



Orchard landscape



D. citri-infected



Uninfected

Fig. S1 The visual symptoms of *D. citri*-infected and uninfected leaves. The infected and uninfected samples were collected from a citrus orchard in August 2019, where the melanose disease (caused by *D. citri*) had been severely occurred for three sequential years.

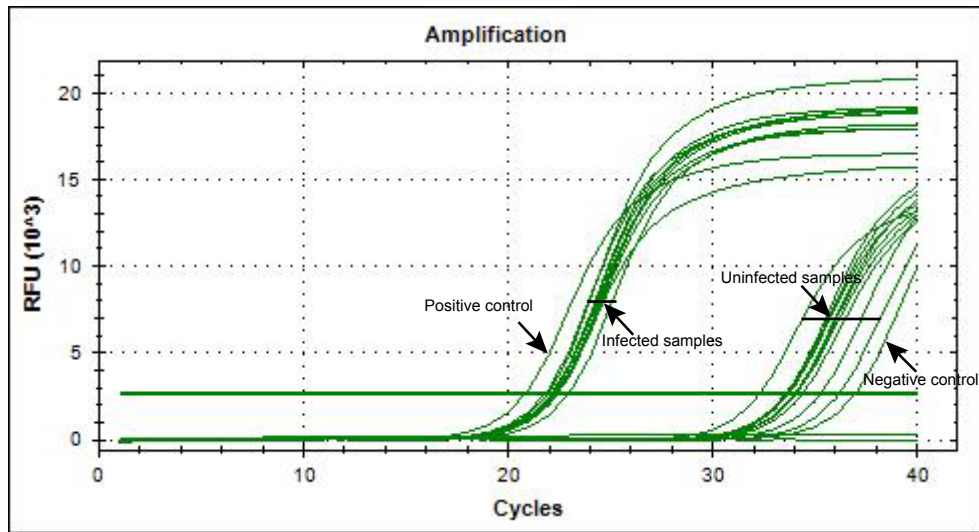


Fig. S2 qPCR amplification of melanose pathogen *D. citri*. The infected (Ct value <30) and uninfected samples (Ct value >30) were identified based on qPCR results. The β -tubulin (TUB) gene was amplified using the forward primer Dc-F (CCCTCGAGGCAT-CATTAC), and reverse primer Dc-R (ATGTTGCAGATGGTCAAATGG).

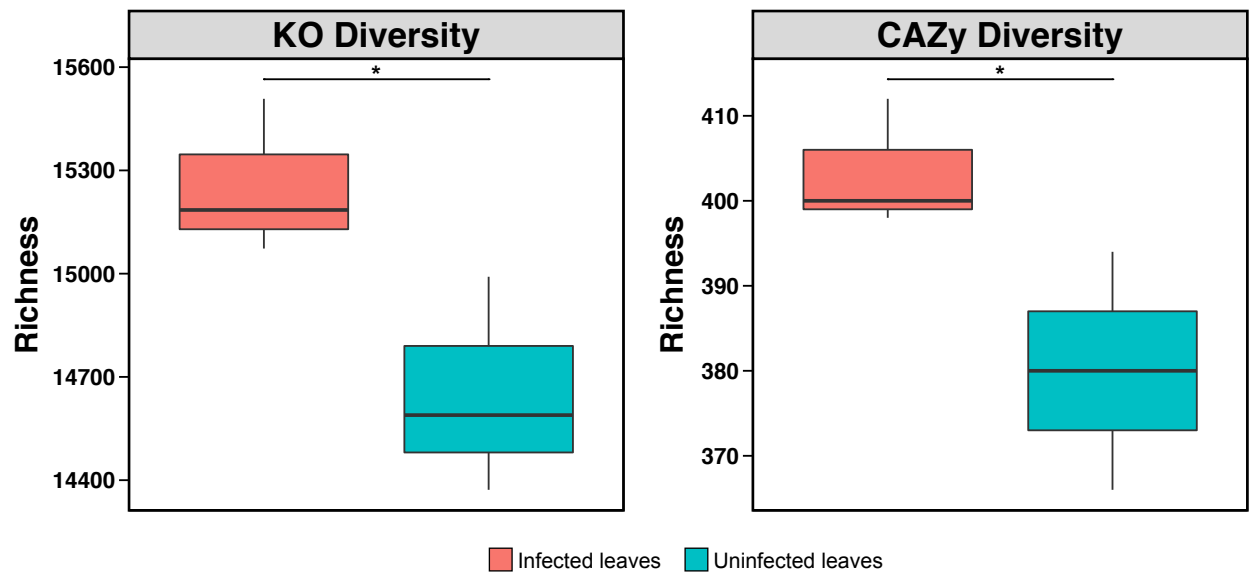


Fig. S3 Functional diversity between infected and uninfected phyllosphere microbiomes. Richness was conducted to characterize the KO and CAZy diversity and analyzed in Kruskal-Wallis to test for differences. Asterisks denote significant differences (*P < 0.05; **P < 0.01; ***P < 0.001) and NS denotes no statistical significance.

