To: 5.1.2e 5.1.2e [5.1.2e @rivm.nl]
From: 5.1.2e 5.1.2e
Sent: Tue 1/12/2021 8:07:53 AM
Subject: RE: FYI prior to publication – ECDC Threat Assessment Brief entitled "Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom"
Received: Tue 1/12/2021 8:08:05 AM
Sample size calculation READING COPY.xlsx

Dear 5.1.2e

After thinking more about your question I did an attempt o make a set of tables for this purpose (attached). We will most likely update our sequencing guidance doc with this information.

Let me know if you have any comments on this.

Best wishes,
5.1.2e

From: 5.1.2e 5.1.2e <5.1.2e @rivm.nl>
Sent: 08 January 2021 12:02
To: 5.1.2e 5.1.2e <5.1.2e @ecdc.europa.eu>
Subject: RE: FYI prior to publication – ECDC Threat Assessment Brief entitled "Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom"

Hi 5.1.2e

Thanks for you answer (I already read it on mondag but still needed to reply). It seems to me there is no rationale or caculations behind what is the needed sequencing level. We are going to try to do that ourselves. What are the questions and what does that mean for sequencing strategy.
Thanks 5.1.2e

From: 5.1.2e 5.1.2e <5.1.2e @ecdc.europa.eu>
Sent: maandag 4 januari 2021 10:40
To: 5.1.2e 5.1.2e <5.1.2e @rivm.nl>
Subject: RE: FYI prior to publication – ECDC Threat Assessment Brief entitled "Rapid increase of a SARS-CoV-2 variant with multiple spike protein mutations observed in the United Kingdom"

Dear 5.1.2e

Sorry for not replying earlier, I took a few days off from all work-related issues over the new year.

I agree that it is not possible to base any conclusions on the percentage of sequences samples alone, the sampling strategy is also crucial.

The statement in the RRA (that only 5.1.2a would be able to detect an emerging or introduced VOC at low levels with <30 days delay) is largely based on these factors and assumptions:

- The GISAID data reflects what is actually produced.
- The UK has a representative sequencing programme with approximately 5% of cases sequenced, it was successful in detecting this VOC at an early stage and follow its increase.
- ECDCs influenza sentinel guidance suggests sequencing 10% of cases to be able to catch the diversity of variants at a high enough resolution.

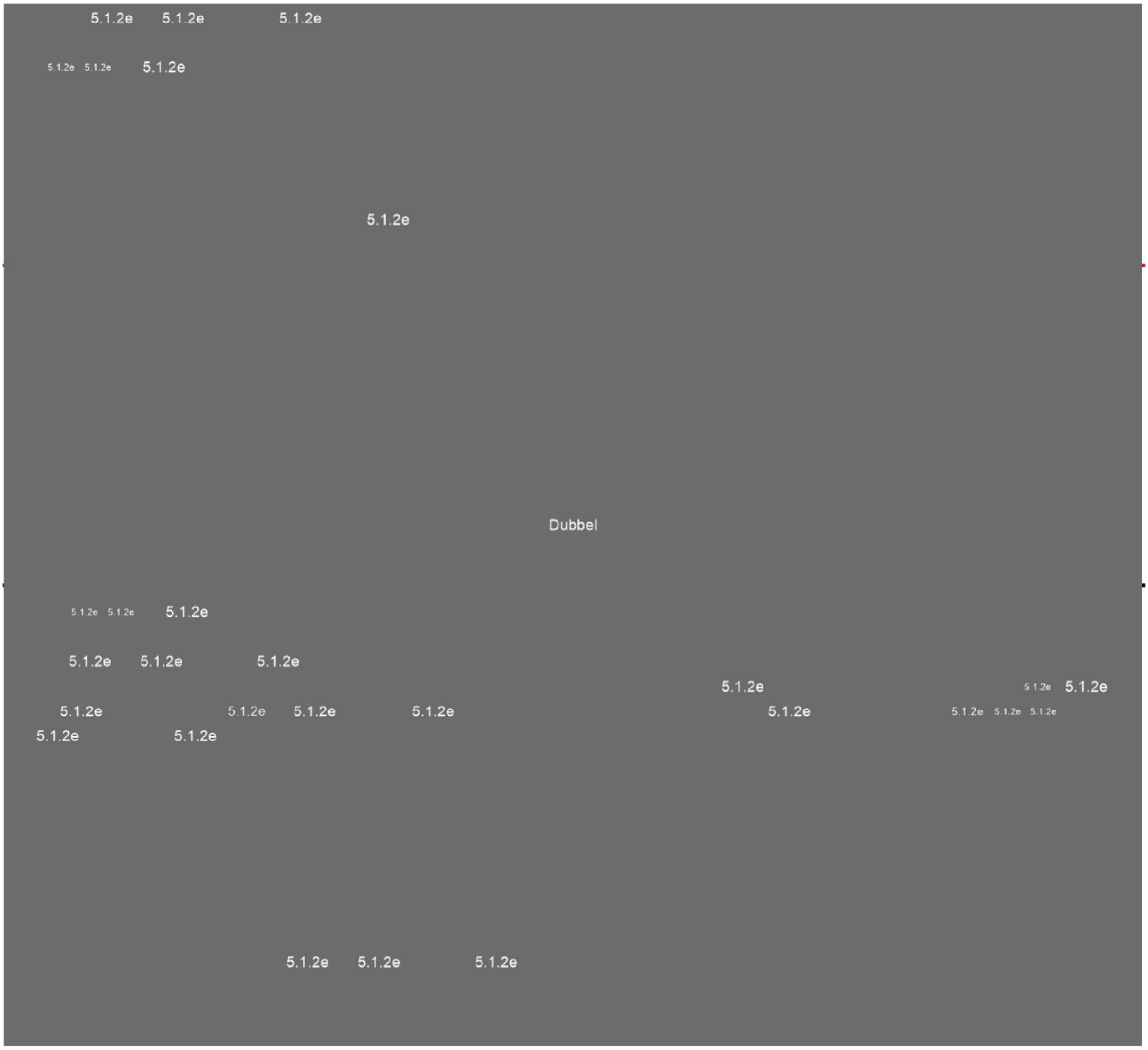
- The jump from 5.1.2a to the other countries is about a factor of 10, it is likely that any reasonable cut-off for a representative sequencing programme would be in this interval.

