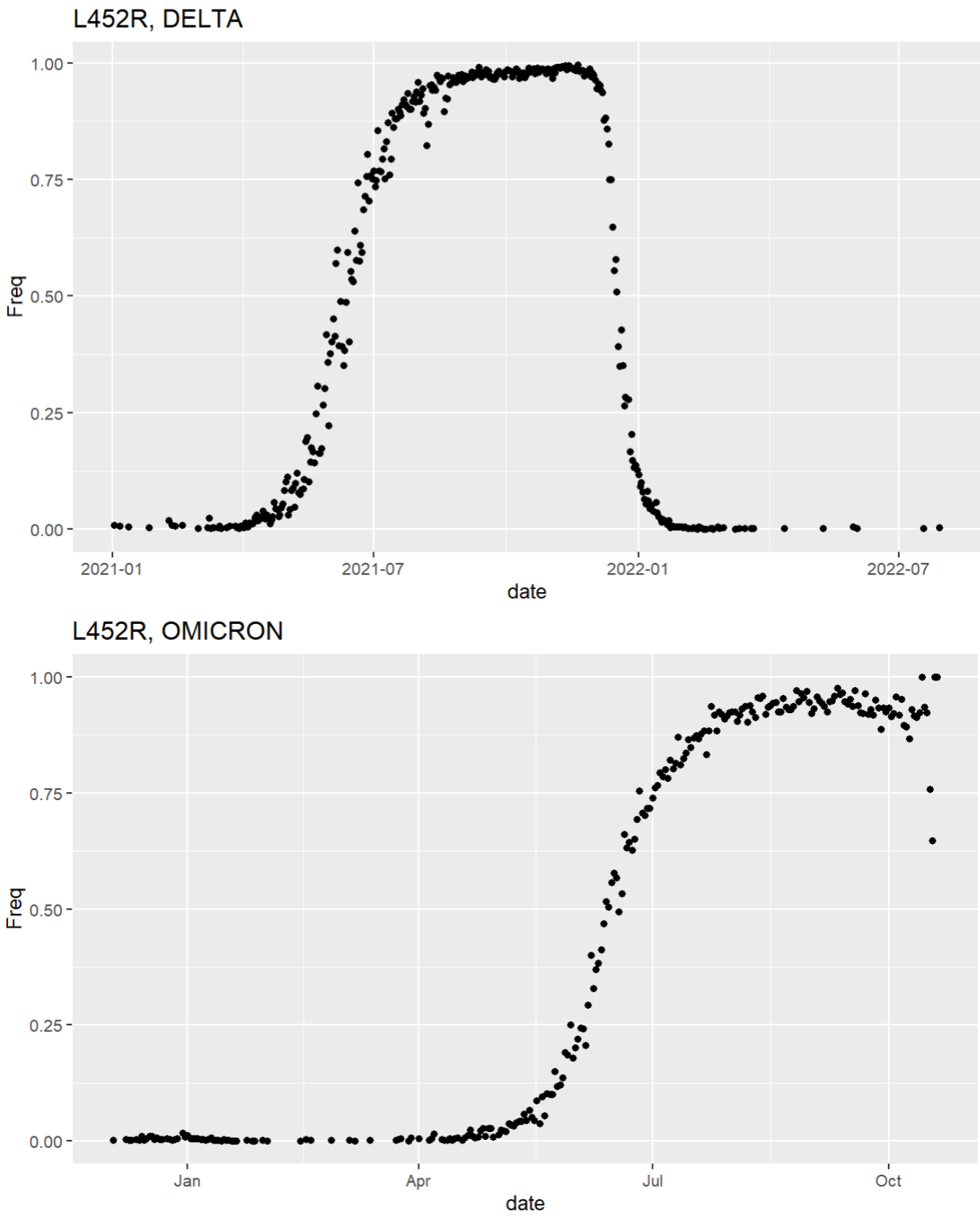
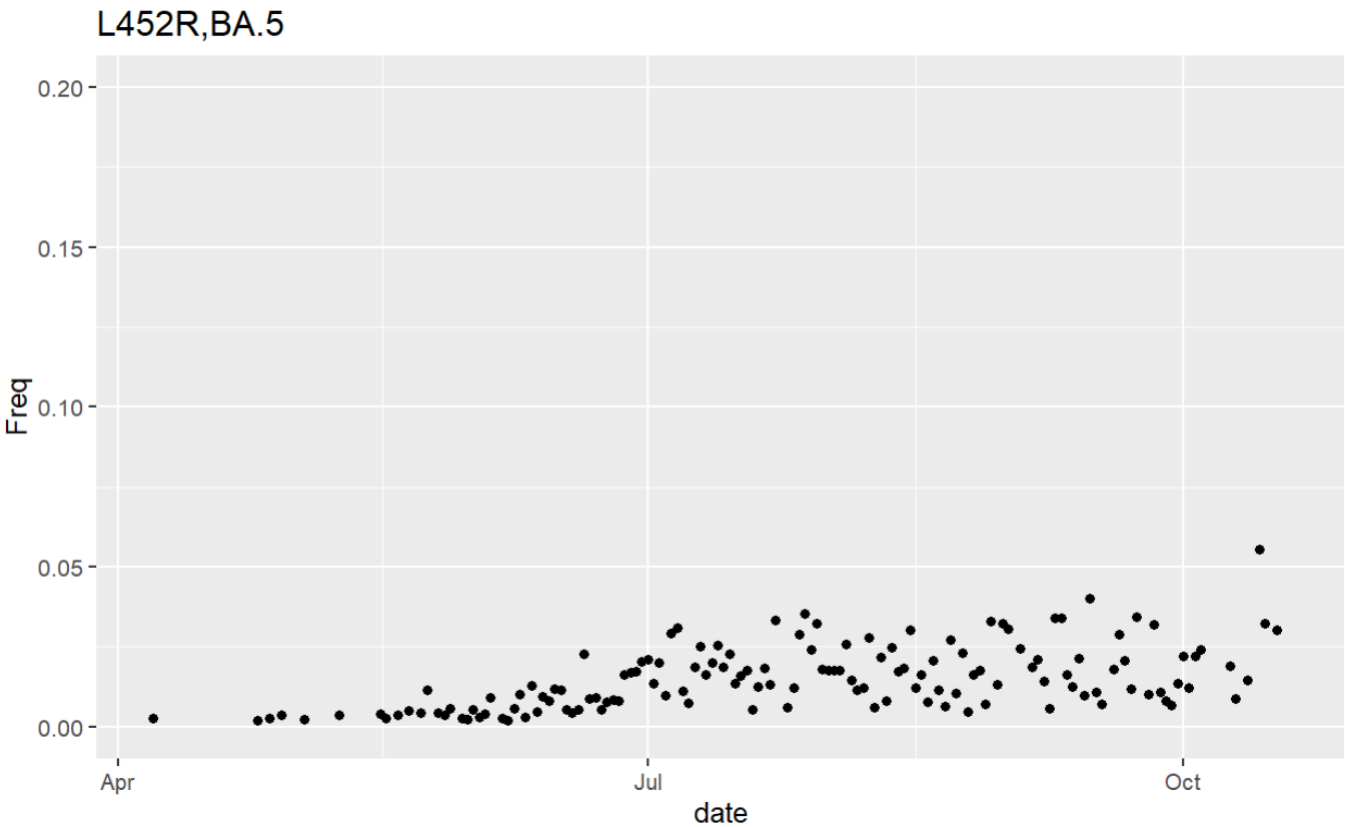
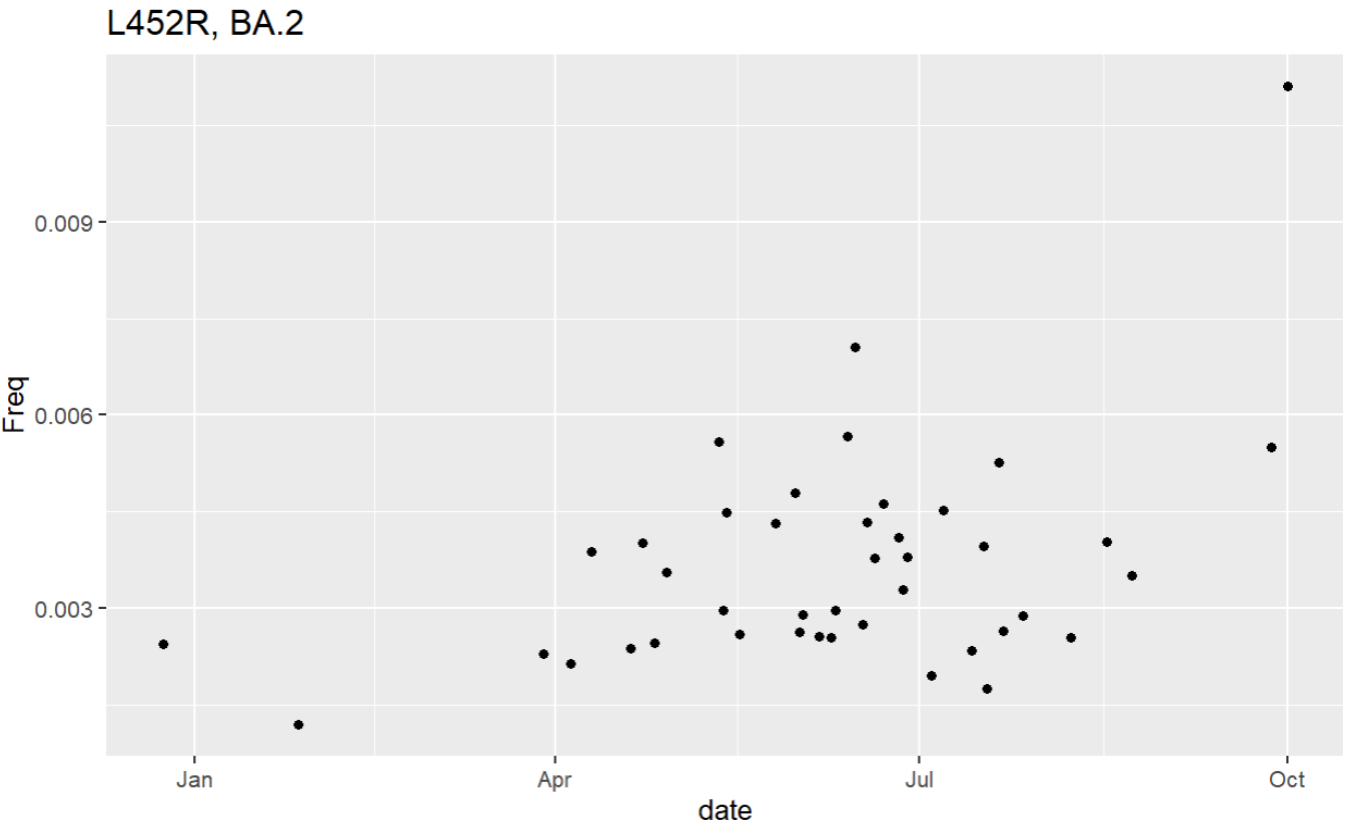


