Supplementary appendix

Supplementary table 1: Cross-tabulation of S-gene target status and variant as identified by whole genome sequencing

Variant	S-gene			Total
	positive	negative	unknown	TOtal
No sequencing result	356	1,574	439	2,369
B.1.1.7	2	5,099	278	5,379
B.1.1351	19	0	4	23
B.1.617.2	666	0	56	722
P.2	7	0	0	7
B.1.617.1	28	0	9	37
B.1.617.3	3	0	0	3
B.1.525	0	12	0	12
B.1.1.318	9	0	1	10
Low quality (likely B.1.617.2)	1	0	1	2
Not VOC/VUI	26	3	3	32
Total	1,117	6,688	791	118,157

Supplementary table 2: Cross-tabulation of S-gene target status and variant as identified by whole genome sequencing after dropping non B.1.1.7 or B.1.617.2 variants and reassignment based on sequencing results

Variant		Total			
variant	positive	negative	unknown	TOLAI	
No sequencing result	356	1,574	439	2,369	
B.1.1.7	0	5,379	0	5,379	
B.1.617.2	722	0	0	722	
Total	1,117	6,688	791	118,157	

	Number	r of cases	Ratio B.1.617.2	aOR	
Vaccination status	B.1.1.7	B.1.617.2	to B.1.1.7		
Days 0-13 post dose 1	551	32	0.058	base	
Any vaccine					
Dose 1	2237	272	0.122	1.30 (0.82-2.08)	
Dose 2	81	25	0.309	1.52 (0.72-3.18)	
Dose 1 or 2	2511	322	0.128	1.33 (0.83-2.11)	
Vaccine type (dose 1 or 2)					
BNT162b2	720	68	0.094	1.10 (0.64-1.90)	
ChAdOx1	1791	254	0.142	1.39 (0.87-2.23)	

Supplementary table 3: Odds ratios for detection of B.1.617.2 relative to B.1.1.7 in vaccinated individuals compared to the <14 days post dose 1

Supplementary table 4: Matched case control analysis

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Vaccination status	Number of cases		Ratio B.1.617.2	aOR compared	aOR compared to
	B.1.1.7	B.1.617.2	to B.1.1.7	to unvaccinated	<14 days post dose
Unvaccinated	2799	534	0.191	base	
<14 days post dose 1	133	21	0.158		base
Any vaccine					
Dose 1	621	173	0.279	1.19 (0.93-1.54)	1.29 (0.74-2.22)
Dose 2	33	13	0.394	1.44 (0.70-2.95)	1.55 (0.65-3.70)
Dose 1 or 2	710	198	0.279	1.18 (0.93-1.51)	1.27 (0.74-2.19)

Matched on Ethnicity, Region, age(10 yrs), week of sample



