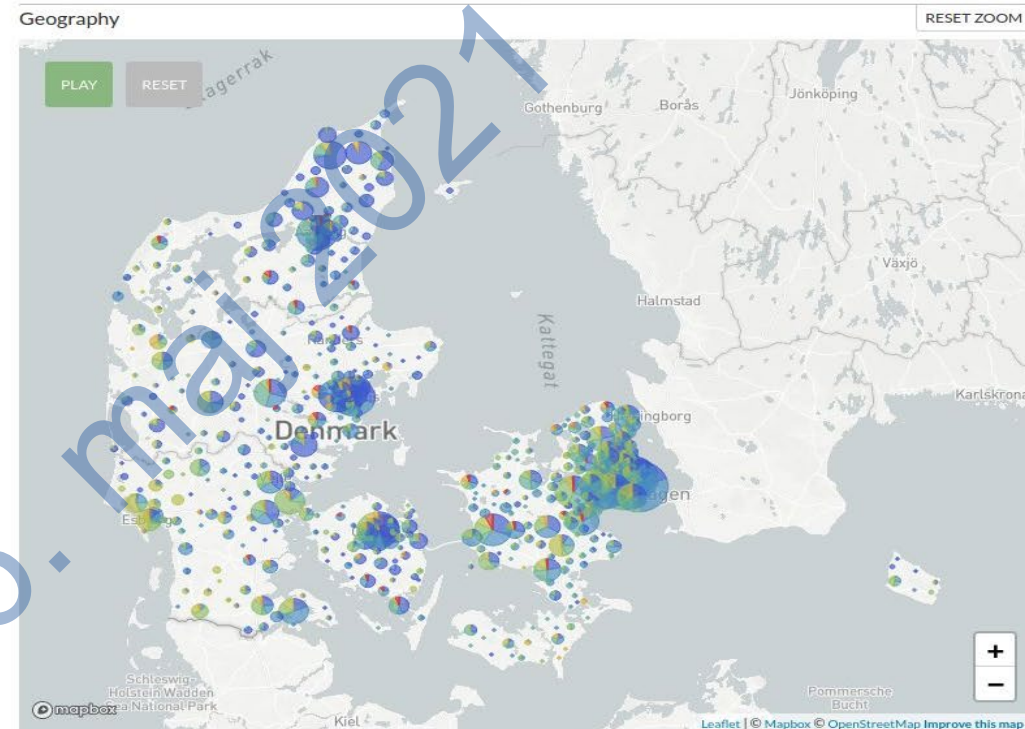
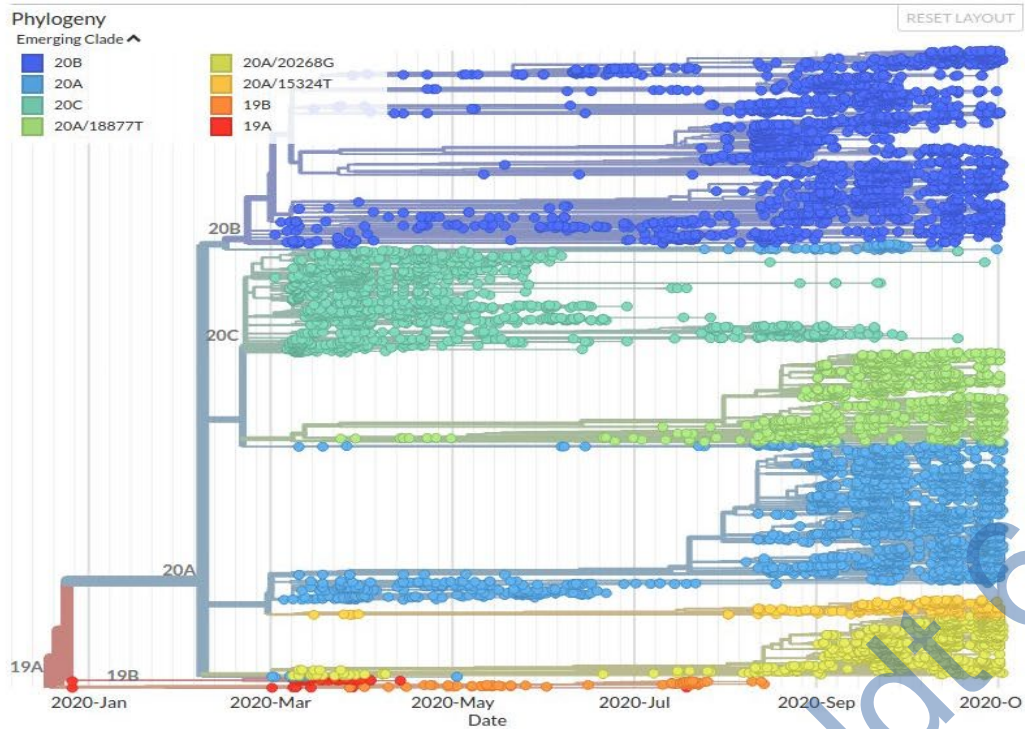


SARS-COV-2 SEKVENTERING I DANMARK

Showing 8945 of 8945 genomes sampled between Dec 2019 and Nov 2020.



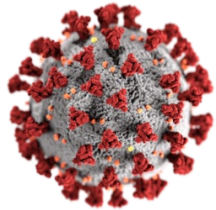
Diversity

ENTROPY EVENTS | AA NT

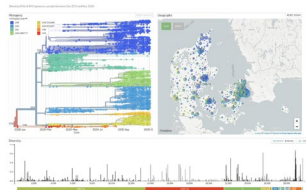
Morten Rasmussen, Seniorforsker, PhD
Virus og Mikrobiologisk Specialdiagnostik, SSI



