

Figure S1. Boxplots showing relative abundance for the most abundant bacterial phyla (A) and for the 20 most abundant bacterial final taxonomies (B). Stars indicate statistically significant differences according to the Kruskal–Wallis test between sampling dates (* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$).

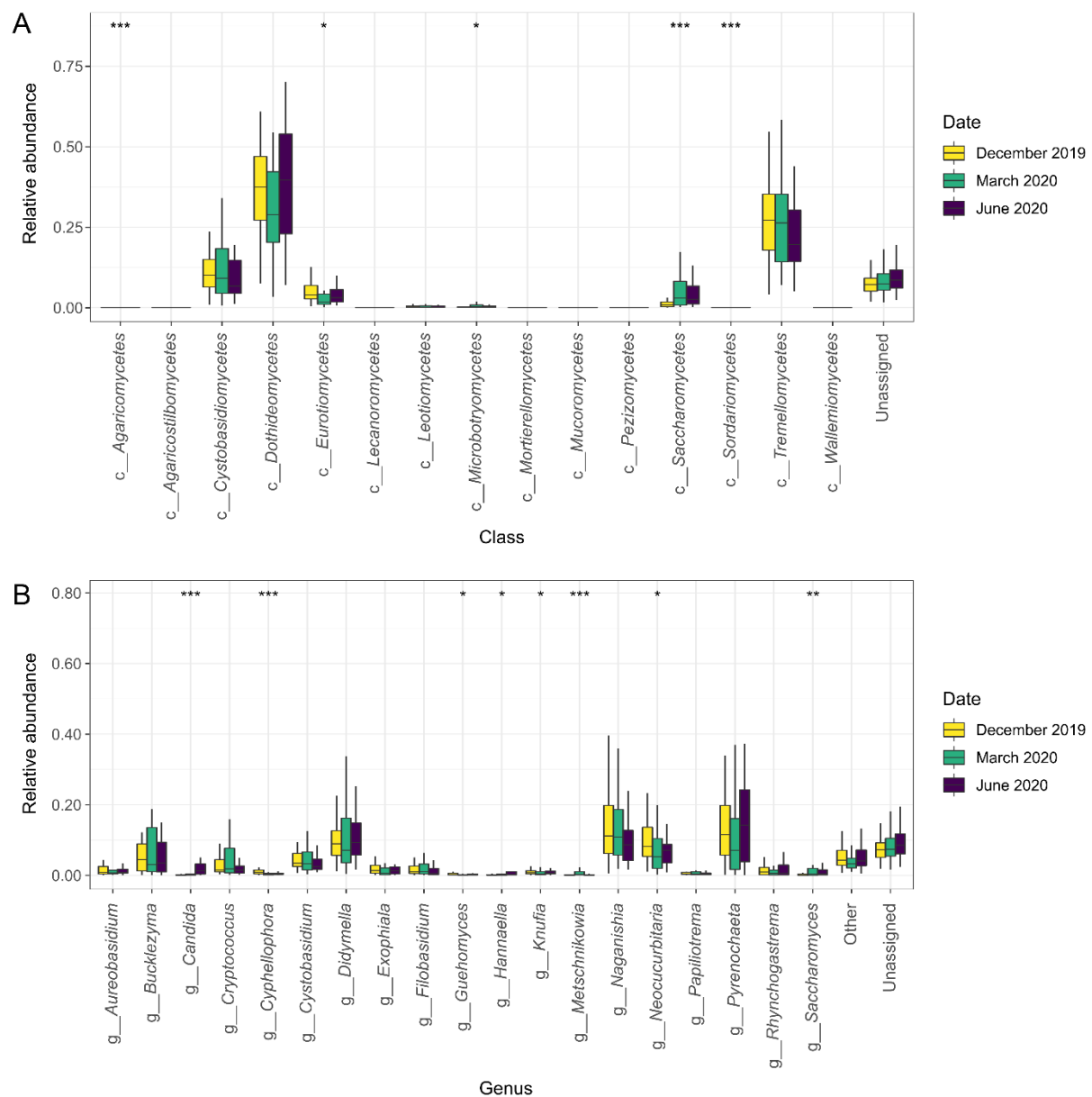


Figure S2. Boxplots showing relative abundance for the most abundant fungal classes (A) and for the 20 most abundant fungal genera (B). Stars indicate statistically significant differences according to the Kruskal–Wallis test between sampling dates (* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$).

