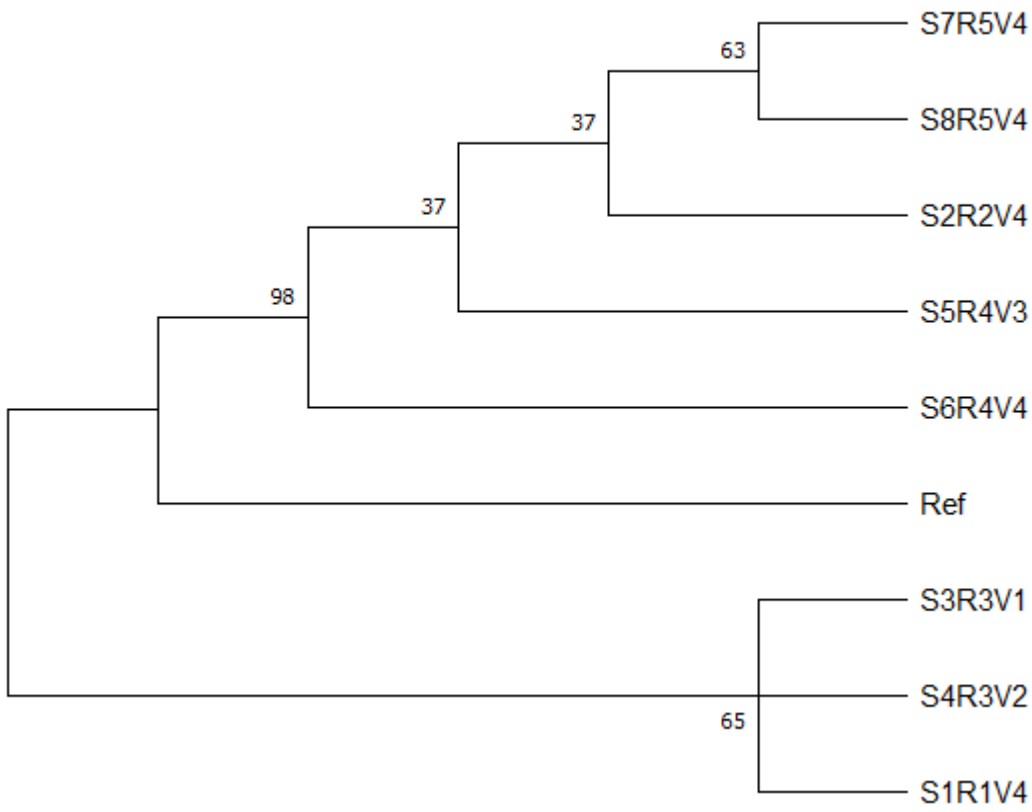


Figure S1. Maximum likelihood tree of *Lac 1* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

