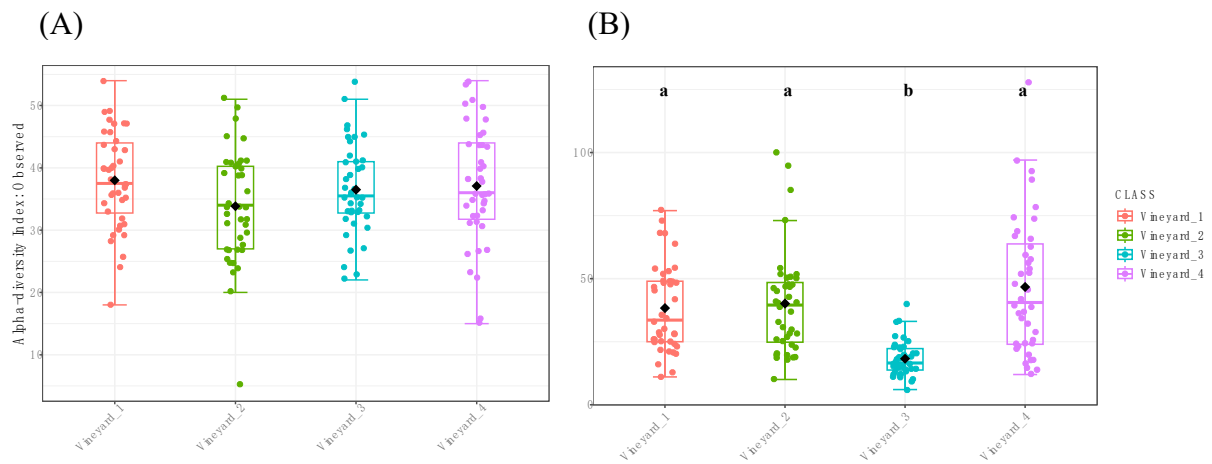


**Figure S1:** Wood sampling from the inner trunk at two different positions (Trunk head and Trunk center)



**Figure S2:** A longitudinal trunk section showing an example of the measured wood necrosis



**Figure S3:** Boxplot illustrating the differences in alpha diversity measures (Observed index) of the fungal (A) and bacterial (B) communities between vineyards

**Table S1:** Pairwise PERMANOVAs of beta diversity indexes between vineyards for fungal and bacterial communities.

	<b>Fungi</b>	<b>Bacteria</b>
	<b>p-value</b>	<b>p-value</b>
<b>Vineyard_1 vs Vineyard_2</b>	0.001	0.07
<b>Vineyard_1 vs Vineyard_3</b>	0.001	0.001
<b>Vineyard_1 vs Vineyard_4</b>	0.001	0.001
<b>Vineyard_2 vs Vineyard_3</b>	0.001	0.001
<b>Vineyard_2 vs Vineyard_4</b>	0.001	0.001
<b>Vineyard_3 vs Vineyard_4</b>	0.001	0.001

**Table S2:** Alpha richness and diversity indexes for fungal (A) and bacterial communities (B) of treatment effect. T1 and T2 correspond to sampling time points, 2- and 10-months after Esquire® WP treatment, respectively. Significant *p values* are shown in bold.

