SUPPLEMENTARY DATA

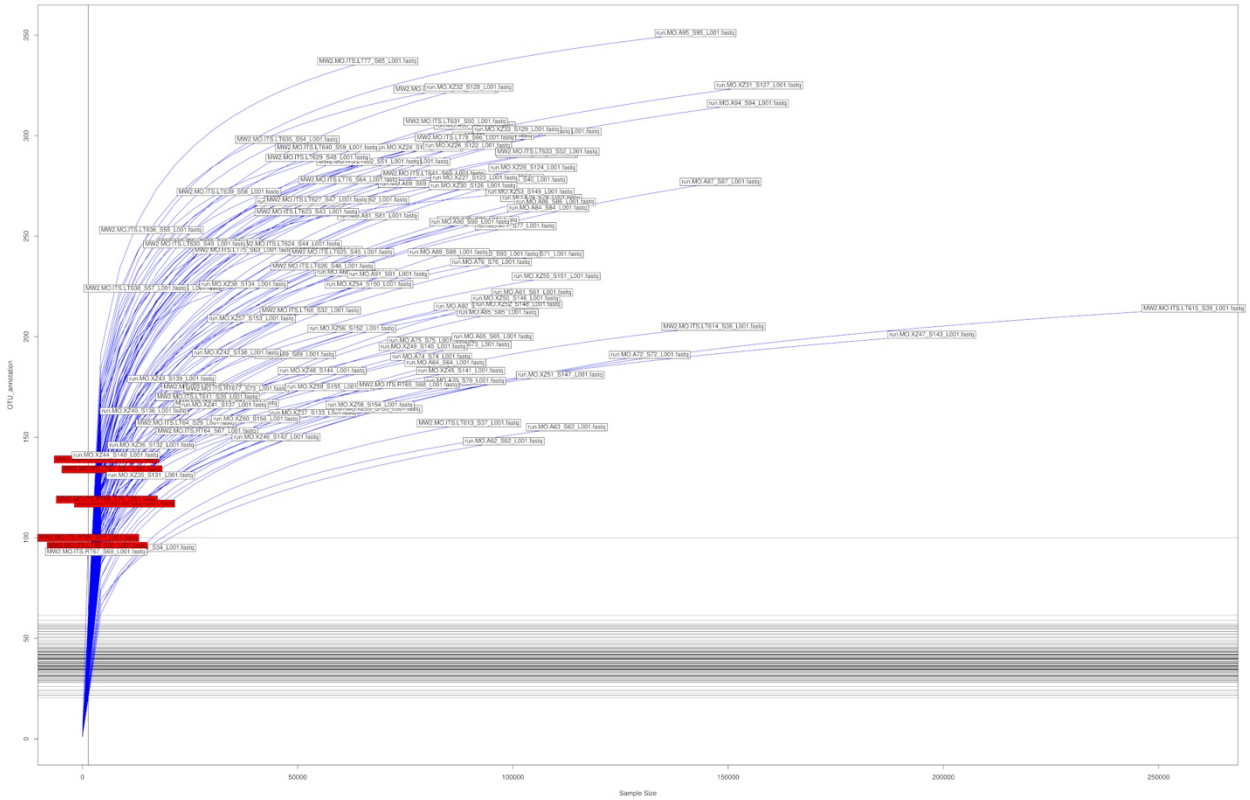


Figure S1. Rarefaction of sequenced samples.

Samples MW2-MO-ITS-RT67_S69, MW2-MO-ITS-RT68_S70, MW2-MO-ITS-RT69_S71, MW2-MO-ITS-RT616_S72, MW2-MO-ITS-LT63_S28 and MW2-MO-ITS-LT67_S31 (red squares) were excluded from the analysis due to the number of assigned OTUs not reaching saturation.