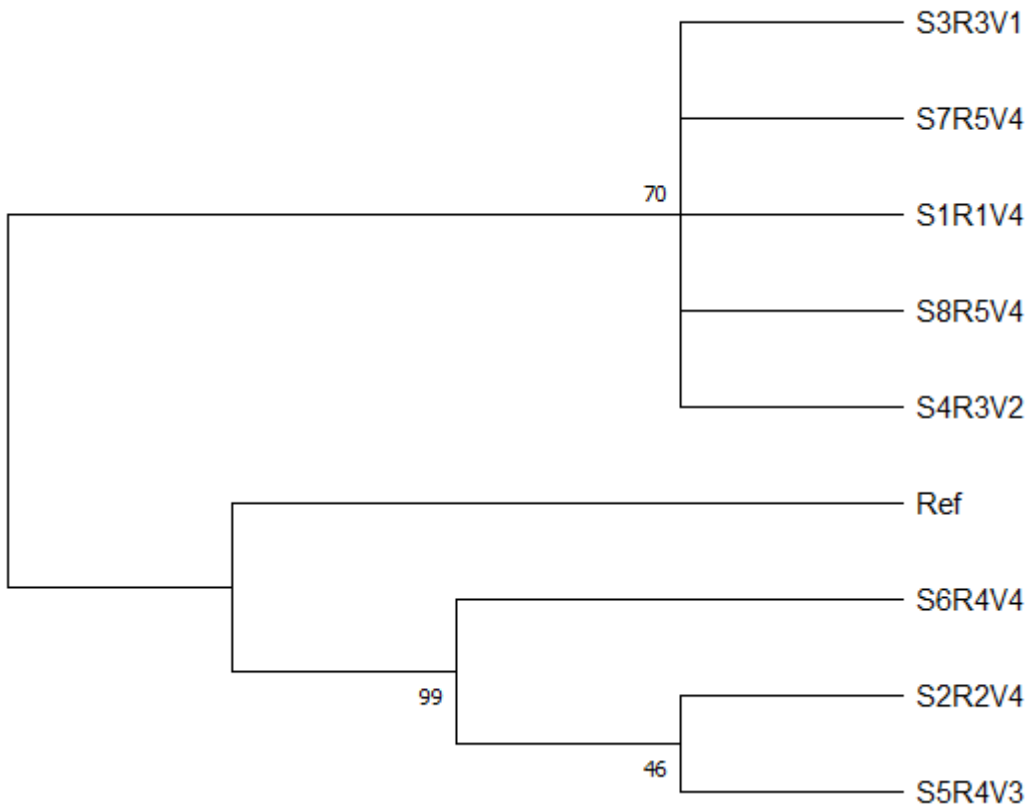


Figure S2. Maximum likelihood tree of *Lac 2* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

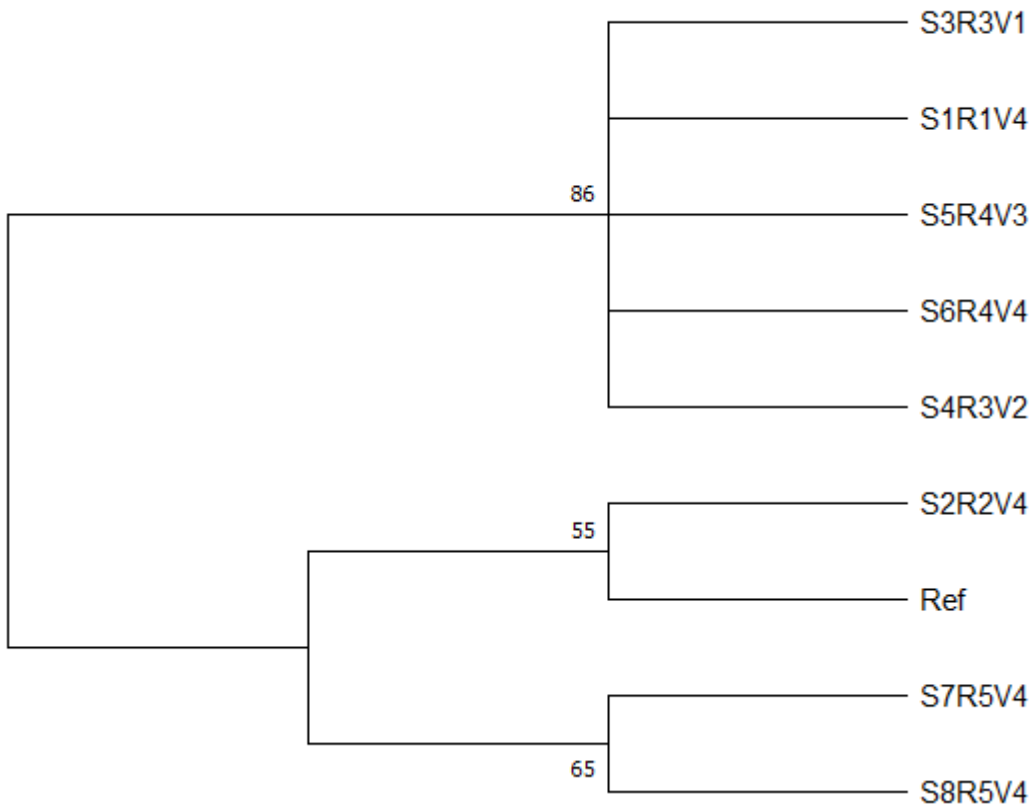


Figure S3. Maximum likelihood tree of *Lac 3* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.



Figure S4. Maximum likelihood tree of *Lac 4* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.



Figure S5. Maximum likelihood tree of *Lac 5* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

