Supplementary Table 1. SARS-CoV-2 Nsps, main characteristics and functions.

Non-structural protein	Function	Reference
Nsp1	Inhibits host gene expression and affects the host viral defense strategy	(Bai et al., 2022; Giovanetti et al., 2021; van de Leemput and Han, 2021)
Nsp2	Regulates the signaling pathways involved in signal transmission within the host	(Kadam et al., 2021)
Nsp3, Papain-like cysteine protease (PLpro)	Transcriptional role of SARS-CoV-2 Involved in pp1a/pp1ab polyprotein proteolysis Dysregulating host inflammation response Impairing the host type I interferon antiviral immune responses	(Chaube et al., 2023, Li et al., 2023; Yang and Rao, 2021)
Nsp4	Viral replication Generates double membrane vesicles Partially in contact with mitochondria	(Chaube et al., 2023; Prasada et al., 2023; Ricciardi et al., 2022)
Nsp5, Main protease (Mpro) or 3C-like protease (3-CLpro)	Involved in the proteolysis of 1a/1ab polyproteins Participates in the degradation of IRF3 Inhibits RIG-I Contains immune escape mechanisms	(Dömling and Gao, 2020; Low et al., 2022; Prasada et al., 2023; van de Leemput and Han, 2021)
Nsp6	Causes apoptosis by acting on the mitochondrion Promotes replication-transcription complexes Involved in the mechanism of immune evasion Inhibits the phosphorylation of IRF3, STAT1, and STAT2	(Low et al., 2022; van de Leemput and Han, 2021; Yoshimoto, 2020)
Nsp7	Involved in blocking the development of autophagosome/autolysosome vesicles Cofactor in processes for the RTC of other proteins	(Frazier et al., 2022; van de Leemput and Han, 2021)
Nsp8	Participates in the assembly of complexes for viral replication, initiating the replication process and operating as a primase Downregulates immune factors (e.g., type I IFN), reduces phosphorylation of TBK1, IRF3, IKKα/β Interferes with mitochondria	(Low et al., 2022; Prasada et al., 2023; Ruan et al., 2021; Vicenti et al., 2021)
Nsp9	RNA-binding protein, reducing the IFN response Interacts with nucleoporin 62 to disturb the translocation of p65 after TNF-α stimulation	(Low et al., 2022; Varghese Edwin and Stanislaus Antony, 2023)

Nsp10	Responsible for the RNA methylation with other complexes Deregulates secretion of pro-inflammatory cytokines Cofactor of two peptides, Nsp14 and Nsp16	(Frazier et al., 2022; Kadam et al., 2021; Low et al., 2022; van de Leemput and Han, 2021; Prasada et al., 2023)
Nsp11	Regulates endoribonuclease, necessary for viral replication	(Tam et al., 2023)
Nsp12	RNA-dependent RNA polymerase, catalyzes the synthesis of viral RNA in complex with other Nsps Viral replication	(Aftab et al., 2020; Bai et al., 2022; Tanimoto et al., 2022)
Nsp13	Changes the structure and function of the cytoskeleton, and participates in the RTC formation Reacts with p125 (catalytic subunit of mammalian DNA polymerase delta), disrupting the proper course of replication	(Frazier et al., 2022; Quan et al., 2023)
Nsp14	Provides the error correction in the RNA synthesis complex	(Bai et al., 2022; van de Leemput and Han, 2021)
Nsp15 (NendoU, a uridylate-specific endoribonuclease)	Inhibits nuclear translocation of IRF3 Involved in evasion of the immune system Involved in prevention of the activation of the dsRNA sensor MDA5	(Frazier et al., 2022; van de Leemput and Han, 2021; Wilson et al., 2022)
Nsp16	Encodes for 2'-*O*-ribose methyltransferase, which may refer to the control of the activity of Nsp15 The role of blocking the recognition of viral RNA	(Saramago et al., 2022)

Supplementary Table 2. Spike protein mutations, detected from 137 samples included in this research.

