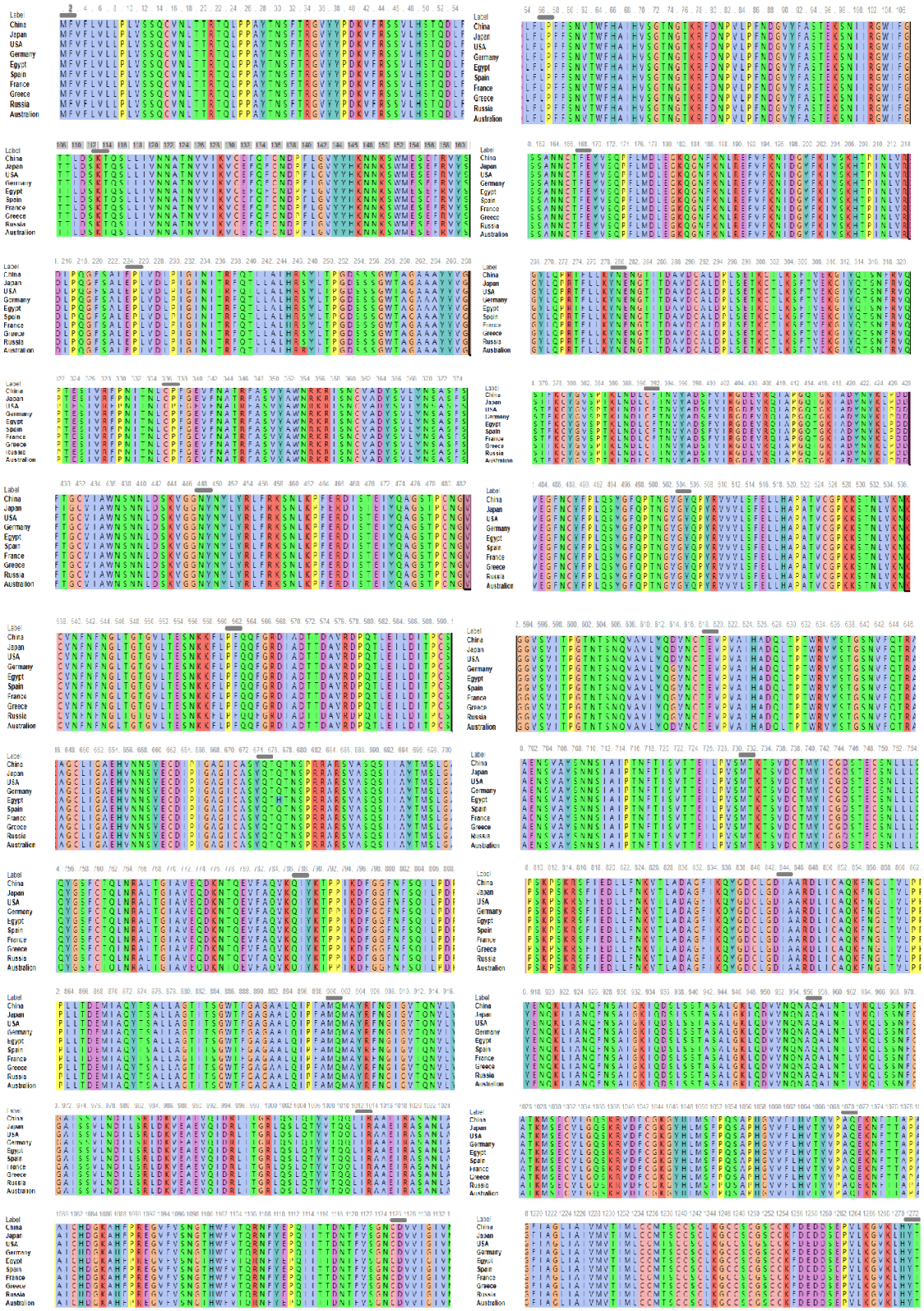

Figure S1. Multiple sequence alignment showing conservation for the S reference protein of SARS-CoV-2 isolated from ten distinct countries.

Table S2 Country Submission Count of N501Y and E484k variants

The following data are as of February 2021 from the website: https://www.gisaid.org/hcov19-variants.

