

The Effects of Heat Treatment on Grapevine Performance in a Chardonnay and a Merlot Vineyard: a Consulting Report

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Abstract

In this report, the effects of agro-thermal heat treatment on various measures of grapevine quality and productivity in the Okanagan Valley are investigated. Specifically, the effects of agro-thermal heat treatment are investigated in a Chardonnay and a Merlot vineyard using data from both 2019 and 2020. With the design of the study that includes a control group and a blocking factor based on the location of the grapevines, a number of parametric and non-parametric two-way analyses are conducted. While the agro-thermal heat treatment does not have a statistically significant effect on most of the measures considered in the study for the Chardonnay grapevines, the heat treatment is shown to have an effect on a number of the measures for the Merlot grapevines. In addition, significant interaction effects between heat and blocking for a number of response variables suggest that the agro-thermal heat treatment effect may vary across different geospatial conditions.

Table of Contents

1	Introduction	1
2	Exploratory data analysis	1
2.1	Response variable description	1
2.2	Correlation among response variables	2
2.3	Visualization of response variables	3
2.3.1	Kaplan-Meier plots	3
2.3.2	Side-by-side boxplots	3
2.4	Preliminary Conclusion	4
3	Handling missing data	5
3.1	Censored data	5
3.2	Non-censored data	5
4	Model-Based Statistical analysis	6
4.1	Censored data analysis	6
4.2	Non-censored data analysis	7
4.2.1	Model description and assumption checks	7
4.2.2	Two-way ANOVA analysis	9
4.2.3	Summary of additional non-censored analysis results	9
4.2.4	Combining both years' data together	10
5	Conclusions and discussion	10
References		12
A	Additional tables and plots in exploratory data analysis	13
A.1	Summary statistics for Chardonnay and Merlot datasets	13
A.2	Correlation plots for outcomes variables	13
A.3	Kaplan-Meier plots	15
A.4	Side-by-side boxplots	16
B	Additional censored data analysis	24
B.1	Cox PH covariate estimates	24
B.2	Interval-censored data method	25
C	Additional non-censored data analysis	27
C.1	Multiple imputation	27
C.2	Chardonnay 2019	28
C.3	Chardonnay 2020	29
C.4	Merlot 2019	31
C.5	Merlot 2020	37
C.6	Three-way ANOVA	43
D	Selective R code	47
D.1	Explorative data analysis	47
D.2	Censored data analysis	48
D.3	Non-censored data analysis	49

1. Introduction

This study investigates the effect of agro-thermal heat treatment on various measures of grapevine quality and productivity in a Chardonnay and a Merlot vineyard in the Okanagan valley. Agro-thermal treatment involves applying a shock-treatment of heat to grapevines by driving a tractor through the vineyard rows that blows extreme heat into the canopy. [AgroThermal Systems](#), the company responsible for this technology, claims their treatment has been shown to increase yield, decrease the use of agro-chemicals used to fight pests, enhance wine quality and improve profits [1]. However, experiments in the Southern Okanagan have indicated these claims may not always hold [2].

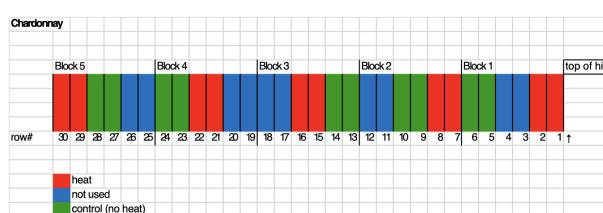
Since this heat treatment has never been tested in the Okanagan Valley or anywhere in Canada, the goal of this study is to identify whether agro-thermal heat treatment influences various measures of the quality and productivity of the Chardonnay and Merlot grapevines grown in the Okanagan Valley. With data collected on Chardonnay and Merlot grapevines in both the 2019 and 2020 growing seasons, the two growing seasons are to be analyzed both separately and jointly.

This report includes exploratory data analysis, handling of missing data, implementation and interpretation of several models used to analyze the effects of the heat treatment on the outcome variables, and a discussion of the implication of the findings in this study. All R code used in this data analysis can be viewed at [STAT 550 Grapevine GitHub repository](#).

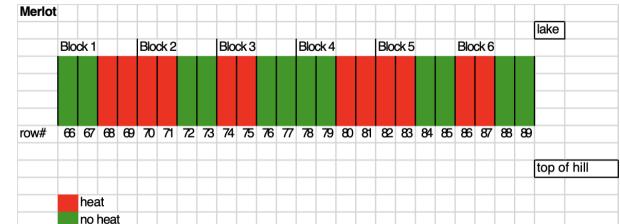
2. Exploratory data analysis

This section examines the outcome variables and the relationships between them. We begin by describing the available data before graphically inspecting the main characteristics of them. Note that for this section, we do not make any assumptions on the distribution of the data.

Figure 1 from the project description shows that both the treatment and block factors have been incorporated in the experimental design. Specifically, the grapevines were grouped by blocks that differ in geospatial conditions. Then within each block, half of the vines received the agro-thermal treatment, and the other half did not. A number of random samples were drawn from each treatment/block combination. Note that across the two growing seasons, the outcome variables were collected on the same set of grapevines. The Chardonnay datasets contain measurements from 40 grapevines (five blocks, four vines per treatment within each block), and the Merlot datasets contain measurements from 60 grapevines (six blocks, five vines per treatment within each block).



(a) Experimental design for Chardonnay Vineyard



(b) Experimental design for Merlot Vineyard

Figure 1. Overview of experimental design in Chardonnay and Merlot vineyards

2.1 Response variable description

The list of variables and their descriptions are shown in Table 1. The vineyard for which each variable is recorded (Chardonnay or Merlot), along with the year(s) in which each variable is recorded (2019, 2020, or both 2019 and 2020), is also noted in the table.

Variable	Definition and collection method	Vineyard	Year
# of clusters	the cluster count for each vine at the time of harvest in October	Both	Both
Yield (kg)	yield in kg for each vine at the time of harvest in October	Both	Both
Average cluster weight (kg)	total grapevine yield divided by number of grape clusters	Both	Both
Leaf greenness (SPAD)	average value of ten randomly subsampled leaves measured in July	Merlot	Both
50% veraison (days after August 1st)	time by which half of the berries on a treatment vine have changed from green to red	Merlot	Both
Average berry weight (kg)	average weight of thirty randomly subsampled berries measured in October	Merlot	Both
Average # of berries per cluster	cluster weight (in grams) divided by the berry weight (in grams)	Merlot	Both
Berry quality: pH, TA, and Brix	measurements from the same set of randomly subsampled berries, may influence quality of wine	Merlot	Both
Brown seed color	visually accessed seed color change once grapes have matured	Merlot	2020
Pruning weight (kg)	the pruned cane weight after harvest	Merlot	Both
Ravaz index	yield divided by pruning weight	Merlot	Both
Fruitfulness	the number of clusters emerged in Spring divided by the number of new shoots	Merlot	2020
50% Bloom (days after June 1st)	time by which half of flowers on a treatment vine have started to bloom	Merlot	2020

Table 1. Descriptions of all outcome variables

The five number summary statistics for all outcome variables in the Merlot 2019 dataset are shown in Table 9. The summary statistics table for the Merlot 2020 dataset and both years' Chardonnay datasets are shown in Appendix A.1. Note that the missing values are removed before calculating the summary statistics for each outcome variable. It is found that the mean and median are quite close for almost all outcome variables, indicating that their distributions may be roughly symmetric. However, considering the small sample size, this may not be the case within each treatment/block combination.

	leaf greenness	veraison	avg. cluster number	yield	avg. cluster weight	avg. # of berries per cluster	avg. berry weight	berry TA	berry pH	berry Brix	pruning weight	Ravaz index
min	35.6	11	9	0.55	0.05	42.78	0.98	4.82	3.17	21.8	0.05	1.26
median	39.9	21.67	18	2.57	0.14	98.18	1.37	7.35	3.3	24.6	0.22	11.69
max	46	25	35	7.07	0.34	205.76	1.78	10.52	3.65	25.7	0.8	35.24
mean	40	20.02	18.55	2.65	0.14	101.62	1.38	7.19	3.32	24.45	0.27	12.34
sd	2.27	4.98	5.36	1.23	0.05	33.23	0.17	1.21	0.09	0.72	0.16	6.74

Table 2. Summary statistics for Merlot 2019

2.2 Correlation among response variables

Based on the description of outcome variables in Table 1, it is likely that some of them may be correlated. To investigate the pairwise correlations among these variables, we use Pearson's correlation coefficient to measure the strength of linear correlations for all response variables in both years' Chardonnay and Merlot datasets. This can help us decide on an appropriate model for further statistical analysis.

Since the assessment of correlations among response variables is similar for each dataset, we discuss the correlations among response variables from the Merlot 2019 dataset as an example. The correlation plots for the other datasets are shown in Appendix A.2. We see in Figure 2 there are strong correlations between yield and average cluster weight ($\text{corr}=0.76$) and between average cluster weight and average number of berries per cluster ($\text{corr}=0.94$) [3]. Both of these high correlations can be reasonably explained: a high average cluster weight implies high yield, and the average number of berries per cluster indeed depends on the average cluster weight.

The high pairwise correlations discussed above suggest that we should be conducting model-based statistical analysis that tests for the treatment effects simultaneously across multiple response variables. If each of the response variables is examined separately, we may fail to incorporate the additional information

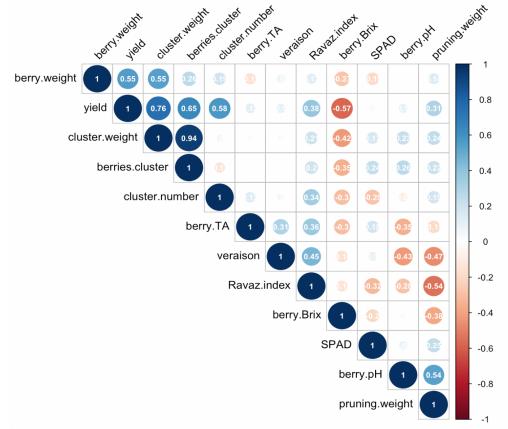


Figure 2. Correlation plot for Merlot 2019

from the correlation structure. However, tests that handles multiple response variables simultaneously usually require the data to follow a multivariate normal distribution. With the small sample size of the available data, particularly within each treatment/block combination, it may be difficult to verify whether this multivariate normality assumption holds. Hence, we conduct our following analysis one outcome variable at a time for both the Chardonnay and Merlot grapevines.

2.3 Visualization of response variables

We now graphically inspect the observations under each treatment/block combination. As is further discussed in Section 3.1, the veraison and bloom variables indicate the time of occurrence of some event. This is unlike all other responses in our datasets that measure some fixed quantitative property of each grapevine. Therefore we use different visualization tools for each of the two types of response variables.

2.3.1 Kaplan-Meier plots

Veraison and bloom measure the occurrence times of each grapevine reaching 50% veraison and 50% bloom. A Kaplan-Meier survival plot can be used here to inspect the probability that grapevines under some treatment/block combination have not reached 50% veraison/bloom at some given time. We call this probability the survival probability. On the Kaplan-Meier plots, the range of the survival probabilities from 95% confidence intervals are indicated by the shaded area. P-values from the log-rank test, which examines the differences between two treatments' survival distributions within each block, are also shown in the plot. The Kaplan-Meier plots for each of the veraison and bloom variables are shown in Appendix A.3.

As an illustration of how these plots can be interpreted, we more closely examine the Kaplan-Meier plot for veraison from the Merlot 2020 dataset (Figure 3). We see that in blocks 2 and 4, the control group seems to have a lower survival probability across the entire period of the study, while most other blocks show that the treatment groups may have lower survival probabilities. Specifically in block 2, the control group's survival probability is shown to reach zero considerably earlier than the treatment group. The corresponding p-value from the log-rank test ($p=0.058$) indeed suggests that the two survival distributions may be different. Compared to the rest of the blocks, the different trends that we have found in blocks 2 and 4 suggest that the effect of the heat treatment on the survival probabilities may be dependent on the blocks that the vines are in. Again, we note that our confidence intervals are wide due to the small sample sizes, indicating that there is considerable uncertainty from our preliminary inspections.

2.3.2 Side-by-side boxplots

For all of the other response variables, side-by-side box plots are used to further visualize the observations in the control and treatment groups within each block (Appendix A.4). A box plot displays the five-number summary of the measurements: the minimum, 1st quartile, median, 3rd quartile and the maximum. Though there are only four or five observations under each treatment/block combination, box plots are still helpful in comparing the location and spread of the data between treatment groups.

The boxplots also include p-values from the t-test and Wilcoxon test to numerically detect differences between the responses from the two treatments within each block. Note that the t-test requires the data to be normally distributed, which may not hold with our small sample size. Therefore, in addition, p-values from the Wilcoxon test are also included. The Wilcoxon test does not make an assumption on the distribution of the data and so it is more appropriate when the normality assumption does not hold or when the data contain outliers.

Since the boxplots for each response variable can be interpreted in a similar way, we discuss the berry pH values from the Merlot 2019 dataset in detail, and provide a summary on all of the other response

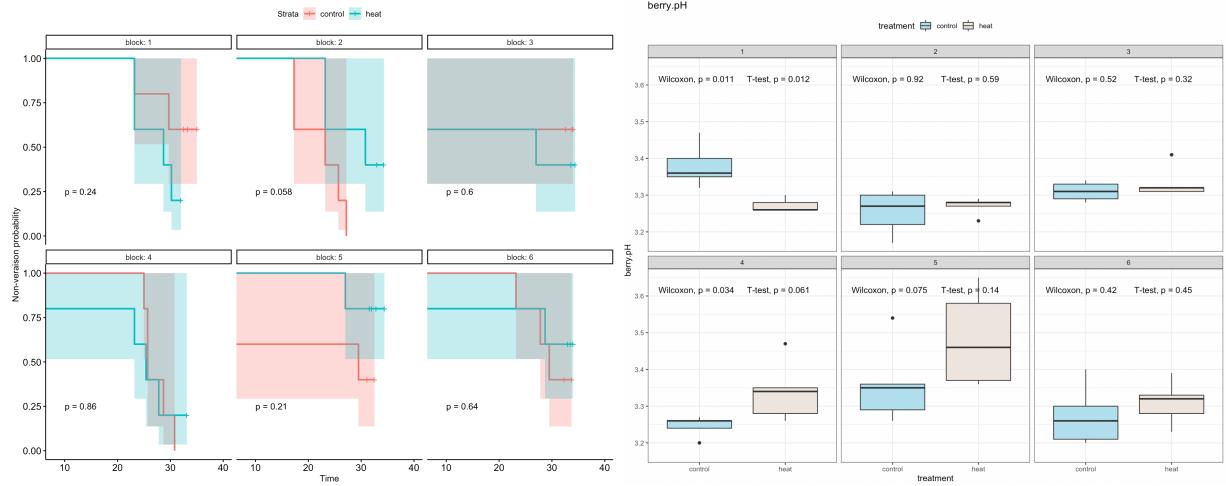


Figure 3. Kaplan-Meier plot for veraison with treatment v.s. control in Merlot 2020, divide by block.

Figure 4. Side-by-side boxplots of berry pH value in Merlot 2019, divided by block: block number is labelled on the top of each window

variables. From Figure 4, we can see that the treatment group seems to have higher berry pH values in all blocks except for the first one. In addition, there is strong evidence against that the berry pH values from the two treatment groups in the first block are the same ($p \approx 0.01$ from both tests). This suggests that the heat treatment may overall lead to a higher berry pH, but this effect is not uniform and depends on the block that the vines are in.

In both of the Chardonnay datasets, most response variables appear to overlap across most treatment/block combinations. However, there are contrasting trends across the different blocks. Notably, the treatment seems to have effects varying from block to block on the number of clusters in both years' Chardonnay datasets. This implies that there may not be an effect of the heat treatment overall, but rather effects that are specific to some of the blocks.

Several outcome variables in the Merlot 2019 dataset seem to have different means between the two treatments. In addition to the berry pH values discussed above, the average number of berries per cluster from the control group seems to be higher across most blocks. In addition, contrasting trends are also found in block 5 of average cluster weight and block 6 of average berry weight. The Merlot 2020 dataset contains many missing values due to zero yield that year. Some plots become less informative after the missing values are dropped. Among all the distributions of outcome variables, the measurements of leaf greenness seem to be higher across all blocks in the control group.

2.4 Preliminary Conclusion

Besides berry pH and average number of berries per cluster from Merlot 2019 and leaf greenness from Merlot 2020, most of the response variables do not seem to differ in their means between the treatment and control groups. However, within particular blocks, some variables have distinct means under different treatment groups. This may indicate the presence of interaction between the geospatial conditions of each block and the treatments (heat/control); that is, the treatment effect may depend on the geospatial locations. To justify these observed differences, a confirmatory analysis needs to be carried out.

3. Handling missing data

There are a number of response variables that contain missing values (Table 3). In addition, 43.3% of the veraison values are also missing from Merlot 2019. Depending on the reason why these values are missing, simply ignoring them may cause the analysis result to be biased. Below, we discuss the outcome variables with missing values in detail, and how we can handle these missing data.

bloom	veraison	yield related measures	berry quality related measures	brown seed color	pruning weight	Ravaz index
11.7%	13.3%	11.7%	13.3%	26.7%	13.3%	38.3%

Table 3. List of response variables and their missing rates in Merlot 2020

3.1 Censored data

Censored data is a special type of missing data where we have some but not all the information about the missing values. This is the case for bloom and veraison. The bloom variable indicates the estimated time when 50% of the flowers on a vine have started to bloom, and the veraison variable indicates the estimated time when 50% of the berries on a vine have changed from green to red. Some of the bloom and veraison data are missing because the plant had already reached 100% bloom or veraison before T1. Other times, data are missing because the plant did not produce any flowers or berries. In either case, the missing values are partially known. In other words, we have some information about when 50% bloom or veraison occurred – either before T1 or after T3, respectively. A summary of this censored data can be seen in Table 4.

Thus, instead of interpreting 50% Bloom and Veraison as occurring on fixed dates, we can interpret these events (50% bloom or veraison) as occurring within certain time intervals. There are three cases:

1. The event did not occur because no berries or flowers grew. This is known as right-censored data. In this case, the event happened in the interval (T_3, ∞)
2. The event had already occurred prior to T1. This is known as left-censored data. In this case, the event happened sometime in the interval $(-\infty, T_1)$.
3. The event was observed. In this case, the “interval” is a fixed number indicating when the event happened.

To achieve better interpretability, a common practice is to only consider right-censored data. Therefore in Section 4.1, we focus on a method which only handles the right-censored data. In this case, left-censored data are interpreted to be “observed” (not censored) at T1. An additional analysis which handles left-censored and right-censored data is also given in Appendix B.2.

