

Supplementary material for:
Vaccine-breakthrough infections with SARS-CoV-2 Alpha mirror
mutations in Delta Plus, Iota and Omicron

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Table S1. Demographic data and preexisting comorbidities in five SARS-CoV-2 infected patients after vaccination.

Characteristics	TOTAL (n=5)
Age mean ± SD, years	61.4 ± 25
Male (%)	2 (40%)
Female (%)	3 (60%)
Hypertension (%)	3 (60%)
Cardiac disease (%)	2 (40%)
Diabetes (%)	1 (20%)
Dyslipidemia (%)	2 (40%)
Pulmonary pathology (%)	1 (20%)
Smoker (%)	0
Hospitalization (%)	1 (20%)
Antibodies after vaccination (%)^a	4 (80%)
Survival 90 days after diagnosis (%)	5 (100%)
Ct (cycle threshold, which is inversely correlated with viral RNA level) ± SD	22.0 ± 4.2

^a Data available for four patients. All patients in whom the level of antibodies was determined after vaccination, the result was greater than 2,000 (>50 it is considered positive).

Table S2. Reference accession numbers of sequences retrieved from the National Center for Biotechnology Information (NCBI) database to design specific oligonucleotides.

NC_045512.2; NC_045512; MN908947.3; MT510727.1; MT510728.1; MT509958.1; MT509959.1; MT509649.1; MT509650.1; MT509651.1; MT509656.1; MT509657.1; MT509658.1; MT509659.1; MT509494.1; MT509495.1; MT509496.1; MT509497.1; MT509498.1; MT509499.1; MT509500.1; MT509501.1; MT509502.1; MT509503.1; MT509504.1; MT509505.1; MT509506.1; MT509507.1; MT509508.1; MT509509.1; MT509510.1; MT509511.1; MT509512.1; MT500122.1; MT502774.1; MT502900.1; MT502901.1; MT502902.1; MT502903.1; MT502904.1; MT502905.1; MT502906.1; MT502907.1; MT502908.1; MT502909.1; MT502910.1; MT502911.1; MT502912.1; MT502913.1; MT502914.1; MT502915.1; MT502916.1; MT502917.1; MT502918.1; MT502919.1; MT502920.1; MT502921.1; MT502922.1; MT502923.1; MT502924.1; MT502925.1; MT502926.1; MT502927.1; MT502928.1; MT502929.1; MT502930.1; MT502931.1; MT502932.1; MT502933.1; MT502934.1; MT502935.1; MT502936.1; MT502937.1; MT502938.1; MT502939.1; MT502940.1; MT502941.1; MT502942.1; MT502943.1; MT502944.1; MT502945.1; MT502946.1; MT502947.1; MT502948.1; MT502949.1; MT502950.1; MT502951.1; MT502952.1; MT502953.1; MT502954.1; MT502955.1; MT502956.1; MT502957.1; MT502958.1; MT502959.1; MT502960.1; MT502961.1; MT502962.1; MT502963.1; MT502964.1; MT502965.1; MT502966.1; MT502967.1; MT502968.1; MT502969.1; MT502970.1; MT502971.1; MT502972.1; MT502973.1; MT502974.1; MT502975.1; MT502976.1; MT502977.1; MT502978.1; MT502979.1; MT502980.1; MT502981.1; MT502982.1; MT502983.1; MT502984.1; MT502985.1; MT502986.1; MT502987.1; MT502988.1; MT502989.1; MT502990.1; MT502991.1; MT502992.1; MT502993.1; MT502994.1; MT502995.1; MT502996.1; MT502997.1; MT502998.1; MT502999.1; MT503000.1; MT503001.1; MT503002.1; MT503003.1; MT503004.1; MT503005.1; MT503006.1; MT503007.1; MT503008.1; MT503009.1; MT503010.1; MT503011.1; MT503012.1; MT503013.1; MT503014.1; MT503015.1; MT503016.1; MT503017.1; MT503018.1; MT503019.1; MT503020.1; MT503021.1; MT503022.1; MT503023.1; MT503024.1; MT503025.1; MT503026.1; MT503027.1; MT503028.1; MT503029.1; MT503030.1; MT503031.1; MT503032.1; MT503033.1; MT503034.1; MT503035.1; MT503036.1; MT503037.1; MT503038.1; MT503039.1; MT503040.1; MT503041.1; MT503042.1; MT503043.1; MT503044.1; MT503045.1; MT503046.1; MT503047.1; MT503048.1; MT503049.1; MT503050.1; MT503051.1; MT503052.1; MT503053.1; MT503054.1; MT503055.1; MT503056.1; MT503057.1; MT503058.1; MT447174.1; MT447175.1; MT447176.1; MT447177.1; MT447188.1; MT447189.1; MT439595.1; MT439596.1; MT439597.1; MT434757.1; MT434758.1; MT434759.1; MT434760.1; MT435079.1; MT435080.1; MT435081.1; MT435082.1; MT435083.1; MT435084.1; MT435085.1; MT435086.1; MT365028.1; MT365029.1; MT365030.1; MT365031.1; MT365032.1; MT428551.1; MT428552.1; MT428553.1; MT428554.1; MT429168.1; MT215193.1; MT215194.1; MT215195.1; MT270814.1; MT270815.1; MT276600.1; MT412134.1; MT415320.1; MT415321.1; MT415322.1; MT415323.1; MT415833.1; MT415834.1; MT415835.1; MT415836.1; MT415837.1; MT415838.1; MT415839.1; MT415366.1; MT415367.1; MT415368.1; MT415369.1; MT415370.1; MT415371.1; MT415372.1; MT415373.1; MT415374.1; MT415375.1; MT415376.1; MT415377.1; MT415840.1; MT415841.1; MT415842.1; MT415843.1; MT415844.1; MT415845.1; MT415846.1; MT396241.1; MT396242.1; MT396243.1; MT396244.1; MT396245.1; MT396246.1; MT396247.1; MT396248.1; MT380726.1; MT380727.1; MT186683.1; MT374101.1; MT374102.1; MT374103.1; MT374104.1; MT374105.1; MT374106.1; MT374107.1; MT374108.1; MT374109.1; MT374110.1; MT374111.1; MT374112.1; MT374113.1; MT374114.1; MT374115.1; MT374116.1; MT370516.1; MT370517.1; MT370518.1; MT371047.1; MT371048.1; MT371049.1; MT371050.1; MT372480.1; MT372481.1; MT372482.1; MT372483.1; LC542976.1; LC542809.1; MT114412.1; MT114413.1; MT114414.1; MT114415.1; MT114416.1; MT114417.1; MT114418.1; MT114419.1; MT230904.1; MT358637.1; MT327745.1; MT039874.1; MT320891.2; MT304474.1; MT304475.1; MT304476.1; MT281577.1; MT291831.1; MT291832.1; MT291833.1; MT291834.1; MT291835.2; MT291836.1; MT281530.2; MT291827.1; MT291828.1; MT291826.1;

