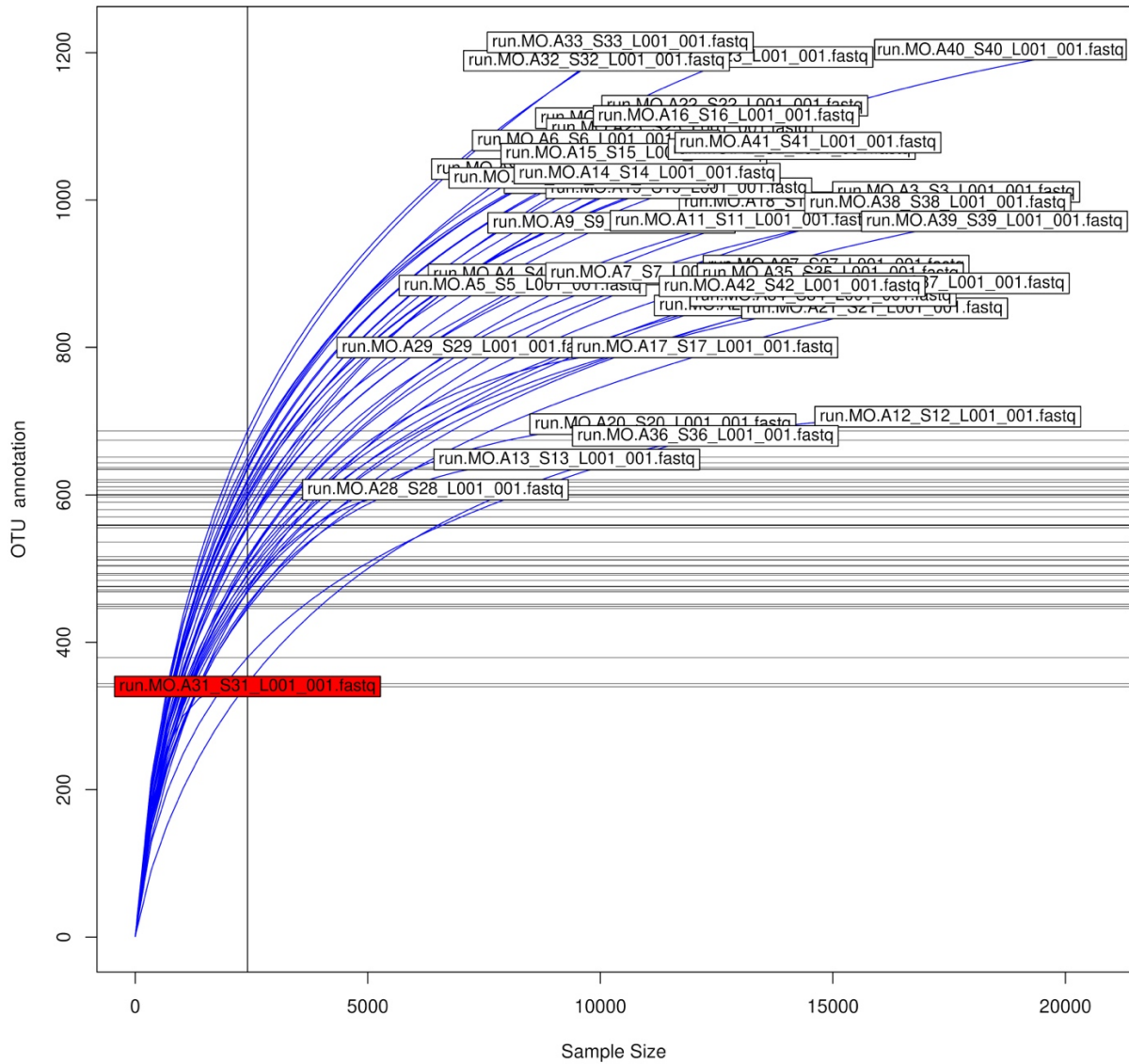