Country	**N501Y.V1 (B.1.1.7)**	**Country**	**E484K.V2 (B.1.1.28)**
United Kingdom	86,457	Brazil	144
Denmark	2,614	Japan	14
USA	1,183	Singapore	13
Belgium	1,070	Italy	12
France	1,007	Switzerland	12
Netherlands	941	United Kingdom	10
Spain	938	Colombia	10
Switzerland	713	USA	10
Italy	659	United Arab Emirates	9
Ireland	595	Belgium	7
Turkey	256	Portugal	7
Israel	246	France	6
Portugal	206	Netherlands	5
Austria	188	India	3
Sweden	173	Czech Republic	3
Australia	115	French Guiana	2
Germany	112	Brunei	2
Finland	97	Denmark	2
Norway	82	Turkey	1
India	81	Australia	1
Romania	35	New Zealand	1
Luxembourg	32	Mexico	1
South Korea	25	Faroe Islands	1
Brazil	22	Canada	1
United Arab Emirate	21	China	1
Iceland	20	Iran	1
Czech Republic	17	Peru	1
Sri Lan	15	South Korea	1
Aruba ka	14	Russia	1
North Macedonia	11	Ireland	1
Vietnam	10		
Total	97955	Total	283

Table S3. B-cell linear epitopes and antigenicity scores predicted via BepiPred-2.0 and Vaxijen 2.0 tool

The following antigenicity is calculated by the axijen 2.0 with a threshold of 0.4. It's indicated that the epitope has favorable antigenicity (above threshold) in the red highlight.The epitopes below the five residues are too short for the software to calculate the results, denoted by "/".

No.	Start	End	Peptide	Length	Antigenicity
1	21	33	RTQLPPAYTNSFT	13	0.5003
2	62	75	VTWFHAIHVSGTNG	14	0.5786
3	141	152	LGVYYHKNNKSW	12	0.8156
4	182	186	KQGNF	5	/
5	208	220	TPINLVRDLPQGF	13	0.4768
6	252	259	GDSSSGWT	8	0.2201
7	315	320	TSNFRV	6	0.3505
8	332	335	ITNL	4	/
9	341	361	VFNATRFASVYAWNRKRISNC	21	0.2783
10	372	374	ASF	3	/
11	384	390	PTKLNDL	7	1.0882
12	405	418	DEVRQIAPGQTGKI	14	0.9312
13	441	448	LDSKVGGN	8	0.8773
14	459	464	SNLKPF	6	0.5943
15	469	478	STEIYQAGST	10	0.0944
16	487	492	NCYFPL	6	0.9960
17	519	523	HAPAT	5	/
18	525	533	CGPKKSTNL	9	0.1363
19	557	560	KKFL	4	/
20	619	625	EVPVAIH	7	0.3624

No.	Start	End	Peptide	Length	Antigenicity
21	657	664	NNSYECDI	8	0.6539
22	674	688	YQTQTNSPRRARSVA	15	0.2617
23	696	709	TMSLGAENSVAYSN	14	0.6780
24	789	798	YKTPPIKDFG	10	0.0200
25	808	813	DPSKPS	6	0.0456
26	833	834	FI	2	/
27	1110	1114	YEPQI	5	/
28	1136	1143	TVYDPLQP	8	0.3135
29	1154	1169	KYFKNHTSPDVDLGDI	16	0.7333
30	1256	1263	FDEDDSEP	8	0.3300