Mutation	Lineage	Additional comments
P26S	P.1	
W64R	BA.2.9.3	
T19I	BA.2.9.3, BA.2.49, BA.2.9, BA.2	
T19R	B.1.617.2	
A27S	BA.2, BA.2.9.3, BA.2.49, BA.2.9, B.1.1.529 XBB.1, XBB.1.5, XBB.11.5.14, BF.7, BA.4.6, BN.1.2, BQ.1.1.18, BN.1.2, BQ.1.1, BQ.1, BA.5.2.1, BA.5.2, BA.5, BA.5.2	This mutation is not present in two BA.5.2 samples from Russia
W64R	BA.2.93	
Del69	B.1.1.7, BA.1, BA.2, BA.1.1, BA.1.1.1, BA.1.17, BA.1.18, BF.7, BA.4.6, BN.1.2, BQ.1.1.18, BQ.1.1, BQ.1, BA.5.2.1, BA.5.2, BA.5.	These deletions were not found in samples from Russia for the BA.5.2 variant In the sample from France for BA.5, the deletion was not found in one sample
Del70	B.1.1.7, BA.1, BA.2, BA.1.1, BA.1.1.1, BA.1.17, BA.1.18, BF.7, BA.4.6, BN.1.2, BQ.1.1.18, BQ.1.1, BQ.1, BA.5.2.1, BA.5.2, BA.5.	
S71F	BQ.1	
D80A	B.1.351	
T95I	BA.1.17, BA.1.18, BA.1.1, BA.1.1.1, B.1.1.529, B.1.617.2, BA.2, BA.1	In a sample from France, B.1.617.2 does not contain this mutation The BA.2 variant contains this mutation (except for one sample from Russia)
Q134H	BQ.1.1.18	
D138Y	P.1	
G142D	BQ.1	
Del144	BQ.1.1, BQ.1, BA.5, BA.1, XBB.1, XBB.1.5.14, XBB.1.5, B.1.1.7.	
Del143	BA.1, BA.2, BA.1.1, BA.1.18, BA.1.17, BA.1.1.1	
Del144	BA.1, BA.2, BA.1.1, BA.1.18, BA.1.17, BA.1.1.1	
Del145	BA.1, BA.2, BA.1.1, BA.1.18, BA.1.17, BA.1.1.1	
H146Q	XBB.1, XBB.1.5, XBB.1.5.14	
K147E	BA.5, BN.1.2	
E156G	B.1.617.2	
DelF157 DelR158	B.1.617.2	

Q183E	XBB.1, XBB.1.5, XBB.1.5.14
Q183L	BA.5.2.1
G184V	BA.5.2
R190S	P.1
T208M	BA.1
Del211	BA.1.17, BA.1.18, BA.2, BA.1
Del215	Alpha, Beta, BA.2, BA.2.9.3, BA.2.49, BA.2.9, BA.1.1.1, B.1.1.529, B.1.617.2, P.1, XBB.1, XBB.1.5, XBB.1.5.14, BF.7, BA.4.6
Del216	Alpha, Beta, BA.2, BA.2.9.3, BA.2.49, BA.2.9, BA.1.1.1, B.1.1.529, B.1.617.2, P.1, XBB.1, XBB.1.5, XBB.1.5.14, BF.7, BA.4.6
Del217	Alpha, Beta, BA.2, BA.2.9.3, BA.2.49, BA.2.9, BA.1.1.1, B.1.1.529, B.1.617.2, P.1, XBB.1, XBB.1.5, XBB.1.5.14, BF.7, BA.4.6
Del214	BA.1.1.1
Del215	BA.1.1.1
Del216	BA.1.1.1
Del217	BA.1.1.1
Del211	BA.1.1, BA.1.1.1, BA.2
V213G	BA.2.9.3, BA.2.49, BA.2.9, BN.1.2, BQ.1.1.18, BQ.1.1, BQ.1, BA.5, BA.5.2.1, BA.5.2
S257F	BA.1.1.1
Del244	Beta variant
Del245	Beta variant
Del246	Beta variant
G260S	BN.1.2, BA.5
G342D	Omicron
D342H	XBB.1, XBB.1.5, XBB.1.5.14, BA.5
R349T	XBB.1, XBB.1.5, XBB.1.5.14. BF7, BA.4.6, BN.1.2, BQ.1.1.18, BQ.1.1, BA.5
S374L	BA.1, BA.1.17, BA.1.18, BA.1.1, BA.1.1.1, BA.1.1.529
S375F	BA.2, BA.2.9, BA.2.9.3, BA.2.49, XBB.1, XBB.1.5 XBB.1.5.14, BF.7, BA.4.6, BN.1.2, BQ.1, BQ.1.1, BQ.1.1.18, BA.5, BA.5.2
D408N	BA.2, BA.2.9.3, BA.2.49, BA.2.9, XBB.1, XBB.1.5, XBB.1.5.14, BF.7, BA.4.6, BN.1.2, BQ.1.1.18, BQ.1.1
S411R	BA.5.2
K420N	BQ.1, Delta, Beta, Alpha

