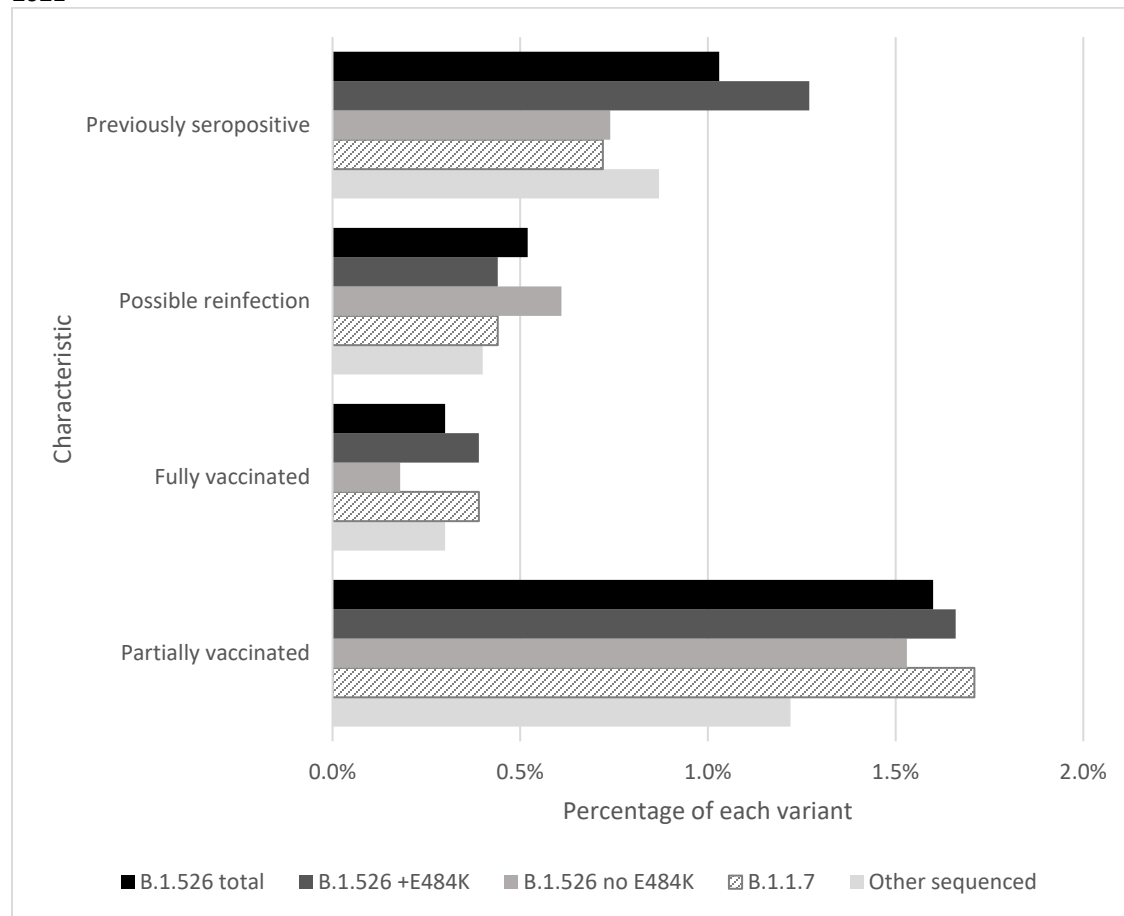


**SUPPLEMENTARY FIGURE. Percentage of persons with B.1.526 total, persons with B.1.526 with the E484K mutation, persons with B.1.526 without the E484K mutation, persons with B.1.1.7 and persons with other sequenced\* non-VOL/VOC with a preceding positive SARS-CoV-2 antibody test, with possible reinfection,† or with a SARS CoV-2 infection after being either fully or partially vaccinated§ — New York City, January 1–April 5, 2021**



**Data table**

Characteristic	Variant, no. (%)				
	B.1.526			B.1.1.7	Other sequenced
	With E484K	Without E484K	Total		
<b>Total</b>	<b>2,050</b>	<b>1,629</b>	<b>3,679</b>	<b>1,815</b>	<b>4,271</b>
Previously seropositive	26 (1.3)	12 (0.7)	38 (1)	13 (0.7)	37 (0.9)
Partially vaccinated	34 (1.7)	25 (1.5)	59 (1.6)	31 (1.7)	52 (1.2)
Fully vaccinated	8 (0.4)	3 (0.2)	11 (0.3)	7 (0.4)	14 (0.3)
Possible reinfection	9 (0.4)	10 (0.6)	19 (0.5)	8 (0.4)	17 (0.4)

**Abbreviation:** WGS = whole genome sequencing; VOI = variant of interest; VOC = variant of concern.

\* All persons had WGS performed at the Public Health Laboratory or the Pandemic Response Laboratory and include New York City Residents with a sequenced specimen collection date during January 1–April 5, 2021.

† A case of possible reinfection was defined as collection of a sequenced specimen from a person ≥90 days after a positive SARS-CoV-2 antigen or NAAT result.

§ Breakthrough infections among partially vaccinated persons were defined as infections in persons with a sequenced specimen collected ≥14 days after the first vaccine dose and <14 days after the second dose (for mRNA vaccines). Breakthrough infections among fully vaccinated persons were defined as infections in persons with a sequenced specimen collected ≥14 days after either a second mRNA vaccine dose or a single dose viral vector vaccine.