

Figure S1. Number of COVID-19 cases and the prevalence of the SARS-CoV-2 Delta variant in the UK, Japan, USA, and Germany. Graphs of the number of cases (blue line) and the percentage of the Delta variant (orange circles) as a function of time. Red circles show the beginning of a new COVID-19 peak case. All data were obtained from World in Data, WHO, CDC, UK Gov and Outbreak [1,148–151].

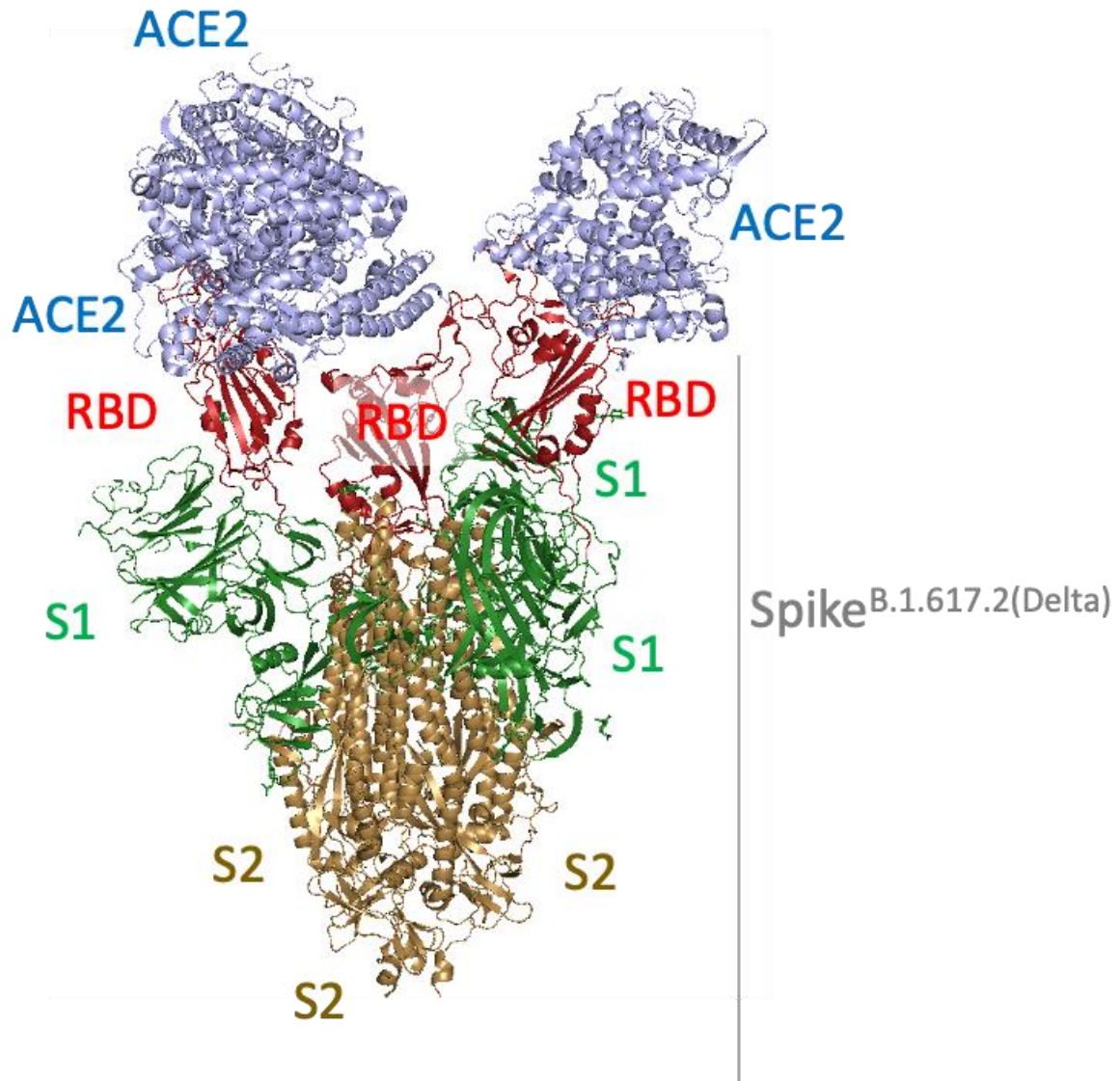
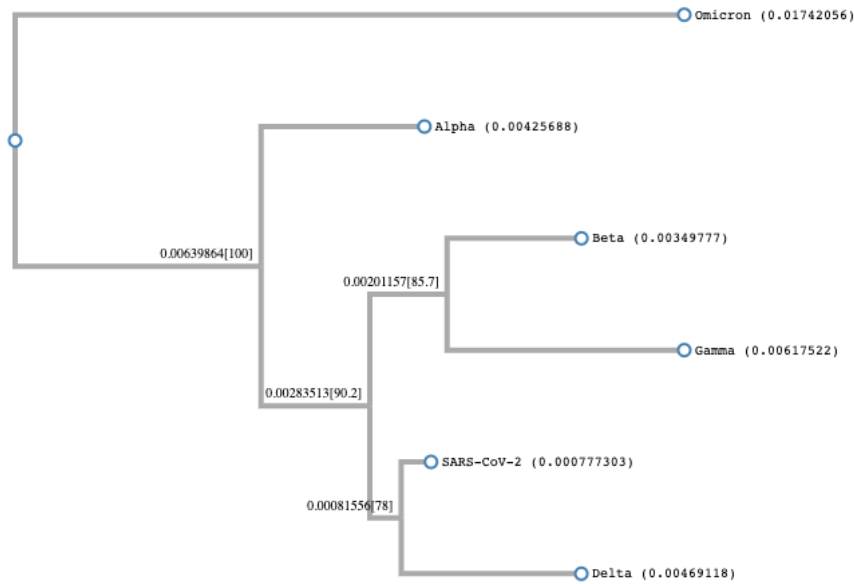


