Twitter Thread by Dr Emma Hodcroft

Dr Emma Hodcroft
@firefoxx66

The latest S:N501 focal build is now up, with data from 28th Dec:

We can see new sequences from Italy, Israel, Spain, France, & Ireland in the SE England variant (501Y.V1) & Switzerland in the South African variant (501Y.V2).

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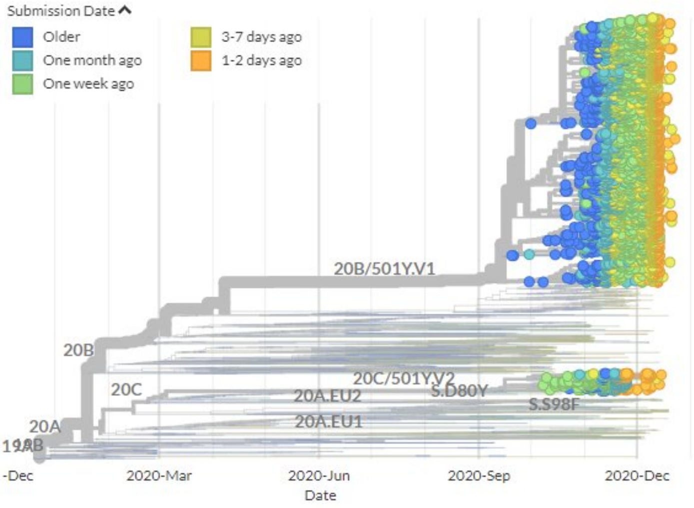
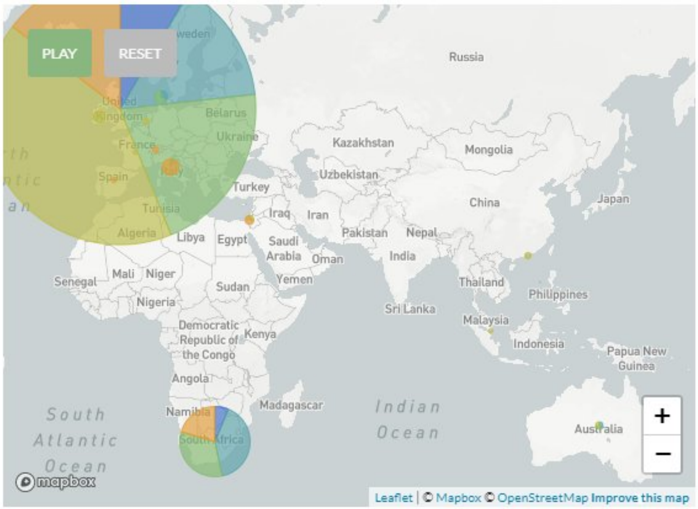
https://t.co/PEU7dhptO6





In 501Y.V1 (SE England variant), we can see 1 new sequence from France & Spain, each. The French sample has a travel history to the UK.

3 new sequences are from Israel (marked 1 & 2). Zooming in on '2' (divergence view) shows they are identical, indicating 1 introduction.