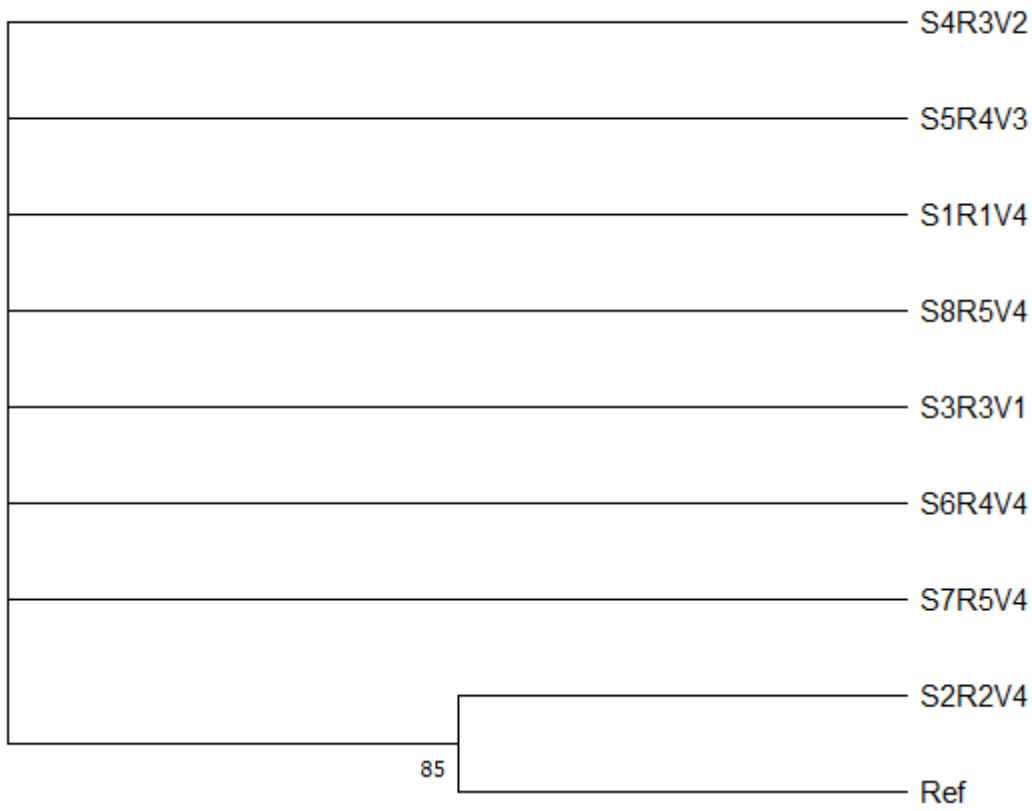


Figure S6. Maximum likelihood tree of *Lac 6* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

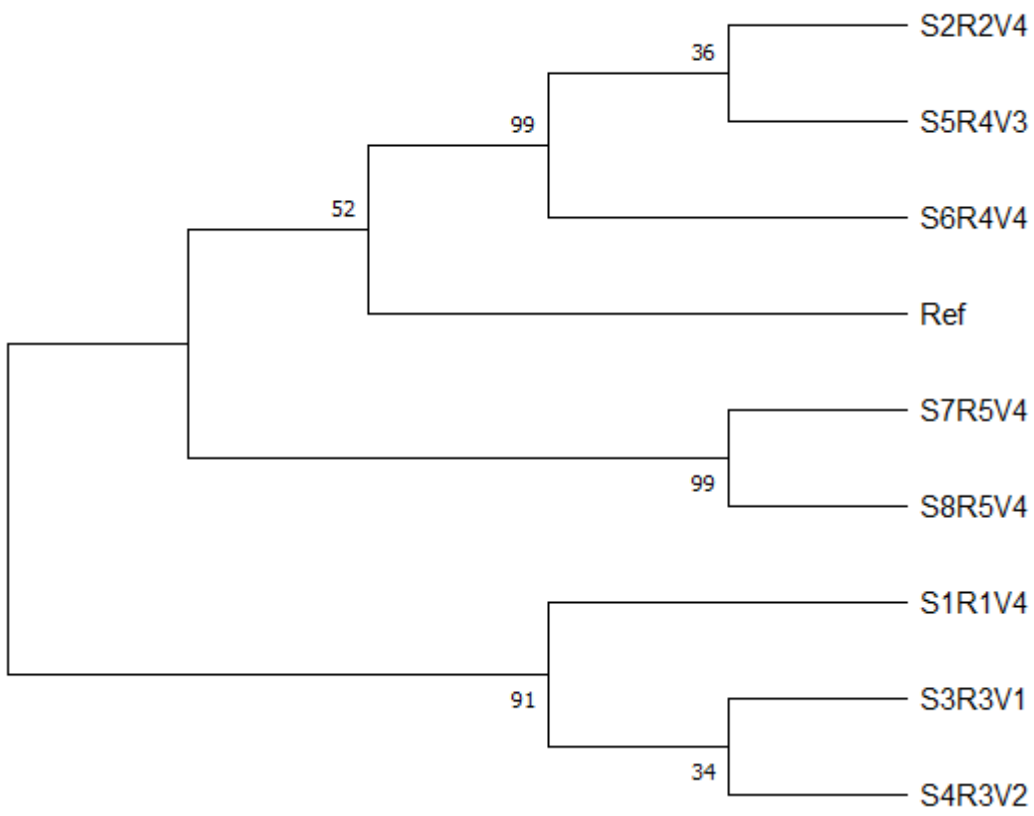


Figure S7. Maximum likelihood tree of *Lac 7* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

