

## Results - B.1.1.7, “UK variant”

14/8/2021

### Phylogeographic mapping

The analyses take a dated phylogeny exported from NextStrain as a starting point for quantifying imports and local transmission of Sars-CoV-2 B.1.1.7 in Norway. Each isolate is assigned to one of two binary categories: “Norway” or “Rest of the world (RoW)”. The output is presented in Fig.1 and ancestral character estimation performed on the dated phylogeny.

**Fig. 1. B.1.1.7 phylogeny colored by binary geographic mappings (Norway, rest of the world [RoW]).** Quantifying introductions and local transmission

**Table 1. Estimated number of infections in Norway resulting from import and local transmission based on the phylogeographic analyses in Figure 1.**

	2.5%	50%	97.5%
Import	208.0000	216.0000	222.5250
Local transmission	1403.4750	1410.0000	1418.0000
Import / Total	0.1279	0.1328	0.1369

Next, we estimate the fraction of introductions relative to local transmission over time. In these and subsequent analyses it is important to keep detection lag into account (see <https://science.sciencemag.org/content/371/6530/708>). There will always be a delay between the introduction and detection, which varies from case to case. In the figures below, the last four weeks prior to the time of sampling of the most recent included isolate is shaded to indicate that estimates in this period is highly uncertain.