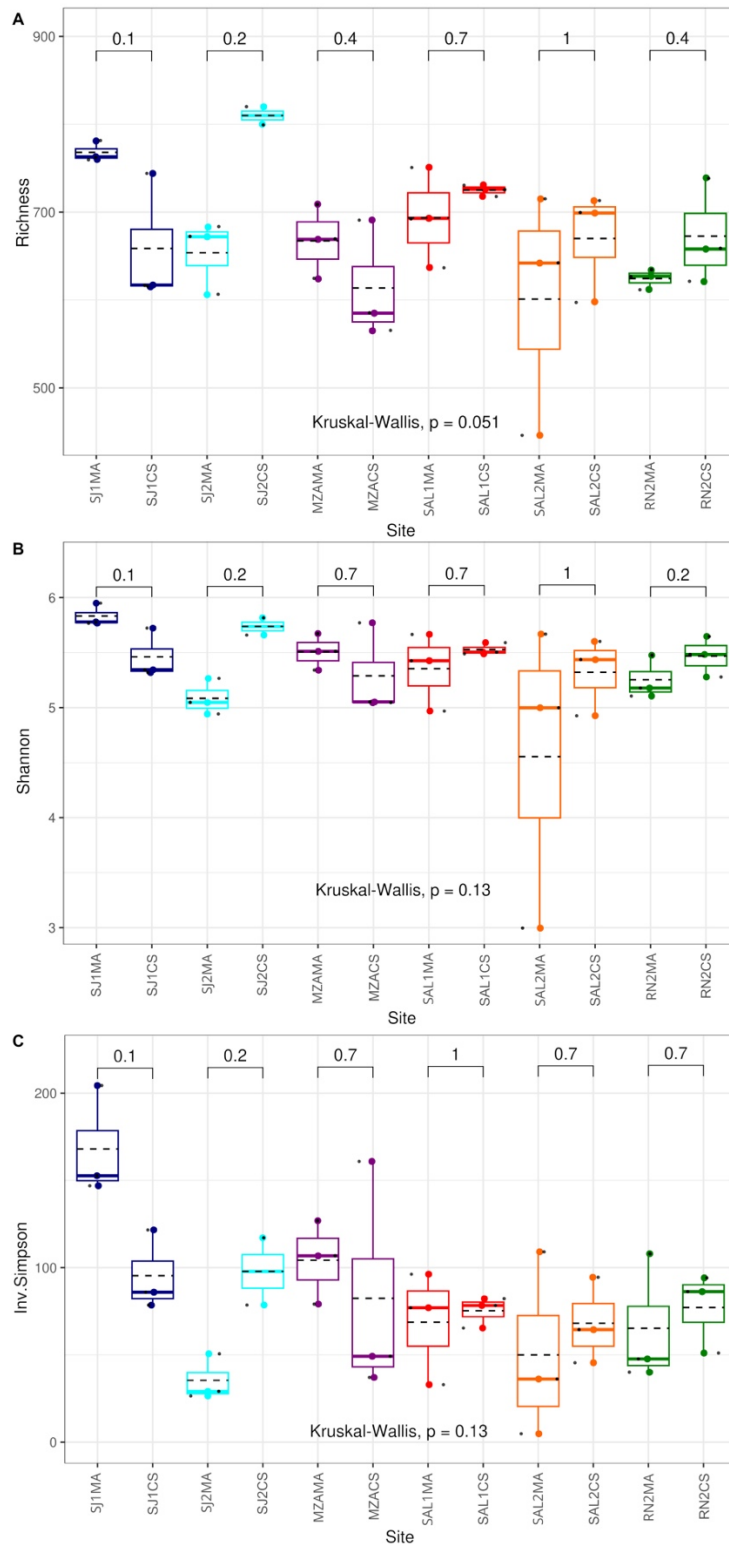