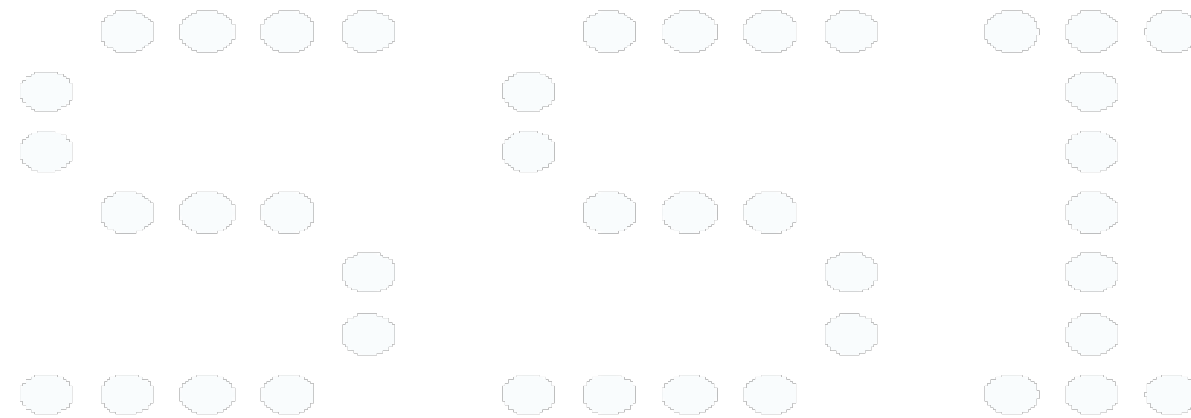
Hvordan det hele startede



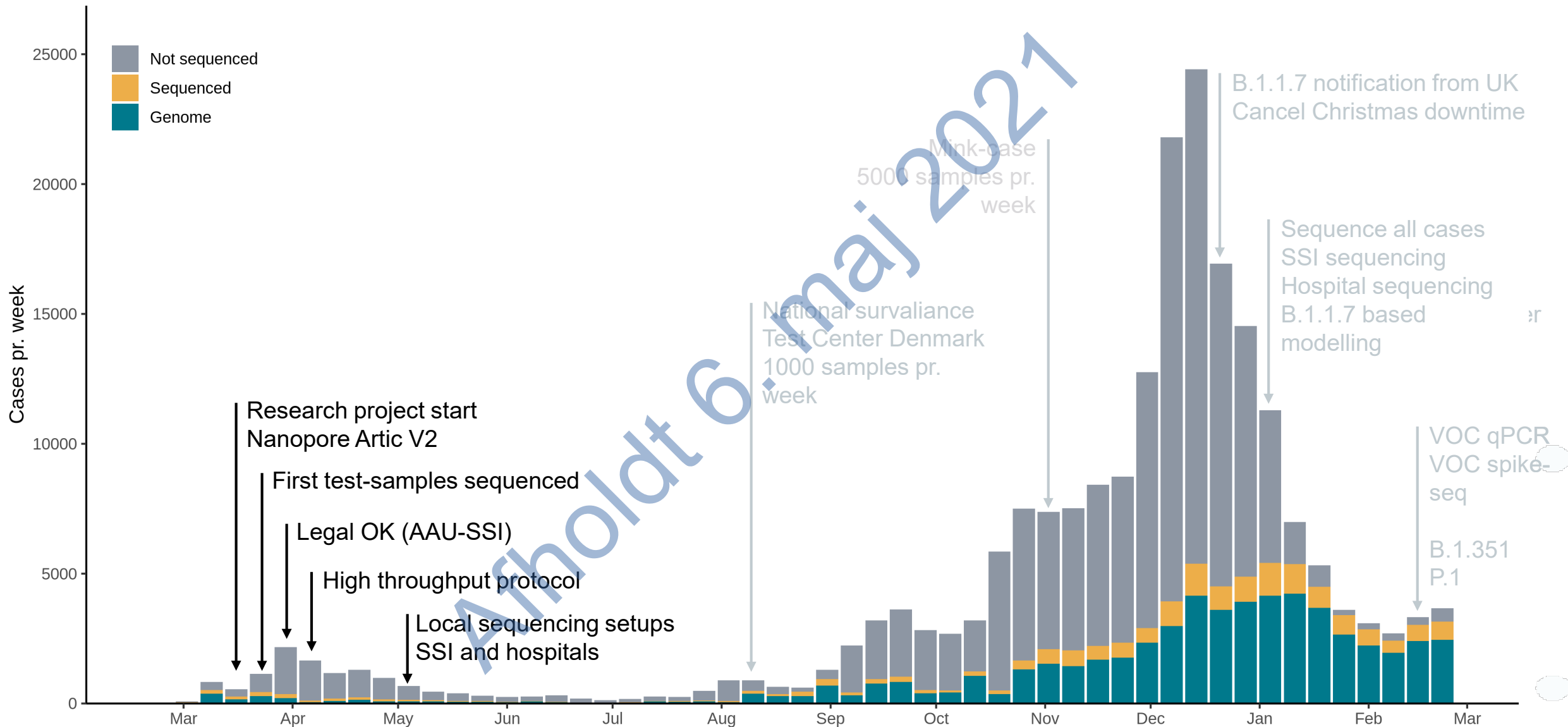
Epidemien set gennem sekventering

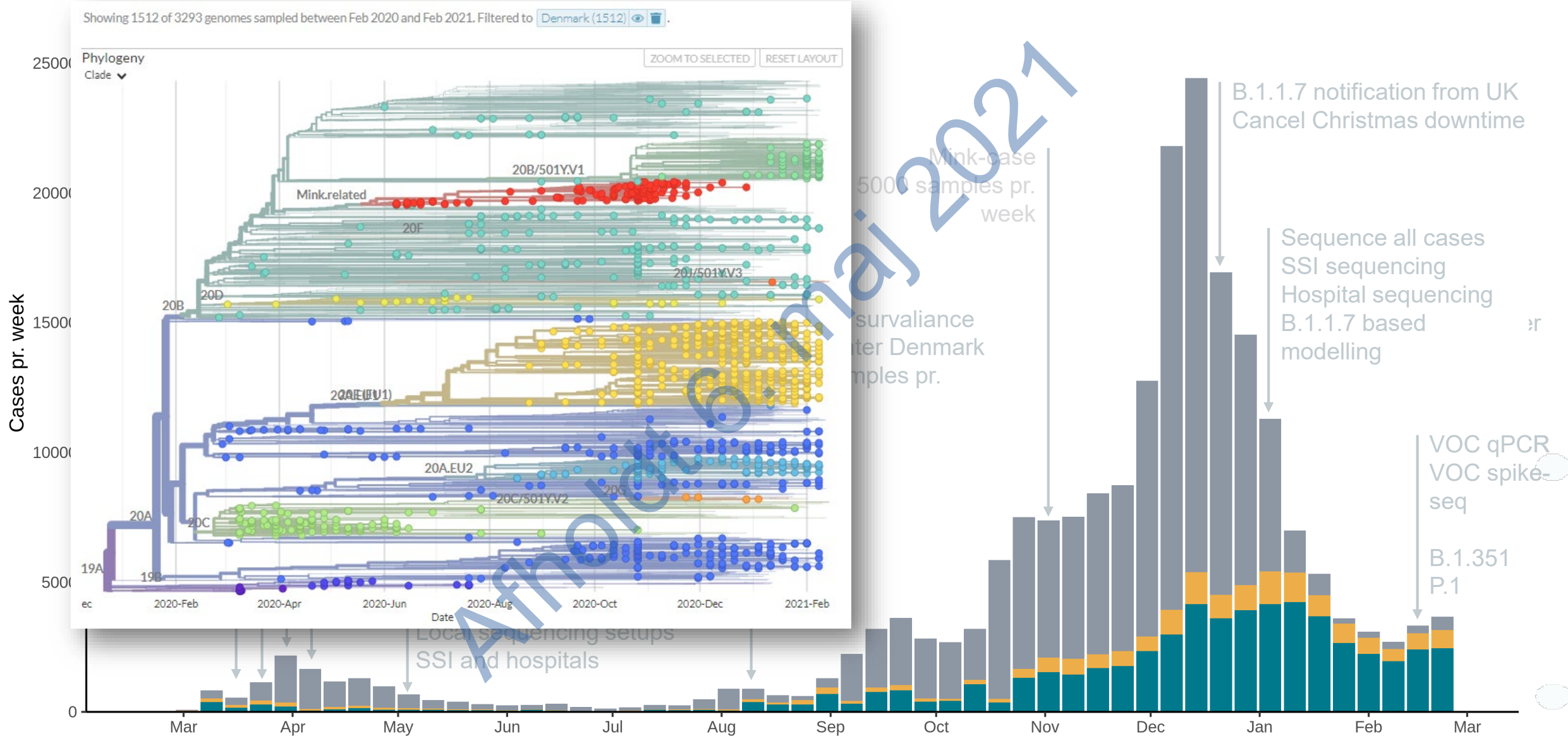


Rapporteringer



