**Figure S1.** Rarefaction curve values for each sample in (a) 110 Richter and (b) 41 Berlandieri rootstocks.

**Figure S2**. Relative abundance of different fungal phyla in (a) 110 Richter and (b) 41 Berlandieri rootstocks.

**Figure S3.** Venn diagram illustrating the overlap of the number of OTUs identified in the fungal microbiota among sampling moments in (a) 110 Richter and (b) 41 Berlandieri rootstocks.

**Figure S4.** Core microbiome analysis showing a limited number of genera prevalent across all the samples in (a) 110R and (b) 41B rootstocks. Sample prevalence threshold is set up above 20%, and relative abundance threshold is set up above 0.01%. The heatmap colors represent the sample prevalence values.

**Figure S5.** Droplet digital PCR amplitude plot showing all accepted droplets with a clear distinction between positives (mostly between 6,500 and 8,000) and negatives (mostly around 750) in each sampling moment of 110R and (b) 41B rootstocks, positive control (*Cadophora luteo-olivacea isolate* BV-0577 DNA), and nontemplate control (NTC), confirming the assay optimization.

**Figure S6.** The distribution of the number of reads and DNA concentration of *Cadophora luteo-olivacea* in (a) 110 Richter and (b) 41 Berlandieri rootstocks are shown on the diagonal. The bivariate scatter plot with a fitted line is displayed on the bottom of the diagonal and the Spearman correlation value (*P*<0.05) is indicated on the top of the diagonal.