

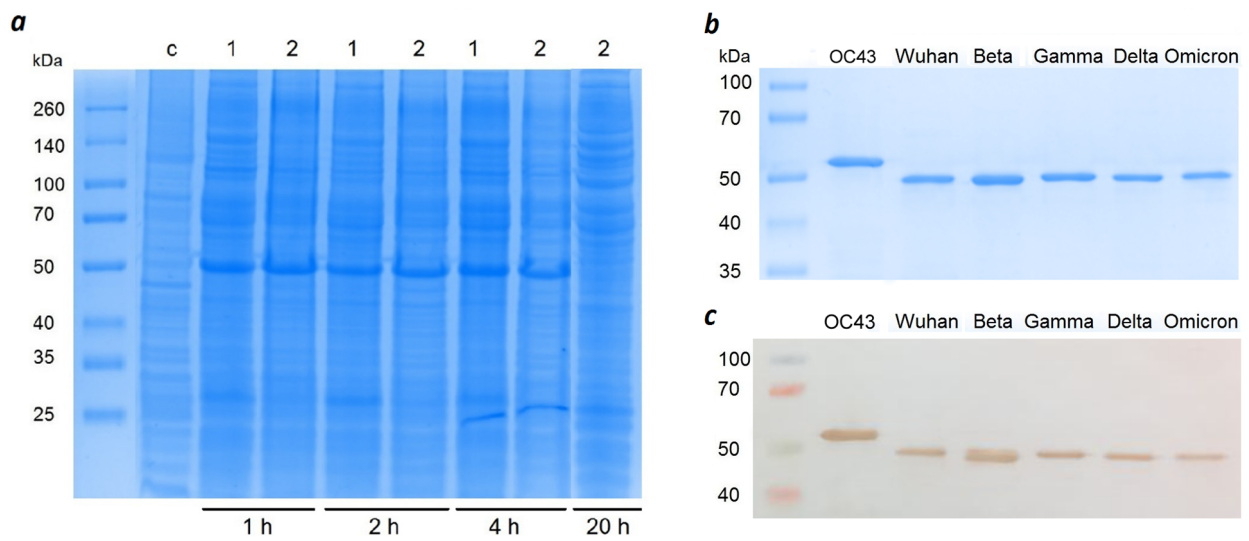
## Supplementary Materials

**Table S1.** Demographic characteristics of the study subjects

Nº	Sex	Age	Date of disease onset	SARS-CoV-2 lineage†	Severity	Month PSO
1	F	31	May 2020	B.1	severe	7
2	F	31	May 2020	B.1	severe	18
3	M	39	May 2020	B.1	severe	4
4	M	39	May 2020	B.1	severe	11
5	M	39	May 2020	B.1	severe	16
6	F	34	May 2020	B.1	mild	7
7	F	40	June 2020	B.1	mild	6
8	M	38	Sep 2020	B.1	moderate	2
9	F	33	Oct 2020	B.1	moderate	6
10	F	33	Oct 2020	B.1	moderate	9
11	F	33	Oct 2020	B.1	moderate	11
12	F	77	Oct 2020	B.1	moderate	1
13	F	77	Oct 2020	B.1	moderate	6
14	F	77	Oct 2020	B.1	moderate	11
15	F	39	Nov 2020	B.1	mild	6
16	M	39	Dec 2020	B.1	moderate	1
17	M	39	Dec 2020	B.1	moderate	5
18	M	39	Dec 2020	B.1	moderate	7
19	F	39	Dec 2020	B.1	mild	5
20	F	39	Feb 2021	B.1	mild	1
21	F	39	Feb 2021	B.1	mild	6
22	F	80	Feb 2021	B.1	moderate	7
23	M	84	Feb 2021	B.1	severe	7
24	F	64	May 2021	B.1.617.2	mild	1
25	F	37	May 2021	B.1.617.2	mild	4
26	M	37	May 2021	B.1.617.2	moderate	4
27	F	45	May 2021	B.1.617.2	mild	1
28	M	26	Aug 2021	B.1.617.2	mild	1
29	M	31	Aug 2021	B.1.617.2	mild	1
30	F	38	Sep 2021	B.1.617.2	mild	1
31	M	31	Oct 2021	B.1.617.2	mild	1
32	F	35	Oct 2021	B.1.617.2	mild	1

† the B.1 (Wuhan D614G) lineage was assigned based on the surveillance data [1], while B.1.617.2 (Delta) lineage assignment was based on the sequencing of Spike protein gene of the RT-PCR positive specimens or recovered live viruses.

PSO – post symptoms onset.



**Figure S1.** Induction and purification of recombinant N proteins. (a) SDS-PAGE analysis of different IPTG concentrations and induction time on the expression intensity of N protein (B.1) at 37 °C (1, 0.1 mM IPTG; 2, 0.5 mM IPTG); (b) SDS-PAGE analysis of N proteins purified by IMAC under non-reducing conditions; (c) Western blot analysis of obtained proteins with HisProbe-HRP. M - molecular weight marker.

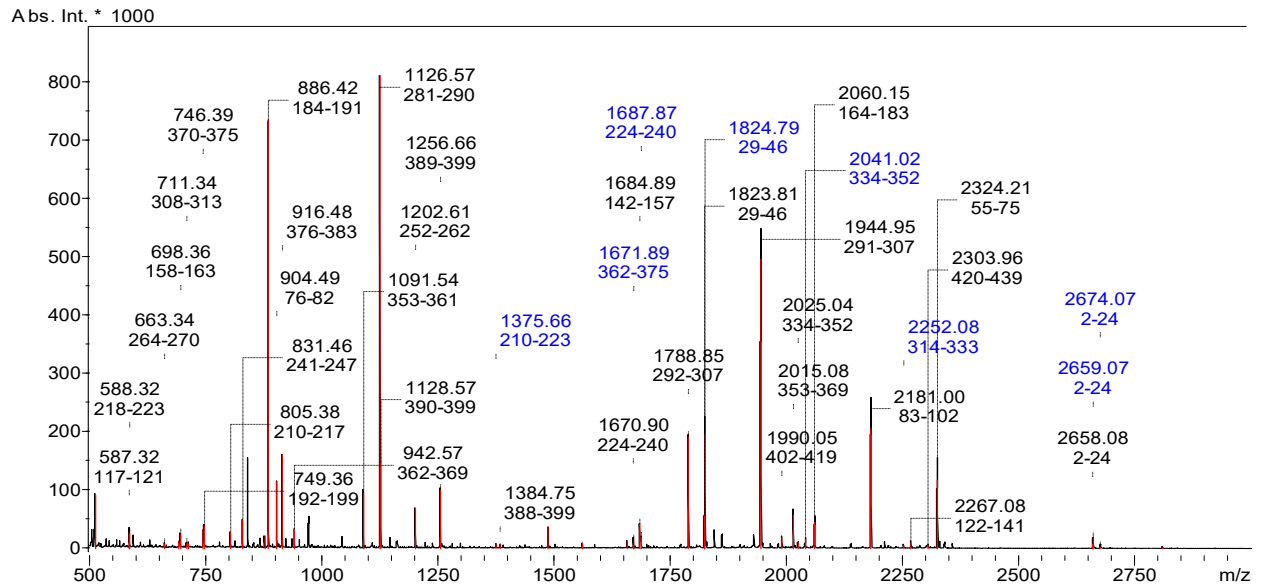
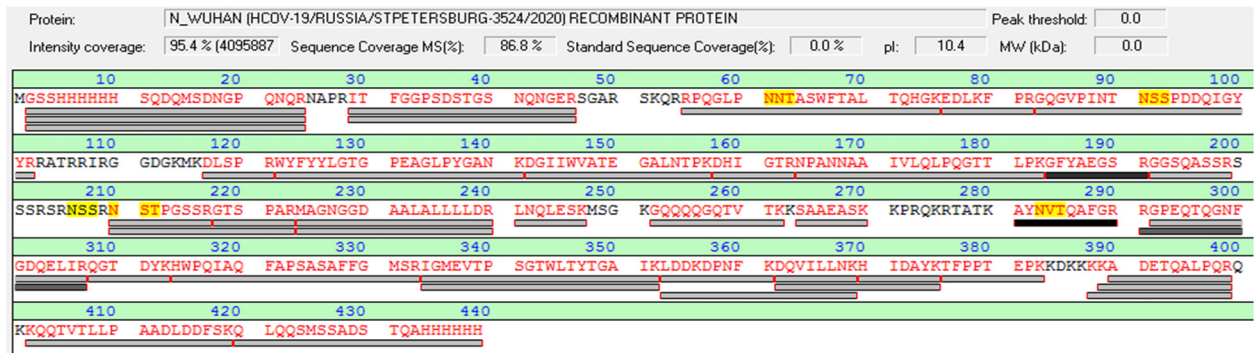
## A

