

**Supplementary Figure S1** – Symptoms taken into account for the esca disease classification on Verdicchio cultivar. Leaves presented the tiger-striped pattern, with a typical yellow band between the green and necrotic tissues (left) and plant with portion of the canopy and clusters desiccated (central). On the right, canopy of a healthy plant.



**Supplementary Figure S2** – Sequence similarity searches using NCBI Blast web site of AMF *R. irregularis* and *F. mosseae* qPCR fragments. (a), Blast alignment according 28SRNA gene of sample S1\_V1 (NCBI accession number, MK513942) and S5\_V3 (MK513943) showing high nucleotide similarity to *R. irregularis* species (HF968988.1 and FJ235574.1), (b) Blast alignment of according to LSU gene of sample S4\_V1 (MK513940) and S10\_V3 (MK513941) homologous to *F. mosseae* species (FN377862.2 and FN37865.1).



**Supplementary Table S1** - Serial dilutions of DNA from I10 and A7 samples analyzed on qPCR for *R. irregularis* and *F. mosseae* genes. The experiments were assessed in triplicate over three independent experiments (n = 9). Cq, quantification cycle; SD, standard deviation; \*less of four replicates amplified of six performed; na, not amplified

		qPCR			
		DNA from grapevine roots (ng)			
	sample	100	50	5	0.5
		Cq mean $\pm$ SD			
<i>R. irregularis</i>	I10	na	na	29.6 $\pm$ 0.3	33.6 $\pm$ 1.2*
	A7	na	na	30.2 $\pm$ 0.5	35.1 $\pm$ *
<i>F. mosseae</i>	I10	na	na	31.2 $\pm$ 1.1*	na
	A7	na	na	33.9 $\pm$ 1.1*	36.1 $\pm$ *

**Supplementary Table S2** - The ddPCR inhibitors investigation and LOD for AMF. Non host roots from oak plants (0, and 50 ng/qPCR reaction) spiked with serial dilutions of AMF qPCR fragments (S1\_V1 and S10\_V3 for *R. irregularis* and *F. mosseae*, respectively) at different concentration. The test was assessed on two independent experiments (n = 2).

ddPCR			
	AMF qPCR fragments from grapevine roots (ng/reaction) +	DNA from oak non-host plant	
		0 ng/reaction	50 ng/reaction
		Concentration (copies/20 L reaction) Mean ± SD	
<i>R. irregularis</i>	$3.5 \times 10^{-8}$	2,940 ± 84.1	2,380 ± 90.5
	$3.5 \times 10^{-9}$	270 ± 32	216 ± 34
	$3.5 \times 10^{-10}$	38 ± 4.1	24 ± 7.1
	$3.5 \times 10^{-11}$	10 ± 3.3	8 ± 3.5
<i>F. mosseae</i>	$2.8 \times 10^{-8}$	3,020 ± 58.3	2,800 ± 68.3
	$2.8 \times 10^{-9}$	364.2 ± 14	424 ± 19
	$2.8 \times 10^{-10}$	30 ± 9.0	56 ± 12
	$2.8 \times 10^{-11}$	5.6 ± 1.1	9.4 ± 21

**Supplementary Table S3** - Serial dilutions of DNA from I10 and A7 samples analyzed on ddPCR with the primers for *R. irregularis* gene and LSU *F. mosseae* genes. The test was assessed over two independent experiments (n = 2). SD, standard deviation; na, not amplified.

qqPCR					
DNA from grapevine roots (ng)					
sample		100	50	5	0.5
Concentration (copies/20µL)					
<i>R. irregularis</i>	I10	na	706 ± 80.4	101 ± 21.1	9 ± 2.1
	A7	na	105.4± 21.7	12.4 ± 6.1	2.2 ± 1.8
<i>F. mosseae</i>	I10	na	36 ± 2.82	4.6 ± 2.1	1.4 ± 0.04
	A7	na	50.4 ± 10.7	6.4 ± 3.1	1.2 ± 1.1