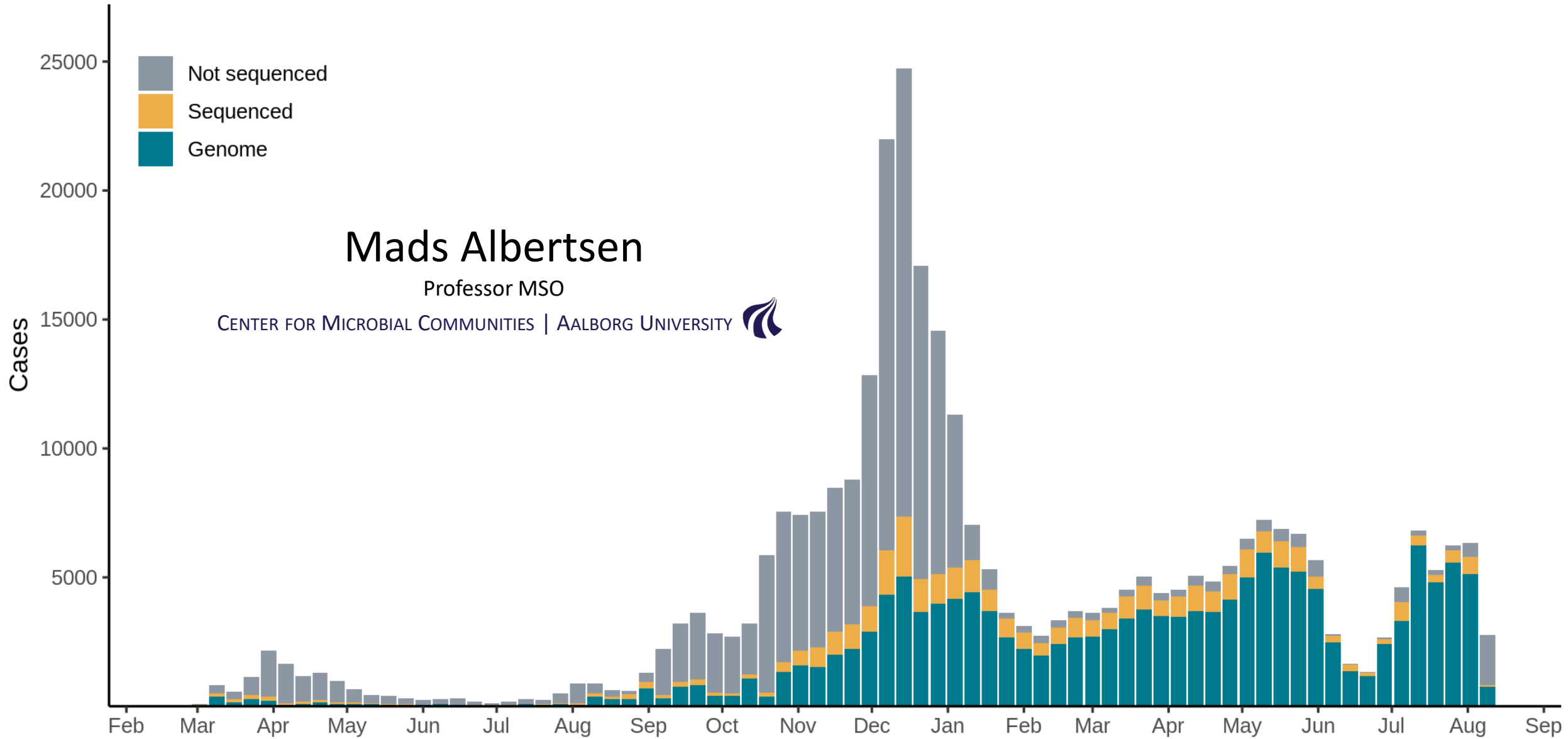


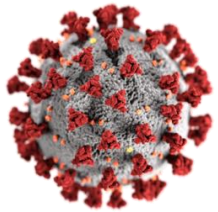
# A brief history of SARS-CoV-2 sequencing in Denmark



# Two small stories



How we started sequencing SARS-CoV-2



The Danish pandemic seen through genomics



# Albertsen lab

*“First movers in applying and developing new methods within DNA sequencing and microbial ecology”*



Mads (PI)



Thomas (PhD)



Emil (PhD)



Vibeke (PD)



Thomas (PhD)



Mantas (PhD)



Simon (RA)



Andre (PD, co)



Morten (MSc)



Mette (MSc)



Søren (MSc)



Sebastian (MSc)



Amalie (MSc)



Erika (MSc)



Frederik (RA)

nature  
biotechnology

Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes

Mads Albertsen<sup>1</sup>, Philipp Hugenholz<sup>2,3</sup>, Adam Skarshewski<sup>4</sup>, Kåre I. Nielsen<sup>1</sup>, Gene W. Tyson<sup>5,6</sup> & Per H. Nielsen<sup>1</sup>

Science  
AAAS

Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation

Hanna Koch<sup>1</sup>, Alexander Galushko<sup>1</sup>, Mads Albertsen<sup>1</sup>, Arno Schintlmeister<sup>1,5</sup>, Christiane Gruber-Dorninger<sup>1</sup>, Sebastian Lüscher<sup>1,5</sup>, Eric Pelletier<sup>1,5,6</sup>, Dennis Le. Paslier<sup>1,5,6</sup>, Eva Spieck<sup>7</sup>, Andreas Richter<sup>8</sup>, Per H. Nielsen<sup>1</sup>, Michael Wagner<sup>1</sup>, Holger Dalmé<sup>1</sup>

nature

Complete nitrification by *Nitrospira* bacteria

Holger Dalmé<sup>1</sup>, Elena V. Lebedeva<sup>2</sup>, Petra Pjevac<sup>1</sup>, Ping Han<sup>1</sup>, Craig Herbold<sup>1</sup>, Mads Albertsen<sup>1</sup>, Nico Jehmlich<sup>1</sup>, Marton Palatinszky<sup>1</sup>, Julia Vierhellig<sup>1</sup>, Alexander Bulavaev<sup>1</sup>, Rasmus H. Kirkegaard<sup>1</sup>, Martin von Bergen<sup>4,5</sup>, Thomas Ratter<sup>6</sup>, Bernd Bendinger<sup>7</sup>, Per H. Nielsen<sup>1</sup> & Michael Wagner<sup>1</sup>

nature

Complete nitrification by a single microorganism

Maartje A. H. J. van Kessel<sup>1</sup>, Daan R. Speth<sup>1</sup>, Mads Albertsen<sup>2</sup>, Per H. Nielsen<sup>2</sup>, Huub J. M. Op den Camp<sup>1</sup>, Boran Kai Mike S. M. Jetten<sup>1,3</sup> & Sebastian Lüscher<sup>1</sup>

nature  
biotechnology

Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias

Soren M. Karst<sup>1,2</sup>, Morten S. Dueholm<sup>1,3,4</sup>, Simon J. McIlroy<sup>1,5</sup>, Rasmus H. Kirkegaard<sup>1,6</sup>, Per H. Nielsen<sup>1,7</sup> & Mads Albertsen<sup>1</sup>

nature

Kinetic analysis of a complete nitrifier reveals an oligotrophic lifestyle

K. Dimitri Kits<sup>1</sup>, Christopher J. Sedlacek<sup>1</sup>, Elena V. Lebedeva<sup>2</sup>, Ping Han<sup>1</sup>, Alexandr Bulavaev<sup>1</sup>, Petra Pjevac<sup>1</sup>, Anne Daebler<sup>1</sup>, Stefano Komano<sup>1</sup>, Mads Albertsen<sup>1</sup>, Lisa Y. Stein<sup>1</sup>, Holger Dalmé<sup>1</sup> & Michael Wagner<sup>1</sup>

“Danish research result of the year 2015”



nature methods  
ARTICLES  
https://doi.org/10.1038/nmeth.4192-025-09141-y

High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing

Soren M. Karst<sup>1,2</sup>, Ryan M. Ziels<sup>1,2,7</sup>, Rasmus H. Kirkegaard<sup>1</sup>, Emil A. Sorensen<sup>1,2</sup>, Daniel McDonald<sup>1,2</sup>, Qiyun Zhu<sup>1,2</sup>, Rob Knight<sup>1,4,5,6</sup> & Mads Albertsen<sup>1,2,8</sup>

High-throughput amplicon sequencing of large genomic regions remains challenging for short-read technologies. Here, we report a high-throughput amplicon sequencing approach combining unique molecular identifiers (UMIs) with Oxford Nanopore Technologies (ONT) or Pacific Biosciences circular consensus sequencing, yielding high-accuracy single-molecule consensus sequences of large genomic regions. We applied our approach to sequence ribosomal RNA operon amplicons (~4,500 bp) and genomic sequences (>10,000 bp) of reference microbial communities in which we observed a chimera rate <0.02%. To reach a mean UMI consensus error rate <0.01%, a UMI read coverage of 15x (ONT R10.3), 25x (ONT R9.4.1) and 3x (Pacific Biosciences circular consensus sequencing) is needed, which provides a mean error rate of 0.0042%, 0.0041% and 0.0007%, respectively.

High-throughput amplicon sequencing is a ubiquitous method for studying genetics with low-abundance variants or high heterogeneity, including cancer driver genes<sup>1,2</sup>, viral populations<sup>3,4</sup> and microbial communities<sup>5</sup>. Short-read Illumina sequencing has dominated amplicon-related research due to its unprecedented throughput and low native error rate of ~0.1%, but its maximum amplicon size of ~500 bp<sup>6</sup> limits important long-range information and assay resolution<sup>7</sup>. UMIs have been applied to enable sequencing of longer amplicons with short-reads via assembly of synthetic long reads<sup>8</sup>. Each template molecule in a sample is tagged with a UMI sequence consisting of 10–20 random bases, which can subsequently be used to sort and analyze reads based on their original template molecule. UMIs can enable sequencing of synthetic long reads up to ~11,000 bp, but this approach cannot resolve amplicons with repeats longer than the short-read length<sup>9</sup>, which limits its application. The high native error rates of ONT (5–25%)<sup>10</sup> and Pacific Biosciences (PacBio) (~1%)<sup>11</sup> have until now, made it difficult to confidently identify true UMI tag sequences that are necessary to accurately assign raw reads to their template molecules. Furthermore, the combination of UMIs with long-read sequencing is relatively unexplored and only recently has this combination been applied with PacBio circular consensus sequencing (CCS)<sup>12</sup>, but without using dual UMIs for chimera filtering<sup>13</sup> and profiling the error of the generated consensus sequences.

Here, we present a simple workflow that combines UMIs with sequencing of long amplicons on the ONT and PacBio platforms to produce highly accurate single-molecule consensus sequences with a low chimera rate. To improve recognition of UMI-tagged error-prone reads, we designed UMIs to contain recognizable internal patterns (Fig. 1a and Supplementary Table 1) that avoid abundant homopolymer stretches<sup>14</sup> (Fig. 1c, step 2). The filtered, high-quality

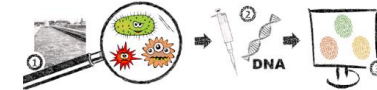
based on UMI length and pattern, allow for robust determination of true UMI sequences in raw error-prone ONT and PacBio data.

### Results

#### Applying dual-UMI tagging for long-read amplicon sequencing.

The DNA template is initially diluted to a target number of output sequences, which is estimated based on the desired single-molecule coverage and expected sequencing yield. This initial dilution step must be optimized for the genomic material of a given study to ensure that the target number of amplifiable target molecules can be achieved, either by trial sequencing or using methods such as semi-quantitative PCR and a suitable amplicon product standard. The genetic region of interest is then targeted using two cycles of PCR with a customized set of tailored primers (Supplementary Table 1), which includes a target-specific primer, a UMI sequence and a synthetic priming site used for downstream amplification (Fig. 1b, step 1). For PCR-free approaches, such as whole-genome or metagenomic DNA sequencing, adapters containing UMIs can be ligated to template DNA molecules. The product from the initial UMI-tagging step is a double-stranded DNA amplicon copy of the genetic target, containing the UMI and synthetic primer sites on both ends. The UMI-tagged molecule is subsequently amplified by PCR targeting the synthetic primer sites (Fig. 1b, step 2) and prepared for long-read sequencing with ONT or PacBio CCS (Fig. 1b, step 3). After sequencing, reads are binned based on the concatenation of the two terminal UMIs (UMI pair) (Fig. 1c, steps 1 and 2). High-quality UMI sequences are detected on the basis of the presence of the designated pattern, as well as the expected UMI length of 18 bp (Fig. 1c). Chimeric sequences are filtered de novo by removing UMI pairs in which either terminal UMI is observed in a more abundant UMI pair<sup>15</sup> (Fig. 1c, step 2). The filtered, high-quality

DNA sense  
more than just the sequence



# We play with new technology...



Rasmus Kirkegaard  
@kirk3gaard

Following

2x @nanopore sequencing power  
#dualMinION



2:13 AM - 20 Sep 2017

8 Retweets 33 Likes



2 8 33

[Early access users since 2014]



Rasmus Kirkegaard @kirk3gaard · Mar 14

The real @nanopore #promethion machine has arrived in #albertsenlab! Looking forward to receive flowcells and put it to the test.



10 18

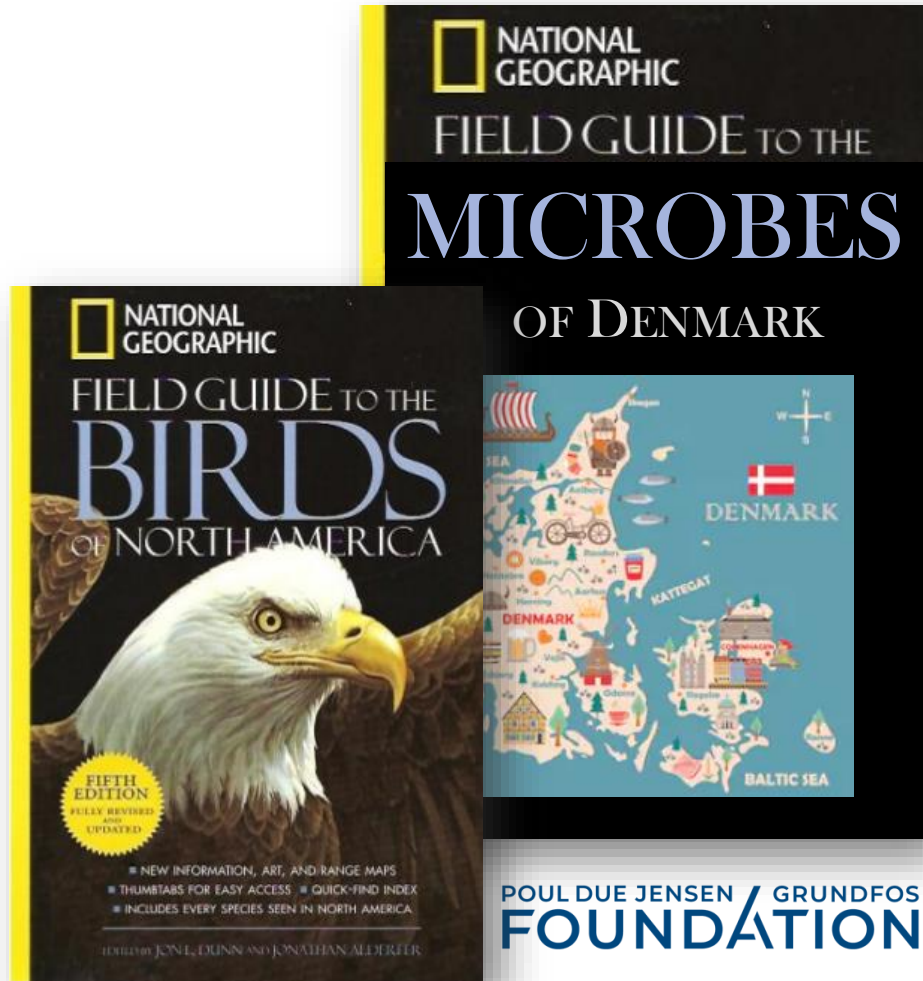
[Early access users since 2017]