10	20	30	40	50	60	70	80	90	100
1: MGSSHHHHHH	SQDQMSDNGP	QNQRNAPRIT	FGGPSDSTGS	NQNGERSGAR	SKQRRPQGLP	NNTASWFTAL	TQHGKEDLKF	PRGQGVPIINT	NSSPDDQIGY
2: MGSSHHHHHH	SQDQMSDNGP	QNQRNAPRIT	FGGPSDSTGS	NQNGERSGAR	SKQRRPQGLP	NNTASWFTAL	TQHGKEDLKF	PRGQGVPIINT	NSSPDDQIGY
3: MGSSHHHHHH	SQDQMSDNGP	QNQRNAPRIT	FGGPSDSTGS	NQNGERSGAR	SKQRRPQGLP	NNTASWFTAL	TQHGKEDLKF	PRGQGVPIINT	NSSPDDQIGY
4: MGSSHHHHHH	SQDQMSDNGP	QNQRNAPRIT	FGGPSDSTGS	NQNGERSGAR	SKQRRPQGLP	NNTASWFTAL	TQHGKEDLKF	PRGQGVPIINT	NSSPDDQIGY
5: MGSSHHHHHH	SQDQMSDNGP	QNQRNAPRIT	FGGPSDSTGS	NQNGERSGAR	SKQRRPQGLP	NNTASWFTAL	TQHGKEDLKF	PRGQGVPIINT	NSSPDDQIGY
110	120	130	140	150	160	170	180	190	200
YRRATRIRRG	GDGKMKDLSP	RWYFYLLGTG	PEAGLPYGAN	KDGIWVATE	GALNTPKDHI	GTRNPANNA	IVLQLPQGT	LPGFYAEGS	RGGSQASSRS
YRRATRIRRG	GDGKMKDLSP	RWYFYLLGTG	PEAGLPYGAN	KDGIWVATE	GALNTPKDHI	GTRNPANNA	IVLQLPQGT	LPGFYAEGS	RGGSQASSRS
YRRATRIRRG	GDGKMKDLSP	RWYFYLLGTG	PEAGLPYGAN	KDGIWVATE	GALNTPKDHI	GTRNPANNA	IVLQLPQGT	LPGFYAEGS	RGGSQASSRS
YRRATRIRRG	GDGKMKDLSP	RWYFYLLGTG	PEAGLPYGAN	KDGIWVATE	GALNTPKDHI	GTRNPANNA	IVLQLPQGT	LPGFYAEGS	RGGSQASSRS
YRRATRIRRG	GDGKMKDLSP	RWYFYLLGTG	PEAGLPYGAN	KDGIWVATE	GALNTPKDHI	GTRNPANNA	IVLQLPQGT	LPGFYAEGS	RGGSQASSRS
210	220	230	240	250	260	270	280	290	300
SSRSRNSSRN	STPGSSRGTS	PARMAGNGGD	AALALLLLDR	LNQLESKMSG	KGQQQQGQTV	TKKSAAEASK	KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF
SSRSRNSSRN	STPGSSRGTS	PARMAGNGGD	AALALLLLDR	LNQLESKMSG	KGQQQQGQTV	TKKSAAEASK	KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF
SSRSRNSSRN	STPGSSRGTS	PARMAGNGGD	AALALLLLDR	LNQLESKMSG	KGQQQQGQTV	TKKSAAEASK	KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF
SSRSRNSSRN	STPGSSRGTS	PARMAGNGGD	AALALLLLDR	LNQLESKMSG	KGQQQQGQTV	TKKSAAEASK	KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF
SSRSRNSSRN	STPGSSRGTS	PARMAGNGGD	AALALLLLDR	LNQLESKMSG	KGQQQQGQTV	TKKSAAEASK	KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF
310	320	330	340	350	360	370	380	390	400
GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGMEVTP	SGTWLTYTGA	IKLDDKDPNF	KDQVILLNKH	IDAYKTFFPT	EPKDKKKKA	DETQALPQRQ
GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGMEVTP	SGTWLTYTGA	IKLDDKDPNF	KDQVILLNKH	IDAYKTFFPT	EPKDKKKKA	DETQALPQRQ
GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGMEVTP	SGTWLTYTGA	IKLDDKDPNF	KDQVILLNKH	IDAYKTFFPT	EPKDKKKKA	DETQALPQRQ
GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGMEVTP	SGTWLTYTGA	IKLDDKDPNF	KDQVILLNKH	IDAYKTFFPT	EPKDKKKKA	DETQALPQRQ
GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGMEVTP	SGTWLTYTGA	IKLDDKDPNF	KDQVILLNKH	IDAYKTFFPT	EPKDKKKKA	DETQALPQRQ
410	420	430							
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	Cov	Score	1 – hCoV-19/Russia/StPetersburg-3524/2020 (B.1 Lineage, Wuhan)			
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	87%	330 / 70	2 – hCoV-19/Russia/SPE-RII-27029S/2021 (B.1.351 Lineage, Beta)			
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	85%	243 / 70	3 – hCoV-19/Japan/TY7-503/2021 (P.1 Lineage, Gamma)			
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	72%	339 / 70	4 – hCoV-19/Russia/SPE-RII-32759S/2021 (B.1.617.2 Lineage, Delta)			
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	71%	238 / 70	5 – hCoV-19/Russia/SPE-RII-6243V1/2021 (B.1.1.529 Lineage, Omicron)			
KKQQTVTLLP	AADLDDFSKQ	LQSMSSADS	TQAHHHHHH	86%	267 / 70	S – hCoV_OC43			