Figure S2. Cryo-EM structure of SARS-CoV-2 Spike^{B.1.617.2(Delta)} in complex with Angiotensin-converting enzyme 2 (ACE2) ectodomain. ACE2 is colored in blue, Spike protein structure in red (RBD domain), green (S1 subunit not considering the RBD domain) and brown (S2 domain) (protein data bank, PDB, 7V8A, not published).

A



B

SARS-CoV-2	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
Delta/B.1.617.2	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
Omicron/B.1.1.529	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
Alpha/B.1.1.7	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
P.1/Gamma	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
Beta/B.1.351	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFS	60
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SARS-CoV-2	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	120
Delta/B.1.617.2	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	120
Omicron/B.1.1.529	NVTWFHVI--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	118
Alpha/B.1.1.7	NVTWFHAI--SGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	118
P.1/Gamma	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	120
Beta/B.1.351	NVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSTQSLIV	120
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SARS-CoV-2	NNATNVVIKVCEFCNDPFLGVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLE	180
Delta/B.1.617.2	NNATNVVIKVCEFCNDPFLDVYHKNKSWMESG--VYSSANNCTFEYVSQPFLLMDLE	180
Omicron/B.1.1.529	NNATNVVIKVCEFCNDPFLD---HKNNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLE	175
Alpha/B.1.1.7	NNATNVVIKVCEFCNDPFLGVY-HKNNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLE	177
P.1/Gamma	NNATNVVIKVCEFCNYPFLGVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLE	180
Beta/B.1.351	NNATNVVIKVCEFCNDPFLGVYHKNKSWMESEFRVYSSANNCTFEYVSQPFLLMDLE	180
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SARS-CoV-2	GKQGNFKNLREFVFNIDGYFKIYKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF	238
Delta/B.1.617.2	GKQGNFKNLREFVFNIDGYFKIYKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF	238
Omicron/B.1.1.529	GKQGNFKNLREFVFNIDGYFKIYKHTPIIVREPEDLPQGFSALEPLVDLPIGINITRF	235
Alpha/B.1.1.7	GKQGNFKNLREFVFNIDGYFKIYKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF	235
P.1/Gamma	GKQGNFKNLSEFVFNIDGYFKIYKHTPINL--VRDLPQGFSALEPLVDLPIGINITRF	238
Beta/B.1.351	GKQGNFKNLREFVFNIDGYFKIYKHTPINL--VRGLPQGFSALEPLVDLPIGINITRF	238
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SARS-CoV-2	QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	298
Delta/B.1.617.2	QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	298
Omicron/B.1.1.529	QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	295
Alpha/B.1.1.7	QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	295
P.1/Gamma	QTLLALHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	298
Beta/B.1.351	QT---LHRSYLT PGDSSSGWTAGAAAYVGYLQPR	TFLLYKNENGTITDAVDCALDPLSE	295
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SARS-CoV-2	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	358
Delta/B.1.617.2	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	358
Omicron/B.1.1.529	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	355
Alpha/B.1.1.7	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	355
P.1/Gamma	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	358