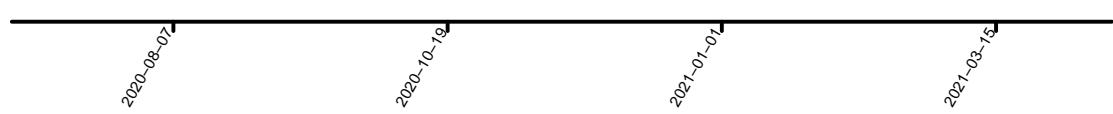
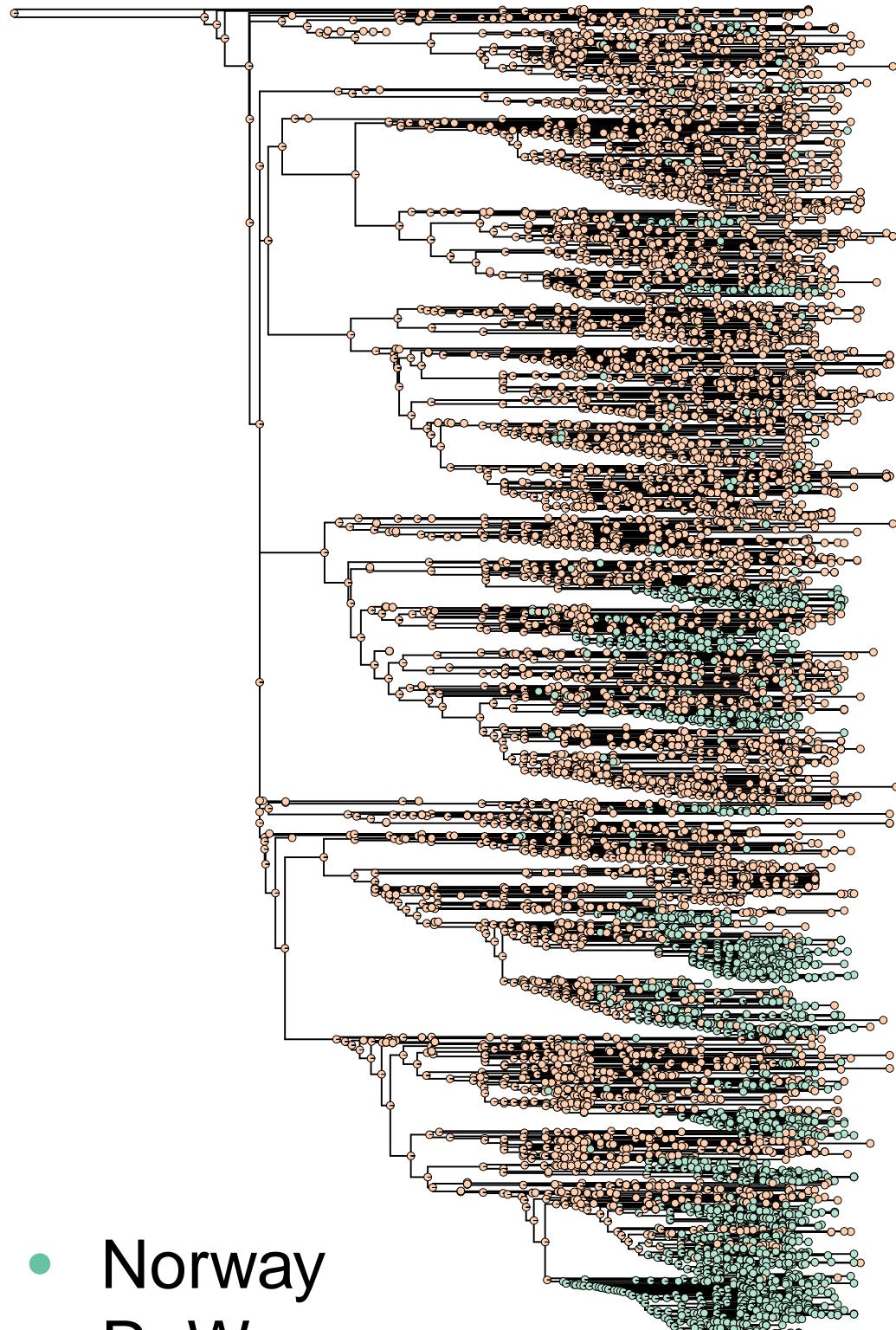