# Microflora Danica: The microbiome of Denmark



Per H. Nielsen



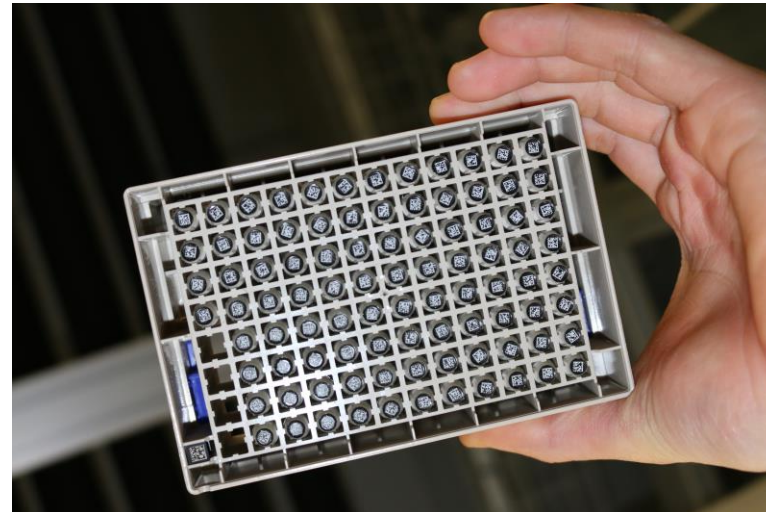
*"Sounds awesome, here is 30 mill. DKK.  
Go do great science."*

# A high-throughput system for analysis of 10.000 samples

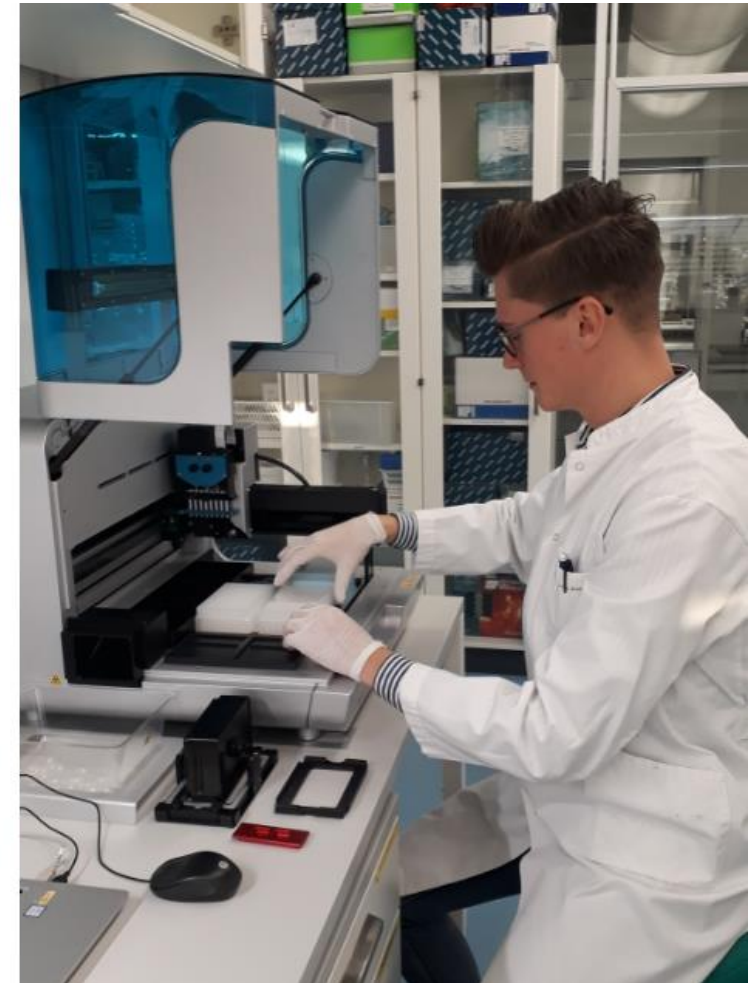
Sample and plate barcoding system



Scanning system  
(collected samples & 96 sample format)



Automated extraction platform  
(96 sample format, 2 hours turnaround)



Thomas BN Jensen

# Ny coronavirus fra Wuhan



Siden december 2019 er der i den kinesiske storby Wuhan fundet flere tilfælde af svær lungebetændelse og dødsfald, som er forårsaget af en ny coronavirus. Der er også fundet tilfælde i andre asiatiske lande hos personer, der har opholdt sig i Wuhan. Sundhedsstyrelsen vurderer, at der er meget lille sandsynlighed for, at sygdommen kommer til Danmark, men følger situationen nøje. Sundhedsstyrelsen anbefaler ikke screeningstiltag i fx lufthavne i forbindelse med indrejse i Danmark. Hvis der mod forventning skulle komme personer til Danmark med mistanke om sygdommen, så er de danske sundhedsmyndigheder og sundhedsvæsenet klar til at håndtere dette.

22 JAN 2020

[sst.dk/da/nyheder/2020/ny-coronavirus-fra-wuhan](https://sst.dk/da/nyheder/2020/ny-coronavirus-fra-wuhan)



**31. december 2019** - Kina advarer WHO om udbrud af, hvad der forventes at være lungebetændelse i Wuhan.

**3. januar** - Øjenlægen Li Wenliang arresteres i Wuhan, da de kinesiske myndigheder mener, at han har spredt falske rygter om coronavirusen. Han dør 6. februar af coronavirus.

**11. januar** - Kina registrerer det første dødsfald som følge af coronavirus i Wuhan.



**22. januar** - WHO: Uenighed om at erklære Covid-19 for en international sundhedskrise.



**23. januar** - Kina: Wuhan lukkes ned.

**24. januar** - Frankrig registrerer første tilfælde af Covid-19 i Europa.

## Article

# A pneumonia outbreak associated with a new coronavirus of probable bat origin


<https://doi.org/10.1038/s41586-020-2012-7>

Received: 20 January 2020

Accepted: 29 January 2020

Published online: 3 February 2020

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 Check for updates

Peng Zhou<sup>1,5</sup>, Xing-Lou Yang<sup>1,5</sup>, Xian-Guang Wang<sup>2,5</sup>, Ben Hu<sup>1</sup>, Lei Zhang<sup>1</sup>, Wei Zhang<sup>1</sup>, Hao-Rui Si<sup>1,3</sup>, Yan Zhu<sup>1</sup>, Bei Li<sup>1</sup>, Chao-Lin Huang<sup>2</sup>, Hui-Dong Chen<sup>2</sup>, Jing Chen<sup>1,3</sup>, Yun Luo<sup>1,3</sup>, Hua Guo<sup>1,3</sup>, Ren-Di Jiang<sup>1,3</sup>, Mei-Qin Liu<sup>1,3</sup>, Ying Chen<sup>1,3</sup>, Xiao-Shuang Zheng<sup>1,3</sup>, Kai Zhao<sup>1,3</sup>, Quan-Jiao Chen<sup>1,3</sup>, Fa-Xian Zhan<sup>4</sup>, Yan-Yi Wang<sup>1</sup>, Geng-Fu Xiao<sup>1</sup> & Zhen

Since the outbreak of severe acute respiratory syndrome (SARS) in 2002, a number of SARS-related coronaviruses (SARSr-CoVs) have been identified in their natural reservoir host, bats<sup>1–4</sup>. Previous studies have shown that these viruses have the potential to infect humans<sup>5–7</sup>. Here we report the characterization of a new coronavirus (2019-nCoV) that caused the acute respiratory syndrome in humans in Wuhan, China, on 12 December 2019, had caused 2,794 laboratory-confirmed deaths by 26 January 2020. Full-length genomes were obtained from 19 patients at an early stage of the outbreak. The sequences share 79.6% sequence identity to SARS-CoV. Full-length genomes are 96% identical at the whole-genome level to a bat coronavirus. Sequence analysis of seven conserved non-structural protein genes shows that the virus belongs to the species of *SARSr-CoV*. In addition, the bronchoalveolar lavage fluid of a critically ill patient was found to contain the receptor–angiotensin converting enzyme II (ACE2) receptor.

Editor's Note: This article was published on January 24, 2020, at NEJM.org.

ORIGINAL ARTICLE BRIEF REPORT

## A Novel Coronavirus from Patients with Pneumonia in China, 2019

Na Zhu, Ph.D., Dingyu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D., Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., *et al.*, for the China Novel Coronavirus Investigating and Research Team

Article Figures/Media

Metrics

17 References 9817 Citing Articles

### Summary

In December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. Human airway epithelial cells were used to isolate a novel coronavirus, named 2019-nCoV, which formed a clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. Different from both MERS-CoV and

February 20, 2020

N Engl J Med 2020; 382:727-733

DOI: 10.1056/NEJMoa2001017

Chinese Translation 中文翻译

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EDITORIAL FEB 20, 2020

Another Decade, Another Coronavirus

S. Perlman

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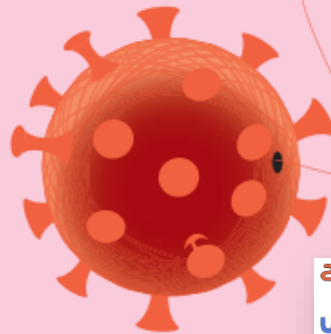
# Using sequencing to understand virus outbreaks

Onsdag 13. januar 2021 | POLITIKEN

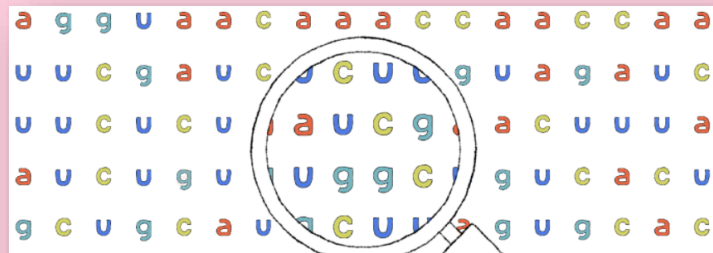
## Her er de 6 virusvarianter, som det nordjyske forskerhold holder øje med

Professor Mads Albertsen og hans 15 mand store forskerstab fra Aalborg Universitet har en tjekliste på alle de varianter af coronavirus, som de skal holde et særligt vågent øje med i Danmark

Tekst: Lasse Foghsgaard Grafik: Jens B. Mørch



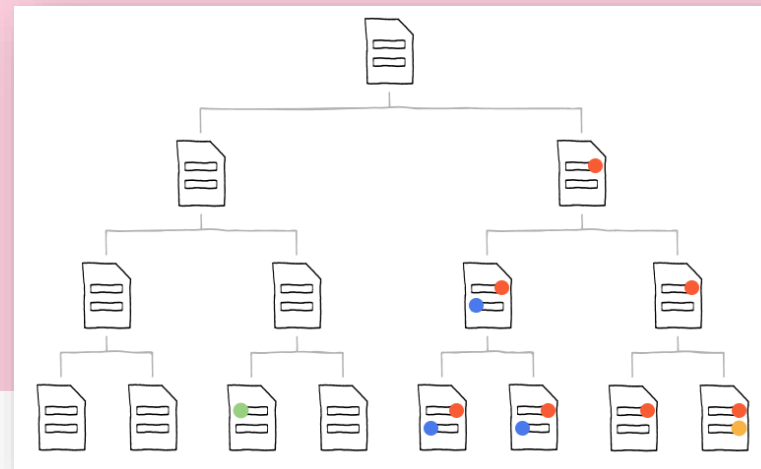
I øjeblikket er den smitsomme **britiske variant B117** øverst på listen, og den er for alvor ved at få fat i Danmark. Derudover er også den smitsomme **sydafrikanske variant** på listen. Den er fundet andre steder i Europa, men er endnu ikke sporet i Danmark. Derudover holder man stadig øje med **danske minkvarianter** af coronavirus samt en **spansk** og en **rumænsk** variant



INDLAND

**Hvor blev jeg smittet?  
Sådan afslører danske forskere, hvem der smitter hvem med corona**

Ved mutationen **N501Y** bliver et **a** ændret til et **t** i kodenstrengen  
`acaatcatatggtttccaaccacttatggtgttggttaccaccatacag`  
(i stedet for **a**)



En person med symptomer på covid-19 får taget en coronatest med et mundskrab



Hvis prøven er positiv, bliver den sendt til Statens Serum Institut, som isolerer virusens arvemasse i form af rna.



Prøven bliver sendt til Aalborg Universitet, hvor rna bliver kopieret til dna og mangfoldiggjort i rigtig mange kopier. En sekvensmaskine bestemmer den præcise rækkefølge af de 30.000 bogstaver, som den genetiske kode består af.

```
acttaacasagccttacattaagtggga  
tttgttaaataatgacttcacggaagaggta-  
aaactcttgaccgttatttaaatat-  
tgggatcagacacttaacaagccttacattaagtgg  
atttgttaaataatgacttcacggaagaggttaaaa
```



# Using sequencing to understand virus outbreaks

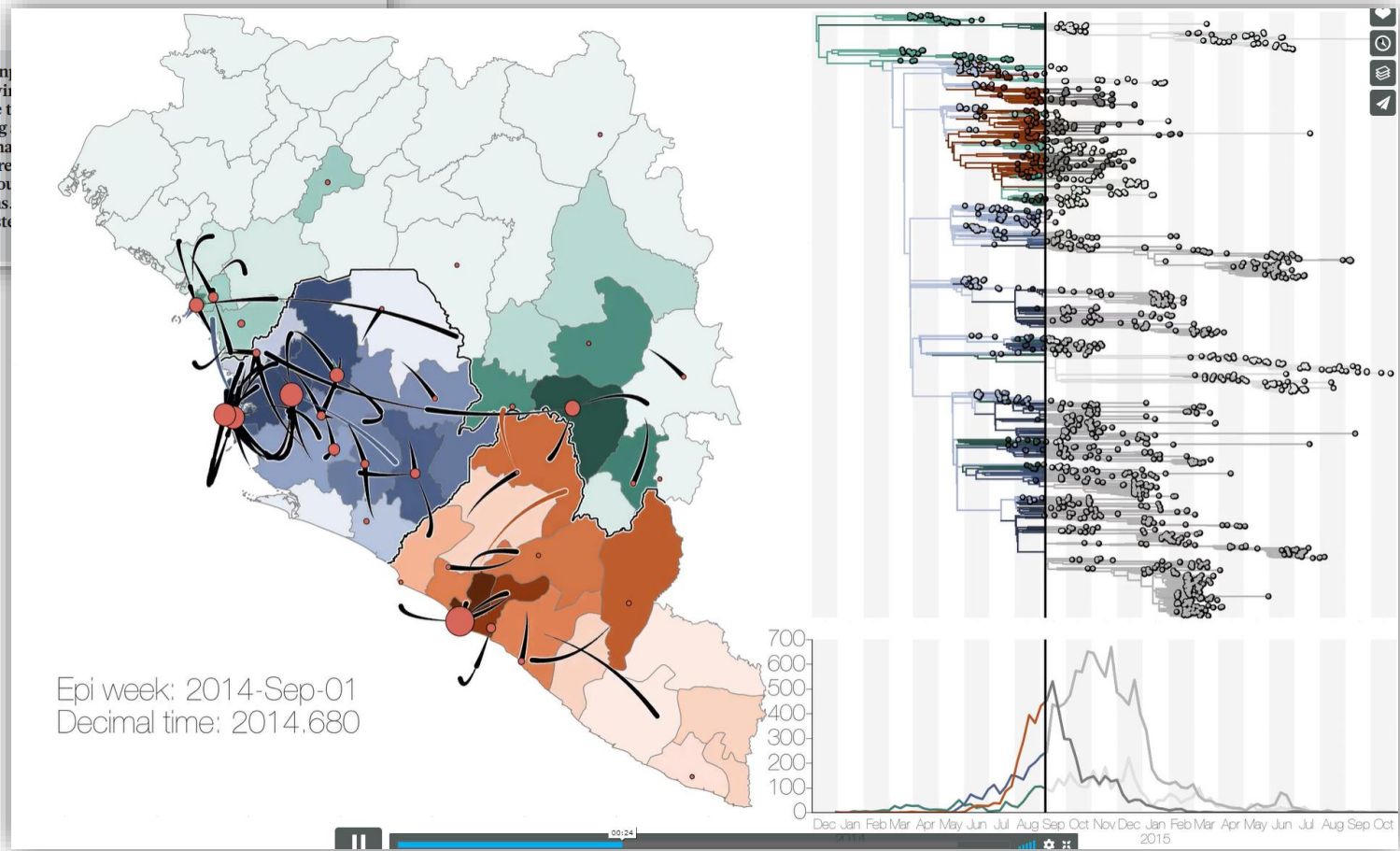
## ARTICLE

doi:10.1038/nature22040

### Virus genomes reveal factors that spread and sustained the Ebola epidemic

A list of authors and their affiliations appears at the end of the paper

The 2013–2016 West African epidemic caused by the Ebola virus was of unprecedented scale. Here we reconstruct the dispersal, proliferation and decline of Ebola virus genomes, which represent over 5% of the known cases. We integrate demographic data with viral movement among administrative regions, inferring transmission routes between larger and closer populations. Despite attenuation of international transmission had already sown the seeds for an international epidemic, regional transmission sustained the epidemic. We address why the epidemic did not spread into neighboring countries, which were susceptible to substantial outbreaks but at lower risk of introductions. These insights will help to inform interventions in future epidemics.