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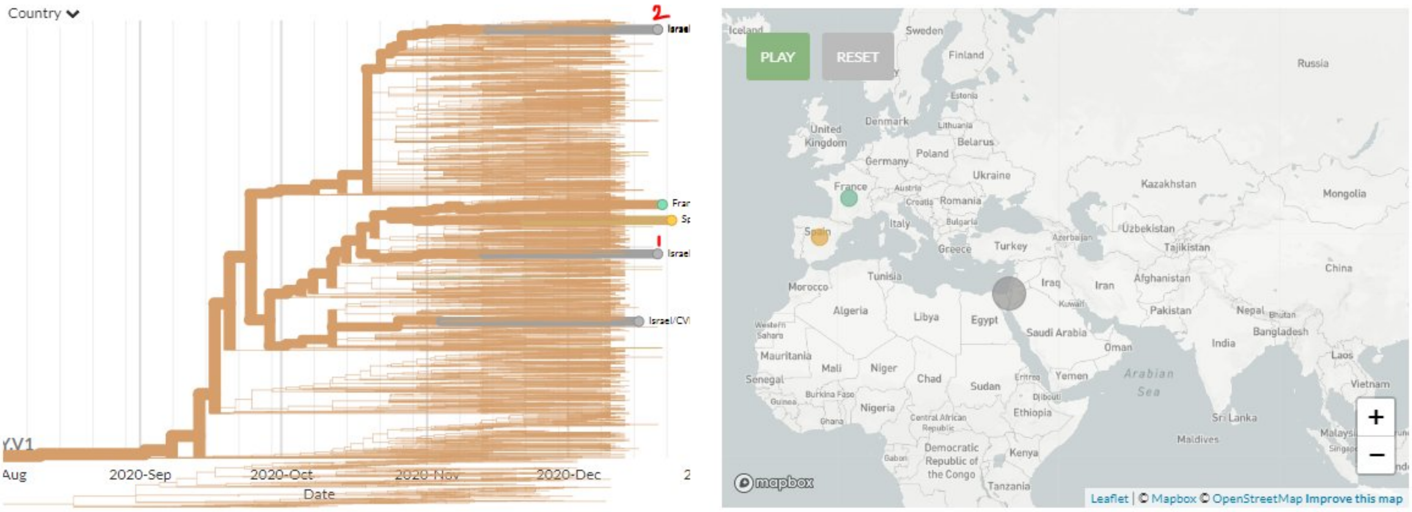

There are 7 new sequences from Ireland, found roughly in 5 places on the tree (4 are singletons, 3 cluster together - 2nd 'group' from the top).

These indicate at least 5 introductions, but we need to zoom in on the 3 that cluster to see more clearly.

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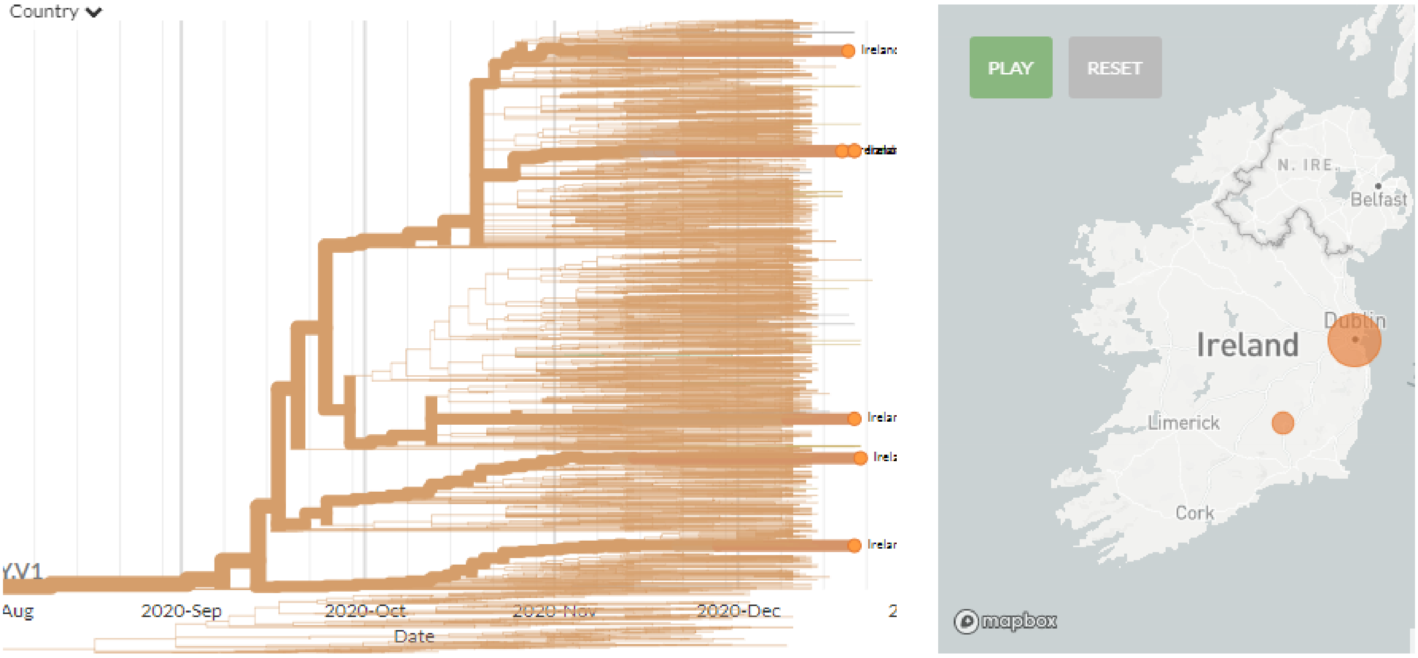