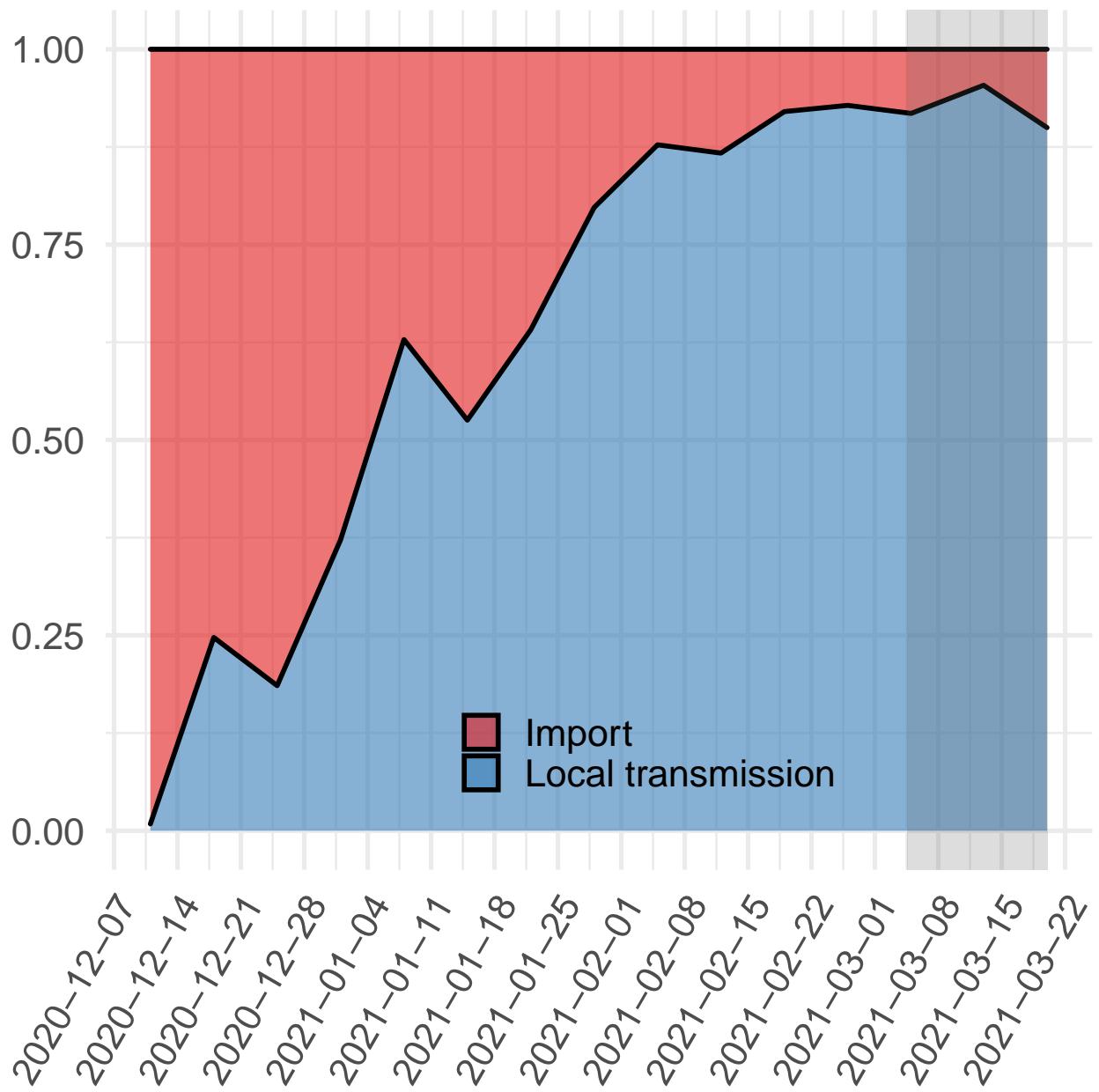
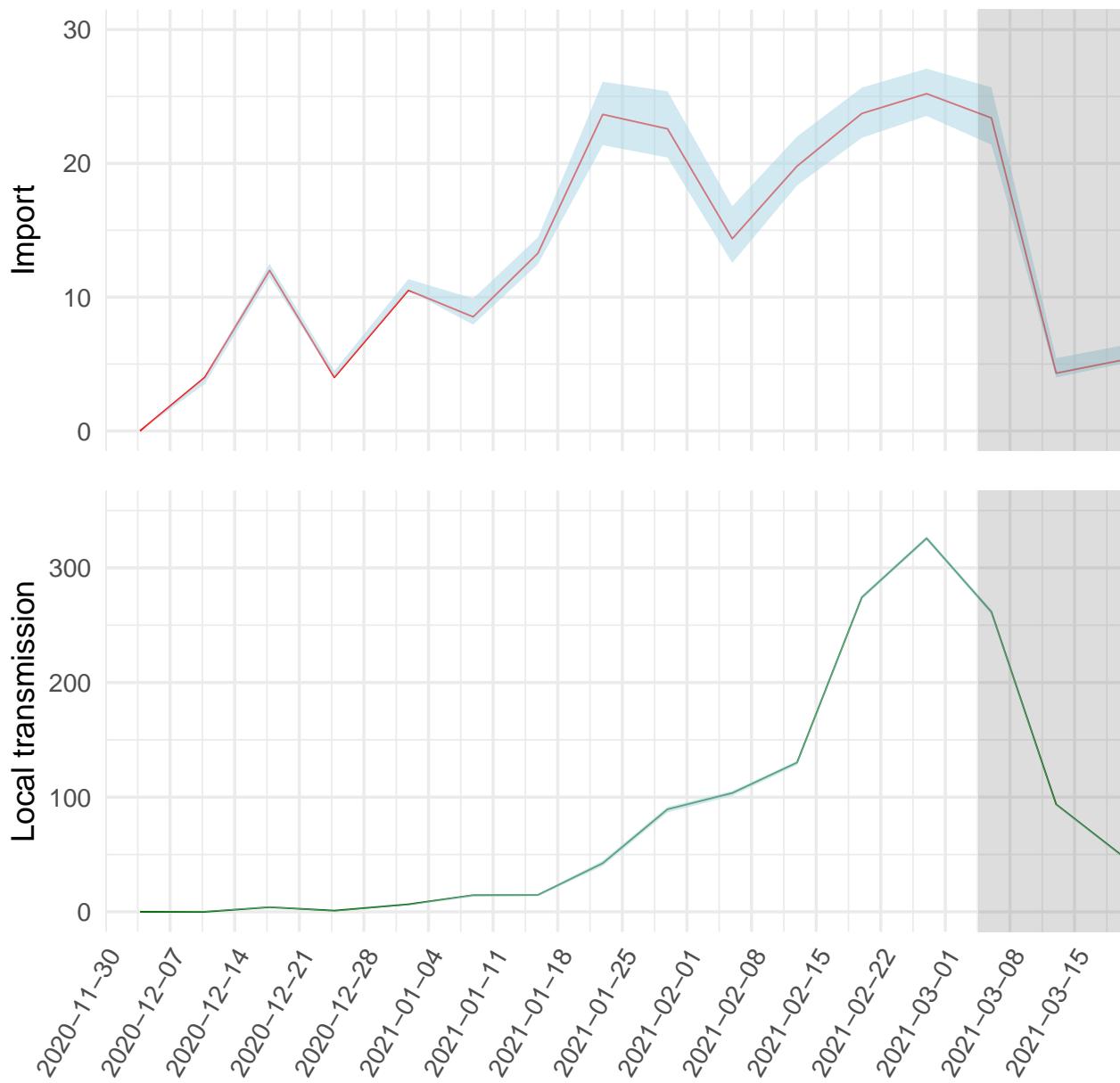