Table S4 B cell Discontinuous epitopes predicted via Discotope 2.0 tool

No.	RP	RN	NC	P-score	D-score	No.	RP	RN	NC	P-score	D-score
1	282	ASN	4	-2.346	-2.537	27	503	VAL	5	-0.472	-0.993
2	415	THR	1	-3.642	-3.338	28	504	GLY	4	-2.462	-2.638
3	439	ASN	14	-2.039	-3.415	29	505	TYR	10	-0.741	-1.806
4	449	ASN	4	-1.934	-2.172	30	556	ASN	0	-3.687	-3.263
5	448	ASN	23	-0.603	-3.178	31	558	LYS	0	-1.282	-1.135
6	449	TYR	4	-0.399	-0.813	32	560	LEU	4	-3.379	-3.45
7	450	ASN	8	-1.453	-2.206	34	561	PRO	0	-3.821	-3.382
8	455	LEU	6	-1.119	-1.68	35	703	ASN	3	-2.182	-2.276
9	456	PHE	5	-0.76	-1.247	36	704	SER	3	-1.361	-1.549
10	457	ARG	22	0.5	-2.087	37	705	VAL	9	-2.785	-3.499
11	458	LYS	4	1.236	0.634	38	793	PRO	0	-1.814	-1.605
12	459	SER	4	1.271	0.665	39	794	ILE	4	-2.148	-2.361
13	460	ASN	13	0.073	-1.43	40	809	PRO	6	-2.403	-2.816
14	462	LYS	1	-3.956	-3.616	41	810	SER	4	0.639	0.106
15	468	ILE	2	-2.185	-2.164	42	811	LYS	18	-0.867	-2.837
16	469	SER	13	-1.347	-2.687	43	914	ASN	7	-0.804	-1.516
17	470	THR	4	-2.13	-2.345	44	917	TYR	9	-2.58	-3.318
18	490	PHE	4	-2.056	-2.279	45	918	GLU	12	-2.383	-3.489
19	492	LEU	18	-1.23	-3.158	46	1140	PRO	8	-0.757	-1.59
20	493	GLN	12	-0.625	-1.933	47	1141	LEU	3	-0.698	-0.963
21	494	SER	8	-1.035	-1.836	48	1142	GLN	6	-0.05	-0.735
22	496	GLY	2	0.335	0.067	49	1143	PRO	6	0.444	-0.297
23	498	GLN	3	1.807	1.254	50	1144	GLU	4	0.587	0.06
24	499	PRO	4	1.917	1.237	51	1145	LEU	5	-0.213	-0.763
25	500	THR	2	3.437	2.811	52	1146	ASP	5	0.694	0.039
26	501	ASN	22	2.379	-0.425	53	1147	SER	6	0	-0.69

RP: position; PN:Residue names; NC:Number of contacts,showing the connection of Residues with others; P-score:Propensity score; D-score:DiscoTope score

Table S5 The comparison of B cell epitopes between prototype and H49Y Spike mutation

Prototype Spike					H49Y mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~152	LGVYYHKNNKSW	12	4.321	0.8156	invariant
208~220	TPINLVRDLPQGF	13	1.534	0.4768	208~220	TPINLVRDLPQGF	13	1.534	0.4768	invariant
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~417	DEVRQIAPGQT	13	3.463	1.1073	Improved

						GK				antigenicity
441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~464	SNLKPF	6	1.239	0.5943	invariant
487~492	NCYFPL	6	0.388	0.9960	487~492	NCYFPL	6	0.388	0.9960	invariant
519~523	HAPAT	5	0.499	/	519~533	HAPATVCGPKKSTNL	15	3.838	0.6650	Extension of epitope sequence,new likely epitope
525~533	CGPKKSTNL	9	2.483	0.1363						
619~625	EVPVAIH	7	0.308	0.3624	618~629	TEVPVAIHADQL	12	1.157	0.4635	Extension of epitope sequence,new likely epitope
657~664	NNSYECDI	8	1.127	0.6539	657~664	NNSYECDI	8	1.127	0.6539	invariant
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	697~709	MSLGAENSVAYSN	13	1.523	0.8525	Improved antigenicity,likely epitope
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

“/”:Residue number</=5,antigenicity can not be calculated the result.Potential dominant epitopes marked in blue. The changes of epitopes were marked in red.

Table S6 The comparison of B cell epitopes between prototype and Y145H Spike mutation

Prototype Spike					Y145H mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	140~153	FLGVYHHKNNKSWM	14	3.808	0.8227	Improved antigenicity,likely epitope
208~220	TPINLVRDLPQGF	13	1.534	0.4768	208~220	TPINLVRDLPQGF	13	1.534	0.4768	invariant
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	invariant

441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~465	SNLKPFE	7	1.507	0.8128	Improved antigenicity,likely epitope
487~492	NCYFPL	6	0.388	0.9960	487~492	NCYFPL	6	0.388	0.9960	invariant
619~625	EVPVAIH	7	0.308	0.3624	618~625	TEVPVAIH	8	1.027	0.4176	Extension of epitope sequence,new likely epitope
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.54	0.8211	Improved antigenicity,likely epitope
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Potential dominant epitopes marked in blue. The epitopes that changed after comparison were marked in red.