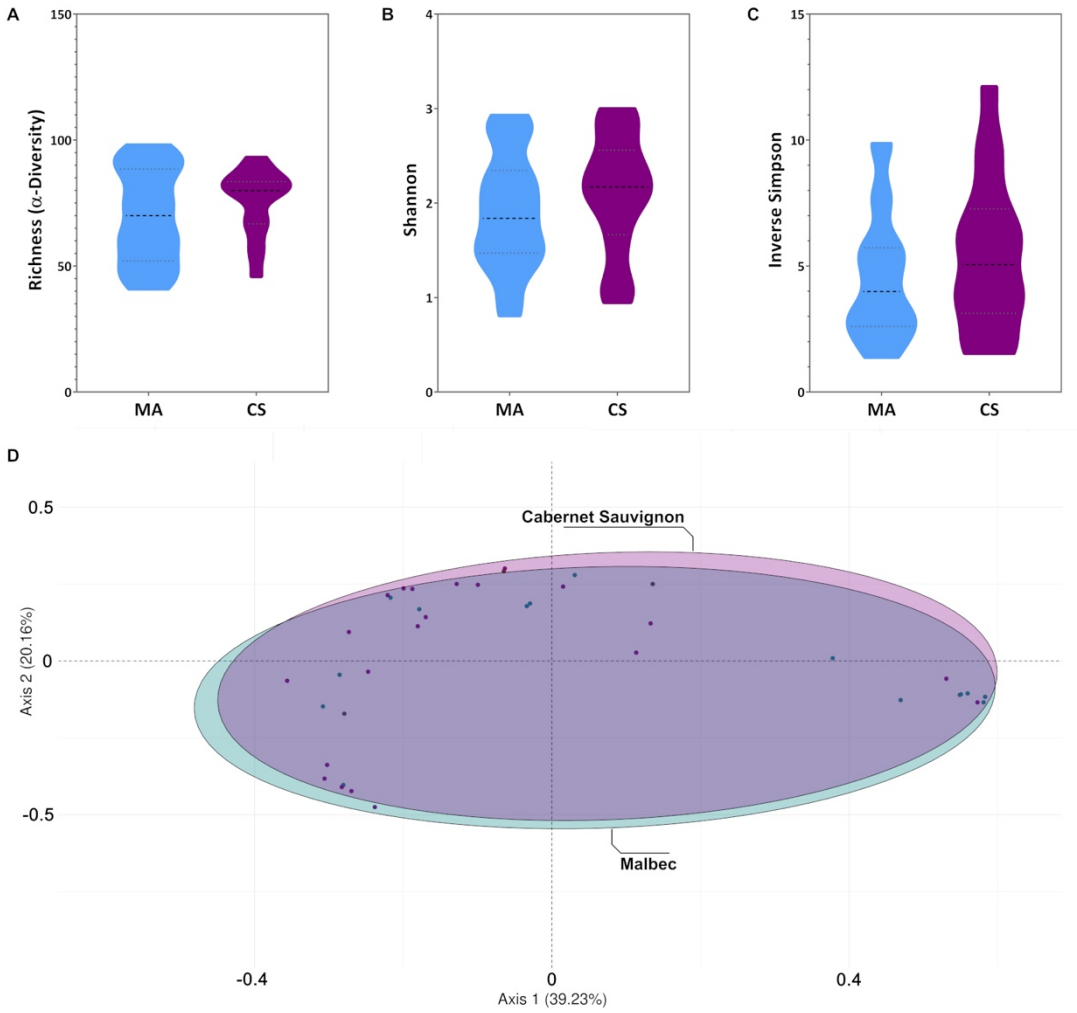


Figure S2. Variation in fungal diversity among grapevine cultivars' rhizospheres.

A. Species richness, B. Shannon diversity, and C. Inverse Simpson indices for MA and CS fungal communities associated with the rhizosphere. D. PCoA summarising the differences in ITS rRNA gene sequences across cultivars (p-value = 0.269). The first two axes are displayed. A PERMANOVA test was used to assess variance based on distance matrices.

