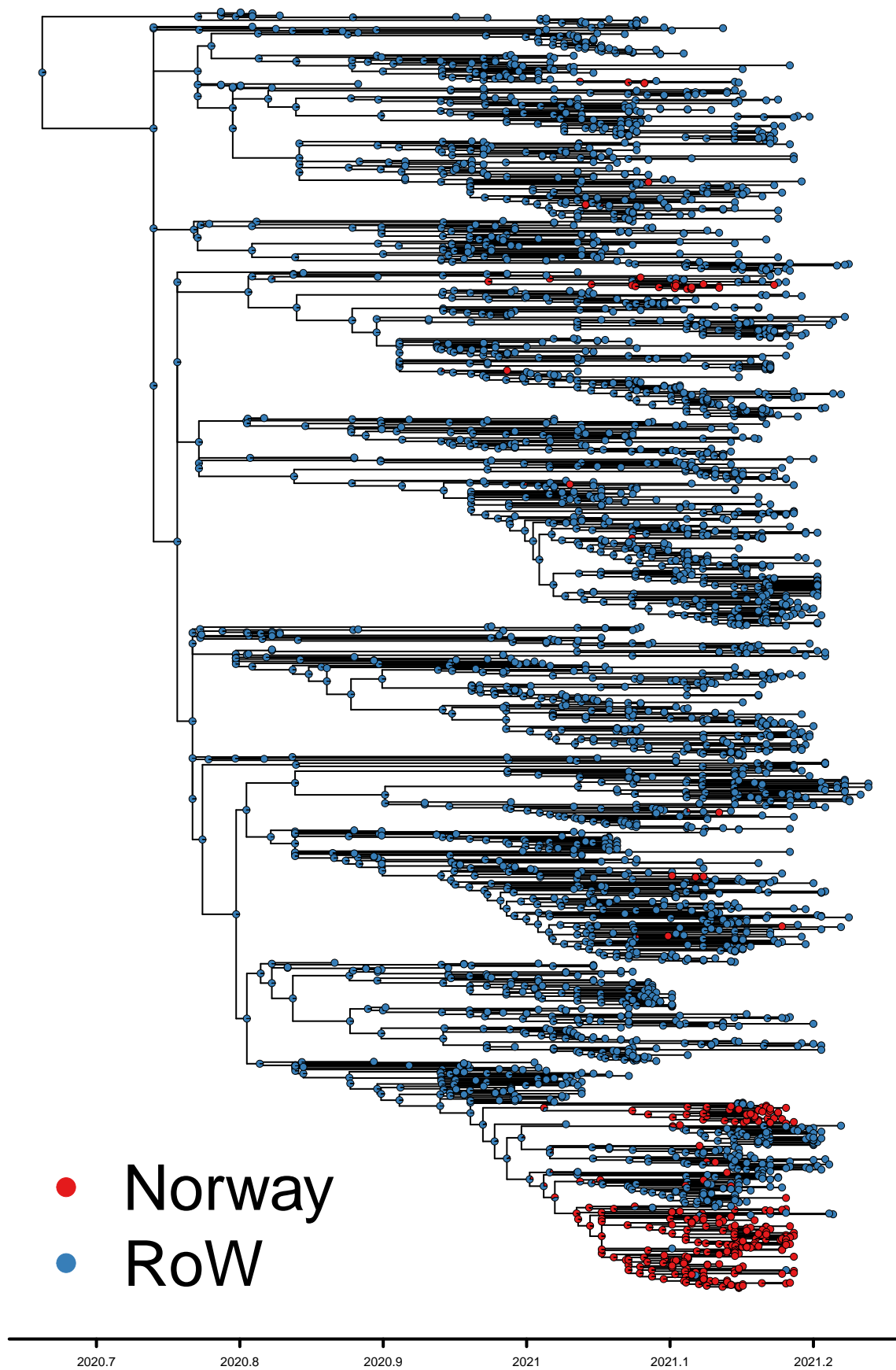


## Results - B.1.351, “South Africa variant”

4/8/2021

### Phylogeographic mapping

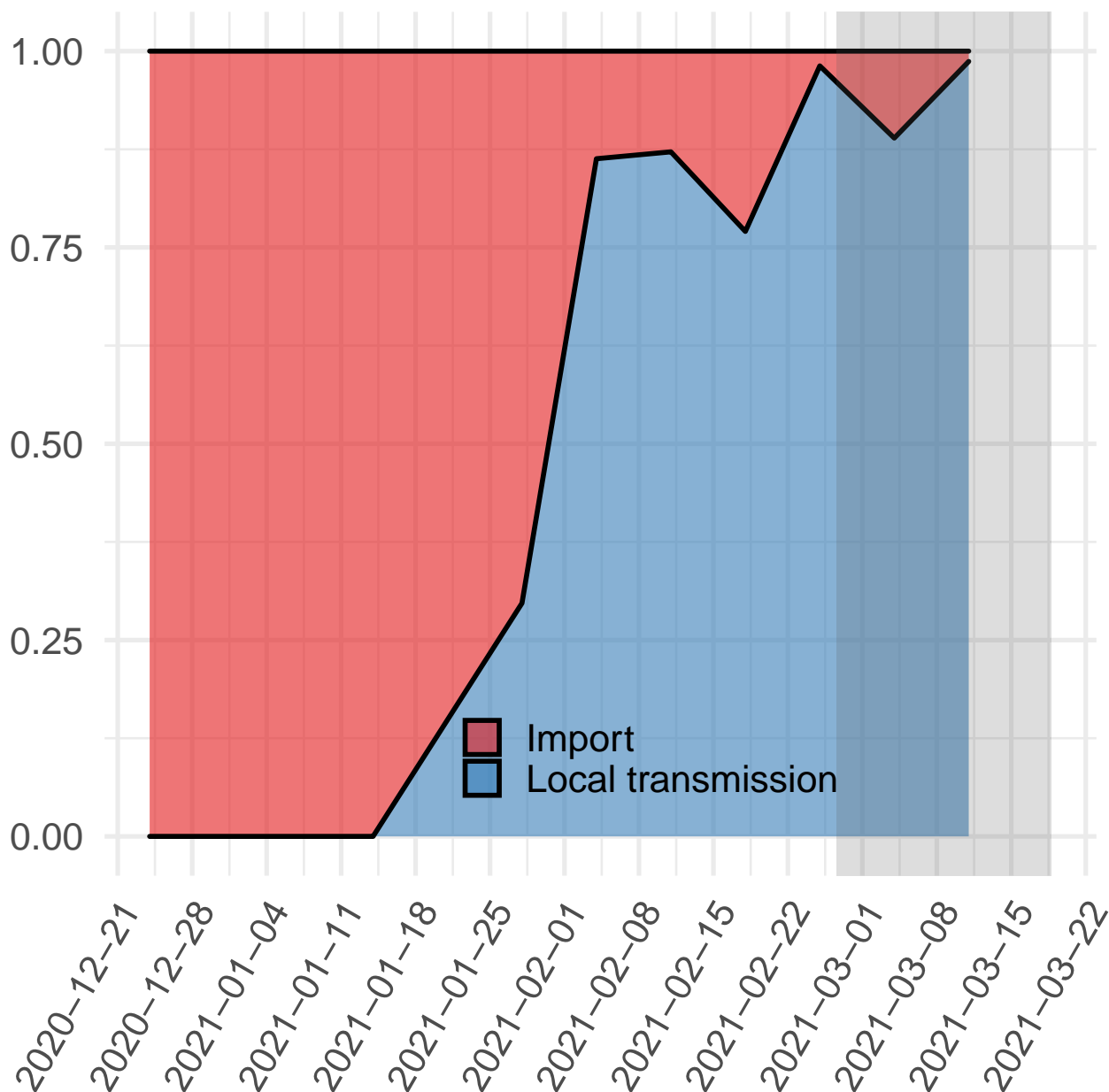
Ancestral character estimation was performed on a dated phylogeny exported from NextStrain. Each isolate was assigned to one of two binary categories: “Norway” or “Rest of the world (RoW)”. The output is presented in Fig.1.



**Fig. 1. B.1.351 phylogeny colored by binary geographic mappings (Norway, rest of the world [RoW]).** The number of Norwegian isolates resulting from local transmission vs introductions from abroad were estimated from the tree and is summarized in Table 1.