Beta/B.1.351	TKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNI	TNLCPFGEVFNATRFASVYAWNRRKI	355
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SARS-CoV-2	SNCVADYSVLYNSASFSTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	418
Delta/B.1.617.2	SNCVADYSVLYNSASFSTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	418
Omicron/B.1.1.529	SNCVADYSVLYNSAPFFTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	415
Alpha/B.1.1.7	SNCVADYSVLYNSASFSTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	415
P.1/Gamma	SNCVADYSVLYNSASFSTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	418
Beta/B.1.351	SNCVADYSVLYNSASFSTFKCYGVSP	TKLNDLCFTNVYADSFVIRGDEV	415
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SARS-CoV-2	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	478
Delta/B.1.617.2	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	478
Omicron/B.1.1.529	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	475
Alpha/B.1.1.7	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	475
P.1/Gamma	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	478
Beta/B.1.351	ADYNYKLDDFTGCVIAWNSNNLDSKVG	SNLYLYLFRKSNLKPFERDISTE	475
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SARS-CoV-2	PCNGVEGFNCYFPLQSYGFQPT	YGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	538
Delta/B.1.617.2	PCNGVEGFNCYFPLQSYGFQPT	YGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	538
Omicron/B.1.1.529	PCNGVAGFNCYFPLRSYSFRPT	YGVGHQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	535
Alpha/B.1.1.7	PCNGVEGFNCYFPLQSYGFQPT	YGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	535
P.1/Gamma	PCNGVKGfNCYFPLQSYGFQPT	YGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	538
Beta/B.1.351	PCNGVKGfNCYFPLQSYGFQPT	YGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKC	535
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SARS-CoV-2	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	598
Delta/B.1.617.2	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	598
Omicron/B.1.1.529	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	595
Alpha/B.1.1.7	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	595
P.1/Gamma	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	598
Beta/B.1.351	VNFNFNGLTGTGVLTESNKKFLPFQ	QFGRDIADTTDAVRDPQTLEILDITPCSFGGVS	595
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SARS-CoV-2	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN	658
Delta/B.1.617.2	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN	658
Omicron/B.1.1.529	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNN	655
Alpha/B.1.1.7	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN	655
P.1/Gamma	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEYVNN	658
Beta/B.1.351	TPGTNTSNQVAVLYQGVNCTEVPV	AIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNN	655
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SARS-CoV-2	SYECDIPIGAGICASYQTQNSPRRAR	SVASQSI IAYTMSLGAENSVAYSNN	718
Delta/B.1.617.2	SYECDIPIGAGICASYQTQNSRRRAR	SVASQSI IAYTMSLGAENSVAYSNN	718
Omicron/B.1.1.529	SYECDIPIGAGICASYQTQTKSHRRAR	SVASQSI IAYTMSLGAENSVAYSNN	715
Alpha/B.1.1.7	SYECDIPIGAGICASYQTQNSHRRAR	SVASQSI IAYTMSLGAENSVAYSNN	715
P.1/Gamma	SYECDIPIGAGICASYQTQNSPRRAR	SVASQSI IAYTMSLGAENSVAYSNN	718
Beta/B.1.351	SYECDIPIGAGICASYQTQNSPRRAR	SVASQSI IAYTMSLGVENSVAYSNN	715

