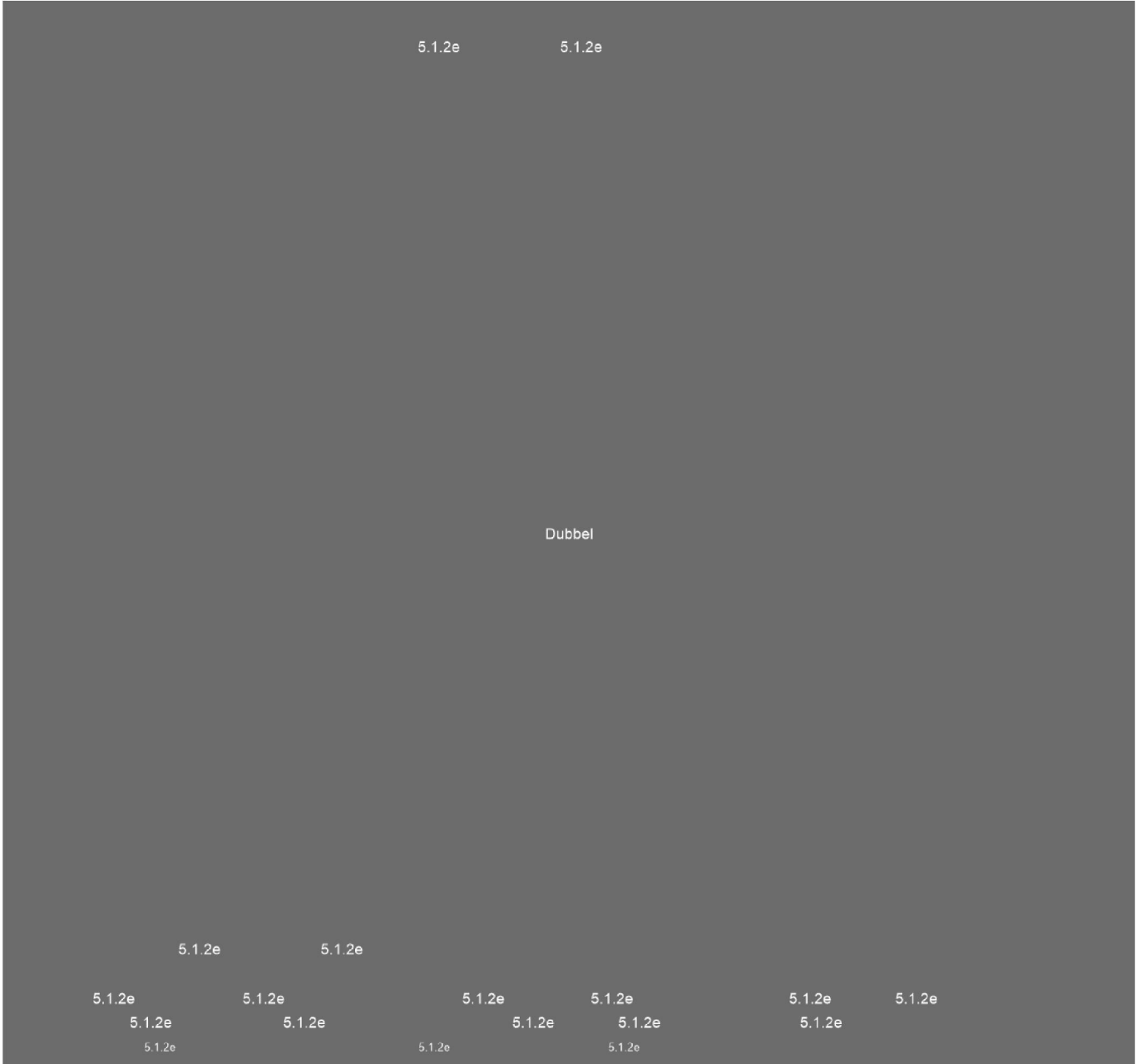


**To:** [redacted] [redacted] @rivm.nl  
**Cc:** [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @etz.nl; [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @rivm.nl; [redacted] [redacted] [redacted] @rivm.nl  
**From:** [redacted] [redacted] [redacted]  
**Sent:** Wed 8/26/2020 4:07:46 PM  
**Subject:** Re: Presentation on reported re-infections at COVID network call on Friday?  
**Received:** Wed 8/26/2020 4:10:36 PM

Als ik de volledige genoom sequenties kan krijgen dan kan ik wel een [redacted] maken samen met andere Nederlandse sequenties van GISAID om fylogenetisch te zien hoe ze clusteren.  
 Groetjes,

[redacted]

Verstuurd vanaf mijn iPhone



[redacted] [redacted]

Dubbel

[redacted] [redacted]  
 [redacted] [redacted] [redacted] [redacted] [redacted] [redacted]  
 [redacted] [redacted] [redacted] [redacted] [redacted] [redacted]  
 [redacted] [redacted] [redacted] [redacted]

2 - 4

Dubbel

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Dubbel