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Supplementary appendix

This appendix formed part of the original submission. We post it as supplied by the authors.

Supplement to: Chu CY, Marais G, Opperman C, et al. Performance of saliva and mid-turbinate swabs for detection of the beta variant in South Africa. *Lancet Infect Dis* 2021; published online August 4. http://dx.doi.org/10.1016/S1473-3099(21)00405-9

Appendix 2

A

	PPA	95% CI	NPA	95% CI	PPV	95% CI	NPV	95% CI	Cohen's kappa
SA pre-Beta VOC replacement	*51.5*	*35.22-67.50*	*98.5*	*96.21-99.42*	*81.0*	*60.00-92.33*	*94.3*	*90.89-96.44*	*0.60*
SA post-Beta VOC replacement	*72.5*	*57.17-83.89*	*98.5*	*92.02-99.92*	*96.7*	*83.33-99.83*	*85.7*	*76.20-91.83*	*0.75*
MT pre-Beta VOC replacement	*75.8*	*58.98-87.17*	*99.3*	*97.31-99.87*	*92.6*	*76.63-98.68*	*97.1*	*94.33-98.51*	*0.82*
MT post-Beta VOC replacement	*77.5*	*62.50-87.68*	*100*	*94.58-100.0*	*100*	*88.97-100.0*	*88.2*	*79.00-93.64*	*0.81*

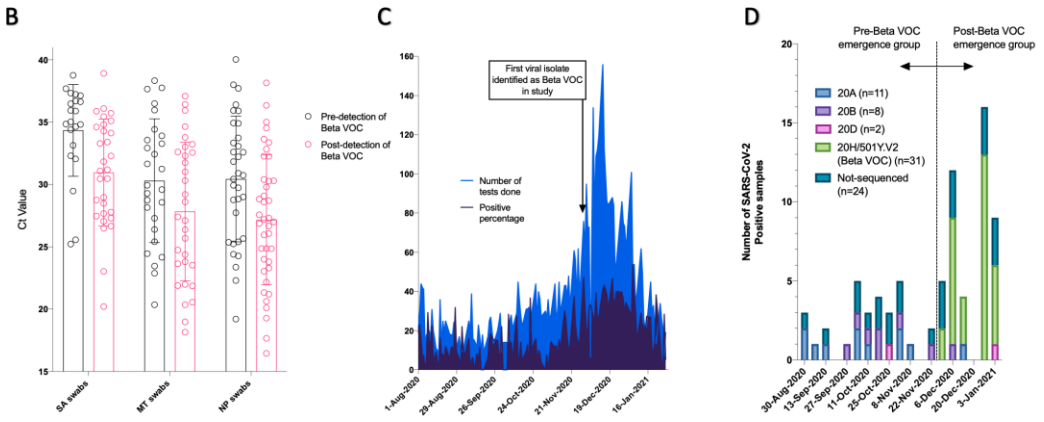

Figure 1.

A: Diagnostic validity.

SA: Saliva; MT: Mid-turbinate; NP: Nasopharyngeal PPA: Positive percent agreement; NPA: Negative percent agreement; PPV: Positive predictive value; NPV: Negative predictive value; 95% CI: 95% Confidence interval; Cohen Kappa: The following nomenclature were used to describe the relative strength of agreement associated with kappa statistics: 0 = poor; 0–0.2 = slight; 0.21–0.4 = fair; 0.41–0.6 = moderate; 0.61–0.8 = substantial; and 0.81– 1 = almost perfect.

Positive and negative percent agreement (PPA, NPA) to NP swab as well as PPV and NPV of SA and MT self-administered swabs as a diagnostic sample for SARS-CoV-2 PCR prior to (n=33/300) and after (n=40/107) replacement with the Beta VOC. Post-emergence, 3 proven non-Beta infected participants were excluded from analysis.

Confidence intervals were calculated using the Wilson-Brown method. The likelihood ratio of having a positive SA swab result pre- and post-emergence of the Beta VOC for participants with a positive NP swab result was 34 and 48 respectively.

B: Mean cycle threshold (Ct) values.

Ct values for SA, MT and NP swabs are shown with 1 standard deviation error bars. Pre-Beta VOC replacement, the mean SA ($p<0.001$) but not the mean MT Ct values were significantly different from mean NP values as assessed by paired t-test. Similarly, post-Beta VOC replacement, the mean Ct values for saliva ($p<0.0001$) and MT swabs ($p<0.01$) were significantly different from mean NP values.

Pre-and post-Beta replacement the Ct values for SA, MT and NP was 34.35 (SD $\pm$ 3.69) and 30.96 (SD $\pm$ 4.28); 30.31 (SD $\pm$ 4.96) and 27.84 (SD $\pm$ 5.57) and 30.44 (SD $\pm$ 5.04) and 27.16 (SD $\pm$ 5.21), respectively. Comparing the periods, mean Ct SA swab values decreased by 3.39 ($p<0.01$) and a comparable 2.47 (NS) and 3.28 ($p<0.01$) for MT and NP swabs, respectively, suggesting a higher viral burden (assessed by unpaired t-test. p: P-value, NS: Not significant)

C: Longitudinal Pre-test probability. For all samples collected at the Groote Schuur Hospital SARS-CoV-2 testing site, the pre-test probability pre- and post-Beta VOC replacement was 11% (n=2148) and 32% (n=2669), respectively.

D: Whole Genome Sequencing. The longitudinal number of isolates sequenced (n=52) and Nextstrain Clades are displayed. Post- Beta VOC emergence, clades 20A, 20B and 20D were excluded from diagnostic validity assessment. The proportion of

positive samples with Ct values ≥ 30 (n=24), not deemed suitable for WGS, are also shown.