3.2 Non-censored data

Outcome variables that contain missing data and can not be interpreted as censored include yield related measures, berry quality measures, pruning weight, and Ravaz index. For all outcome variables that are related to yield (yield, average cluster weight, average number of berries per cluster, average berry weight), the reason for missing is that the vine had no yield. Consequently, these data are not truly

Variable	Left-censored	Observed	Right-censored
Veraison (2019)	26	34	0
Veraison (2020)	2	52	6
Bloom (2020)	2	53	5

Table 4. Overview of the number of censored data points for each censored variable considered.

“missing” – they have a “true” value of zero to indicate zero yield. The missingness in berry quality related measures (including berry brix, TA, and pH; and brown seed color) are precisely due to zero yield. In other words, these measurements could not have been taken because the corresponding vines produced no berries. On the other hand, some of the entries of pruning weight are missing because the winery had started to prune canes before any data could be collected. Finally, the Ravaz index is the ratio between yield and pruning weight, for any vine that has its yield or pruning weight missing, its Ravaz index is also be missing.

The missing values present in our datasets are either missing completely at random (pruning weight), or due to other responses of the corresponding vine being missing (berry quality related measures and Ravaz index). That is, none of the missingness is dependent on the missing values themselves. Statistically speaking, these missing values are considered ignorable, meaning that excluding these missing values does not result in our subsequent analysis being biased.

Therefore, when conducting model-based analysis for non-censored data, we focus on the complete case analysis where all of the missing values are simply discarded. To check whether our analysis results are sensitive to the missing values, another set of tests are run after addressing the missing values using the multiple imputation method. The details of the use of multiple imputation are shown in Appendix C.1.

4. Model-Based Statistical analysis

With the strategies for both types of missing data laid out, the model-based statistical analysis is carried out in this section for both censored and non-censored data.

4.1 Censored data analysis

We use a Cox Proportional Hazards (Cox PH) model to investigate the effects of treatment and blocking on the censored variables: time to the events of 50% veraison and bloom. This model is one of the most commonly used models for survival analysis, which precisely studies the expected duration of time until some event happens. As mentioned in Section 3.1, only right-censoring is considered for the analysis below.

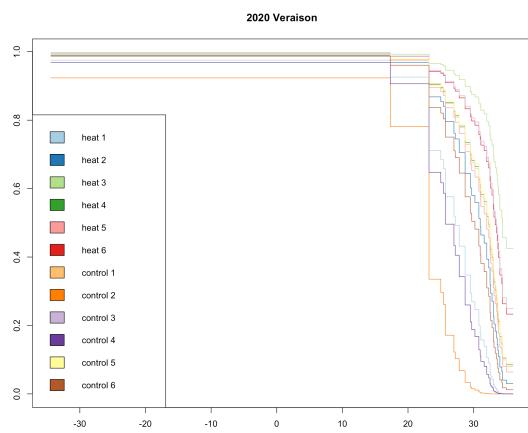


Figure 5. Survival function for 50% veraison from the Merlot 2020 data. “Survival” indicates the probability the event has not yet occurred by time t .

A Cox PH model is expressed by a hazard function, $h(t)$, that can be interpreted as the instantaneous risk of the event (in this case, “risk” of reaching 50% veraison or bloom) occurring at time t , based on a set of covariates x that specify the treatment that the corresponding vine received and the block it was in:

$$h(t) = h_0(t) \times \exp(\beta_{trt}x_{trt} + \beta_{block}x_{block} + \beta_{trt:block}x_{trt:block})$$

In this equation, $h_0(t)$ represents the baseline hazard function, which is the hazard function for when all covariates equal zero. In this case, the baseline hazard represents the hazard function for the control group in block 1.

The covariates in this model include the treatment, block, and the interaction (combination) of the factors. The interaction term checks whether the effect of the agro-thermal heat treatment on veraison or bloom depends on the block that the vines are in. The Cox PH model estimates the coefficients for

these covariates. Then much like for a linear regression model, we can look at the significance of the coefficients to see if treatment, blocking, or their interaction influence 50% veraison or bloom.

The only assumption of Cox PH models is the assumption of proportional hazards: that the covariates only affect the chance of 50% veraison or bloom, and not the timing of periods of high blooming/veraison. In other words, the β 's are constant for all t . This assumption can be checked by inspecting the Kaplan-Meier plots for each treatment/block combination. If survival functions (probability that 50% veraison/bloom has not yet occurred by a given time) do not overlap, the proportional hazards assumption is said to approximately hold. As an example, by Figure 5, we can see that the proportional hazards assumption approximately holds for the veraison variable in the Merlot 2020 dataset. This is also the case for our other two censored response variables (veraison in Merlot 2019 and bloom in Merlot 2020, shown in Figure 21).

We note that the blocking factor is mostly to help isolate effects of the two treatments, and so we are not primarily interested in the effects of the blocking factors. Then of all censored response variables, there is only evidence against that the treatment effects are the same for veraison from the Merlot 2020 dataset (Appendix B.1). By Table 5, we see that there is strong evidence (p -values as small as 0.00) against that the effect of the heat treatment does not depend on the block that the vines are in, and that there is weak evidence ($p=0.07$) against that the two treatments (heat and no heat) have the same effect. The significant interaction effects align with our preliminary conclusions from the exploratory data analysis. Overall, the heat treatment seems to make the vines reach 50% veraison earlier than those that did not receive the heat treatment. Again from Table 5, the 95% confidence interval indicates that the instantaneous probability of reaching 50% veraison among vines that received the heat treatment ranges from 0.92 to 12.17 times of that among vines in the control group.

4.2 Non-censored data analysis

From Figure 1, we see that both the treatment and blocking factors are included in the design of the experiment. In addition, Section 2 has also discussed that since the number of observations within each treatment/block combination is small, analyzing each response variable separately would be preferred rather than simultaneously analyzing multiple response variables. Considering these characteristics of the experimental design and the data available, fitting a two-way ANOVA model on each response variable separately is most appropriate. Since the method of analysis is similar, if not identical, across all non-censored response variables, here we focus on the berry pH response variable in the Merlot 2019 dataset. At the end of this section, a summary of the analysis results on all other non-censored responses is provided, the details of which can be found in Appendix C.

4.2.1 Model description and assumption checks

Under the two-way ANOVA model, the berry pH value of the l th vine in block j receiving treatment i , denoted y_{ijl} , is decomposed as the following:

$$y_{ijl} = \eta + \alpha_i + \beta_j + \omega_{ij} + \varepsilon_{ijl}, \forall i = 1, 2; j = 1, \dots, 5; l = 1, \dots, 5.$$

explanatory	HR	L95	U95	p
heat	3.35	0.92	12.17	0.07
heat:block 2	0.04	0.01	0.27	0.00
heat:block 3	0.18	0.03	1.36	0.10
heat:block 4	0.07	0.01	0.50	0.01
heat:block 5	0.34	0.05	2.16	0.26
heat:block 6	0.10	0.01	0.65	0.02

Table 5. Output for veraison 2020: HR-hazard ratio, L95/U95 - lower/upper bound of 95% confidence interval

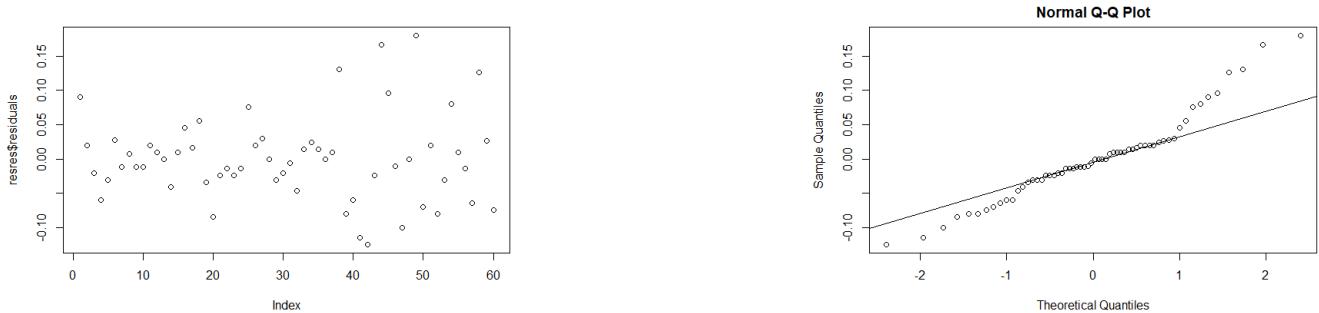


Figure 6. Residual plot and residual QQ plot of berry pH in Merlot 2019

In our case, α_1 and α_2 denote the respective effects on berry pH of being in the group receiving and not receiving heat treatment, and β_j denotes the effect on berry pH of being in block j . Note each of the α_i and β_j terms are independent of the other factor in the study. In practice, it may not be the case that the effect of each factor can be decomposed into independent terms. The interaction effect ω_{ij} then accounts for when the treatment effect depends on the block that the vines are in. Finally, ε_{ijl} describes the remaining variation that is unexplained by any of the factors considered in the model. Note that the effects described above are all relative to η , which is the mean berry pH value across all vines in the study.

Under this setup, we can test whether both treatment effects α_1 and α_2 are different from zero by comparing the amount of variation explained by the treatment effects against the remaining unexplained variation. Similarly, the same tests can be applied to the blocking effects and the interaction effects. It is worth noting that we are not primarily interested in the blocking factor. However, incorporating this blocking factor in the above model ensures that the influence on berry pH caused by the blocking factor has been extracted when testing for the treatment effects.

The two-way ANOVA model assumes that the variances present across all treatment/block combinations are the same, and that the error terms ε_{ijl} across all values of i, j, l are normally distributed with a mean of zero. We now check whether these two assumptions hold for the berry pH response.

Looking at Figure 4, it is clear that the variance of the berry pH values of vines receiving heat treatment in block 5 is higher than all other groups. Indeed, the Levene test, which simultaneously tests whether the variance across all treatment/block combinations are equal, returns a p-value of 0.08, indicating that there is weak evidence against that the variances across all groups considered are equal. By Figure 6, we see that although the residual terms are randomly scattered around zero, there seems to be some severe departure from the assumed normal distribution. If the residuals were indeed normally distributed, we should have the observations represented as empty dots roughly following the slanted line in the QQ plot. Therefore, both the equal variance and normality assumptions are violated for the berry pH variable in Merlot 2019.

One potential source of the assumption violations is the outliers present in the data, which can be seen as the dots shown in Figure 4. However, without further knowledge of whether these points reflect the natural variation among different vines or some experimental error, we refrain from removing these outliers for our analysis. A common fix for the violation of distribution assumptions is to apply the log transformation on the data. However, this does not seem to help with this particular set of data.

As a result, we decide to run another model, alongside two-way ANOVA, that tests the same set of hypotheses without making the above assumptions that are shown to be violated. If the two sets of results are similar, it indicates that the conclusions made from these results are reliable and not very sensitive to the violations of the above assumptions.

The alternative model of choice is the Aligned Rank Transform (ART) ANOVA model described in [4]. This model can be seen as a rank-based two-way ANOVA model: instead of comparing variations among

	sum of squares	degrees of freedom	F value	P value
intercept	661.14	1	141500	0.00
treatment	0.01	1	3.09	0.09
block	0.15	5	6.56	0.00
treatment:block	0.08	5	3.45	0.01
residuals	0.22	48		

Table 6. ANOVA table for berry pH in Merlot 2019

the observed berry pH values, variations among the data's ranks of magnitude are compared between different groups to draw conclusions. Unlike the actual data, the data's ranks of magnitude are not as sensitive to the extremely large or small values. Therefore, the ART ANOVA model does not require the equal variance and normality assumptions described above. Note that the ART ANOVA model is preferred over the possibly more familiar Kruskal-Wallis test because the ART ANOVA model considers two factors simultaneous, while each Kruskal-Wallis model can only handle one factor.

4.2.2 Two-way ANOVA analysis

The two-way ANOVA table for berry pH in Merlot 2019 is shown in Table 6. As expected, we have very strong evidence ($p = 0.00$) against that the effects of each block on the berry pH values are the same. We also have weak evidence ($p = 0.09$) against that the two treatment effects are the same. Finally, there is strong evidence against that ($p = 0.01$) that the interaction effects are all the same. This means that the treatment effects vary depending on which block the vines are in. This set of results is consistent compared to the results obtained from the ART ANOVA model shown in Table 7, indicating that the conclusions drawn above are reliable despite the assumption violations.

To quantify the difference between the two treatment effects, as well as the uncertainty around this difference obtained using the available data, the estimated difference between the two treatment effects and its 95% confidence interval can be computed. We get that, compared to the overall mean across all berry pH values, receiving heat treatment on average increases the berry pH value by 0.02. On the other hand, not receiving heat treatment on average decreases the berry pH value by the same amount compared to the overall mean. The 95% confidence interval on the difference between these two effects is shown to be (0.00, 0.07). This aligns with our conclusion that there is weak evidence against that the two treatment effects are the same as the 95% confidence interval is non-negative after rounding.

Our conclusions above also indicates that the interaction effect is significant. In other words, the treatment effect differs across the blocks. To see this, we again refer to the boxplot shown in Figure 4. While we have found that overall, those vines that received heat treatment on average have a higher berry pH value than those that did not, this is not the case for the first block. In fact, in the first block, receiving heat treatment actually results in the vines having lower berry pH values. From Figure 1, we see that the first block is the furthest away from the lake and is not at the top of the hill.

To conclude, while generally the berry pH values among Merlot vines in the 2019 growing season is on average higher when the agro-thermal heat treatment is applied, this trend depends on the geospatial conditions present in each block. Specifically, if the vines were grown far away from the lake and the top of the hill, applying the agro-thermal heat treatment results in a decrease in the berry pH values.

4.2.3 Summary of additional non-censored analysis results

The same set of analysis can be applied to all other non-censored response variables without missing values. For those responses that contain missing values, some special care is needed to address the missing values. The details of the handling of missing values can be found in Appendix C.1.

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	4.85	0.03
block	5	48	5.94	0.00
treatment:block	5	48	4.26	0.00

Table 7. ART ANOVA table for berry pH in Merlot 2019

After inspecting the output from both the parametric and non-parametric models, we have found that there is evidence against that the effects of the two treatments (with and without heat) are the same on a number of the response variables. The estimated difference in the effects of the two treatments, its 95% confidence interval, as well as the corresponding p-values are shown in the first four rows of Table 8. We find that, during the 2019 growing season, for the Merlot grapes, by applying the heat treatment, the vines' average number of berries per cluster decreases and berry pH values increases compared to those that did not receive the heat treatment. During the 2020 growing season, the heat treatment seems to have made the Merlot vines' leaf greenness decrease and the pruning weight increase compared to those that did not receive the heat treatment.

Besides these treatment effects, we have also found that for some other response variables, although there is no evidence against that there is no overall difference in the treatment effects, the effect of the heat treatment seems to vary according to the block that the vines are in. Particularly, from Figure 15d, we see that unlike the other blocks, the heat treatment increases pruning weight in blocks that are close to the water and the top of the hill (blocks 5 and 6). This interaction effect between the treatment and blocking factors are confirmed by a p-value that is 0.03. Consequently, the Ravaz index, which is the ratio between yield and pruning weight, is lower in blocks 5 and 6 for those that received the heat treatment (Figure 16a).

4.2.4 Combining both years' data together

Finally, we note that since the sampled grapevines are the same across both growing seasons, and that many of the response variables have been collected in both years. This allows us the combine both years' data for both the Chardonnay and Merlot grapevines by introducing year as a third factor. Then the same set of analysis described above for non-censored response variables can be conducted for both the combined Chardonnay and Merlot datasets. The only difference is that three factors, including year, are analyzed at the same time. Out of all response variables that have been collected in both years, we have found that, for the Merlot grapevines, the leaf greenness and Ravaz index are lower, and the pruning weight is slightly higher among those that received the heat treatment (Table 8).

Note that leaf greenness and pruning weight are found to be impacted by the heat treatment from the Merlot 2020 dataset alone. This further confirms the effect of the heat treatment on these two measures. As we combine both years' data, the dataset contains more information. This may explain the inconsistent results of the average number of berries per cluster, berry pH and the Ravaz index.

	diff. of effects (heat - control)	lower bound of 95% C.I.	upper bound of 95% C.I.	P value
avg.# berries/cluster (2019)	-13.68	-28.18	0.81	0.06
berry pH (2019)	0.03	0.00	0.07	0.09
leaf greenness (2020)	-1.26	-2.56	0.03	0.06
pruning weight (2020)	0.09	0.00	0.18	0.03
leaf greenness (both)	-0.92	-1.73	-0.10	0.03
pruning weight (both)	0.08	0.03	0.14	0.01
Ravaz index (both)	-2.75	-5.26	-0.24	0.05

Table 8. Estimated effects of sig. main factors from additional ANOVA analysis for the Merlot datasets

5. Conclusions and discussion

Overall, the agro-thermal heat treatment does not seem to affect the productivity of the Chardonnay grapevines or the quality of the berries that they produce. However, by analyzing the Merlot grapevines from the 2019 and 2020 growing seasons, we see that the heat treatment is shown to increase the probability of reaching 50% veraison at any given time. This indicates that the heat treatment has the effect to make the Merlot grapes ripen earlier. However, this comes at the cost of getting less green leaves and clusters that on average have fewer berries. The heat treatment is also shown to increase the pruning weight and berry pH values for the Merlot grapevines. In addition, for a number of measures, the effect of the heat

treatment is shown to depend on the geospatial conditions of the specific blocks that the vines are in.

It is important to note that the above conclusions are drawn from a statistical perspective. The effects are said to be different if there is sufficient evidence (statistical significance) against the treatment effects being equal. Particularly, a statistically significant conclusion says nothing about the magnitude of the estimated effects. Therefore, the estimated effects need to be more closely examined in the context of viticulture before deciding whether it is worth investing in the agro-thermal heat treatment.

Finally, we note that one limitation of this study is the small sample size. As a direction for future studies, we suggest collecting a larger sample of vines receiving each treatment under each block. This enables the incorporation of the correlation information through conducting analysis that handles multiple response variables simultaneously. At the same time, having more observations can also help with outlier detection. A larger sample can also make most of the model-based statistical analysis more powerful. In other words, the models can be more sensitive to smaller differences of the effects of any of the factors considered.