Zooming in to the 3 that cluster together (divergence view), shows it can be difficult to distinguish introductions sometimes, especially as we expect strong travel links between the UK & Ireland, & may only be sampling the total diversity present in Ireland.

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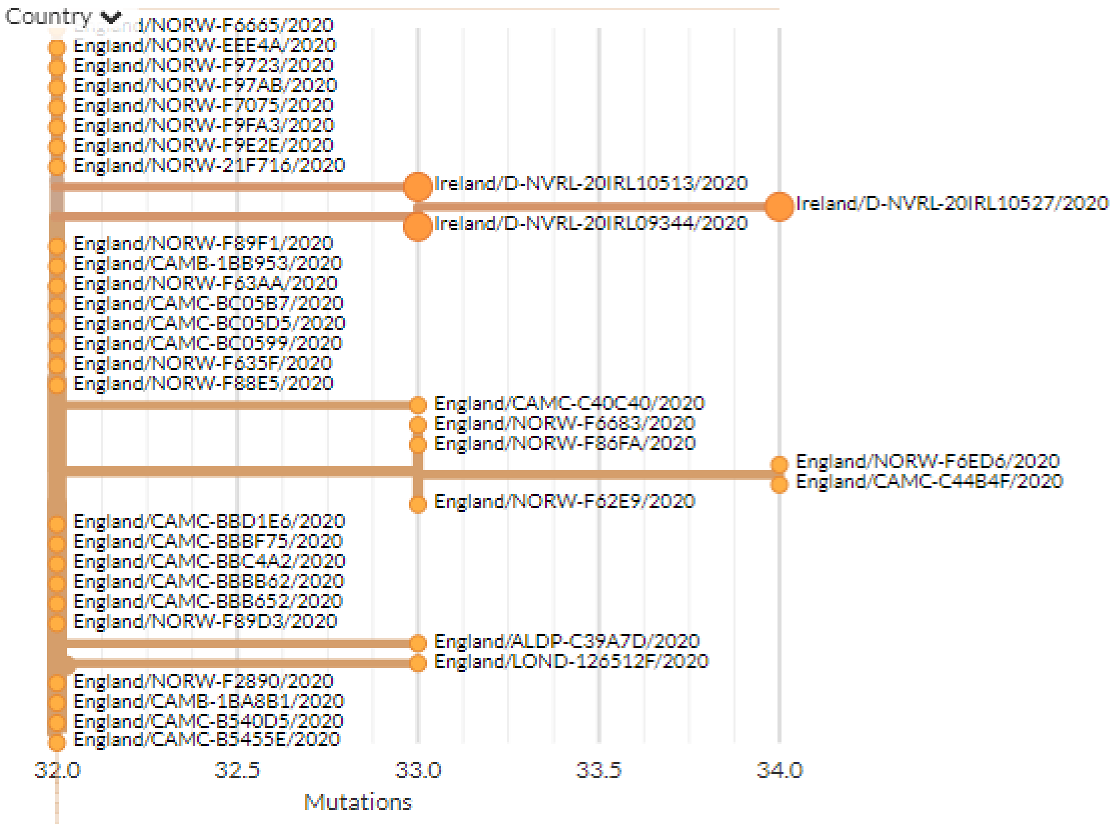

14 new sequences from Italy are scattered across the tree - some alone & some clustering.

Zooming in on a few clusters shows some seem to be linked, while others are harder to determine.
4 seem to be clearly linked as 1 introduction.