Table S7 The comparison of B cell epitopes between prototype and V367F Spike mutation

Prototype Spike					V367F mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	140~154	FLGVYYHKNNKSWME	15	6.623	0.4793	Highly Reduced antigenicity,likely epitope
208~220	TPINLVRDLPQGF	13	1.534	0.4768	210· 221	INLVRDLPQGFS	12	1.247	0.3874	Reduced antigenicity,likely epitope
384~390	PTKLNDL	7	2.602	1.0882	385~392	TKLNDLCF	8	2.602	3.0542	Highly Improved antigenicity,likely epitope

405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	404~416	GDEVRQIAPGQTG	13	2.605	1.0883	Improved antigenicity,likely epitope
441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~464	none				Lost, likely epitope
487~492	NCYFPL	6	0.388	0.9960	487~489	NCY	3	0.201	/	likely epitope failure
657~664	NNSYECDI	8	1.127	0.6539	657~664	NNSYECDI	8	1.127	0.6539	invariant
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

“/”:Residue number</=5,antigenicity can not be calculated the result due to too few residues.
Potential dominant epitopes marked in blue.
The epitopes that changed after comparison were marked in red.
“None” meaning the loss of the epitope.

Table S8 The comparison of B cell epitopes between prototype and G476S Spike mutation

Prototype Spike					G476S mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	None				Loss of likely epitope
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~152	LGVYYHKNNKSW	12	4.321	0.8156	invariant
208~220	TPINLVRDLPQGF	13	1.534	0.4768	216~221	LPQGFS	6	0.659	0.3694	reduced antigenicity,unlikely epitope
315~320	TSNFRV	6	1.019	0.3505	314~321	QTSNFRVQ	8	2.781	0.852	Improved antigenicity,likely epitope
372~374	ASF	3	0.256	/	368~390	LYNSASFSTFKCYGVSPTKLNDL	23	3.649	0.8344	Two epitopes fused into one epitope, reduced antigenicity
384~390	PTKLNDL	7	2.602	1.0882						

405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	406~417	EVRQIAPGQTGK	12	2.669	1.5279	Improved antigenicity,likely epitope
441~448	LDSKVGGN	8	1.156	0.8773	440~450	NLDSKVGGNYN	11	1.911	0.8998	Improved antigenicity,likely epitope
459~464	SNLKPF	6	1.239	0.5943	none					Loss of likely epitope
487~492	NCYFPL	6	1.388	0.9960	486~492	FNCYFPL	7	1.463	0.8045	reduced antigenicity, likely epitope
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.537	0.8211	Improved antigenicity,likely epitope
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

“/”:Residue number</=5,antigenicity can not be calculated the result.

Potential dominant epitopes marked in blue.

The epitopes that changed after comparison were marked in red.

Table S9 The comparison of B cell epitopes between prototype and V483A Spike mutation

Prototype Spike					V483A mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~30	CVNLTTRTQLPPAYTN	16	4.32	1.3820	Improved antigenicity,likely epitope
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	none					Loss of likely epitope
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~152	LGVYYHKNNKSW	12	4.321	0.8156	invariant
182~186	KQGNF	5	2.07	/	181~186	GKQGNF	6	1.229	2.1342	New likely epitope
208~220	TPINLVRDLPQGF	13	1.534	0.4768	210~221	INLVRDLPQGFS	12	1.247	0.3874	Reduced antigenicity,unlikely epitope

341~361	VFNATRFASVYAWNRKRISNC	21	2.369	0.2783	342~353	FNATRFASVYAW	12	1.331	0.4633	Improved antigenicity,likely epitope
					363~377	ADYSVLYNSASFSTF	15	1.85	0.8252	New likely epitope
384~390	PTKLNDL	7	2.602	1.0882	379~389	CYGVSPTKLND	11	2.904	1.4360	Improved antigenicity,likely epitope
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~413	DEVRQIAPG	9	1.806	0.7216	Reduced antigenicity,likely epitope
441~448	LDSKVGGN	8	1.156	0.8773	442~447	DSKVGG	6	1.846	1.3825	Improved antigenicity,likely epitope
459~464	SNLKPF	6	1.239	0.5943	458~463	KSNLKP	6	2.859	2.5009	Highly Improved antigenicity,likely epitope
487~492	NCYFPL	6	0.388	0.9960	None					Loss of likely epitope
619~625	EVPVAIH	7	0.308	0.3624	617~628	CTEVPVAIHADQ	12	1.029	0.4112	Improved antigenicity,likely epitope