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A. Additional tables and plots in exploratory data analysis

A.1 Summary statistics for Chardonnay and Merlot datasets

	# of clusters	yield	avg. cluster weight
min	15	2.9	0.12
median	31	5.9	0.18
max	48	10.34	0.3
mean	31.18	6.05	0.19
sd	7.29	1.89	0.04

Table 9. Summary statistics for Chardonnay 2019

	# of clusters	yield	avg. cluster weight
min	15	2.26	0.1
median	25	4.73	0.2
max	57	11.32	0.38
mean	27.4	5.41	0.2
sd	8.94	2.25	0.05

Table 10. Summary statistics for Chardonnay 2020

	fruitfulness	bloom	SPAD	veraison	cluster.number	yield	cluster.weight	berries.cluster	berry.weight	berry.Brix	berry.TA	berry.pH	brown.seed.color	pruning.weight	Ravaz.index
min	0	23.9	30.3	17.3	0	0.04	0.01	20.5	0.67	21.6	5.6	3.03	60	0.02	0.29
median	0.45	27.5	38.2	29.95	5	0.61	0.12	101.44	1.2	25.8	8.22	3.22	80	0.16	3
max	2	33	44.9	35	23	4.84	0.24	192.63	1.77	27	10.65	3.5	90	0.62	11.6
mean	0.52	27.62	38.27	29.11	6.25	0.96	0.12	96.32	1.2	25.24	8.17	3.22	78.46	0.22	3.88
sd	0.56	1.36	3	4.53	5.47	0.99	0.05	38.26	0.23	1.35	1.32	0.12	8.2	0.16	2.96

