

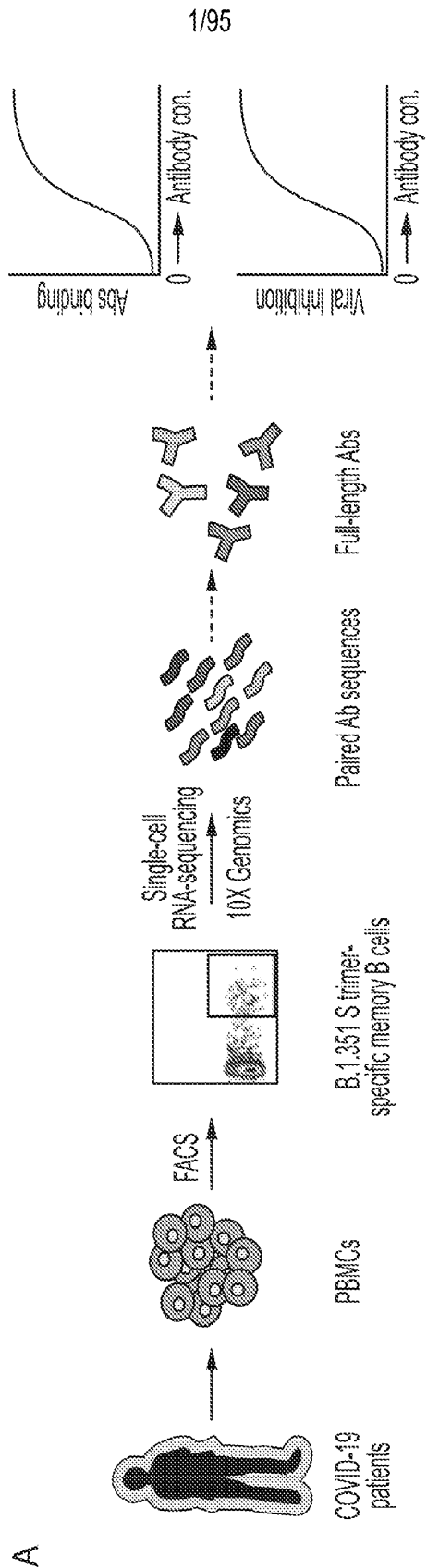


FIG. 1A

A

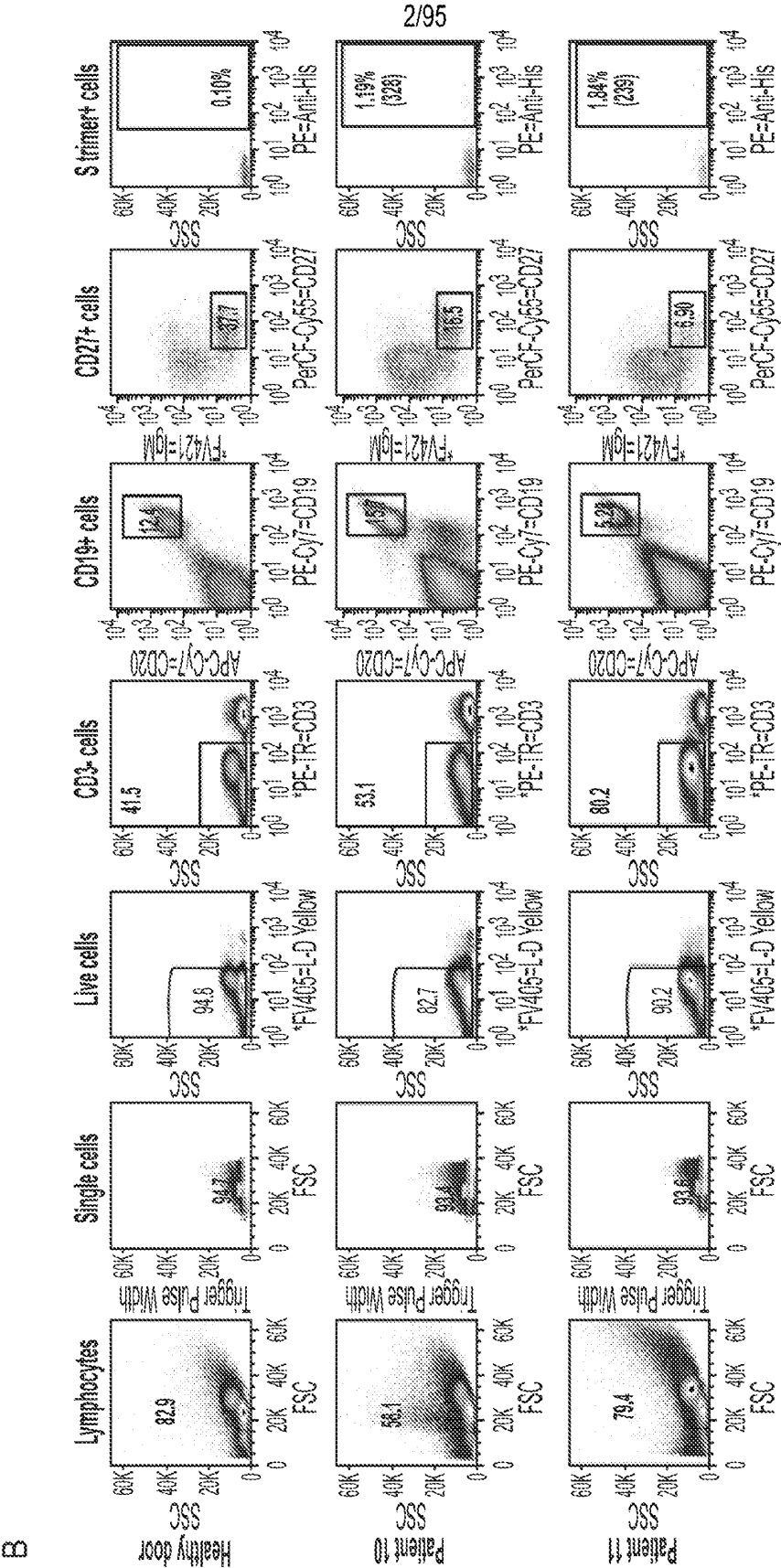


FIG. 1B

B

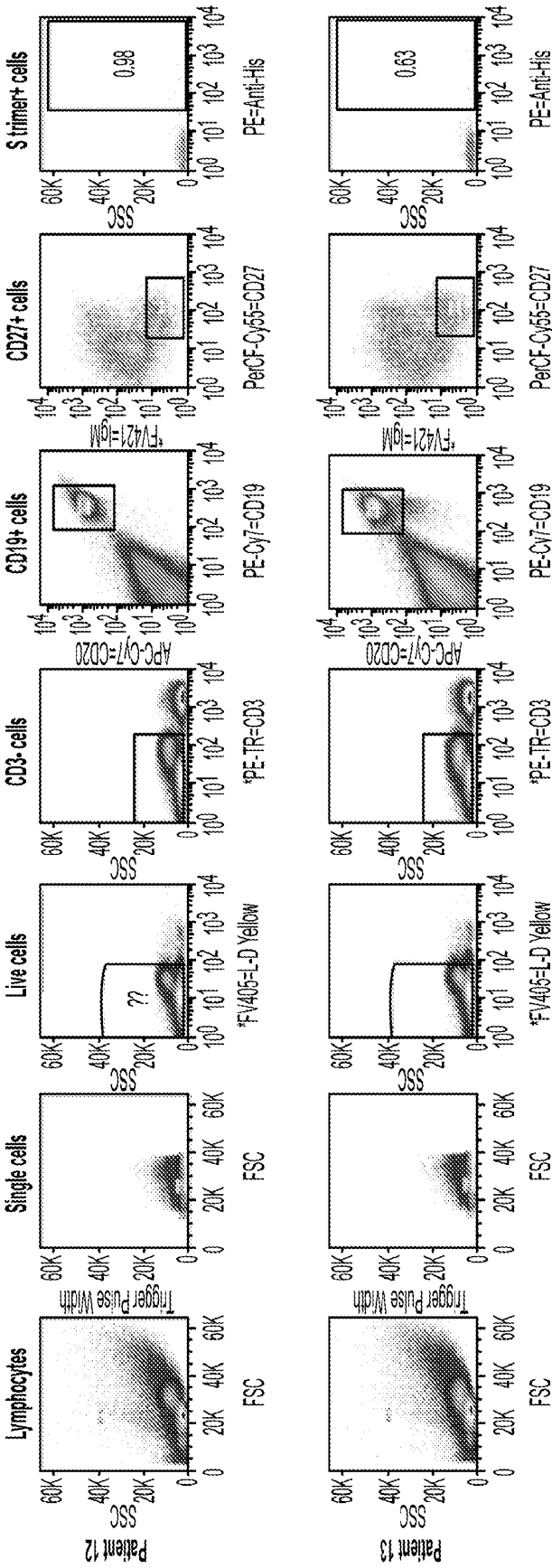


FIG. 1B
CONTINUED

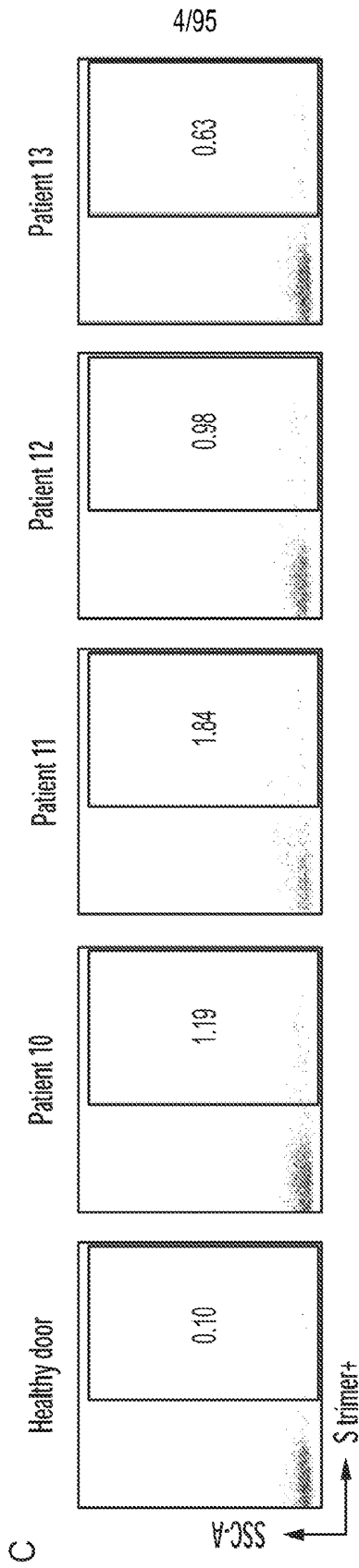
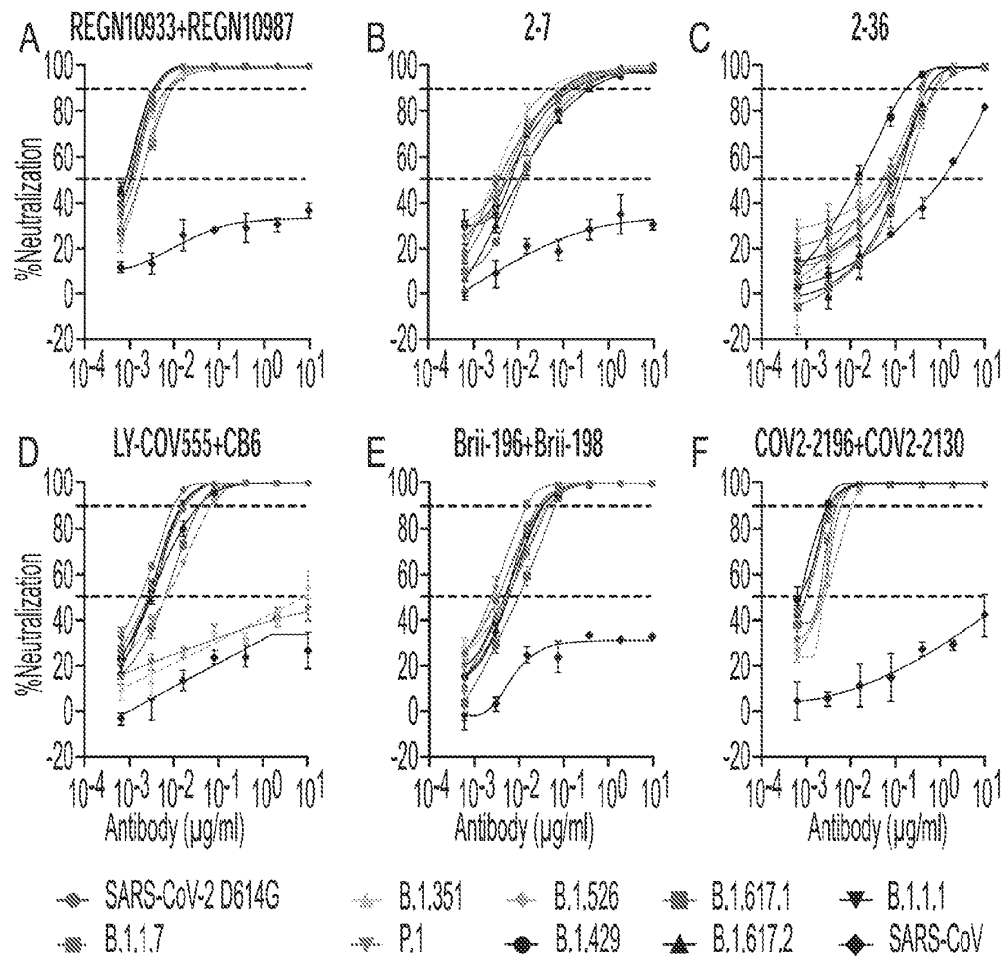
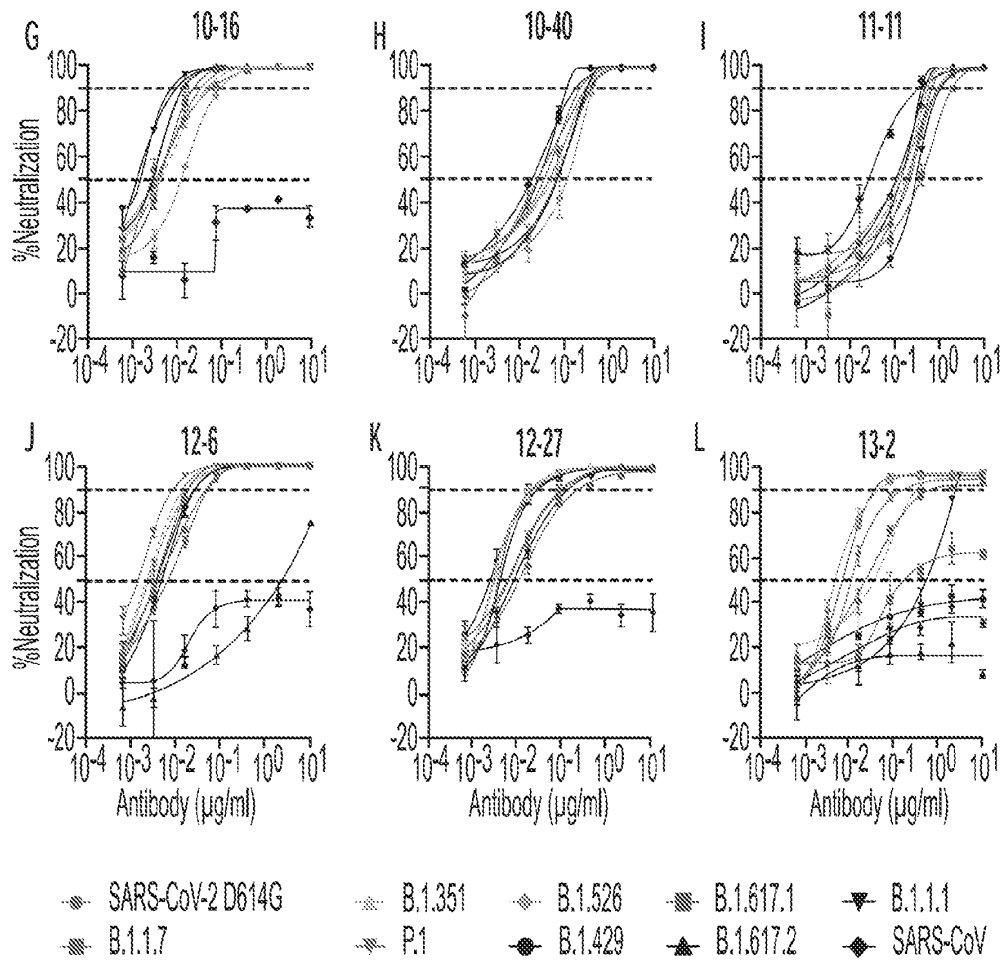