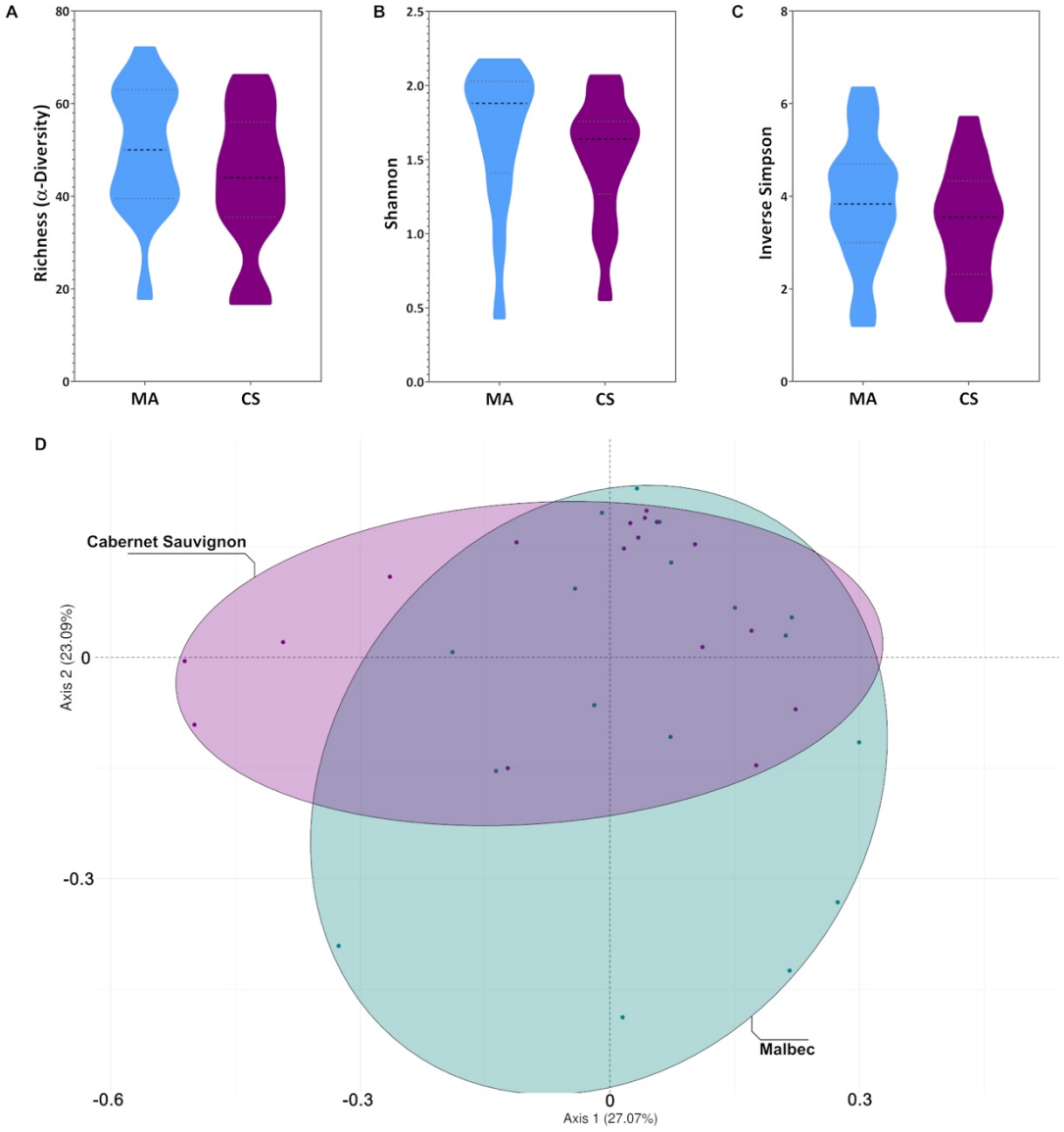


Figure S3. Variation in fungal diversity among the leaves of grapevine cultivars.