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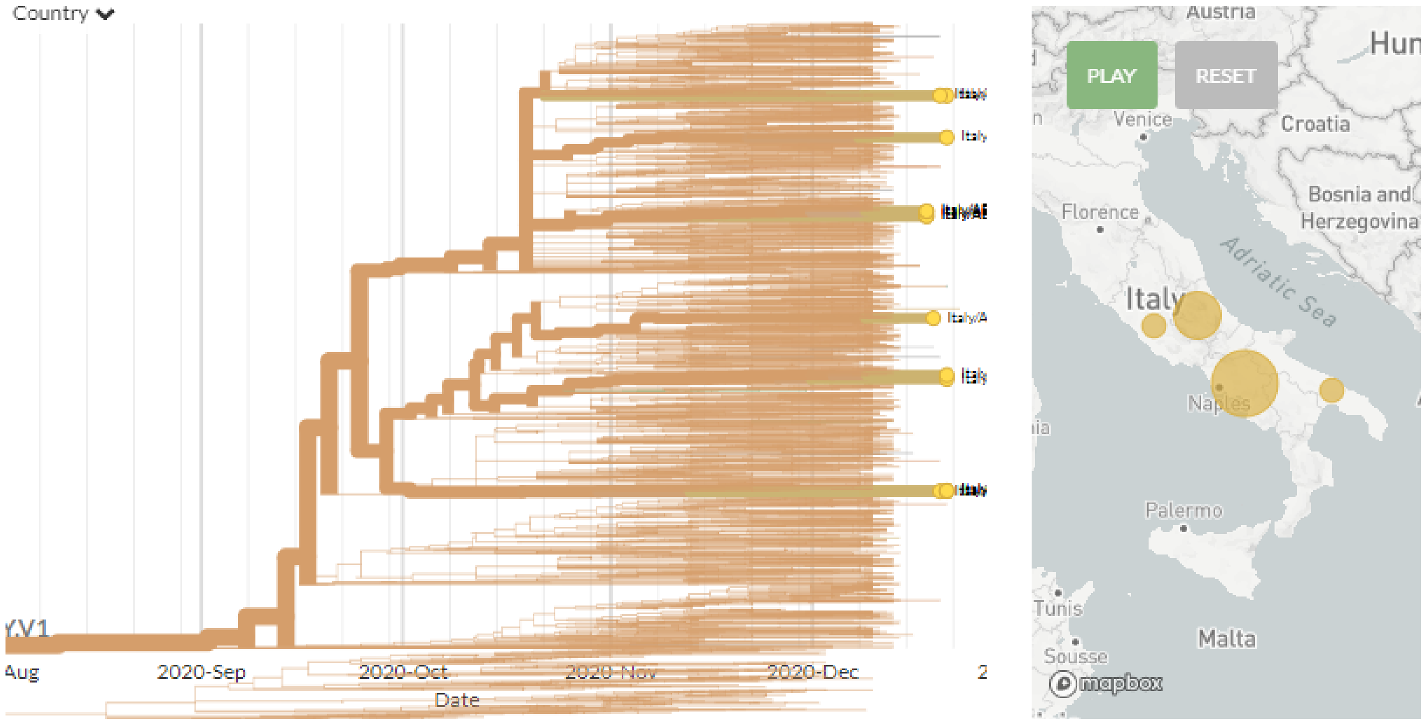

In 501Y.V2 (SA variant), there are 2 new sequences from Switzerland. As they sit quite separately within this cluster, this indicates two separate introductions to Switzerland.

