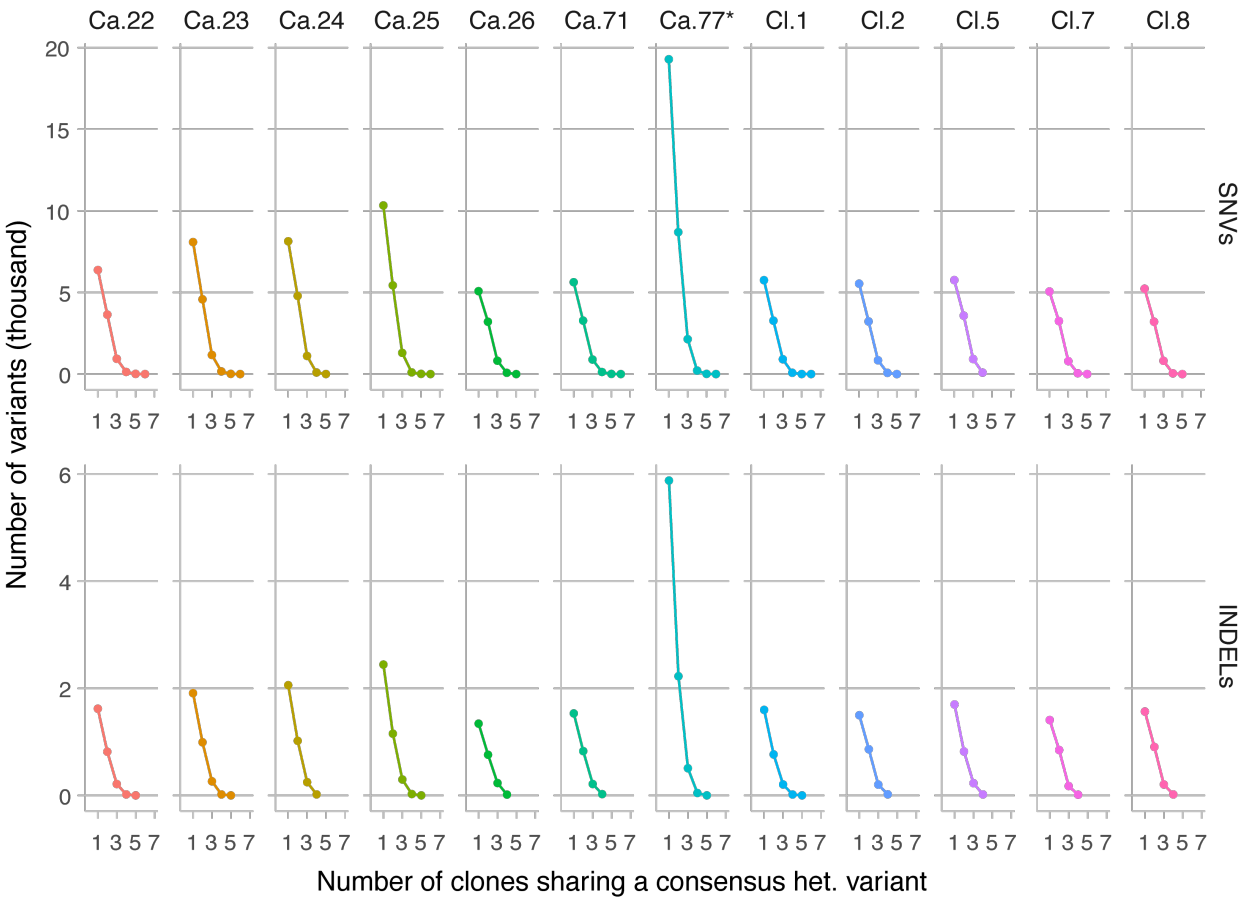

Figure S5. Per-clone contribution of SNVs and INDELs across sharing levels.