A. Species richness, B. Shannon diversity, and C. Inverse Simpson indices for MA and CS fungal communities associated with leaves. D. PCoA summarising the differences in ITS rRNA gene sequences across cultivars (p-value = 0.058). The first two axes are displayed. A PERMANOVA test was used to assess variance based on distance matrices.

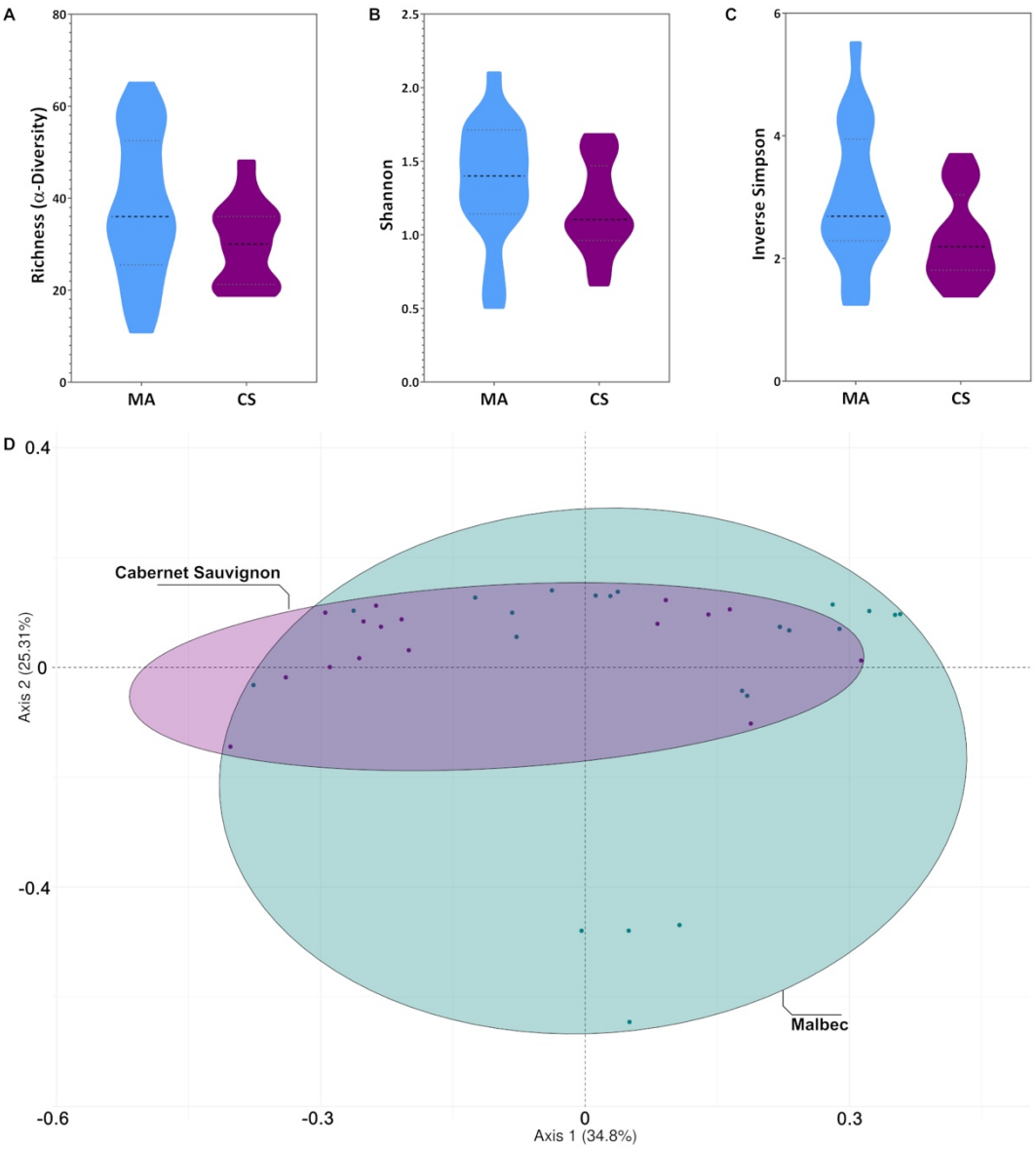


Figure S4. Fungal diversity variation among grapevine cultivar must samples.