## B

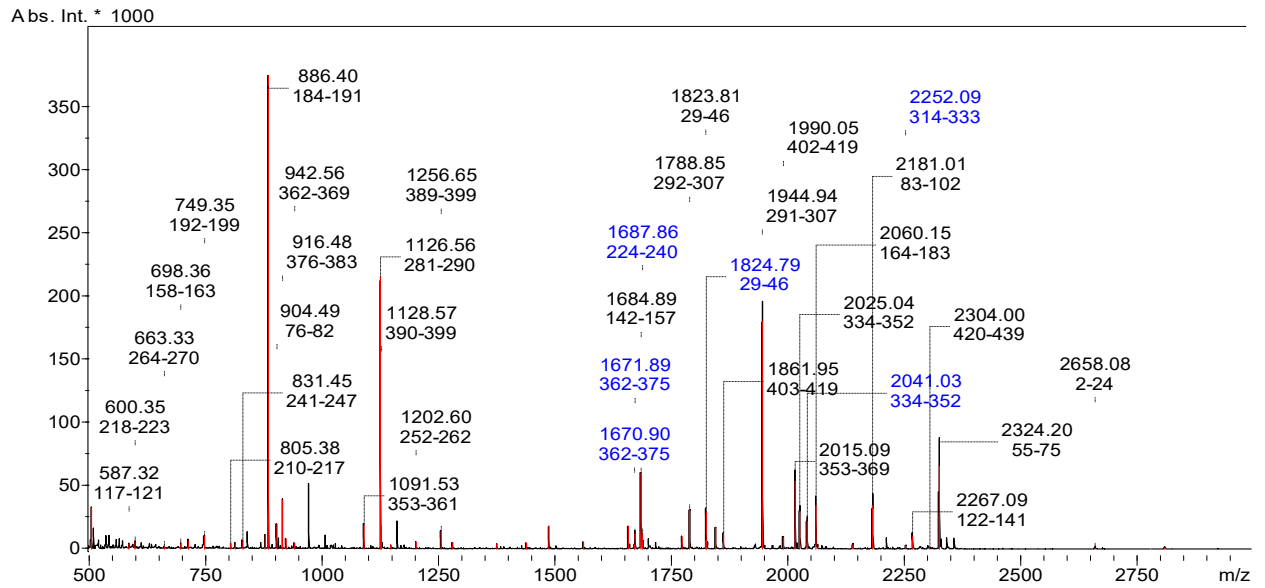
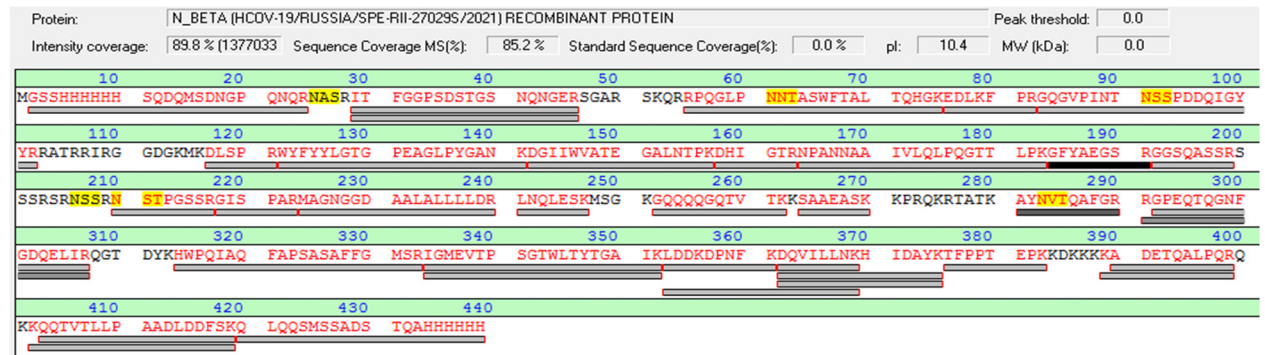
10	20	30	40	50	60	70	80	90	100
1: MGSSHHHHHH	SQDQMS	-----D	NGPQNQRNAP	RIITFGGPSDS	TGSNQNGERS	GARSQRRPQ	GLPNNTASWF	TALTQHGK-E	DLKFPRGQGV
S: MGSSHHHHHH	SQDQMS	FTPG	KQSSSRASSG	NRSNGILKW	ADQSDQVRNV	QTRGRRAQPK	QTATSQQPSG	GNVVPYYSWF	SGITQFQKKG
110	120	130	140	150	160	170	180	190	200
PINTNSSPDD	QIGYYRRATR	R-IRGGDGKM	KDLSRPRWYF	YLGTPGEAGL	PYGANKDGI	WVATEGA-LN	TPKDHIHTRN	PANNAIVLQ	LPQGTTLPGK
PIAPGVPATE	AKGYWYRHR	RSFKTADGNQ	RQLLPRWYF	YLGTPGPHAKD	QYGTIDIGVY	WVASNQADV	TPAD-IVDRD	PSSDEAIPTR	FPPGTVLPGQ
210	220	230	240	250	260	270	280	290	300
FYAEGS----	-----RGGS	QASSRSSRS	RNSSRNSTPG	SSRGTSPTM	AGNGGDAALA	LLLLDLRLNQL	ESKMSGKQQQ	QQGQTVTKKS	AAEASK----
YYIEGSGRSA	PNSRSTSRIS	SRASSAGRS	RANSNRTPT	S--GVTPD-M	ADQ-----IA	SLVLAKLGKD	ATK-----	--PQVTKHT	AKEVRQKILN
310	320	330	340	350	360	370	380	390	400
KPRQKRTATK	AYNVTQAFGR	RGPEQTQGNF	GDQELIRQGT	DYKHWPQIAQ	FAPSASAFFG	MSRIGM----	-----EVT	PSGTWLTYTGA	AIKLDDKDPN
KPRQKRSQNK	QCTVQCFQK	RGPNQ---NF	GGGEMLKLGT	SDPQFPILAE	LAPTAGAFF	GSRLAKLVQ	NLSGNPDPEQ	KDVEYLRYNG	AIRFDSTLSG
410	420	430	440	450	460	470	480		
FKDQVILLNK	HIDAYKTFFP	TEPKDKKKK	ADETQALPQR	QKQQTVTLL	PAADLDDFSK	QLQSMSSAD	STQA-----	-----HHHHHH	Cov
FETIMKVLNE	NLNAYQODG	MMNMSPKQR	QRGHKNGQGE	NDNISVAVPK	SRVQNKRSRE	LTAEDISLLK	KMDEPYTEDT	SEIHHHHHH	Score
									79%
									316 / 70

**Figure S2.** Comparison of amino acid sequences of recombinant N proteins based on the results of mass spectrometric study. **A.** Alignment of five sequences of SARS-CoV-2 strains used in the study. **B.** Comparison of the N proteins sequences of B.1 SARS-CoV-2 (1) and a seasonal OC43 (S) coronavirus. Identified amino acid residues are marked in red. Yellow and blue colors indicate residues that differ in the analyzed proteins. Areas that distinguish at least one of the proteins are marked in bold red, and unique regions allowing to unambiguously identify the proteins are underlined. Unique regions that distinguish the N proteins of SARS-CoV-2 and OC43 viruses are shown in frames. Coverage and identification score (value/threshold) for each protein are indicated; the identification is considered reliable ( $p < 0.05$ ) if the score exceeds the threshold.