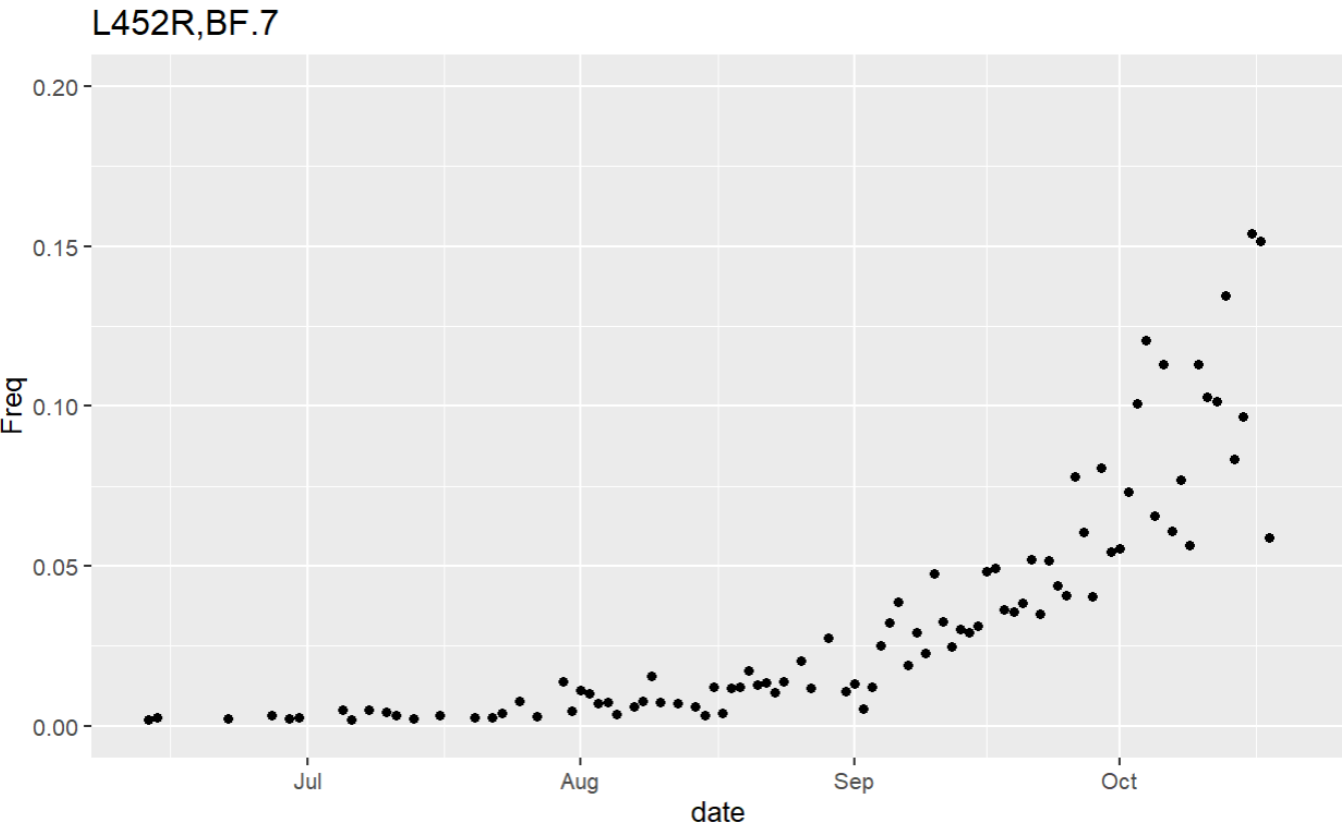
Week 11

Update the data before

1. L452R







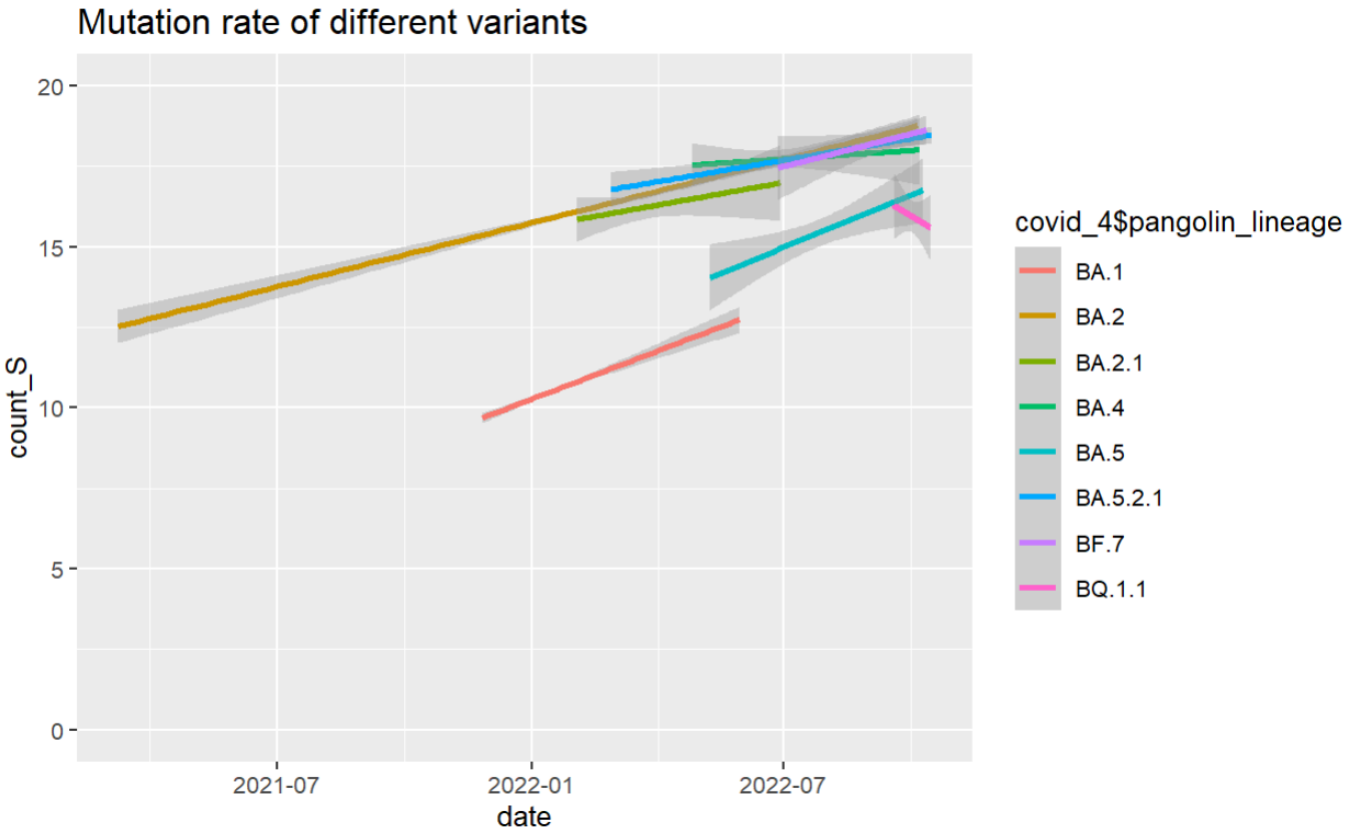
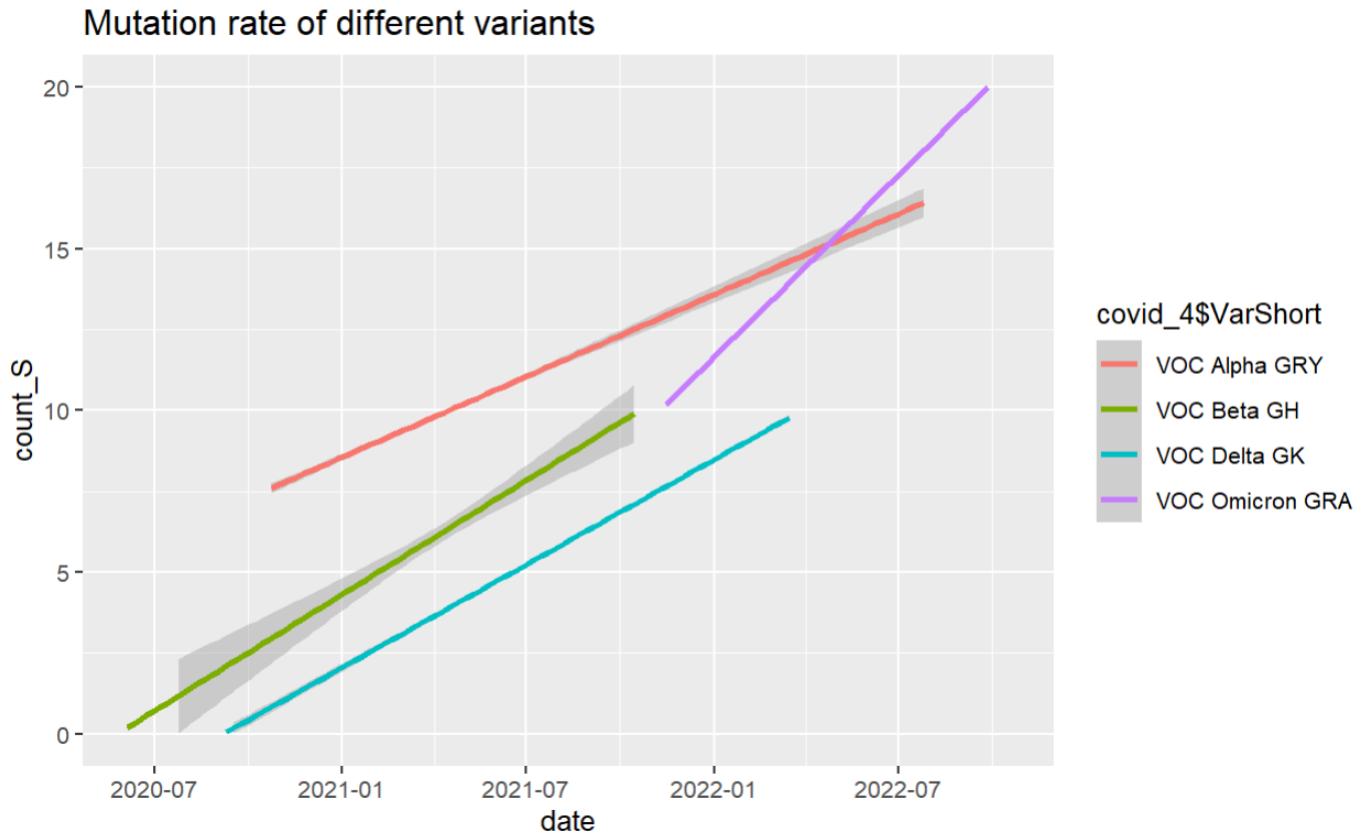
2. PrepViralLineageAmongInfection