## SUPPLEMENTARY DATA



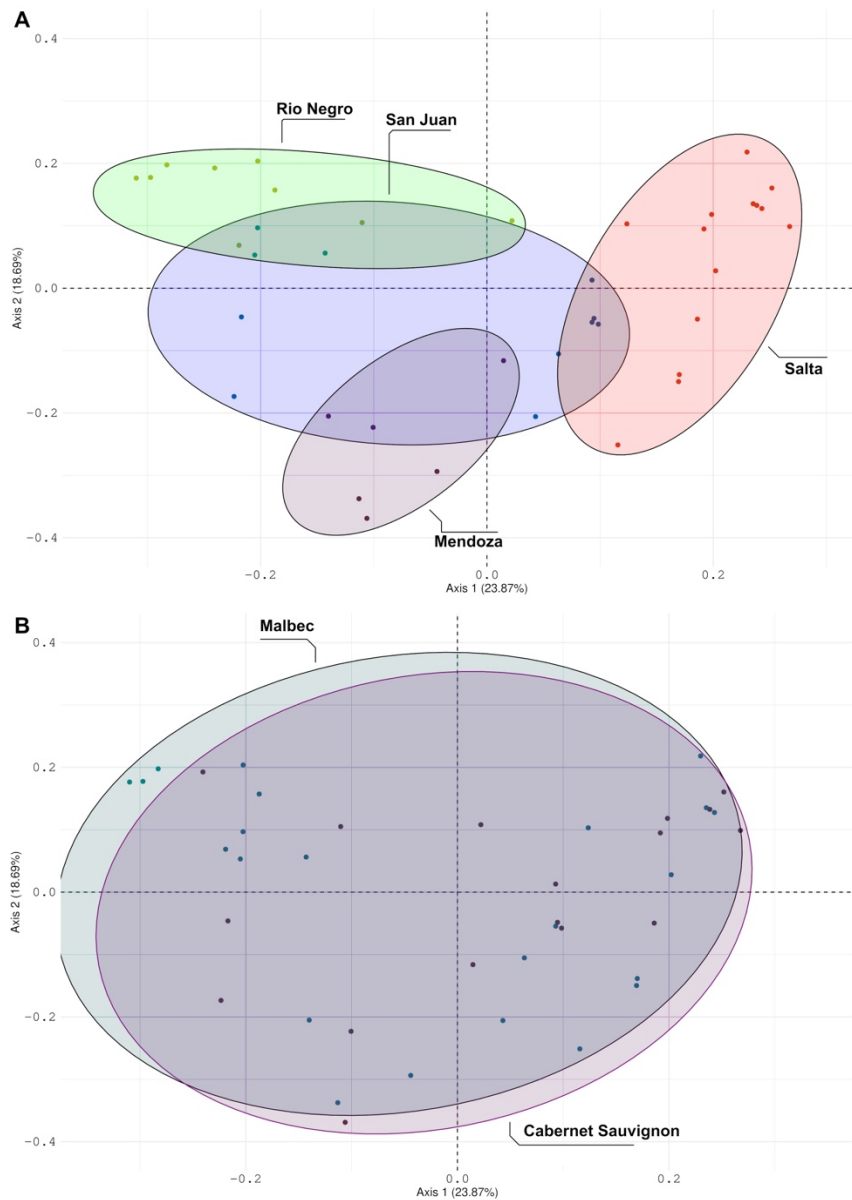
**Figure S1. Rarefaction of sequenced samples.**

Sample run.MO.A31\_S31\_L001\_001.fastq (red square) was excluded from the analysis due to the number of assigned OTUs not reaching saturation.



**Figure S2. Boxplot for microbial species Richness (S), Shannon (H') and Inverse Simpson (1/D) Index values sorted by grape cultivars.**

Boxplots (A), (B) and (C) represent the prokaryotic species  $\alpha$ -diversity indexes. The statistical analysis was done using a Kruskal Walli's test. The identified pairwise-comparisons results were obtained through a post hoc Mann–Whitney Bonferroni adjusted test.