FIG. 1C



FIGS. 2A-F



FIGS. 2G-L

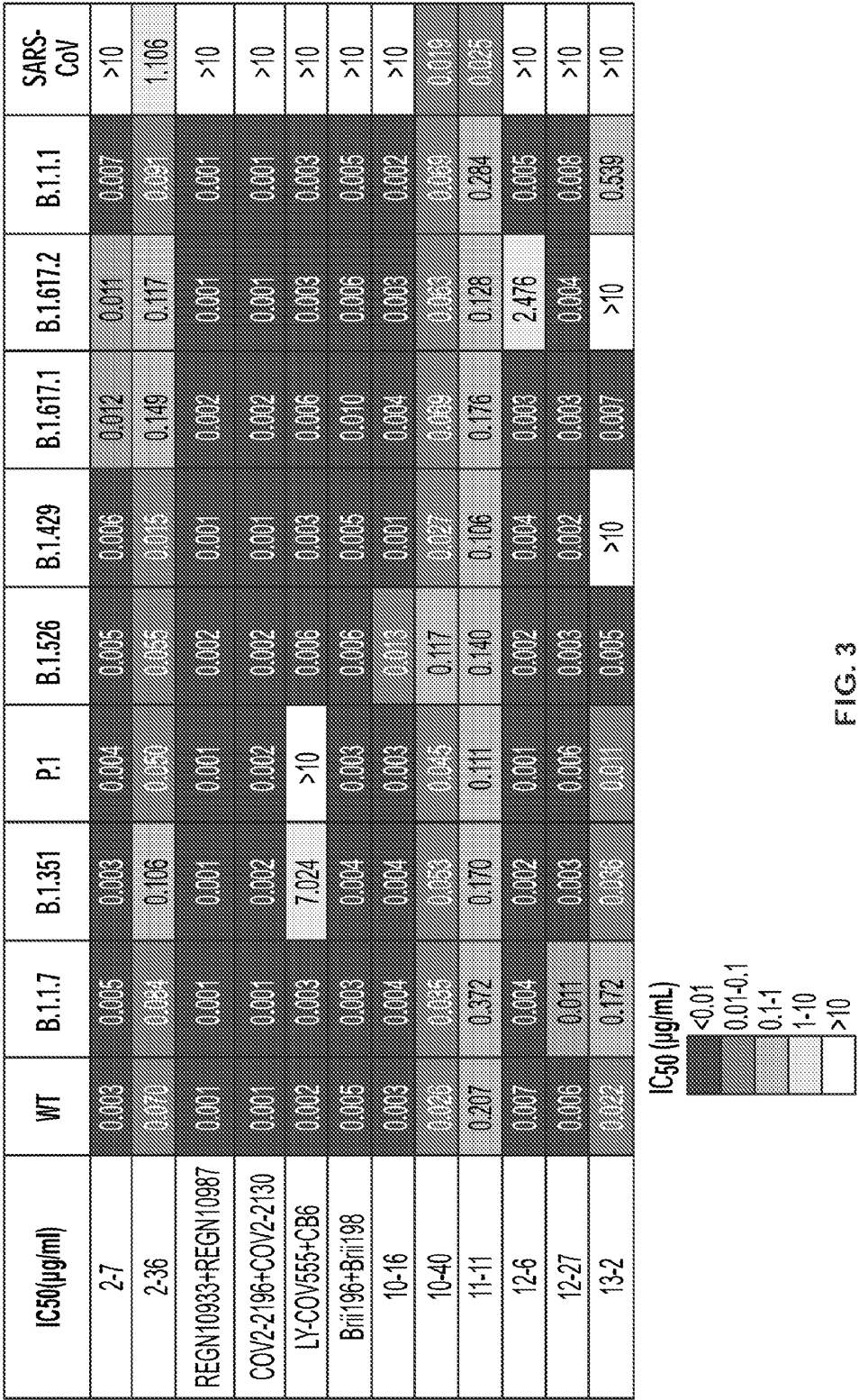
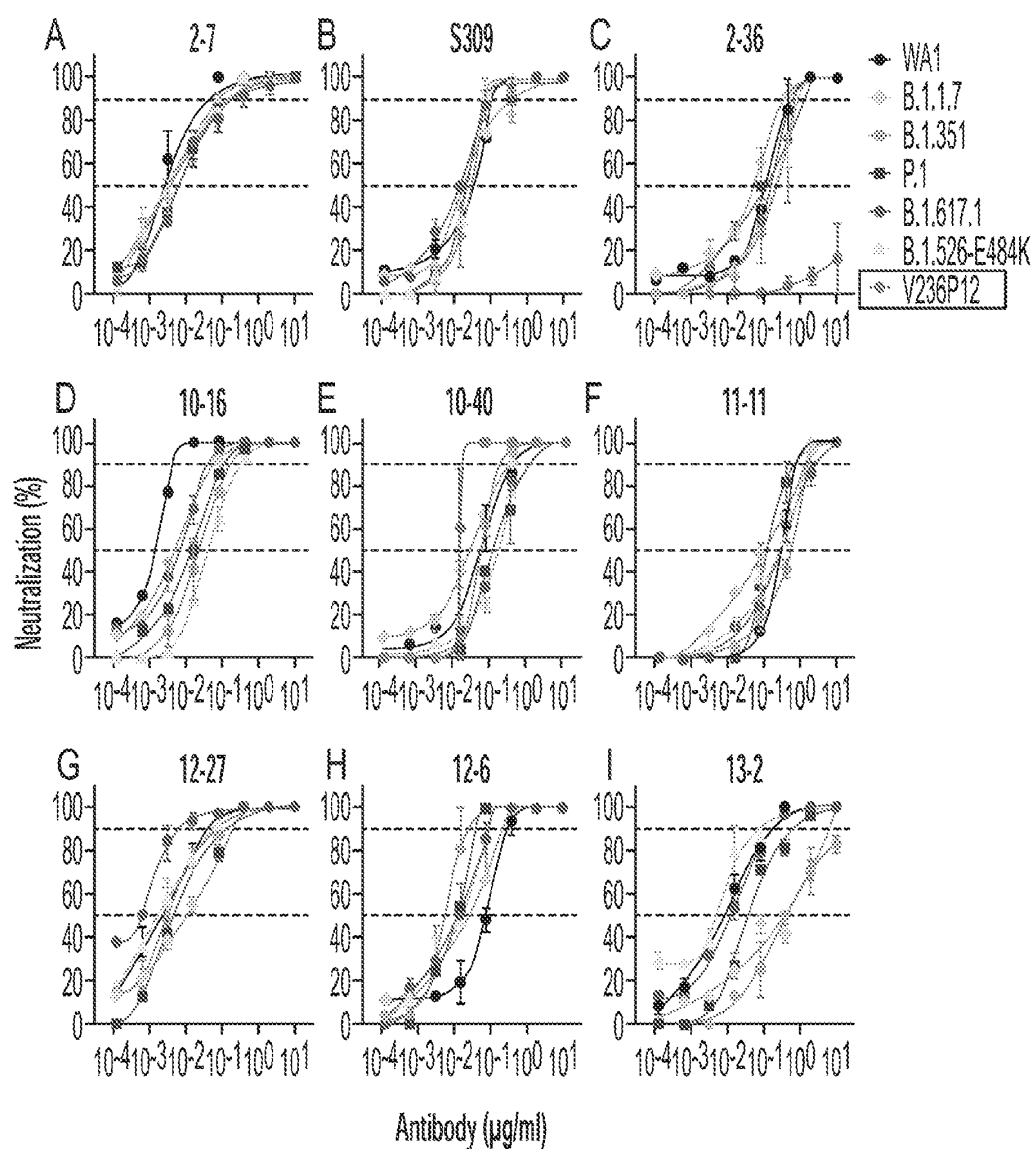


FIG. 3

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FIGS. 4A-I

mAb	Potency (IC50) µg/mL						
	WA1	B.1.1.7	B.1.351	P.1	B.1.617.1	B.1.526-E484K	V236P12 **
2-7	0.003	0.003	0.004	0.006	0.006	0.003	
S309	0.037	0.019	0.032	0.024	0.015	0.024	
2-36	0.114	0.052	0.215	0.109	0.149	0.21	50
10-16	0.002	0.005	0.024	0.016	0.007	0.042	
10-40	0.06	0.031	0.054	0.134	0.156	0.198	0.015
11-11	0.309	0.111	0.55	0.126	0.283	0.289	
12-6	0.085	0.027	0.006	0.013	0.014	0.018	
12-27	0.003	0.012	0.003	0.005	0.001	0.002	
13-2	0.008	6.399	59.316	0.038	0.012	0.005	