Table 11. Summary statistics for Merlot 2020

A.2 Correlation plots for outcomes variables

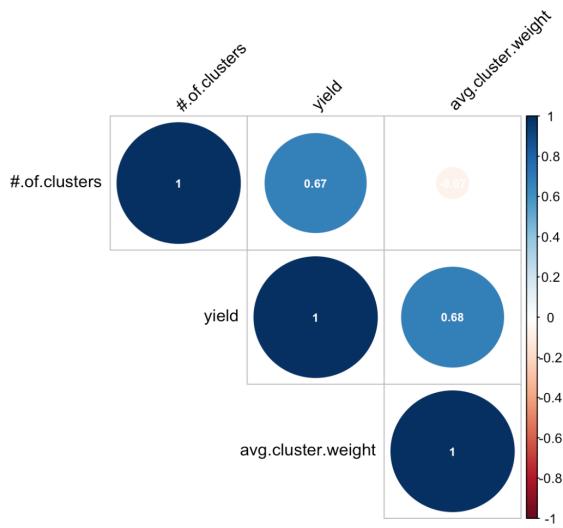


Figure 7. Correlation plot for Chardonnay 2019

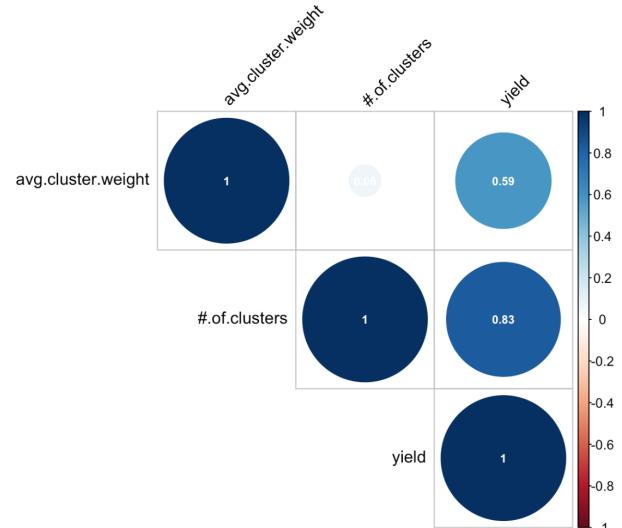


Figure 8. Correlation plot for Chardonnay 2020

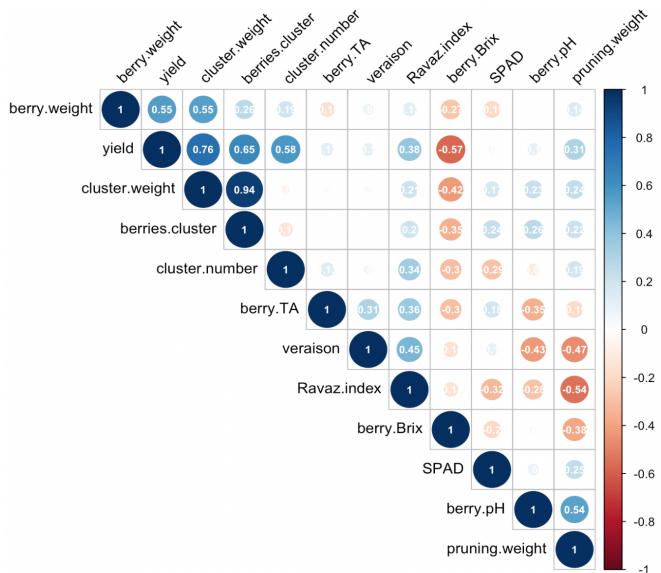


Figure 9. Correlation plot for Merlot 2019

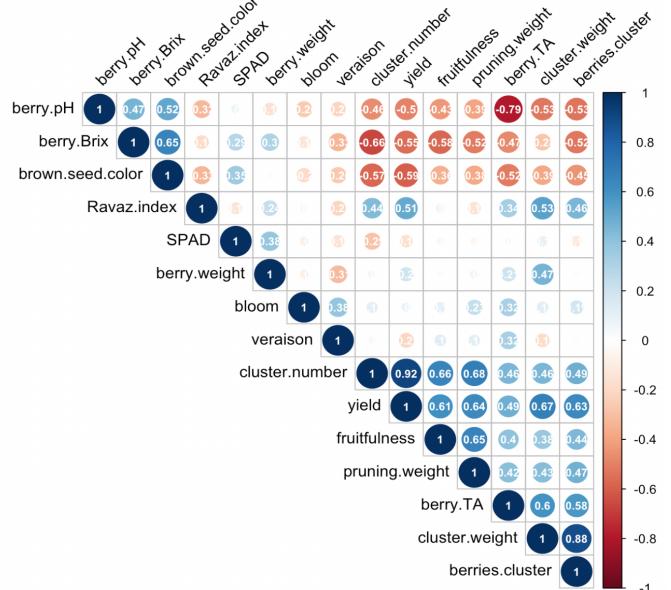


Figure 10. Correlation plot for Merlot 2020

A.3 Kaplan-Meier plots

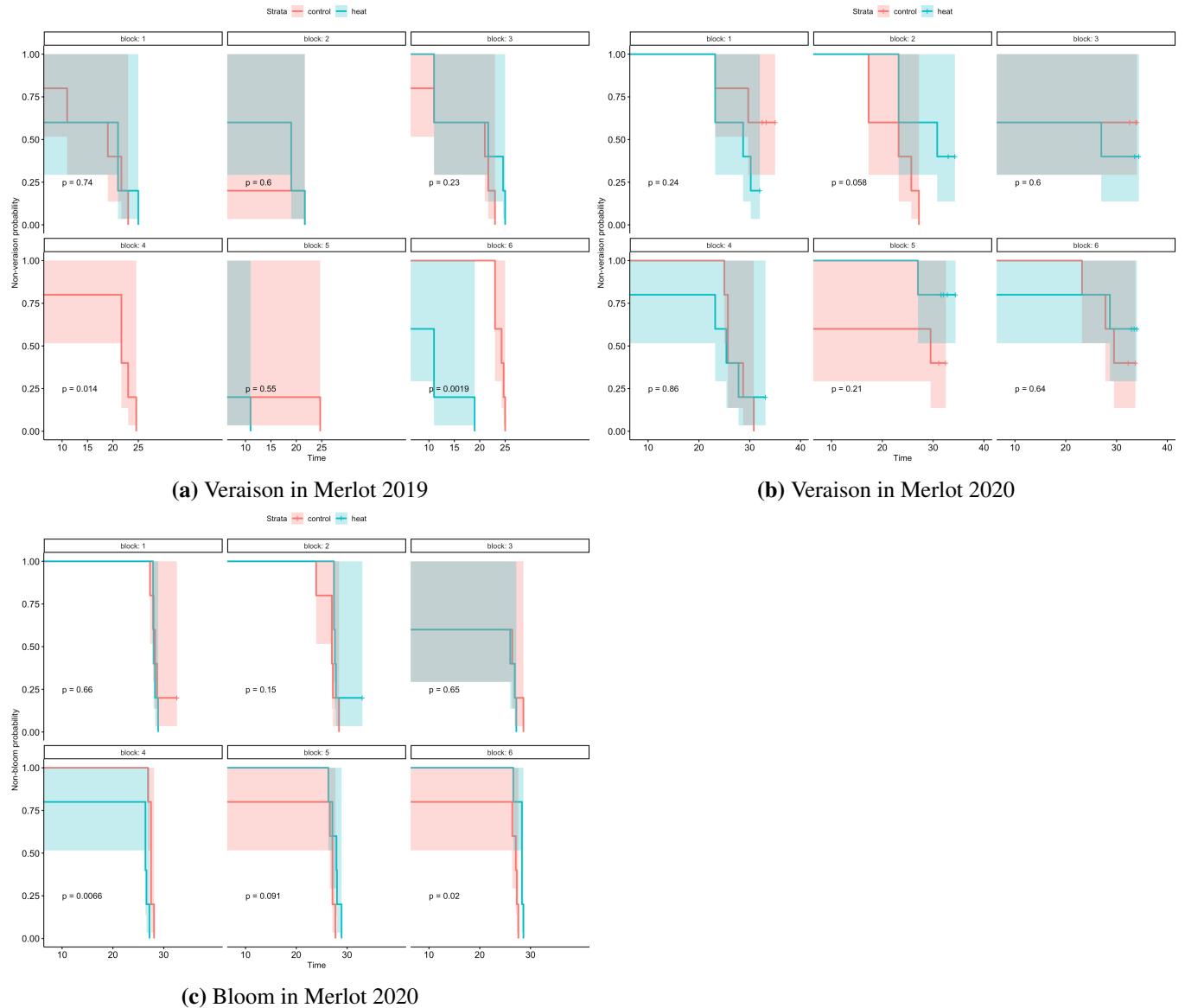


Figure 11. Kaplan Meier plots for each censored response variable

A.4 Side-by-side boxplots

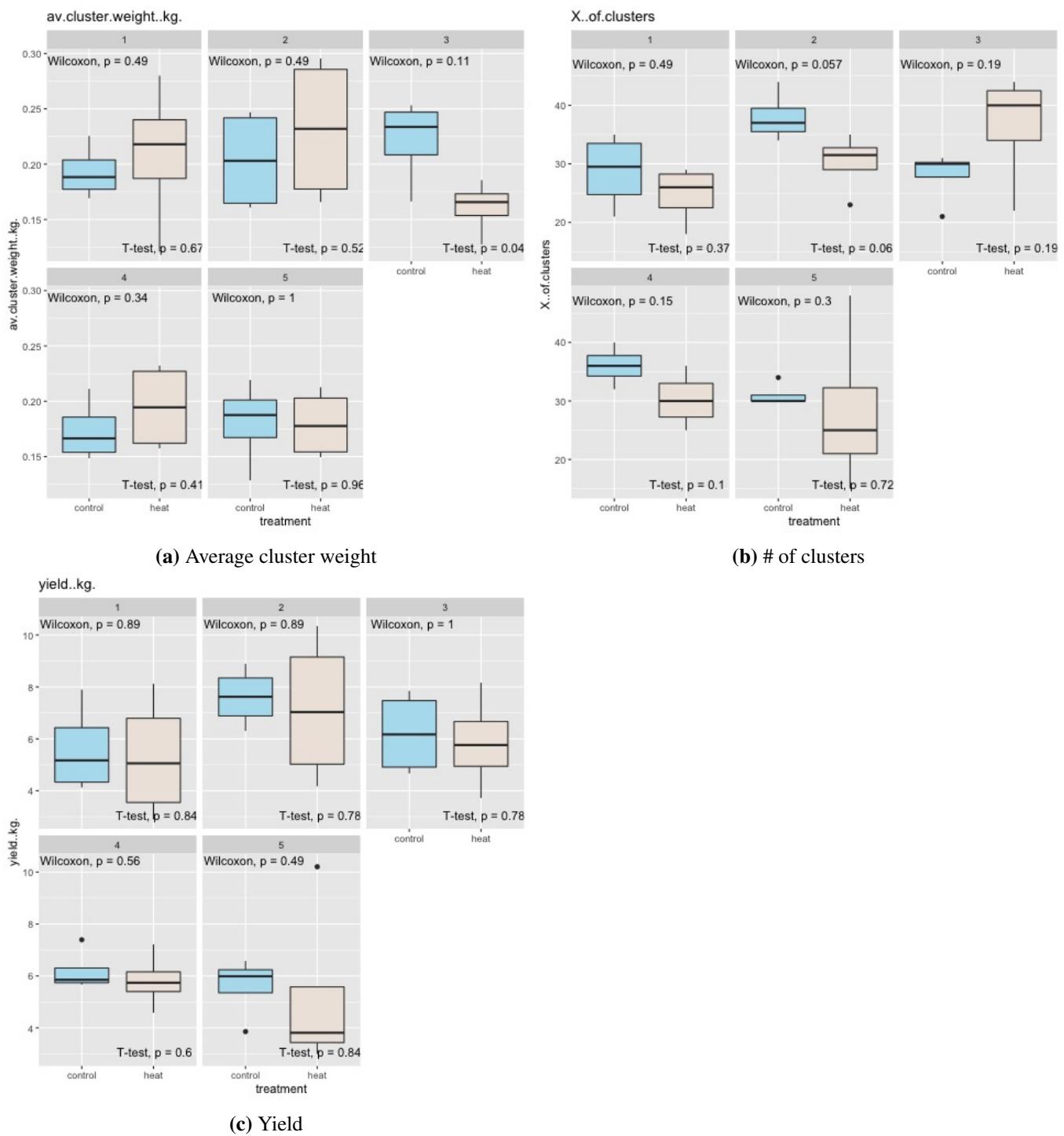


Figure 12. Boxplots for Chardonnay 2019 under treatment and block combination

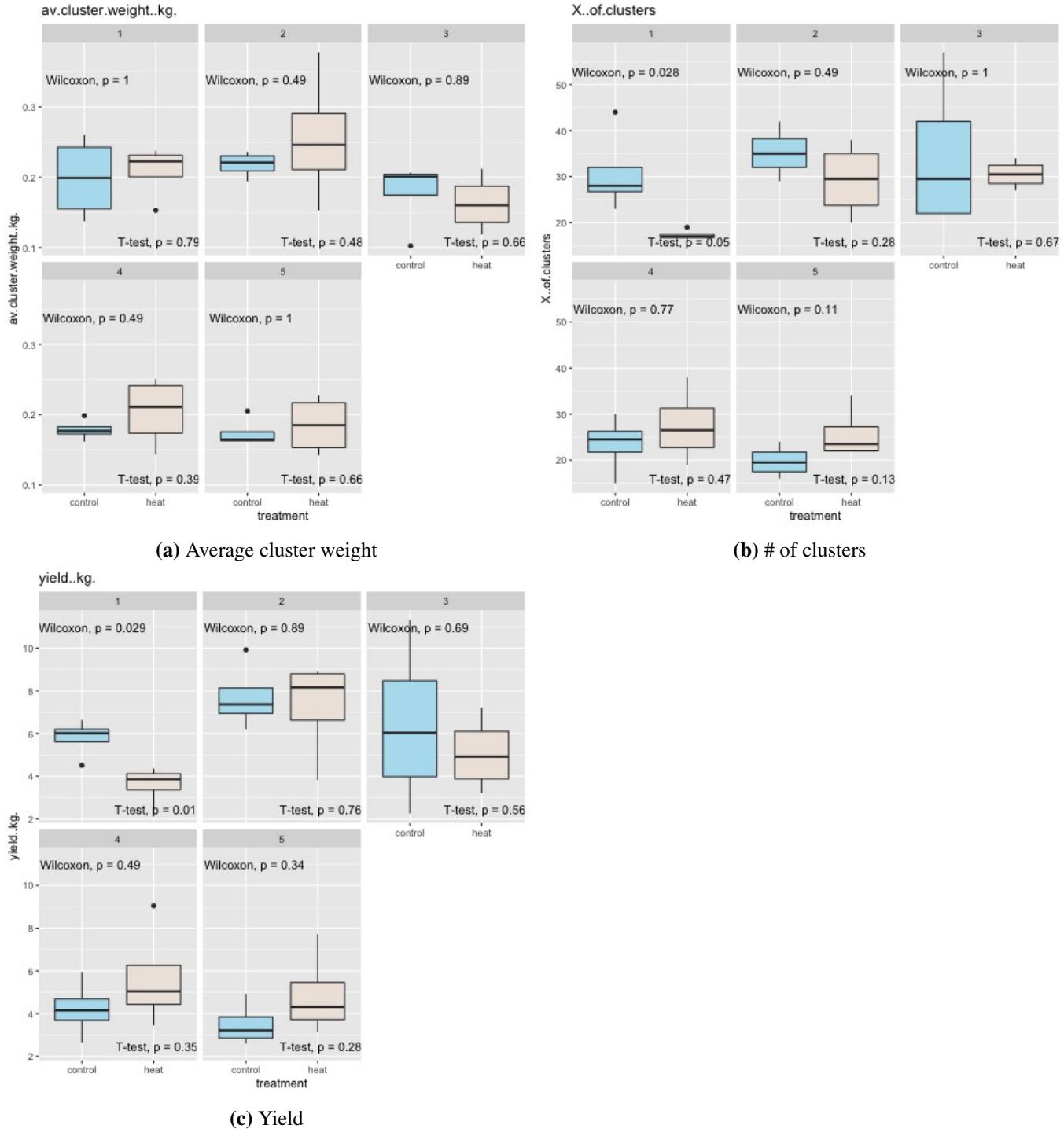


Figure 13. Boxplots for Chardonnay 2020 under treatment and block combination

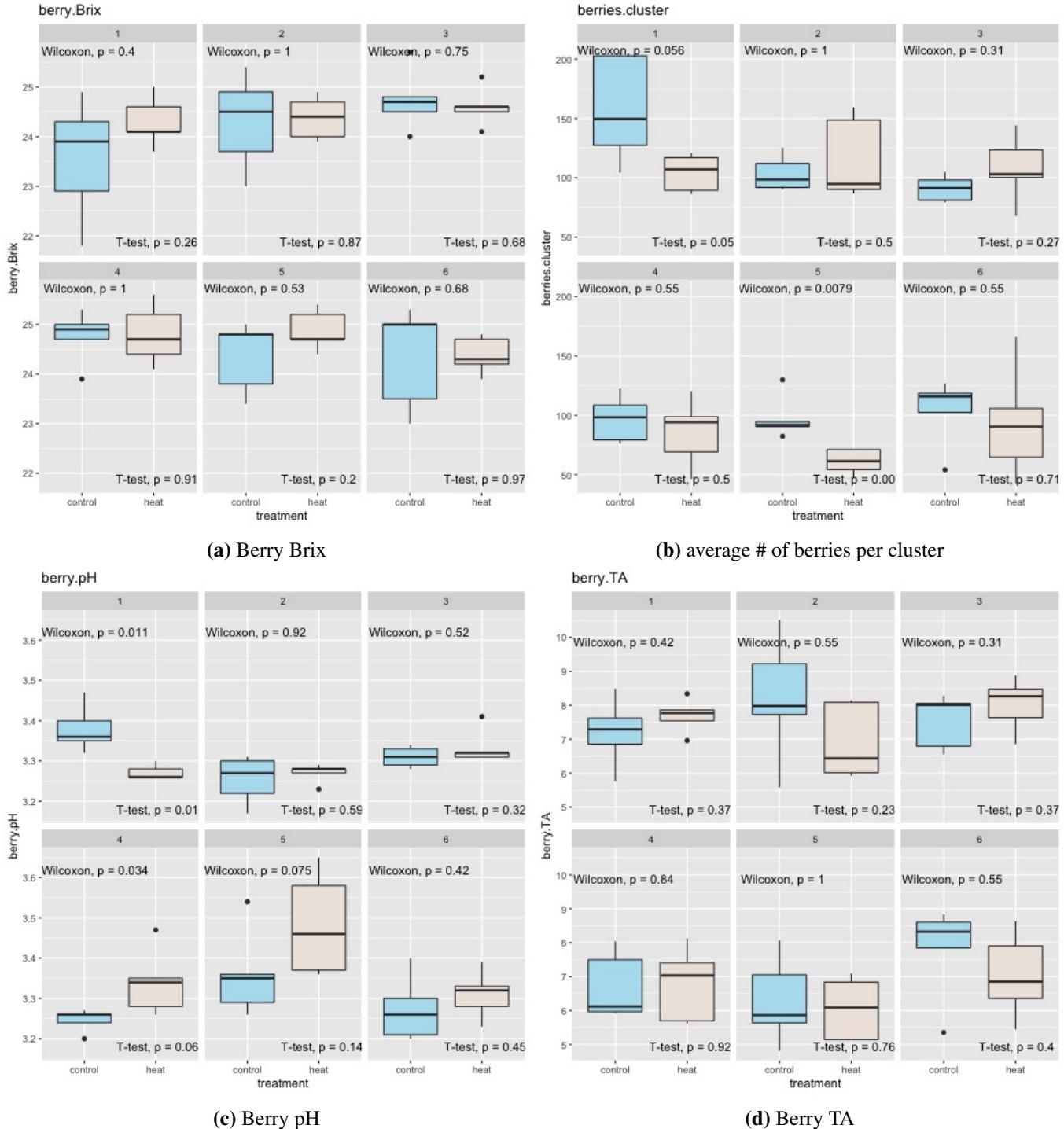
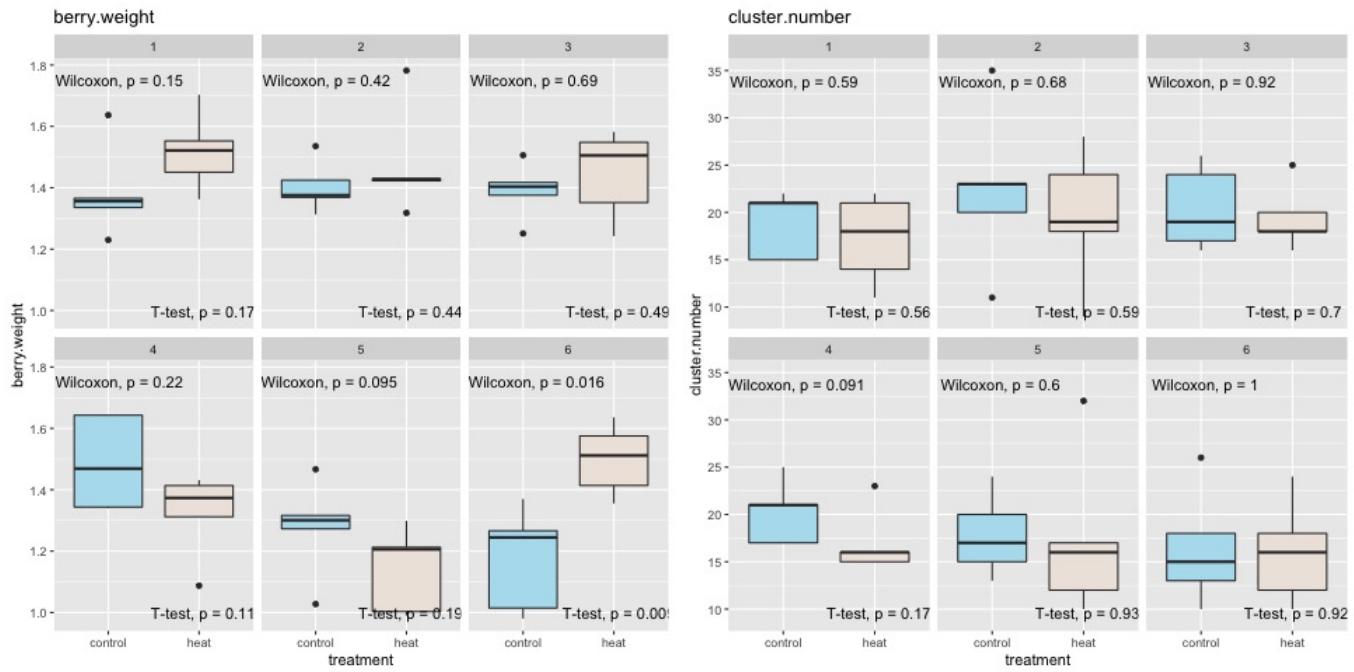
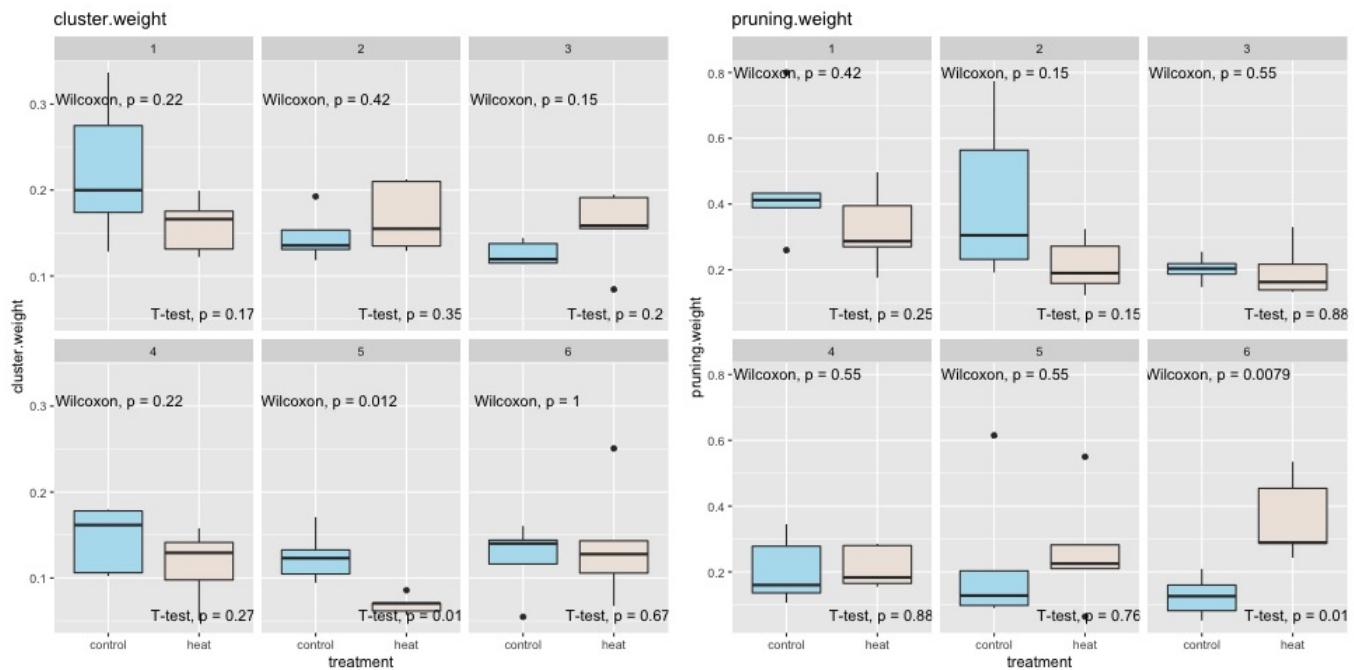


Figure 14. Boxplots for Merlot 2019 under treatment and block combination (Part 1 of 3)



(a) Average berry weight



(c) Average cluster weight

(b) # of clusters

(d) Pruning weight

Figure 15. Boxplots for Merlot 2019 under treatment and block combination (Part 2 of 3)

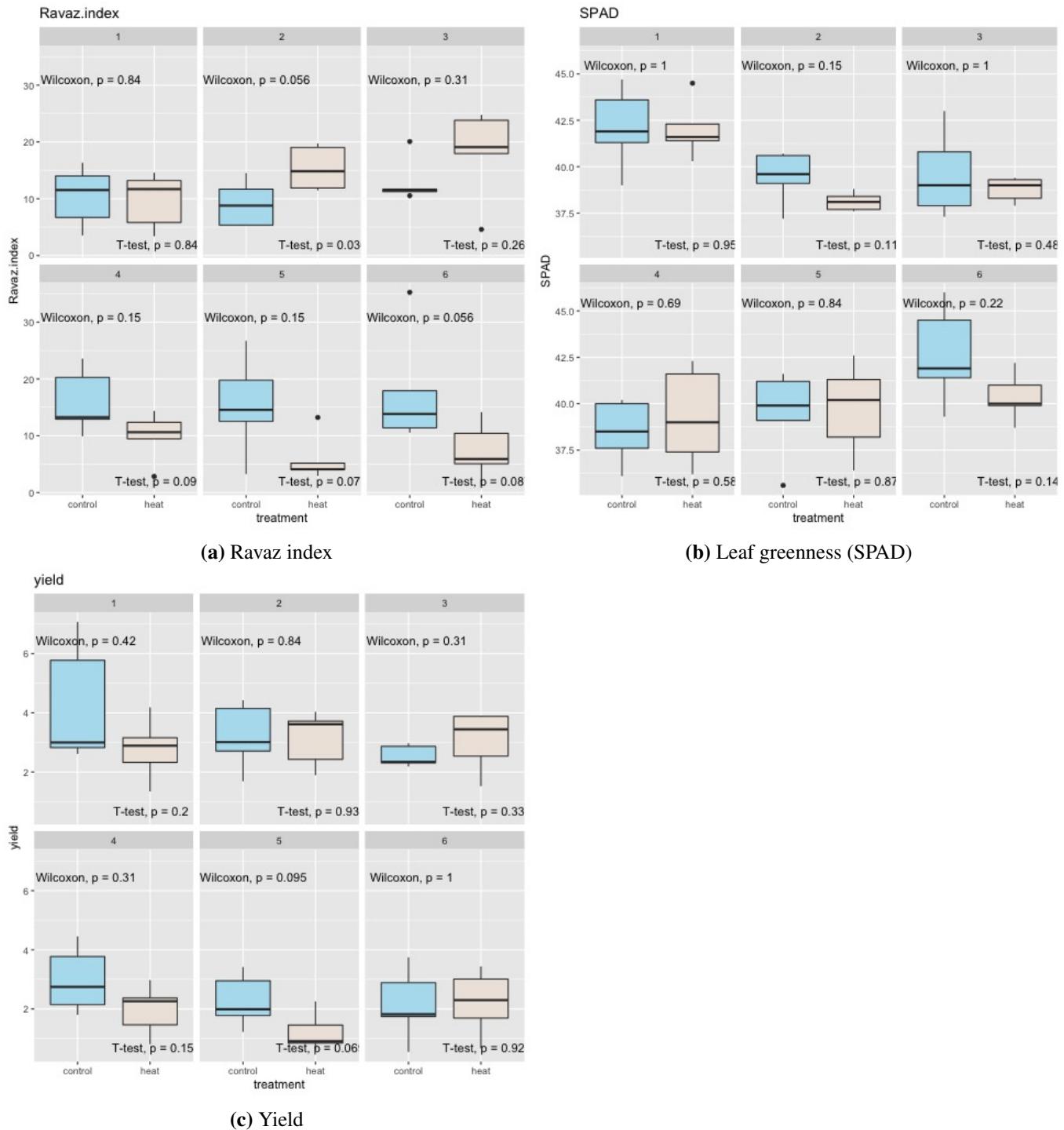


Figure 16. Boxplots for Merlot 2019 under treatment and block combination (Part 3 of 3)

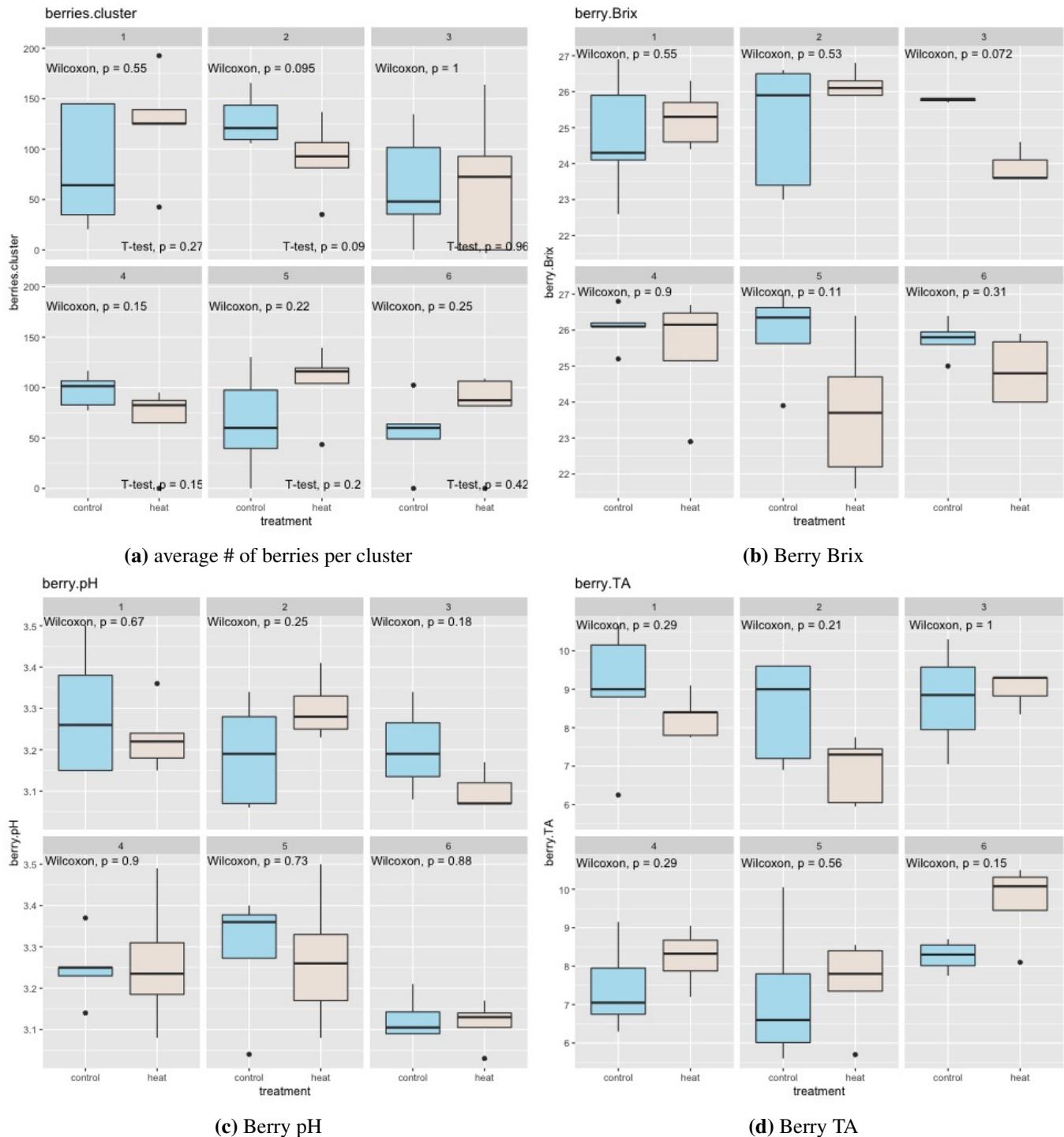


Figure 17. Boxplots for Merlot 2020 under treatment and block combination (Part 1 of 4)

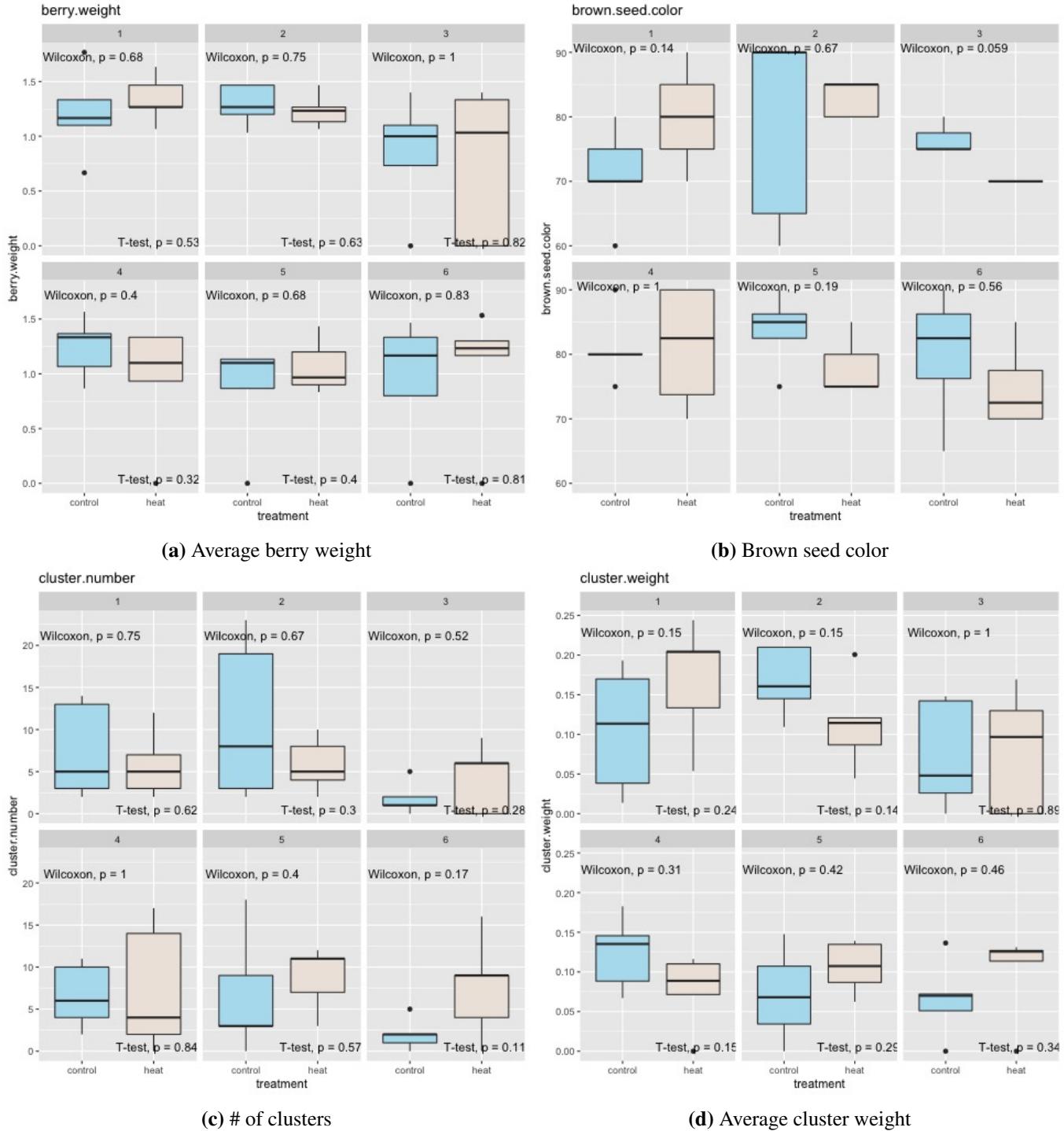


Figure 18. Boxplots for Merlot 2020 under treatment and block combination (Part 2 of 4)