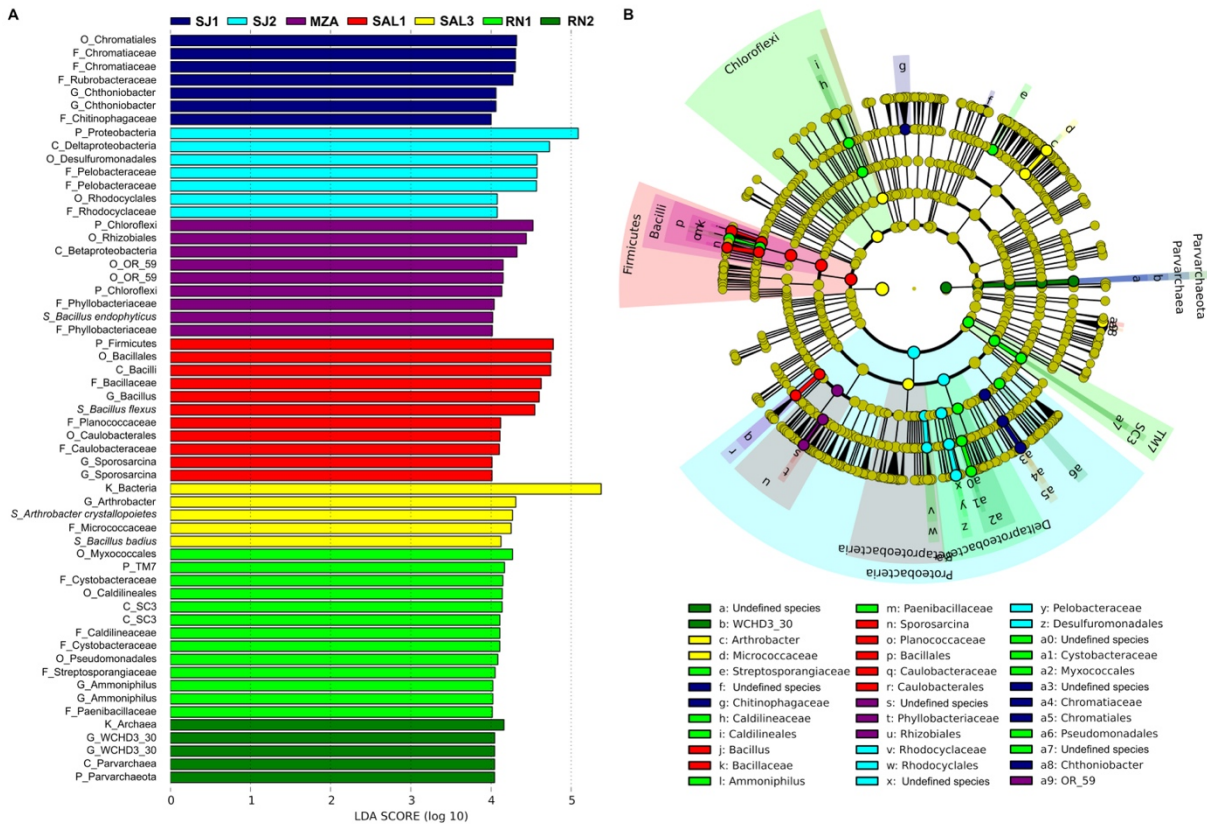
**Figure S3. PCoA of prokaryotic OTUs sorted by regions and grape cultivars.**

PCoA summarises the differences between rhizospheric bacterial 16S rRNA gene sequence analysed in (A) regions and (B) grape cultivars.

Permanova test was performed for the analysis of variance using distance matrices. p-value = 0.001.