Date: after 2022-09-01

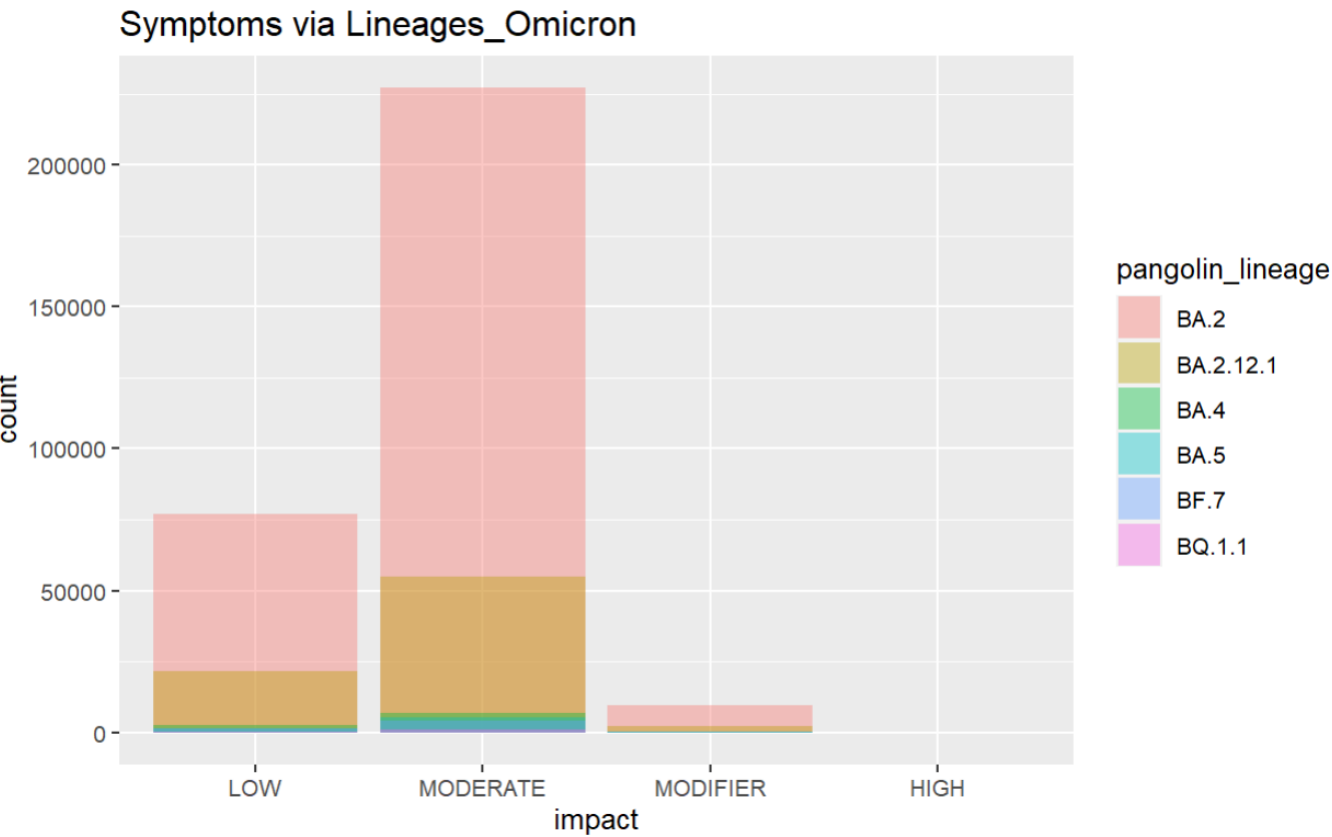
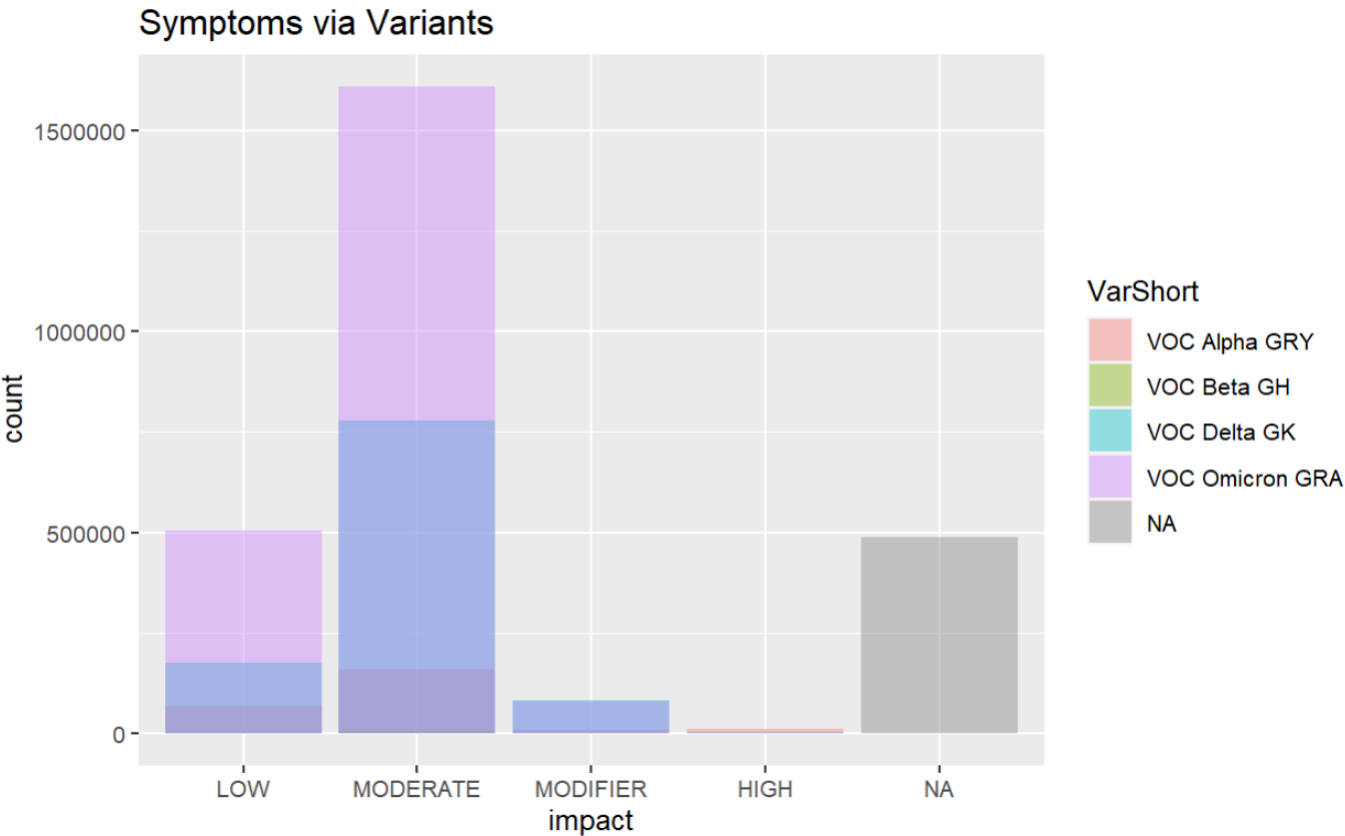