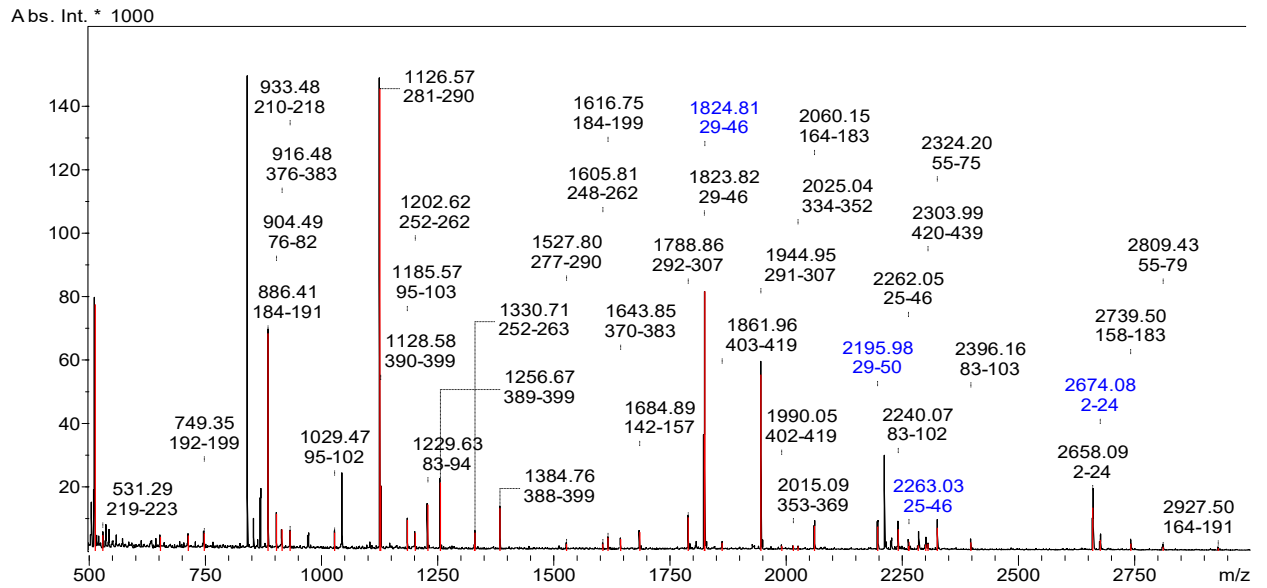
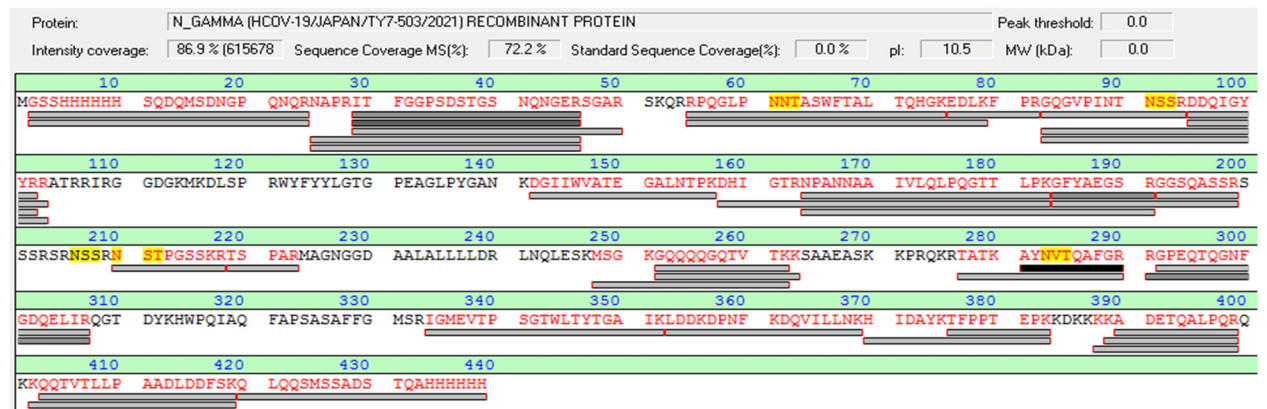
**A****B**

**Figure S3.** Mass spectrometry analysis of N protein (B.1). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (hCoV-19/Russia/StPetersburg-3524/2020) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.



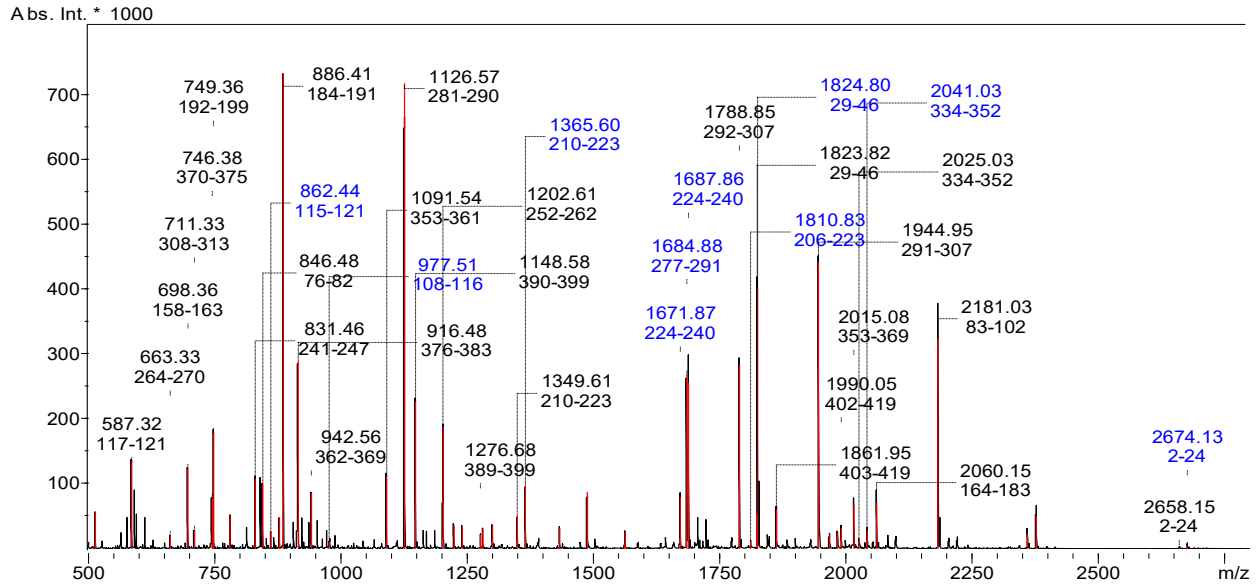
**A****B**

**Figure S4.** Mass spectrometry analysis of N protein (B.1.351). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (hCoV-19/Russia/SPE-R11-27029S/2021) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.

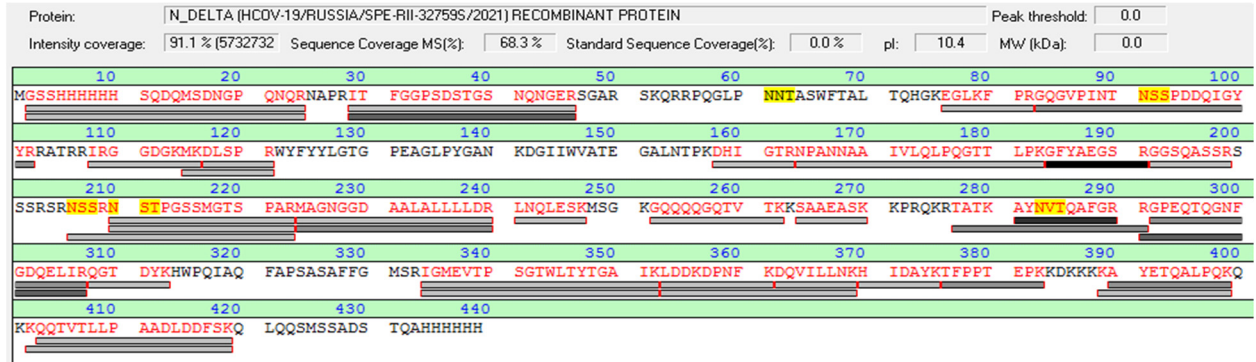
**A****B**

**Figure S5.** Mass spectrometry analysis of N protein (P.1). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (hCoV-19/Japan/TY7-503/2021) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.