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Table S3. Specific oligonucleotides designed to amplify and sequence the spike-coding region of SARS-CoV-2.

Primer name	Sense	Sequence (5' – 3')	Genome positions ^a	Tm (°C)
Spk-CoV2-u21424	Fw	GGTACTGCTGTTATGTCTTAAAA	21424-21447	50.6
Spk-CoV2-d21867	Rv	CTTATTATGTTAGACTTCTCAGTGGAA	21867-21842	53.2
Spk-CoV2-u21701	Fw	GTTTTACATTCAACTCAGGACTTGT	21701-21726	53.2
Spk-CoV2-d22154	Rv	CAATATTCTAACACAAATTCCCTAA	22154-22128	50.6
Spk-CoV2-u22088	Fw	CTTATGGACCTTGAAGGAAAACA	22088-22110	51.7
Spk-CoV2-d22536	Rv	GATTCTGTTGGTTGGACTCTA	22536-22516	50.5
Spk-CoV2-u22464	Fw	GTACGTTGAAATCCTTCAGTGT	22464-22486	51.7
Spk-CoV2-d22902	Rv	CCACCAACCTTAGAATCAAGAT	22902-22881	51.1
spk-CoV2-u22853	Fw	GGCTGCGTTATAGCTTGGAA	22853-22871	51.1
spk-CoV2-d23288	Rv	CAGCATCAGTAGTGTCAGCA	23288-23269	51.8
spk-CoV2-u23236	Fw	GTTCCTGCCTTCCAACAATTG	23236-23258	51.7
spk-CoV2-d23666	Rv	CTGCACCAAGTGACATAGTGT	23666-23646	52.4

^aThe SARS-CoV-2 genome residue numbering according to the NCBI reference sequence (accession number NC_045512.2).

Table S4. Repertoire of substitutions and deletions in the spike-coding region of SARS-CoV-2 (amino acid positions 1–694)^a, analyzed by ultra-deep sequencing (UDS).

Region	Amino Acid substitution ^b	PAM250 ^c	Number of patients	Domain
spike A1	L5F	2	1	Signal peptide
spike A2	F157L	2	1	N-terminal
spike A3	A222V	0	2	N-terminal
spike A4	K417R	3	5	RBD
spike A5	L452P	-3	3	RBD
spike A5	N501Y	-2	5	RBD
spike A5	T547A	1	2	-
spike A6	A570D	1	5	-
spike A6	D614G	1	5	-
spike A6	N679K	1	1	-
spike A6	P681H	0	5	S1/S2
spike A6	P681R	0	1	S1/S2
Region	Affected amino acid positions ^b	Amino acid reference sequence ^d	Amino acid sequence detected ^h	Number of patients
spike A1/ A2	69-70	AI <u>H</u> VSG	AISG	5
spike A2	144	GV <u>YY</u> H	GVYH	5

^a The SARS-CoV-2 genome residue numbering according to the NCBI reference sequence (accession number NC 045512.2).

^b Amino acid residues (single letter code) are numbered from N- to the C-terminus of each region.

^c PAM250 substitution matrix values are take from Feng and Doolittle (Methods in Enzymology 266: 368-382, 1996): PAM250<0, lower acceptability than expected, meaning a rare replacement; PAM250=0, acceptability as expected; PAM250>0 acceptability higher than expected.

^d Underline amino acids are the ones affected by the deletion.

^h Amino acid sequence detected in patients.