*Each panel displays the number of consensus heterozygous variants attributed to a given clone, broken down by sharing level k, where k denotes the number of clones carrying the variant. A consensus heterozygous variant was defined as a site heterozygous in at all replicates of a given clone. Name abbreviations are as follows: Ca., Carménère clones named Carolina in the study; Carménère clones named Clone in the study. *The elevated count of clone-private variants (k = 1) observed in Ca.77 reflects the fact that this clone was represented by only two replicates, such that consensus required agreement across two samples rather than three, lowering the stringency threshold relative to all other clones.*

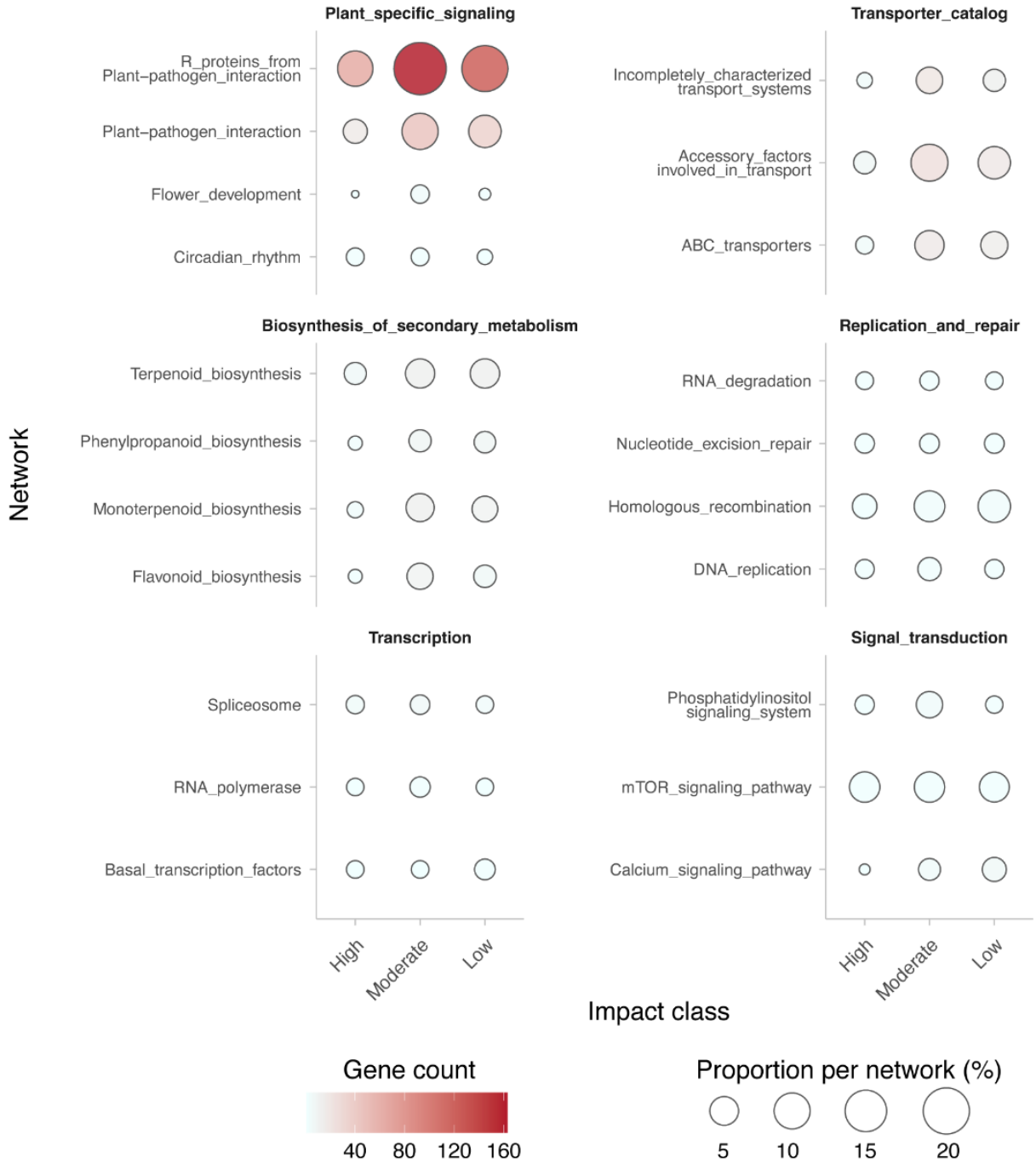

Figure S6. Functional networks of genes affected by consensus heterozygous variants across predicted impact classes.