** V236P12 tested for 10-40 and 10-28 only

FIG. 4J

0.000
0.010
1.000
50.000
>50

J

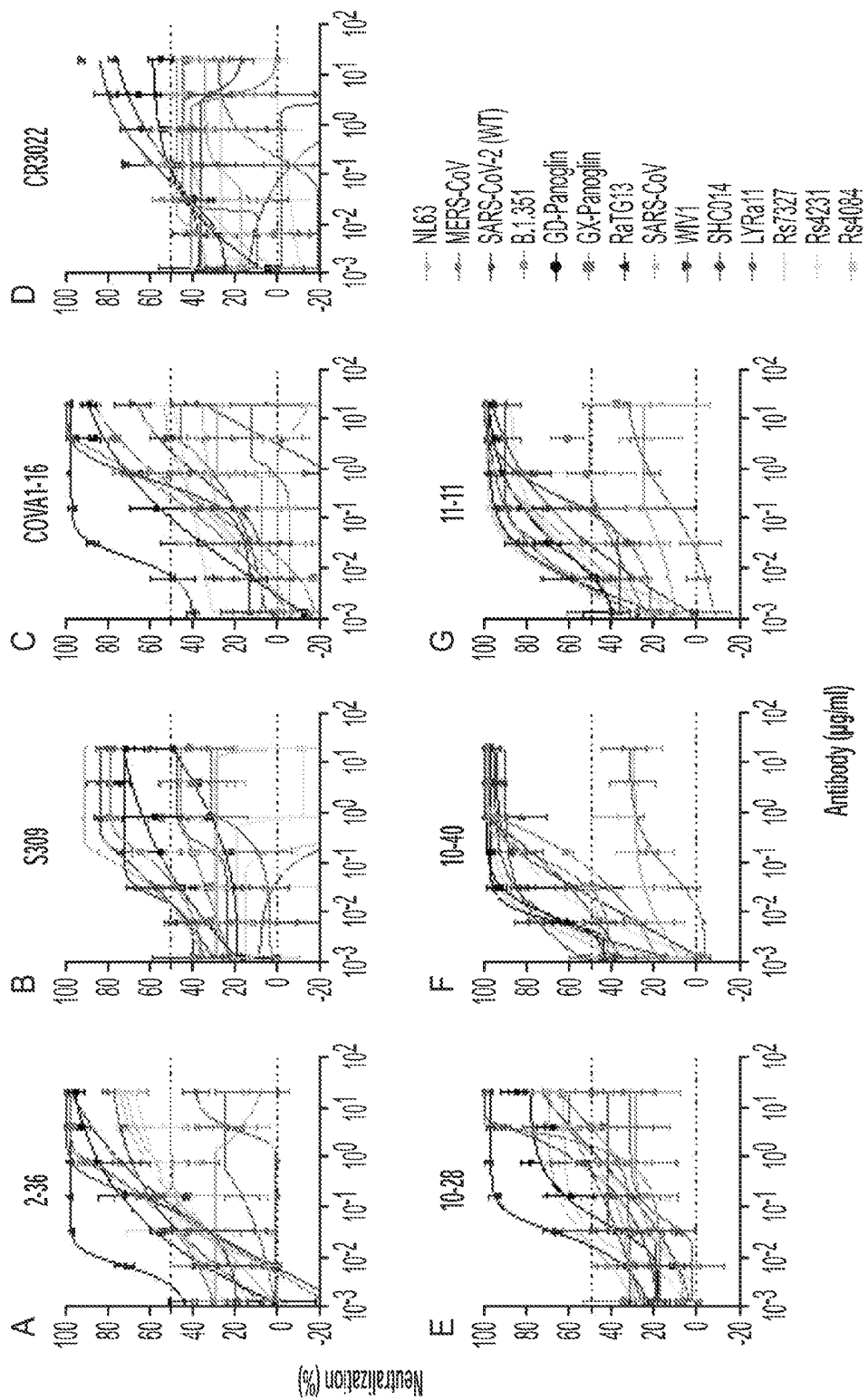
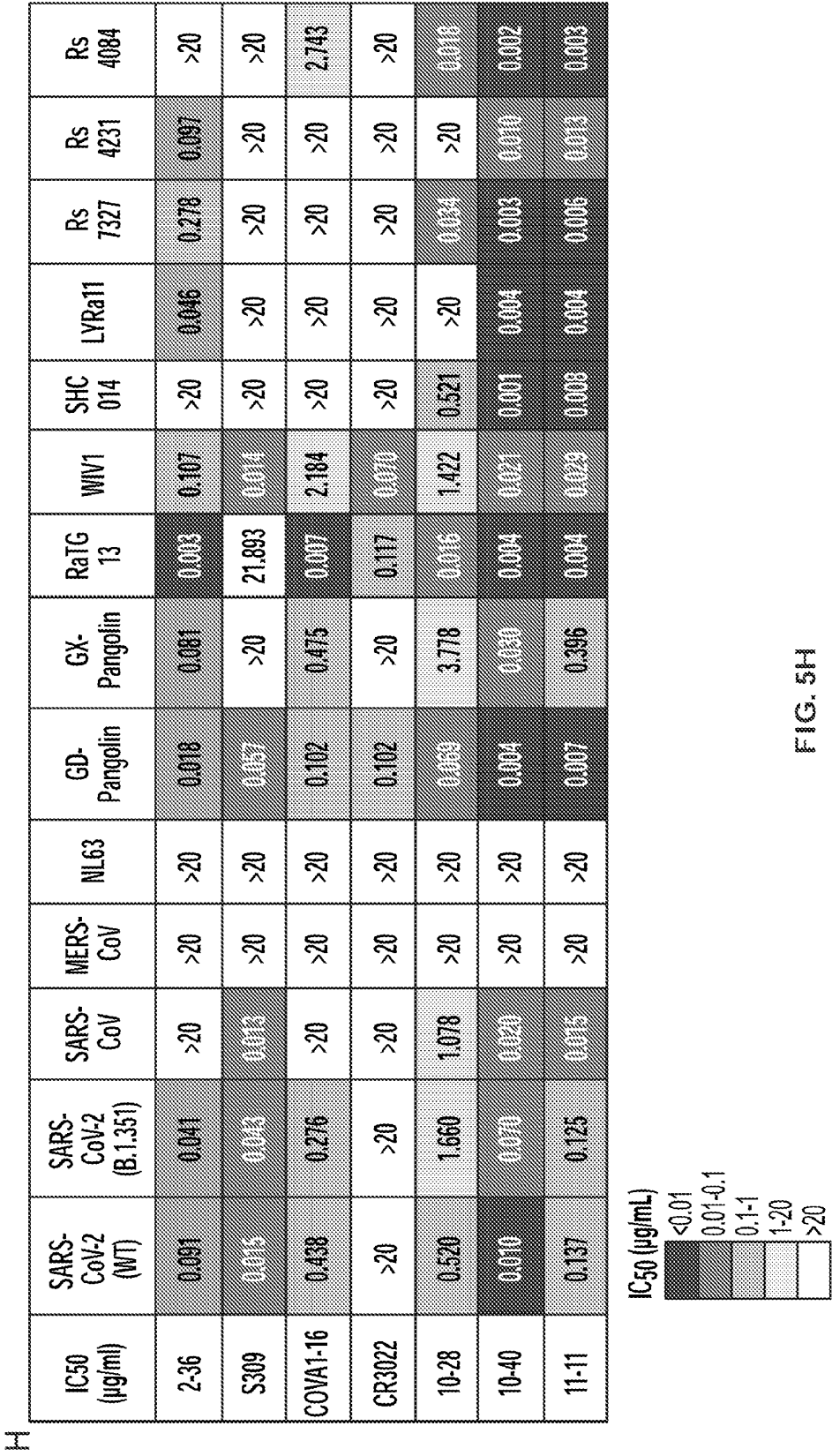
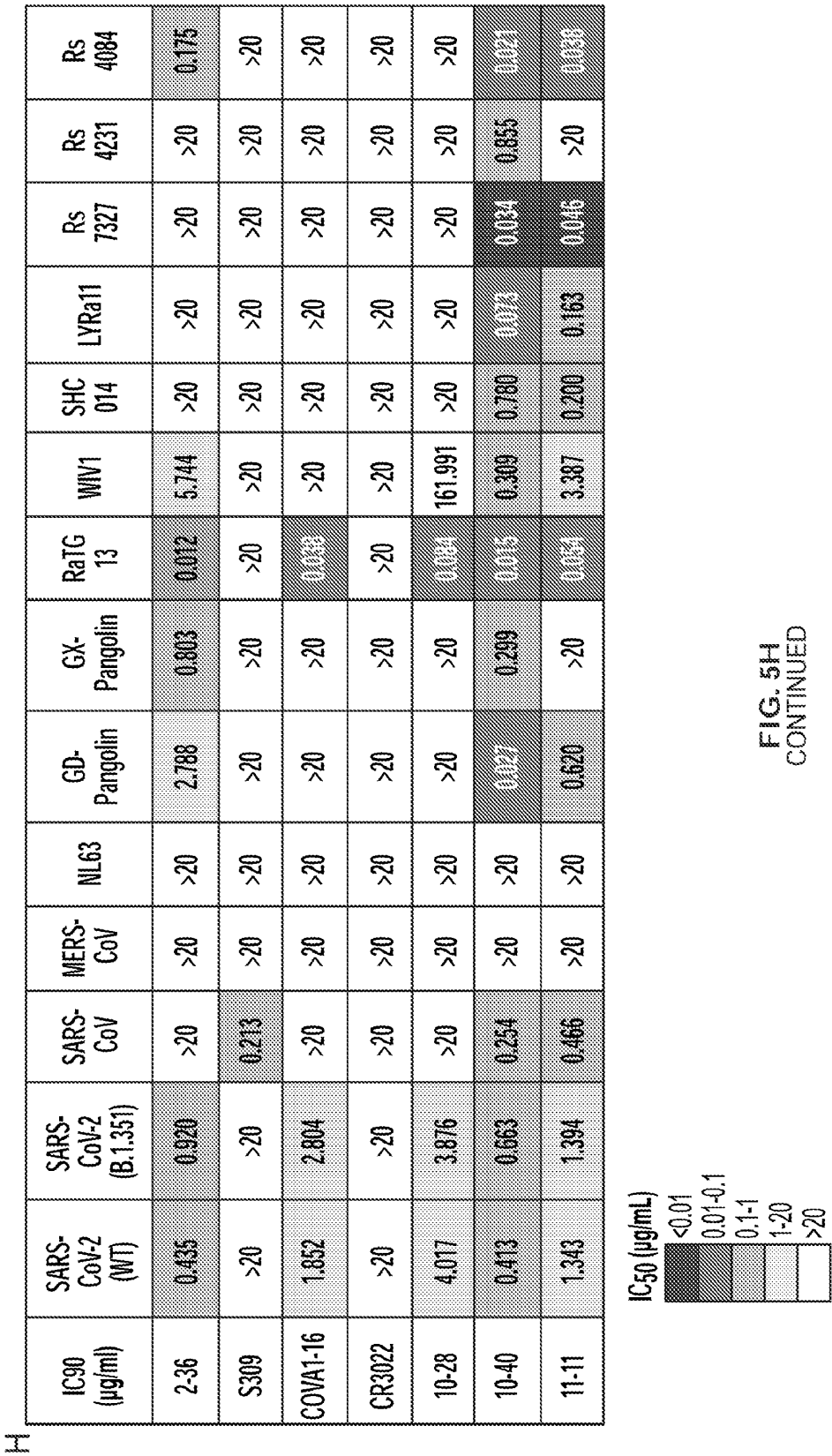
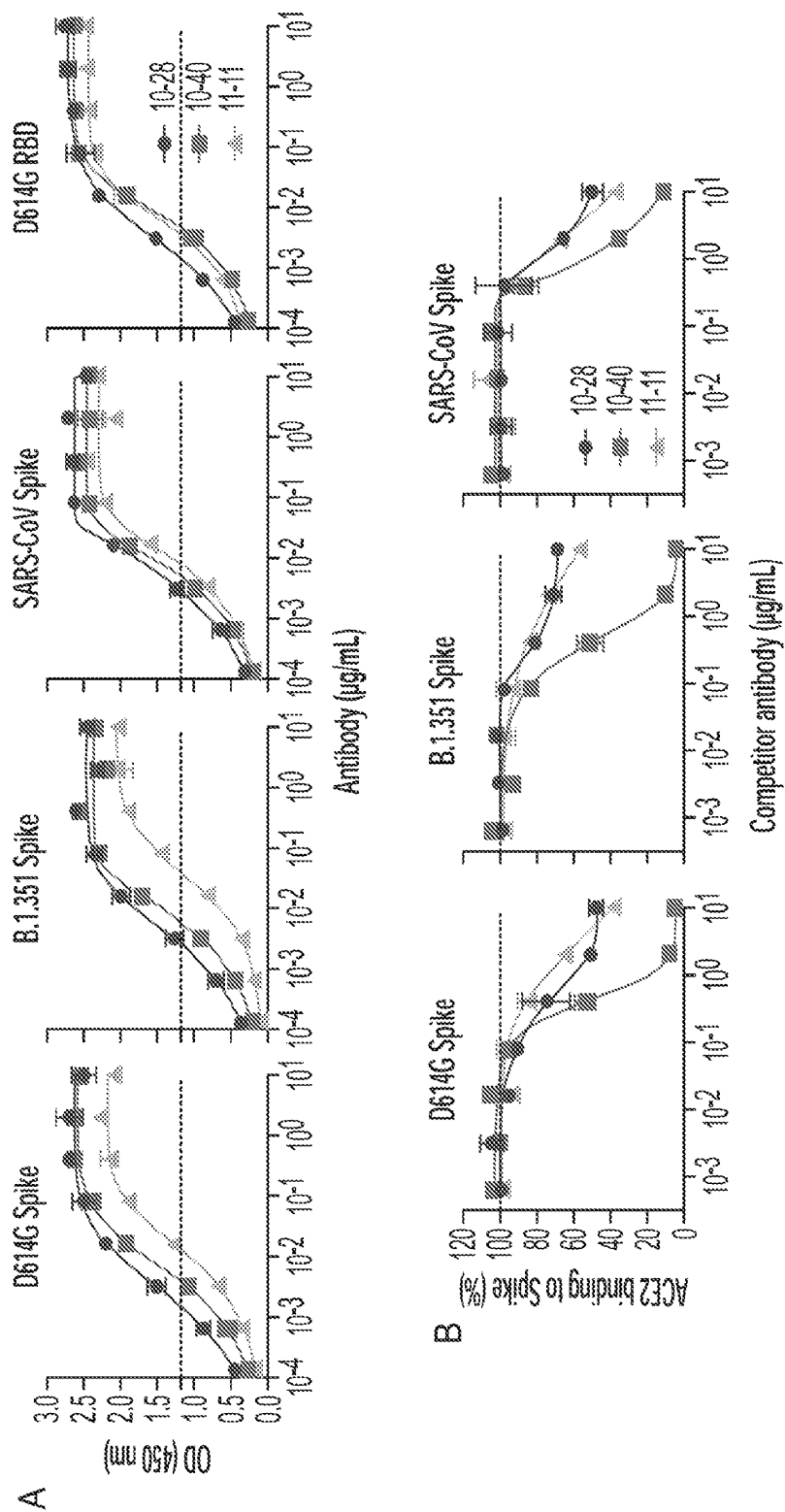