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SARS-CoV-2	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	778
Delta/B.1.617.2	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	778
Omicron/B.1.1.529	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	775
Alpha/B.1.1.7	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	775
P.1/Gamma	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	778
Beta/B.1.351	TISVTTEILPVSMTKTSVDCTMYICGDSTEC SNLLQYGSFCTQLNRALTGIAVEQDKNT	775
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SARS-CoV-2	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	838
Delta/B.1.617.2	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	838
Omicron/B.1.1.529	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	835
Alpha/B.1.1.7	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	835
P.1/Gamma	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	838
Beta/B.1.351	QEVFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLDAGFIKQYG	835
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SARS-CoV-2	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	898
Delta/B.1.617.2	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	898
Omicron/B.1.1.529	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	895
Alpha/B.1.1.7	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	895
P.1/Gamma	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	898
Beta/B.1.351	DCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPF	895
	*****:*****	
SARS-CoV-2	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	958
Delta/B.1.617.2	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	958
Omicron/B.1.1.529	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	955
Alpha/B.1.1.7	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	955
P.1/Gamma	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	958
Beta/B.1.351	AMQMAYRFNGIGVTONVLYENQKLIANQFN SAIGKIQDSLSTASALGKLQDVVNQNAQA	955
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SARS-CoV-2	LNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1018
Delta/B.1.617.2	LNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1018
Omicron/B.1.1.529	LNTLVKQLSSKFGAISSVLNDIFSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1015
Alpha/B.1.1.7	LNTLVKQLSSNFGAISSVLNDILAR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1015
P.1/Gamma	LNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1018
Beta/B.1.351	LNTLVKQLSSNFGAISSVLNDILSR LDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEI	1015
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SARS-CoV-2	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1078
Delta/B.1.617.2	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1078
Omicron/B.1.1.529	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1075
Alpha/B.1.1.7	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1075
P.1/Gamma	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1078
Beta/B.1.351	RASANLAATKMSECVLGQSKRVDFCGKG YHLSFPQSAPHGVVFLHVTVYPAQEKNFTTA	1075
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SARS-CoV-2	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY	1138
Delta/B.1.617.2	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY	1138
Omicron/B.1.1.529	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY	1135
Alpha/B.1.1.7	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTHNTFVSGNCDVVIGIVNNTVY	1135
P.1/Gamma	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY	1138
Beta/B.1.351	PAICHDGKAHFPREGV FVSN GTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVY	1135
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SARS-CoV-2	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1198
Delta/B.1.617.2	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1198
Omicron/B.1.1.529	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1195
Alpha/B.1.1.7	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1195
P.1/Gamma	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1198
Beta/B.1.351	DPLQPELDSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLI	1195
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SARS-CoV-2	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1258
Delta/B.1.617.2	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1258
Omicron/B.1.1.529	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1255
Alpha/B.1.1.7	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1255
P.1/Gamma	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1258
Beta/B.1.351	DLQELGKYEQYIKWFWYIWLGFIAGLIAIVMTIMLCCMTSCCCLKGCCSCGSCCKFDE	1255

SARS-CoV-2	DDSEPVLLKGVKLHYT	1273
Delta/B.1.617.2	DDSEPVLLKGVKLHYT	1273
Omicron/B.1.1.529	DDSEPVLLKGVKLHYT	1270
Alpha/B.1.1.7	DDSEPVLLKGVKLHYT	1270
P.1/Gamma	DDSEPVLLKGVKLHYT	1273
Beta/B.1.351	DDSEPVLLKGVKLHYT	1270