A. Species richness, B. Shannon diversity, and C. Inverse Simpson indices for MA and CS fungal communities in must samples. D. PCoA summarising the differences in ITS rRNA gene sequences across cultivars (p-value = 0.008). The first two axes are displayed. A PERMANOVA test was used to assess variance based on distance matrices.

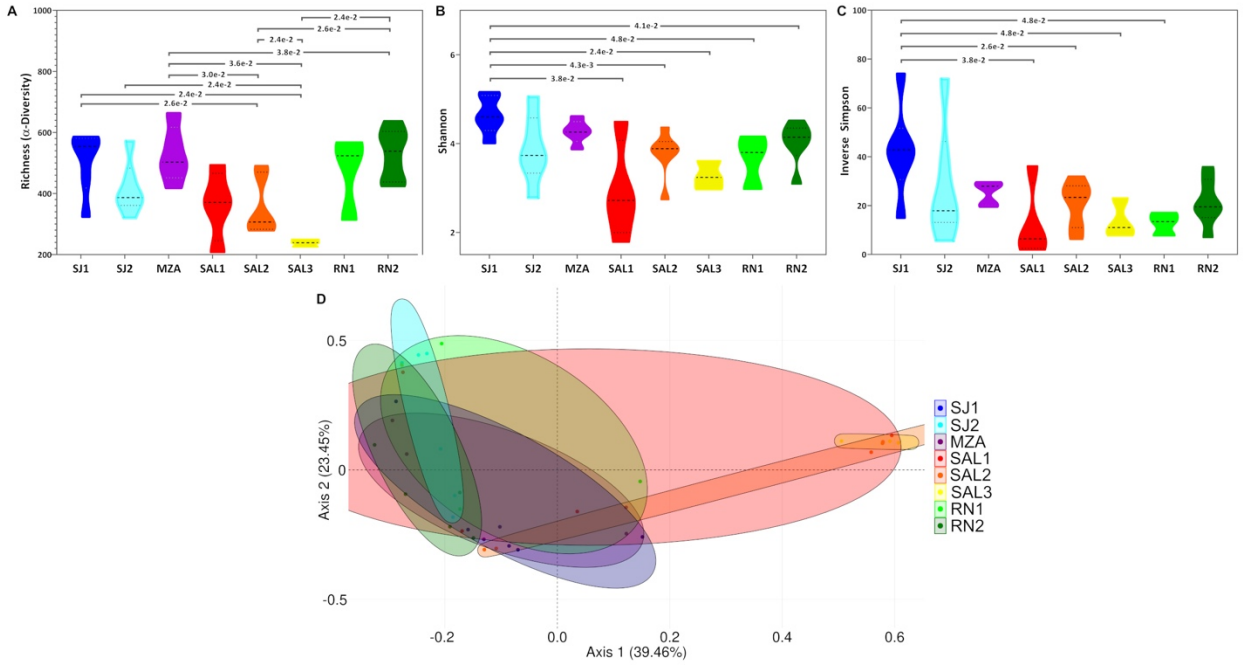


Figure S5. Analysis of fungal diversity in rhizosphere samples from the study sites.

A. Species richness, B. Shannon diversity, and C. Inverse Simpson indices for fungal communities in rhizosphere samples. D. PCoA summarising the differences in ITS rRNA gene sequences across root samples (p-value = 0.001). The first two axes are displayed. A PERMANOVA test was used to assess variance based on distance matrices.