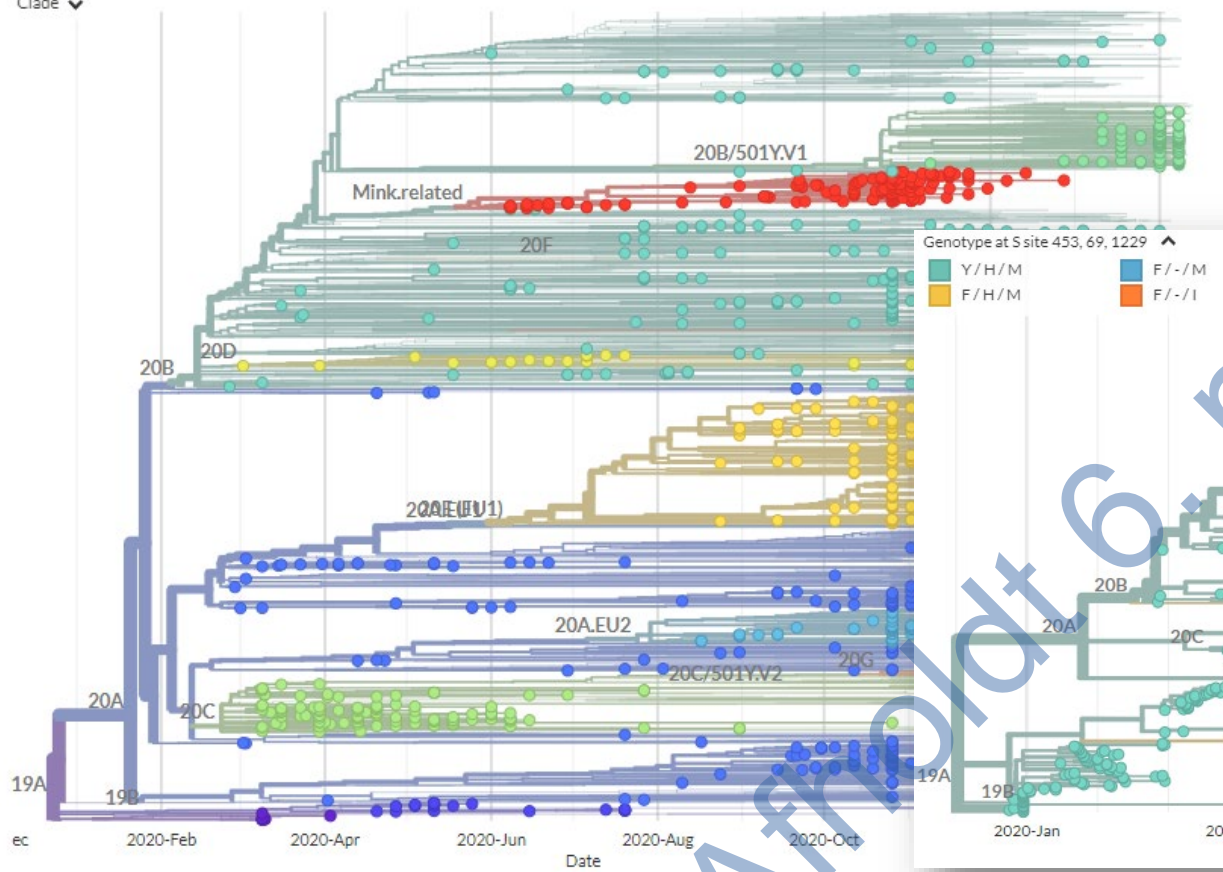
DEN FØRSTE BØLGE



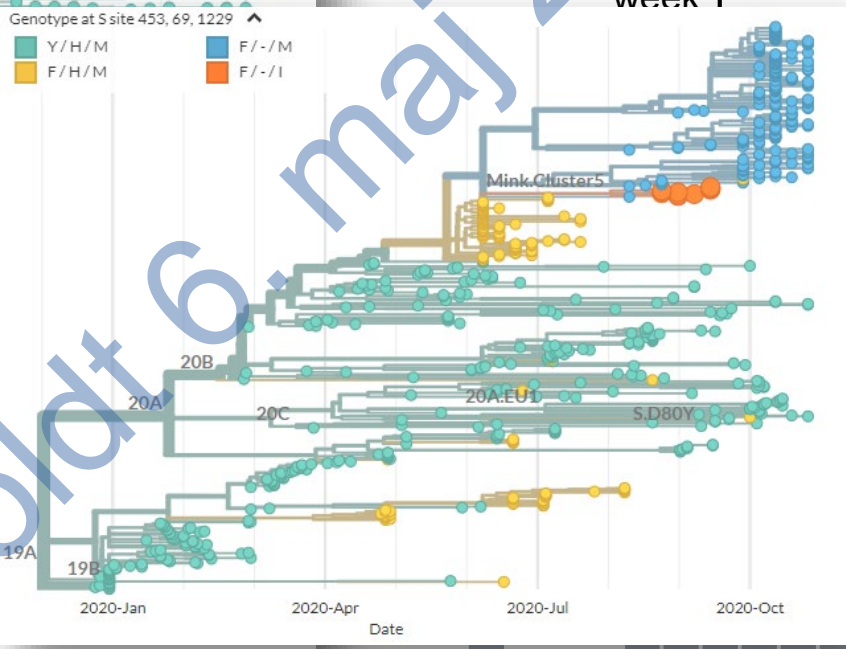


Showing 1512 of 3293 genomes sampled between Feb 2020 and Feb 2021. Filtered to Denmark (1512)