FIG. 5A-G







FIGS. 6A-B

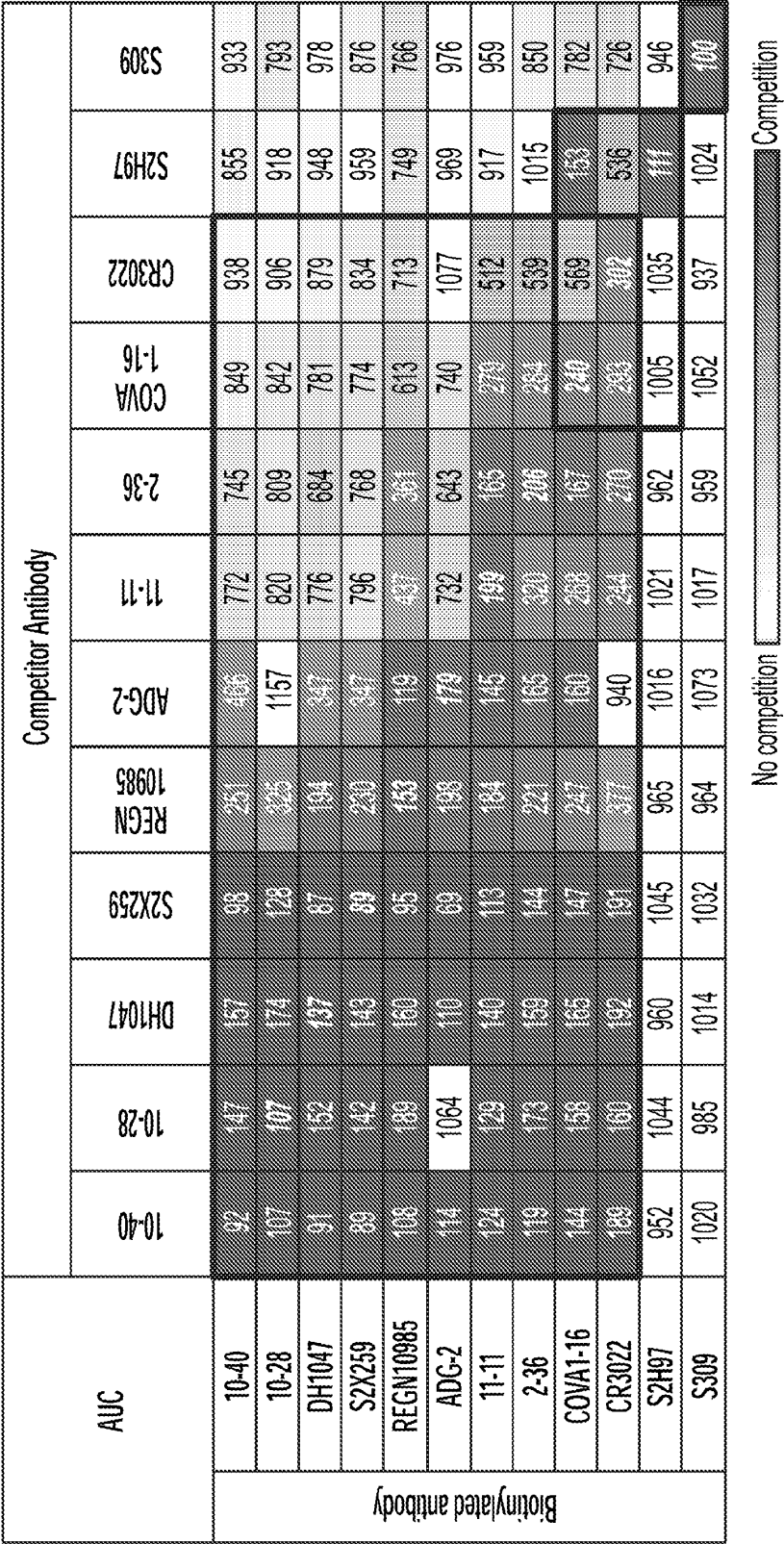


FIG. 6C

A

Pseudoviruses IC ₅₀ (µg/mL)		10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2197	S309
D614G B.1.1.7 B.1.351 P.1 B.1.526 B.1.429 B.1.617.1 B.1.617.2 B.1.1.1 R.1		0.059	0.741	0.603	0.125	0.075	0.050	0.034	0.006	0.034	>10	0.504	0.020
		0.050	0.631	1.074	0.115	0.065	0.040	0.039	0.006	0.251	>10	0.281	0.062
		0.092	0.456	0.258	0.197	0.024	0.040	0.021	0.007	0.161	>10	0.355	0.026
		0.084	0.398	0.285	0.148	0.022	0.030	0.019	0.007	0.048	>10	0.100	0.024
		0.126	0.782	0.271	0.205	0.045	0.053	0.026	0.007	0.175	>10	0.708	0.022
		0.048	0.503	0.229	0.056	0.027	0.025	0.013	0.003	0.070	>10	0.216	0.032
		0.029	0.983	0.256	0.219	0.035	0.041	0.027	0.004	0.166	>10	0.414	0.027
		0.088	0.500	0.154	0.179	0.045	0.045	0.025	0.005	0.139	>10	0.244	0.032
		0.095	1.024	0.425	0.161	0.076	0.071	0.037	0.003	0.188	>10	0.440	0.057
		0.034	0.855	0.263	0.117	0.030	0.054	0.018	0.005	0.126	>10	0.283	0.030
		<0.01	0.01-0.1	0.1-1	1-10	>10							

FIG. 7A

B

Live viruses IC ₅₀ (µg/mL)		10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2H97	S309
WAI B.1.1.7 B.1.351 P.1 B.1.617.2	0.037	1.484	0.583	0.117	0.091	0.049	0.072	0.001	0.410	>50	0.101	0.039	
	0.045	0.874	0.629	0.053	0.038	0.039	0.026	0.001	0.391	>50	0.075	0.017	
	0.104	1.907	0.776	0.204	0.042	0.064	0.019	0.003	0.509	>50	0.237	0.027	
	0.079	1.141	0.336	0.009	0.053	0.152	0.032	0.002	0.621	>50	0.176	0.021	
	0.298	0.921	1.017	0.171	0.092	0.033	0.054	0.009	0.458	>50	0.314	0.024	
SARS-CoV	0.151	NA	NA	13.790	0.221	0.170	3.801	0.008	NA	NA	NA	NA	

<0.01	0.01-0.1	0.1-1	1-10	>10
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FIG. 7B

C

Pseudoviruses IC ₅₀ (µg/mL)	10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2H97	S309
GD-Pangolin	0.011	0.493	0.066	0.076	0.035	0.010	0.006	0.004	0.388	>10	>10	0.140
GX-Pangolin	0.090	5.359	>10	0.197	0.032	4.043	>10	0.029	0.763	>10	5.684	3.526
RaTG13	0.006	0.014	0.008	0.005	0.013	0.009	0.003	>10	0.009	1.401	>10	>10
SARS-CoV	0.046	1.023	0.063	1.597	0.037	0.042	1.259	0.003	6.330	1.561	0.698	0.028
WIV1	0.013	1.175	0.076	0.667	0.107	0.039	0.647	0.005	7.058	1.659	0.956	1.117
SHC014	0.008	0.225	0.024	0.142	0.021	0.022	1.947	0.006	>10	>10	>10	>10
LYRa11	0.005	5.074	0.008	0.832	0.009	0.008	1.092	0.002	2.888	>10	>10	>10
Rs7327	0.004	4.669	0.011	>10	0.011	0.003	0.484	0.002	>10	>10	>10	>10
RS4231	0.236	>10	0.016	>10	0.215	0.248	0.408	0.009	>10	>10	>10	>10
Rs4084	0.006	>10	0.014	3.195	0.017	0.007	0.133	0.005	>10	>10	>10	>10
MERS	>10	>10	>10	>10	>10	>10	>10	>10	>10	>10	>10	>10

<0.01	0.01-0.1	0.1-1	1-10	>10
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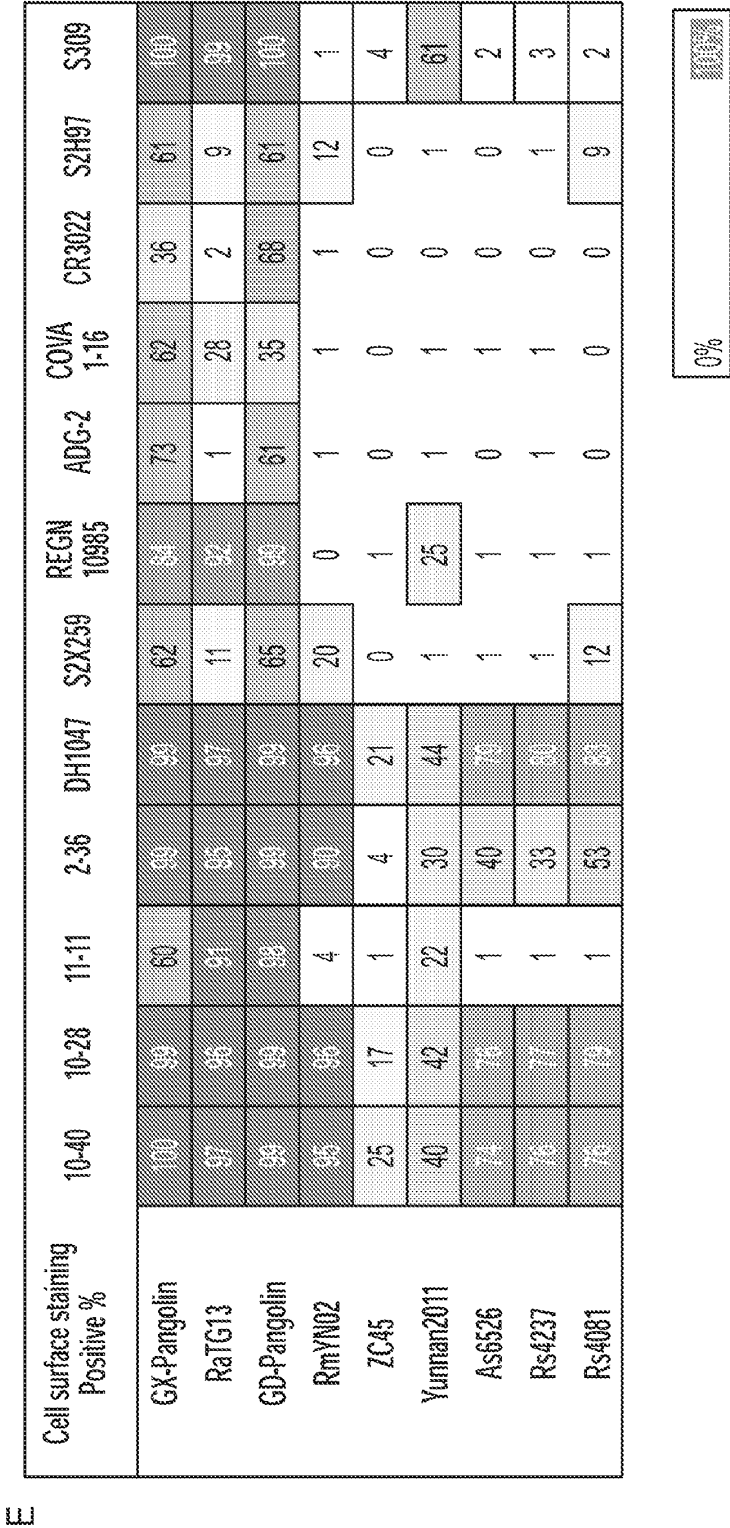
FIG. 7C

RBD ELISA EC ₅₀ (µg/mL)	10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2H97	S309
	10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2H97	S309
BM-4831	0.003	0.002	1.503	>10	0.002	0.005	0.720	0.711	>10	>10	0.009	0.286
BiKY72	0.004	0.004	0.007	1.035	0.003	0.004	0.001	0.005	>10	0.005	0.005	>10
SHC014	0.005	0.002	0.006	0.002	0.003	0.007	0.003	0.003	0.049	0.006	>10	0.018
WIV1	0.004	0.003	0.006	0.026	0.003	0.005	0.003	0.005	>10	0.004	0.540	0.023
SARS-CoV	0.008	0.005	0.009	>10	0.008	0.005	>10	0.002	>10	0.009	0.005	0.011
GX-Pangolin	0.004	0.004	>10	0.003	0.006	0.005	3.296	0.089	0.043	0.030	0.026	0.052
RaTG13	0.003	0.002	>10	0.009	0.003	>10	>10	>10	0.614	0.262	0.008	>10
SARS-CoV-2	0.005	0.003	0.006	0.003	0.004	0.003	0.001	0.003	0.004	0.004	0.003	0.007
B.1.351	0.007	0.004	0.030	0.007	0.009	0.006	0.002	0.007	0.014	0.008	0.005	0.021
Rf1	0.004	0.004	>10	2.455	>10	>10	>10	>10	7.072	>10	0.005	>10
RmYN02	0.010	0.006	>10	1.071	0.010	>10	>10	>10	>10	>10	0.011	>10
Rs4081	0.009	0.007	>10	5.449	0.003	2.287	>10	>10	>10	0.826	0.009	>10
Yunnan2011	0.007	0.009	>10	>10	0.011	>10	>10	>10	>10	0.307	0.124	>10

<0.01	0.01-0.1	0.1-1	1-10	>10
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FIG. 7D