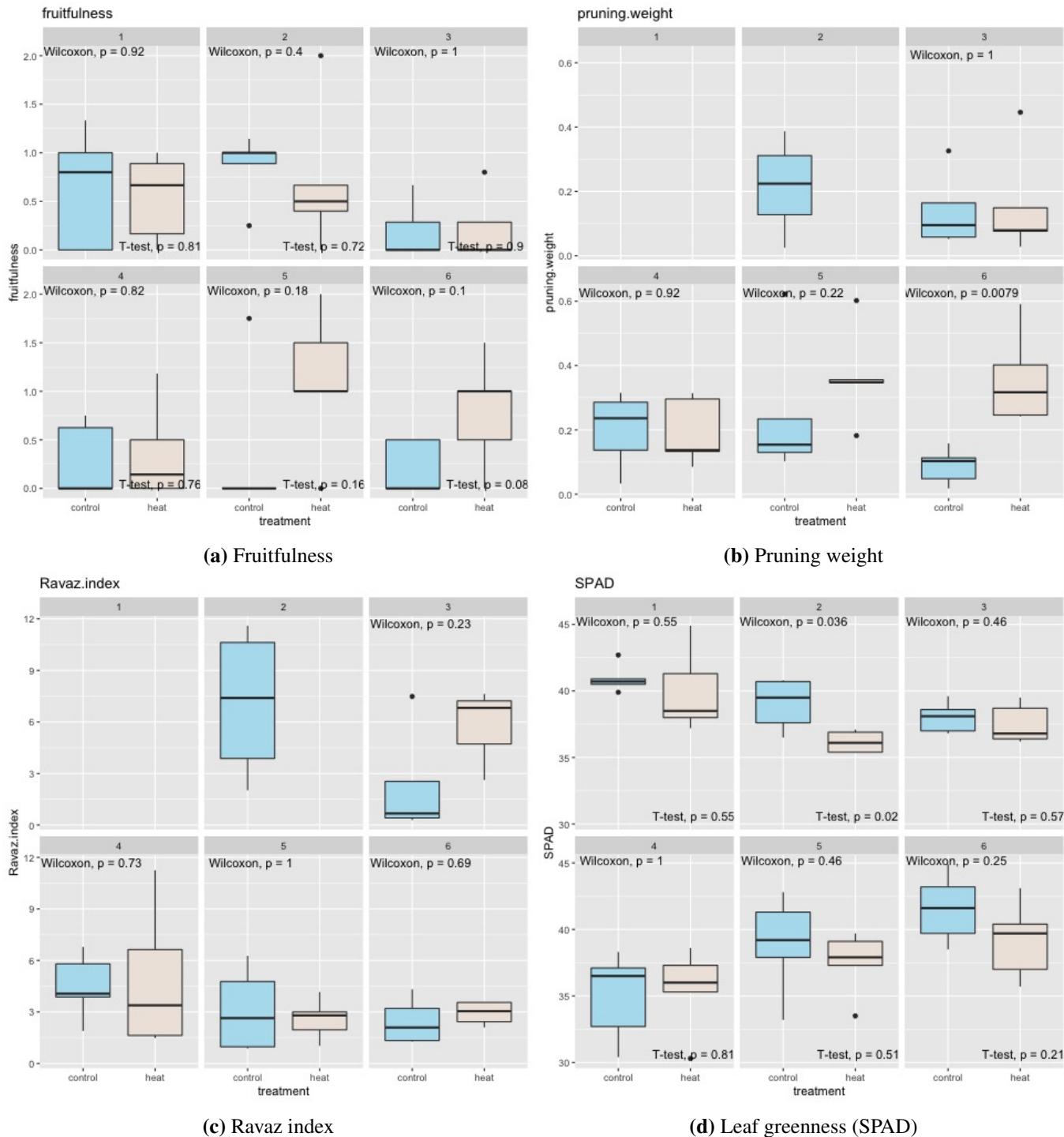
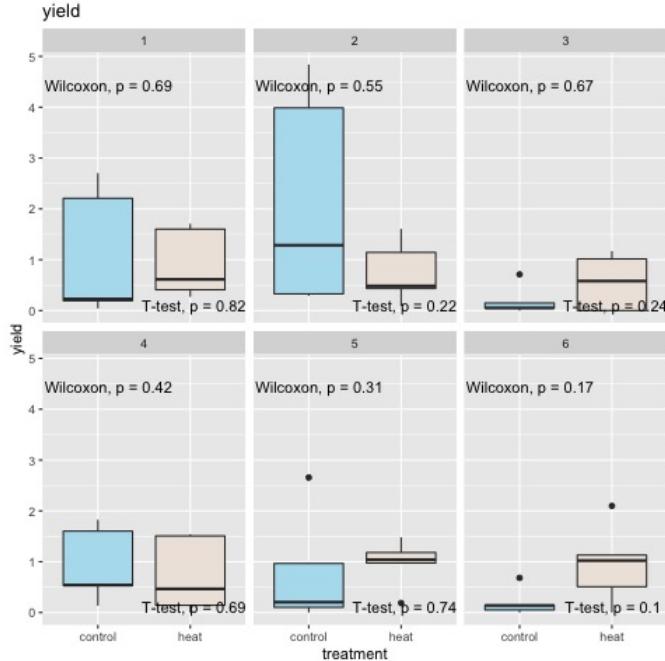


Figure 19. Boxplots for Merlot 2020 under treatment and block combination (Part 3 of 4)



(a) Yield

Figure 20. Boxplots for Merlot 2020 under treatment and block combination (Part 4 of 4)

B. Additional censored data analysis

B.1 Cox PH covariate estimates

explanatory	HR	L95	U95	p
heat	0.57	0.16	1.98	0.38
heat:block 2	3.18	0.55	18.43	0.20
heat:block 3	3.11	0.53	18.38	0.21
heat:block 4	0.63	0.11	3.63	0.60
heat:block 5	1.88	0.32	10.85	0.48
heat:block 6	1.12	0.19	6.64	0.90

Table 12. Output from Cox PH model for Merlot 2019
Veraison: HR-hazard ratio, L95/U95 - lower/upper bound
of 95% confidence interval

explanatory	HR	L95	U95	p
heat	1.17	0.33	4.12	0.81
heat:block 2	0.32	0.05	2.09	0.23
heat:block 3	0.54	0.08	3.85	0.54
heat:block 4	0.74	0.12	4.71	0.75
heat:block 5	0.91	0.15	5.61	0.92
heat:block 6	0.24	0.04	1.45	0.12

Table 13. Output from Cox PH model for Merlot 2020
Bloom: HR-hazard ratio, L95/U95 - lower/upper bound
of 95% confidence interval

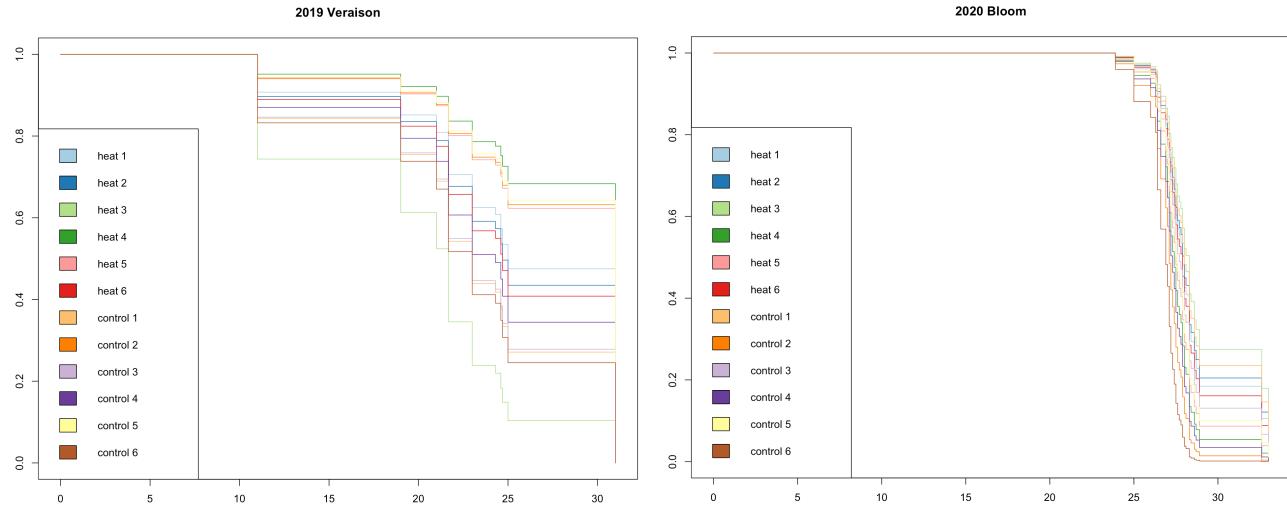


Figure 21. Survival functions for the Cox PH models constructed for 50% bloom in 2020 and 50% veraison in 2019 for the Merlot vineyard. “Survival” indicates the probability that, at time t , the event (50% bloom or veraison) has not yet occurred.

B.2 Interval-censored data method

There are several methods for dealing with censored data that has both left-censoring and right-censoring. One such method is implemented with the R package IcenReg, which allows for construction of Cox PH models using interval-censored (i.e. both left- and right-censored) data. Using this method, the left-censored data may be more properly addressed.

The specific R package used to implement the Cox PH models uses bootstrapping so we can make these inferences on the coefficients.

By Figure 22, we see that the proportional hazards assumption is not severely violated as there is minimal overlapping across the survival functions. By Tables 14 to 16, we see that there is minimal evidence against that there are no treatment or interaction effects. This differs from the analysis in the main text, which is likely due to the different treatment of the left-censored data.

explanatory	HR	Std.Error	p
heat	0.22	8.820	0.86
heat:block 2	9.32	14.920	0.88
heat:block 3	1.39	11.780	0.98
heat:block 4	0.00	15.490	0.36
heat:block 5	4949	20.720	0.68
heat:block 6	177	10.370	0.62

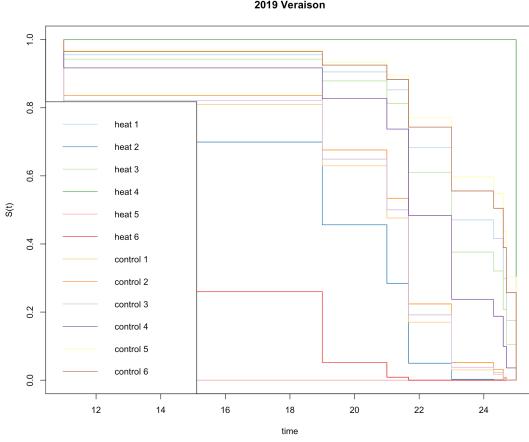
Table 14. Output from Cox PH model for Merlot 2019
veraison: HR-hazard ratio

explanatory	HR	Std.Error	p
heat	3.41	0.91	0.18
heat:block 2	0.03	3.21	0.29
heat:block 3	0.17	2.09	0.40
heat:block 4	0.06	2.59	0.29
heat:block 5	0.37	1.95	0.61
heat:block 6	0.09	2.23	0.29

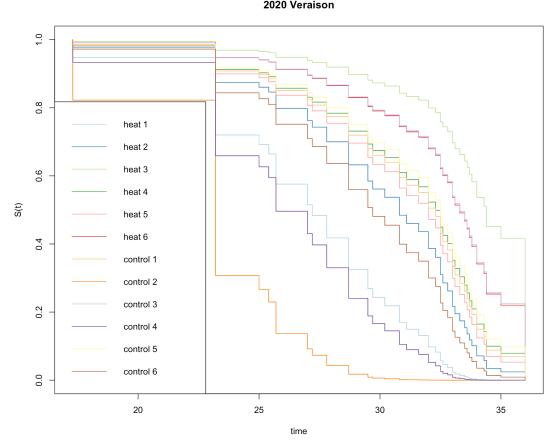
Table 15. Output from Cox PH model for Merlot 2020
veraison: HR-hazard ratio

explanatory	HR	Std.Error	p
heat	1.14	0.49	0.79
heat:block 2	0.30	6.60	0.86
heat:block 3	0.55	2.99	0.84
heat:block 4	0.74	2.19	0.89
heat:block 5	0.95	1.99	0.98
heat:block 6	0.24	0.83	0.09

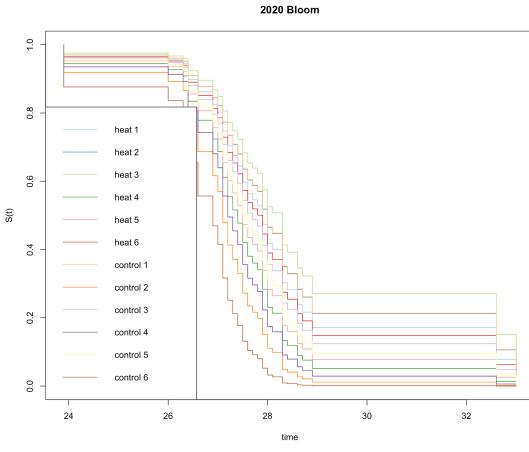
Table 16. Output from Cox PH model for Merlot 2020
bloom: HR-hazard ratio



(a) Merlot 2019 veraison Kaplan-Meier plot:
proportional hazard assumption holds if KM
curves do not cross



(b) Merlot 2020 veraison Kaplan-Meier plot:
proportional hazard assumption holds if KM
curves do not cross



(c) Merlot 2020 bloom Kaplan-Meier plot:
proportional hazard assumption holds if KM
curves do not cross

Figure 22. Survival functions for the Cox PH models constructed for 50% bloom and 50% veraison for the Merlot 2019 and 2020 datasets. “Survival” indicates the probability that, at time t , the event (50% bloom or veraison) has not yet occurred.

C. Additional non-censored data analysis

C.1 Multiple imputation

Multiple imputation is used to deal with the missing values present in our datasets. Multiple imputation involves using the observed values to make several predictions on each of the missing values. This approach is suitable for this study as it does not remove any of the observed values, so the balanced structure stays intact. By having multiple predicted values on each value that is missing, we can reflect the additional uncertainties introduced by not observing these missing data. Finally, once the predictions are made on each missing value, we construct several of complete datasets. Standard analyses can be carried out on each of these complete datasets and final conclusions can be drawn after the results from each of the complete datasets are pooled together.

For simplicity, linear regression models are used to make predictions of the missing values. And as suggested by [5], the final conclusions of the subsequent analyses will be drawn after combining five

imputed datasets. We use the method described in [6] to combine pool the two-way and three-way analysis results.