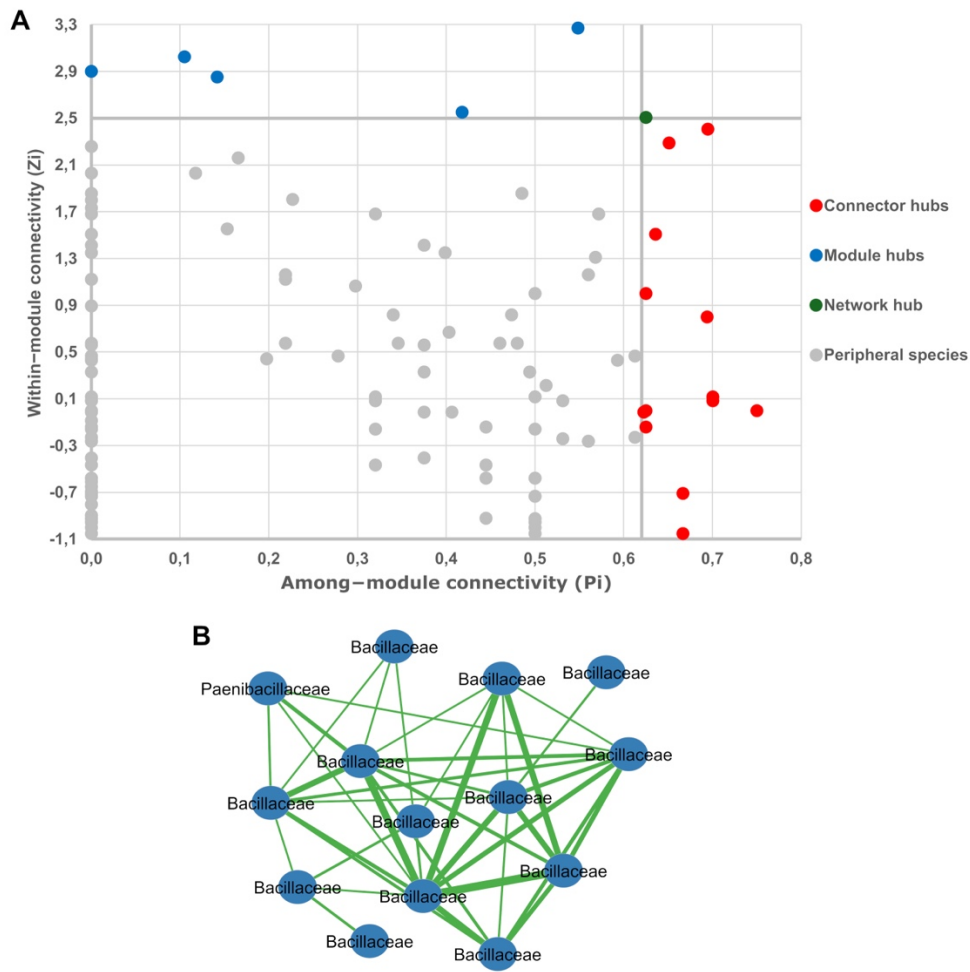
SUPPLEMENTARY DATA

Toscani, A. M., Oyuela Aguilar, M., Rey, C., Rocco Welsh, R. E., Gobbi, A., del Papa, M. F., ... Pistorio, M. (2025). Prokaryotic diversity of the rhizosphere from Argentinean wine-producing regions. *OENO One*, 59(1). <https://doi.org/10.20870/oeno-one.2025.59.1.8130>