# Da lyden af død begyndte i Bergamo, var Italien for længst blevet Europas patient 0

På blot en måned har coronaepidemien bragt Italien ud i landets værste krise siden Anden Verdenskrig. Overhørte advarsler og skødesløshed har givet virussen mulighed for at løbe løbsk. Dermed har Italien vist andre europæiske nationer, hvad man skal og ikke skal gøre, hvis man vil undgå den skarpt opadgående dødelige kurve



En overfyldt hospitalsgang i Bergamo, Italien, hvor patienter, der er formodet smittet med COVID-19, er indlagt.

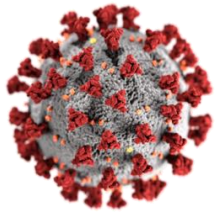
## Tidslinje: Corona i Italien

- 20. februar: En 38-årig mand bliver registreret som den første, der er smittet med COVID-19 i Italien.
- 23. februar: Ti mindre byer med i alt 50.000 indbyggere i Norditalien bliver sat i karantæne. Skoler lukker i Norditalien.
- 4. marts: Skoler og universiteter lukker i hele landet.
- 8. marts: 16 mio. italienere i Lombardiet, Veneto og Emilia-Romagna bliver sat i karantæne.
- 10. marts: Alle Italiens 60 mio. indbyggere bliver sat i karantæne.
- 19. marts: For første gang er der samlet flere coronadøde i Italien (3.405) end i Kina (3.245).
- 22. marts: Alle fabrikker og al produktion, der ikke er absolut nødvendig, lukkes ned.
- 27. marts: I alt 86.498 tilfælde af coronavirus er registreret i Italien. Af dem er 10.950 meldt raske og 9.134 er døde.