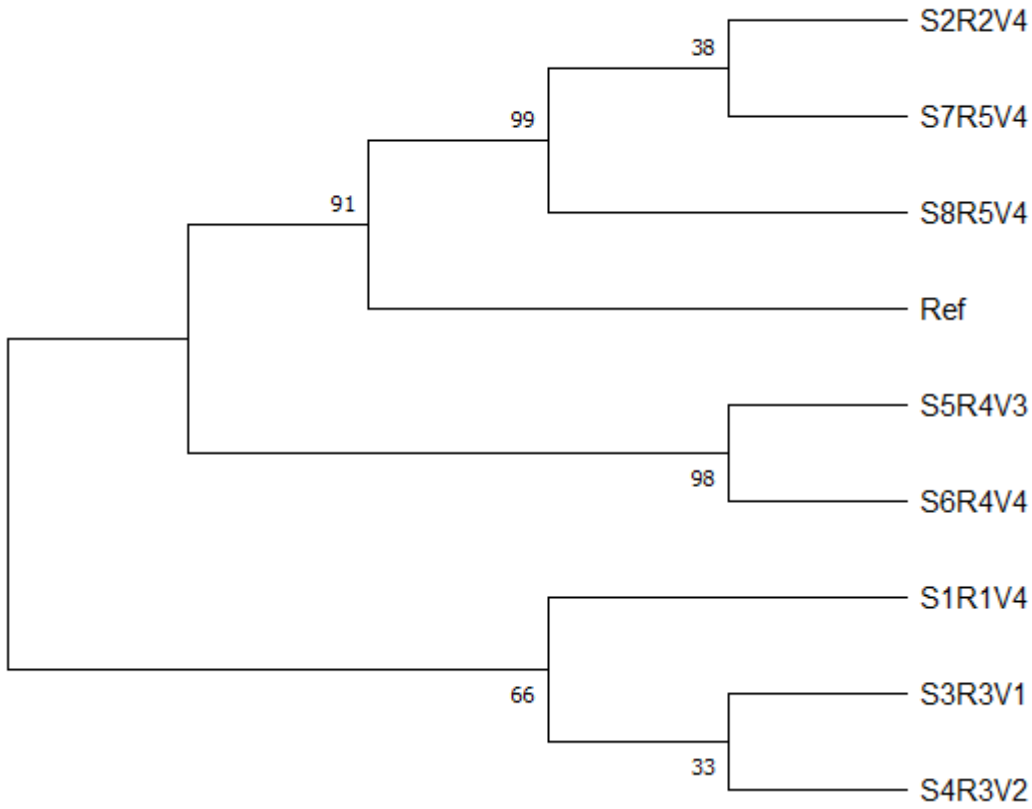


Figure S8. Maximum likelihood tree of *Lac 8* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