C.2 Chardonnay 2019

	# of clusters	yield	avg. cluster weight
P value	0.46	0.41	0.15

Table 17. P values of Levene tests for responses in Chardonnay 2019



Figure 23. Residual plot and residual QQ plot of # of clusters in Chardonnay 2019

	sum of squares	degrees of freedom	F value	P value
intercept	38875	1	827.87	0.00
treatment	55	1	1.18	0.29
block	285	4	1.52	0.22
treatment:block	323	4	1.72	0.17
residuals	1409	30		

Table 18. ANOVA table for # of clusters in Chardonnay 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	1.2226	0.28
block	4	30	2.4189	0.07
treatment:block	4	30	2.4056	0.07

Table 19. ART ANOVA table for # of clusters in Chardonnay 2019

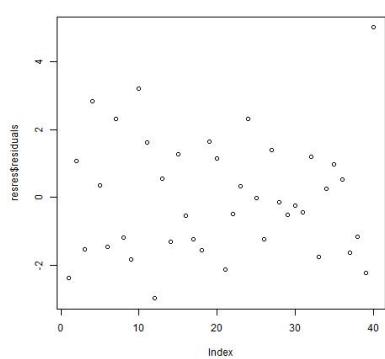
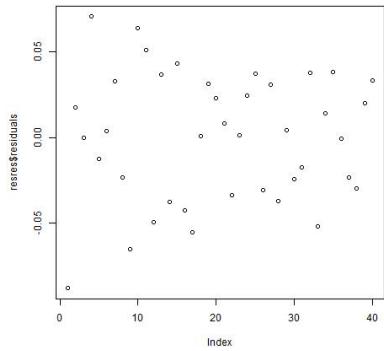


Figure 24. Residual plot and residual QQ plot of yield in Chardonnay 2019

	sum of squares	degrees of freedom	F value	P value
intercept	1464.55	1	376.00	0.00
treatment	1.45	1	0.37	0.55
block	20.44	4	1.31	0.29
treatment:block	0.03	4	0.00	1.00
residuals	116.85	30		

Table 20. ANOVA table for yield in Chardonnay 2019



	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	0.99	0.33
block	4	30	1.36	0.27
treatment:block	4	30	0.05	1.00

Table 21. ART ANOVA table for yield in Chardonnay 2019

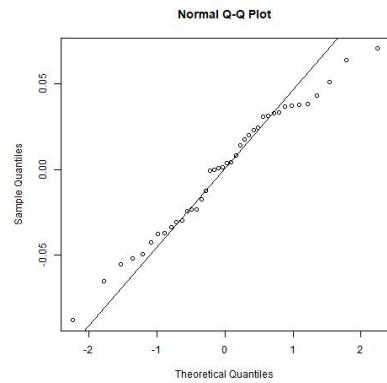


Figure 25. Residual plot and residual QQ plot of average cluster weight in Chardonnay 2019

	sum of squares	degrees of freedom	F value	P value
intercept	1.52	1	816.91	0.00
treatment	0.00	1	0.00	0.96
block	0.01	4	0.96	0.44
treatment:block	0.01	4	1.39	0.26
residuals	0.06	30		

Table 22. ANOVA table for average cluster weight in Chardonnay 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	0.01	0.92
block	4	30	0.65	0.63
treatment:block	4	30	1.37	0.27

Table 23. ART ANOVA table for average cluster weight in Chardonnay 2019

C.3 Chardonnay 2020

	# of clusters	yield	avg. cluster weight
P value	0.12	0.27	0.19

Table 24. P values of Levene tests for responses in Chardonnay 2020



Figure 26. Residual plot and residual QQ plot of # of clusters in Chardonnay 2020

	sum of squares	degrees of freedom	F value	P value
intercept	30030.40	1	486.32	0.00
treatment	72.90	1	1.18	0.29
block	690.60	4	2.80	0.04
treatment:block	499.60	4	2.02	0.12
residuals	1852.50	30		

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	1.00	0.33
block	4	30	2.96	0.04
treatment:block	4	30	2.81	0.04

Table 25. ANOVA table for # of clusters in Chardonnay 2020

Table 26. ART ANOVA table for # of clusters in Chardonnay 2020

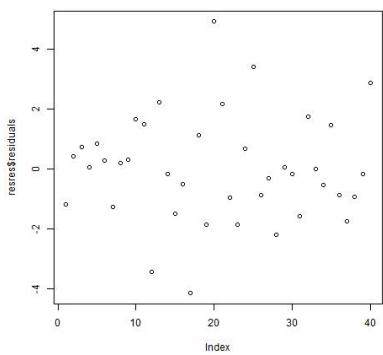


Figure 27. Residual plot and residual QQ plot of yield in Chardonnay 2020

	sum of squares	degrees of freedom	F value	P value
intercept	1170.70	1	286.90	0.00
treatment	0.54	1	0.13	0.72
block	53.14	4	3.26	0.02
treatment:block	20.75	4	1.27	0.30
residuals	122.41	30		

Table 27. ANOVA table for yield in Chardonnay 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	0.11	0.74
block	4	30	2.99	0.03
treatment:block	4	30	1.51	0.23

Table 28. ART ANOVA table for yield in Chardonnay 2020

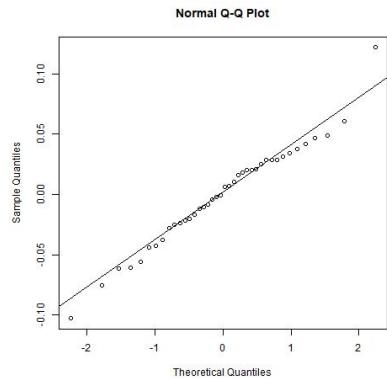
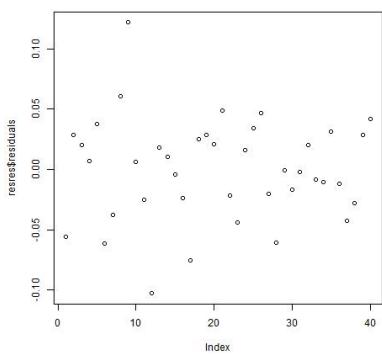


Figure 28. Residual plot and residual QQ plot of average cluster weight in Chardonnay 2020

	sum of squares	degrees of freedom	F value	P value
intercept	1.54	1	668.64	0.00
treatment	0.00	1	0.82	0.37
block	0.02	4	2.33	0.08
treatment:block	0.00	4	0.34	0.85
residuals	0.07	30		

Table 29. ANOVA table for average cluster weight in Chardonnay 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	30	0.72	0.40
block	4	30	2.45	0.07
treatment:block	4	30	0.36	0.83

Table 30. ART ANOVA table for average cluster weight in Chardonnay 2020

C.4 Merlot 2019

	SPAD	# of clusters	yield	avg. cluster weight	avg. # of berries per cluster	avg. berry weight	berry TA	berry pH	berry Brix	pruning weight	Ravaz index
P value	0.37	0.89	0.78	0.34	0.32	1.00	0.92	0.08	0.56	0.72	0.90

Table 31. P values of Levene tests for responses in Merlot 2019

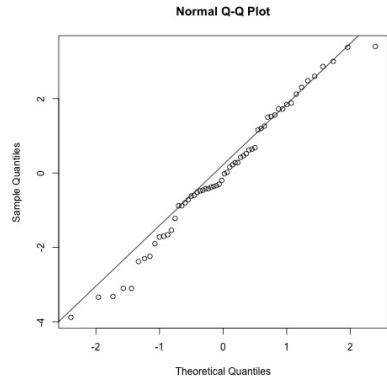
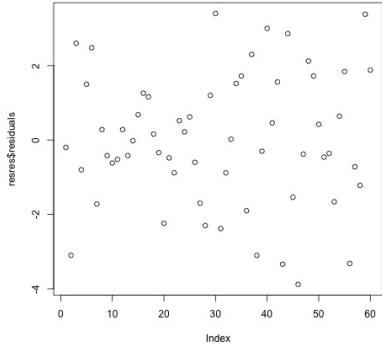
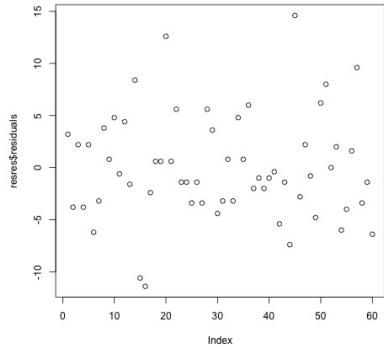


Figure 29. Residual plot and residual QQ plot of leaf greenness in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	96016.00	1	25219.80	0.00
treatment	4.82	1	1.27	0.27
block	99.92	5	5.25	0.00
treatment:block	15.86	5	0.83	0.53
residuals	182.74	48		

Table 32. ANOVA table for leaf greenness in Merlot 2019



	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.23	0.27
block	5	48	5.16	0.00
treatment:block	5	48	0.69	0.64

Table 33. ART ANOVA table for leaf greenness in Merlot 2019

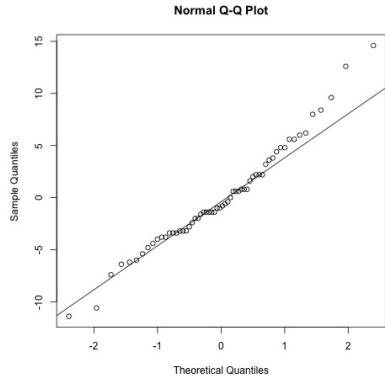


Figure 30. Residual plot and residual QQ plot of # of clusters in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	20646.15	1	663.15	0.00
treatment	36.82	1	1.18	0.28
block	145.55	5	0.94	0.47
treatment:block	18.08	5	0.12	0.99
residuals	1494.40	48		

Table 34. ANOVA table for # of clusters in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.15	0.29
block	5	48	1.09	0.38
treatment:block	5	48	0.15	0.98

Table 35. ART ANOVA table for # of clusters in Merlot 2019

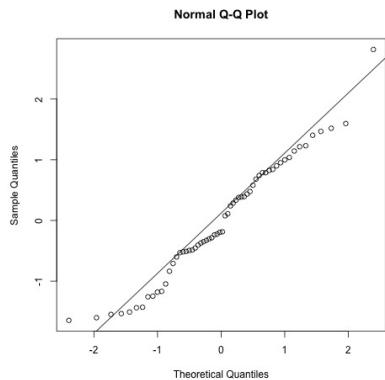
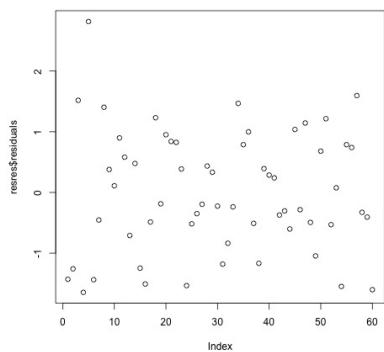


Figure 31. Residual plot and residual QQ plot of yield in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	420.96	1	351.68	0.00
treatment	3.77	1	3.15	0.08
block	21.03	5	3.51	0.01
treatment:block	7.71	5	1.29	0.28
residuals	57.46	48		

Table 36. ANOVA table for yield in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.75	0.19
block	5	48	3.30	0.01
treatment:block	5	48	0.89	0.49

Table 37. ART ANOVA table for yield in Merlot 2019

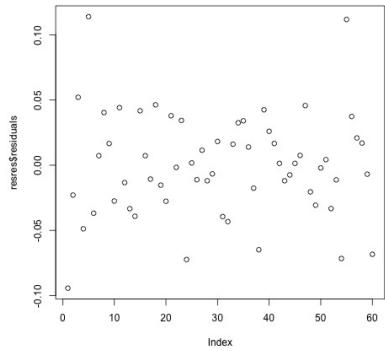
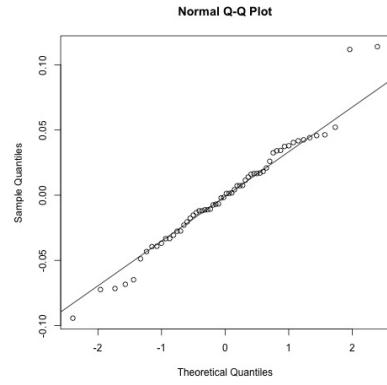


Figure 32. Residual plot and residual QQ plot of average cluster weight in Merlot 2019



	sum of squares	degrees of freedom	F value	P value
intercept	1.20	1	619.63	0.00
treatment	0.00	1	1.43	0.24
block	0.05	5	5.04	0.00
treatment:block	0.02	5	2.25	0.06
residuals	0.09	48		

Table 38. ANOVA table for average cluster weight in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.76	0.19
block	5	48	4.83	0.00
treatment:block	5	48	2.41	0.05

Table 39. ART ANOVA table for average cluster weight in Merlot 2019

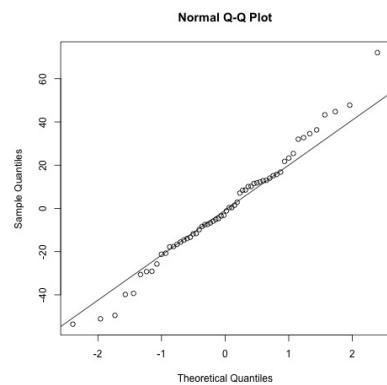
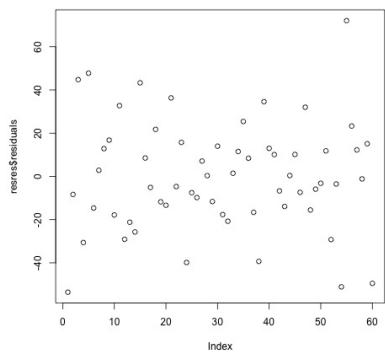
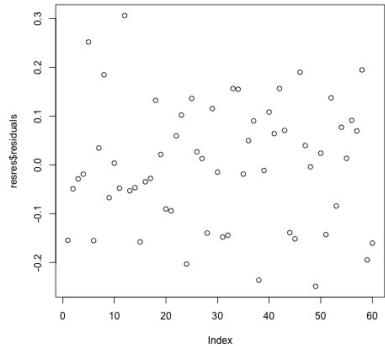


Figure 33. Residual plot and residual QQ plot of average # of berries per cluster in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	619585.26	1	794.83	0.00
treatment	2808.83	1	3.60	0.06
block	15480.23	5	3.97	0.00
treatment:block	9453.78	5	2.43	0.05
residuals	37416.84	48		

Table 40. ANOVA table for average # of berries per cluster in Merlot 2019



	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	3.97	0.00
block	5	48	4.17	0.00
treatment:block	5	48	2.34	0.06

Table 41. ART ANOVA table for average # of berries per cluster in Merlot 2019

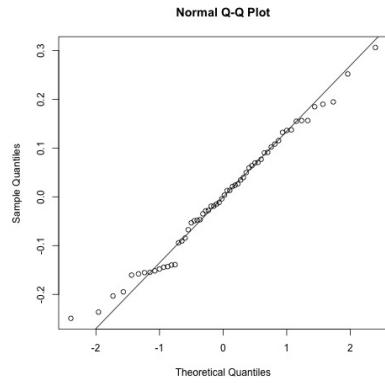


Figure 34. Residual plot and residual QQ plot of average berry weight in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	113.75	1	5816.51	0.00
treatment	0.03	1	1.73	0.19
block	0.42	5	4.27	0.00
treatment:block	0.41	5	4.15	0.00
residuals	0.94	48		

Table 42. ANOVA table for average berry weight in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.36	0.25
block	5	48	3.65	0.01
treatment:block	5	48	3.71	0.01

Table 43. ART ANOVA table for average berry weight in Merlot 2019

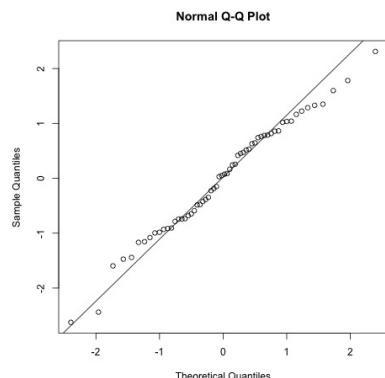
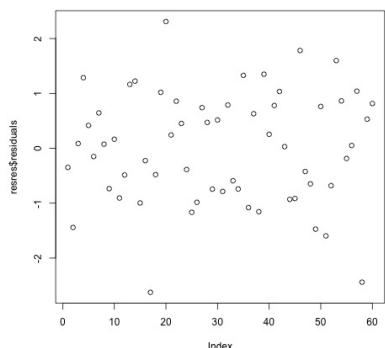
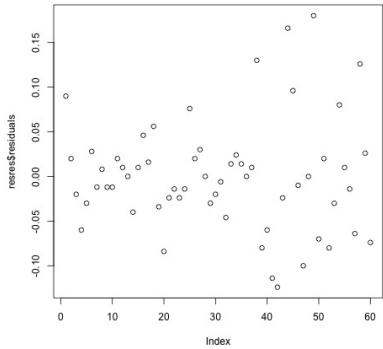


Figure 35. Residual plot and residual QQ plot of berry TA in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	3100.26	1	2419.60	0.00
treatment	0.62	1	0.48	0.49
block	18.36	5	2.87	0.02
treatment:block	6.25	5	0.98	0.44
residuals	61.50	48		

Table 44. ANOVA table for berry TA in Merlot 2019



	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.65	0.42
block	5	48	2.80	0.03
treatment:block	5	48	1.00	0.43

Table 45. ART ANOVA table for berry TA in Merlot 2019

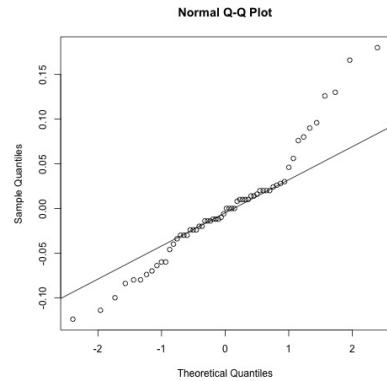


Figure 36. Residual plot and residual QQ plot of berry pH in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	661.14	1	141497.02	0.00
treatment	0.01	1	3.09	0.09
block	0.15	5	6.56	0.00
treatment:block	0.08	5	3.45	0.01
residuals	0.22	48		

Table 46. ANOVA table for berry pH in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	4.85	0.03
block	5	48	5.94	0.00
treatment:block	5	48	4.26	0.00

Table 47. ART ANOVA table for berry pH in Merlot 2019

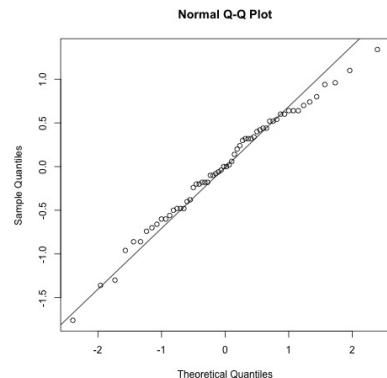
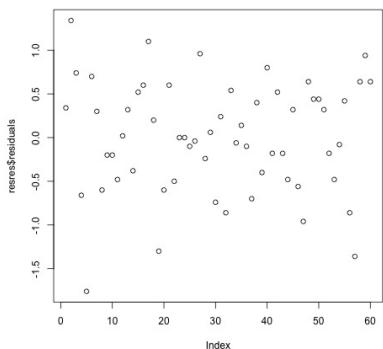


Figure 37. Residual plot and residual QQ plot of berry Brix in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	35873.04	1	72703.34	0.00
treatment	0.66	1	1.34	0.25
block	4.75	5	1.93	0.11
treatment:block	1.45	5	0.59	0.71
residuals	23.68	48		

Table 48. ANOVA table for berry Brix in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.30	0.58
block	5	48	1.56	0.19
treatment:block	5	48	0.42	0.83

Table 49. ART ANOVA table for berry Brix in Merlot 2019

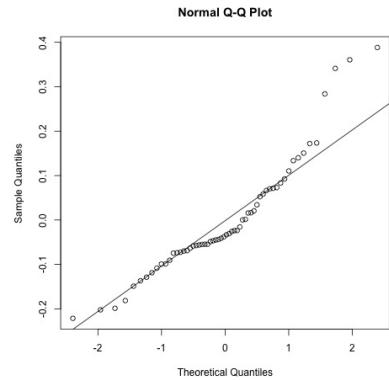
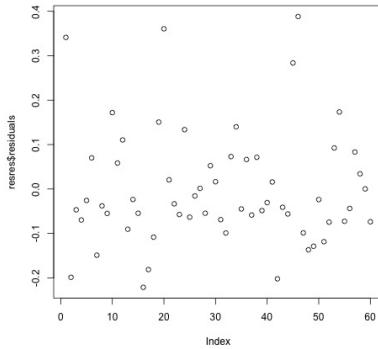


Figure 38. Residual plot and residual QQ plot of pruning weight in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	4.29	1	207.78	0.00
treatment	0.00	1	0.06	0.80
block	0.27	5	2.58	0.04
treatment:block	0.29	5	2.77	0.03
residuals	0.99	48		

Table 50. ANOVA table for pruning weight in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.02	0.88
block	5	48	2.93	0.02
treatment:block	5	48	3.36	0.01