# Two small stories

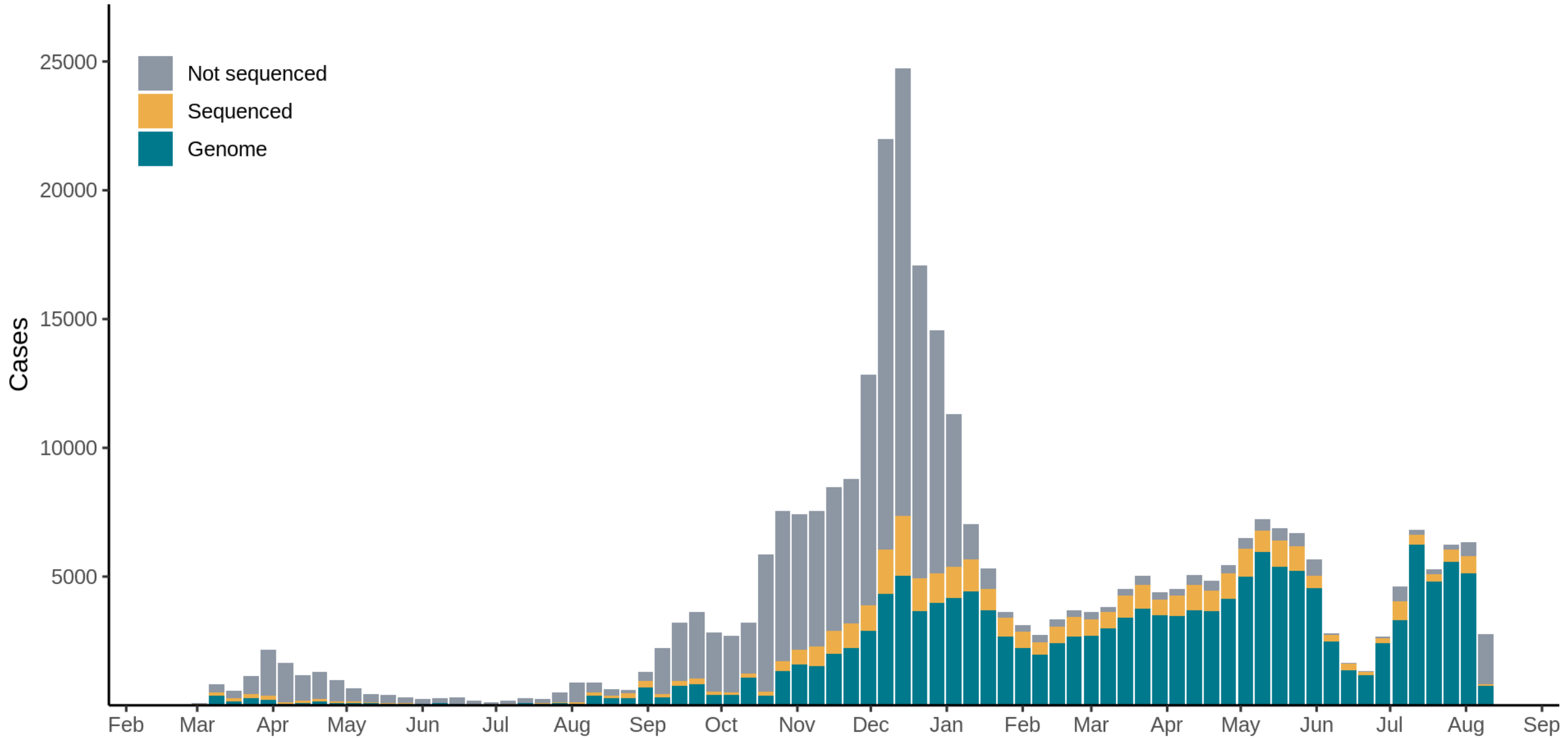


How we started sequencing SARS-CoV-2

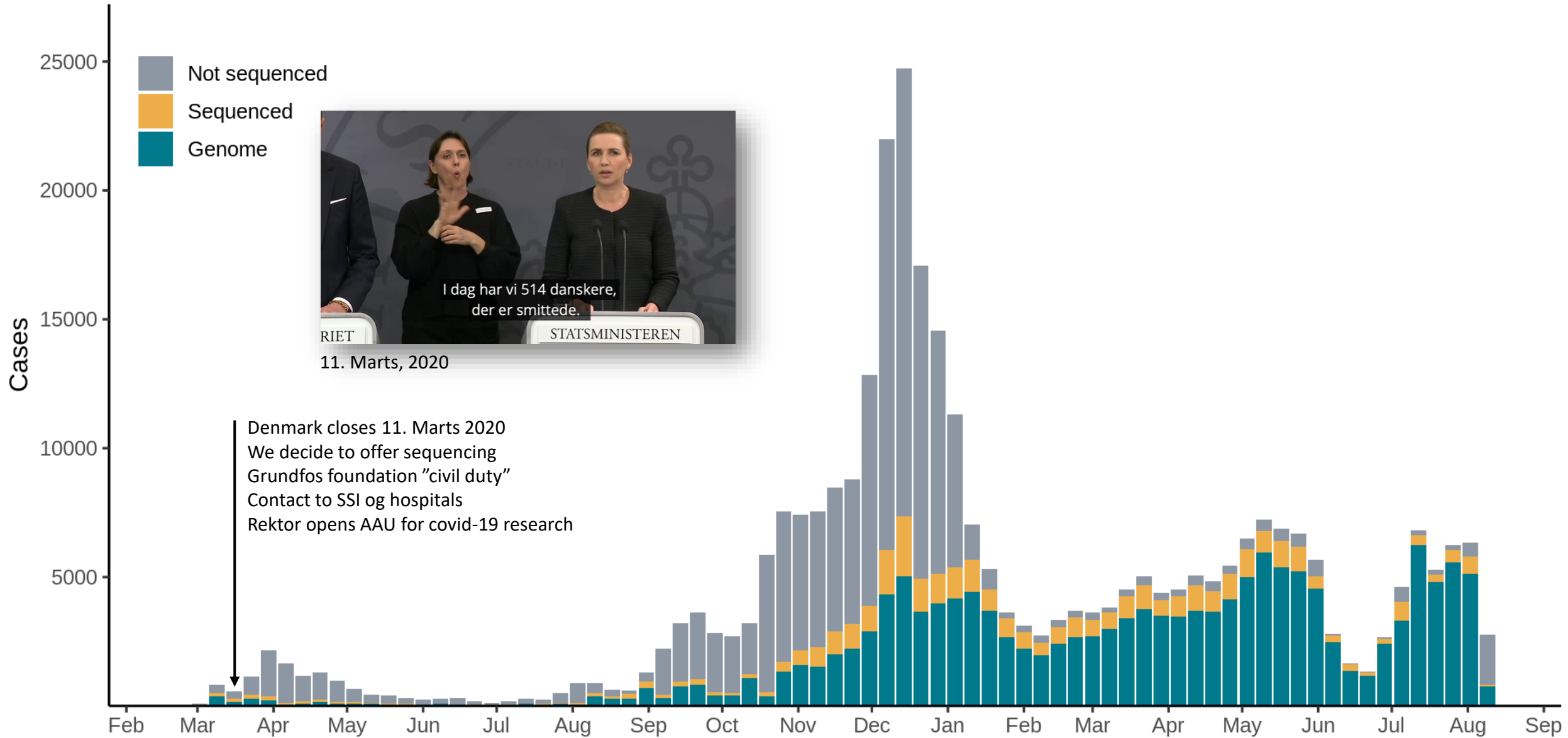


The Danish pandemic seen through genomics

# A brief history of SARS-CoV-2 sequencing in Denmark

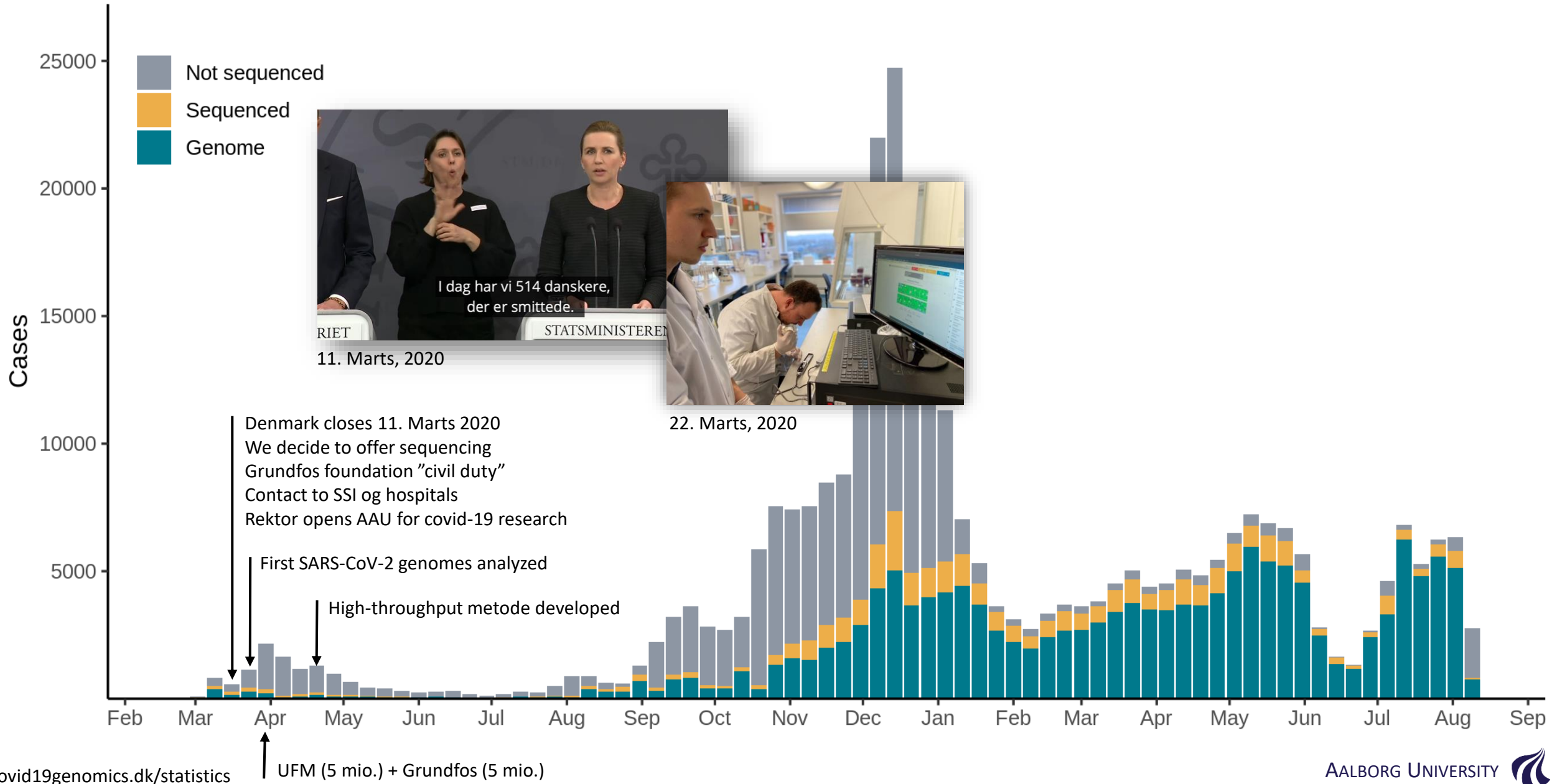


# A brief history of SARS-CoV-2 sequencing in Denmark

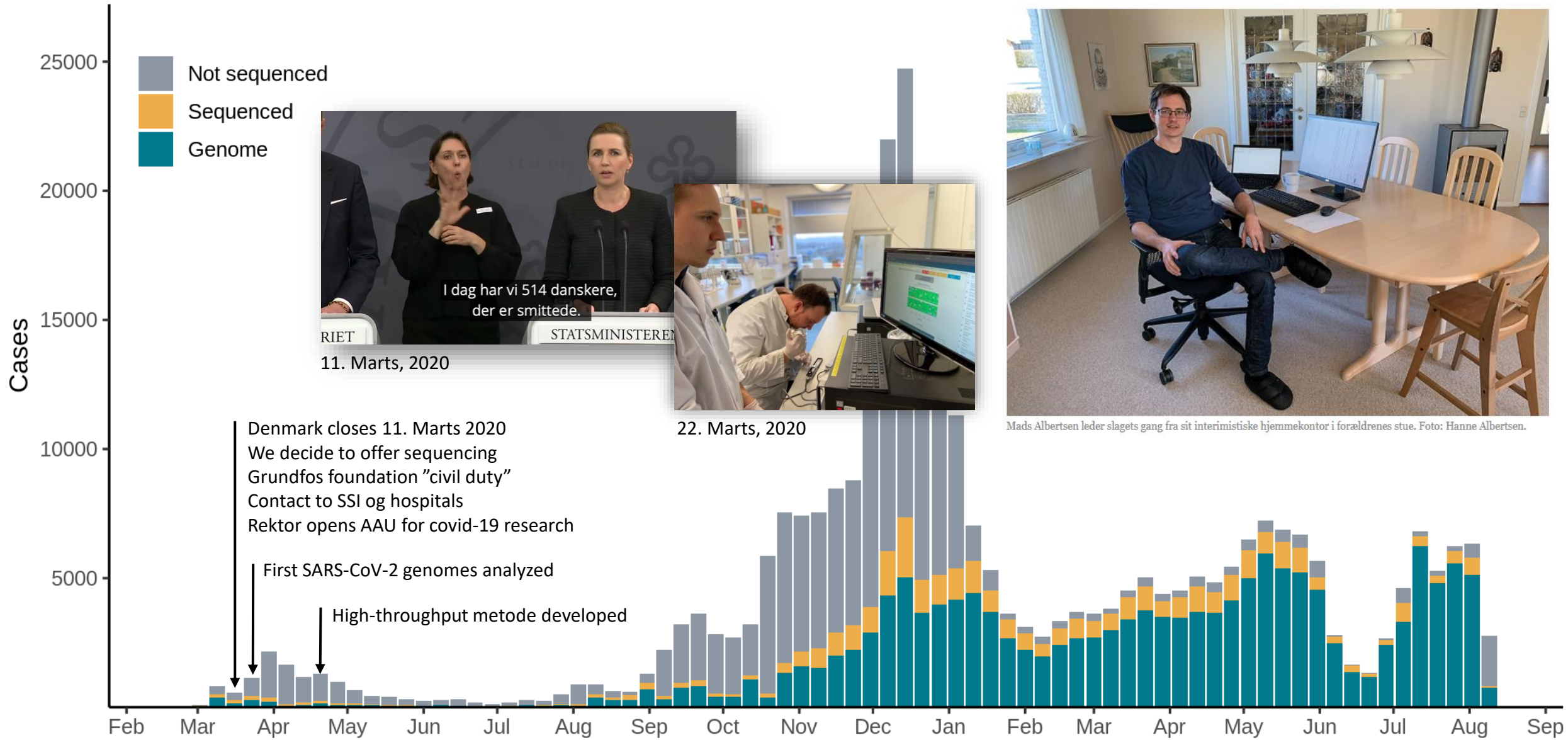


Denmark closes 11. Marts 2020  
We decide to offer sequencing  
Grundfos foundation "civil duty"  
Contact to SSI og hospitals  
Rektor opens AAU for covid-19 research

# A brief history of SARS-CoV-2 sequencing in Denmark



# A brief history of SARS-CoV-2 sequencing in Denmark





# A brief history of SARS-CoV-2 sequencing in Denmark

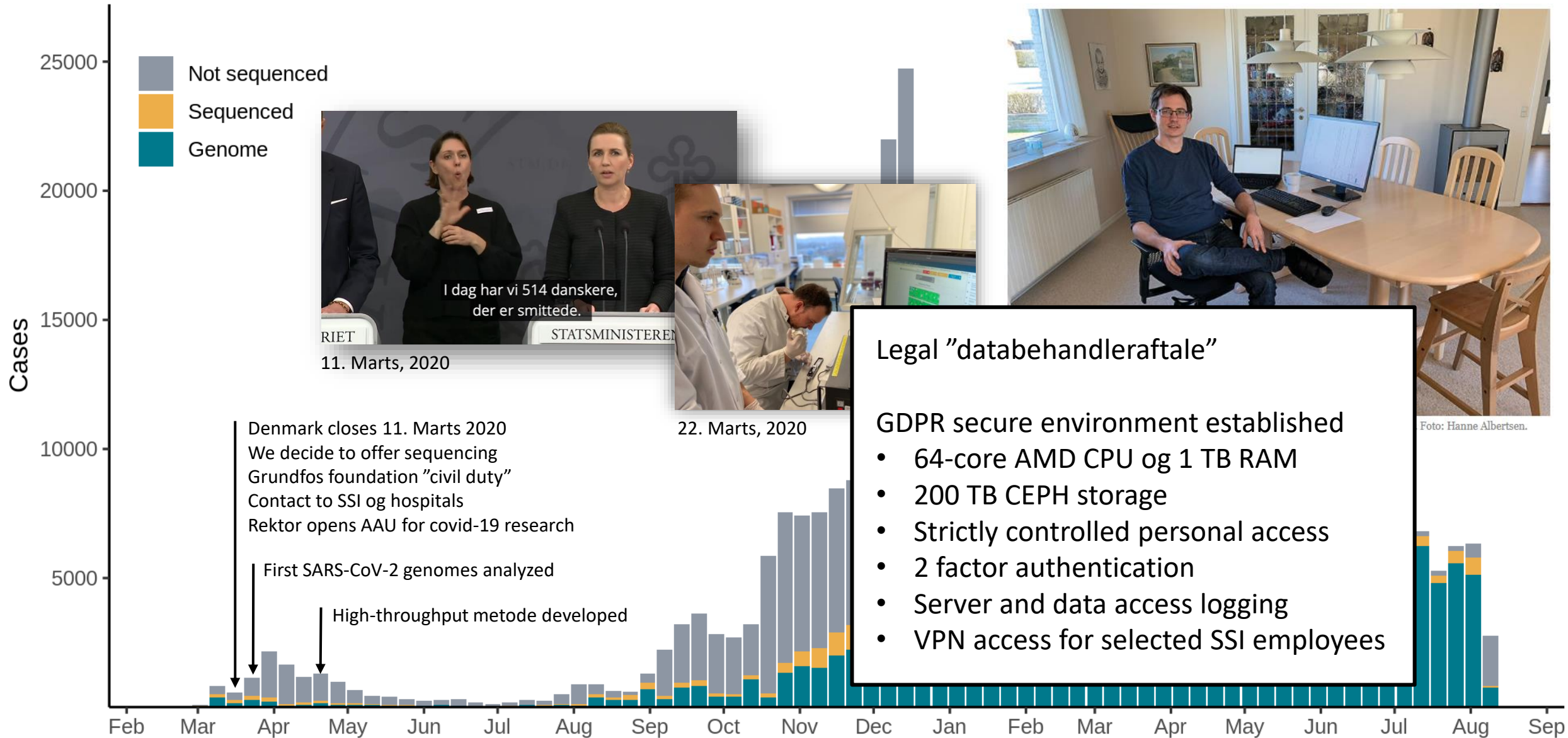


Foto: Hanne Albertain.

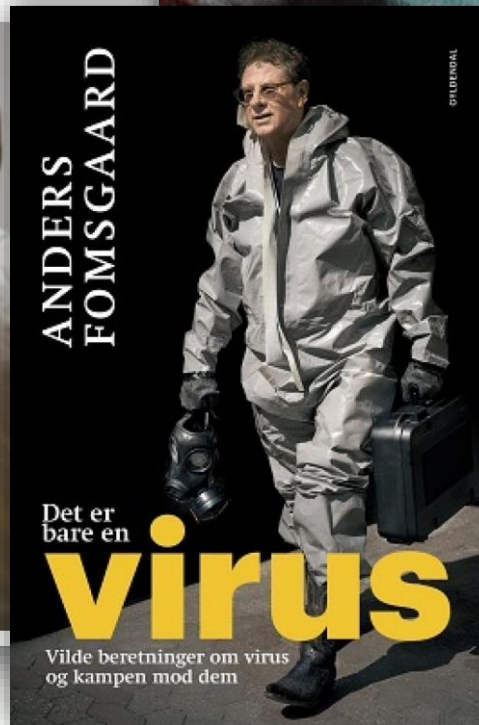
# A brief history of SARS-CoV-2 sequencing in Denmark



# A brief history of SARS-CoV-2 sequencing in Denmark

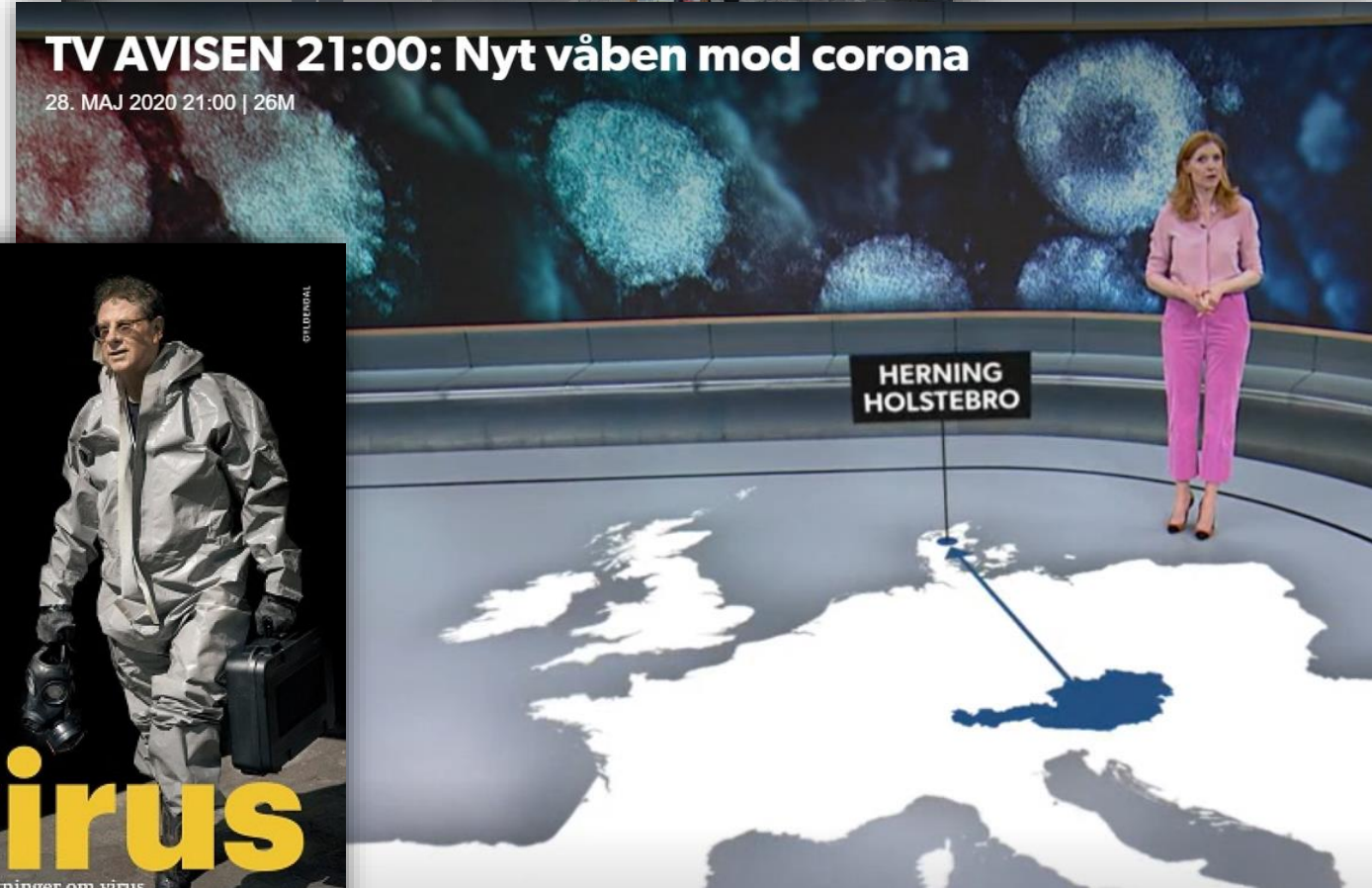
## Ny genforskning afslører: Sådan endte Midt- og Vestjylland med at blive hotspot for corona

Herning og Holstebro blev kaldt lille-Bergamo, og området flød med rygter om årsag til udbredt corona-smitte.