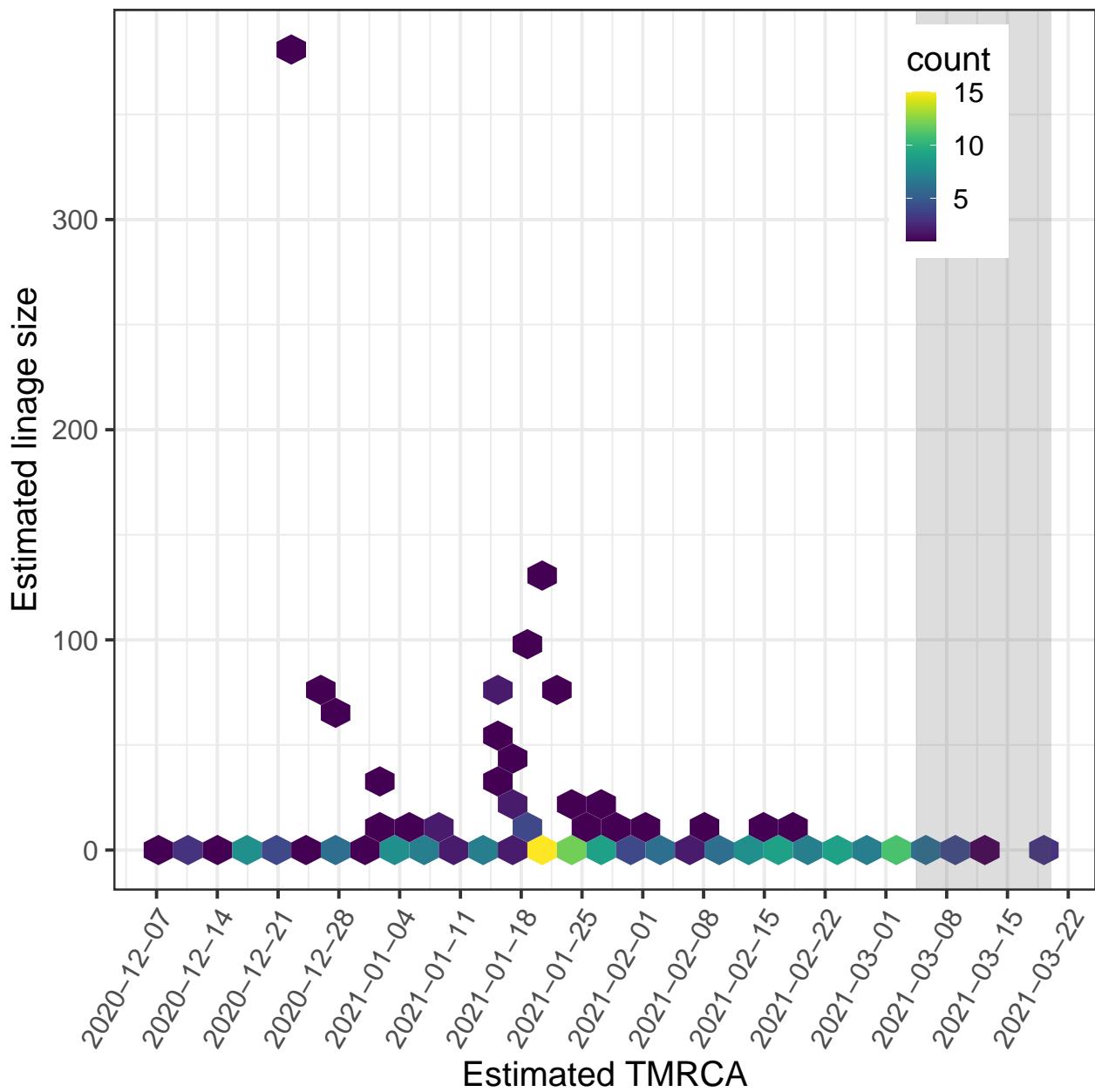
Figure 1: Test  
2



**Fig. 2. Relative quantification of infection source (new introduction / import vs local transmission).** The same output is visualized as absolute numbers in Fig. 3 below. It should be noted that absolute estimates will be significantly shaped by sampling density.



**Fig. 3. Absolute quantification of imports and local transmission events.** Perhaps the most interesting aspect of quantifying introductions, is to investigate the fate of individual inferred imports. Mandatory testing at the border and/or mandatory quarantines etc will obviously have a bearing on the fate of newly introduced infections from abroad. The plot below visualizes the number of infections in Norway resulting from each individual import over time, stratified by inferred TMRCA of each introduced lineage.



**Fig. 4.** Transmission lineage sizes as a function of time of introduction. “TMRCA” = time of most recent common ancestor.