657~664	NNSYECDI	8	1.127	0.6539	657~664	NNSYECDI	8	1.127	0.6539	invariant
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	698~709	SLGAENSVAYSN	12	1.683	0.7274	Improved antigenicity,likely epitope
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Potential dominant epitopes marked in blue.The epitopes that changed after comparison were marked in red.

Table S10 The comparison of B cell epitopes between prototype and E484K Spike mutation

Prototype Spike					E484K mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~154	LGVYYHKNNKSWME	14	4.993	0.5658	Reduced antigenicity
182~186	KQGNF	5	2.07	/	179~186	LEGKQGNF	8	1.671	1.9202	New epitope
208~220	TPINLVRDLPQGF	13	1.534	0.4768	209~220	PINLVRDLPQGF	12	1.366	0.4926	Slightly Increasing antigenicity
252~259	GDSSSGWT	8	1.339	0.2201	249~259	LTPGDSSSGWT	11	2.001	0.6744	Increasing

										antigenicity
372~374	ASF	3	0.256	/	370~376	NSASFST	7	1.013	0.4420	New likely epitope
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	410~416	IAPGQTG	7	0.871	2.2057	Improved antigenicity
441~448	LDSKVGGN	8	1.156	0.8773	439~447	NNLDSKVGG	9	2.9075	0.8904	Slightly Increasing antigenicity
459~464	SNLKPF	6	1.239	0.5943	458~481	KSNLKPFERDISTEIYQAGSTPCN	24	4.973	0.2557	Non-antigenicity
487~492	NCYFPL	6	0.388	0.9960	/					epitopes lost
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.542	0.8211	Improved antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Table S11 The comparison of B cell epitopes between prototype and N501Y Spike mutation

Prototype Spike					N501Y mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~74	VTWFHAIHVSGTN	13	1.217	0.5728	decreasing antigenicity
141~152	LGVYYHKNNKSW	12	4.321	0.8156	140~154	FLGVYYHKNNKSWME	15	6.263	0.4793	decreasing antigenicity
					176~186	LMDLEGKQGNF	11	1.731	1.5671	New epitope
208~220	TPINLVRDLPQGF	13	1.534	0.4768	214~221	RDLPQGFS	8	2.081	1.0718	Increasing antigenicity
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	invariant

441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943						loss
487~492	NCYFPL	6	0.388	0.9960						loss
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.542	0.8211	Increasing antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Table S12 The comparison of B cell epitopes between prototype and D614G Spike mutation

Prototype Spike					D614G mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~152	LGVYYHKNNKSW	12	4.321	0.8156	invariant
208~220	TPINLVRDLPQGF	13	1.534	0.4768	208~220	TPINLVRDLPQGF	13	1.534	0.4768	invariant
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	invariant

441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~464	SNLKPF	6	1.239	0.5943	invariant
487~492	NCYFPL	6	0.388	0.9960	487~492	NCYFPL	6	0.388	0.9960	invariant
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.542	0.8211	Increasing antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Potential dominant epitopes marked in blue.

The epitopes that changed after comparison were marked in red.

Table S13 The comparison of B cell epitopes between prototype and V615I Spike mutation

Prototype Spike					V615I mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~152	LGVYYHKNNKSW	12	4.321	0.8156	invariant
208~220	TPINLVRDLPQGF	13	1.534	0.4768	208~220	TPINLVRDLPQGF	13	1.534	0.4768	invariant
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	invariant

441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~464	SNLKPF	6	1.239	0.5943	invariant
487~492	NCYFPL	6	0.388	0.9960	487~492	NCYFPL	6	0.388	0.9960	invariant
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.542	0.8211	Improved antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Potential dominant epitopes marked in blue.