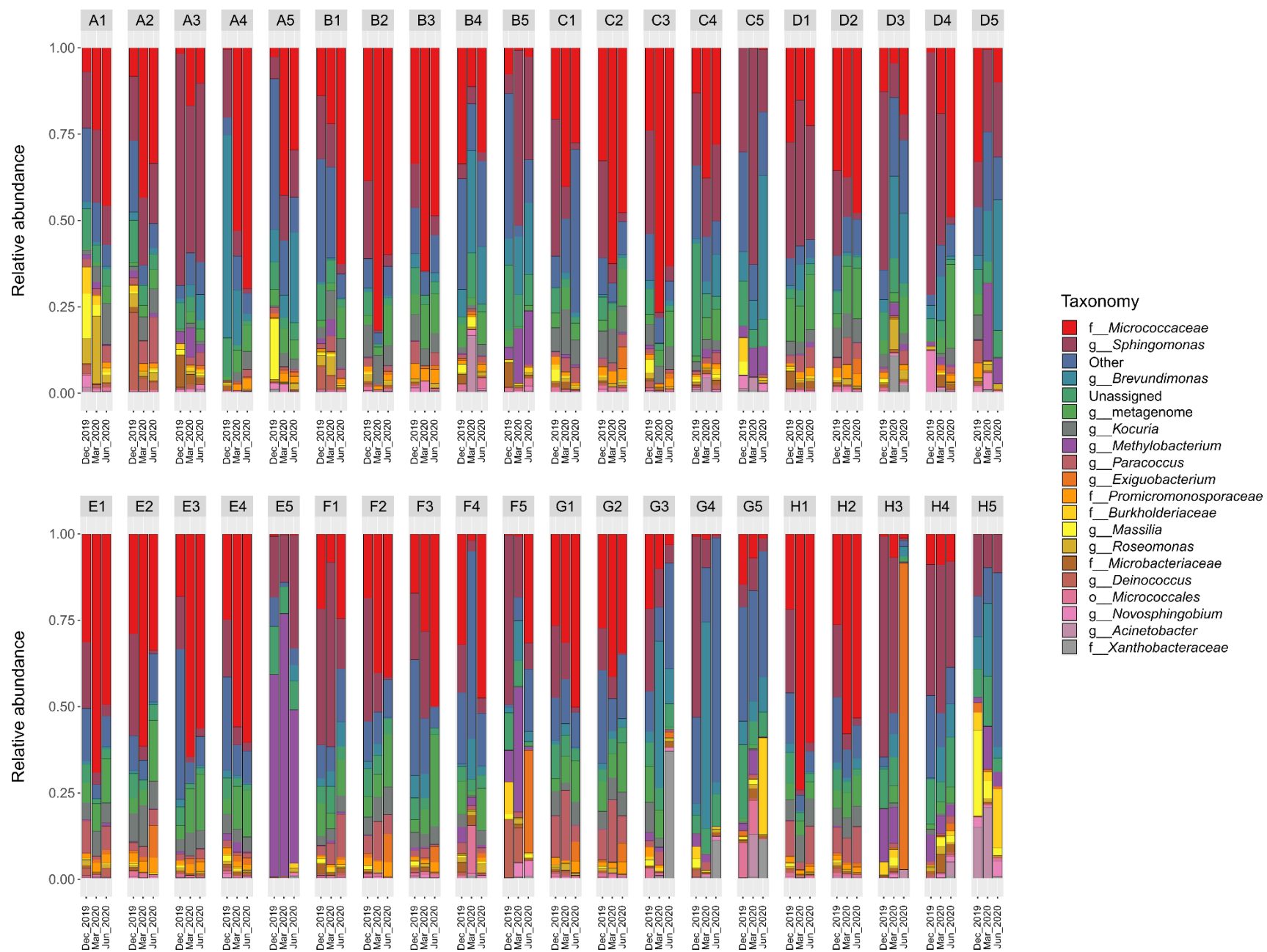