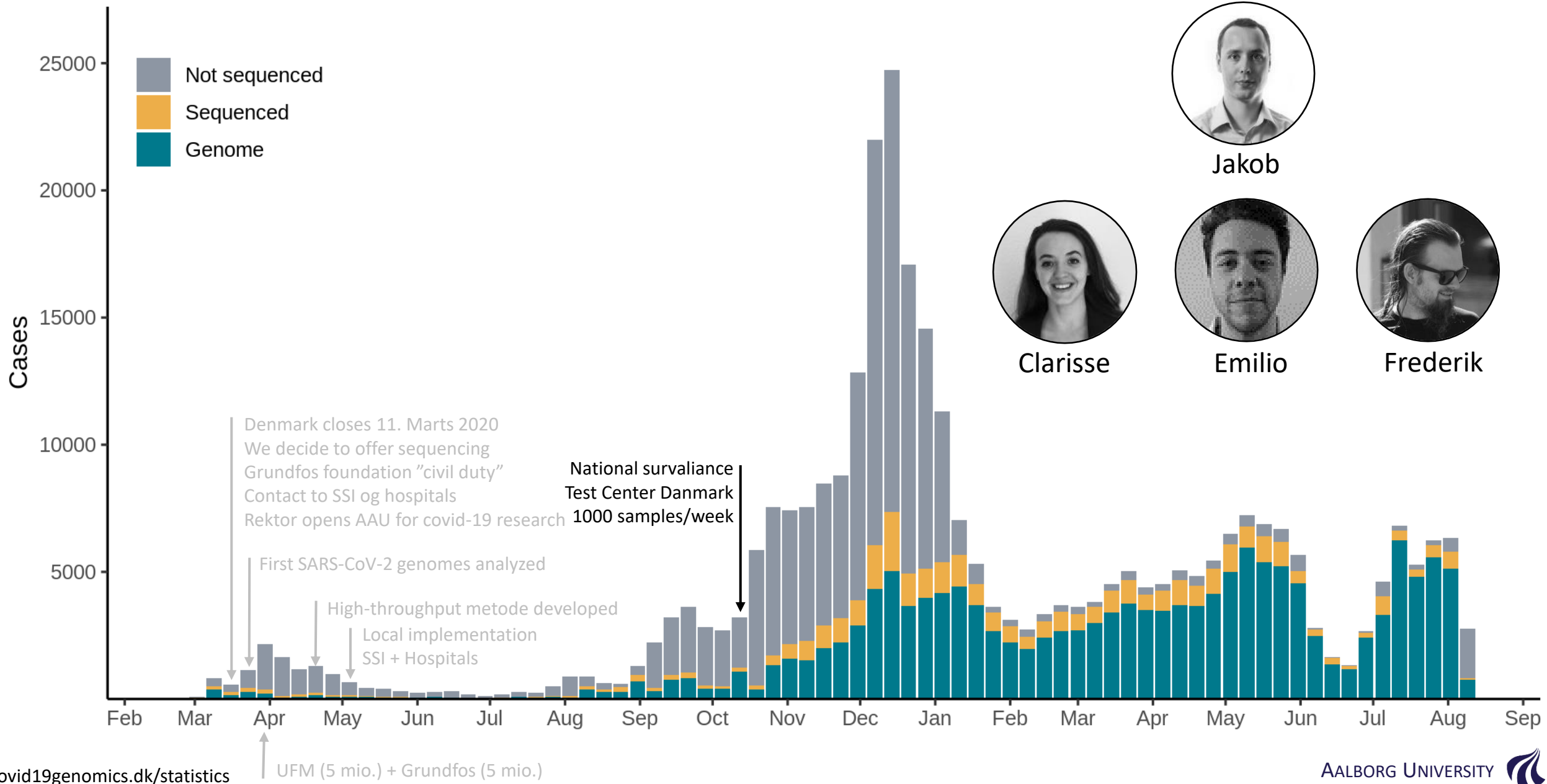


## TV AVISEN 21:00: Nyt våben mod corona

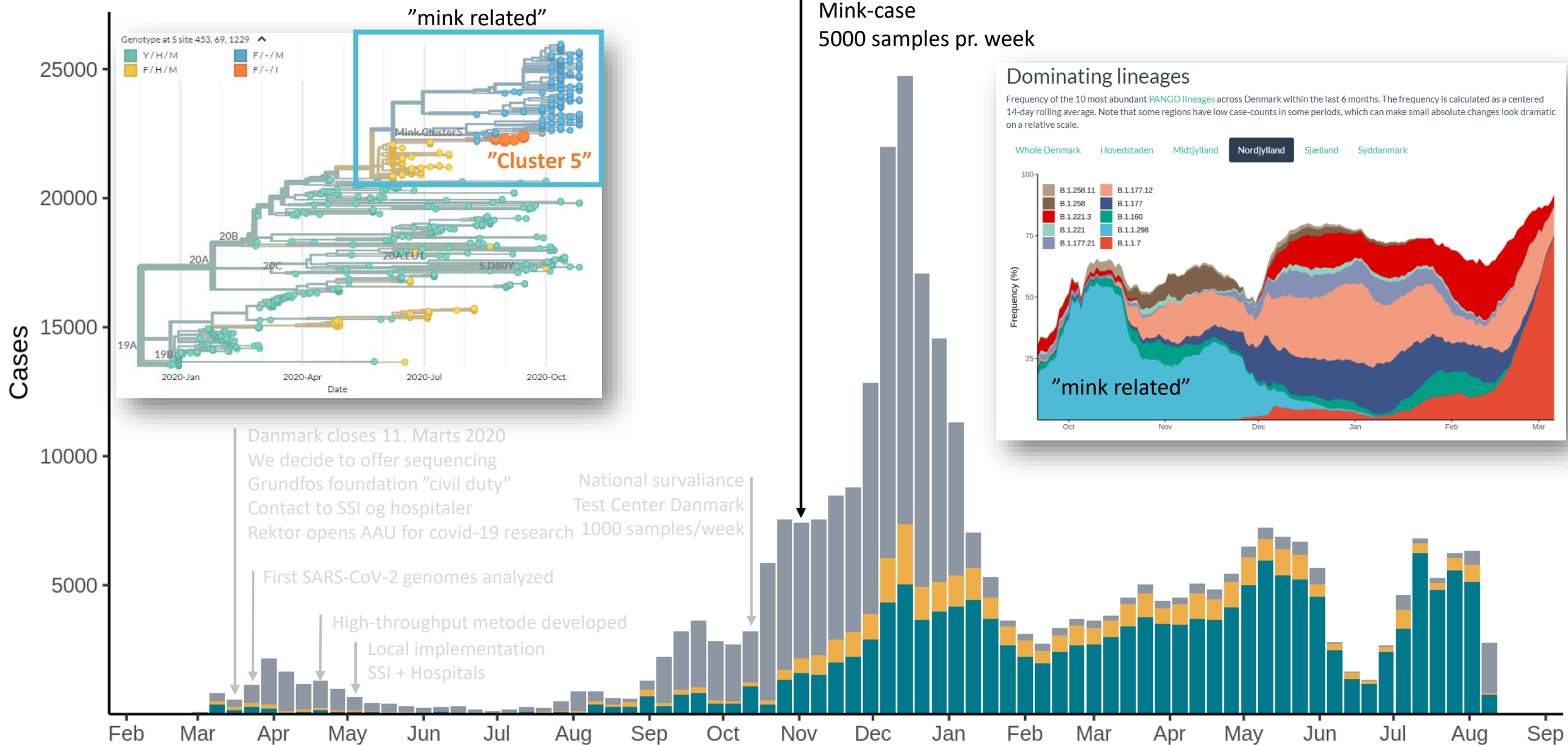
28. MAJ 2020 21:00 | 26M



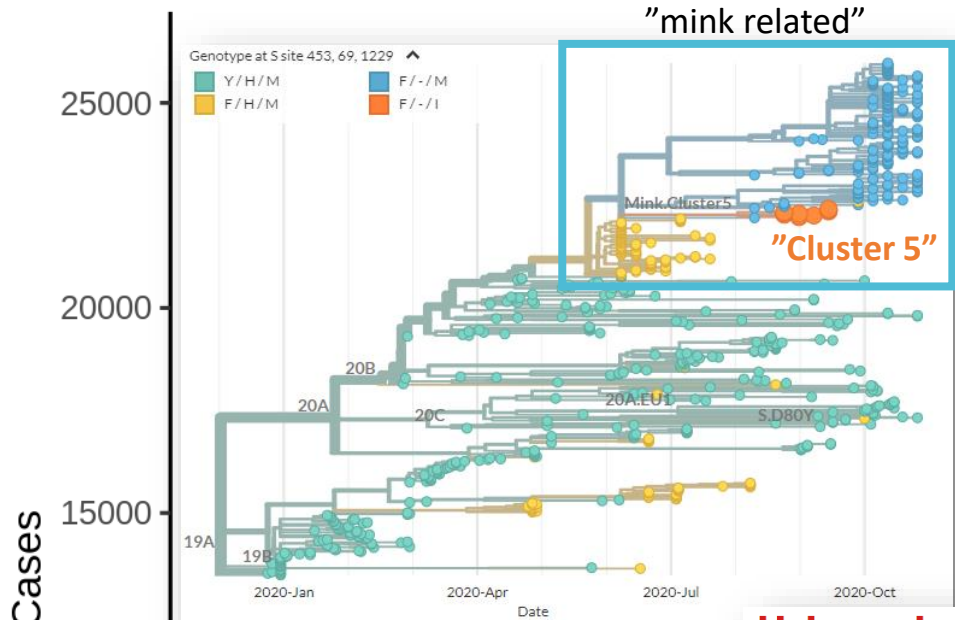
# A brief history of SARS-CoV-2 sequencing in Denmark



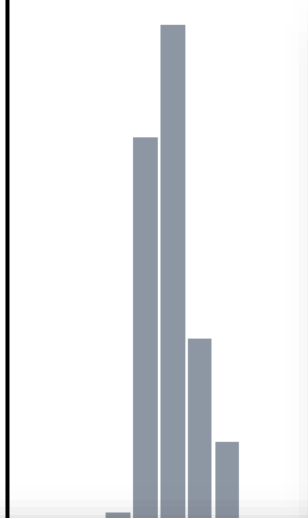
# A brief history of SARS-CoV-2 sequencing in Denmark



# A brief history of SARS-CoV-2 sequencing in Denmark

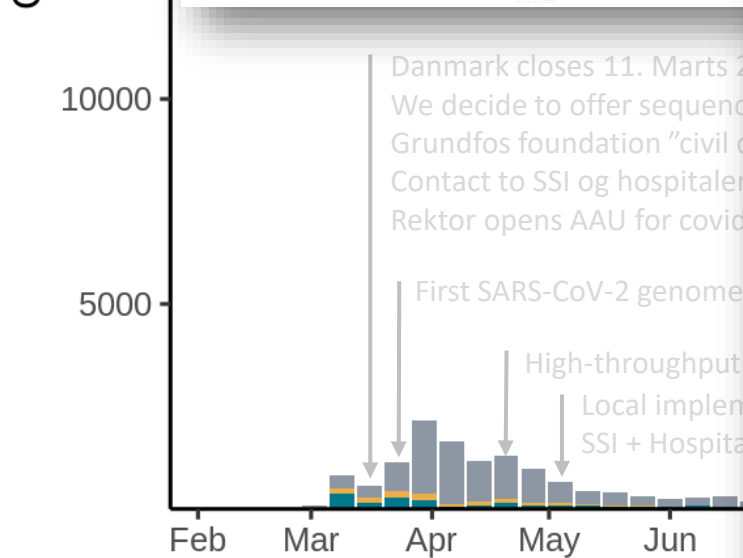
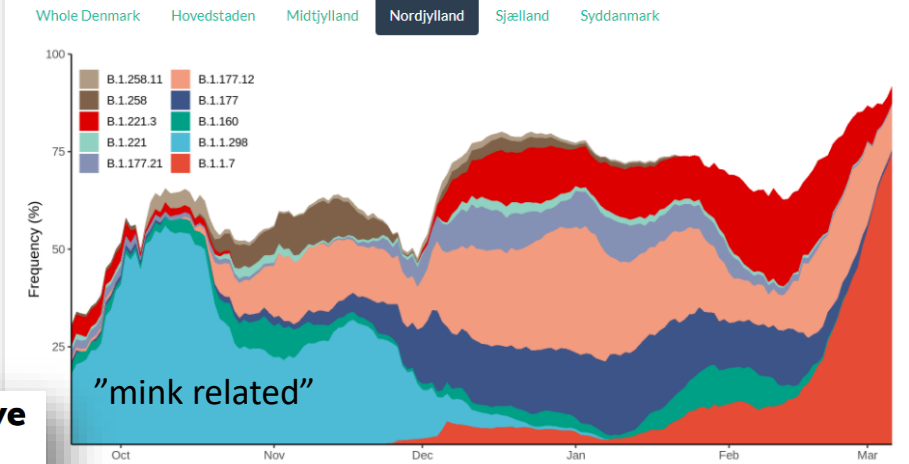


Mink-case  
5000 samples pr. week



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.



## Hele verden holder vejret: Nordjylland kan blive et nyt Wuhan

Et plejehjem i Sindal og nogle minkfarme i nærheden var startskuddet til den situation, der har ført til en delvis nedlukning af Nordjylland - for at undgå et nyt Wuhan.

Lyt til artiklen

05. nov 2020, kl. 14:27

af Emma Fjordbak  
Journalist

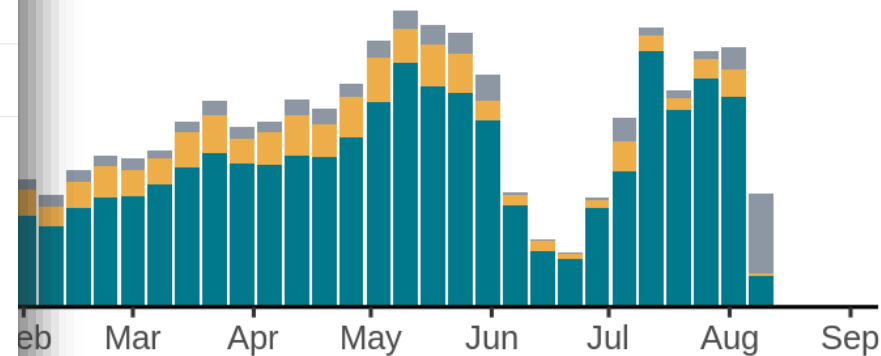
Nordjylland har på mindre end et døgn trukket overskrifter i de største nyhedsmedier verden over.

Danmark vil dræbe alle opdrættede mink: Regeringen oplyste onsdag, at en mutation i virussen kan påvirke vaccineeffektiviteten hos mennesker, skrev [The New York Times](#) blandt andet.

Det sker efter, regeringen på et pressemøde onsdag oplyste, at den muterede coronavirus fra mink udgør en trussel for en fremtidig vaccine og folkesundheden. Ikke bare i Danmark, men i hele verden.

”Worst case-scenariet er, at vi har en pandemi, som starter forfra med udgangspunkt i Danmark.

Kåre Mølbak, faglig direktør i Statens Serum Institut.



# Blitz-scaling



**Mads Albertsen**  
@MadsAlbertsen85

Testing our new brute-force high-throughput setup for SARS-CoV-2 sequencing. Emilio and the lab-team just started 14 @nanopore flowcells. 5 on GridION and 9 MinIONs with raw data streamed to our Tesla V100 GPU node. Also asked for 300 TB extra storage: IT - sure, mounting it now!



8:05 PM · Nov 12, 2020 · Twitter Web App

||| View Tweet activity

52 Retweets 8 Quote Tweets 320 Likes



# Blitz-scaling



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50% of a NVIDIA DGX-2 server (KVM VM):

- **8 NVIDIA Tesla V100 GPU's**
- 750 GB RAM
- Intel Xeon CPU 24 cores
- 15 TB intern NVMe file-storage

750 TB CEPH storage

2 servers:

- 64-core AMD CPU og 1 TB RAM (main)
- 36-core Intel CPU og 768 GB RAM (test)

≈ **200 GB signal-level data pr. hour**

1000 samples pr. day (max 2304)

Overnight data turnaround

Live signal processing

Workflow triggers

Direct metadata from SSI

Direct metadata from Test Center Denmark

Daily data-release before 12.00

- SSI, Modelling, Contact-tracing





# A brief history of SARS-CoV-2 sequencing in Denmark



SUNDHEDS- OG ÆLDREMINISTERIET

TEMAER Sundhed Ældre Sundhedsprofessionelle Ministeriet Ministeren

Du er her: Forside **De fleste restriktioner lempes i Nordjylland**

NYHEDER

- Pressekontakt
- Om hjemmesiden
- Privatlivspolitik
- Abonner på nyheder
- Lovstof
- Publikationer

## De fleste restriktioner lempes i Nordjylland

19-11-2020

PRESSEMEDDELELSE - På baggrund af nye smittedata og resultater fra sekventeringen af de positive prøver, der viser en faldende tendens af minkvarianter i Nordjylland, vurderer Indsatsgruppen for Covid-19-håndtering, at de fleste lokale restriktioner i syv nordjyske kommuner kan lempes. Regeringen har besluttet at følge anbefalingen.

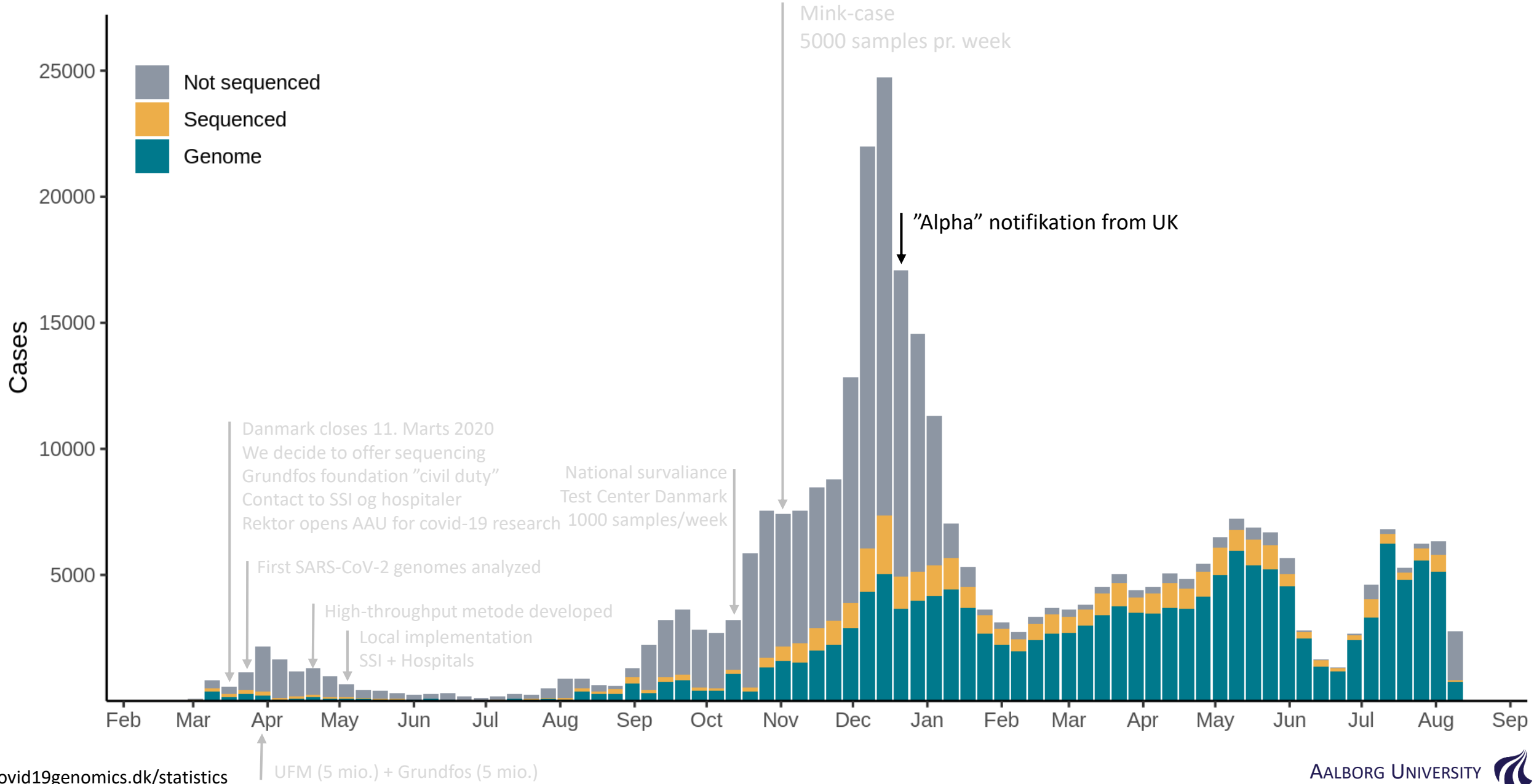
Sundhedsmyndighederne har på baggrund af nyeste data for smittespredning og sekventering af positive prøver fundet basis for en lempelse af langt de fleste restriktionerne i Frederikshavn, Vesthimmerland, Jammerbugt, Thisted, Brønderslev, Hjørring og Læsø kommuner.