Phylogeny Clade ZOOM TO SELECTED RESET LAYOUT



Mink-case
5000 samples pr.
week

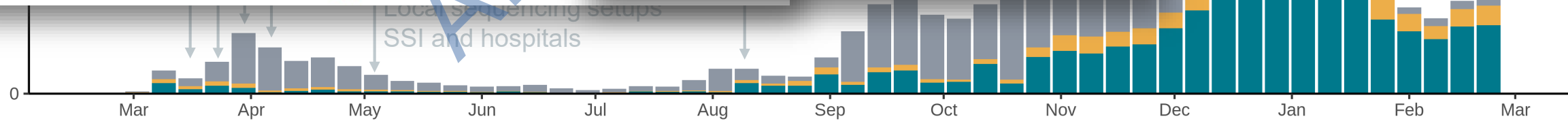


B.1.1.7 notification from UK
Cancel Christmas downtime

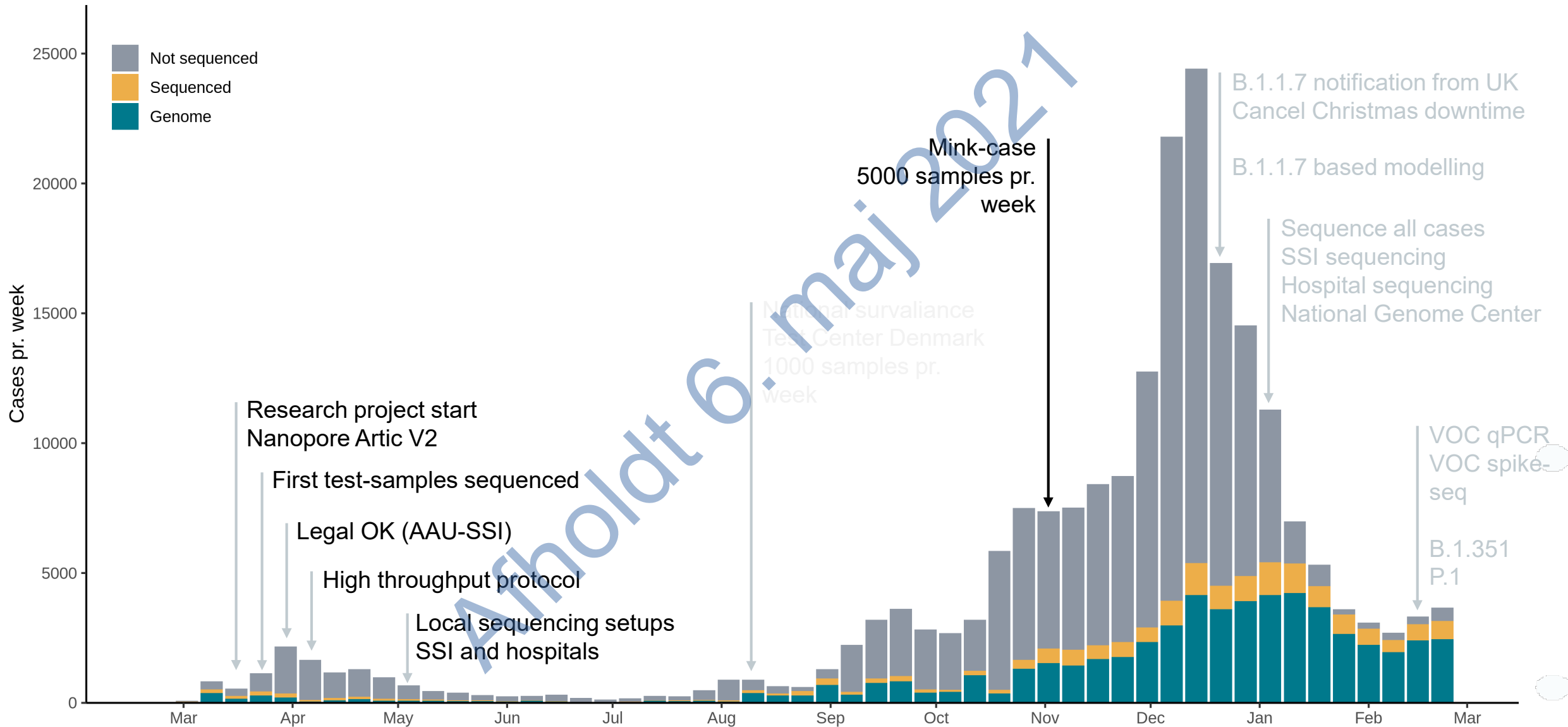
Sequence all cases
SSI sequencing
Hospital sequencing
B.1.1.7 based
modelling