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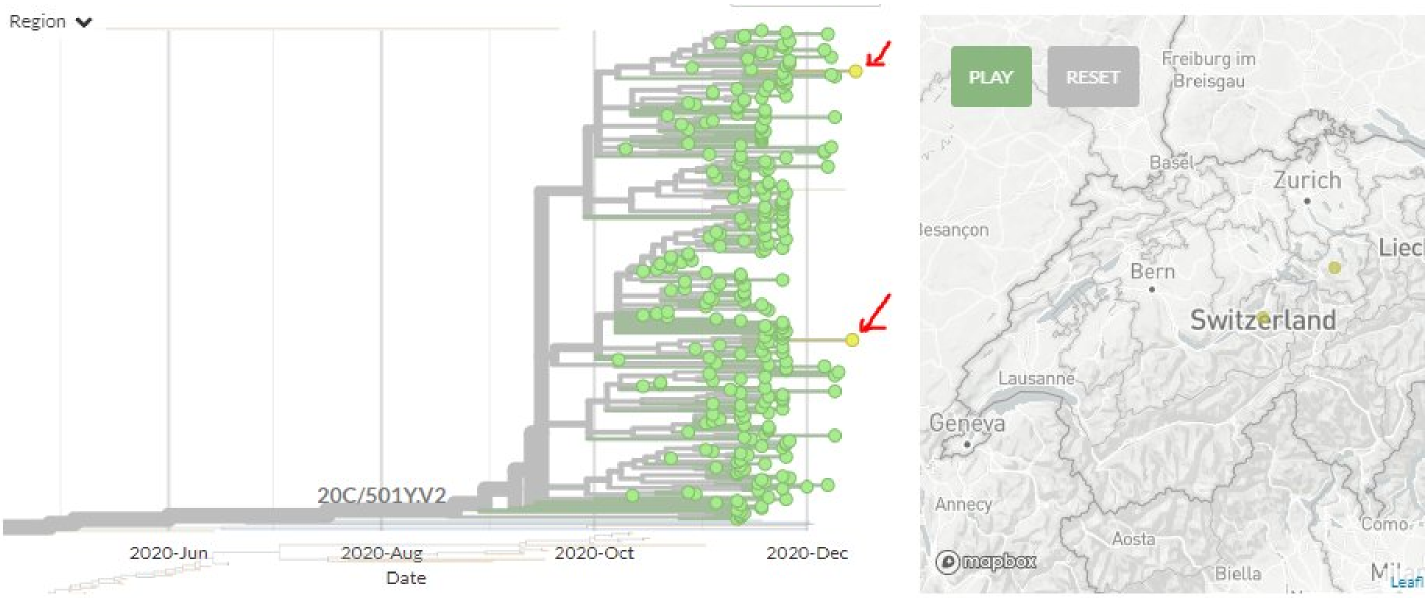
https://t.co/6Cux2E3Y6y



Additionally, a new graph showing the proportion of different variants in selected countries is also up.

Note the sharp in increase of N501 (bright pink) at the end of many graphs: this indicates increased interest in sequencing N501 samples.