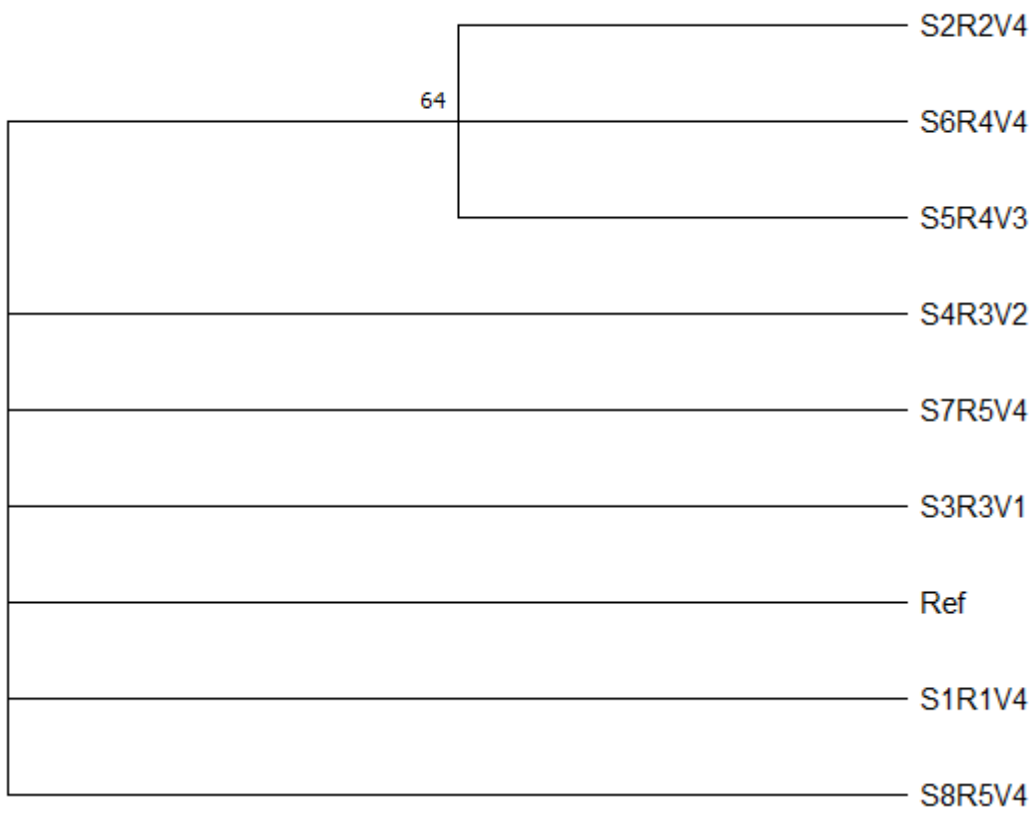


Figure S9. Maximum likelihood tree of *Lac 9* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

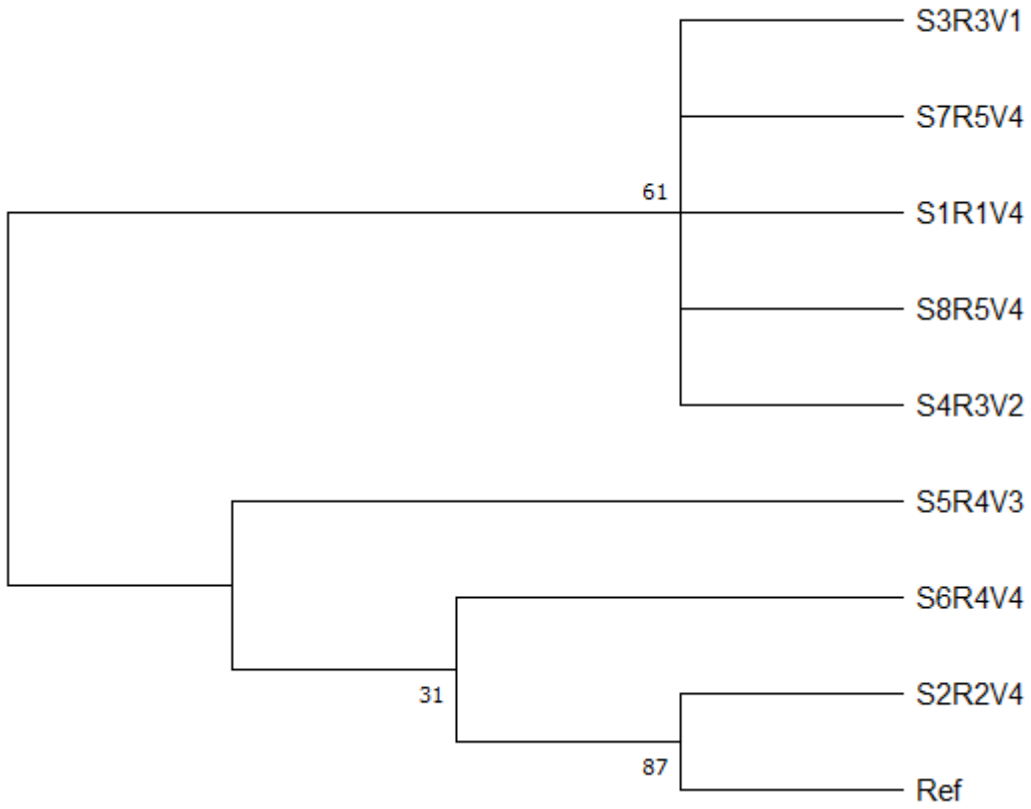


Figure S10. Maximum likelihood tree of *Lac 10* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