VOC qPCR
VOC spike-
seq

B.1.351
P.1

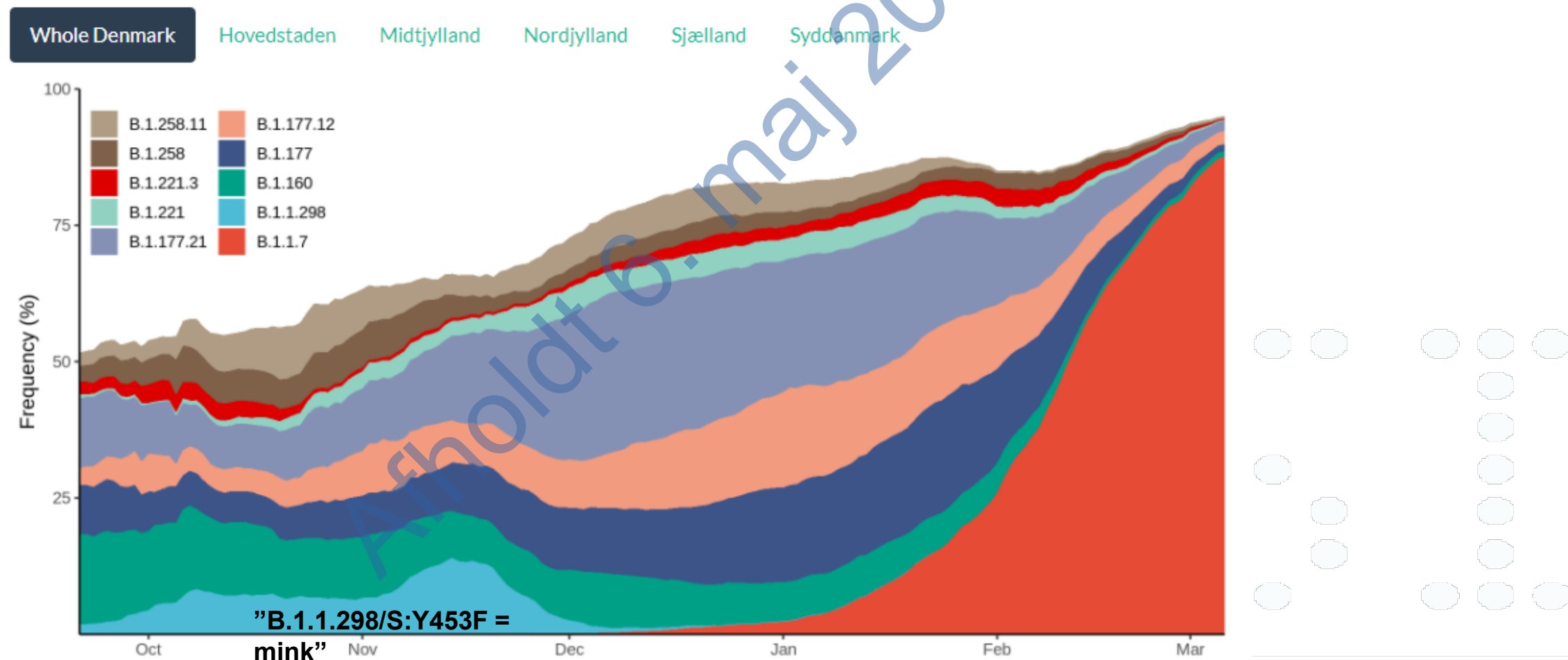


OVERSIGT SARS-COV-2 SEKVENTERING



Dominating lineages

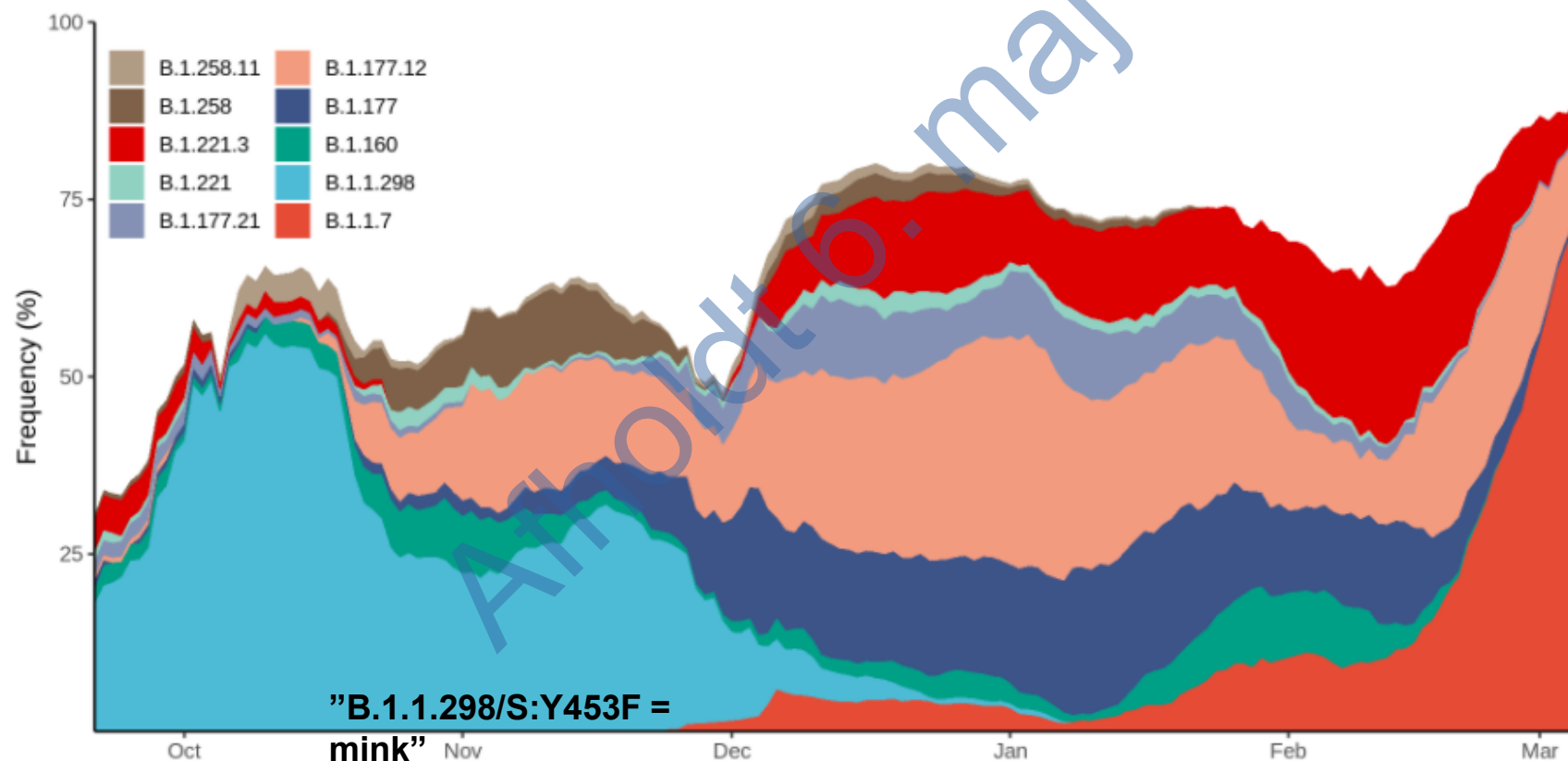
Frequency of the 10 most abundant PANGO lineages across Denmark within the last 6 months. The frequency is calculated as a centered 14-day rolling average. Note that some regions have low case-counts in some periods, which can make small absolute changes look dramatic on a relative scale.