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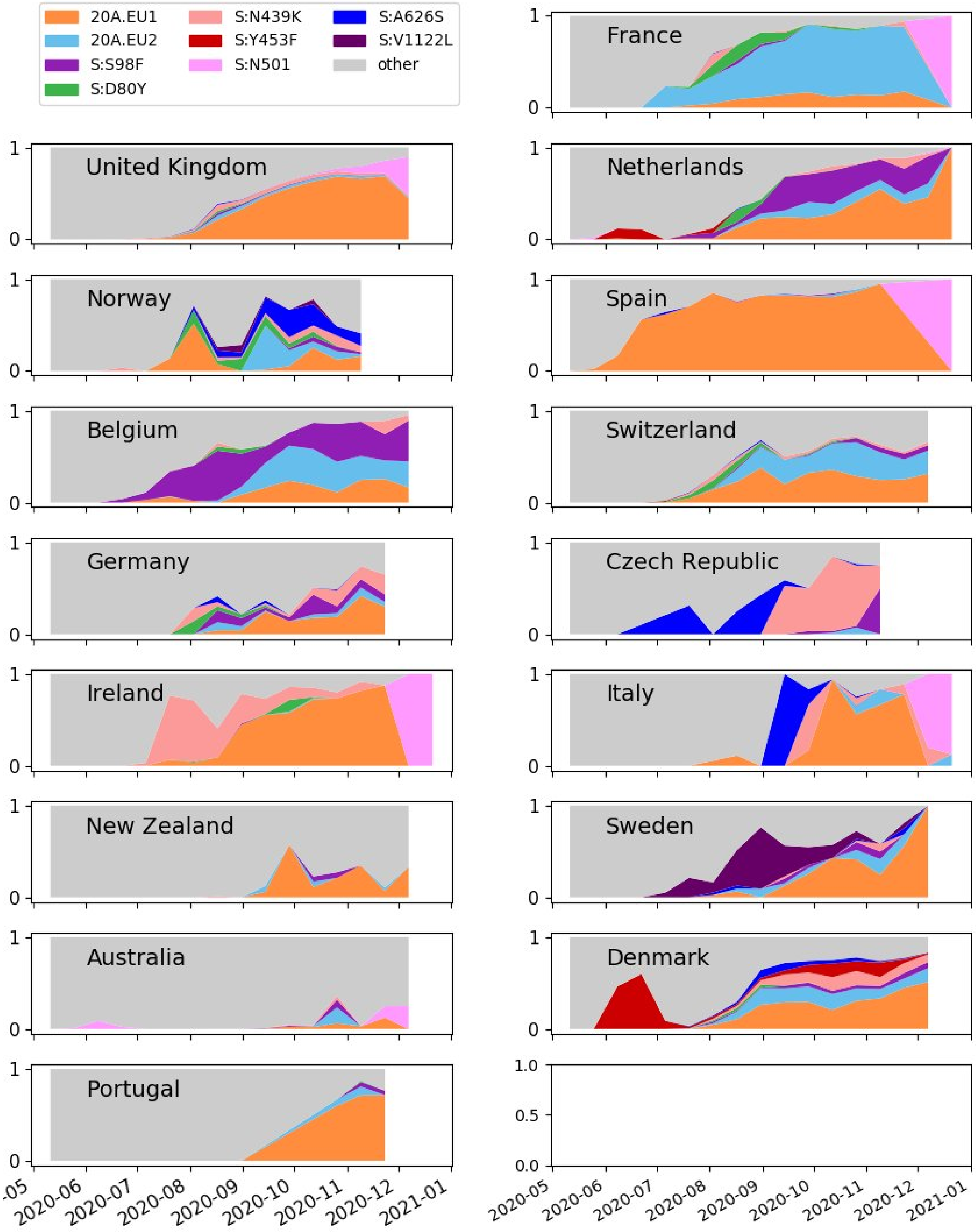
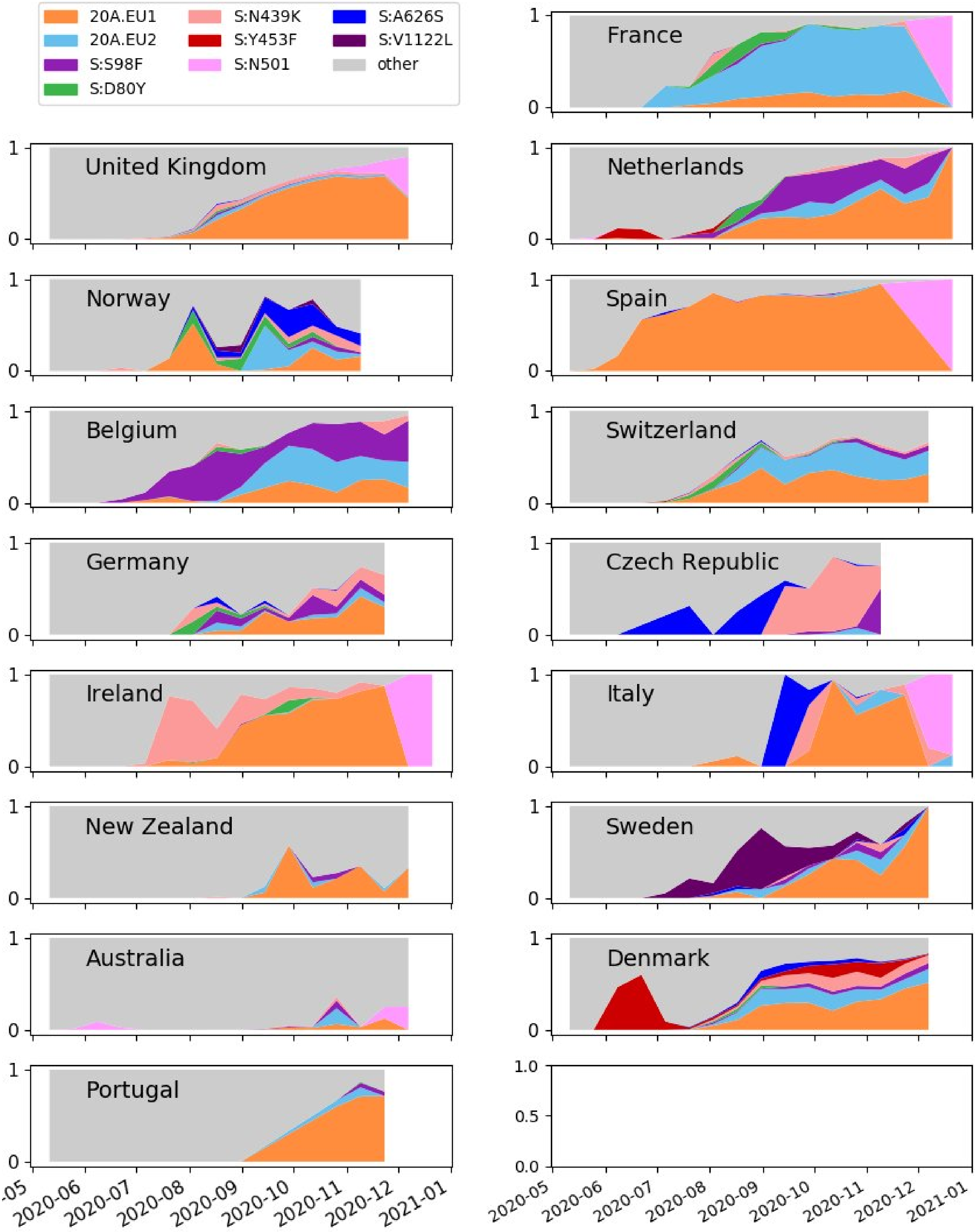
https://t.co/AUkR60o0GO