The epitopes that changed after comparison were marked in red.

Table S14 The comparison of B cell epitopes between prototype and V615F Spike mutation

Prototype Spike					V615F mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	140~154	FLGVYYHKNNKSWME	15	6.263	0.4793	Reduced antigenicity
182~186	KQGNF	5	2.07	/	180~186	EGKQGNF	7	2.667	1.9334	Highly improved antigenicity,new
208~220	TPINLVRDLPQGF	13	1.534	0.4768	209~212	PINL	4	0.363	/	Reduced antigenicity,lost
					214~221	RDLPQGFS	8	2.083	1.0718	New epitope

					374~389	FSTFKCYGVSPTKLND	16	3.579	0.9650	New epitope
384~390	PTKLNDL	7	2.602	1.0882	None					Loss of likely epitope
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	404~418	GDEVRQIAPGQTGKI	15	3.579	0.9650	improved antigenicity
441~448	LDSKVGGN	8	1.156	0.8773	441~444	LDSK	4		/	Reduced antigenicity,lost
459~464	SNLKPF	6	1.239	0.5943	458~466	KSNLKPFER	9	3.84	0.9490	improved antigenicity
487~492	NCYFPL	6	0.388	0.9960	487~497	NCYFPLQSYGF	11	1.259	0.7616	Reduced antigenicity
657~664	NNSYECDI	8	1.127	0.6539	656~664	VNNSYECDI	9	2.117	0.7935	improved antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	697~709	MSLGAENSVAYSN	13	1.524	0.8525	improved antigenicity
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

"/":Residue number</=5,antigenicity can not be calculated the result.

Potential dominant epitopes marked in blue. The epitopes that changed after comparison were marked in red.

Table S15 The comparison of B cell epitopes between prototype and A831V Spike mutation

Prototype Spike					A831V mutation					Change results
Position	Peptide	Length	Accessibility	Antigenicity	Position	Peptide	Length	Accessibility	Antigenicity	
15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	15~31	CVNLTTRTQLPPAYTNS	17	4.781	1.2219	invariant
62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	62~75	VTWFHAIHVSGTNG	14	1.114	0.5786	invariant
141~152	LGVYYHKNNKSW	12	4.321	0.8156	141~153	LGVYYHKNNKSWM	13	4.636	0.7113	Reduced antigenicity
208~220	TPINLVRDLPQGF	13	1.534	0.4768	208~220	TPINLVRDLPQGF	13	1.534	0.4768	invariant
384~390	PTKLNDL	7	2.602	1.0882	384~390	PTKLNDL	7	2.602	1.0882	invariant
405~418	DEVRQIAPGQTGKI	14	2.716	0.9312	405~417	DEVRQIAPGQTGK	13	2.654	1.1073	Improved antigenicity,likely

										epitope
441~448	LDSKVGGN	8	1.156	0.8773	441~448	LDSKVGGN	8	1.156	0.8773	invariant
459~464	SNLKPF	6	1.239	0.5943	459~465	SNLKPFE	7	1.506	0.8128	Improved antigenicity,likely epitope
487~492	NCYFPL	6	0.388	0.9960	487~492	NCYFPL	6	0.388	0.9960	invariant
619~625	EVPVAIH	7	0.308	0.3624	618~625	TEVPVAIH	8	1.031	0.4076	Improved antigenicity,likely epitope(new)
657~664	NNSYECDI	8	1.127	0.6539	657~663	NNSYECD	7	1.542	0.8211	Improved antigenicity
696~709	TMSLGAENSVAYSN	14	1.674	0.6780	696~709	TMSLGAENSVAYSN	14	1.674	0.6780	invariant
1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	1154~1169	KYFKNHTSPDVDLGDI	16	4.097	0.7333	invariant

Potential dominant epitopes marked in blue.

The epitopes that changed after comparison were marked in red.