Figure S3. Multiple sequence alignment and construction of the phylogenetic tree of SARS-CoV-2 VOCs. A) Phylogenetic tree of SARS-CoV-2 Spike protein VOCs. **B)** Multiple sequence alignment of the Spike protein VOCs. The domains are colored as: signal peptide (orange); N-terminal domain (green), RBD (red), SD1 (pink) and SD2 (purple), cleavage sites (S1/S2 and S2' are colored in black) the fusion peptide (brown), HR1 (cyan and blue), HR2 (dark green), a transmembrane domain (grey), and cytoplasm domain (not colored) [5,6]. The predominant residues D614G and N501Y are pointed using arrows. The residues of the Spike protein involved in hACE2 interaction are highlighted: E1 region in yellow (corresponds to residues 417, 455-456, 470-490) and E2 region in light blue (made up of residues 444-454 and 493-505) [55]. Multiple sequence alignment and the phylogenetic tree were performed using the ClustalW server [14].

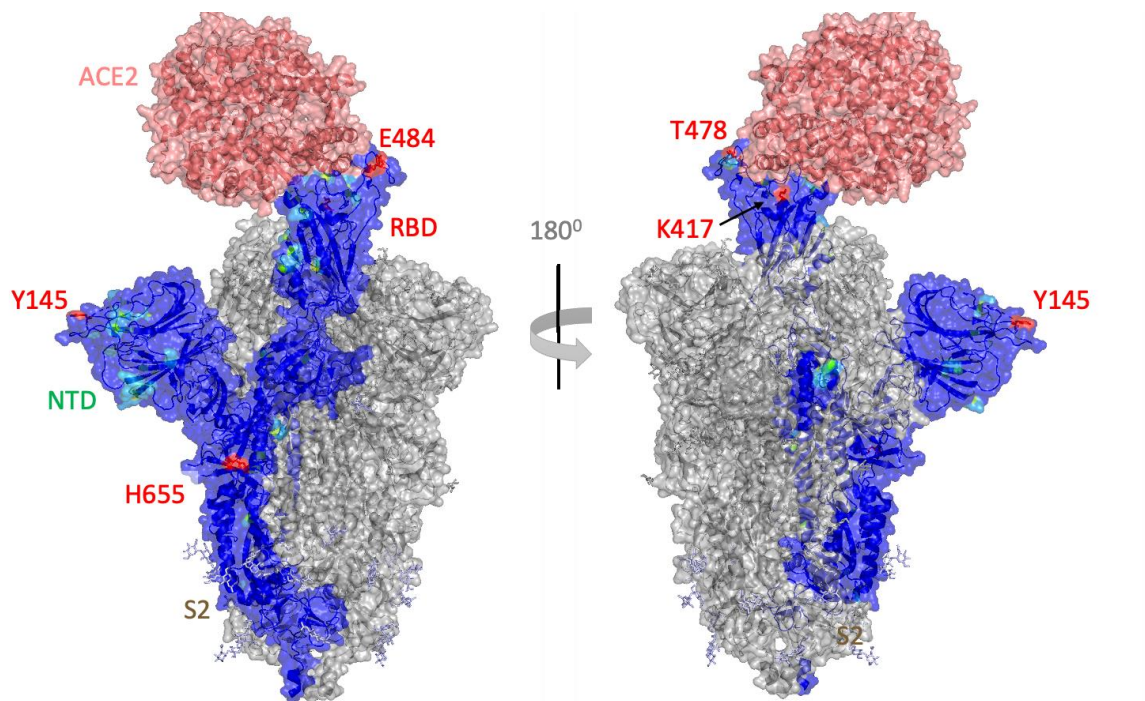


Figure S4. Conservation profile of the Spike protein among VOCs. The surface of the structure of the Spike^{WT} protein in complex with ACE2 (PDB ID: 7DF4 [17]) is colored based on the conservation profile. The ACE2 structure is colored in salmon, and the chains A and C in the trimeric form of Spike protein are colored in grey. The residues Y145, K417, T478, E484 and H655 are colored in red and correspond to the residues in the SARS-CoV-2 VOCs with more variability.