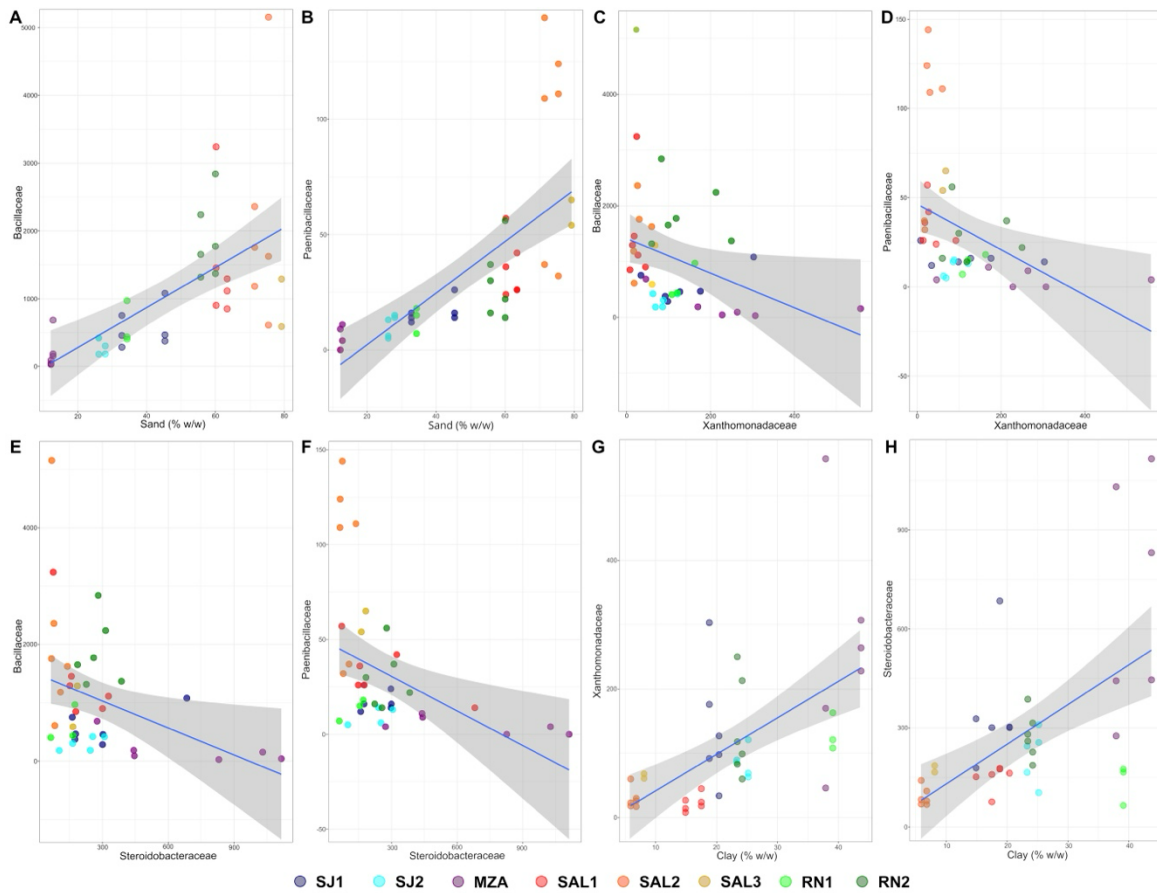
**Figure S4. Linear discriminant analysis effect size (LEfSe) analysis.**

A) 57 taxonomic units above a logarithmic LDA score of 4 OTUs are shown. B) The cladogram depicts the phylogenetic distribution of microbial lineages in sampled sites.



**Figure S5. SparCC OTUs' network 2.**

(A ZP graph showing Connector, Module, Network, and Peripheral hubs. (B Network for OTUs assigned to *Bacillaceae* and *Paenibacillaceae* families. Blue colour indicates their belonging to Module 2.



**Figure S6. Scatter plot of bacterial families' association.**

(A Correlation of bacterial presence with sand content for *Bacillaceae* (Pearson's correlation coefficient (PCC): 0.79). B) Sand vs. *Paenibacillaceae* (PCC: 0.85). C) *Xanthomonadaceae* family negatively correlates with *Bacillaceae* (PCC: -0.52). D) *Xanthomonadaceae* vs. *Paenibacillaceae* family (PCC: -0.55). E) *Steroidobacteraceae* family negatively correlates with *Bacillaceae* (PCC: -0.56). F) *Steroidobacteraceae* vs. *Paenibacillaceae* family (PCC: -0.65). G) Correlation of bacterial number with clay content for *Xanthomonadaceae* (PCC: 0.67). H) Clay vs. *Steroidobacteraceae* (PCC:0.58).