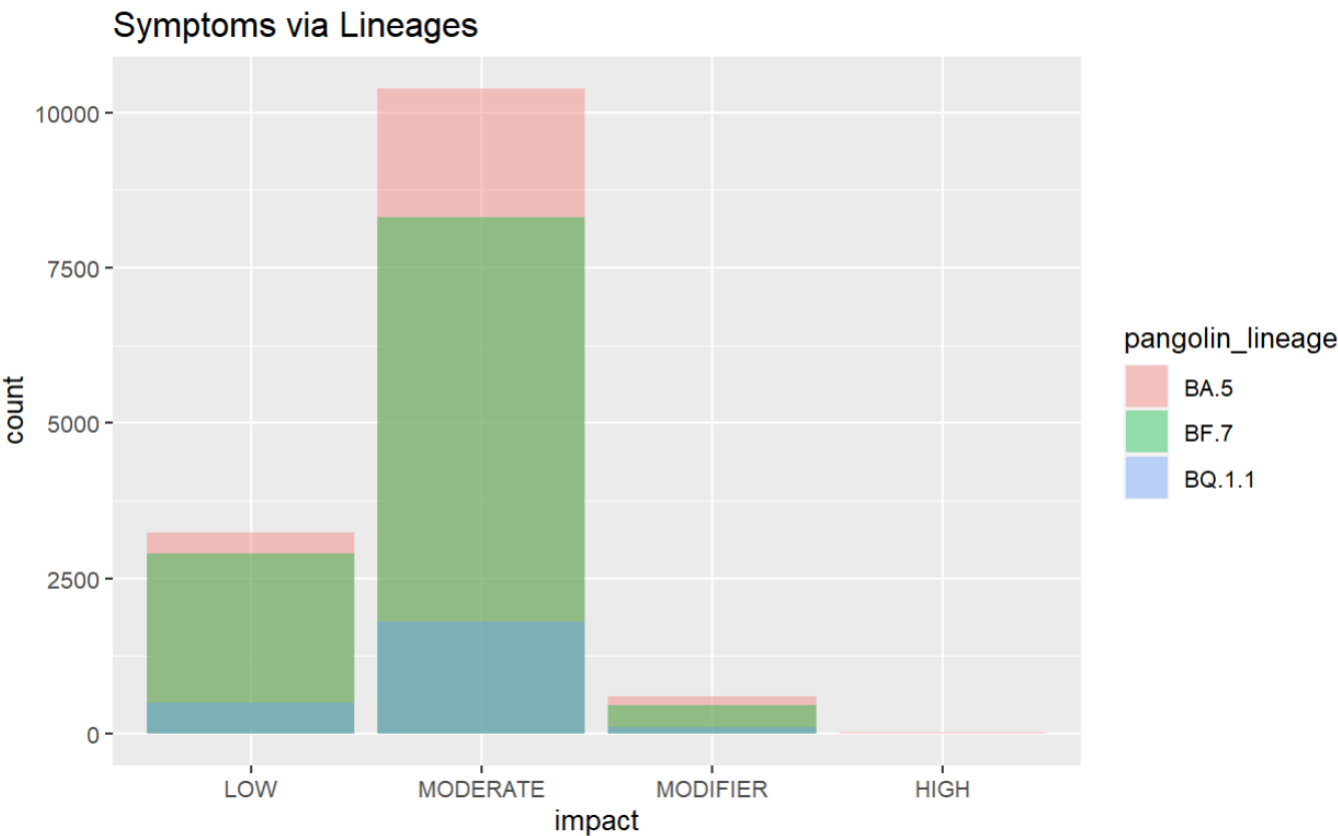
3. Mutation rate of different *

$y = XW + b$



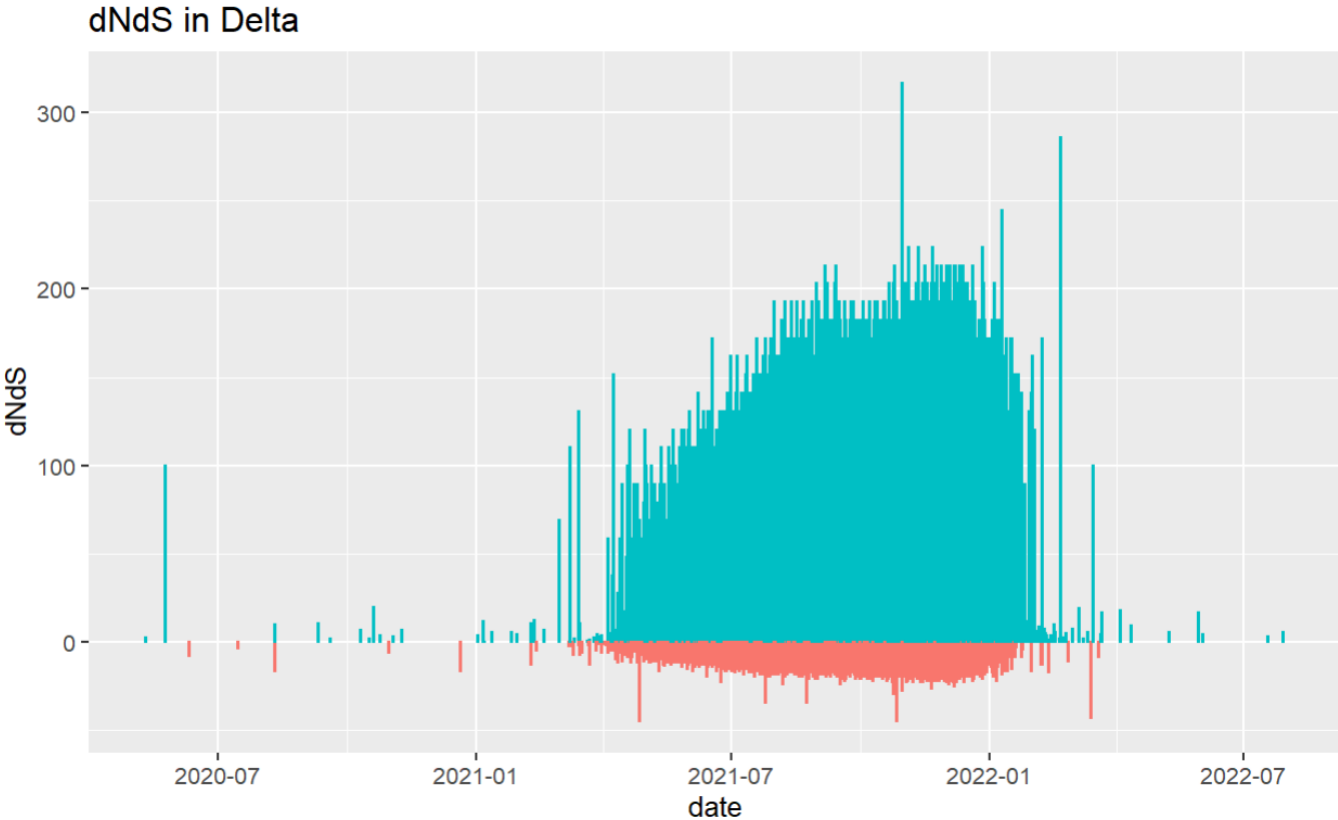
4. Symptoms via *