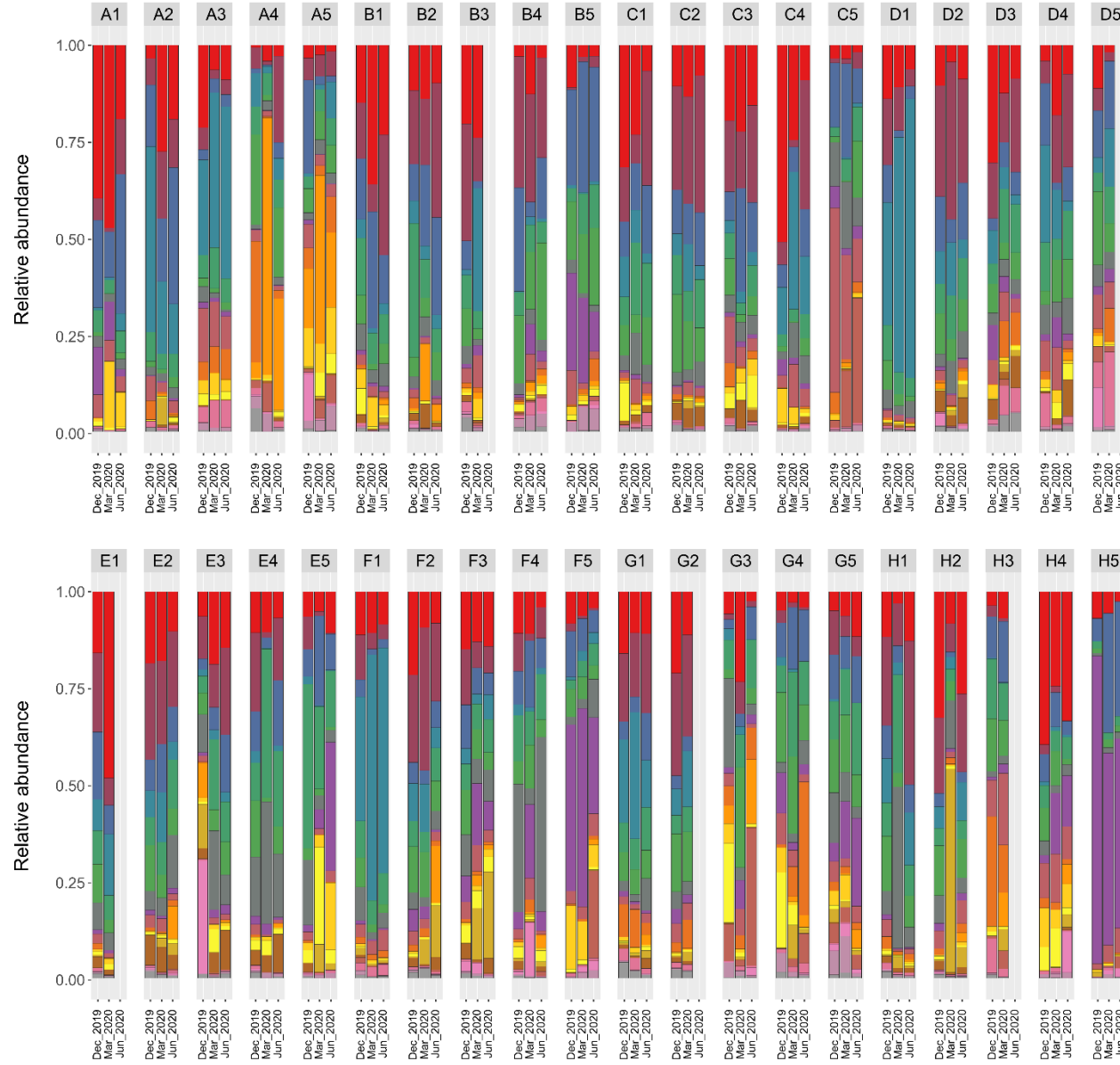