D



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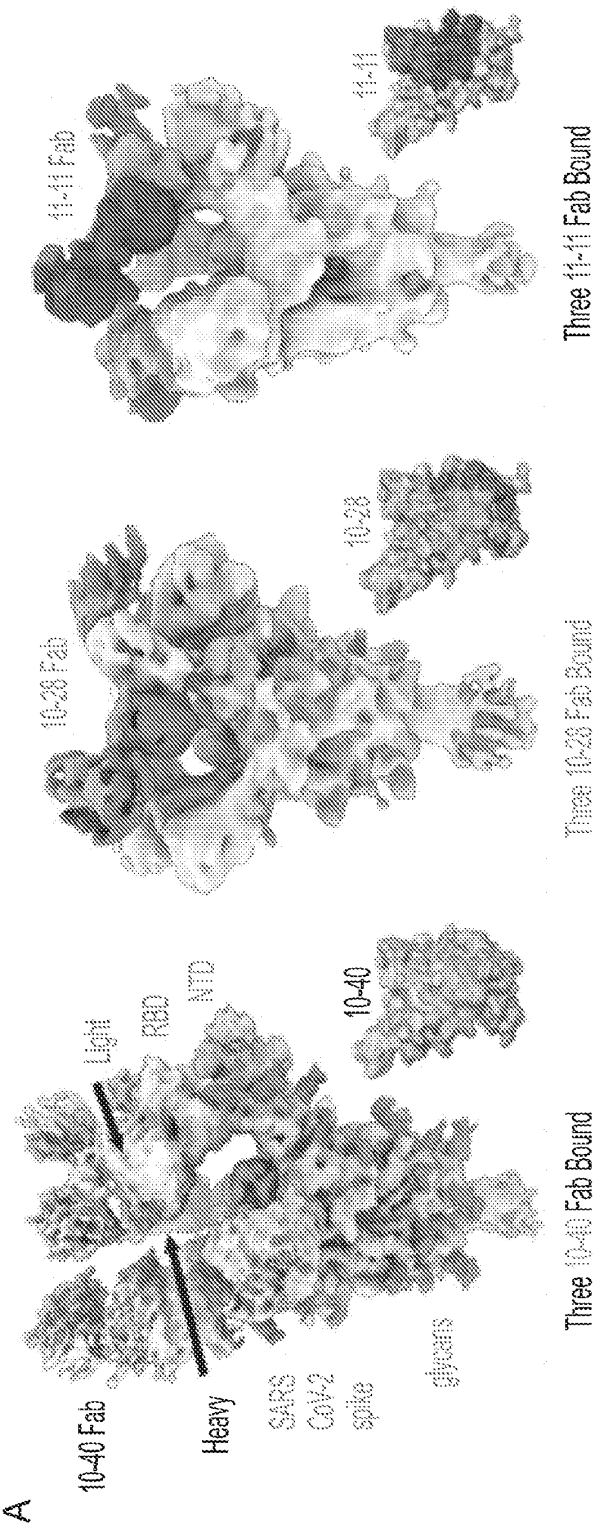
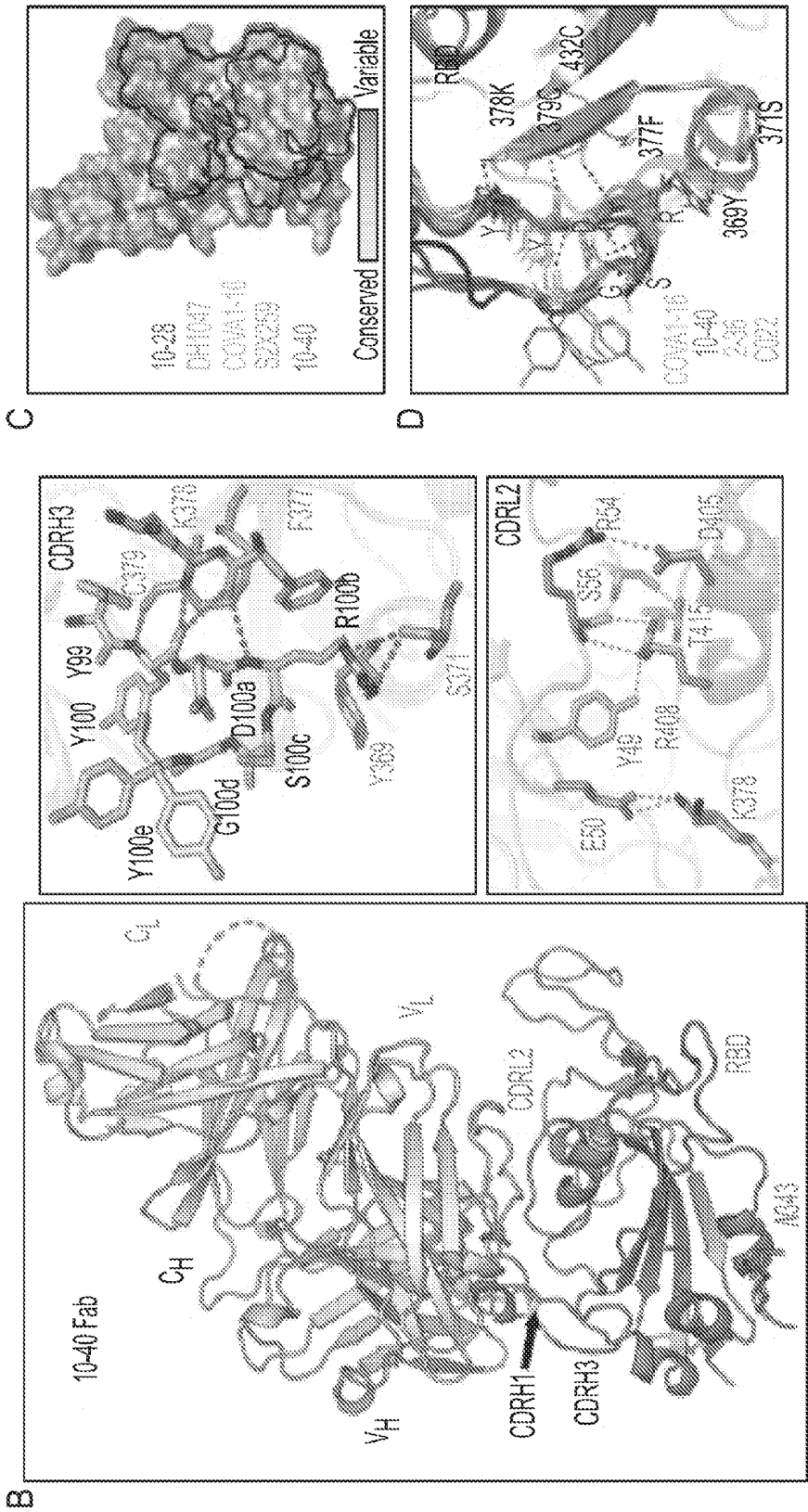


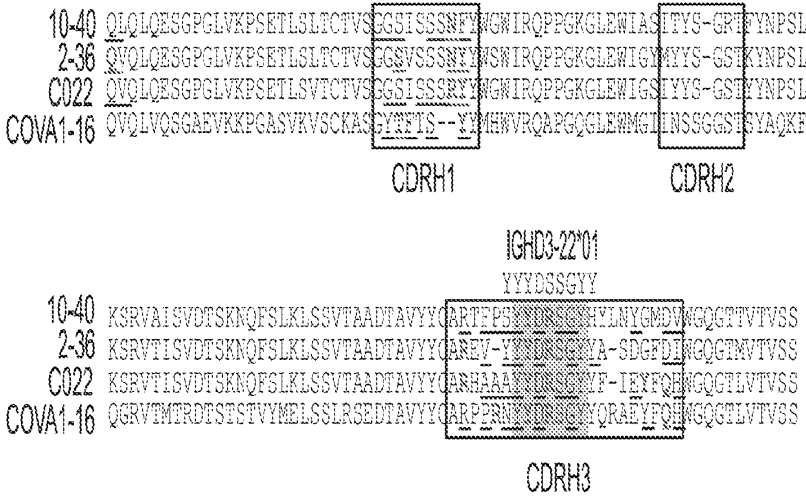
FIG. 8A



FIGS. 8B-D

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E



F

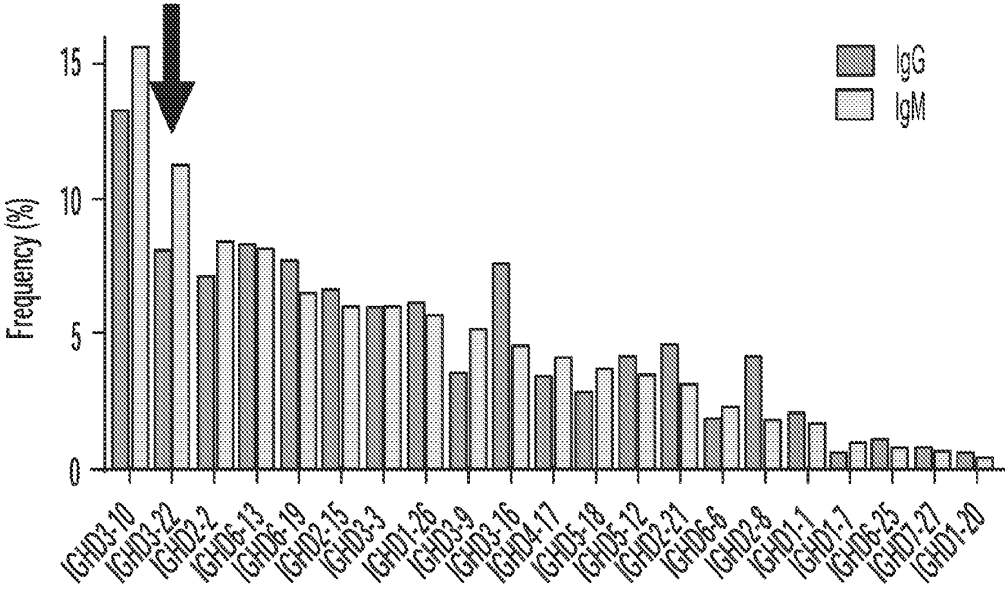
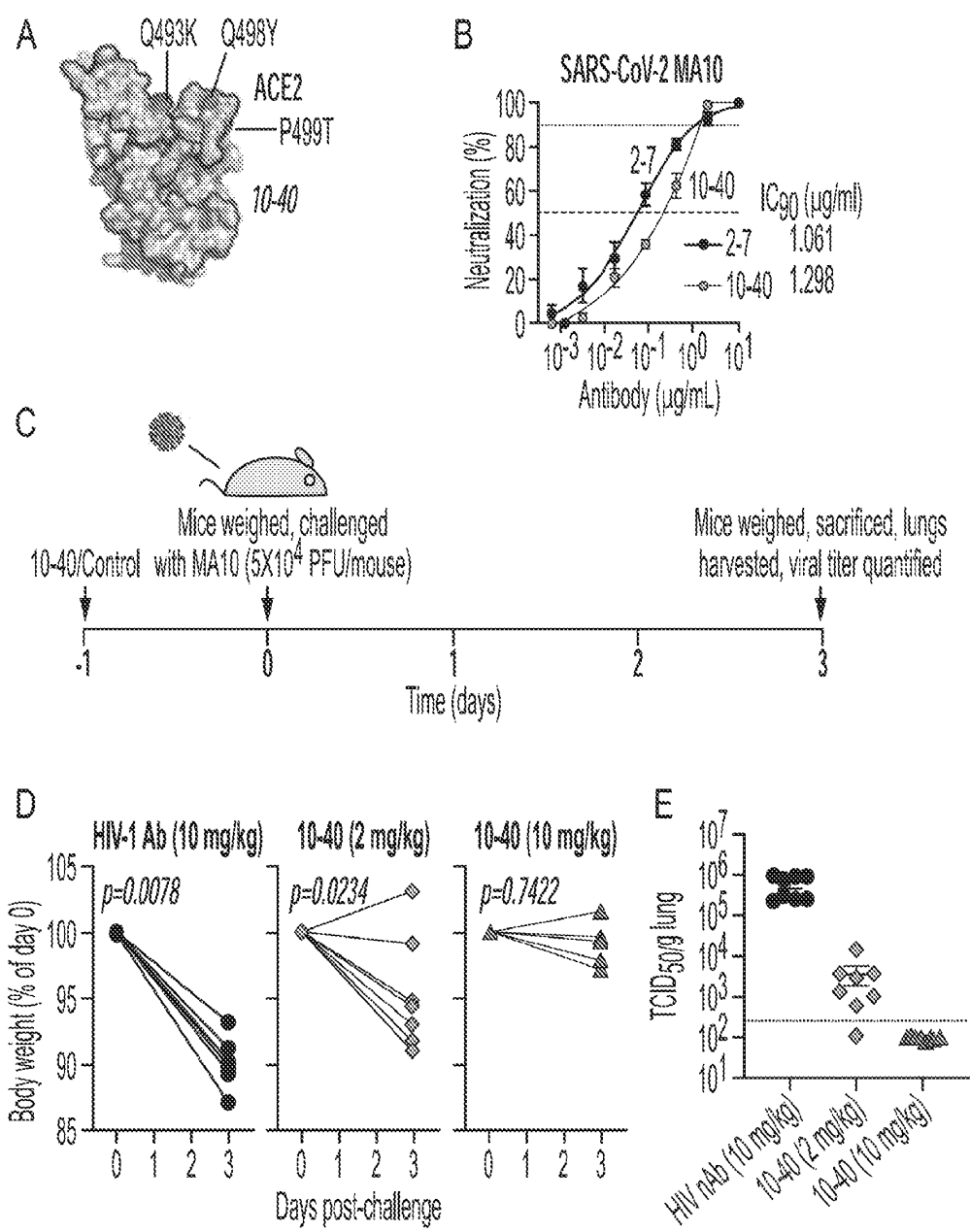