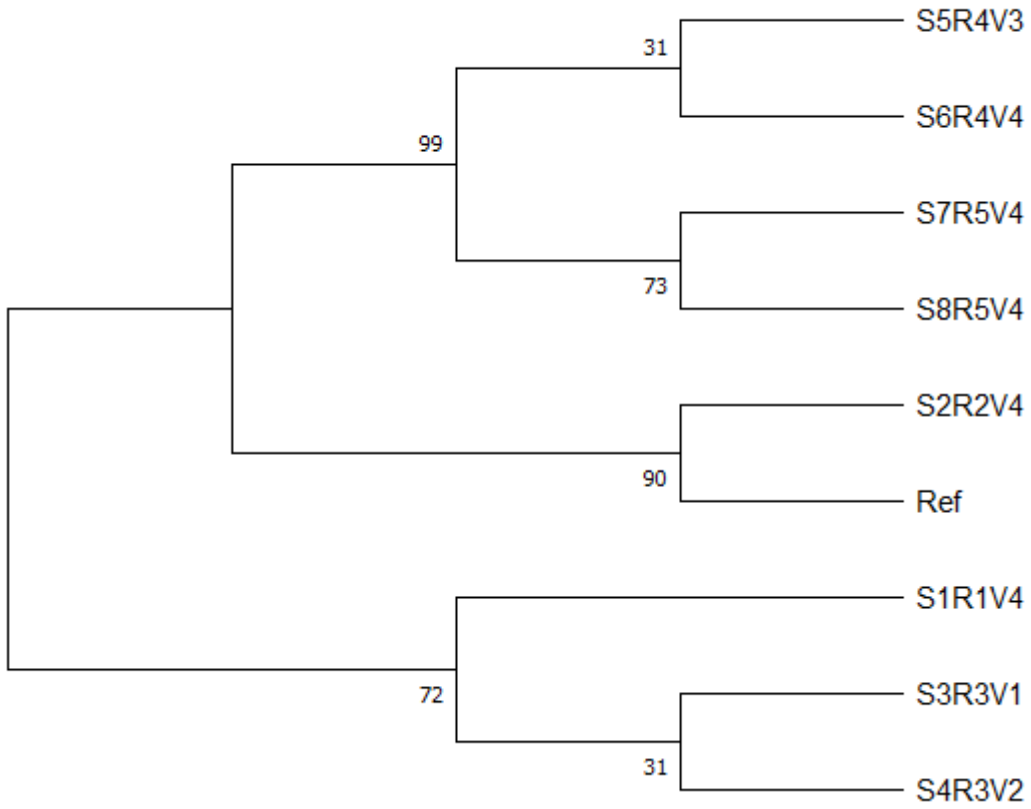


Figure S11. Maximum likelihood tree of *Lac 11* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

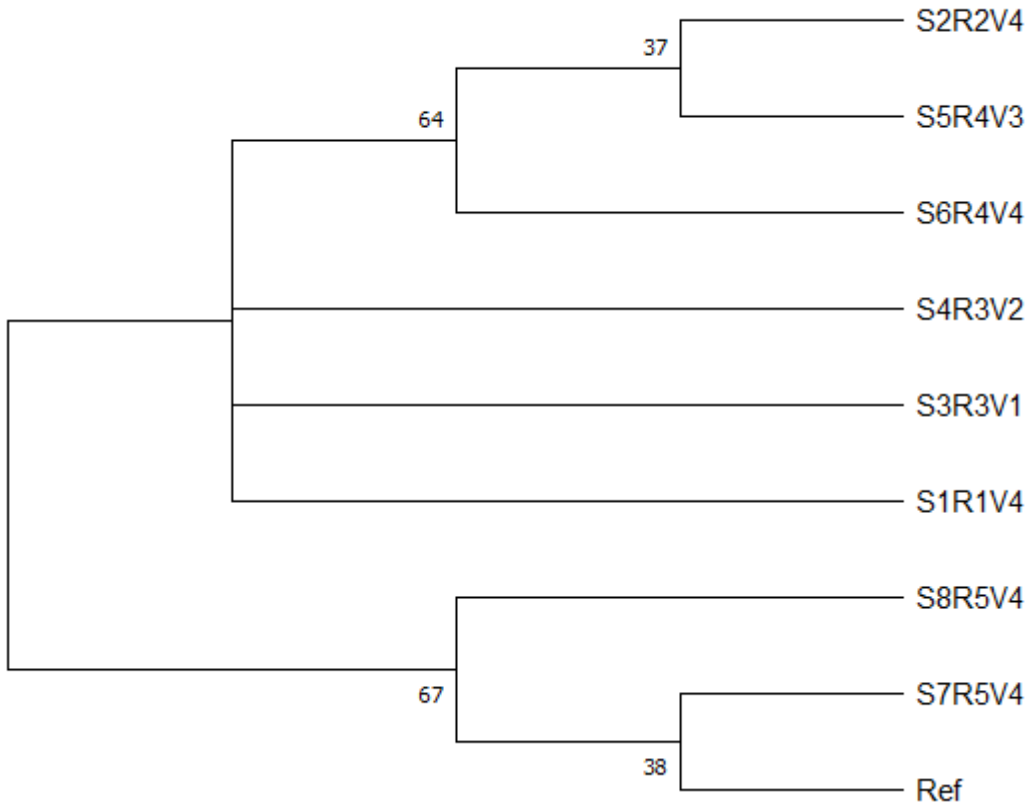


Figure S12. Maximum likelihood tree of *Lac 12A* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