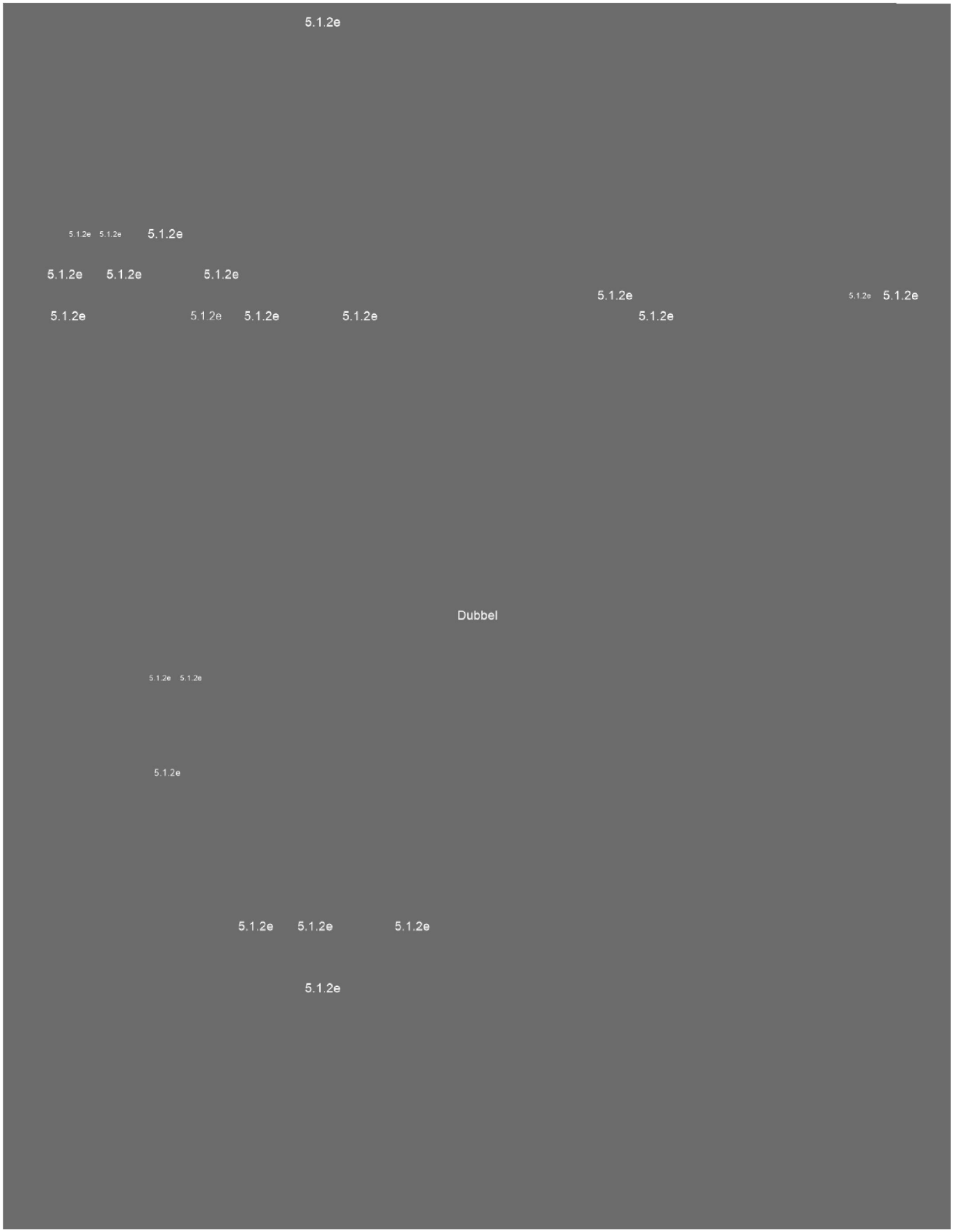
In the RRA we also suggest that if representative sequencing at a level similar to 5.1.2a though they have not been submitting to GISAID) is not possible, a smarter sampling strategy needs to be employed to catch VOCs, and we outline some suggestions.

