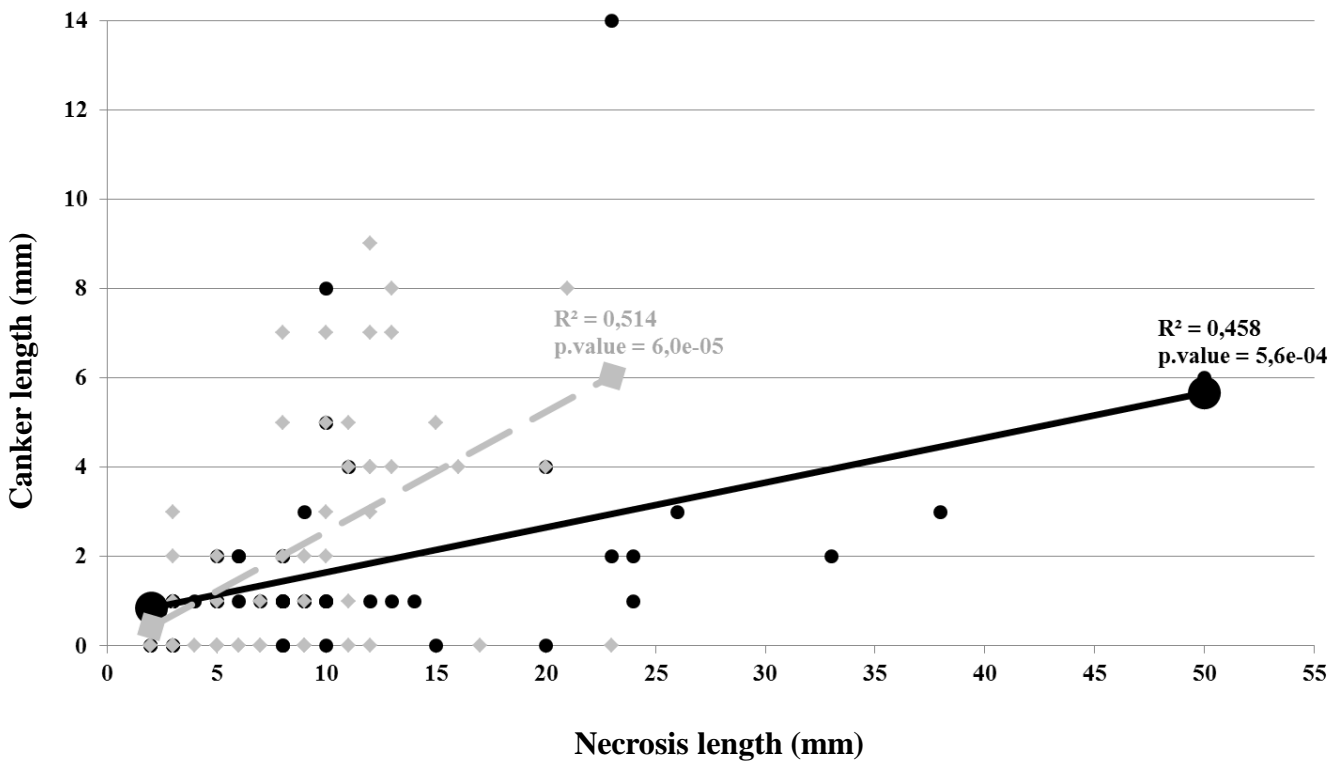


Figure S1. Correlations between Botryosphaeriaceae canker and necrosis length in five grapevine cultivars and genotypes. (a) Correlations with Merlot (black circle and full line) and Cabernet Sauvignon (grey shape and dash line). (b) Correlations with Ugni-Blanc (black circle, black full line) and with the two genotypes RV4 (grey shape and black dotted line) and RV5 (grey triangle and black dotted line). Correlations made independently of inoculated isolate, in each cultivar or genotype.