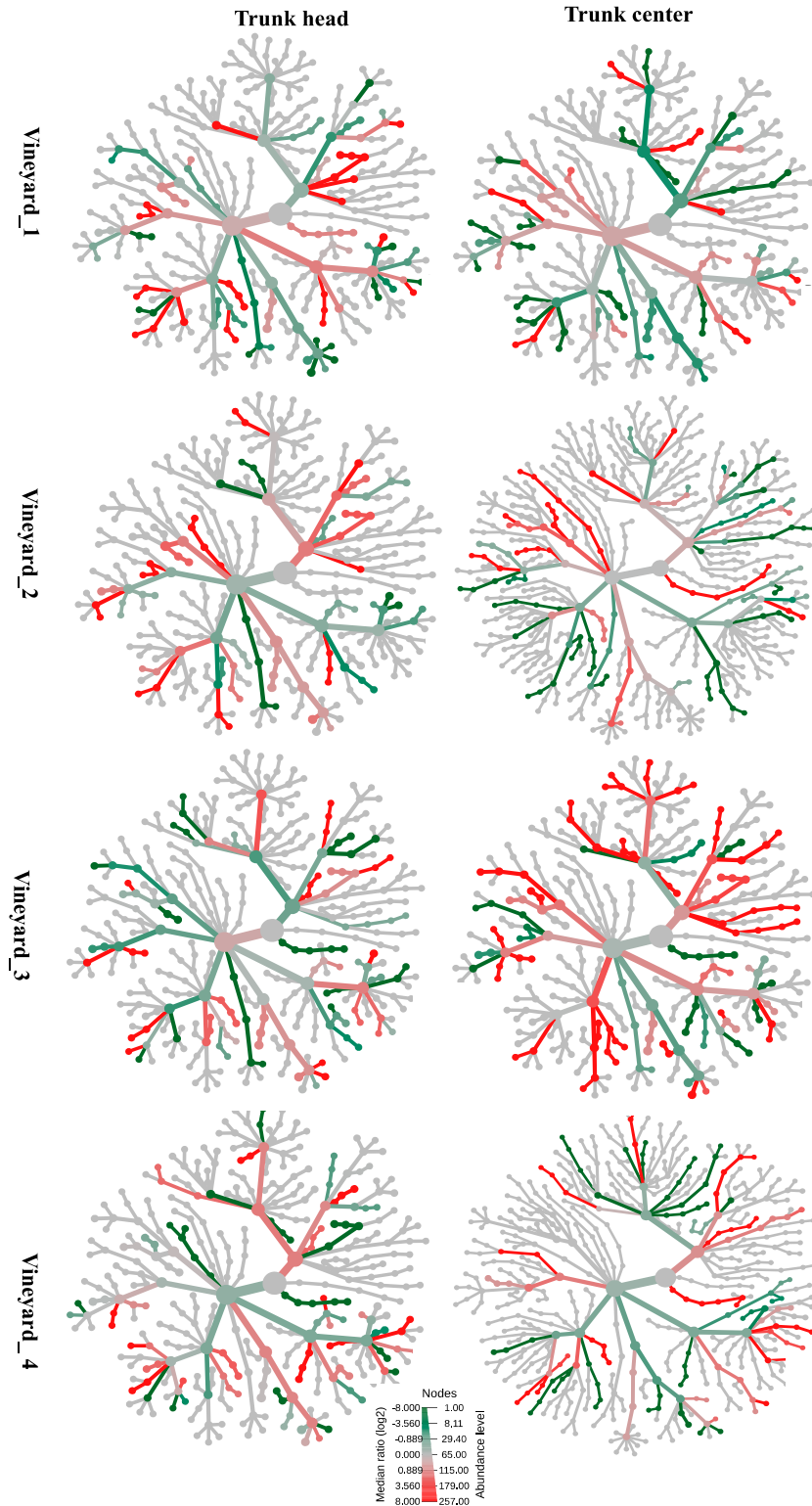
(A)	Bacteria							
	Observed				Shannon			
	T1		T2		T1		T2	
	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center
Vineyard_1	0.82	0.96	0.46	0.2	0.7	0.36	0.72	0.26
Vineyard_2	0.32	0.81	0.67	0.6	0.3	0.04	0.84	0.45
Vineyard_3	0.63	0.7	0.97	0.12	0.58	0.42	0.27	0.11
Vineyard_4	0.97	0.35	0.36	0.23	<b>0.001</b>	0.64	0.52	0.83

(B)	Fungi							
	Observed				Shannon			
	T1		T2		T1		T2	
	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center
Vineyard_1	0.9	0.34	0.79	0.55	0.61	0.6	0.2	0.2
Vineyard_2	0.99	0.77	0.6	0.67	0.49	0.71	0.95	0.72
Vineyard_3	0.85	0.39	0.59	0.7	<b>0.01</b>	0.54	0.83	0.75
Vineyard_4	0.1	0.1	0.4	0.16	0.67	0.21	0.9	0.9