Table S16 Comparison of epitopes of various variants

No mutation				D614G mutation				Major changes
Position	**Peptide**	**Length**	**Antigenicity**	**Position**	**Peptide**	**Length**	**Antigenicity**	
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**H49Y mutation**				
405~418	DEVRQIAPGQTGKI	14	0.9312	405~417	DEVRQIAPGQTGK	13	1.1073	Improved antigenicity
519~523	HAPAT	5	/	519~533	HAPATVCGPKKSTNL	15	0.6650	Extension of epitope sequence,new epitope
525~533	CGPKKSTNL	9	0.1363					
619~625	EVPVAIH	7	0.3624	618~629	TEVPVAIHADQL	12	0.4635	Extension of epitope sequence,new epitope
696~709	TMSLGAENSVAYSN	14	0.6780	697~709	MSLGAENSVAYSN	13	0.8525	Improved antigenicity
No mutation				**Y145H mutation**				
141~152	LGVYYHK	12	0.8156	140~153	FLGVYHHK	14	0.8227	Improved

	NNKSW				NNKSWM			antigenicity
459~464	SNLKPF	6	0.5943	459~465	SNLKPFE	7	0.8128	Improved antigenicity
619~625	EVPVAIH	7	0.3624	618~625	TEVPVAIH	8	0.4176	Improved antigenicity
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**A831V mutation**				
141~152	LGVYYHK NNKSW	12	0.8156	141~153	LGVYYHKN NKSWM	13	0.7113	Reduced antigenicity
405~418	DEVRQIAP GQTGKI	14	0.9312	405~417	DEVRQIAPG QTGK	13	1.1073	Improved antigenicity
459~464	SNLKPF	6	0.5943	459~465	SNLKPFE	7	0.8128	Improved antigenicity
619~625	EVPVAIH	7	0.3624	618~625	TEVPVAIH	8	0.4076	Improved antigenicity
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**V483A mutation**				
15~31	CVNLTTRT QLPPAYTN S	17	1.2219	15~30	CVNLTTRT QLPPAYTN	16	1.3820	Improved antigenicity
62~75	VTWFHAIH VSGTNG	14	0.5786	62~75	None			Loss of epitope
182~186	KQGNF	5	/	181~186	GKQGNF	6	2.1342	New likely epitope

208~220	TPINLVRDLPQGF	13	0.4768	210~221	INLVRDLPQGFS	12	0.3874	Reduced antigenicity
341~361	VFNATRFASVYAWNRKRISNC	21	0.2783	342~353	FNATRFASVYAW	12	0.4633	Improved antigenicity
				363~377	ADYSVLYNSASFSTF	15	0.8252	New epitope
384~390	PTKLNDL	7	1.0882	379~389	CYGVSPTKLND	11	1.4360	Improved antigenicity
405~418	DEVRQIAPGQTGKI	14	0.9312	405~413	DEVRQIAPG	9	0.7216	Reduced antigenicity
441~448	LDSKVGGN	8	0.8773	442~447	DSKVGG	6	1.3825	Improved antigenicity
459~464	SNLKPF	6	0.5943	458~463	KSNLKP	6	2.5009	Highly Improved antigenicity
487~492	NCYFPL	6	0.9960		None			Loss of epitope
619~625	EVPVAIH	7	0.3624	617~628	CTEVPVAIHADQ	12	0.4112	Improved antigenicity
696~709	TMSLGAENSVAYSN	14	0.6780	698~709	SLGAENSVAYSN	12	0.7274	Improved antigenicity
No mutation				**E484K mutation**				
141~152	LGVYYHKNNKSW	12	0.8156	141~154	LGVYYHKNNKSWME	14	0.5658	Reduced antigenicity
182~186	KQGNF	5	/	179~186	LEGKQGNF	8	1.9202	New epitope
208~220	TPINLVRDLPQGF	13	0.4768	209~220	PINLVRDLPQGF	12	0.4926	Slightly Increasing