A

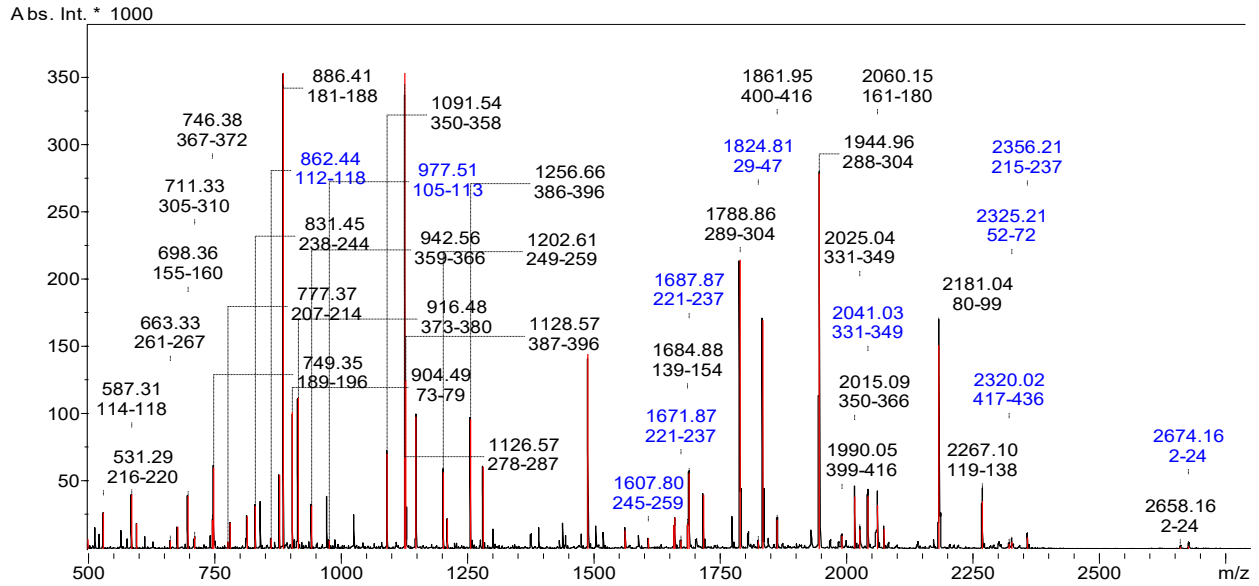


B

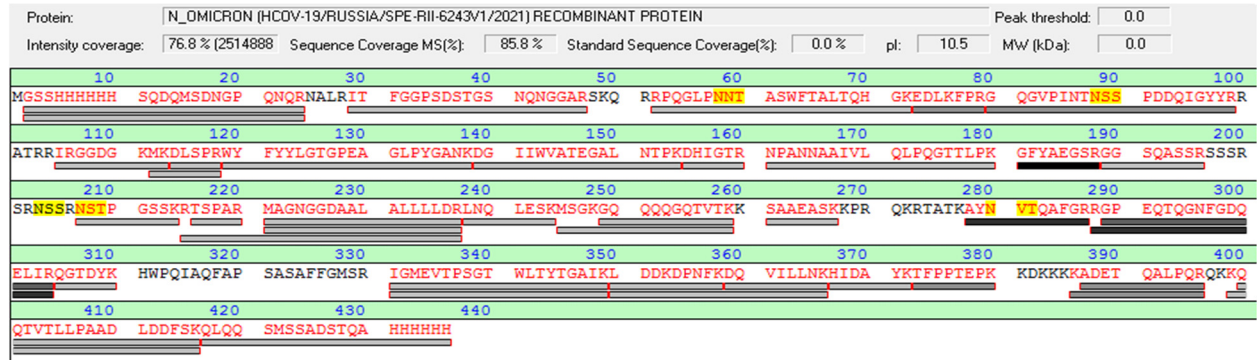


**Figure S6.** Mass spectrometry analysis of N protein (B.1.617.2). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (hCoV-19/Russia/SPE-RII-32759S/2021) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.

A



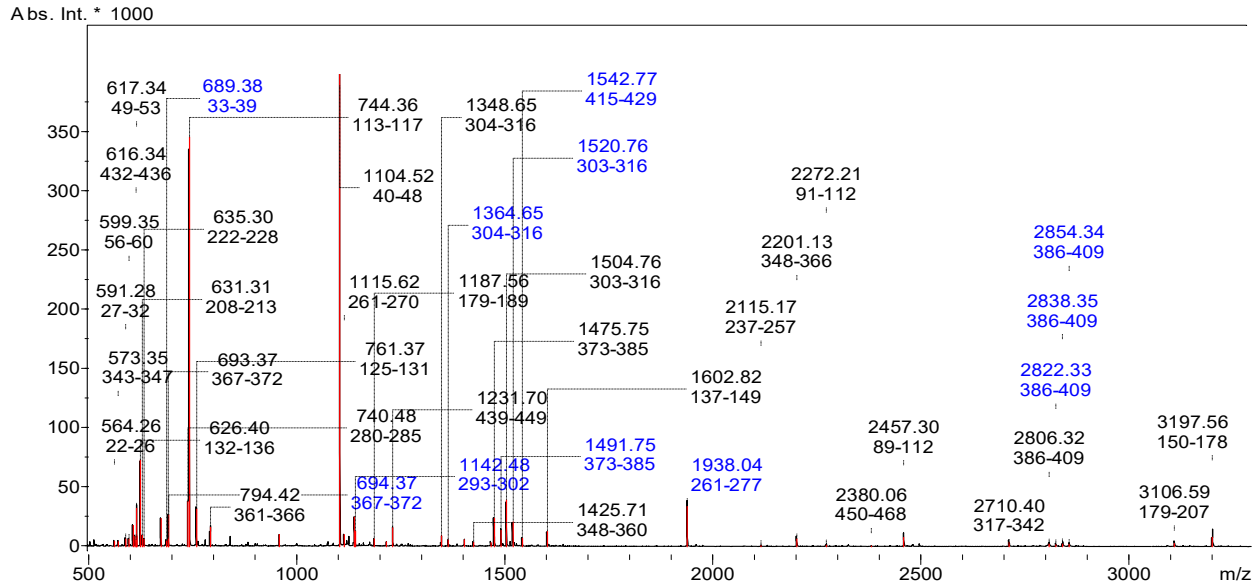
B



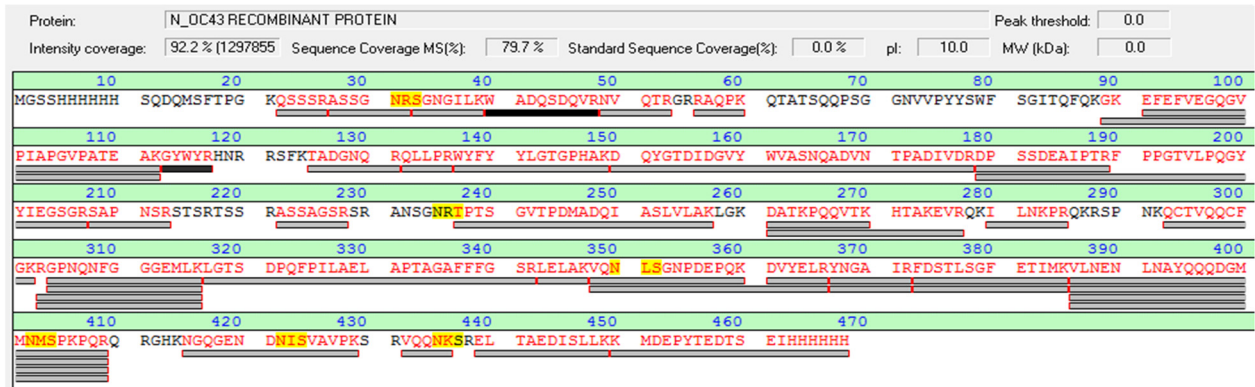
**Figure S7.** Mass spectrometry analysis of N protein (B.1.1.529). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (hCoV-19/Russia/SPE-RII-6243V1/2021) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.



**A**



**B**



**Figure S8.** Mass spectrometry analysis of N protein (HCoV OC43). **A.** Fragment of MALDI mass spectrum of hydrolyzed protein. Ions associated with fragments of the amino acid sequence (OC43) and the corresponding ranges are indicated; **B.** The amino acid sequence of protein: the fragments found in the spectrum are marked in red, gray underlined regions are matched with registered ions.