Figure S3. Relative abundance for the most abundant bacterial final taxonomies found at the Hickinbotham Roseworthy Wine Science Laboratory according to location and sampling date.



Taxonomy

- g__Naganishia
- g__Pyrenochaeta
- g__Didymella
- g__Buckleyzyma
- Unassigned
- g__Neocucurbitaria
- Other
- g__Cryptococcus
- g__Cystobasidium
- g__Exophiala
- g__Candida
- g__Filobasidium
- g__Aureobasidium
- g__Saccharomyces
- g__Rhynchogastrema
- g__Hannaella
- g__Knufia
- g__Guehomyces
- g__Papiliotrema
- g__Cyphellophora

Figure S4. Relative abundance for the most abundant fungal genera found at the Hickinbotham Roseworthy Wine Science Laboratory according to location and sampling date.

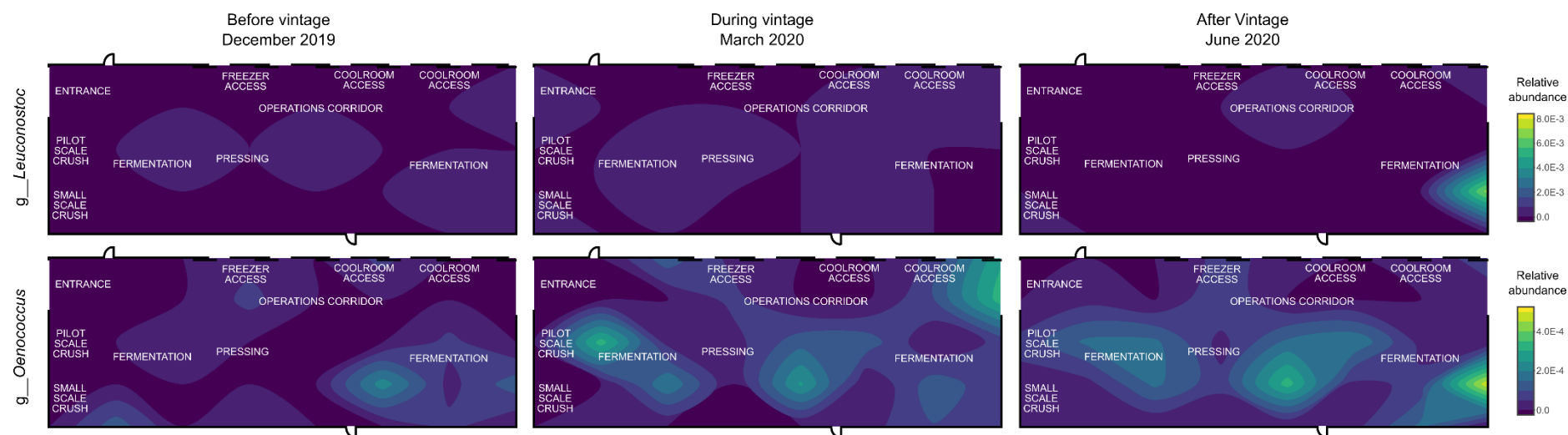


Figure S5. Mapping of the wine-related bacterial genera *Leuconostoc* and *Oenococcus*, before, during and after vintage.