FIG. 8E-F

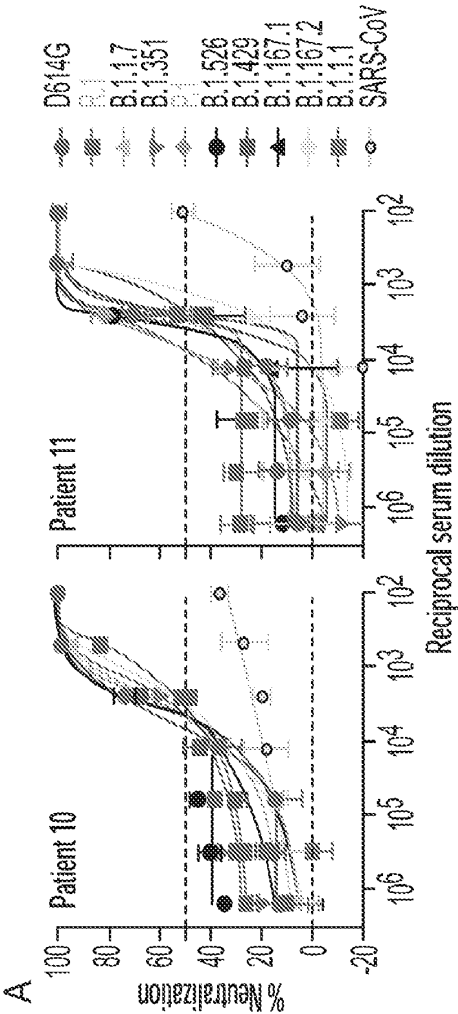
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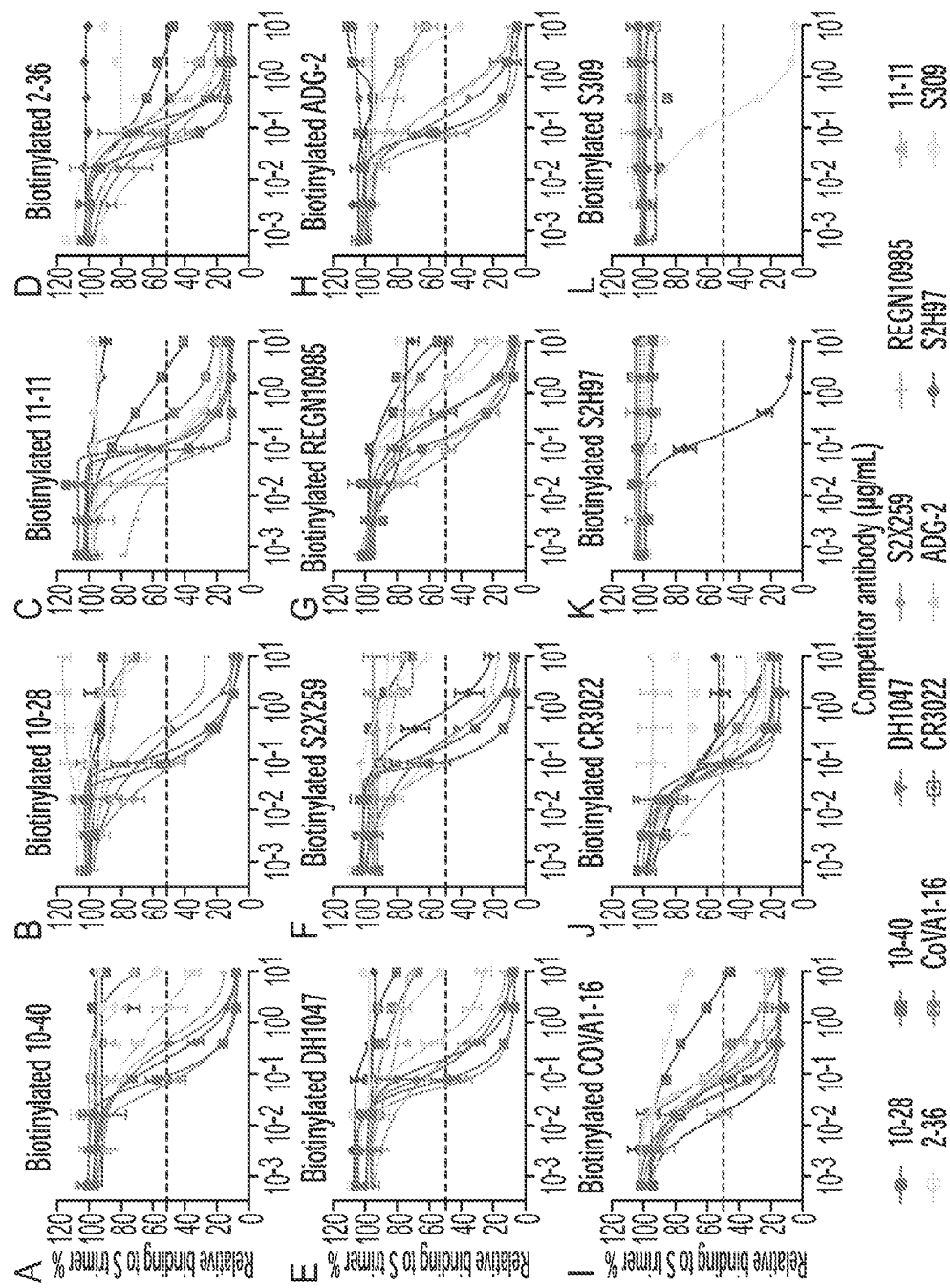
FIGS. 9A-E

ID ₅₀	Patient 10	Patient 11
D614G	6911	3635
R1	3567	2641
B.1.1.7	4354	2967
B.1.1.351	4326	7147
P.1	4225	6625
B.1.526	4657	3562
B.1.429	7515	2112
B.1.617.1	4112	2238
B.1.617.2	3544	1126
B.1.1.1	4837	2781
SARS-CoV	>100	102

B



FIGS. 10A-B



FIGS. 11A-L

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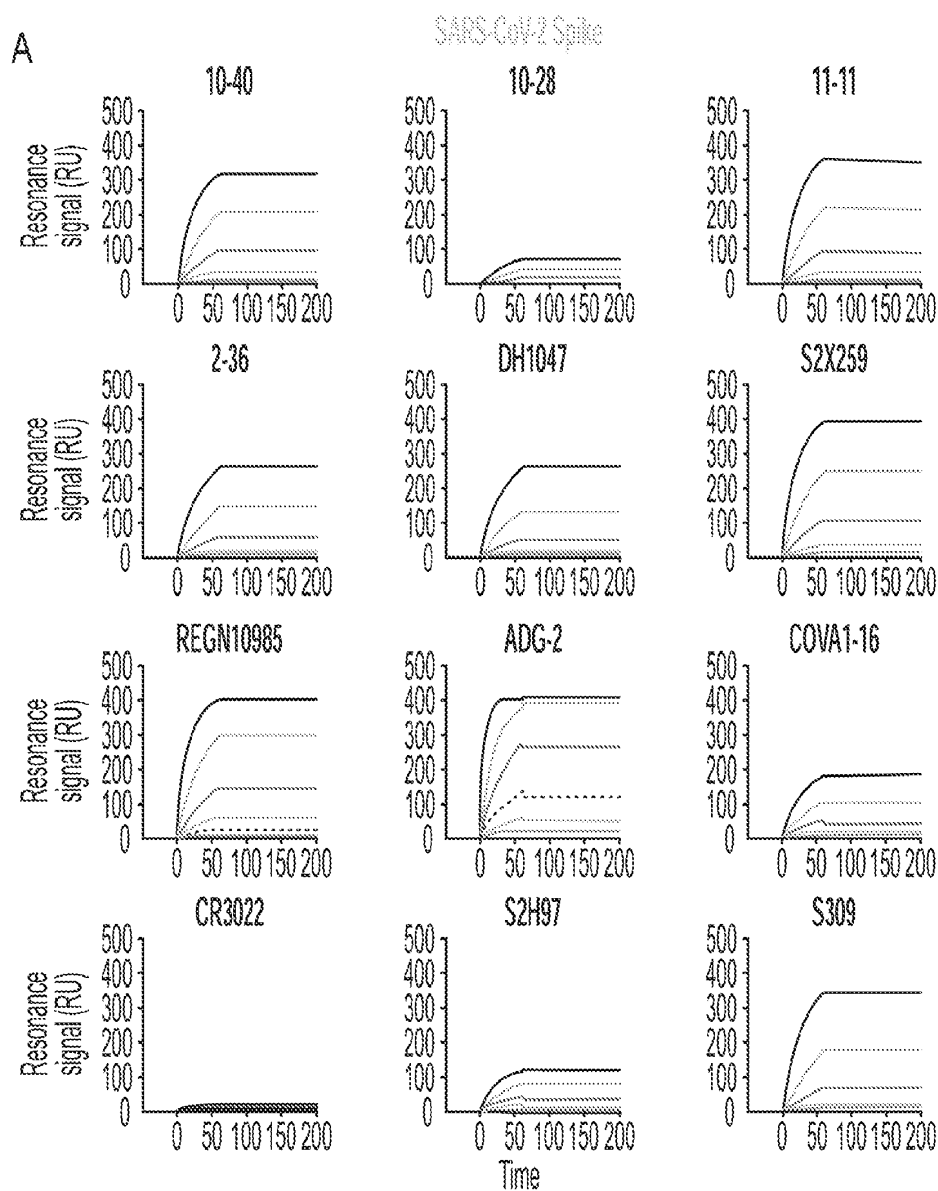


FIG. 12A

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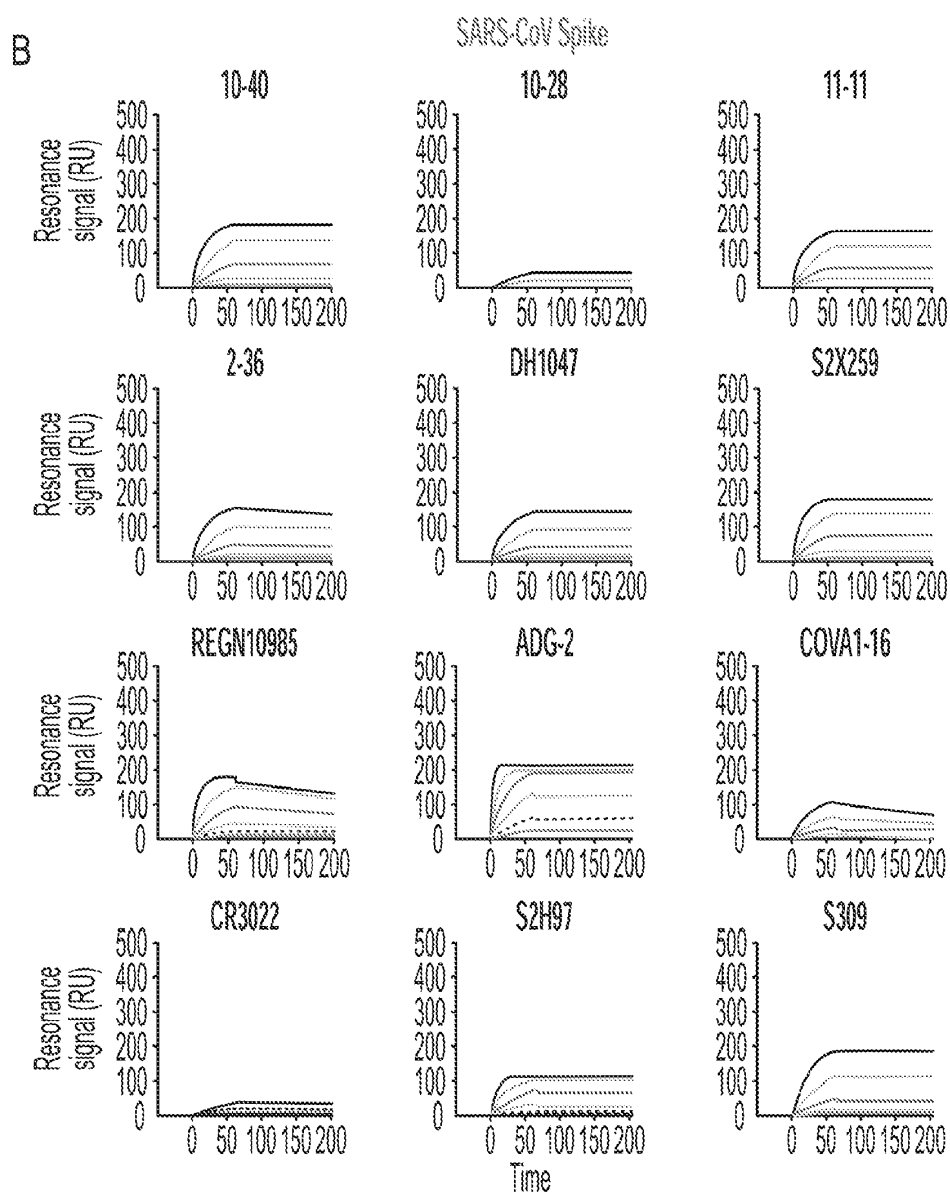


FIG. 12B

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C

mAb	SARS-CoV-2 Spike			SARS-CoV Spike		
	ka (1/Ms)	kd (1/s)	KD (M)	ka (1/Ms)	kd (1/s)	KD (M)
10-40	1.60E+05	7.22E-07	4.52E-12	2.05E+05	4.54E-07	2.21E-12
10-28	9.17E+04	7.17E-08	7.82E-13	5.44E+04	2.01E-07	3.69E-12
11-11	1.36E+05	2.09E-04	1.54E-09	1.85E+05	8.34E-07	4.51E-12
2-36	1.11E+05	1.68E-06	1.51E-11	1.69E+05	4.99E-04	2.96E-09
DH1047	8.59E+04	9.10E-08	1.06E-12	1.52E+05	1.69E-07	1.11E-12
S2X259	1.54E+05	1.38E-07	8.95E-13	2.41E+05	8.78E-07	3.65E-12
REGN10985	2.10E+05	1.83E-06	8.72E-12	4.08E+05	1.90E-03	4.65E-09
ADG-2	5.09E+05	5.00E-07	9.83E-13	1.23E+06	1.73E-06	1.41E-12
COVA1-16	1.03E+05	1.33E-07	1.29E-12	1.64E+05	3.20E-03	1.95E-08
CR3022	2.71E+05	4.85E-04	1.79E-09	8.59E+04	6.52E-08	7.59E-13
S2H97	1.64E+05	7.42E-07	4.53E-12	5.20E+05	3.67E-05	7.06E-11
S309	9.18E+04	1.78E-07	1.94E-12	1.35E+05	2.63E-07	1.95E-12