Bubble plot showing the number and proportion of genes per functional network affected by consensus heterozygous variants. For each impact class, the three general functional categories with the highest proportion of affected genes were selected. Within each general category, the top three networks with the highest numbers of affected genes are shown. Bubble size represents the number of affected genes per network, and colour indicates the proportion relative to the total number of genes annotated in that network.

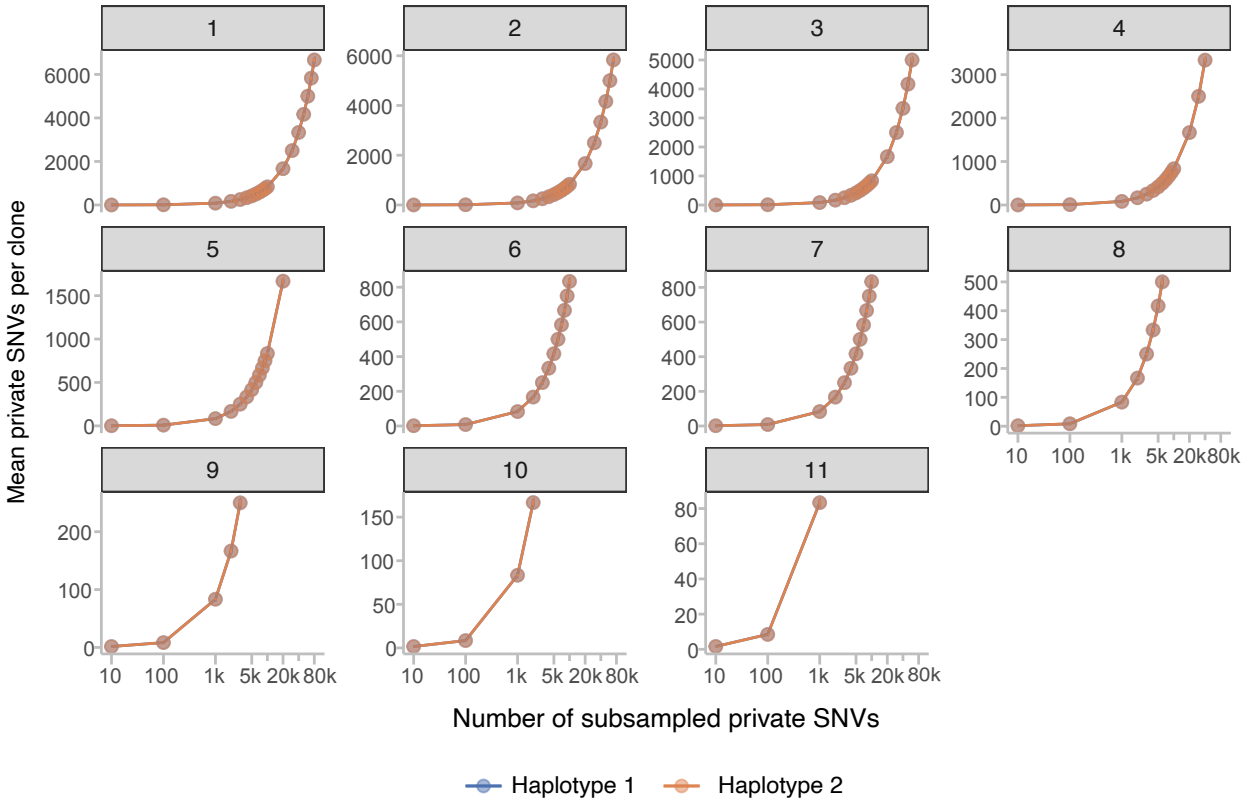

Figure S7. Contribution of private SNVs per clone across in silico marker subsampling analyses. *Candidate marker sets as previously described were generated using progressively increasing stringency thresholds. Panels 1–11 indicate the minimum number of the remaining clones required to carry a consensus homozygous reference genotype at sites where only a single clone was classified as consensus heterozygous. For each marker set, SNVs were randomly subsampled at increasing sizes (x-axis), and the mean number of private SNVs contributed by each clone to the subsampled marker set is shown on the y-axis. Points represent the mean contribution across 100 independent subsampling replicates, and error bars indicate the standard error of the mean. This figure is complimentary to Figure S6 and the numbers were calculated on exactly the same sets used for Figure S6.*