Hovedparten af lempelserne vil være gældende fra den 19. november 2020. Der er følgende undtagelser:

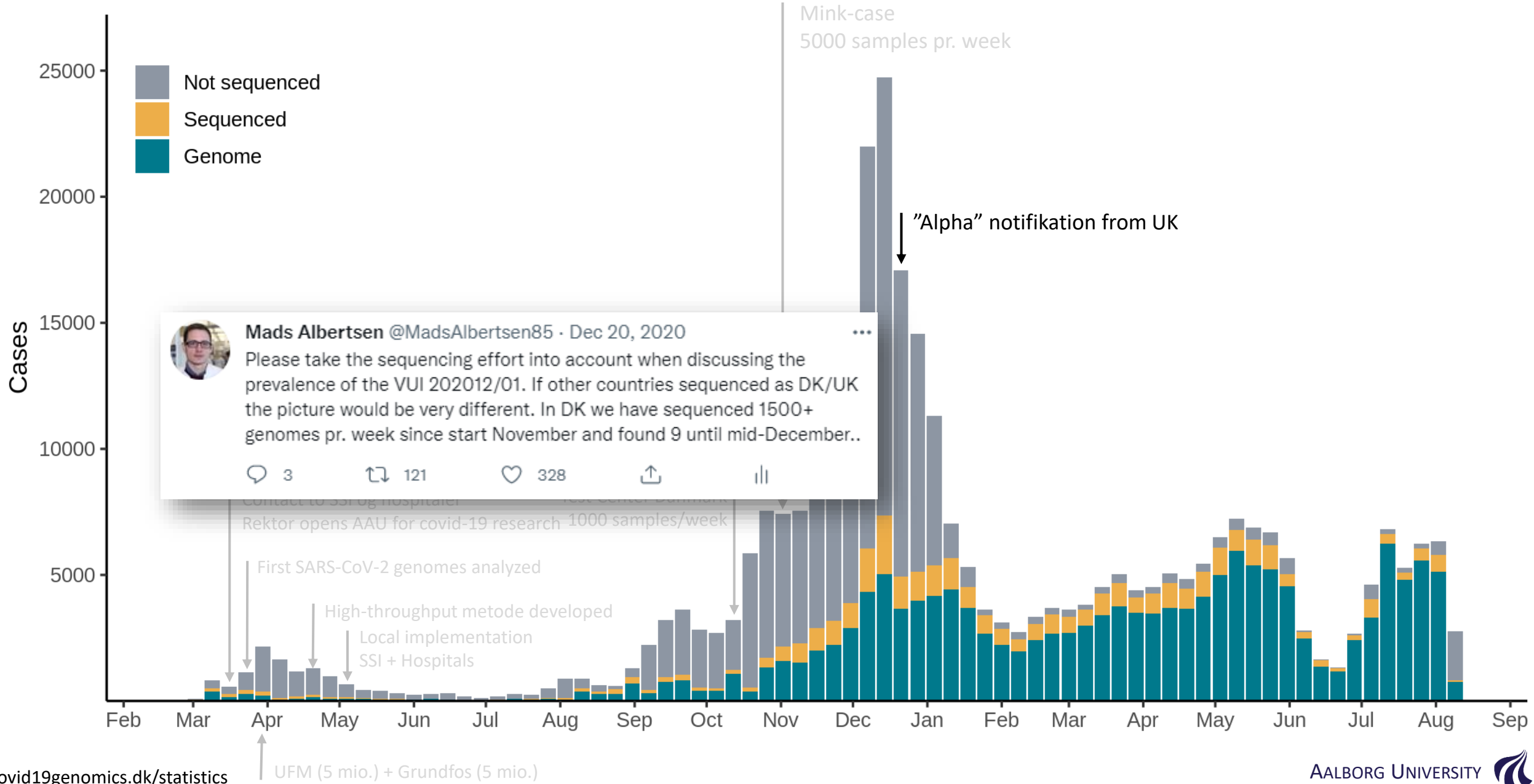
LÆS MERE PÅ CORONASMITTE.DK

De danske myndigheder har samlet alle informationer om coronavirus på [coronasmitte.dk](https://coronasmitte.dk). Hvis du ikke kan finde svar her, kan du ringe til: telefon-hotline 7020 0233

# A brief history of SARS-CoV-2 sequencing in Denmark



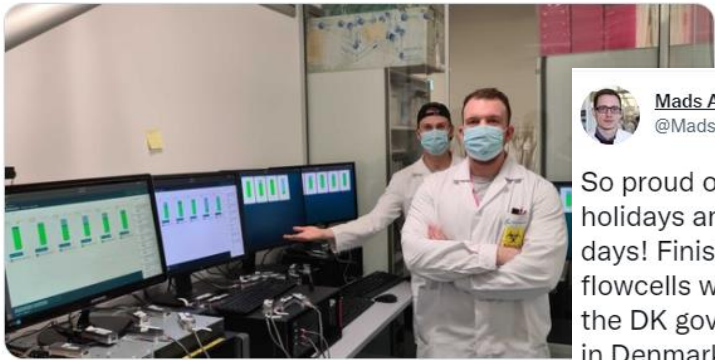
# A brief history of SARS-CoV-2 sequencing in Denmark



# A brief history of SARS-CoV-2 sequencing in Denmark

Mads Albertsen  
@MadsAlbertsen85

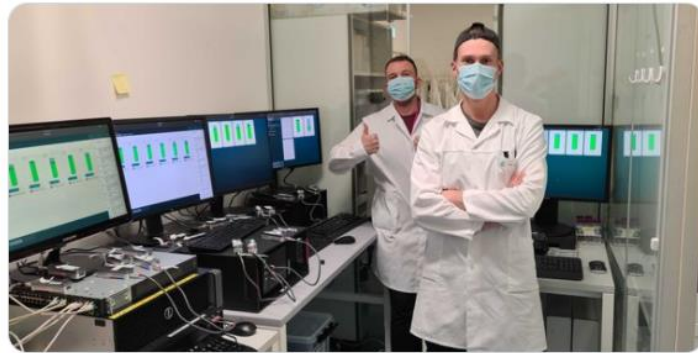
The @aauengineering SARS-CoV-2 lab-team ends the year strong with 24 @nanopore flowcells running 2304 samples! Cheers to @SSI\_dk and DK hospitals for feeding us with samples throughout 2020. Hats off to the bioinformatic, admin, and legal teams that work behind the scenes.



10:30 PM · Dec 30, 2020 · Twitter Web App

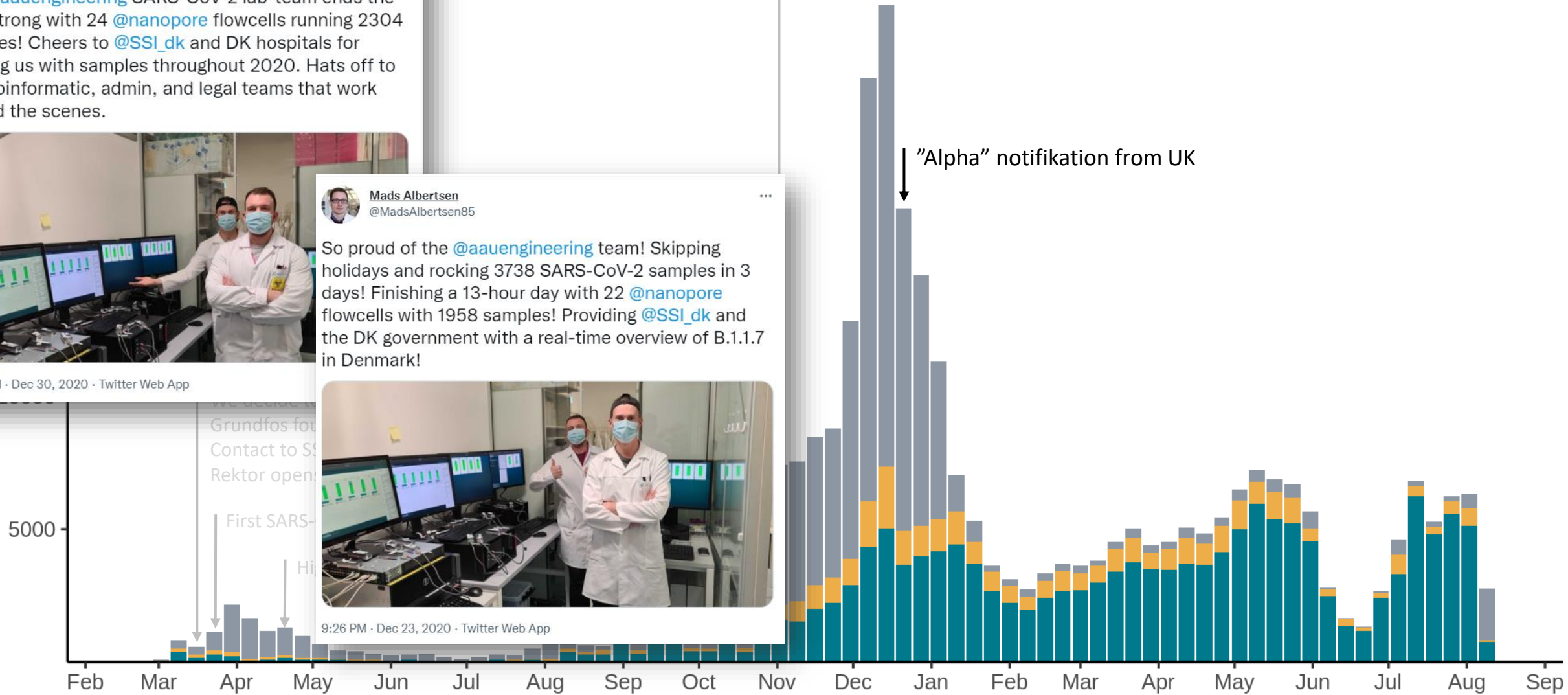
Mads Albertsen  
@MadsAlbertsen85

So proud of the @aauengineering team! Skipping holidays and rocking 3738 SARS-CoV-2 samples in 3 days! Finishing a 13-hour day with 22 @nanopore flowcells with 1958 samples! Providing @SSI\_dk and the DK government with a real-time overview of B.1.1.7 in Denmark!

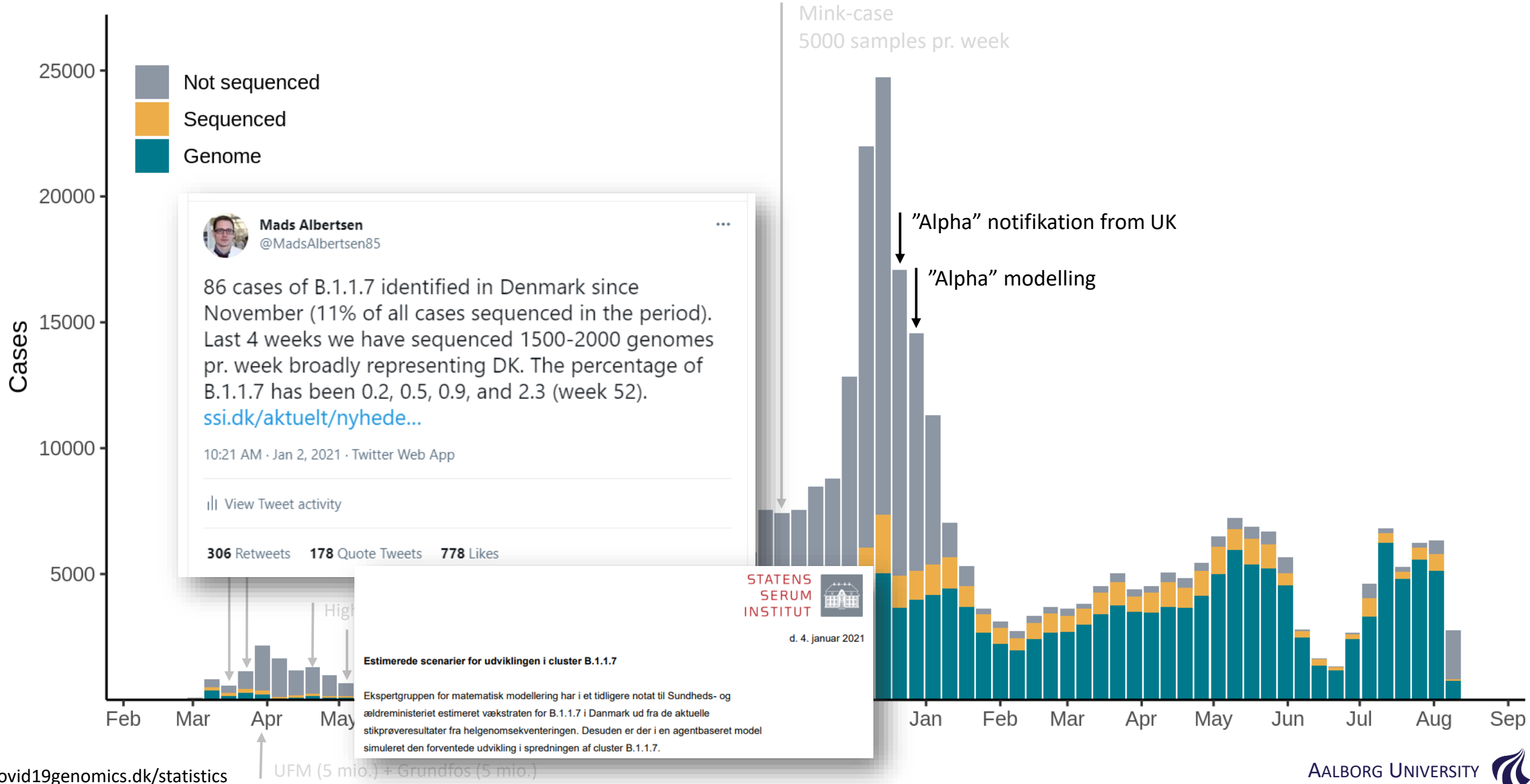


9:26 PM · Dec 23, 2020 · Twitter Web App

Mink-case  
5000 samples pr. week



# A brief history of SARS-CoV-2 sequencing in Denmark



**Mads Albertsen**  
@MadsAlbertsen85

86 cases of B.1.1.7 identified in Denmark since November (11% of all cases sequenced in the period). Last 4 weeks we have sequenced 1500-2000 genomes pr. week broadly representing DK. The percentage of B.1.1.7 has been 0.2, 0.5, 0.9, and 2.3 (week 52).