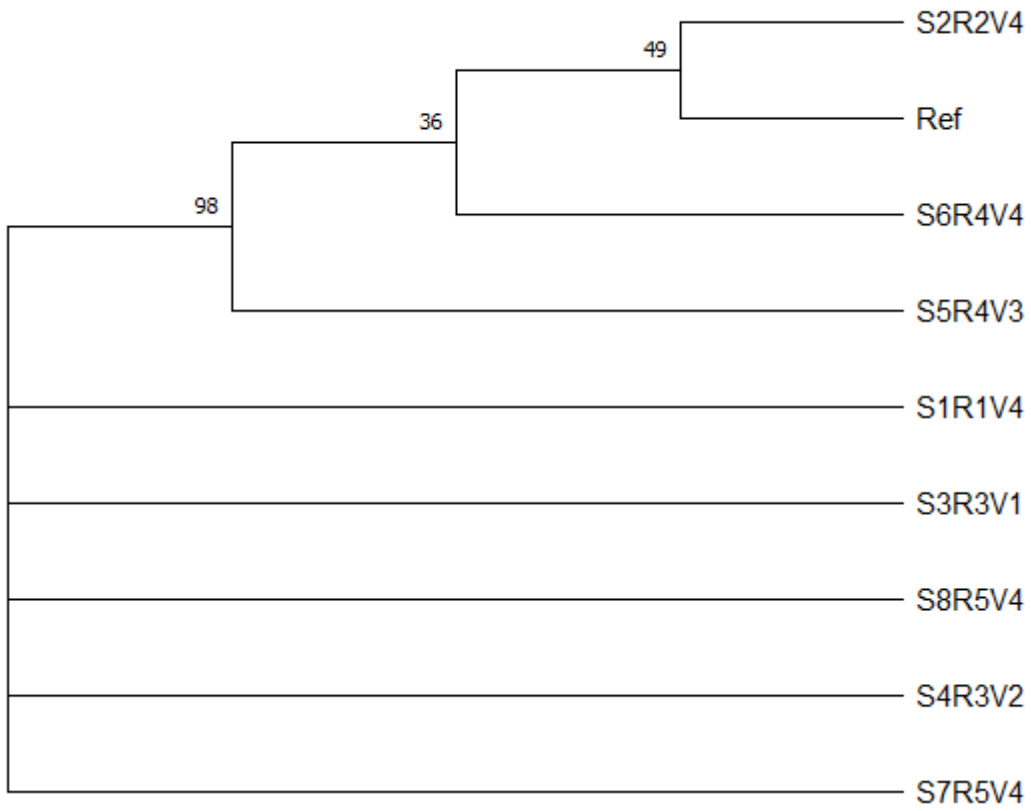


Figure S13. Maximum likelihood tree of *Lac 12B* Gene sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