**Table 1. Estimated number of Norwegian infections that are caused by import and local transmission in geographically mapped phylogeny in Figure 1.**

	2.5%	50%	97.5%
Import	19.0000	20.0000	22.0000
Local transmission	132.0000	134.0000	135.0000
Import / Total	0.1234	0.1299	0.1429



**Fig. 2. Forhold mellom import og lokaltransmisjon av B.1.351 over tid i Norge.** OBS, ingen sekvenserte

isolater som er nyere enn 10. mars.

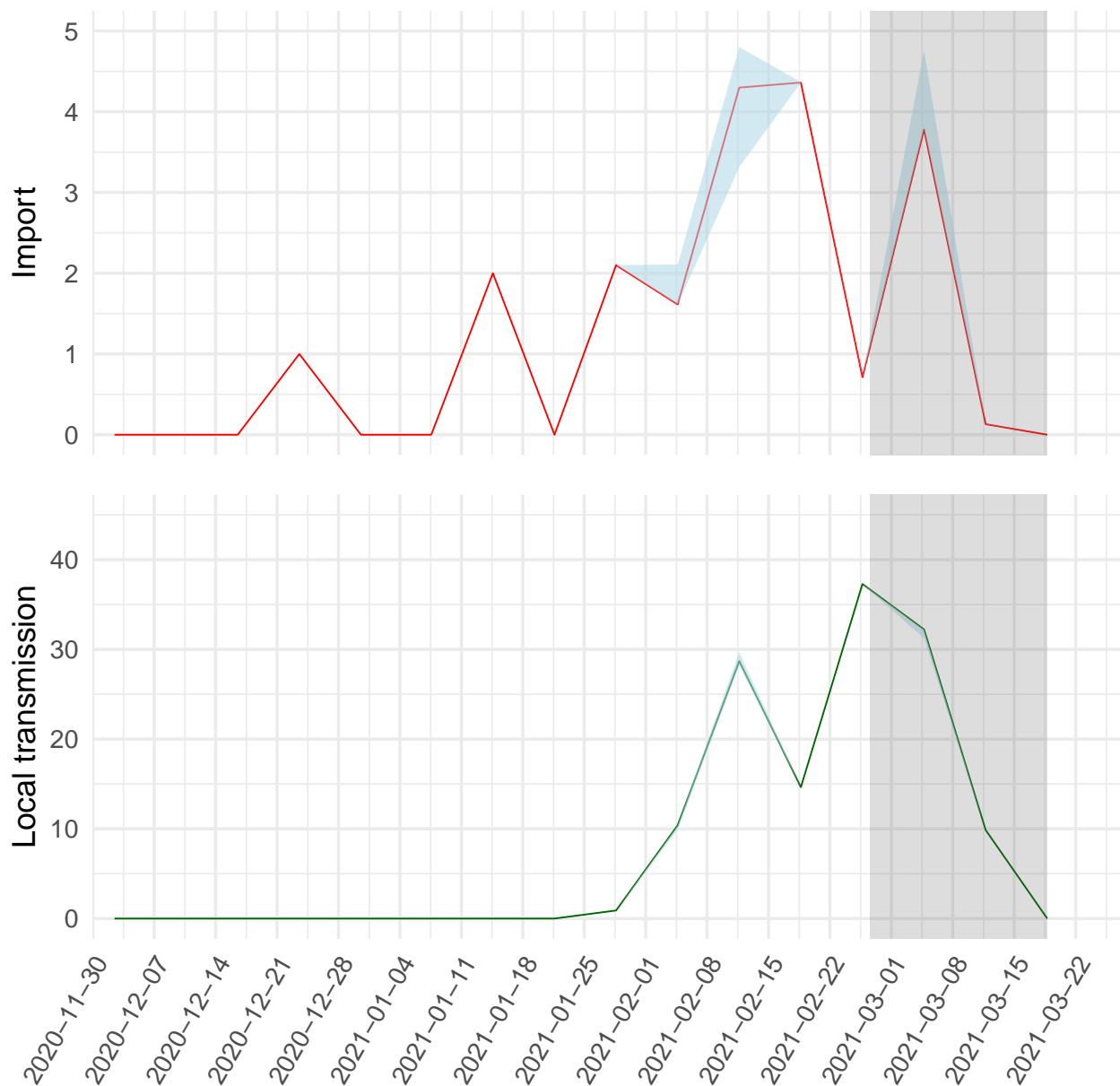


Fig. 3. Import og transmisjon av B.1.351. Estimert antall import-hendelser (øverst) og lokale transmisjoner (nederst) per uke. Det er knyttet stor usikkerhet rundt estimater i perioden skravert i grått.