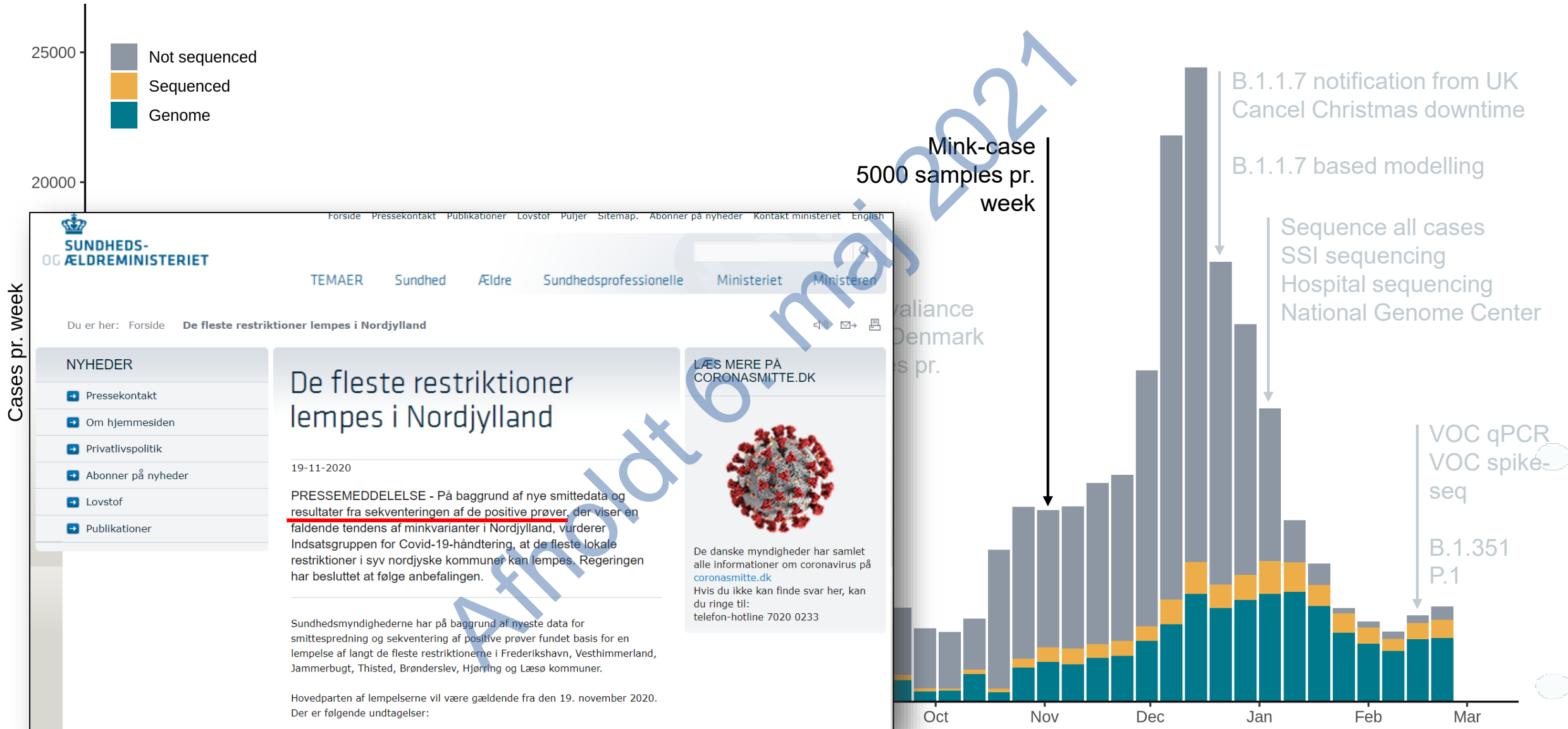


Dominating lineages

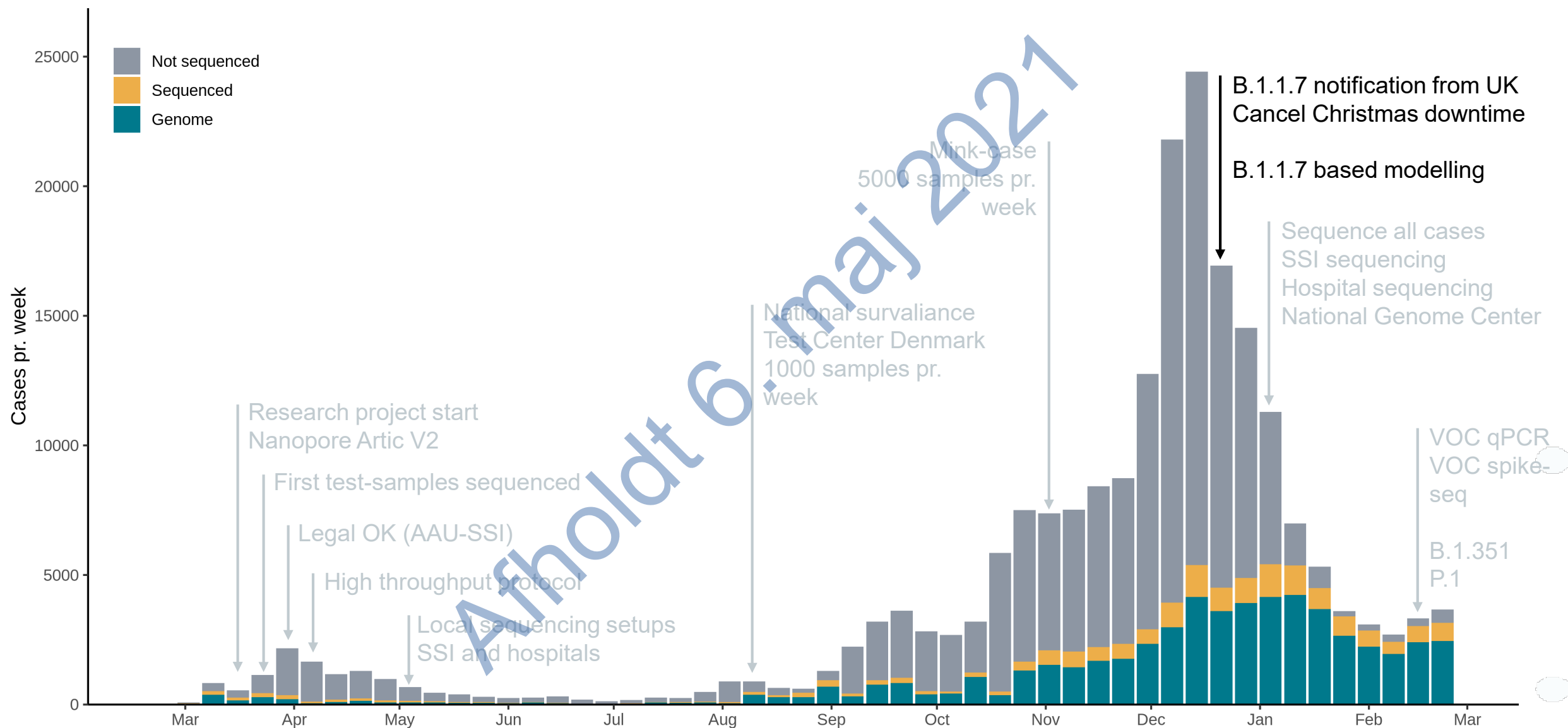
Frequency of the 10 most abundant PANGO lineages across Denmark within the last 6 months. The frequency is calculated as a centered 14-day rolling average. Note that some regions have low case-counts in some periods, which can make small absolute changes look dramatic on a relative scale.