**Table S2.** Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (B.1) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Matched peptide
587.31	27512.69	11.37	117 - 121	DLSPR
<b>588.31</b>	<b>25817.61</b>	<b>9.47</b>	<b>218 - 223</b>	<b>GTSPAR</b>
663.33	8914.68	12.56	264 - 270	SAAEASK
698.36	25481.97	6.72	158 - 163	DHIGTR
711.33	9493.81	10.66	308 - 313	QGTDYK
746.38	31731.21	6.74	370 - 375	HIDAYK
749.35	39593.38	3.67	192 - 199	GGSQASSR
<b>805.38</b>	<b>28000.48</b>	<b>1.61</b>	<b>210 - 217</b>	<b>NSTPGSSR</b>
831.46	49533.04	6.3	241 - 247	LNQLESK
886.41	733180.94	12.52	184 - 191	GFYAEGSR
<b>904.49</b>	<b>115198.42</b>	<b>4.06</b>	<b>76 - 82</b>	<b>EDLKFPK</b>
916.48	160751.78	7.68	376 - 383	TFPTEPK
942.56	33435.58	3.63	362 - 369	DQVILLNK
1091.54	95118.6	4.06	353 - 361	LDDKDPNFK
1126.56	830947.64	5.7	281 - 290	AYNVTQAFGR
<b>1128.56</b>	<b>145732.46</b>	<b>5.78</b>	<b>390 - 399</b>	<b>ADETQALPQR</b>
1202.61	69095.96	-4.59	252 - 262	GQQQQGQTVTK
<b>1256.66</b>	<b>101407.45</b>	<b>-0.38</b>	<b>389 - 399</b>	<b>KADETQALPQR</b>
<b>1375.66</b>	<b>8647.57</b>	<b>-0.21</b>	<b>210 - 223</b>	<b>NSTPGSSRGTSAPAR 1: Deamidated (NQ)</b>
<b>1384.75</b>	<b>7247.41</b>	<b>-1.36</b>	<b>388 - 399</b>	<b>KKADETQALPQR</b>
1670.89	6429	6.47	224 - 240	MAGNGGDAALALLLDR
1671.9	15410.38	-5.26	362 - 375	DQVILLNKHIDAYK 2: Deamidated (NQ) 7: Deamidated (NQ)
1684.89	42657.95	1.67	142 - 157	DGIWVATEGALNTPK
1687.87	19729.67	-1.68	224 - 240	MAGNGGDAALALLLDR 1: Oxidation (M) 4: Deamidated (NQ)
1788.85	192022.96	1.82	292 - 307	GPEQTQGNFGDQELIR
<b>1823.82</b>	<b>56772</b>	<b>-5.18</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER</b>
<b>1824.8</b>	<b>195305.65</b>	<b>-5.61</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER 13: Deamidated (NQ)</b>
1944.95	495320.52	-1.67	291 - 307	RGPEQTQGNFGDQELIR
1990.05	18602.11	0.26	402 - 419	KQQTVTLLPAADLDDFSK
2015.08	57246.82	-1.74	353 - 369	LDDKDPNFKDQVILLNK
2025.04	10393.14	0.49	334 - 352	IGMEVTPSGTWLTYTGAIK
2041.03	16691.14	-5.29	334 - 352	IGMEVTPSGTWLTYTGAIK 3: Oxidation (M)
2060.15	45208.99	-0.72	164 - 183	NPANNAAIVLQLPQGTTLPK
<b>2181.02</b>	<b>205942.06</b>	<b>-7.23</b>	<b>83 - 102</b>	<b>GQGVPIINTNSSPDDQIGYYR</b>

2252.07	5949.45	3.89	314 - 333	HWPQIAQFAPSASAFFGMSR 18: Oxidation (M)
2267.08	10286.59	1.87	122 - 141	WYFYLLGTGPEAGLPYGANK
<b>2304.01</b>	<b>6300</b>	<b>-19.61</b>	<b>420 - 439</b>	<b>QLQQSMSSADSTQAHHHHHH</b>
2324.19	117640.71	8.28	55 - 75	RPQGLPNNTASWFTALTQHGK
2658.11	8524	-11.62	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR
2659.09	18997	-9.85	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR 11: Deamidated (NQ)
2674.11	3614	-14.13	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR 14: Oxidation (M)

**Table S3** - Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (B.1.351) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Sequence
587.31	4137.63	2.93	117 - 121	DLSPR
<b>600.35</b>	<b>5917.54</b>	<b>3.05</b>	<b>218 - 223</b>	<b>GISPAR</b>
663.33	2329	3.04	264 - 270	SAAEASK
698.36	4479.49	-0.38	158 - 163	DHIGTR
749.35	10225.64	-1.96	192 - 199	GGSQASSR
<b>805.38</b>	<b>4407.71</b>	<b>-1.79</b>	<b>210 - 217</b>	<b>NSTPGSSR</b>
831.46	6944.56	-3.12	241 - 247	LNQLESK
886.41	390911.05	-2.2	184 - 191	GFYAEGSR
<b>904.49</b>	<b>19787.71</b>	<b>0.5</b>	<b>76 - 82</b>	<b>EDLKFPR</b>
916.48	38991.55	-2.62	376 - 383	TFPTEPK
942.56	4561.42	-0.32	362 - 369	DQVILLNK
1091.54	18783.54	-4.54	353 - 361	LDDKDPNFK
1126.56	215077.87	-4.21	281 - 290	AYNVTQAFGR
<b>1128.56</b>	<b>18023.5</b>	<b>6.14</b>	<b>390 - 399</b>	<b>ADETQALPQR</b>
1202.61	5850.88	-8.65	252 - 262	GQQQQGQTVTK
<b>1256.66</b>	<b>14265.01</b>	<b>-5.78</b>	<b>389 - 399</b>	<b>KADETQALPQR</b>
1670.91	3870	-4.73	362 - 375	DQVILLNKHIDAYK 2: Deamidated (NQ)
1671.9	12166.27	-3.28	362 - 375	DQVILLNKHIDAYK 2: Deamidated (NQ) 7: Deamidated (NQ)
1684.89	60314.71	-2.75	142 - 157	DGIWVATEGALNTPK
1687.87	12211.43	-2.68	224 - 240	MAGNGGDAALALLLDLR 1: Oxidation (M) 4: Deamidated (NQ)
1788.85	31278.36	-2.27	292 - 307	GPEQTQGNFGDQELIR
<b>1823.82</b>	<b>6976</b>	<b>-0.94</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER</b>
<b>1824.8</b>	<b>28961.85</b>	<b>-2.56</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER 13: Deamidated (NQ)</b>
1861.95	12083.4	-2.51	403 - 419	QQTVTLLPAADLDDFSK
1944.95	180056.74	-5.54	291 - 307	RGPEQTQGNFGDQELIR
1990.05	9214.58	-0.87	402 - 419	KQQTVTLLPAADLDDFSK

2015.08	53623.51	2.75	353 - 369	LDDKDPNFKDQVILLNK
2025.04	30090.62	0.06	334 - 352	IGMEVTPSGTWLTYTGAIK
2041.03	22198.44	-2.68	334 - 352	IGMEVTPSGTWLTYTGAIK 3: Oxidation (M)
2060.15	34543.96	-0.75	164 - 183	NPANNAIAIVLQLPQGTTLPK
<b>2181.02</b>	<b>34538.78</b>	<b>-4.81</b>	<b>83 - 102</b>	<b>GQGVPIINTNSSPDDQIGYYR</b>
2252.07	2553.02	6.62	314 - 333	HWPQIAQFAPSASAFFGMSR 18: Oxidation (M)
2267.08	10035.9	2.33	122 - 141	WYFYLLGTGPEAGLPYGANK
<b>2304.01</b>	<b>1250</b>	<b>-1.06</b>	<b>420 - 439</b>	<b>QLQQSMSSADSTQAHHHHHH</b>
2324.19	65313.93	5.77	55 - 75	RPQGLPNNTASWFTALTQHGK
2658.11	1057	-12.64	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR