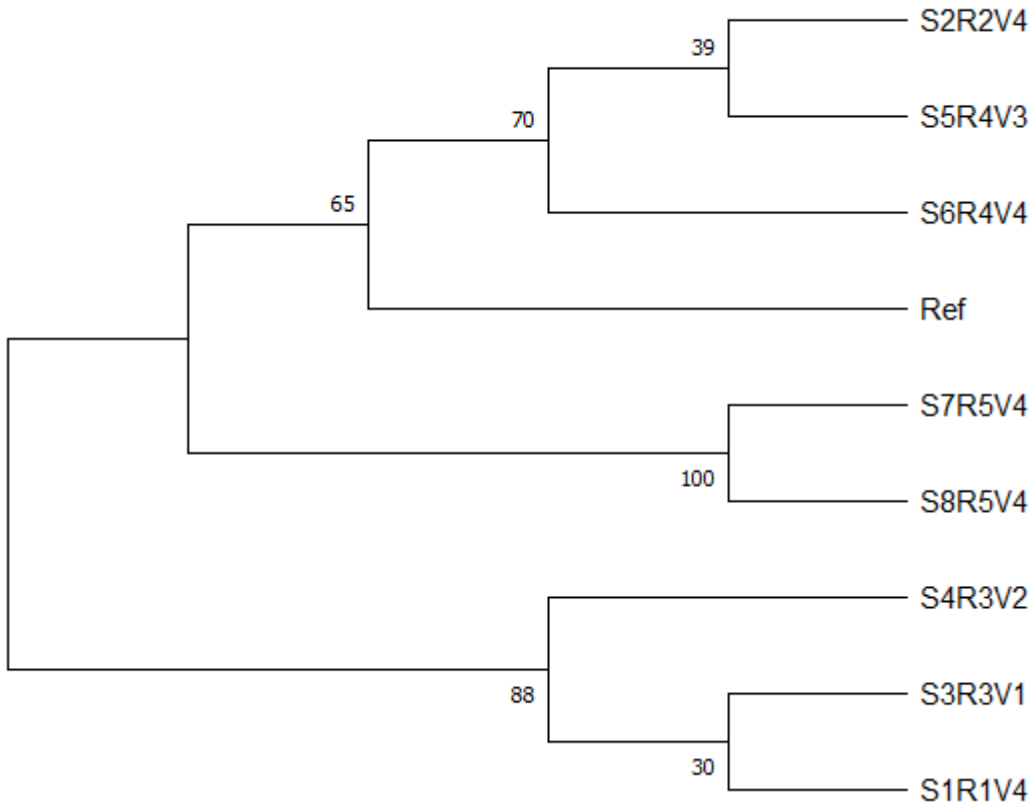


Figure S14. Maximum likelihood tree of *Lac 13* sequences of *Botrytis cinerea* combined and compared for every strain. The strains selected were from different regions and vintages. Bootstrap values were calculated from 1000 iterations and are displayed in %.

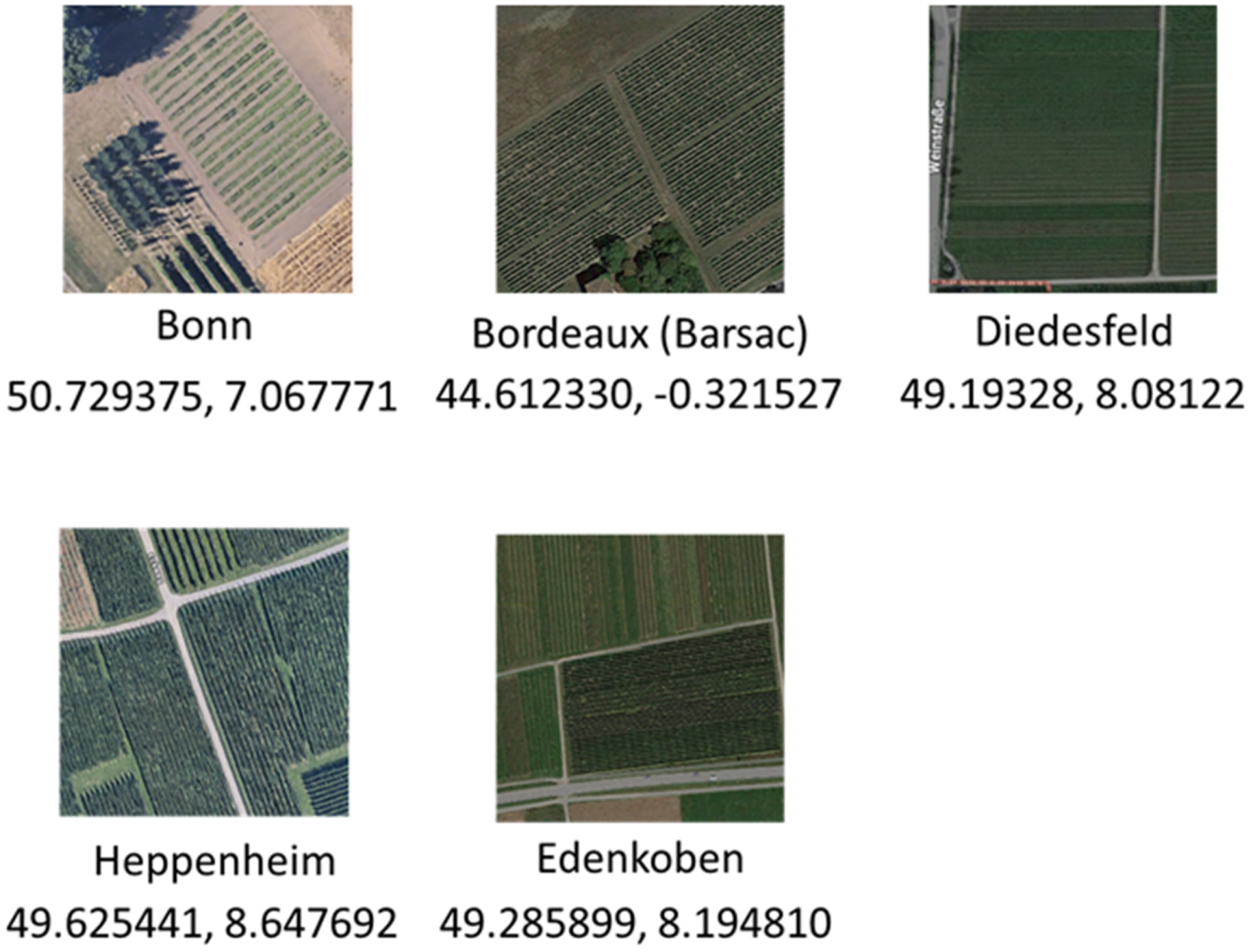


Figure S15. Satellite images of the collection sites. The images do not represent the vineyard at the collection time.