								antigenicity
252~259	GDSSSGWT	8	0.2201	249~259	LTPGDSSSGWT	11	0.6744	Increasing antigenicity
372~374	ASF	3	/	370~376	NSASFST	7	0.4420	New likely epitope
405~418	DEVRQIAPGQTGKI	14	0.9312	410~416	IAPGQTG	7	2.2057	Improved antigenicity
441~448	LDSKVGGN	8	0.8773	439~447	NNLDSKVGG	9	0.8904	Slightly Increasing antigenicity
459~464	SNLKPF	6	0.5943	458~481	KSNLKPFERDISTEIYQAGSTPCN	24	0.2557	Non-antigenicity
487~492	NCYFPL	6	0.9960	/				Loss of epitope
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**N501Y mutation**				
62~75	VTWFHAIHVSGTNG	14	0.5786	62~74	VTWFHAIHVSGTN	13	0.5728	Reduced antigenicity
141~152	LGVYYHKNNKSW	12	0.8156	140~154	FLGVYYHKNNKSWME	15	0.4793	Reduced antigenicity
				176~186	LMDLEGKQGNF	11	1.5671	New epitope
208~220	TPINLVRDLPQGF	13	0.4768	214~221	RDLPQGFS	8	1.0718	Improved antigenicity
459~464	SNLKPF	6	0.5943					Loss of epitope

487~492	NCYFPL	6	0.9960					Loss of epitope
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**V615I mutation**				
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity
No mutation				**V615F mutation**				
141~152	LGVYYHK NNKSW	12	0.8156	140~154	FLGVYYHK NNKSWME	15	0.4793	Reduced antigenicity
182~186	KQGNF	5	/	180~186	EGKQGNF	7	1.9334	Highly Improved antigenicity
208~220	TPINLVRDL PQGF	13	0.4768	209~212	PINL	4	/	Reduced antigenicity
				214~221	RDLPQGFS	8	1.0718	New epitope
				374~389	FSTFKCYGV SPTKLND	16	0.9650	New epitope
384~390	PTKLNDL	7	1.0882	None				Loss of epitope
405~418	DEVRQIAP GQTGKI	14	0.9312	404~418	GDEVRQIAP GQTGKI	15	0.9741	Improved antigenicity
441~448	LDSKVGGN	8	0.8773	441~444	LDSK	4	/	Reduced antigenicity(epitope didn’t work)
459~464	SNLKPF	6	0.5943	458~466	KSNLKPFER	9	0.9490	Highly Improved antigenicity
487~492	NCYFPL	6	0.9960	487~497	NCYFPLQSY GF	11	0.7616	Reduced antigenicity

657~664	NNSYECDI	8	0.6539	656~664	VNNSYECDI	9	0.7935	Improved antigenicity
696~709	TMSLGAENSVAYSN	14	0.6780	697~709	MSLGAENSVAYSN	13	0.8525	Improved antigenicity
No mutation				**V367F mutation**				
141~152	LGVYYHKNNKSW	12	0.8156	140~154	FLGVYYHKNNKSWME	15	0.4793	Highly Reduced antigenicity
208~220	TPINLVRDLPQGF	13	0.4768	210~221	INLVRDLPQGFS	12	0.3874	Didn’t work
384~390	PTKLNDL	7	1.0882	385~392	TKLNDLCF	8	3.0542	Highly Improved antigenicity
405~418	DEVRQIAPGQTGKI	14	0.9312	404~416	GDEVRQIAPGQTG	13	1.0883	Improved antigenicity
459~464	SNLKPF	6	0.5943	459~464			None	Loss of epitope
487~492	NCYFPL	6	0.9960	487~489	NCY	3	/	Didn’t work
No mutation				**G476S mutation**				
62~75	VTWFHAIHVSGTNG	14	0.5786	73~74	TN	2	/	Loss of antigenicity
208~220	TPINLVRDLPQGF	13	0.4768	216~221	LPQGFS	6	0.3694	Reduced antigenicity
315~320	TSNFRV	6	0.3505	314~321	QTSNFRVQ	8	0.7823	Highly Improved antigenicity
384~390	PTKLNDL	7	1.0882	368~390	LYNSASFSTFKCYGVSPTKLNDL	23	0.8344	Reduced antigenicity

405~418	DEVRQIAPGQTGKI	14	0.9312	406~417	EVRQIAPGQTGK	12	1.5279	Highly Improved antigenicity
441~448	LDSKVGGN	8	0.8773	440~450	NLDSKVGGNYN	11	0.8998	Slightly Improved antigenicity
459~464	SNLKPF	6	0.5943	None				Loss of epitope
487~492	NCYFPL	6	0.9960	486~492	FNCYFPL	7	0.8045	Reduced antigenicity
657~664	NNSYECDI	8	0.6539	657~663	NNSYECD	7	0.8211	Improved antigenicity