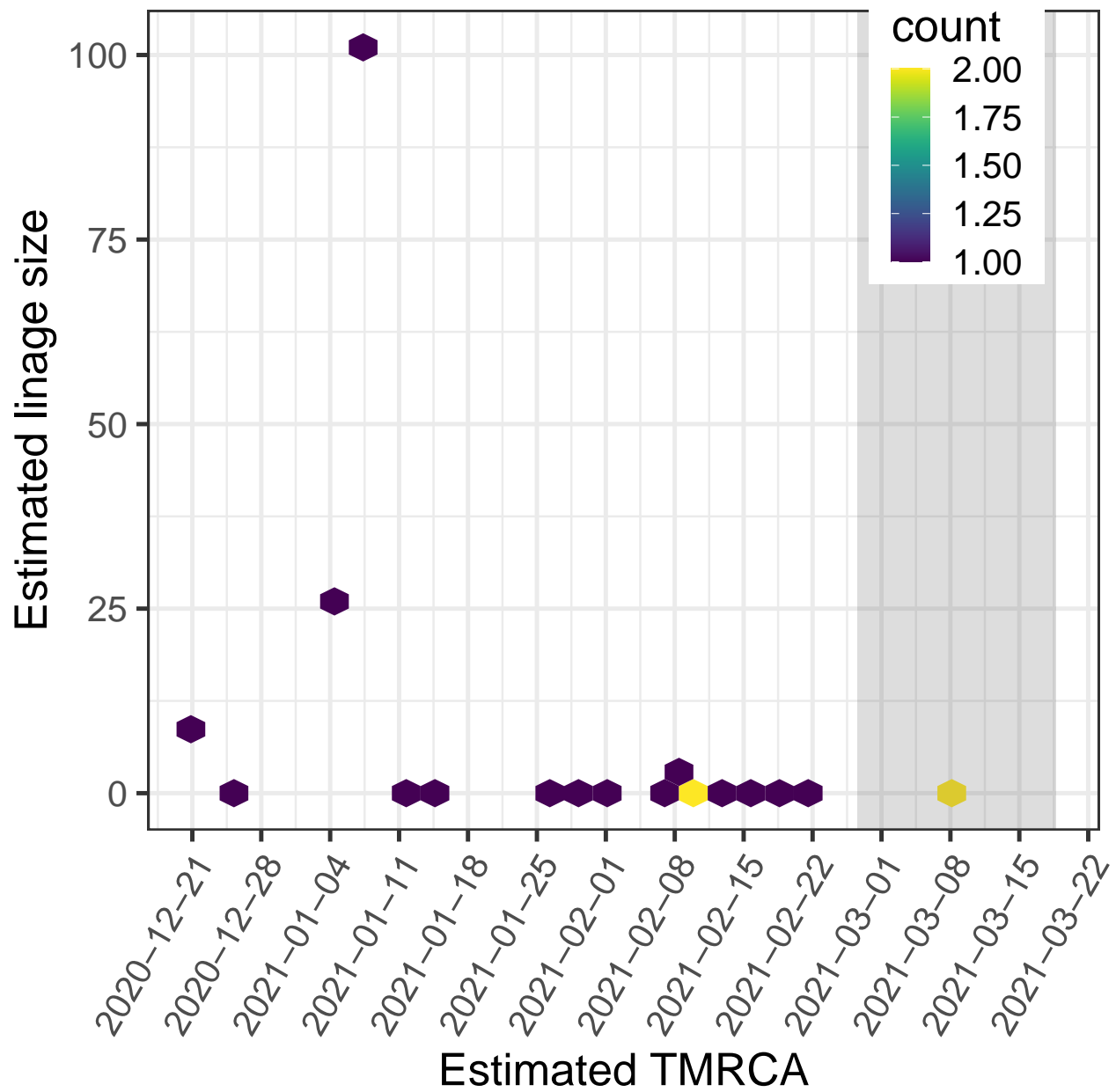


Fig. 4. Klyngestørrelser som funksjon av importtidspunkt, B.1.351 “TMRCA” = time of most recent common ancestor, og indikerer estimert tidspunkt for hver enkelt import. Den store klyngen som skiller seg ut her tilsvarer Bodø-utbruddet.