Table 51. ART ANOVA table for pruning weight in Merlot 2019

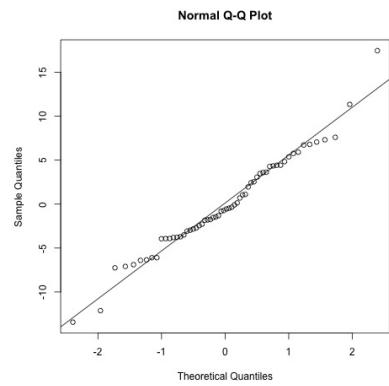
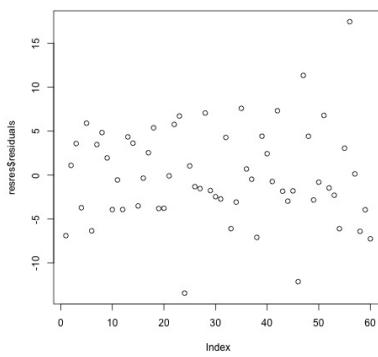


Figure 39. Residual plot and residual QQ plot of Ravaz index in Merlot 2019

	sum of squares	degrees of freedom	F value	P value
intercept	9132.28	1	251.01	0.00
treatment	98.01	1	2.69	0.11
block	185.93	5	1.02	0.42
treatment:block	651.81	5	3.58	0.01
residuals	1746.33	48		

Table 52. ANOVA table for Ravaz index in Merlot 2019

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	1.98	0.17
block	5	48	1.17	0.34
treatment:block	5	48	3.59	0.01

Table 53. ART ANOVA table for Ravaz index in Merlot 2019

C.5 Merlot 2020

	fruitfulness	SPAD	# of clusters	yield	avg. cluster weight	avg. # of berries per cluster	avg. berry weight	berry Brix	berry TA	berry pH	brown seed color	pruning weight	Ravaz index
P value	1.00	0.60	0.83	0.53	0.87	0.61	0.68	0.37	0.72	0.69	0.42	0.81	0.82

Table 54. P values of Levene tests for responses in Merlot 2020

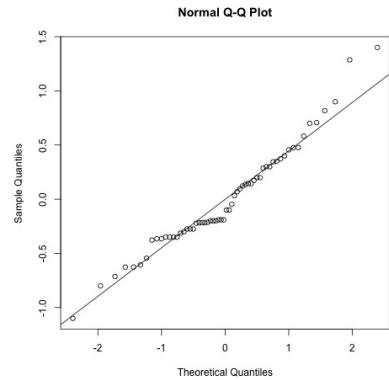
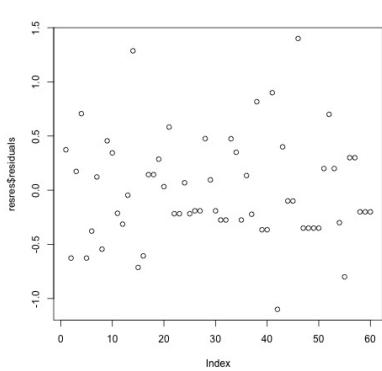


Figure 40. Residual plot and residual QQ plot of fruitfulness in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	16.22	1	56.84	0.00
treatment	0.64	1	2.25	0.14
block	2.57	5	1.80	0.13
treatment:block	1.75	5	1.23	0.31
residuals	13.69	48		

Table 55. ANOVA table for fruitfulness in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	3.30	0.08
block	5	48	2.14	0.08
treatment:block	5	48	1.75	0.14

Table 56. ART ANOVA table for fruitfulness in Merlot 2020

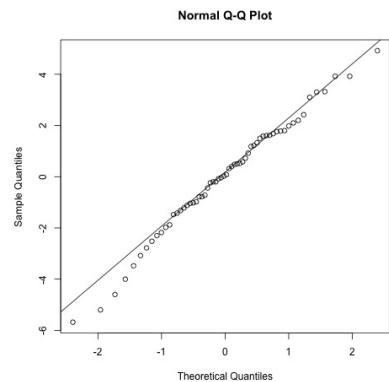
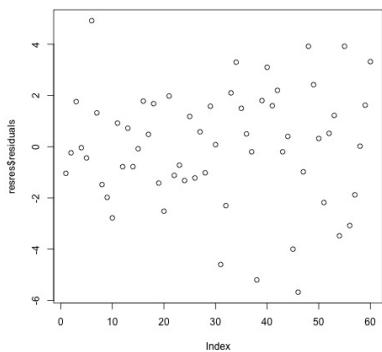


Figure 41. Residual plot and residual QQ plot of leaf greenness in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	87898.54	1	14130.84	0.00
treatment	23.94	1	3.85	0.06
block	190.74	5	6.13	0.00
treatment:block	18.94	5	0.61	0.69
residuals	298.58	48		

Table 57. ANOVA table for leaf greenness in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	4.21	0.05
block	5	48	6.31	0.00
treatment:block	5	48	0.65	0.66

Table 58. ART ANOVA table for leaf greenness in Merlot 2020

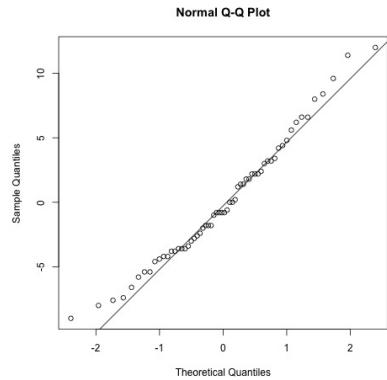
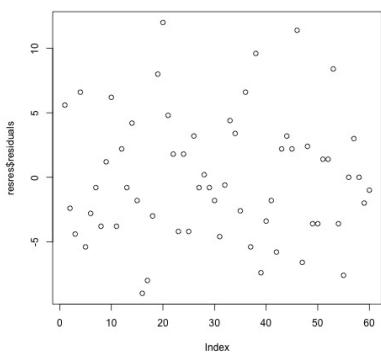


Figure 42. Residual plot and residual QQ plot of # of clusters in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	2343.75	1	81.17	0.00
treatment	7.35	1	0.25	0.62
block	200.75	5	1.39	0.24
treatment:block	173.15	5	1.20	0.32
residuals	1386.00	48		

Table 59. ANOVA table for # of clusters in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.19	0.67
block	5	48	1.10	0.37
treatment:block	5	48	0.85	0.52

Table 60. ART ANOVA table for # of clusters in Merlot 2020

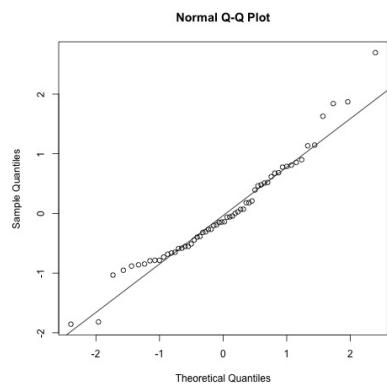
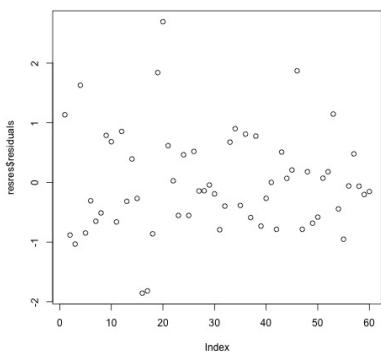


Figure 43. Residual plot and residual QQ plot of yield in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	43.42	1	48.92	0.00
treatment	0.08	1	0.09	0.76
block	6.83	5	1.54	0.20
treatment:block	6.75	5	1.52	0.20
residuals	42.60	48		

Table 61. ANOVA table for yield in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.07	0.80
block	5	48	1.05	0.40
treatment:block	5	48	1.07	0.39

Table 62. ART ANOVA table for yield in Merlot 2020



Figure 44. Residual plot and residual QQ plot of average cluster weight in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	0.65	1	186.65	0.00
treatment	0.00	1	0.16	0.69
block	0.04	5	2.22	0.07
treatment:block	0.03	5	1.58	0.18
residuals	0.17	48		

Table 63. ANOVA table for average cluster weight in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.15	0.70
block	5	48	1.92	0.11
treatment:block	5	48	1.60	0.18

Table 64. ART ANOVA table for average cluster weight in Merlot 2020

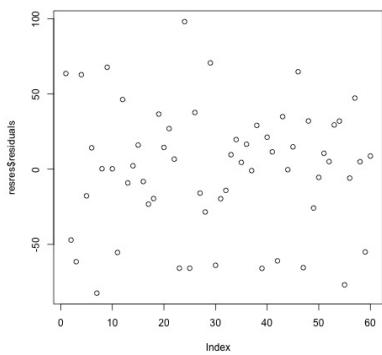


Figure 45. Residual plot and residual QQ plot of average # of berries per cluster in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	434347.89	1	207.61	0.00
treatment	544.41	1	0.26	0.61
block	17350.84	5	1.66	0.16
treatment:block	15175.91	5	1.45	0.22
residuals	100420.01	48		

Table 65. ANOVA table for average # of berries per cluster in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.89	0.35
block	5	48	1.77	0.14
treatment:block	5	48	1.64	0.17

Table 66. ART ANOVA table for average # of berries per cluster in Merlot 2019

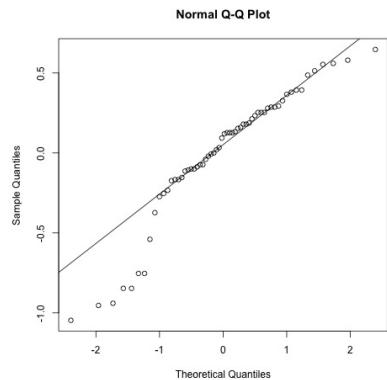
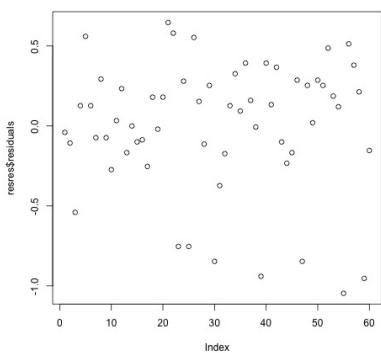


Figure 46. Residual plot and residual QQ plot of average berry weight in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	67.84	1	336.23	0.00
treatment	0.00	1	0.00	1.00
block	1.68	5	1.67	0.16
treatment:block	0.44	5	0.44	0.82
residuals	9.68	48		

Table 67. ANOVA table for average berry weight in Merlot 2020

	degrees of freedom	residual degrees of freedom	F value	P value
treatment	1	48	0.01	0.91
block	5	48	1.38	0.25
treatment:block	5	48	0.33	0.90

Table 68. ART ANOVA table for average berry weight in Merlot 2020

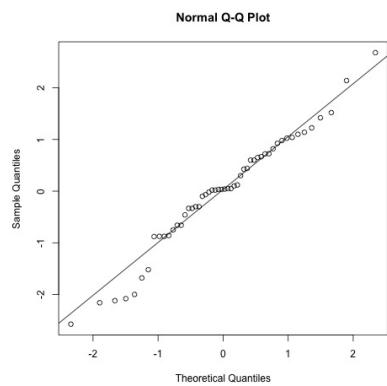
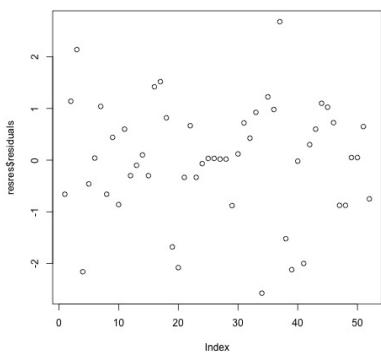


Figure 47. Residual plot and residual QQ plot of berry Brix in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	31984.13	1	20566.48	0.00
treatment	5.23	1	3.37	0.07
block	7.28	5	0.94	0.47
treatment:block	18.30	5	2.35	0.06
residuals	62.21	40		

Table 69. ANOVA table for berry Brix in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.21	0.43	0.06
ART ANOVA	0.18	0.38	0.12

Table 70. P values of pooled analyses from multiple imputation for berry Brix in Merlot 2020

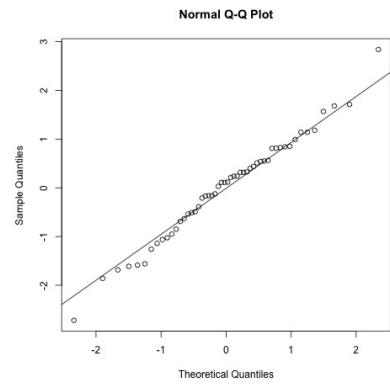
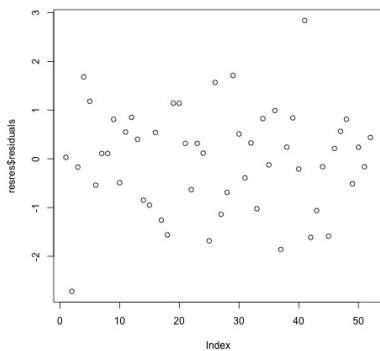


Figure 48. Residual plot and residual QQ plot of berry TA in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	3399.93	1	2403.73	0.00
treatment	0.11	1	0.08	0.78
block	19.01	5	2.69	0.03
treatment:block	13.03	5	1.84	0.13
residuals	56.58	40		

Table 71. ANOVA table for berry TA in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.90	0.12	0.25
ART ANOVA	0.82	0.09	0.20

Table 72. P values of pooled analyses from multiple imputation for berry TA in Merlot 2020

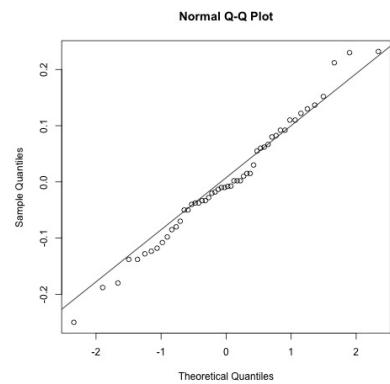
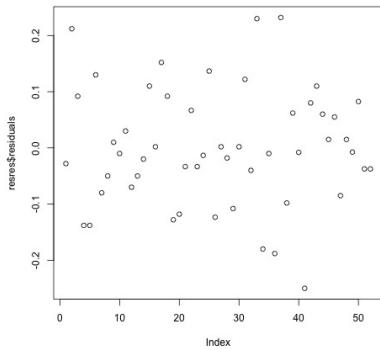


Figure 49. Residual plot and residual QQ plot of berry pH in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	520.32	1	36952.95	0.00
treatment	0.00	1	0.12	0.73
block	0.17	5	2.35	0.06
treatment:block	0.06	5	0.80	0.56
residuals	0.56	40		

Table 73. ANOVA table for berry pH in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.87	0.60	0.70
ART ANOVA	0.98	0.48	0.68

Table 74. P values of pooled analyses from multiple imputation for berry pH in Merlot 2020



Figure 50. Residual plot and residual QQ plot of brown seed color in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	307358.76	1	4776.05	0.00
treatment	6.06	1	0.09	0.76
block	432.05	5	1.34	0.27
treatment:block	432.77	5	1.34	0.27
residuals	2574.17	40		

Table 75. ANOVA table for brown seed color in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.79	0.03	0.24
ART ANOVA	0.64	0.03	0.26

Table 76. P values of pooled analyses from multiple imputation for brown seed color in Merlot 2020

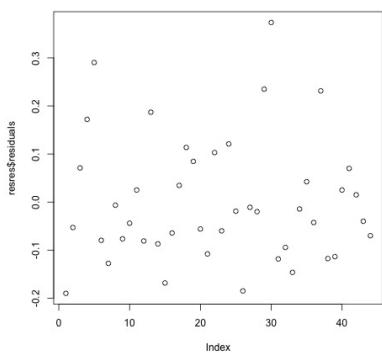


Figure 51. Residual plot and residual QQ plot of pruning weight in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	1.92	1	97.05	0.00
treatment	0.10	1	5.02	0.03
block	0.14	3	2.28	0.10
treatment:block	0.12	3	2.04	0.13
residuals	0.63	32		

Table 77. ANOVA table for pruning weight in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.07	0.21	0.10
ART ANOVA	0.10	0.29	0.05

Table 78. P values of pooled analyses from multiple imputation for pruning weight in Merlot 2020

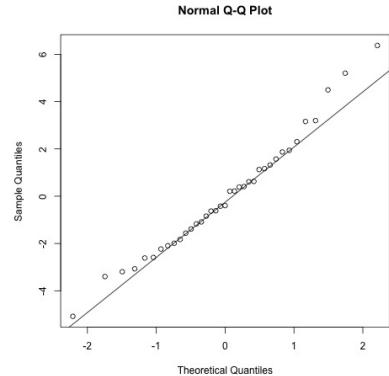
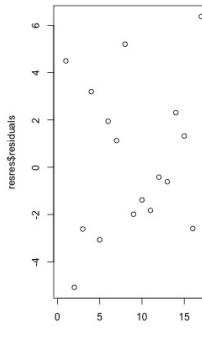


Figure 52. Residual plot and residual QQ plot of Ravaz index in Merlot 2020

	sum of squares	degrees of freedom	F value	P value
intercept	407.01	1	62.99	0.00
treatment	7.22	1	1.12	0.30
block	22.90	3	1.18	0.34
treatment:block	16.06	3	0.83	0.49
residuals	161.53	25		

Table 79. ANOVA table for Ravaz index in Merlot 2020

	treatment	block	treatment:block
two-way ANOVA	0.82	0.00	0.94
ART ANOVA	0.93	0.01	0.84

Table 80. P values of pooled analyses from multiple imputation for Ravaz index in Merlot 2020

C.6 Three-way ANOVA

	sum of squares	degrees of freedom	F value	P value
intercept	68620.61	1	1262.47	0.00
block	794.58	4	3.65	0.01
treatment	127.51	1	2.35	0.13
year	285.01	1	5.24	0.03
block:treatment	401.67	4	1.85	0.13
block:year	181.17	4	0.83	0.51
treatment:year	0.61	1	0.01	0.92
block:treatment:year	420.58	4	1.93	0.12
residuals	3261.25	60		

Table 81. ANOVA table for # of clusters for both years' Chardonnay data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	60	1881.80	39671.50	2.85	0.10
block	4	60	9984.34	31925.75	4.69	0.00
year	1	60	5216.45	36815.88	8.50	0.00
treatment:block	4	60	5348.23	36560.00	2.19	0.08
treatment:year	1	60	0.80	41655.75	0.00	0.97
block:year	4	60	1700.77	39484.75	0.65	0.63
treatment:block:year	4	60	5740.11	35919.75	2.40	0.06