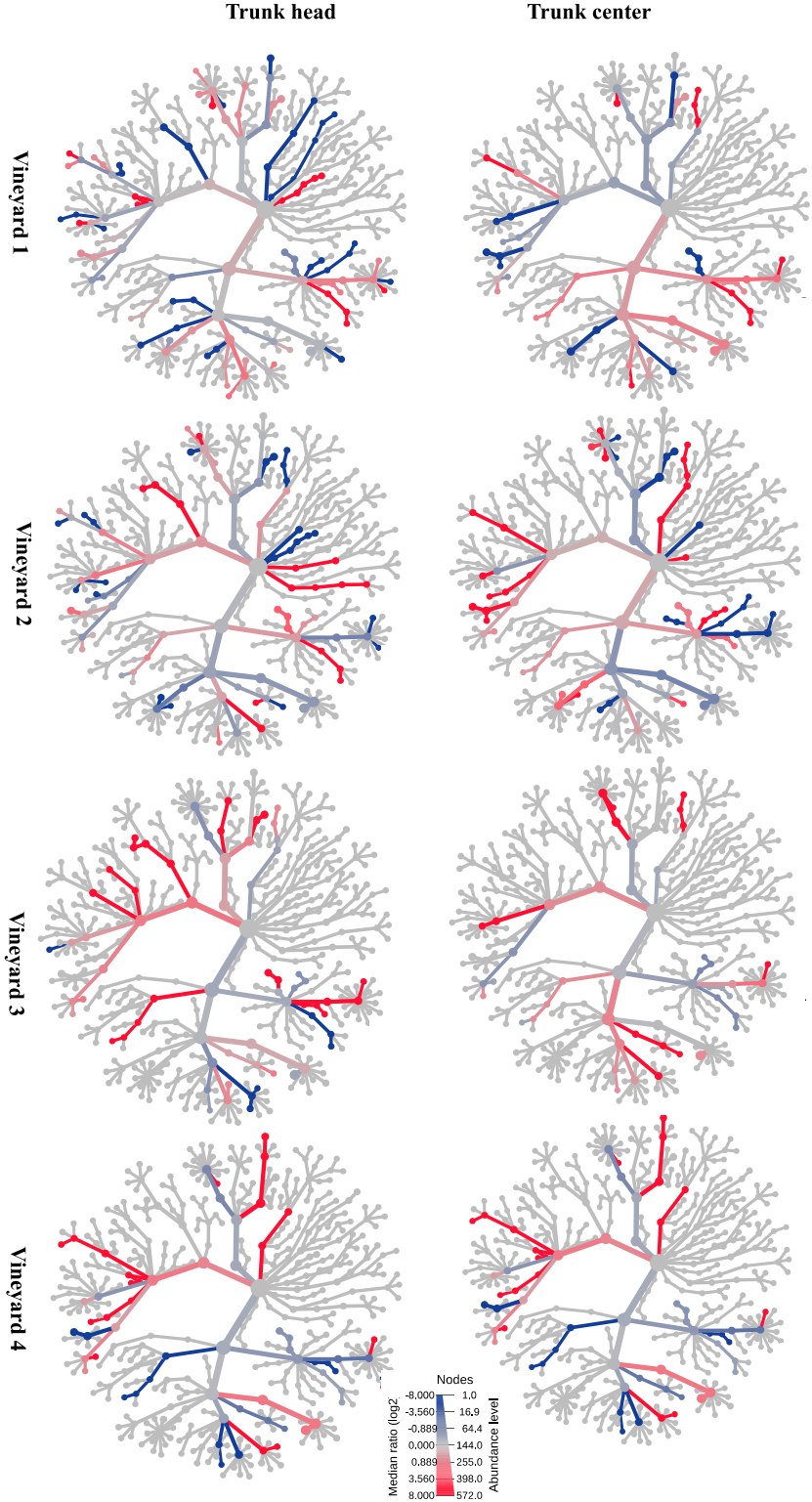
**Table S3:** PERMANOVAs of beta diversity indexes for fungal and bacterial communities. T1 and T2 correspond to sampling time points, 2- and 10-months after Esquire® WP treatment, respectively. Showed values correspond to *p values*.

	Bacteria				Fungi			
	T1		T2		T1		T2	
	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center	Trunk head	Trunk center
	Vineyard_1	0.42	0.65	0.79	0.45	0.5	0.39	0.68
Vineyard_2	0.132	0.125	0.878	0.41	0.11	0.4	0.28	0.35
Vineyard_3	0.26	0.07	0.06	0.57	0.6	0.39	0.8	0.71
Vineyard_4	0.06	0.76	0.73	0.46	0.833	0.82	0.8	0.35



**Figure S4:** Heat tree of factor Treatment. Heat Trees report the effect of treatment on hierarchical structure of taxonomic fungal classifications in Esquire<sup>®</sup> WP treated and control plants, 10 months post-inoculation. Each cladogram shows pairwise comparisons between treatments (Esquire<sup>®</sup> WP vs control), in the different vineyards, at two different tissues (trunk head and trunk center). The indicated taxa with red nodes were significantly abundant in the

Esquive® WP -treated plants, while green nodes significantly more abundant in fungal communities of control plants.



**Figure S5:** Heat tree of factor Treatment. Heat Trees report the effect of treatment on hierarchical structure of taxonomic bacterial classifications in Esquive® WP treated and control plants, 10 months post-inoculation. Each cladogram shows pairwise comparisons between treatments (Esquive® WP vs control), in the different vineyards, at two different tissues (trunk head and trunk center). The indicated taxa with red nodes were significantly abundant in the

Esquive® WP -treated plants, while green nodes significantly more abundant in bacterial communities of control plants.