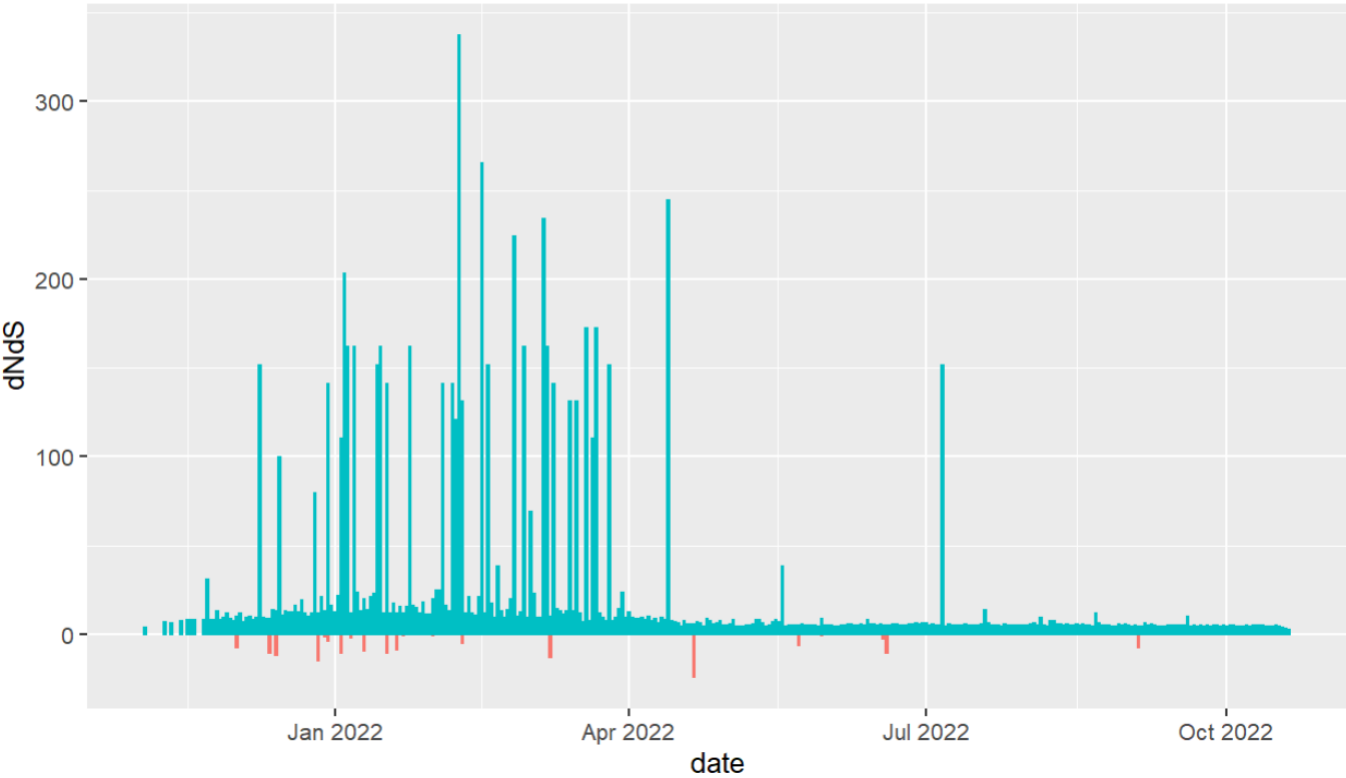


5. dNdS by date

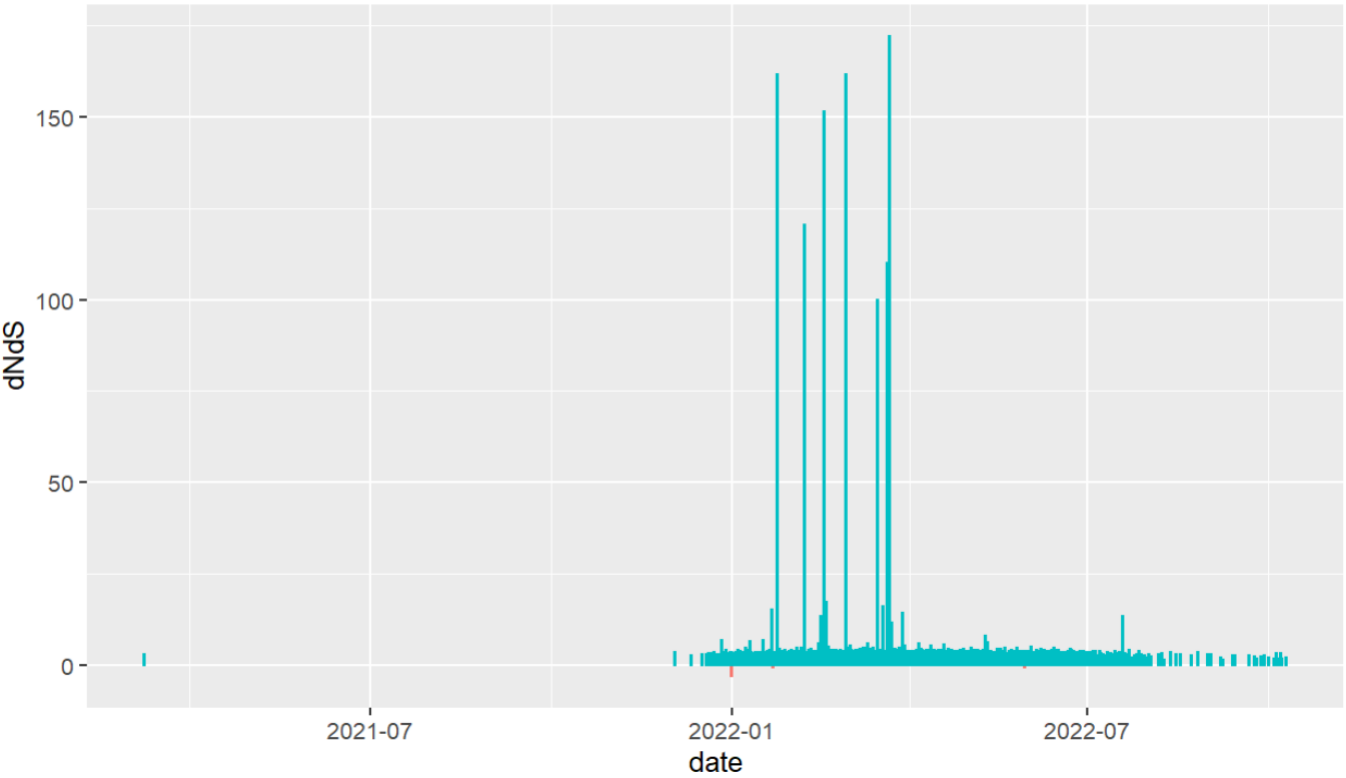
$$dNdS = \frac{\text{NumN} - \text{NumN}_{\beta}}{\text{NumS} - \text{NumS}_{\beta}}$$