**Table S4** - Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (P.1) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Sequence
<b>531.29</b>	<b>4914.45</b>	<b>3.81</b>	<b>219 - 223</b>	<b>TSPAR</b>
749.35	5600.24	0.23	192 - 199	GGSQASSR
886.41	68324.31	0.93	184 - 191	GFYAEGSR
<b>904.49</b>	<b>11590.49</b>	<b>3.49</b>	<b>76 - 82</b>	<b>EDLKFPK</b>
916.48	6706.34	4.58	376 - 383	TFPPTPEPK
<b>933.47</b>	<b>6341.02</b>	<b>2.08</b>	<b>210 - 218</b>	<b>NSTPGSSKR</b>
<b>1029.46</b>	<b>5834.65</b>	<b>2.06</b>	<b>95 - 102</b>	<b>DDQIGYYR</b>
1126.56	145246.58	4.16	281 - 290	AYNVTQAFGR
<b>1128.56</b>	<b>20454.76</b>	<b>10.83</b>	<b>390 - 399</b>	<b>ADETQALPQR</b>
<b>1185.56</b>	<b>9703.26</b>	<b>4.26</b>	<b>95 - 103</b>	<b>DDQIGYYRR</b>
1202.61	5605.11	4.04	252 - 262	GQQQQGQTVTK
<b>1229.62</b>	<b>14521.15</b>	<b>5.99</b>	<b>83 - 94</b>	<b>GQGVPIINTNSSR</b>
<b>1256.66</b>	<b>21467.25</b>	<b>6.69</b>	<b>389 - 399</b>	<b>KADETQALPQR</b>
1330.71	5722.49	4.46	252 - 263	GQQQQGQTVTKK
<b>1384.75</b>	<b>13517.71</b>	<b>3.92</b>	<b>388 - 399</b>	<b>KKADETQALPQR</b>
1527.79	2245.15	4.54	277 - 290	TATKAYNVTQAFGR
1605.8	2216.66	6.82	248 - 262	MSGKGQQQQGQTVTK
1616.74	4199.39	3.83	184 - 199	GFYAEGSRGGSQASSR
1643.84	3705.69	1.61	370 - 383	HIDAYKTFPPTPEPK
1684.89	5885.92	1.25	142 - 157	DGIWVATEGALNTPK
1788.85	10577.79	4.52	292 - 307	GPEQTQGNFGDQELIR
<b>1823.82</b>	<b>36601</b>	<b>2.45</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER</b>
<b>1824.8</b>	<b>81532</b>	<b>6.82</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER 13: Deamidated (NQ)</b>

1861.95	2471.9	1.07	403 - 419	QQTVTLLPAADLDDFSK
1944.95	55336.74	0.62	291 - 307	RGPEQTQGNFGDQELIR
1990.05	1560.49	-1.42	402 - 419	KQQTVTLLPAADLDDFSK
2015.08	1671	3.46	353 - 369	LDDKDPNFKDQVILLNK
2025.04	1452	-0.23	334 - 352	IGMEVTPSGTWLTYTGAIK
2060.15	7809.62	-1.11	164 - 183	NPANNAAIVLQLPQGTTLPK
2195.99	7738.64	-4.31	29 - 50	ITFGGPSDSTGSNQNGERSGAR 13: Deamidated (NQ)
2240.07	6763.77	0.26	83 - 102	<b>GQGVPIINTSSRDDQIGYYR</b>
2262.05	1649	0.84	25 - 46	NAPRITFGGPSDSTGSNQNGER
2263.03	2903.23	-1.03	25 - 46	NAPRITFGGPSDSTGSNQNGER 1: Deamidated (NQ)
2304.01	2247	-6.29	420 - 439	QLQQSMSSADSTQAHHHHHH
2324.19	7252.47	5.37	55 - 75	RPQGLPNNTASWFTALTQHGK
2396.17	2686.4	-5.64	83 - 103	<b>GQGVPIINTSSRDDQIGYYR</b>
2658.11	13583.29	-6.24	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR
2674.11	3517.95	-10.12	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR 14: Oxidation (M)
2739.49	2364.49	4.96	158 - 183	DHIGTRNPANNAAIVLQLPQGTTLPK
2809.44	1317.17	-3.08	55 - 79	<b>RPQGLPNNTASWFTALTQHGKEDLK</b>
2927.54	839.91	-11.71	164 - 191	NPANNAAIVLQLPQGTTLPKGFYAEGSR

**Table S5** - Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (B.1.617.2) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Sequence
587.32	135990.03	4.92	117 - 121	DLSPR
663.33	19335.88	3.89	264 - 270	SAAEASK
698.36	122556.76	1.98	158 - 163	DHIGTR
711.33	27967.01	2.6	308 - 313	QGTDYK
746.38	77014.8	1.9	370 - 375	HIDAYK
749.36	177458.24	2	192 - 199	GSQASSR
831.46	108199.36	1.08	241 - 247	LNQLESK
846.48	99291.25	0.1	76 - 82	<b>EGLKFPR</b>
862.44	25509.04	-1.44	115 - 121	MKDLSPR 1: Oxidation (M)
886.41	756710.07	4.72	184 - 191	GFYAEGSR
916.48	287194.01	2.08	376 - 383	TFPPTEPK
942.56	85270.98	1.59	362 - 369	DQVILLNK
977.51	10530.36	-13.02	108 - 116	IRGGDGKMK 8: Oxidation (M)
1091.54	112672.57	-0.66	353 - 361	LDDKDPNFK
1126.57	715453.11	2.1	281 - 290	AYNVTQAFGR



<b>1148.58</b>	<b>226752.4</b>	<b>-9.83</b>	<b>390 - 399</b>	<b>AYETQALPQK</b>
1202.61	186911.59	-0.82	252 - 262	GQQQQGQTVTK
<b>1276.68</b>	<b>20324.61</b>	<b>-5.59</b>	<b>389 - 399</b>	<b>KAYETQALPQK</b>
<b>1349.61</b>	<b>50180.87</b>	<b>-2</b>	<b>210 - 223</b>	<b>NSTPGSSMGTSPAR</b>
<b>1365.6</b>	<b>97730.22</b>	<b>-4.01</b>	<b>210 - 223</b>	<b>NSTPGSSMGTSPAR 8: Oxidation (M)</b>
1671.87	79458.02	-3.37	224 - 240	MAGNGGDAALALLLLDR 4: Deamidated (NQ)
1684.88	266414.18	2.92	277 - 291	TATKAYNVTQAFGR 7: Deamidated (NQ)
1687.86	255134.92	-4.31	224 - 240	MAGNGGDAALALLLLDR 1: Oxidation (M) 4: Deamidated (NQ)
1788.85	283129.9	-0.66	292 - 307	GPEQTQGNFGDQELIR
<b>1810.83</b>	<b>11259.8</b>	<b>15.18</b>	<b>206 - 223</b>	<b>NSSRNSTPGSSMGTSPAR 1: Deamidated (NQ) 12: Oxidation (M)</b>
<b>1823.82</b>	<b>53543</b>	<b>0.15</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER</b>
<b>1824.8</b>	<b>399973.72</b>	<b>-0.52</b>	<b>29 - 46</b>	<b>ITFGGPSDSTGSNQNGER 13: Deamidated (NQ)</b>
1861.95	61168.59	-4.54	403 - 419	QQTVTLLPAADLDDFSK
1944.95	441339.68	-0.78	291 - 307	RGPEQTQGNFGDQELIR
1990.05	31220.51	-1.16	402 - 419	KQQTVTLLPAADLDDFSK
2015.08	66803.83	-1.51	353 - 369	LDDKDPNFKDQVILLNK
2025.03	12975.21	-1.71	334 - 352	IGMEVTPSGTWLTYTGAIK
2041.03	28249.29	-1.55	334 - 352	IGMEVTPSGTWLTYTGAIK 3: Oxidation (M)
2060.15	71424.99	-2.3	164 - 183	NPANNAIAIVLQLPQGTTLPK
<b>2181.03</b>	<b>323546.63</b>	<b>4.97</b>	<b>83 - 102</b>	<b>GQGVPIINTNSSPDDQIGYYR</b>
2658.15	1205	13.92	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR
2674.13	2832	8.77	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR 14: Oxidation (M)

**Table S6** - Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (B.1.1.529) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Sequence
531.29	26371.43	-3.03	216 - 220	TSPAR
587.31	40219	-1.59	114 - 118	DLSPR
663.33	5896.69	-1.44	261 - 267	SAAEASK
698.36	38888.37	-2.08	155 - 160	DHIGTR
711.33	8824.8	-3.23	305 - 310	QGTDYK
746.38	21175.67	-2.63	367 - 372	HIDAYK
749.35	59926.69	-0.86	189 - 196	GSQASSR
<b>777.37</b>	<b>4846</b>	<b>-3.1</b>	<b>207 - 214</b>	<b>NSTPGSSK</b>
831.45	31441.7	-2.71	238 - 244	LNQLESK
862.44	7317.23	-3.59	112 - 118	MKDLSR 1: Oxidation (M)
886.41	363197.76	2.38	181 - 188	GFYAEGSR

