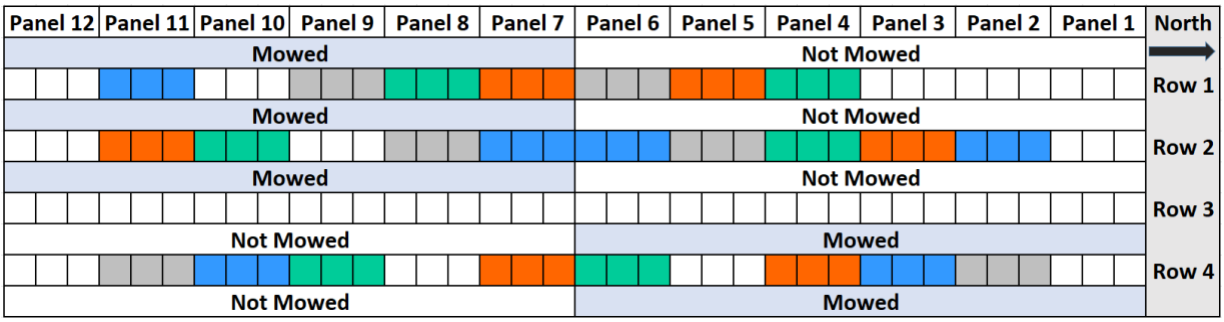
SUPPLEMENTARY DATA



Supplementary Figure 1. Map of vineyard layout with treatment application assignments.

- Control (CTL), - Phenylalanine (Phe), - Prohexadione Calcium (ProCa), and - ProCa+Phe. Mowed/Not Mowed were included in the modelling, but data were not presented on those groups.

Supplementary Table 1. Collection dates and Growing Degree Days (GDD) for five phenological time points throughout berry development and ripening in 2022 and 2023.

Year	Time Point	Date	GDD[b]
2022	1 wk PFS[a]	24 June	582
	3 wks PFS	7 July	751
	Véraison	25 July	1000
	Mid-ripening	9 August	1191
	Harvest	26 August	1389
2023	1 wk PFS	15 June	503
	3 wks PFS	3 July	731
	Véraison	19 July	903
	Mid-ripening	7 August	1157
	Harvest	31 August	1456

[a]PFS: post fruit set. [b]Growing degree days (base 10°C).

Supplementary Table 2. Pruning weights and number of buds retained for each treatment in 2022 and 2023.

Year	Treatment	Pruning weight (kg/vine)	Number of buds retained per vine
2022	CTL	0.8 ± 0.4	33.8 ± 4.7
	Phe	0.9 ± 0.4	35.6 ± 4.9
	ProCa	0.8 ± 0.4	31.1 ± 1.6
	ProCa+Phe	1.0 ± 0.4	35.0 ± 4.2
2023	CTL	0.7 ± 0.3	39.0 ± 7.1
	Phe	0.8 ± 0.3	41.4 ± 8.5
	ProCa	0.6 ± 0.2	37.7 ± 7.3
	ProCa+Phe	0.8 ± 0.3	42.4 ± 8.3
p-value	Year	0.0056	<0.0001
	Treatment	n.s	0.0123
	Year*Treatment	n.s	n.s.

Values are means ± standard deviation across 18 vines per treatment. Significant p-values were taken after a two-way ANOVA with $\alpha = 0.05$.

Supplementary Table 3. Yeast assimilable nitrogen (YAN) and calcium concentration in juice at harvest in 2022 and 2023.

Treatment	YAN (mg N/L)		Calcium (mg/L)	
Year	2022	2023	2022	2023
CTL	401 ± 4	269 ± 93	124 ± 7	97 ± 6 a
Phe	393 ± 15	273 ± 102	124 ± 3	85 ± 5 b
ProCa	359 ± 46	281 ± 136	126 ± 5	92 ± 5 ab
ProCa+Phe	395 ± 7	301 ± 96	121 ± 4	87 ± 7 ab
n	4	6	5-6	6
p-value for *t*-test between years	0.0002		<0.0001	

Values are means ± standard deviation. Different letters within a column indicates significant differences at α = 0.05 between treatments by Tukey's HSD following a one-way analysis of variance. "n" corresponds to the number of replicates for each value in that column.

Supplementary Table 4. Composition of tannins from skins and seeds of Marquette CTL at 1 week post fruit set in 2022 and 2023, obtained after acid-catalysis with an excess of phloroglucinol.

Tissue Type	Skin			Seed		
Year	2022	2023	*p*-value	2022	2023	*p*-value
mDP	46.8 ± 13.5	44.2 ± 8.7	n.s.	10.5 ± 1.4	9.1 ± 1.7	n.s.
%Tri-OH	30.4 ± 1.8	30.8 ± 1.8	n.s.	4.0 ± 0.3	4.5 ± 1.3	n.s.
%Galloylation	5.3 ± 1.5	5.6 ± 1.5	n.s.	22.3 ± 0.8	34.0 ± 1.7	<0.0001
EGC-ext (mole %)	30.4 ± 1.8	30.8 ± 1.8	n.s.	4.0 ± 0.3	4.5 ± 1.3	n.s.
C-ext (mole %)	2.8 ± 0.5	3.0 ± 0.5	n.s.	8.1 ± 0.3	7.7 ± 0.7	n.s.
EC-ext (mole %)	59.2 ± 2.6	58.2 ± 1.5	n.s.	58.3 ± 1.5	46.3 ± 2.2	<0.0001
ECG-ext (mole %)	5.3 ± 1.5	5.6 ± 1.5	n.s.	7.3 ± 1.3	7.6 ± 1.1	<0.0001
C-term (mole %)	2.3 ± 0.7	2.4 ± 0.5	n.s.	19.9 ± 0.4	30.3 ± 2.4	n.s.
EC-term (mole %)	n.d.	n.d.	---	n.d.	n.d.	---
ECG-term (mole %)	n.d.	n.d.	---	2.4 ± 0.5	3.6 ± 0.9	0.0115

Values are means ± standard deviation of six biological replicates. The p-values are from a pooled t-test (α = 0.05) comparing year for skins and seeds. mDP: mean degree of polymerisation. %Tri-OH: percent of B ring tri-hydroxylation. EGC-ext: epigallocatechin extension subunit. C-ext: catechin extension subunit. EC-ext: epicatechin extension subunit. ECG-ext: epicatechin-gallate extension subunit. C-term: catechin terminal subunit. EC-term: epicatechin terminal subunit. ECG-term: epicatechin-gallate terminal subunit. n.s.: not significant. n.d.: not detected.

R Code

The additive effects linear regression model. Example is for the harvest time point.

```
var_mod_harv <- lme(response ~ mow + year*ProCa*Phe,
                    random = ~1|rows/mow/panels,
                    data = var_data_harv,
                    na.action = na.omit)
anova(var_mod_harv)
```