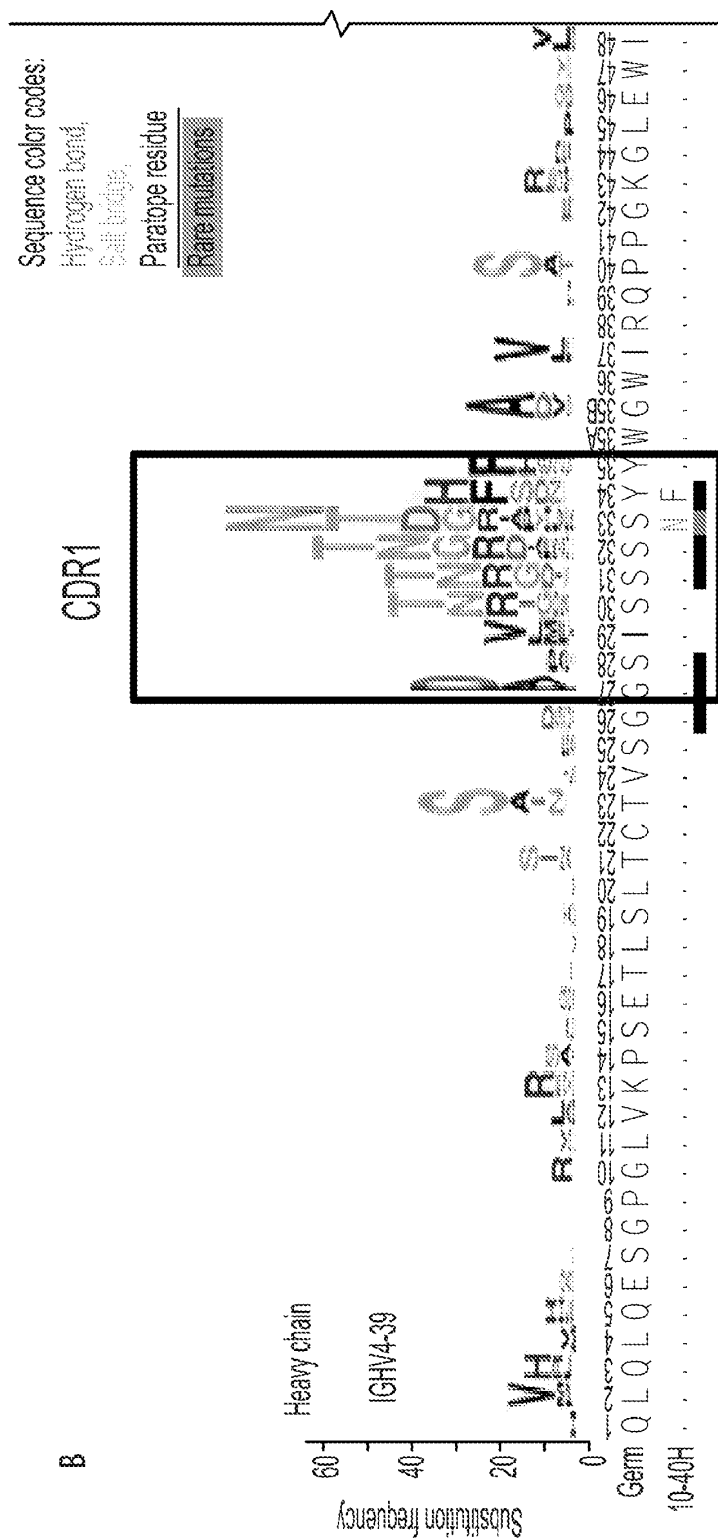
FIG. 12C

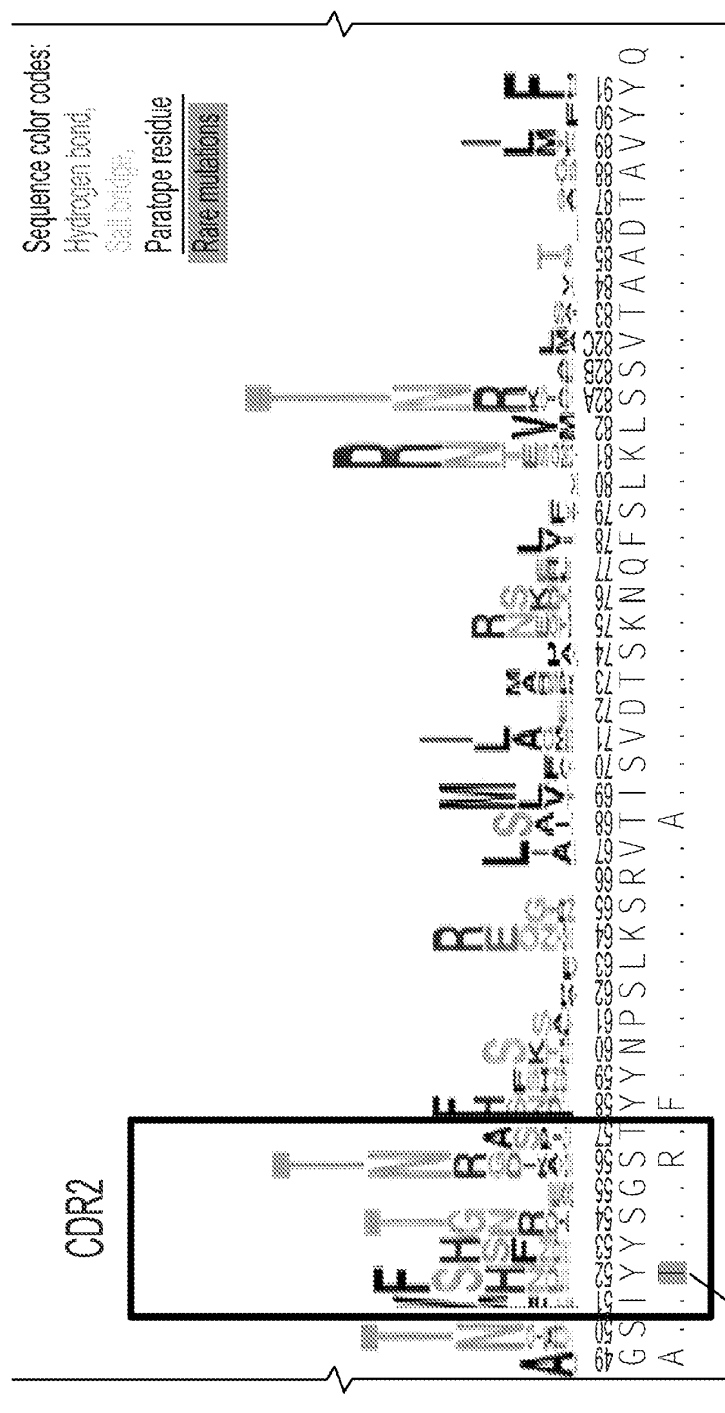
A

mAbs	HV	HD	HJ	Isotype	H_SHM(%)	H_CDR3_len	HCDR3
10-28	IGHV3-30*18	IGHD2-2*03	IGHJ4*02	IGHG1*04	2.4	13	CVKDGQLVPLFDYW
10-40	IGHV4-39*01	IGHD3-22*01	IGHJ6*02	IGHG1*04	3	22	CARTFPSYDRSGYHILNYGMDVW
11-11	IGHV4-31*03	IGHD3-22*01	IGHJ6*02	IGHM*03	0.7	21	CASSNYDGGSYNLLSYGMDVW

mAbs	LV	LJ	L_SHM(%)	L_CDR3_len	LCDR3
10-28	IGKV1-39*01	IGKJ3*01	0.4	10	CQQSYSTPGVTF
10-40	IGLV6-57*01	IGLJ3*02	0.3	9	CQSYDSSSWVF
11-11	IGLV1-40*01	IGLJ3*02	1	12	CQSYDSSLGSWVF