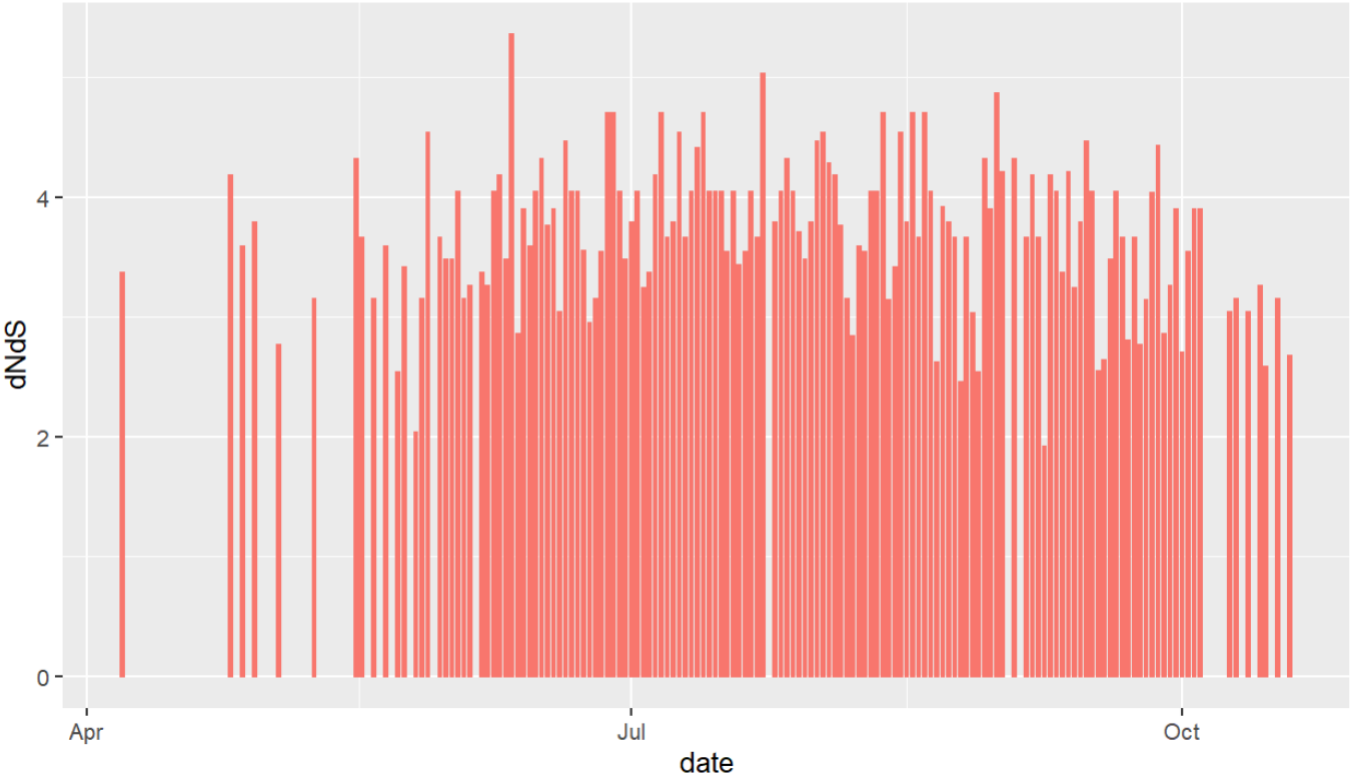
dNdS in Omicron



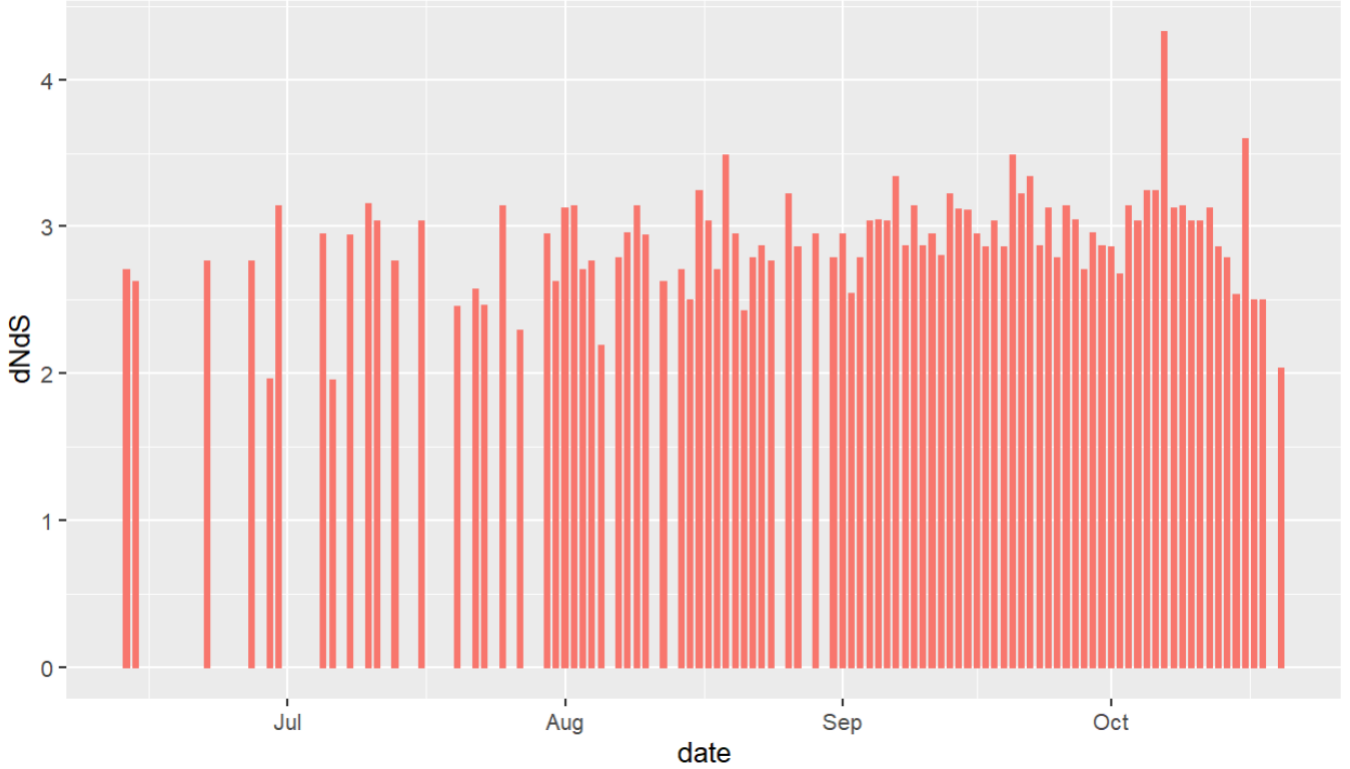
dNdS in BA.2

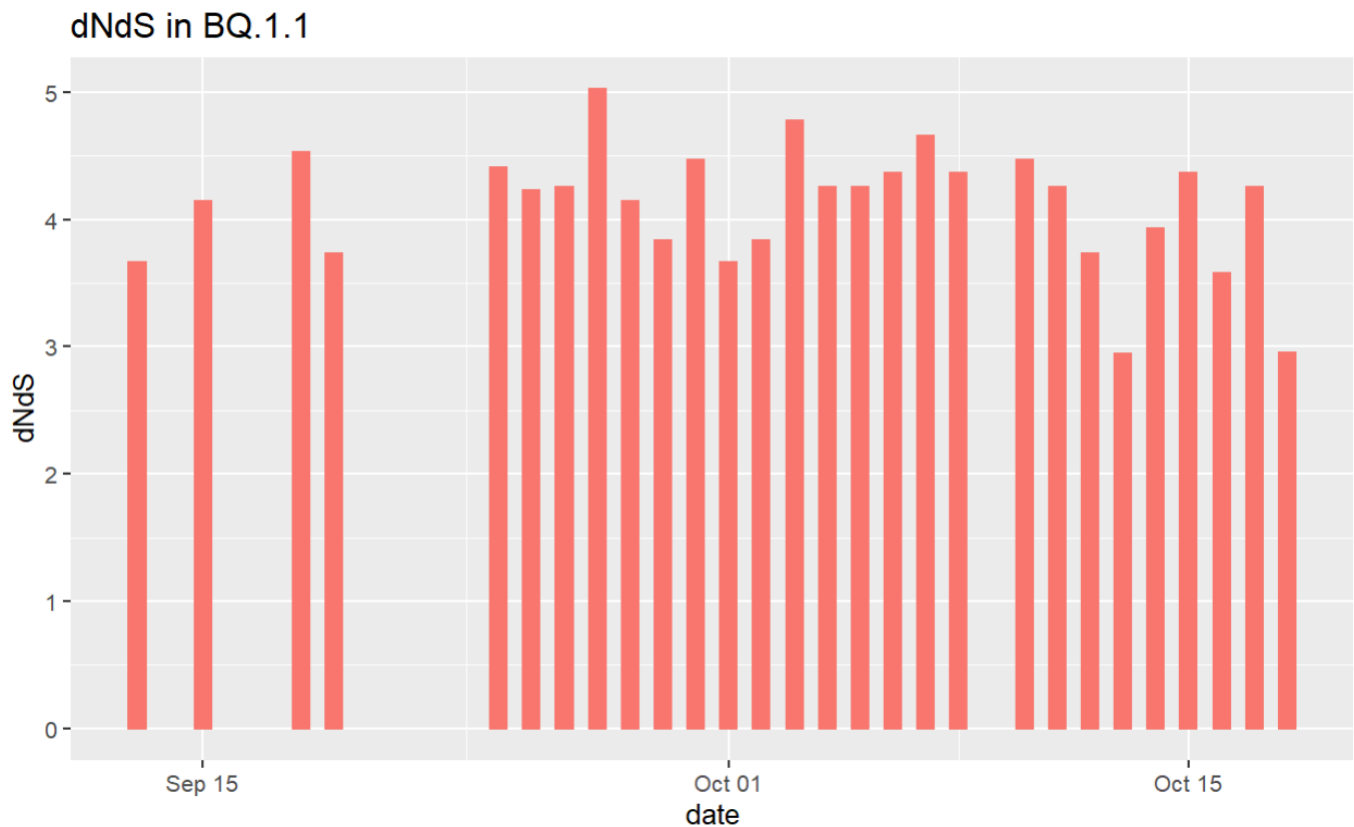


dNdS in BA.5

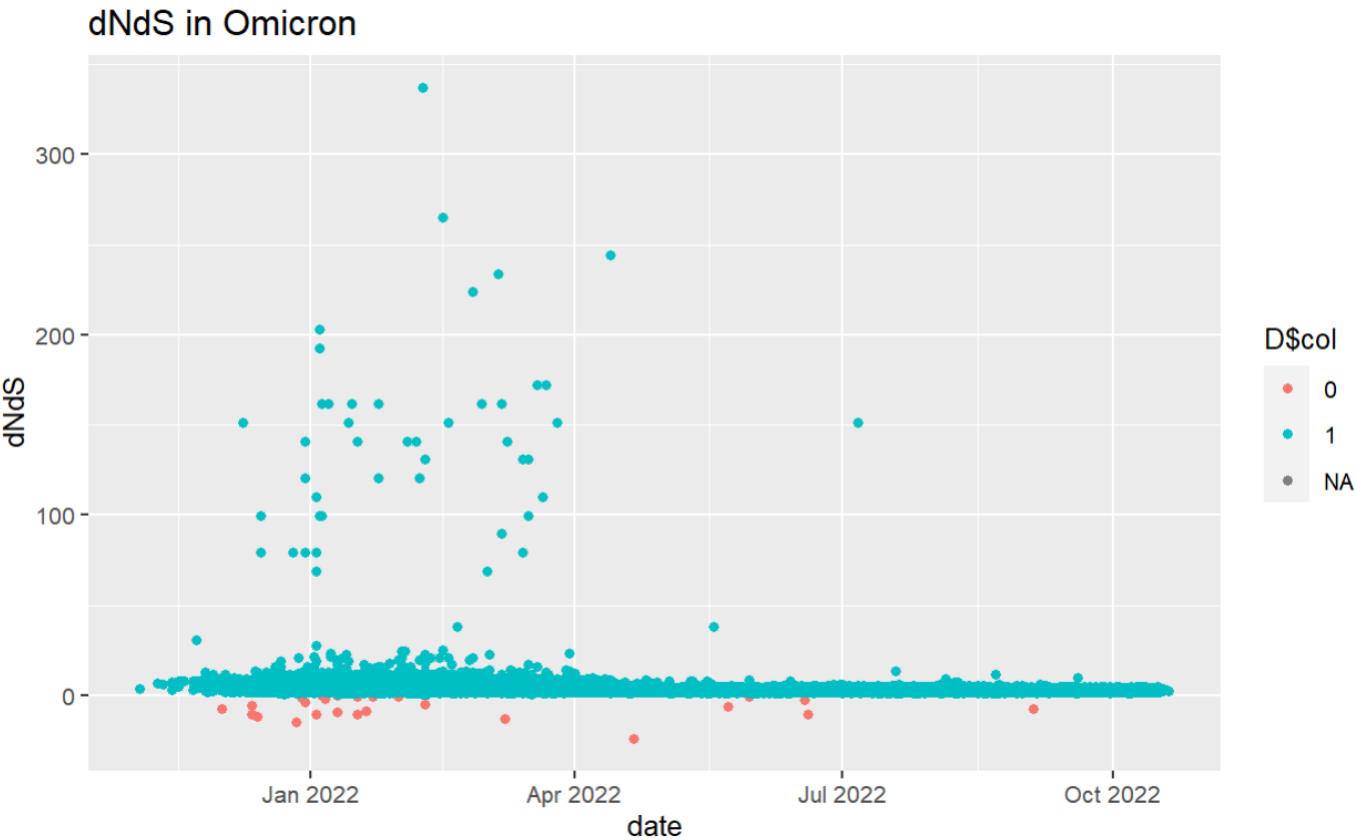
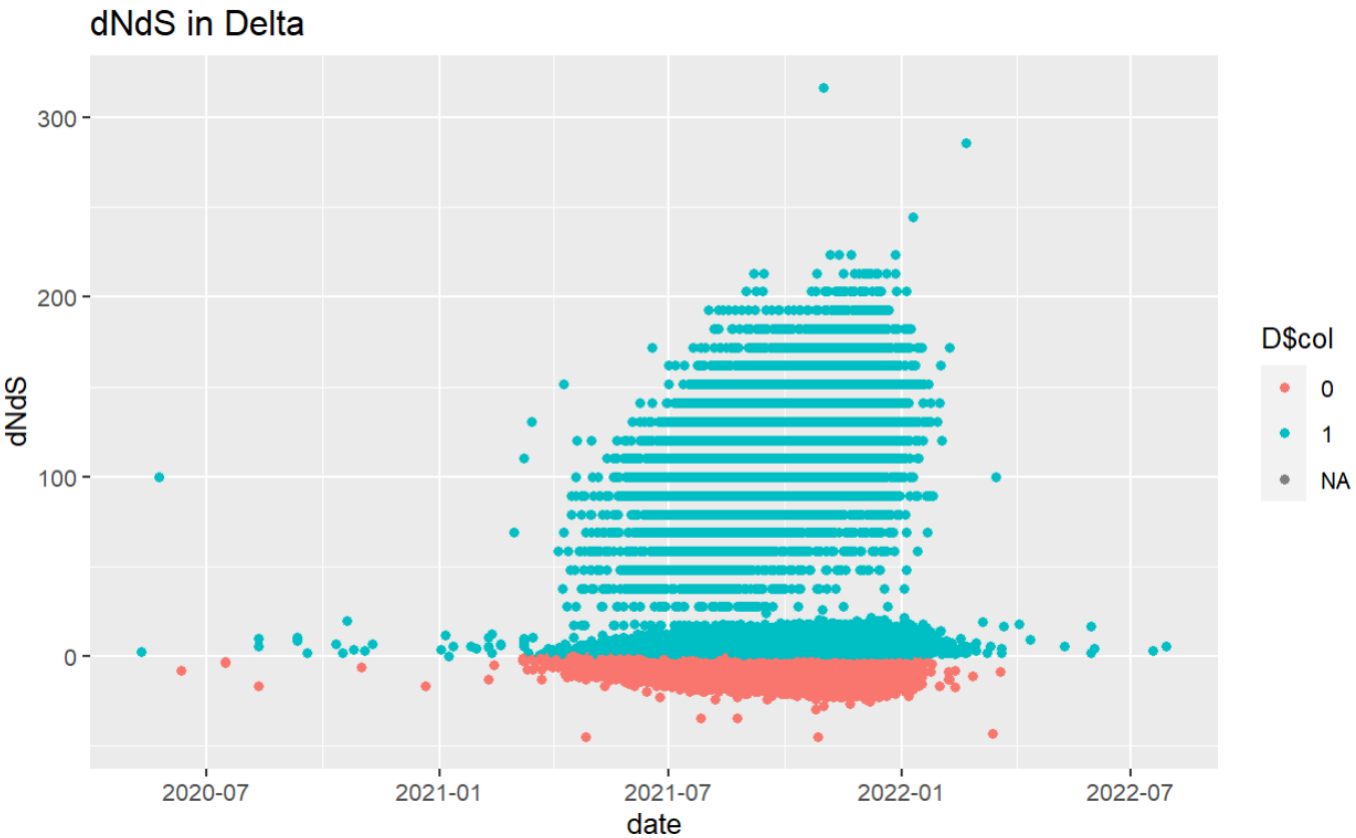


dNdS in BF.7





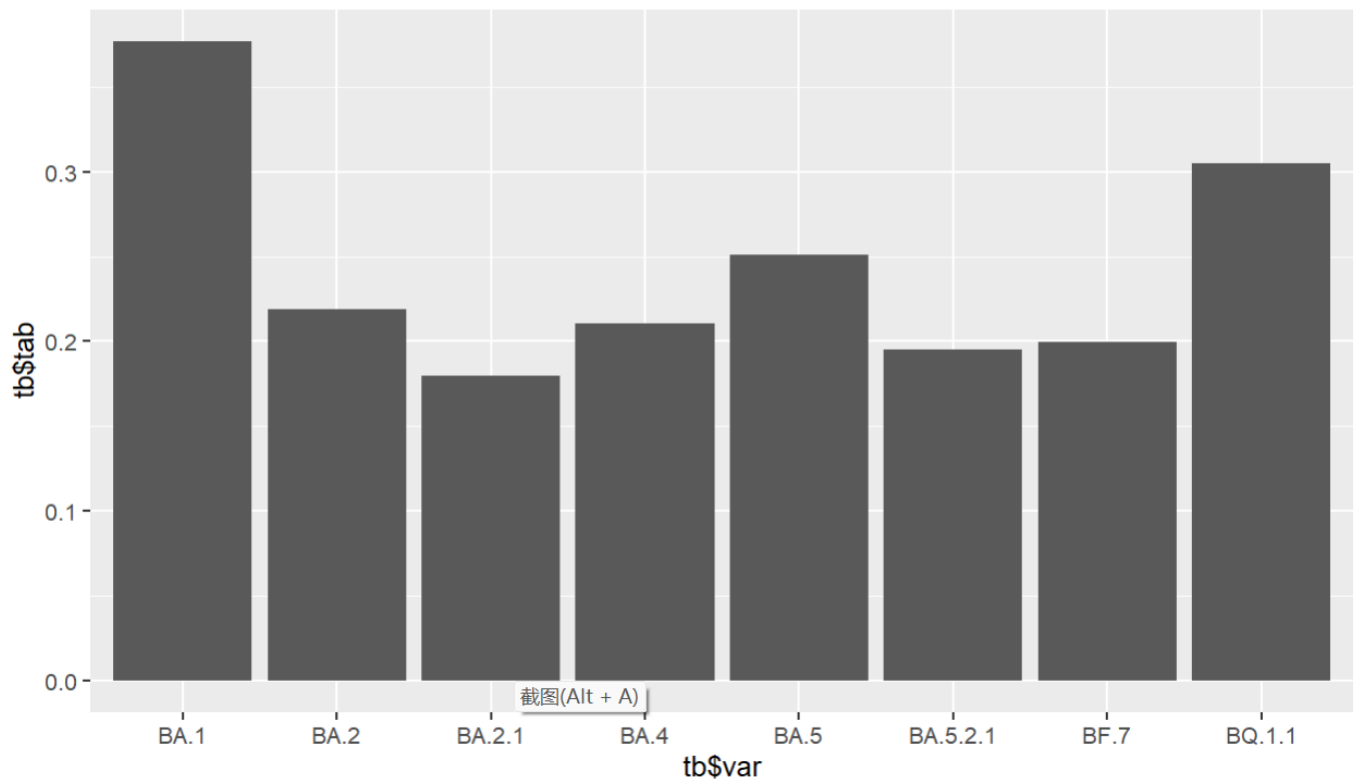
We can infer that dNdS in most proportion of Delta are much higher than those of Omicron, while in Delta there are also more with negative value, meaning $dnds_delta$ smaller than $dnds_beta$. **While a strong stratification can be seen in point plot of Delta**



rdNdS comparing to Delta

$$\text{rdNdS} = \frac{\text{dNdS}_L}{\text{dNdS}_\Delta}$$

rdNdS: lineages / Delta



Next

1. How to improve on dNdS analysis?

In articles I read, they just used dnds and MK test, with checking p-value(by which test?).

Other than this, I don't have idea. Can I implement it with neural network or machine learning?

2. Quantify on others?