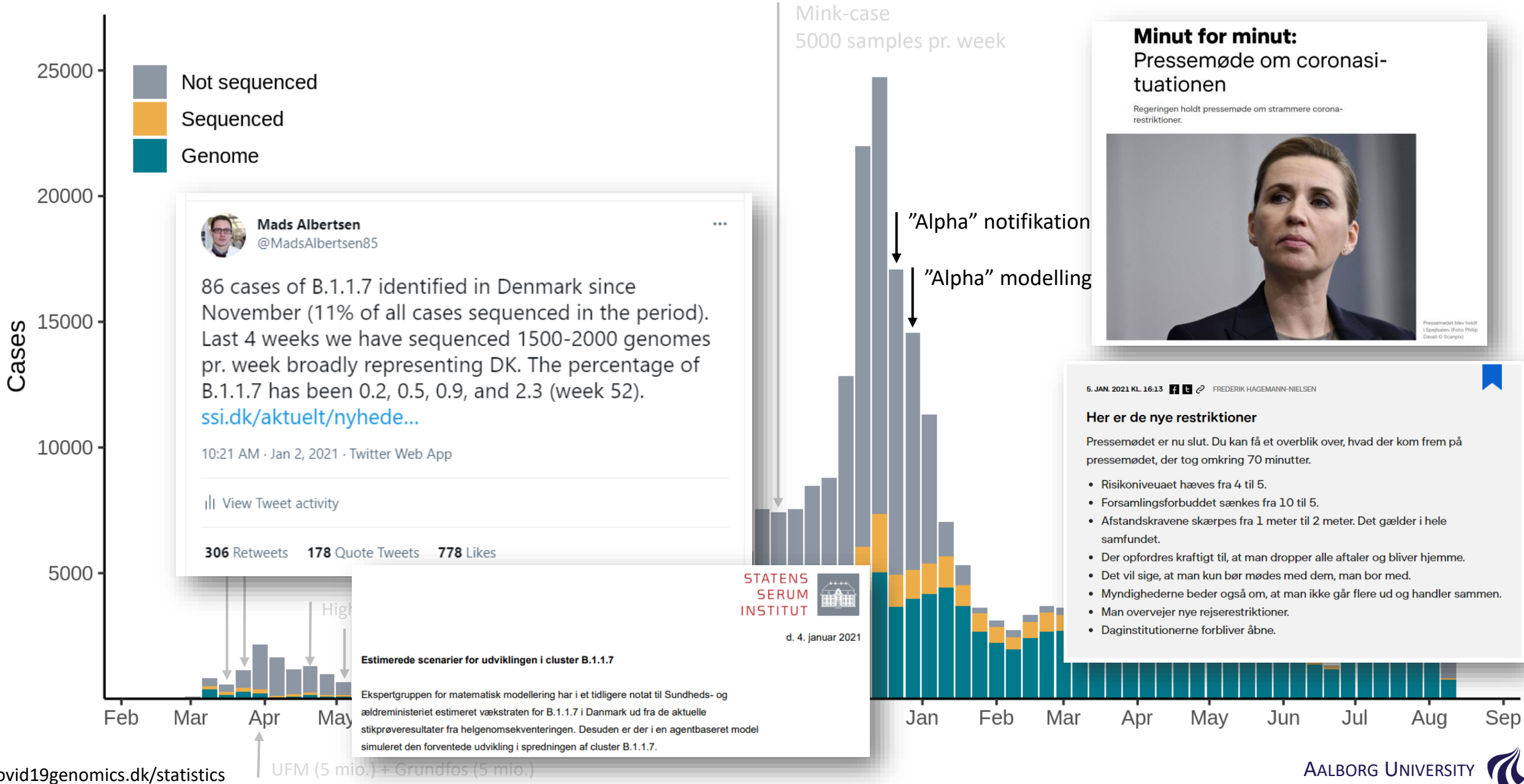
[ssi.dk/aktuelt/nyhede...](https://ssi.dk/aktuelt/nyhede...)

10:21 AM · Jan 2, 2021 · Twitter Web App

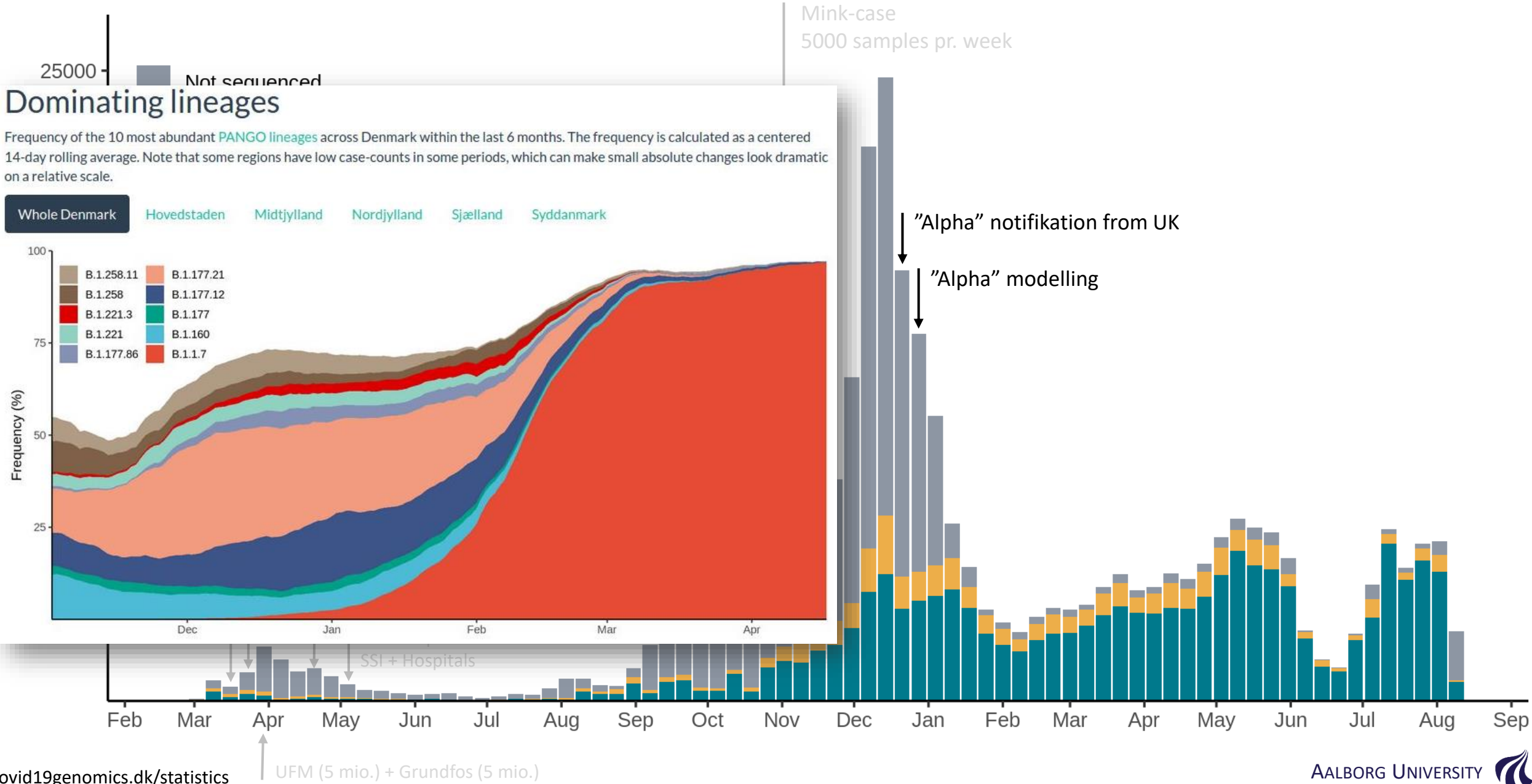
View Tweet activity

306 Retweets 178 Quote Tweets 778 Likes

# A brief history of SARS-CoV-2 sequencing in Denmark



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# A brief history of SARS-CoV-2 sequencing in Denmark



**Mads Albertsen** @MadsAlbertsen85  
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[ssi.dk/aktuelt/nyhede...](https://www.ssi.dk/aktuelt/nyhede...)

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**Mads Albertsen** @MadsAlbertsen85  
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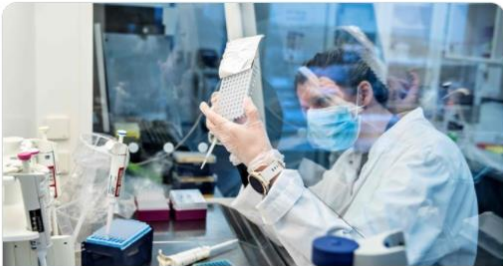
**Eksponeringer** 1.095.597  
 antal gange, brugere har set dette Tweet på Twitter

**Medievisninger** 77  
 der foretages optælling af alle visninger (automatiske afspilninger og klik) af dine medier på tværs af videoer, vines, GIF-filer og billeder

**Engagementer i alt** 22.838  
 antal gange personer har interageret med dette Tweet



**Nick Loman** @pathogenomick · Jan 23  
 "Without this variant, we would be in really good shape,"



Denmark is sequencing all coronavirus samples and has an alarming vi...  
 Cases are exploding exponentially and lockdowns may not be enough.  
[washingtonpost.com](https://www.washingtonpost.com)



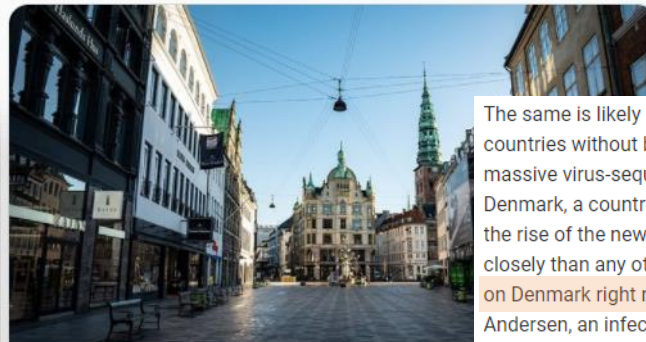
**Eric Topol** @EricTopol · Jan 6  
 The rapid spread of B.1.1.7 in the UK, Ireland and Denmark, as confirmed by sequencing, and need for aggressive action  
[sciencemag.org/news/2021/01/v...](https://www.sciencemag.org/news/2021/01/v...) by @kakape @ScienceMagazine w/ @firefoxx66 @JeremyFarrar @BillHanage @ViolaPriesemann @AdamJKucharski @MadsAlbertsen85 @EvolveDotZoo



Viral mutations may cause another 'very, very bad' COVID-19 wave,



**Kai Kupferschmidt** @kakape · Feb 3  
 As most of you know, I've been following the #b117 data closely which has meant watching Denmark and talking to researchers there. So here is a piece of Danish situation, why it is important and what we are learning from it. (thread to come tomorrow)



Danish scientists see tough times ahead as they wait  
 Some say the country should reopen—even if it causes  
 —once vulnerable populations are vaccinated  
[sciencemag.org](https://www.sciencemag.org)

The same is likely happening in many countries without being noticed. But a massive virus-sequencing effort has allowed Denmark, a country of 5.8 million, to track the rise of the new COVID-19 variant more closely than any other country. "All eyes are on Denmark right now," says Kristian Andersen, an infectious diseases researcher at Scripps Research who is advising the Danish government. "When it comes to B.1.1.7, is there a way in which ... we can prevent the kind of calamity that we have seen in the U.K. and Ireland, for example?" he asks.



**Theis Ehler Molin** @theisemol · Jan 12  
 Mette synes min artikel er "lidt lang, men til gengæld meget interessant 😊"

Jeg synes, det er det perfekte slogan for os på @ZetlandMagasin!



**Mette Frederiksen**  
 32 min ·  
 Kære alle  
 Denne artikel beskriver meget godt, hvorfor den engelske variant af corona er så alvorlig. Og at vi står et svært sted i Danmark netop nu: Andelen, der er smittede – ud af dem, der testes – er faldet. Det er selvsagt godt. Men! Hvis vi dermed tror, at vi kan ånde lettet op og slække på restriktioner og adfærd, så risikerer vi først, at det går helt galt. For "nedenunder" de overordnede smittetal kan vi se, at den engelske variant spreder sig. Og den er mere – mege... Se mere



**Henrik Ullum** @henrik\_ullum · Jan 12  
 #COVID19 pandemien har bragt forskere og eksperter sammen på nye måder. I vores kamp med B117 og andre nye varianter er indsatsen fra @MadsAlbertsen85 og hans gruppe uvurderlig.



**Kim Nohr Skibsted** @kimsbibsted · Jan 11  
 Covid-19 krævede hurtig handling, fleksibilitet & ansvarlighed. Grundfos Fonden ændrede allerede d 11.3.20 betingelserne for vores projekter. Det har givet samfundet mere viden til at håndtere er krisen. Sådan. [berlingske.dk/samfund/en-hid...](https://berlingske.dk/samfund/en-hid...) #dkpol #dkbib #dkforskning #pdf #grundfos



**Lasse Foghsgaard** @Foghsgaard · Jan 13  
 Professor Mads Albertsen og hans forskerhold arbejdede før pandemien på bakterierne svar på Flora Danica. Nu spiller de en central rolle i beredskabet mod den smitsomme britiske variant @politiken #dkvid



Nordjysk virusdetektiv er blevet kendt for at opdage britisk variant i Da...  
 Et forskerhold fra Aalborg Universitet havde travlt med at studere den danske bakteriefiora, før coronapandemien bankede på døren. Nu ...  
[politiken.dk](https://www.politiken.dk)





# A brief history of SARS-CoV-2 sequencing in Denmark



**Per Michael Johansen** @aaurektor · Mar 11

Verden kigger mod AAU's unikke sekventeringsforskning, der hjælper regeringer med at redde menneskeliv. Minister [@AneHalsboe](#) tog sig i dag tid til at hylde de dygtige forskere [@MadsAlbertsen85](#) og team. Tak for jeres enorme indsats og til ministeren for besøg [#dkforsk](#) [#COVID19dk](#)



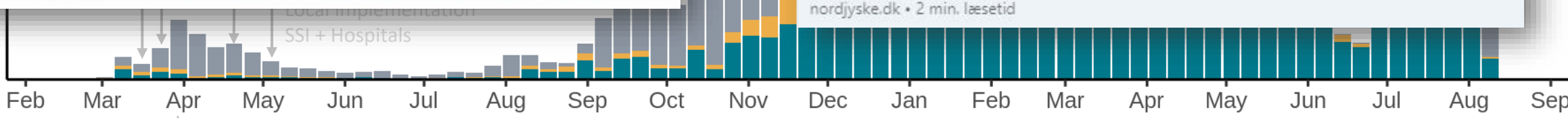
Mink-case  
5000 samples pr. week

**Mads Albertsen**  
Professor MSO hos Aalborg University  
4md. • 🌐

I dag havde vi Statsminister Mette Fredriksen på besøg i laboratoriet [Aalborg Universitet](#) til en snak om hvordan vi har opbygget et af verdens bedste programmer til overvågning af virus-varianter i Danmark i samarbejde i ... se mere



Mette F. 'totalt imponeret' af nordjyske forskere - nu takker hun dem  
nordjyske.dk • 2 min. læsetid