Table 82. ART ANOVA table for # of clusters for both years' Chardonnay data

	sum of squares	degrees of freedom	F value	P value
intercept	2627.03	1	658.77	0.00
block	68.74	4	4.31	0.00
treatment	1.88	1	0.47	0.49
year	8.22	1	2.06	0.16
block:treatment	10.07	4	0.63	0.64
block:year	4.85	4	0.30	0.87
treatment:year	0.11	1	0.03	0.87
block:treatment:year	10.71	4	0.67	0.61
residuals	239.27	60		

Table 83. ANOVA table for yield for both years' Chardonnay data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	60	627.20	41363.5	0.91	0.34
block	4	60	9443.00	32858.5	4.31	0.00
year	1	60	1328.45	40455.5	1.97	0.17
treatment:block	4	60	1269.38	40721.5	0.47	0.76
treatment:year	1	60	204.80	41771.5	0.29	0.59
block:year	4	60	955.68	41149.0	0.35	0.84
treatment:block:year	4	60	2168.30	39802.5	0.82	0.52

Table 84. ART ANOVA table for yield for both years' Chardonnay data

	sum of squares	degrees of freedom	F value	P value
intercept	3.06	1	1469.47	0.00
block	0.03	4	3.02	0.02
treatment	0.00	1	0.51	0.48
year	0.00	1	0.03	0.87
block:treatment	0.01	4	1.43	0.23
block:year	0.00	4	0.42	0.79
treatment:year	0.00	1	0.41	0.53
block:treatment:year	0.00	4	0.18	0.95
residuals	0.12	60		

Table 85. ANOVA table for average cluster weight for both years' Chardonnay data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	60	336.20	42081.0	0.48	0.49
block	block	4	60	5535.00	36496.0	2.27
0.07						
year	1	60	0.45	42458.5	0.00	0.98
treatment:block	4	60	3889.12	38561.5	1.51	0.21
treatment:year	1	60	259.20	42125.5	0.37	0.55
block:year	4	60	805.45	41619.5	0.29	0.88
treatment:block:year	4	60	566.93	41938.5	0.20	0.94

Table 86. ART ANOVA table for average cluster weight for both years' Chardonnay data

	sum of squares	degrees of freedom	F value	P value
intercept	183824.92	1	36664.16	0.00
block	267.94	5	10.69	0.00
treatment	25.12	1	5.01	0.03
year	89.61	1	17.87	0.00
block:treatment	30.94	5	1.23	0.30
block:year	22.72	5	0.91	0.48
treatment:year	3.64	1	0.73	0.40
block:treatment:year	3.86	5	0.15	0.98
residuals	481.32	96		

Table 87. ANOVA table for leaf greenness for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	8167.50	134551.5	5.83	0.02
block	5	96	53075.27	89342.1	11.41	0.00
year	1	96	21280.03	120639.4	16.93	0.00
treatment:block	5	96	7900.03	134450.0	1.13	0.35
treatment:year	1	96	1241.63	141758.9	0.84	0.36
block:year	5	96	3606.87	138934.7	0.50	0.78
treatment:block:year	5	96	1131.44	141450.5	0.15	0.98

Table 88. ART ANOVA table for leaf greenness for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	18451.20	1	614.95	0.00
block	200.70	5	1.34	0.25
treatment	5.63	1	0.19	0.67
year	4538.70	1	151.27	0.00
block:treatment	134.67	5	0.90	0.49
block:year	145.60	5	0.97	0.44
treatment:year	38.53	1	1.28	0.26
block:treatment:year	56.57	5	0.38	0.86
residuals	2880.40	96		

Table 89. ANOVA table for # of clusters for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	320.13	141989.3	0.22	0.64
block	5	96	7573.45	134325.9	1.08	0.38
year	0.00	1	96	90750.00	52750.6	165.15
treatment:block	5	96	4837.79	137188.8	0.68	0.64
treatment:year	1	96	1888.13	140318.3	1.29	0.26
block:year	5	96	8577.92	133951.9	1.23	0.30
treatment:block:year	5	96	2001.89	140777.1	0.27	0.93

Table 90. ART ANOVA table for # of clusters for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	367.39	1	352.49	0.00
block	18.64	5	3.58	0.01
treatment	2.49	1	2.39	0.13
year	96.99	1	93.06	0.00
block:treatment	8.05	5	1.55	0.18
block:year	9.22	5	1.77	0.13
treatment:year	1.37	1	1.31	0.26
block:treatment:year	6.41	5	1.23	0.30
residuals	100.06	96		

Table 91. ANOVA table for yield for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	1598.70	139799.1	1.10	0.30
block	5	96	17163.90	122986.7	2.68	0.03
year	1	96	75100.03	68100.3	105.87	0.00
treatment:block	5	96	7665.70	133349.1	1.10	0.36
treatment:year	1	96	2201.63	140279.5	1.51	0.22
block:year	5	96	12211.67	129869.9	1.81	0.12
treatment:block:year	5	96	6672.40	134456.3	0.95	0.45

Table 92. ART ANOVA table for yield for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	1.81	1	666.96	0.00
block	0.08	5	5.53	0.00
treatment	0.00	1	0.15	0.69
year	0.04	1	15.30	0.00
block:treatment	0.01	5	1.00	0.42
block:year	0.01	5	0.92	0.47
treatment:year	0.00	1	1.08	0.30
block:treatment:year	0.04	5	2.65	0.03
residuals	0.26	96		

Table 93. ANOVA table for average cluster weight for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	1045730.06	1	728.33	0.00
block	25272.63	5	3.52	0.01
treatment	440.03	1	0.31	0.58
year	8203.09	1	5.71	0.02
block:treatment	3410.26	5	0.48	0.79
block:year	7558.44	5	1.05	0.39
treatment:year	2913.21	1	2.03	0.16
block:treatment:year	21219.43	5	2.96	0.02
residuals	137836.85	96		

Table 95. ANOVA table for average # of berries per cluster for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	58.80	142839.8	0.04	0.84
block	5	96	29815.20	112781.4	5.08	0.00
year	1	96	16473.63	125869.8	12.56	0.00
treatment:block	5	96	7228.57	136184.6	1.02	0.41
treatment:year	1	96	2253.33	140724.2	1.54	0.22
block:year	5	96	5533.47	136997.8	0.78	0.57
treatment:block:year	5	96	17345.07	125315.8	2.66	0.03

Table 94. ART ANOVA table for average cluster weight for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	56.03	142282.3	0.04	0.85
block	5	96	22671.80	118297.1	3.68	0.00
year	1	96	6336.53	136268.7	4.46	0.04
treatment:block	5	96	3960.47	138609.5	0.55	0.74
treatment:year	1	96	5413.63	137603.9	3.78	0.05
block:year	5	96	9331.17	132981.5	1.35	0.25
treatment:block:year	5	96	22378.40	119620.3	3.59	0.01

Table 96. ART ANOVA table for average # of berries per cluster for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	178.64	1	1614.31	0.00
block	1.43	5	2.59	0.03
treatment	0.02	1	0.15	0.70
year	2.95	1	26.66	0.00
block:treatment	0.57	5	1.03	0.40
block:year	0.67	5	1.21	0.31
treatment:year	0.02	1	0.15	0.70
block:treatment:year	0.28	5	0.50	0.78
residuals	10.62	96		

Table 97. ANOVA table for average berry weight for both years' Merlot data

Term	Df	Df.res	Sum Sq	Sum Sq.res	F value	Pr(>F)
treatment	1	96	360.53	136298.9	0.25	0.62
block	5	96	21349.40	111692.9	3.67	0.00
year	1	96	32802.13	104009.7	30.28	0.00
treatment:block	5	96	10581.37	126281.5	1.61	0.17
treatment:year	1	96	440.83	135760.3	0.31	0.58
block:year	5	96	8593.37	124948.7	1.32	0.26
treatment:block:year	5	96	2738.97	133480.3	0.39	0.85

Table 98. ART ANOVA table for average berry weight for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	5936.23	1	4236.24	0.00
block	28.30	5	4.04	0.00
treatment	0.01	1	0.01	0.93
year	29.31	1	20.92	0.00
block:treatment	12.36	5	1.76	0.13
block:year	5.93	5	0.85	0.52
treatment:year	0.34	1	0.24	0.62
block:treatment:year	7.83	5	1.12	0.36
residuals	112.10	80		

Table 99. ANOVA table for berry TA for both years' Merlot data

	treatment	block	treatment:block
three-way ANOVA	0.59	0.00	0.25
ART ANOVA	0.67	0.00	0.20

Table 100. P values of pooled analyses from multiple imputation for berry TA for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	1074.00	1	113433.34	0.00
block	0.24	5	4.98	0.00
treatment	0.00	1	0.19	0.66
year	0.26	1	27.79	0.00
block:treatment	0.08	5	1.75	0.13
block:year	0.09	5	1.93	0.10
treatment:year	0.01	1	1.06	0.31
block:treatment:year	0.05	5	1.02	0.41
residuals	0.76	80		

Table 101. ANOVA table for berry pH for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	61993.71	1	60692.86	0.00
block	7.30	5	1.43	0.22
treatment	1.10	1	1.08	0.30
year	15.48	1	15.15	0.00
block:treatment	10.66	5	2.09	0.08
block:year	5.56	5	1.09	0.37
treatment:year	4.77	1	4.67	0.03
block:treatment:year	8.48	5	1.66	0.15
residuals	81.71	80		

Table 103. ANOVA table for berry Brix for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	3.94	1	224.03	0.00
block	0.12	3	2.23	0.09
treatment	0.14	1	8.12	0.01
year	0.00	1	0.04	0.85
block:treatment	0.21	3	3.99	0.01
block:year	0.03	3	0.65	0.58
treatment:year	0.00	1	0.26	0.61
block:treatment:year	0.01	3	0.11	0.95
residuals	1.13	64		

Table 105. ANOVA table for pruning weight for both years' Merlot data

	sum of squares	degrees of freedom	F value	P value
intercept	4006.78	1	155.55	0.00
block	94.95	3	1.23	0.31
treatment	104.38	1	4.05	0.05
year	1208.82	1	46.93	0.00
block:treatment	141.98	3	1.84	0.15
block:year	46.29	3	0.60	0.62
treatment:year	196.45	1	7.63	0.01
block:treatment:year	58.57	3	0.76	0.52
residuals	1287.96	50		

Table 107. ANOVA table for Ravaz index for both years' Merlot data

	treatment	block	treatment:block
three-way ANOVA	0.40	0.03	0.34
ART ANOVA	0.38	0.01	0.14

Table 102. P values of pooled analyses from multiple imputation for berry pH for both years' Merlot data

	treatment	block	treatment:block
three-way ANOVA	0.55	0.12	0.12
ART ANOVA	0.38	0.08	0.08

Table 104. P values of pooled analyses from multiple imputation for berry Brix for both years' Merlot data

	treatment	block	treatment:block
three-way ANOVA	0.26	0.02	0.00
ART ANOVA	0.16	0.02	0.00

Table 106. P values of pooled analyses from multiple imputation for pruning weight for both years' Merlot data

	treatment	block	treatment:block
three-way ANOVA	0.18	0.14	0.01
ART ANOVA	0.29	0.03	0.00

Table 108. P values of pooled analyses from multiple imputation for Ravaz index for both years' Merlot data

D. Selective R code

D.1 Explorative data analysis

```
1 # EDA: correlation plot for merlot 2019
2 merlot19.resp <- select(merlot2019,(-1:-5))
3 merlot19.resp %>%
4   drop_na() %>%
5   cor() %>%
6   corplot(type = "upper", order = "hclust", tl.col = "black", tl.srt = 45,
7         addCoef.col="white", number.cex=0.7)
8
9 # EDA: summary statistics for merlot 2019
10 ## helper function
11 summary.cont<-function(data, x){
12   data %>%
13     summarise(min = round(min(x,na.rm=TRUE),2),
14               median = round(median(x,na.rm=TRUE), 2),
15               max= round(max(x,na.rm=TRUE), 2),
16               mean = round(mean(x,na.rm=TRUE),2),
17               sd = round(sd(x,na.rm=TRUE),2))
18 }
19
20 var.desc3=sapply(merlot19.resp, summary.cont, data=merlot19.resp)
21 kable(var.desc3, "latex", align ="c")
22
23 # EDA: Side by side box plots (treatment and blocks combination)
24 ## helper function
25 plot.trt.blk=function(data, resp)
26   data %>%
27     ggplot(aes(x=treatment, y = .data[[resp]], fill=treatment))+ 
28     scale_fill_manual(values=c("lightblue2", "seashell2"))+
29     geom_boxplot()+
30     labs(title = resp) +
31     ylab(resp)+ 
32     facet_wrap(~block)+ 
33     theme(legend.position = "top")+
34     stat_compare_means(method = "wilcox.test", label.x = 0.7,
35                         label.y = quantile(data[[resp]], probs=c(0.99), na.rm=TRUE)
36                       )+
37     stat_compare_means(method = "t.test", label.x = 1.7,
38                         label.y = quantile(data[[resp]], probs=c(0.99), na.rm=TRUE)
39                       )
40
41 ## draw side-by-side boxplots for response variables in merlot2019
42 for (i in colnames(merlot2019[c(-1:-5,-7)])){
43   print(plot.trt.blk(merlot2019, i))
44 }
45
46 # EDA: Censored data analysis
47 ## draw KM curves for veraison 2020
48 ver20<-merlot2020 %>%
49   select(treatment, veraison, block) %>%
50   mutate(veraison = replace_na(veraison, 0),
51         status = ifelse(veraison <= 31, 1, 0))
```

```

50 fit2<-survfit(Surv(veraison, status) ~ treatment, data=ver20)
51 ggsurvplot(fit2, facet.by = "block", xlim = c(8, 40), pval=TRUE,
52             data=ver20, pval.coord=c(10,0.25), conf.int=TRUE,
53             font.title=11, font.x=11, font.y=11, ylab="Non-veraison probability")

```

D.2 Censored data analysis

```

1
2 # right censored only: merlot2020
3
4 # Let's consider what happens if we only treat the data as right-censored or
5 # observed
6 icen.mer20$bloom.rc <- ifelse(icen.mer20$bloom.start==Inf, icen.mer20$bloom.end
7 , icen.mer20$bloom.start)
8 icen.mer20$verais.rc <- ifelse(icen.mer20$verais.start==Inf, icen.mer20$verais.
9 end, icen.mer20$verais.start)
10 icen.mer20$bloom.indicator.rc <- ifelse(icen.mer20$bloom.indicator=="right-
11 censored", 0, 1)
12 icen.mer20$verais.indicator.rc <- ifelse(icen.mer20$verais.indicator=="right-
13 censored", 0, 1)
14
15
16
17 # Build a model for the bloom data
18 rc.coxph.bloom20 <- coxph(Surv(bloom.rc,bloom.indicator.rc) ~
19                 as.factor(trt) * as.factor(block),
20                 data=icen.mer20)
21
22
23 # Build a model for the veraison merlot 2020 data
24 rc.coxph.ver20 <- coxph(Surv(verais.rc,verais.indicator.rc) ~
25                 as.factor(trt) * as.factor(block),
26                 data=icen.mer20)
27
28
29 # CI
30 exp(confint(rc.coxph.ver20))[1,] # 0.9200849 12.1712735
31
32
33 # right censored only: merlot2019
34
35 # First define our dataset of start and end times for our event intervals
36 icen.mer19$verais.rc <- ifelse(icen.mer19$verais.start==Inf, icen.mer19$verais.
37 end, icen.mer19$verais.start)
38 icen.mer19$verais.indicator.rc <- ifelse(icen.mer19$verais.indicator=="right-
39 censored", 0, 1)
40
41
42 # Build a model for the veraison data
43 rc.coxph.ver19 <- coxph(Surv(verais.rc,verais.indicator.rc) ~ as.factor(trt) *
44                 as.factor(block),
45                 data=icen.mer19)
46
47
48 # print summaries
49
50 summary(rc.coxph.ver19)
51
52 summary(rc.coxph.ver20)
53
54 summary(rc.coxph.bloom20)

```

```

43
44 # assumption check
45
46 newdata <- data.frame(trt=c(rep("heat", 6), rep("control", 6)), "block"=as.character(1:6))
47 rownames(newdata) <- paste(newdata$trt, newdata$block)
48
49 plot(rc.coxph.ver19, newdata, main="2019 Veraison", col=rainbow(12), lgdLocation = "bottomleft")
50
51 plot(rc.coxph.ver20, newdata, main="2020 Veraison", col=rainbow(12), lgdLocation = "bottomleft")
52
53 plot(rc.coxph.bloom20, newdata, main="2020 Bloom", col=rainbow(12), lgdLocation = "bottomleft")

```

D.3 Non-censored data analysis

```

1 # check equal variance
2 with(merlot2019, levene.test(SPAD, paste(treatment, block)))$p
3
4 # fit two-way ANOVA
5 options(contrasts = c("contr.sum", "contr.poly"))
6 resres = aov(SPAD ~ treatment * block, data=merlot2019)
7 options(contrasts = c("contr.sum", "contr.poly"))
8 library(car)
9 resres = Anova(resres, type = "III")
10 print(resres)
11
12 # plot residual
13 plot(resres$residuals)
14 qqnorm(resres$residuals)
15 qqline(resres$residuals)
16
17 # compute CI for difference in treatment effects
18 print(tukey_hsd(resres, which="treatment"))
19
20 # fit art ANOVA
21 model = art(SPAD ~ treatment * block, merlot2019)
22 res = anova(model, type = 3)
23 print(res)
24
25 # combining datasets
26 merlot2019$year <- 2019
27 merlot2020$year <- 2020
28 merlot2019$year <- as.factor(merlot2019$year)
29 merlot2020$year <- as.factor(merlot2020$year)
30 names(merlot2019)[[1]] <- "Key"
31 merlot.bothyr <- rbind(merlot2019[,c(1:6, 8:18)], merlot2020[,c(1:5,8, 10:17, 19:21)])
32 merlot.bothyr[117,1] <- "M57"
33 merlot.bothyr$Key <- as.factor(merlot.bothyr$Key)
34
35 # fit three way ANOVA
36 dat = merlot.bothyr[,c(1:3,6,17)]
37 options(contrasts = c("contr.sum", "contr.poly"))
38 res = aov(SPAD ~ block*treatment*year, data=dat)

```

```
39 resres = Anova(res, type = "III")
40 print(resres)
41
42 # compute CI for difference in treatment effects
43 print(tukey_hsd(res, which="treatment"))
44
45 # fit three way art ANOVA
46 dat = merlot.bothyr[,c(1:3,6,17)]
47 options(contrasts = c("contr.sum", "contr.poly"))
48 res.art = anova(art(eval(parse(text=names(merlot.bothyr)[i]))) ~ treatment *
49   block * year,
50   data = merlot.bothyr), type = 3)
51 print(res.art)
```