N443K	BA.1, BA.1.17, BA.1.18, BA.2.49, BA.1.1, BA.1.1.1, BA.2, XBB.1, XBB.1.5, XBB.1.5.14, BN.1.2, BQ.1.1, BQ.1.1.18, BA.5, BA.5.2	
K447T	BQ.1, BQ.1.1, BQ.1.1.18	
V448P	XBB.1, XBB.1.5	
L455R	Delta, BF.7, BA.4.6, BQ.1.1, BQ.1.1.18	
G449S	P.1, BA.1.17, BA.1.18, BA.1.1, BA.1.1.1, BA.1.1.529, BA.1, XBB.1, XBB.1.5, XBB.1.5.14, BN.1.2	
N480D	XBB.1	
T481K	Delta, Omicron	This mutation was not found in Omicron BA.1 from Ireland
E487K	Beta, Gamma	
E487A	Omicron	
E487Q	Delta	Detected in just one sample from Delta variant
F489S	XBB.1	
F489P	XBB.1.4, XBB.1.5.14	
Q496R	Omicron, Gamma	
G499S	BA.1.17, BA.1.18, BA.1.1, B.1.1.529, BA.1	
Q501R	Alpha, Beta, Gamma	
N504Y	Delta	
Y508H	Omicron	
P524T	XBB.1	
T550K	BA.1, BA.1.17, BA.1.18., BA.1.1, BA.1.1.1	
T575I	BQ.1	
E557G	XBB.1	
A573D	Alpha	
D617G	Present in all samples compared to the RefSeq	
H658Y	Gamma, Omicron	No H658Y mutation was observed in BA.1.18
Q678H	XBB.1.5.14	
R680Q	BA.5.2.1	
K682N	Omicron	
P684H	Gamma	
T719I	Alpha	
N767K	Omicron	This mutation was not found in the sample from Ireland
D799Y	Omicron	
P810S	XBB.1.5.14	
P812S	Alpha	

A848S	BN.1.2	
N859K	BA.1.17, BA.1.1, BA.1.1.1, BA.2, BA.1	
S946P	Beta, BA.2, XBB.1	
D953N	Delta	
Q957H	Gamma, Omicron	
N972K	Omicron	Omicron variant B.1.1.529 from Russia does not contain this mutation
S985A	Alpha	Two Alpha samples do not have this mutation
T1030I	Gamma	
G1088E	BQ.1.1.18	
D1121H	Alpha	Except sample QTC10214.1
P1266L	BQ.1	

Supplementary Table 3. Envelope protein mutations, detected from 120 samples included in this research.

Mutation	Lineage
T9I	B.1.1.529, B.1.1.52, BA.1, BA.2, BA.1.1, BA.5, BA.5.1, BA.5.2, BA.5.2.1, BQ.1, BQ .1.1, BQ.1.1.18, BA.1.17.2, BA.1.17, BA.1.18, BA.1.1.1, BA.2.3, BA.2.9, BA.2.9.3, BA.2.23
S50I	BA.1.1.1
V62F	B.1.617.2
P71L	B.1.351

Supplementary Table 4. RdRp mutations, detected in 42 sequences in this research and sequence IDs in which mutations were identified.

Mutation	Sample IDs
M196R	WBE23697.1
P323L	B.1 lineage, including IDs WBE23697.1, WBE23695.1, WBE23684.1, WBE23682.1, WBE23680.1, WBE23676.1, WBE23672.1
C645G	WBE23697.1
G671S	WBE23676.1