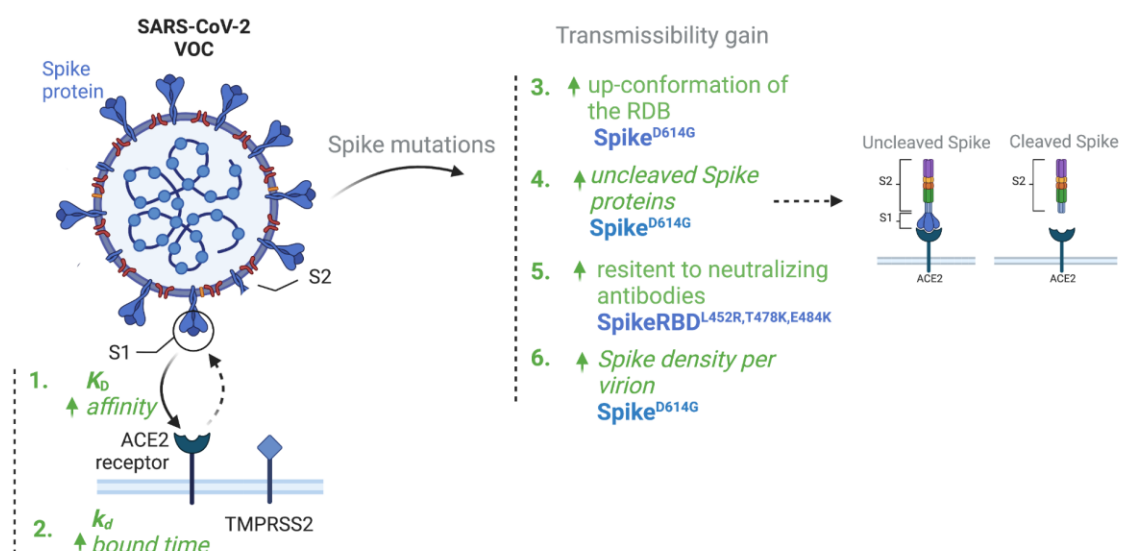


Figure S5: Mutations in the Spike protein of SARS-CoV-2 VOCs result in different mechanisms to evade the immune system, increase the infectiveness, and spread the virus faster in the population. Spike protein of SARS-CoV-2 VOCs increase the hACE2 affinity (K_D) (1); increase the time that the Spike protein is bound to hACE2 (k_d), favoring the process of membrane fusion (2); increase the up conformation of the RBD in the trimeric state of the Spike protein, a conformation that is able to bind to hACE2 (3); increase the amount of the uncleaved form of the Spike protein in virion particles (4); different mutations in the RBD improve resistance to neutralizing antibodies (5); and expand the concentration of Spike proteins per viral particles (6). All mechanisms described contribute to Spike's access to hACE2 and to membrane fusion. In the topic 4 spike cleaved protein refers to the spike protein that is naturally cleaved in the mature viral particle. Mutations in the Spike protein result in greater protection from the proteolysis of the spike protein resulting in an increased amount of complete Spike protein (uncleaved) on the virion surface.

Table S1. Conservation score in the Consurf Server analysis [15,16]. The Spike protein residues with the highest values are listed. High values meaning not conserved residues in the Spike protein among SARS-CoV-2 VOCs.

Spike Residue	Conservation Score
L18	4.5
T19	4.0
P26	4.4
H69	4.1
D80	4.2
T95	4.0
D138	4.2
Y145	7.5
H146	4.3
E156	4.3

R190	4.2
N211	4.3
L212	4.5
V213	4.7
R214	5.0
D215	4.2
G339	4.6
S371	4.2
G339	4.6
S371	4.2
S373	4.0
S375	4.1
K417	8.6
N440	4.1
G446	4.4
L452	4.5
S477	3.9
T478	7.2
E484	7.3
Q493	4.3
G496	4.4
Q498	4.3
N501	4.5
Y505	4.4
T547	4.2
D614	4.5
H655	7.2
A701	4.0

T716	4.0
N764	4.1
D796	4.4
N856	4.1
D950	4.1
Q954	4.2
N969	4.1
L981	4.5
S982	3.9
T1027	4.0
D1118	4.2