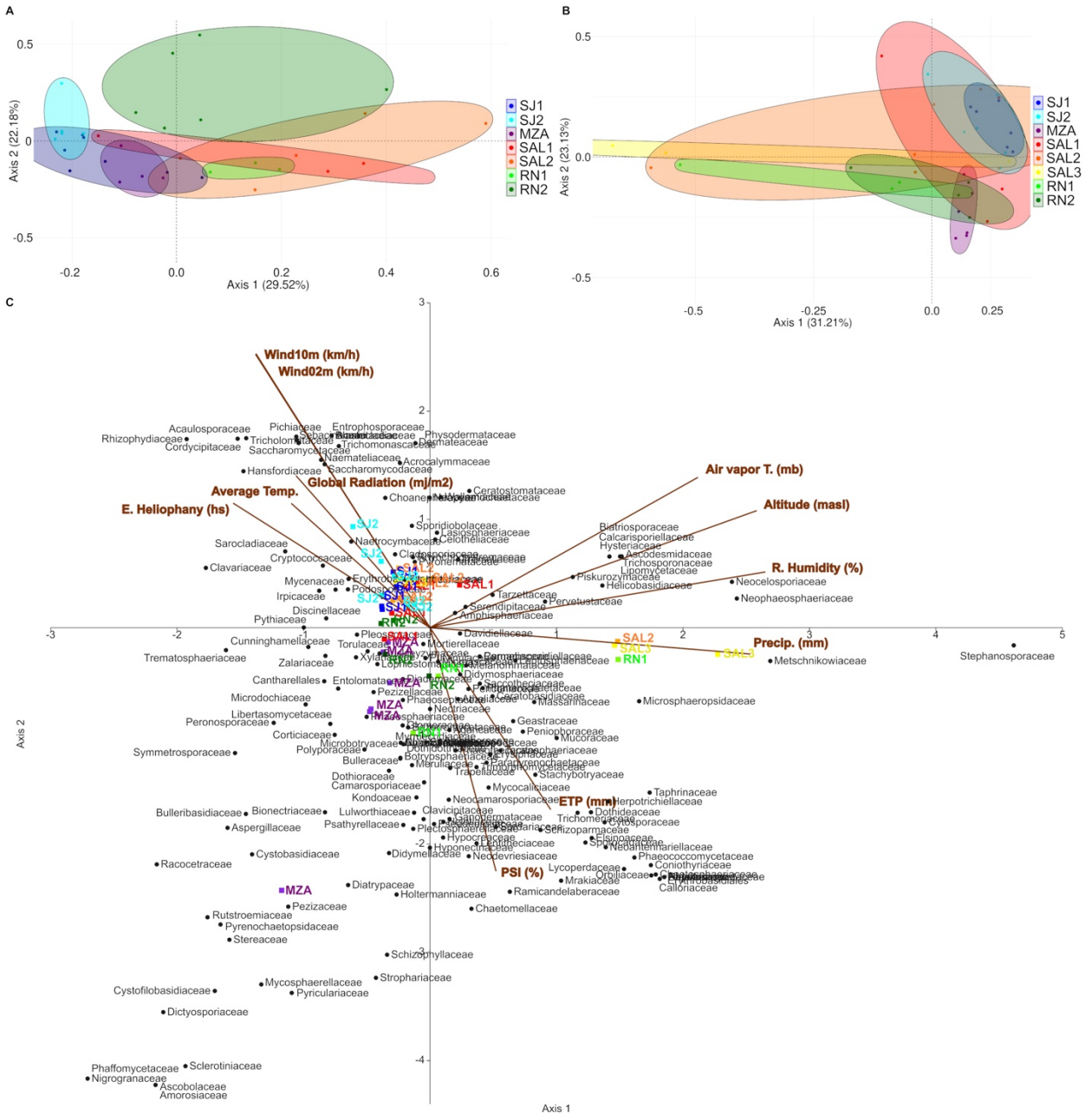


Figure S6. Supplementary rhizosphere and must.

PCoA summarising the differences in ITS rRNA gene sequences across: A. Leaf samples (p-value = 0.001), B. Must samples (p-value = 0.001). The first two axes are displayed. A PERMANOVA test was used to assess variance based on distance matrices. C. CCA plot of the most abundant fungal families in must samples and their relationship with environmental features. Perm (n = 999) Trace = 0.6306, p = 0.028.