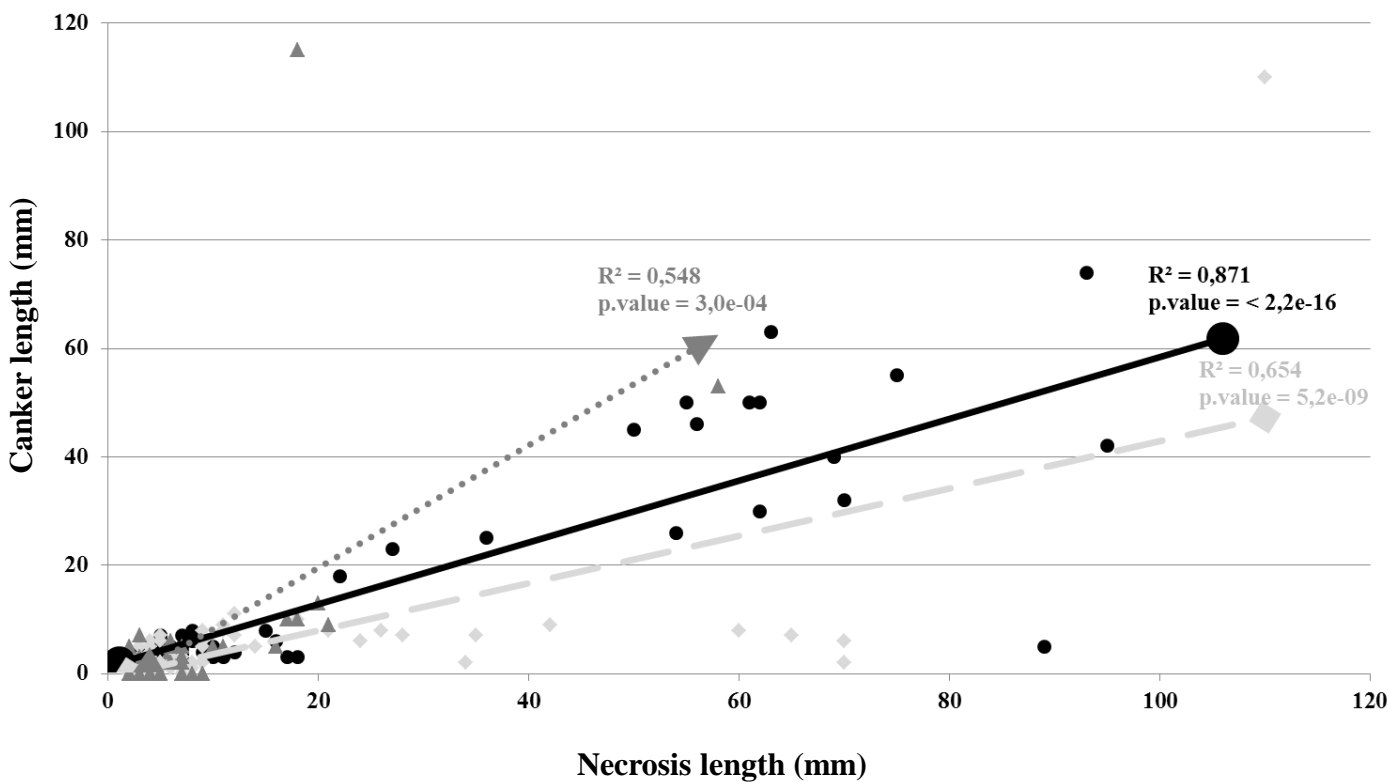
Figure S2. Relative gene expression with log₂ transformation in grapevine cultivar and hybrid leaves, 6 days after inoculation of wood with five Botryosphaeriaceae isolates. Gene expression of wounded but noninoculated plants was used as a reference to calculate the relative expression. Each column represents a combination of one of the five cultivars and genotypes (Merlot, Cabernet Sauvignon, Ugni-Blanc, RV4 and RV5) inoculated with one of the five Botryosphaeriaceae isolates (LAG05, PER20, F98-1, LAT16 and BRA08). Each line corresponds to one gene represented by a single row of boxes. The colour scale bars represent the ratio values corresponding to the mean of three independent experiments. Over-expressed genes appear in shades of red, with expression level higher than five in bright red, while those with reduced expression appear in shades of blue, with intensity lower than -5 in dark blue. Numbers in boxes represent significant changes in gene expression ($P \leq 0.05$) compared to the wounded but noninoculated control.

Figure S3. Relative gene expression with log₂ transformation in grapevine cultivar and hybrid leaves, 17 days after inoculation of wood with five Botryosphaeriaceae isolates. Gene expression of wounded noninoculated plants was used as a reference to calculate relative expression. Each column represents a combination of one of the five cultivars and genotypes (Merlot, Cabernet Sauvignon, Ugni-Blanc, RV4 and RV5) inoculated with one of the five Botryosphaeriaceae isolates (LAG05, PER20, F98-1, LAT16 and BRA08). Each line corresponds to one gene represented by a single row of boxes. The colour scale bars represent the ratio values corresponding to the mean of three independent experiments. Over-expressed genes appear in shades of red, with expression level higher than 5 in bright red, while those with reduced expression appear in shades of blue, with intensity lower than -5 in dark blue. Numbers in boxes represent significant changes in gene expression ($P \leq 0.05$) compared to noninoculated wounded control.

a)



b)





Merlot

LAG05
PER20
F98-1
LAT16
BRA08

<i>VvPR1</i>					
<i>VvPR2</i>				3,5	-0,8
<i>VvPR3</i>	-2,4		-1,1		
<i>VvPR5</i>					
<i>VvPR6</i>			2,3	1,8	2,1
<i>VvPR8</i>	3,9			2,0	
<i>VvPR10</i>			2,6	-0,9	
<i>VvPAL</i>		-1,0			-1,2
<i>VvSTS</i>	3,9			2,3	
<i>VvCHS</i>	-2,2				
<i>VvANTS</i>					
<i>VvCHORM</i>					
<i>VvCHORS</i>		-0,8			
<i>VvCALS</i>					
<i>VvPER</i>					1,3

Cab.-Sauv.

LAG05
PER20
F98-1
LAT16
BRA08

-1,5			-0,9	-1,3	
2,7		2,8	2,2	2,1	
2,8	6,4		3,0	-1,2	
-3,5	-2,8		-2,7	-1,7	
			0,8		
		-1,7	-0,8		
	1,4		1,4		
	-2,2				
	2,0				

Ugni-Blanc

LAG05
PER20
F98-1
LAT16
BRA08

	-1,6				
	-1,7				
	-0,6				
					1,3
3,5			0,8		
	-1,3				
0,4			0,7	0,6	
			1,8	2,0	
1,3					1,2
					1,6
	-0,9				
			0,7	1,5	

RV4

LAG05
PER20
F98-1
LAT16
BRA08

2,1				1,6	
1,9		4,7		2,1	
-1,0	-1,4				
2,7	-1,2	4,3		-1,7	
			-0,9		
					0,9
	-0,6				

RV5

LAG05
PER20
F98-1
LAT16
BRA08

	2,7		1,9	0,9	
	3,6			1,3	
-1,4					
		-1,4		-1,0	
-4,3			2,2	0,9	
	2,6				
		1,6	1,5	1,3	
	-1,3	-2,0	-1,7	-3,1	
-4,0		3,0			
-1,4					
-3,3	1,5	1,4	1,4	1,1	
	2,3	1,9	2,9	1,5	
		1,8	2,0	1,8	