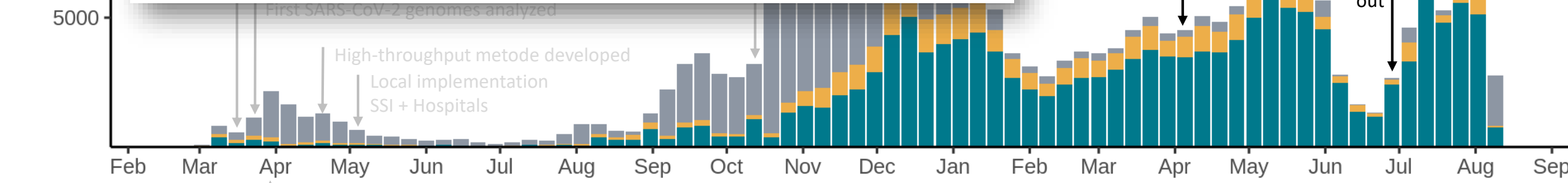
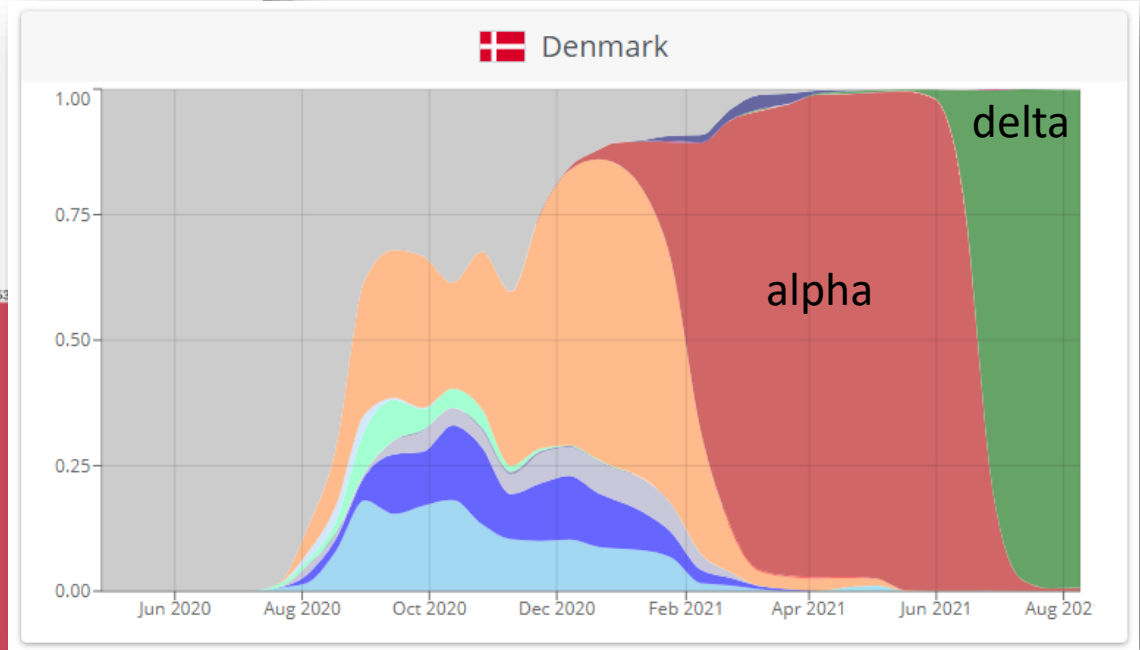
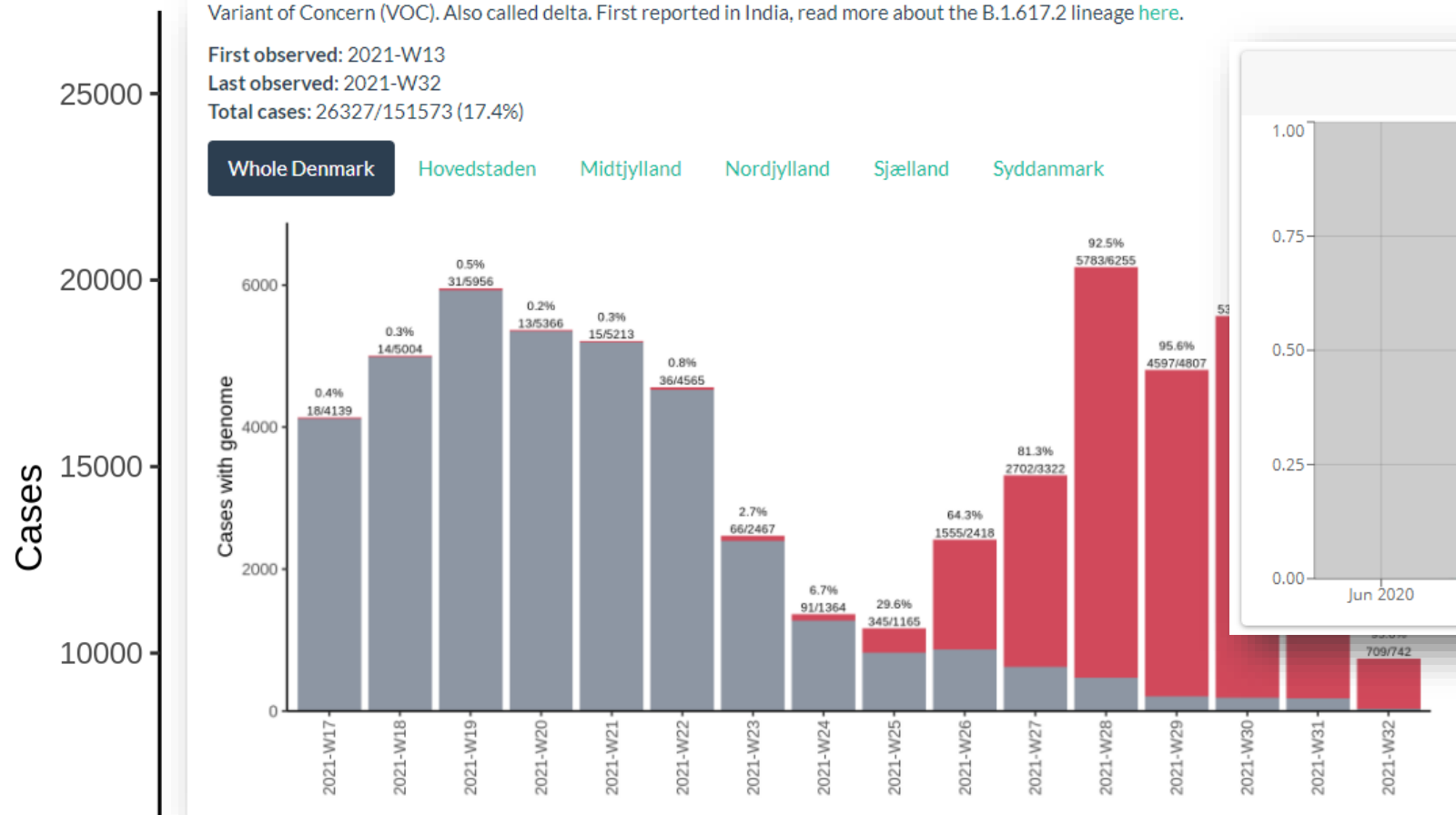
# A brief history of SARS-CoV-2 sequencing in Denmark

Covariants.org

Variant of Concern (VOC). Also called delta. First reported in India, read more about the B.1.617.2 lineage [here](#).

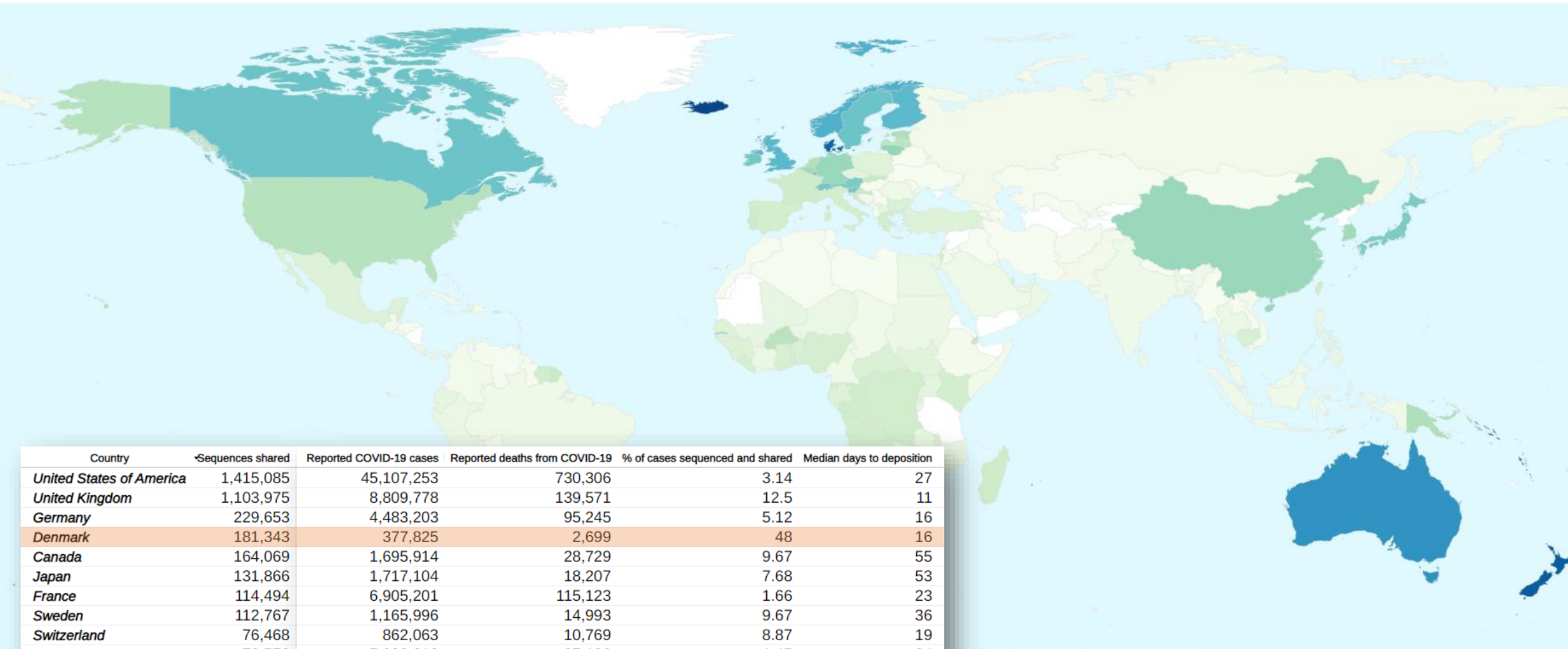
First observed: 2021-W13  
 Last observed: 2021-W32  
 Total cases: 26327/151573 (17.4%)

Whole Denmark Hovedstaden Midtjylland Nordjylland Sjælland Syddanmark



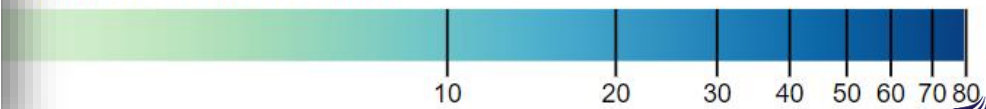
# Denmark has the worlds most comprehensive dataset

4,616,355 sequences shared via GISAID since 10 January 2020.

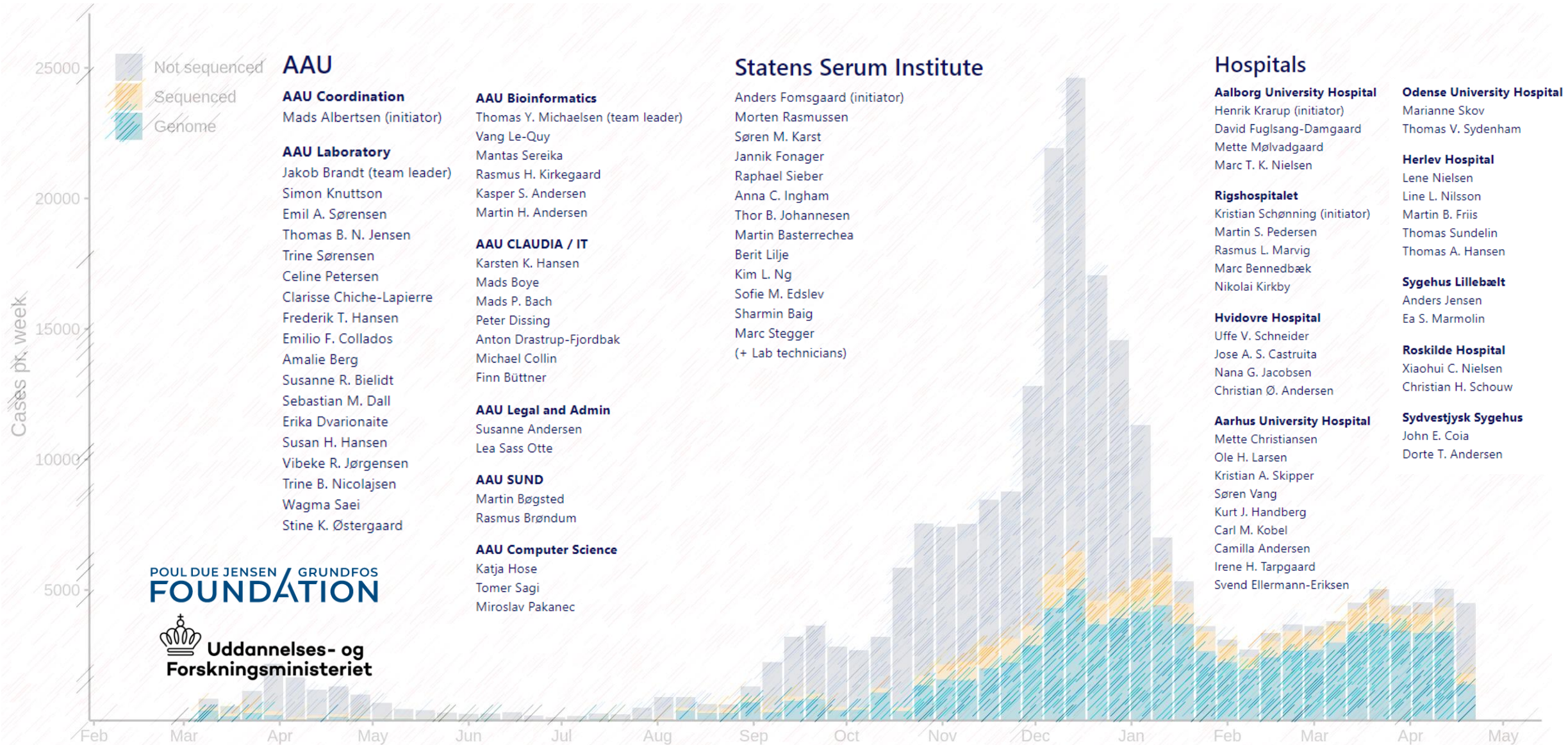


Country	Sequences shared	Reported COVID-19 cases	Reported deaths from COVID-19	% of cases sequenced and shared	Median days to deposition
<i>United States of America</i>	1,415,085	45,107,253	730,306	3.14	27
<i>United Kingdom</i>	1,103,975	8,809,778	139,571	12.5	11
<i>Germany</i>	229,653	4,483,203	95,245	5.12	16
<b>Denmark</b>	<b>181,343</b>	<b>377,825</b>	<b>2,699</b>	<b>48</b>	<b>16</b>
<i>Canada</i>	164,069	1,695,914	28,729	9.67	55
<i>Japan</i>	131,866	1,717,104	18,207	7.68	53
<i>France</i>	114,494	6,905,201	115,123	1.66	23
<i>Sweden</i>	112,767	1,165,996	14,993	9.67	36
<i>Switzerland</i>	76,468	862,063	10,769	8.87	19
<i>Spain</i>	72,576	5,002,218	87,186	1.45	34
<i>India</i>	70,720	34,202,202	455,068	0.207	61
<i>Italy</i>	69,022	4,743,720	131,856	1.46	17
<i>Netherlands</i>	67,335	2,087,859	18,320	3.23	21
<i>Turkey</i>	66,218	7,879,468	69,344	0.84	8

COVID-19 cases shared via GISAID



# Danish Covid-19 Genome Consortium





Institut for Kemi og Biovidenskab  
Department of Chemistry and Bioscience