I think these issues needs to be discussed further, I do not see the RRA as a guidance document for sequencing programmes, and I agree with you that with more time we could have put more thought into this. I hope we will be able to discuss further in the ECOVID lab network in the near future.

Best wishes and happy new year,

5.1.2e

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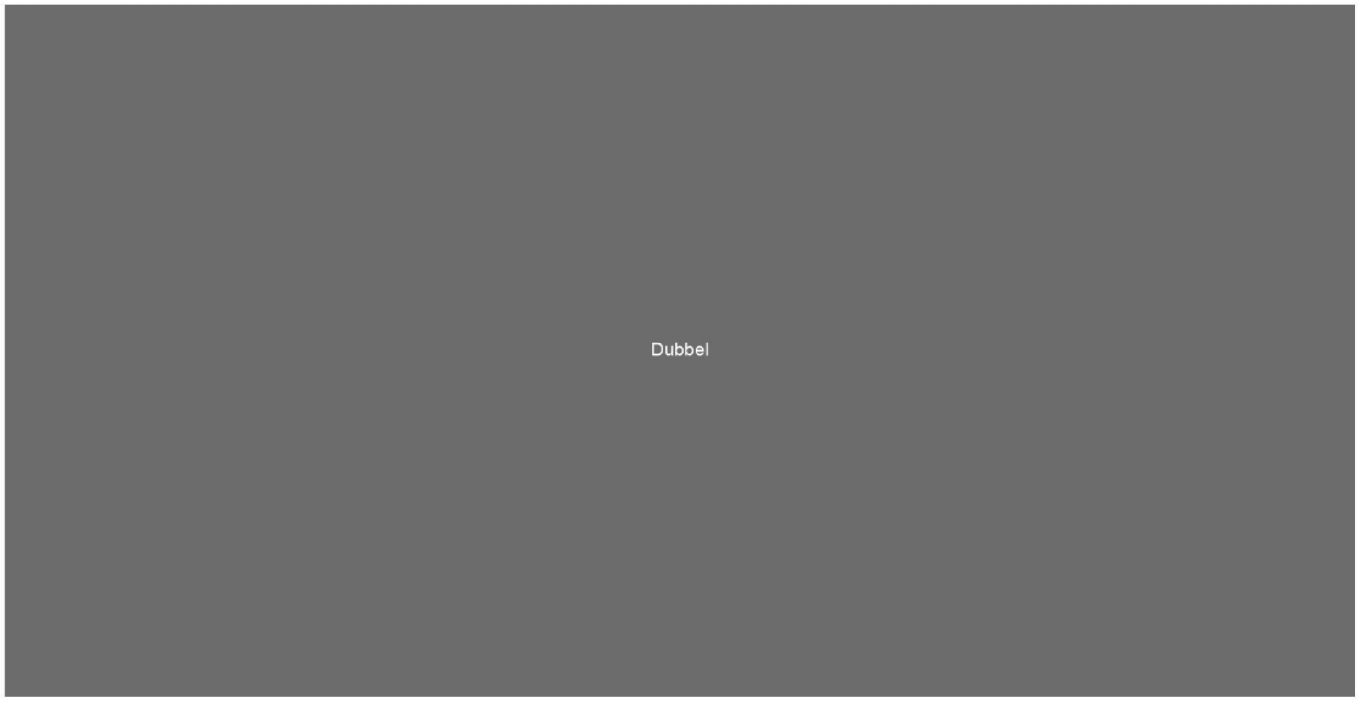
Dubbel