While more sequencing is great, you can see how switching to preferentially sequencing N501 samples will distort our ability to track other variants, both current & emerging.

Long-term, we need coordinated & regular sequencing of many samples to track #SARSCoV2 variants!



For those for whom it's helpful, there's also a new 'N501-noUK' build up which reduces the number of UK sequences. *Importantly* one /should not/ use this tree to discern connections between sequences - use in conjunction with the full

N501 tree!

https://t.co/9md0yn9Qgp

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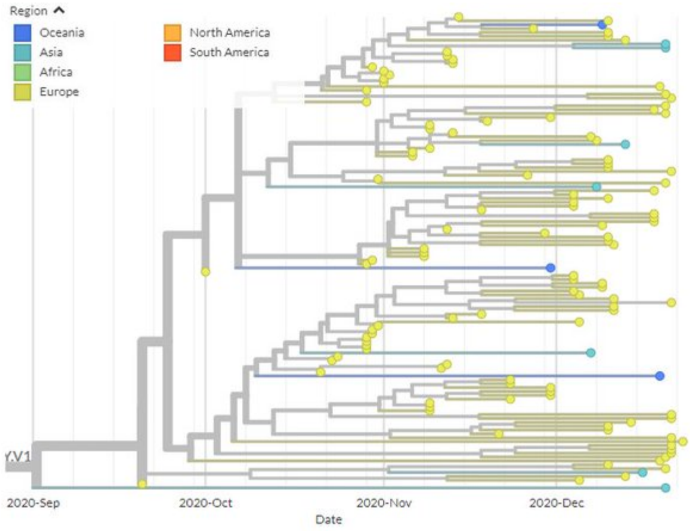

Notably, in the '501-noUK' build, an Israeli sequence seems to 'stick out' from the main 501Y.V1 cluster - we've already been in touch with Israeli scientists & there issues with this sequence (mixed base frequencies at some sites) - do not read much into its position!

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