Whole Denmark Hovedstaden Midtjylland Nordjylland Sjælland Syddanmark

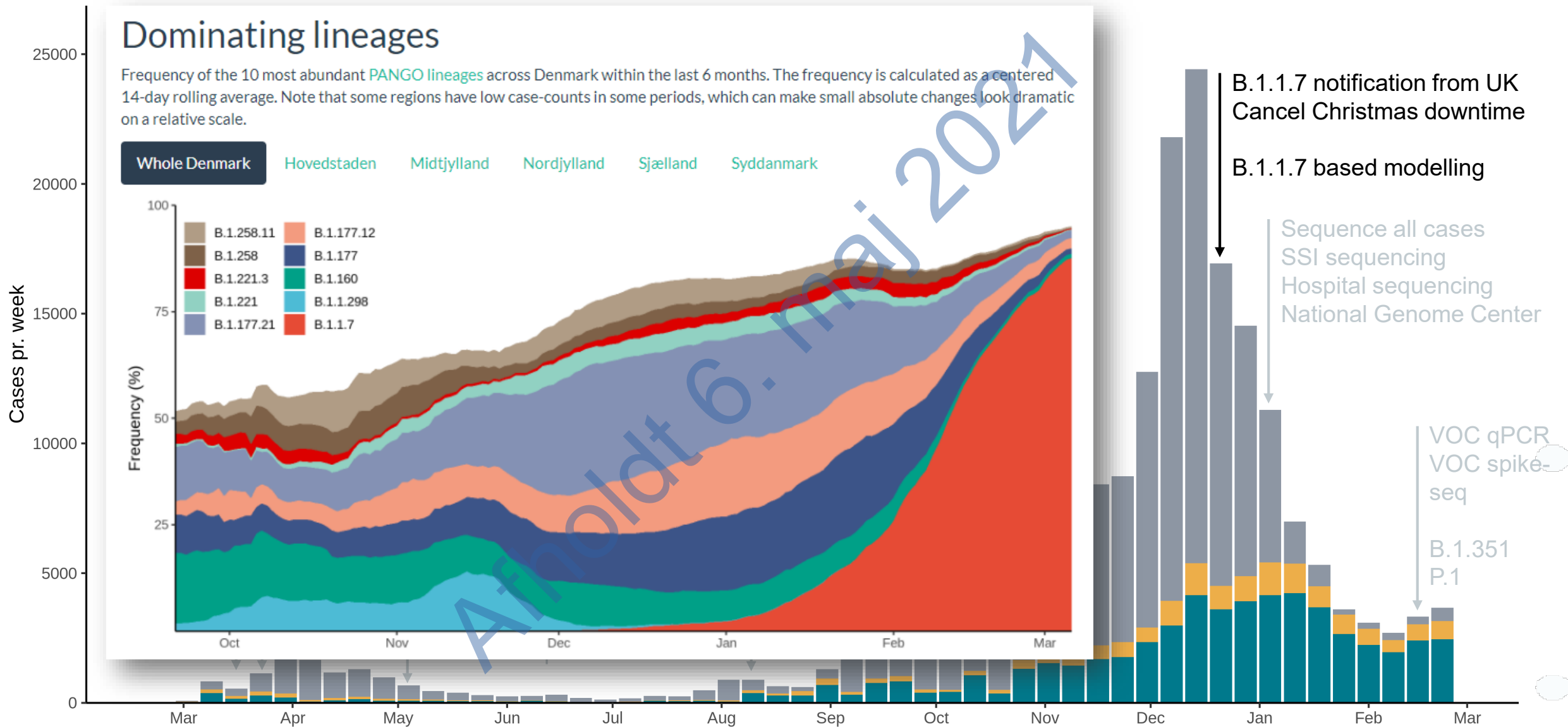




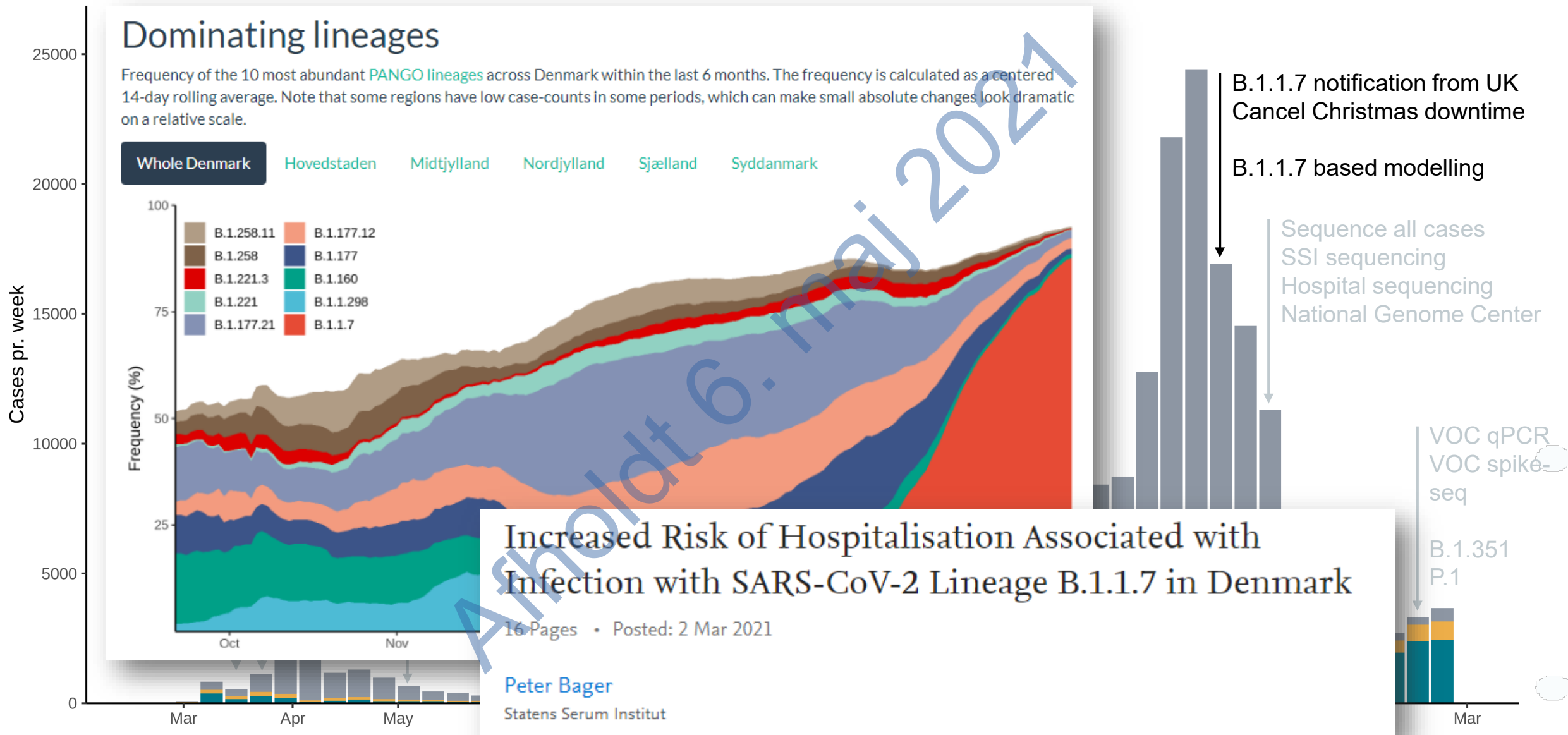
DEN ENGELSKE VARIANT



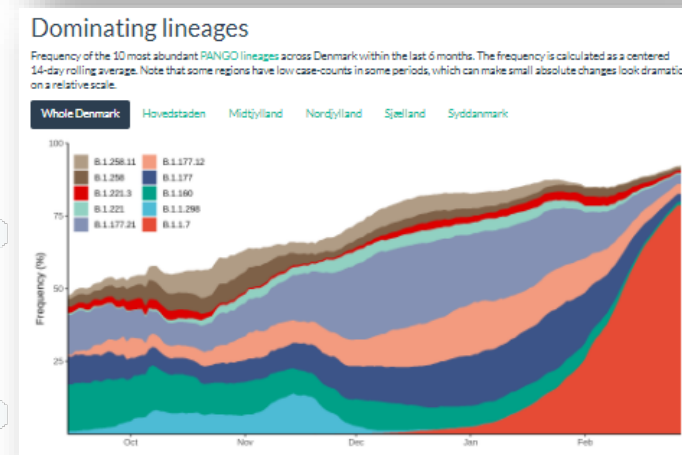
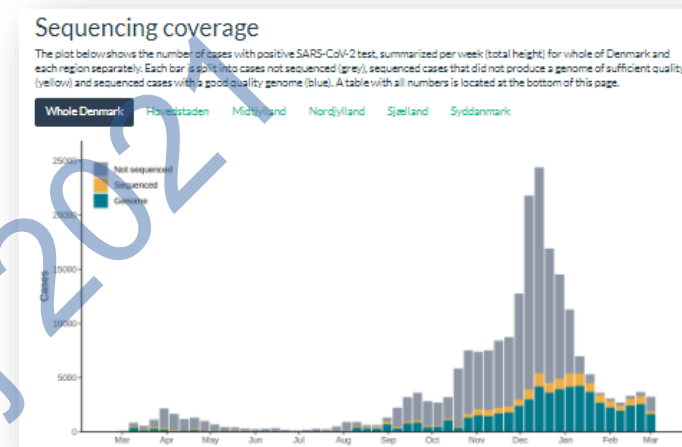
DEN ENGELSKE VARIANT



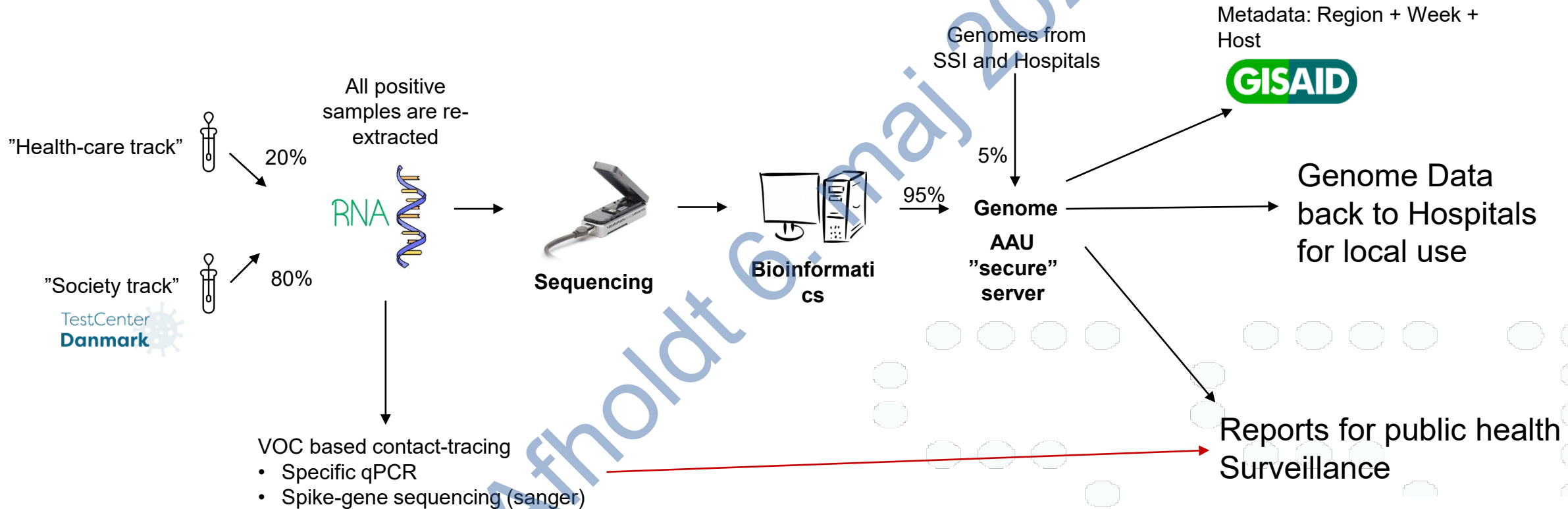
DEN ENGELSKE VARIANT



- ❖ **Daglige data opdateringer kl 12.**
- ❖ **Oversigtsrapporter**
 - Status på sekventering og VOC/VOIs
- ❖ **Udbruds og variant rapporter**
 - Epikurver + fylogeni
- ❖ **Data til modelleringsgruppen**
 - Beregning af kontakttal
- ❖ **Breakthrough infektioner**
 - Overvågning af infektioner post vaccination
- ❖ **Overvågning af diagnostiske assays**
 - Primer/probe statistikker.