904.49	101311.12	-0.54	73 - 79	EDLKFP
916.48	112029.82	-1.69	373 - 380	TFPPTEPK
942.56	32096.42	-1.03	359 - 366	DQVILLNK
977.51	6207.8	-14.97	105 - 113	IRGGDGKMK 8: Oxidation (M)
1091.54	70287.24	-1.49	350 - 358	LDDKDPNFK
1126.57	363043.29	2.15	278 - 287	AYNVTQAFGR
1128.57	124535.85	5.55	387 - 396	ADETQALPQR
1202.61	56376.21	-2.56	249 - 259	GQQQQGQTVTK
1256.66	95743.6	1.25	386 - 396	KADETQALPQR
1607.8	7144.16	17.56	245 - 259	MSGKGQQQQGQTVTK 6: Deamidated (NQ) 7: Deamidated (NQ)
1671.87	5943.5	-2.39	221 - 237	MAGNGGDAALALLLLDR 4: Deamidated (NQ)
1684.88	18260.63	-3.3	139 - 154	DGIIWVATEGALNTPK
1687.87	55851.77	-0.67	221 - 237	MAGNGGDAALALLLLDR 1: Oxidation (M) 4: Deamidated (NQ)
1788.86	213813.42	2.74	289 - 304	GPEQTQGNFGDQELIR
1824.81	5665.32	3.03	29 - 47	ITFGGSPDSTGSNQNGGAR 13: Deamidated (NQ) 14: Deamidated (NQ)
1861.95	21329.44	-3.79	400 - 416	QQTVTLTPAADLDDFSK
1944.96	278052.48	3.29	288 - 304	RGPEQTQGNFGDQELIR
1990.05	9373.06	-0.08	399 - 416	KQQTVTLTPAADLDDFSK
2015.09	38544.41	2.13	350 - 366	LDDKDPNFKDQVILLNK
2025.04	14201.32	0.26	331 - 349	IGMEVTPSGTWLTYTGAIK
2041.03	38807.02	-0.83	331 - 349	IGMEVTPSGTWLTYTGAIK 3: Oxidation (M)
2060.15	32199.1	-0.24	161 - 180	NPANNAAIVLQLPQGTTLPK
2181.04	150735.97	9.55	80 - 99	GQGVPIINTNPPDDQIGYYR
2267.1	35118.93	7.33	119 - 138	WYFYLLGTGPEAGLPYGANK
2320.02	3520.32	8.72	417 - 436	QLQQSMSSADSTQAHHHHHH 6: Oxidation (M)
2325.21	5091.31	17.86	52 - 72	RPQGLPNNTASWFTALTQHGK 3: Deamidated (NQ)
2356.21	8503.4	-14.58	215 - 237	RTSPARMAGNGGDAALALLLLDR 7: Oxidation (M) 10: Deamidated (NQ)
2658.16	1069	18.2	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR
2674.16	1927	19.57	2 - 24	GSSHHHHHHSQDQMSDNGPQNQR 14: Oxidation (M)

**Table S7** - Detected ions (MH<sup>+</sup>) and matched peptides from the recombinant N protein (HCoV OC43) according to peptide mapping. The range of residues corresponding to the peptides, the relative intensity of the ion, the mass deviation (in parts per million, ppm), as well as possible peptide modifications (oxidation and deamidation) are indicated. Peptides that differ in at least one of the studied N proteins are marked in red, and unique peptides for this recombinant proteins are marked in bold red.

MH <sup>+</sup>	Intensity (RU)	Mass deviation (ppm)	Range of residues	Matched peptide
564.26	4639.77	-28.41	22 - 26	QSSSR
573.35	4359.95	-25.83	343 - 347	LELAK

591.28	6763.99	-9.95	27 - 32	ASSGNR
599.35	6470.51	-26.62	56 - 60	RAQPK
616.34	5974.3	-6.71	432 - 436	VQQNK
617.34	32674.01	-2.34	49 - 53	NVQTR
626.4	73147.01	7.78	132 - 136	QLLPR
631.31	9566.58	-10.94	208 - 213	SAPNSR
635.3	6551.06	-13.28	222 - 228	ASSAGSR
689.38	5090.85	-3.54	33 - 39	SGNGILK 3: Deamidated (NQ)
693.37	6743	5.34	367 - 372	YNGAIR
694.37	27035	22.8	367 - 372	YNGAIR 2: Deamidated (NQ)
740.48	37929.29	7.79	280 - 285	ILNKPR
744.36	344721.45	19.17	113 - 117	GYWYR
761.37	31912.34	19.78	125 - 131	TADGNQR
794.42	16695.59	18.86	361 - 366	DVYELR
1104.52	417839.94	14.61	40 - 48	WADQSDQVR
1115.62	10261.13	12.64	261 - 270	DATKPQQVTK
1142.48	13506.72	-13.49	293 - 302	QCTVQQCFGK 1: Deamidated (NQ)
1187.56	6595.45	8.3	179 - 189	DPSSDEAIPTR
1231.7	15975.26	21	439 - 449	ELTAEDISLLK
1348.65	9673.61	14.84	304 - 316	GPNQNFSGGEMLK
1364.65	5895.44	17.36	304 - 316	GPNQNFSGGEMLK 11: Oxidation (M)
1425.71	3826.23	10.57	348 - 360	VQNLSGNPDEPQK
1475.75	24007.45	26.79	373 - 385	FDSTLSGFETIMK
1491.75	13844.14	32.7	373 - 385	FDSTLSGFETIMK 12: Oxidation (M)
1504.76	39343.8	15.37	303 - 316	RGPNQNFSGGEMLK
1520.76	20933.59	24.5	303 - 316	RGPNQNFSGGEMLK 12: Oxidation (M)
1542.77	7187.07	20.36	415 - 429	NGQGENDNISVAVPK 1: Deamidated (NQ)
1602.82	12880.19	27.65	137 - 149	WYFYLLGTGPHAK
1938.04	33934.73	-2.64	261 - 277	DATKPQQVTKHTAKEVR 6: Deamidated (NQ)
2115.17	1108.38	34.72	237 - 257	TPTSGVTPDMADQIASLVLAKE
2201.13	6827.92	21.93	348 - 366	VQNLSGNPDEPQKDVYELR
2272.21	1618.75	27.64	91 - 112	EFEFVEGQGVPIAPGVPATEAK
2380.06	707	19.36	450 - 468	KMDEPYTEDTSEIHSHHHHH
2457.3	8076.09	13.44	89 - 112	GKEFEFVEGQGVPIAPGVPATEAK
2710.4	3728.05	5.36	317 - 342	LGTSDPQFPILAEAPTAGAFFFGSR
2806.32	2412.79	4.64	386 - 409	VLNENLNAYQQQDGMMNMSPKPQR
2822.33	1805.77	10.24	386 - 409	VLNENLNAYQQQDGMMNMSPKPQR 15: Oxidation (M)
2838.35	2526.04	18.5	386 - 409	VLNENLNAYQQQDGMMNMSPKPQR 15: Oxidation (M) 16: Oxidation (M)
2854.34	2133.97	17.73	386 - 409	VLNENLNAYQQQDGMMNMSPKPQR 15: Oxidation (M) 16: Oxidation (M) 18: Oxidation (M)
3106.59	2833.05	24.96	179 - 207	DPSSDEAIPTRFPPGTVPQGYIEGSGR

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3197.56	8097.49	30.52	150 - 178	DQYGTDIDGVYWVASNQADVNTPADIVDR
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## References

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