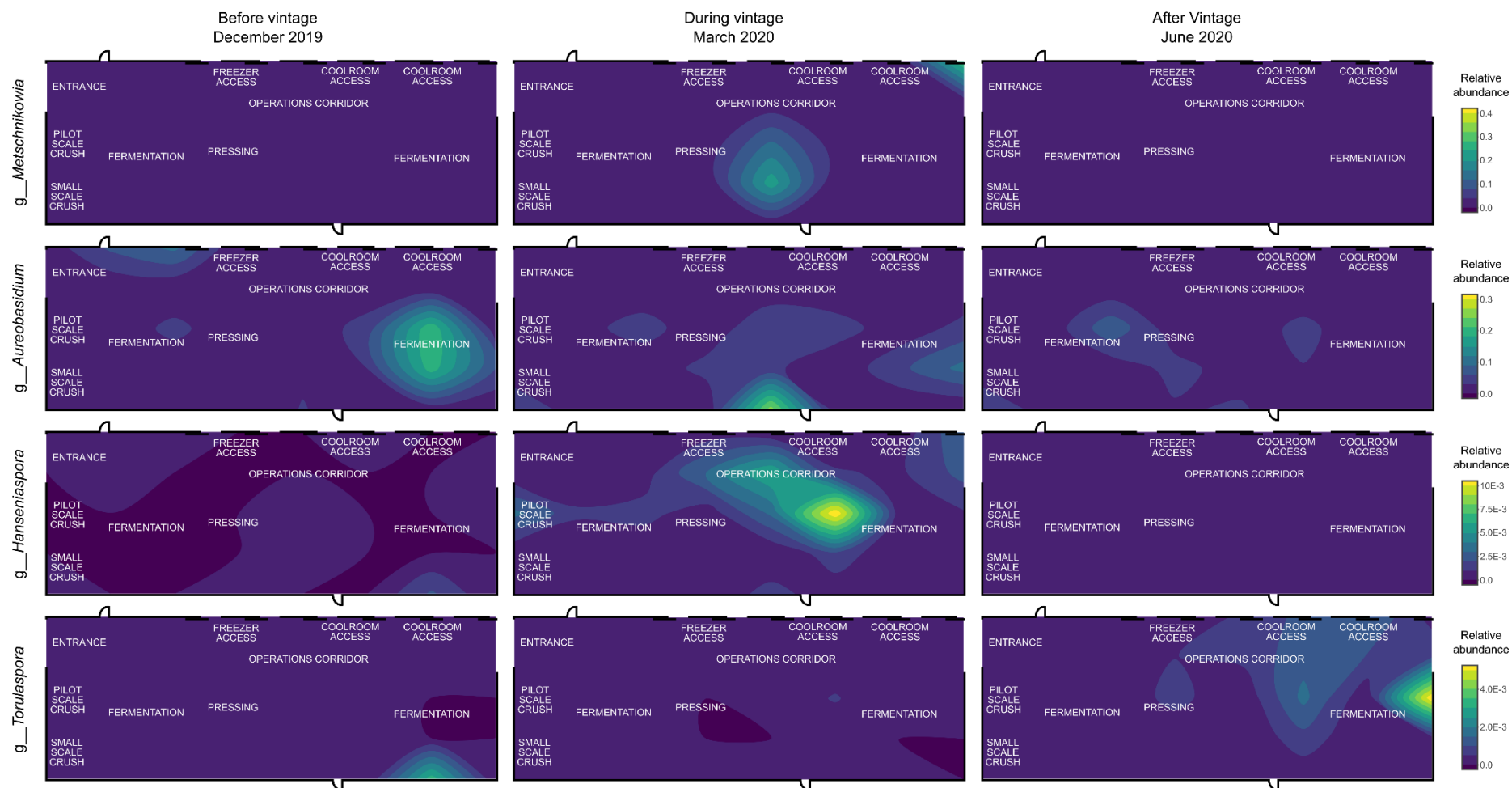


Figure S6. Mapping of the wine-related fungal genera *Metschnikowia*, *Aureobasidium*, *Hanseniaspora* and *Torulaspora*, before, during and after vintage.