FROM PATIENT TO DATA



All tests are free and results < 24 h

RT-qPCR: 150.000 test/day

Antigen: 150.000 test/day

0.3% positive

Sekvensdata i brug

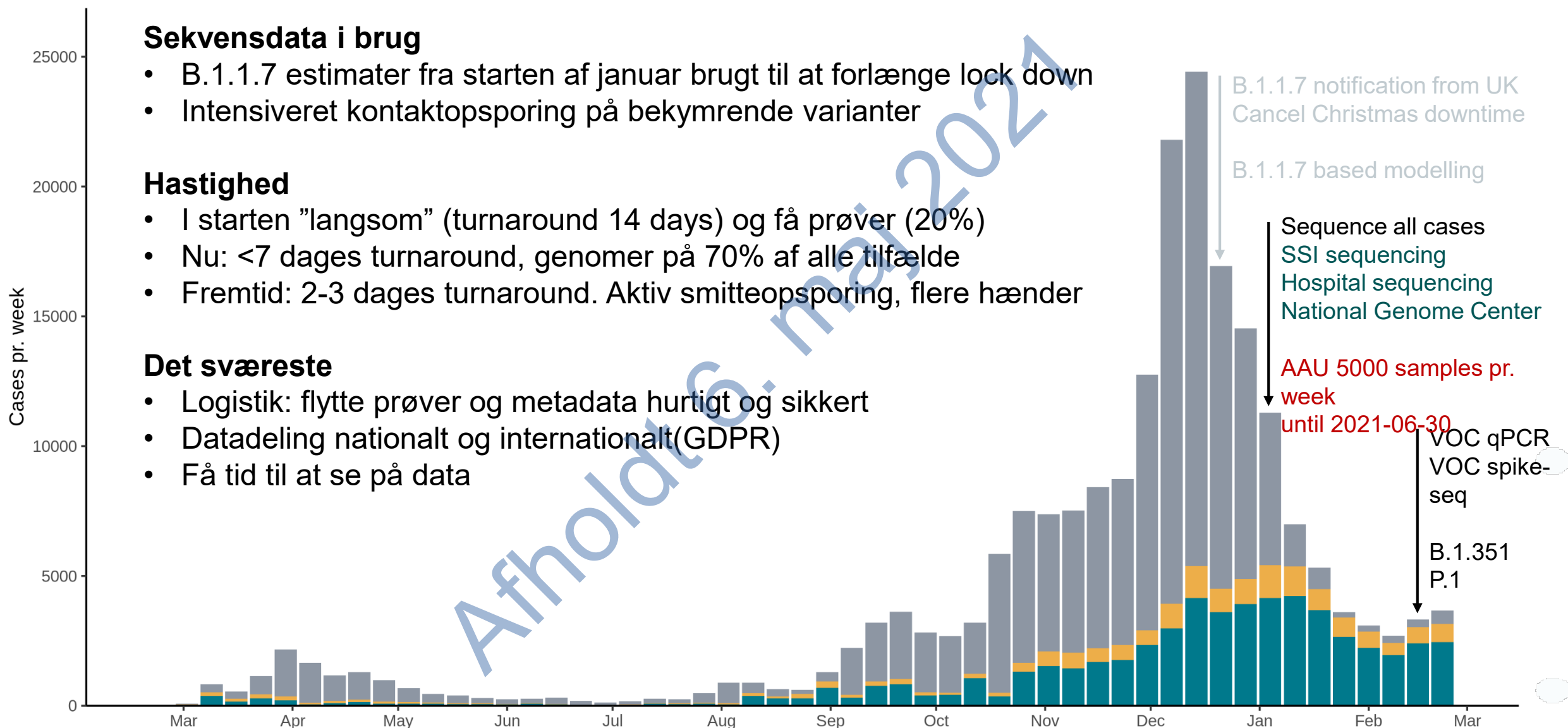
- B.1.1.7 estimerer fra starten af januar brugt til at forlænge lock down
- Intensiveret kontaktopsporing på bekymrende varianter

Hastighed

- I starten "langsom" (turnaround 14 days) og få prøver (20%)
- Nu: <7 dages turnaround, genomer på 70% af alle tilfælde
- Fremtid: 2-3 dages turnaround. Aktiv smitteopsporing, flere hænder

Det sværeste

- Logistik: flytte prøver og metadata hurtigt og sikkert
- Datadeling nationalt og internationalt(GDPR)
- Få tid til at se på data



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Laboratory (AAU)

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Emil A. Sørensen

Trine Sørensen

Celine Petersen

Jakob Brandt

Clarisse Chiche-Lapierre

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Emilio Fuster Collados

Mantas Serika

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Thor Bech Johannesen

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(+ Lab technicians, bioinformaticians)

Hvidovre Hospital

Kristian Schønning (PI)

Martin S. Pedersen

Sarah Mollerup

Nana Gry Jacobsen

Aalborg University Hospital

Henrik Krarup (PI)

Danish Hospitals

All local KMA's shipping samples to SSI

All local KMA's conducting sequencing

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Mads P. Bach

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Michael Collin

Finn Büttner

AAU legal

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Tomer Sagi

Miroslaw Pakanec

AAU SUND

Martin Bøgsted

Rasmus Brøndum

Danish Covid-19 Genome Consortium

HOME NEXTSTRAIN STATISTICS ABOUT US CONTACT

Who are we?

The mission of the Danish Covid-19 Genome Consortium (DCGC) is to assist public health authorities to monitor the spread of SARS-CoV-2. The project was established in March 2020 through the coordinated effort of Aalborg University, Statens Serum Institute, Hvidovre Hospital, and Aalborg University Hospital. Large-scale SARS-CoV-2 sequencing capacity was initially established at Aalborg University and local sequencing capacity at Statens Serum Institute and Hvidovre Hospital. Since June 2020, the consortium has established additional local sequencing nodes at Aalborg University Hospital, Aarhus University Hospital, Slagelse Hospital, Rigshospitalet, Sygehus Lillebælt, and Odense University Hospital.

Last update: 2021-05-03

Sequenced Samples



112562

High-quality Genomes



87918

Uploaded to GISAID



41390

www.covid19genomics.dk/

POUL DUE JENSEN GRUNDFOS
FOUNDATION



Uddannelses- og
Forskningsministeriet

• Formål

- Opbygning af sekventeringskapacitet
- Bruge helgenomsekventering aktivt som overvågningsværktøj
- Assistere med at etablere Nanopore sekventering på landets sygehuse

Afholdt 6. maj 2021



❖ Outbreak report

- In depth reports covering specific outbreaks

❖ Data to modelling group

- Modelling R-numbers and reopening scenarios

❖ Breakthrough infections after vaccination

- Surveillance of infections post vaccination

❖ Surveillance of diagnostic assays

- Primer/probe statistics

❖ Information to ministry of health