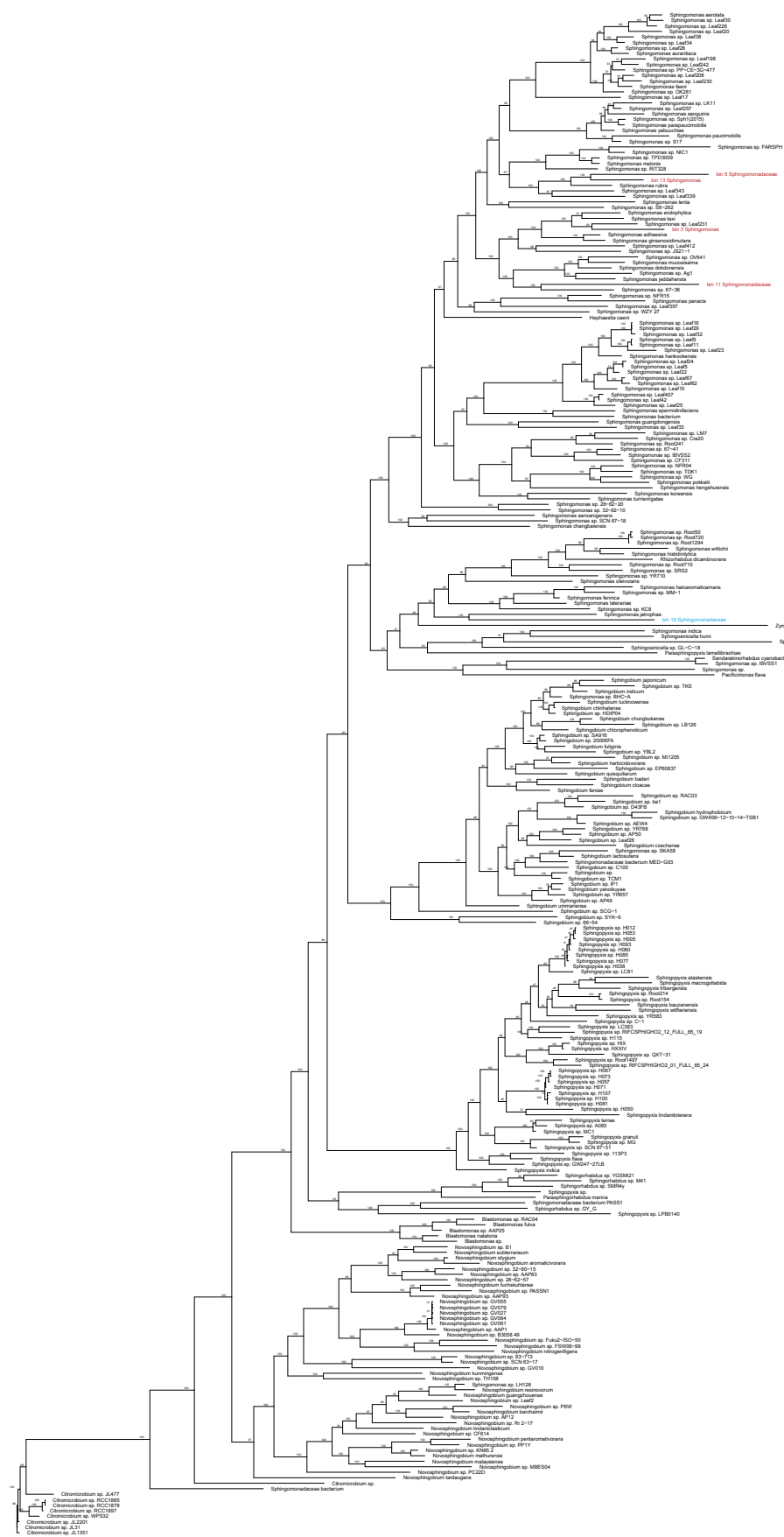


Fig. S4 A high-resolution phylogenetic tree of Sphingomonadaceae bins. 272 Sphingomonadaceae representative genomes and the bin 3, 5, 11, 13 and 19 were selected to further construct a phylogenetic tree using PhyloPhlAn.