FIG. 13A



FIG. 13B
CONTINUED

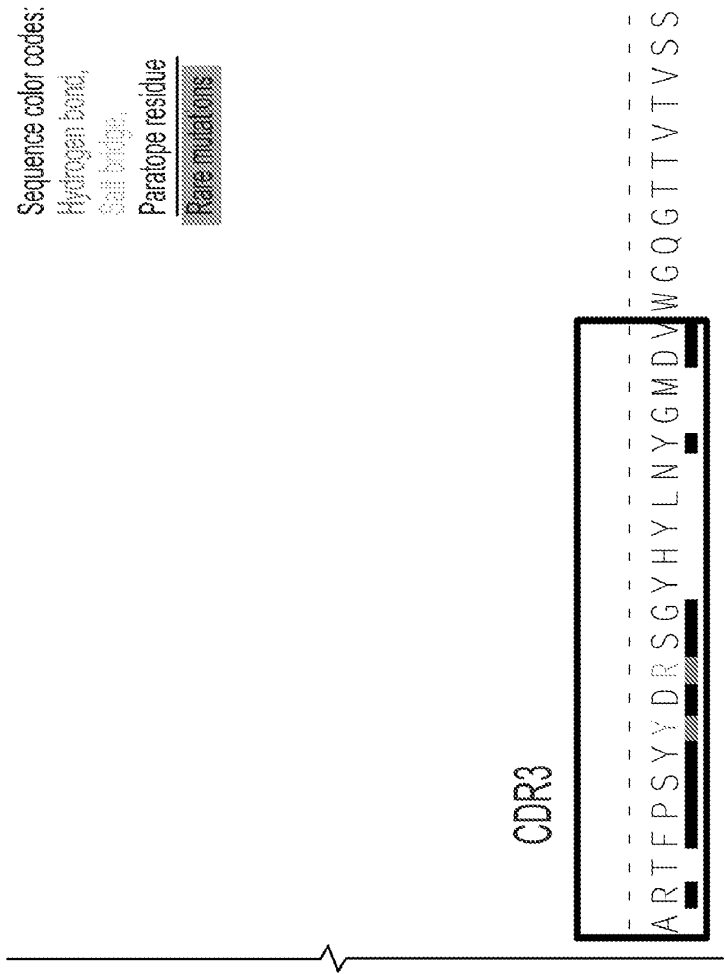


FIG. 13B
CONTINUED

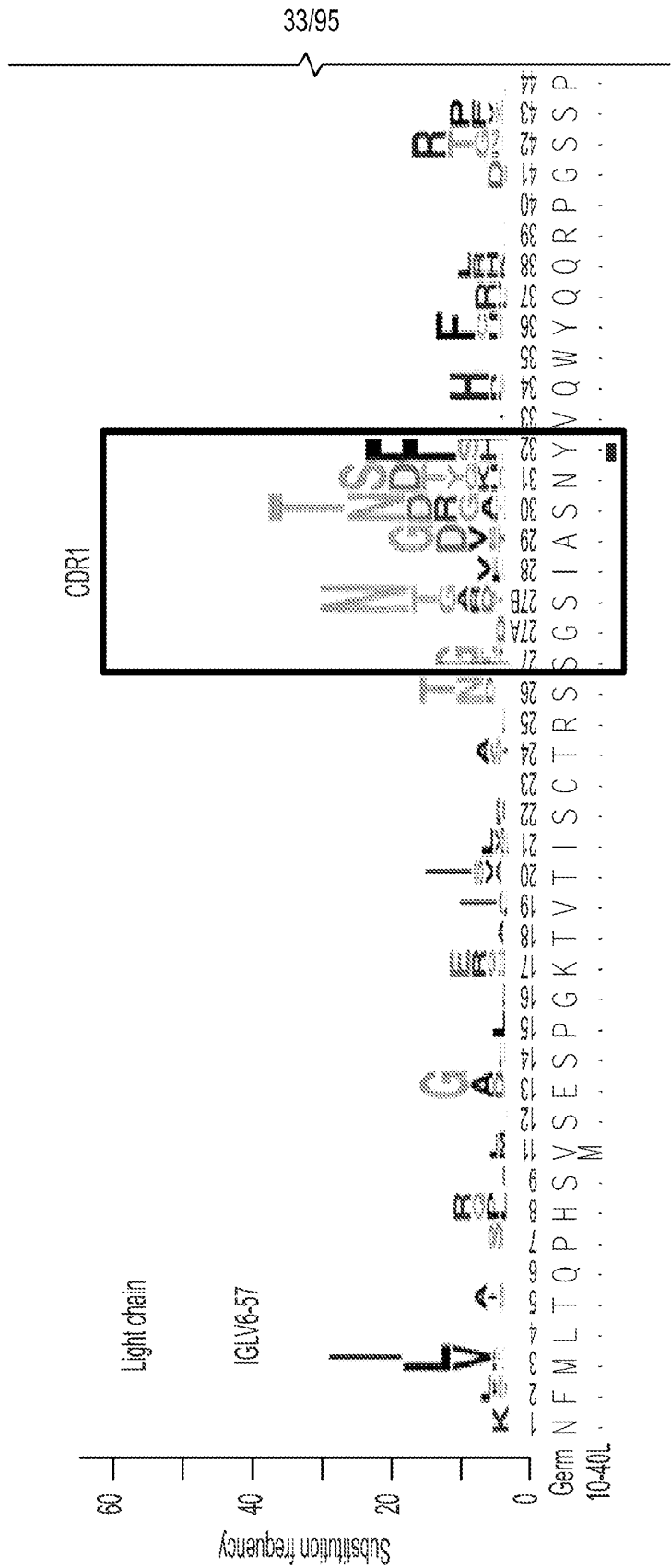


FIG. 13B
CONTINUED

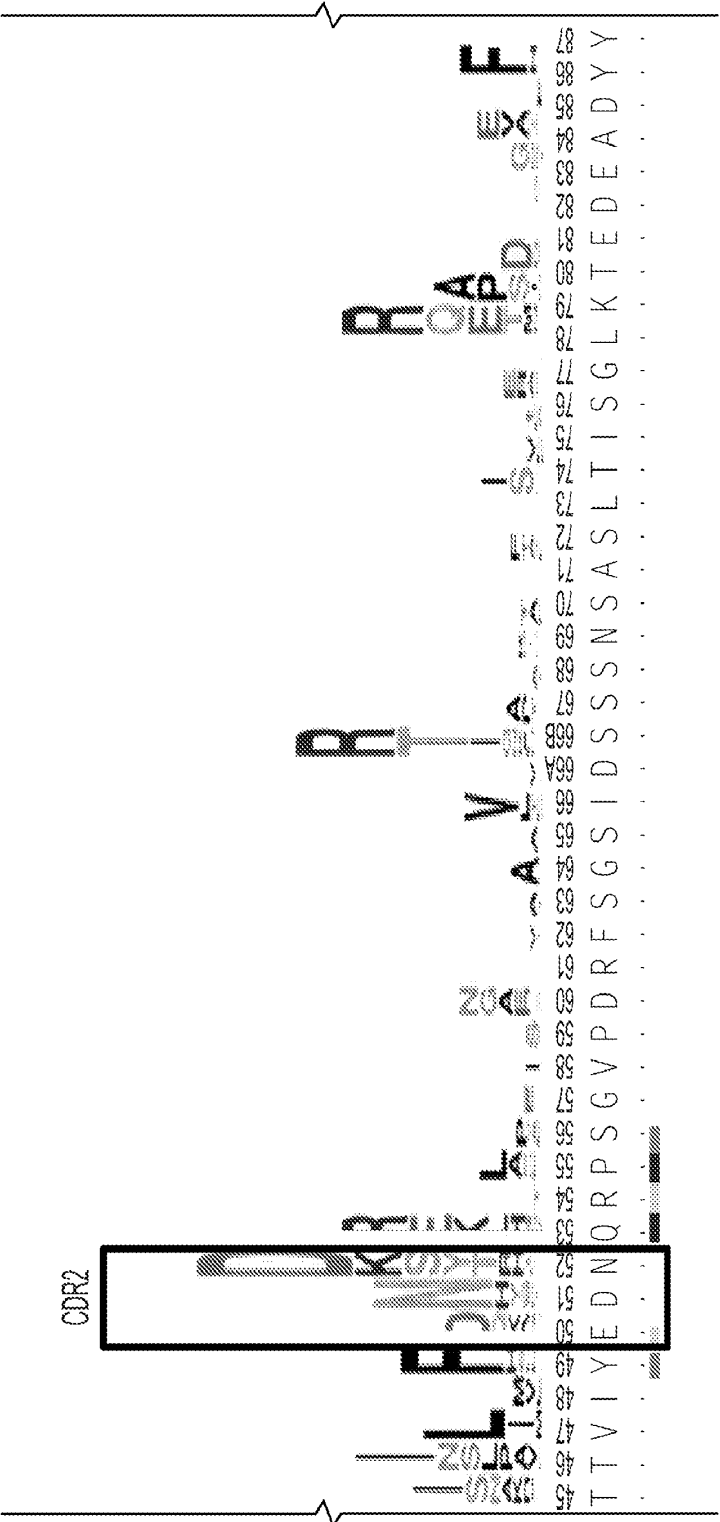
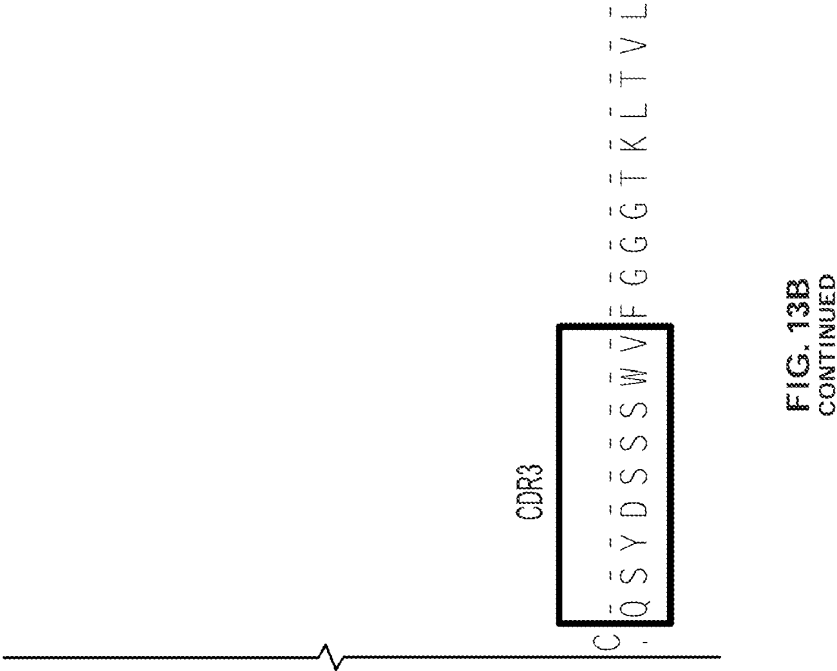


FIG. 13B
CONTINUED

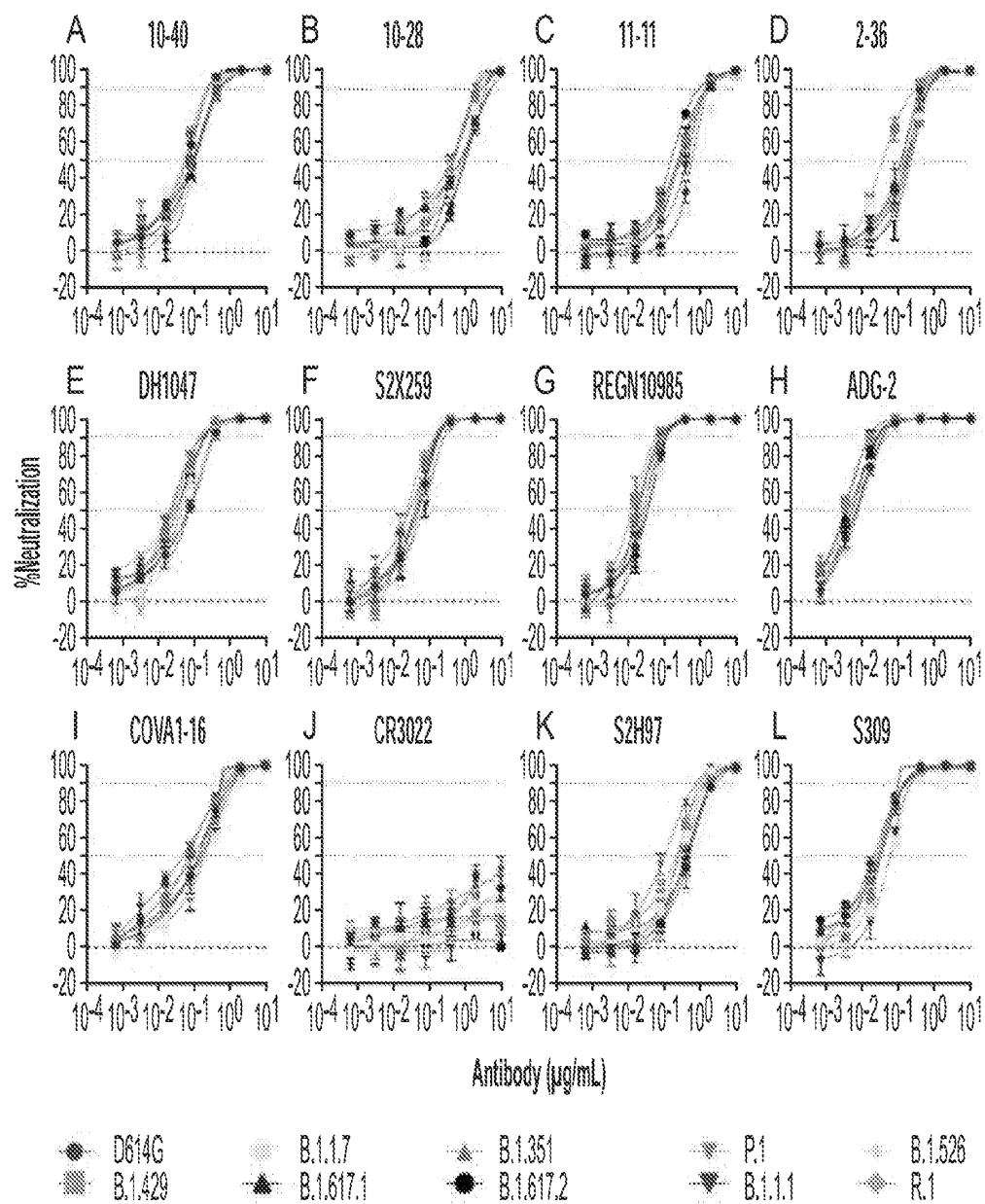


C

Region	Signature motifs	Compatible genes	Critical
CDRH1	GG[IV]SS[NR][FY] GYTFTSY	IGHV4-39, IGHV4-61, IGHV4-31, IGHV4-30-2/4 IGHV1-46, IGHV1-2 IGHD3-22*01	No No Yes
CDRH3 Light Chain	ARx(4-5)YYDRSGYx(8-9) NA	IGLV6-57, IGKV3-20, IGKV1-33, IGKV1-9	No

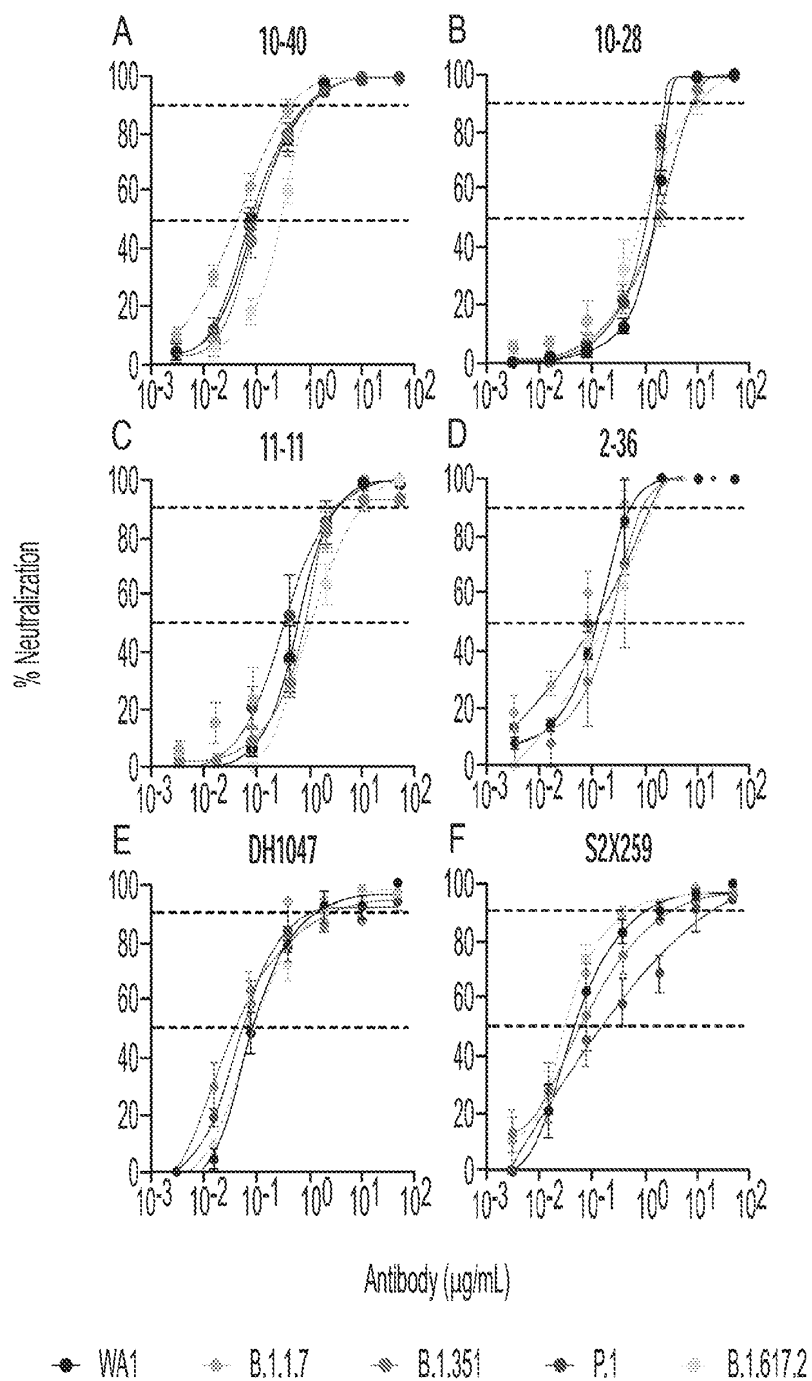
FIG. 13C

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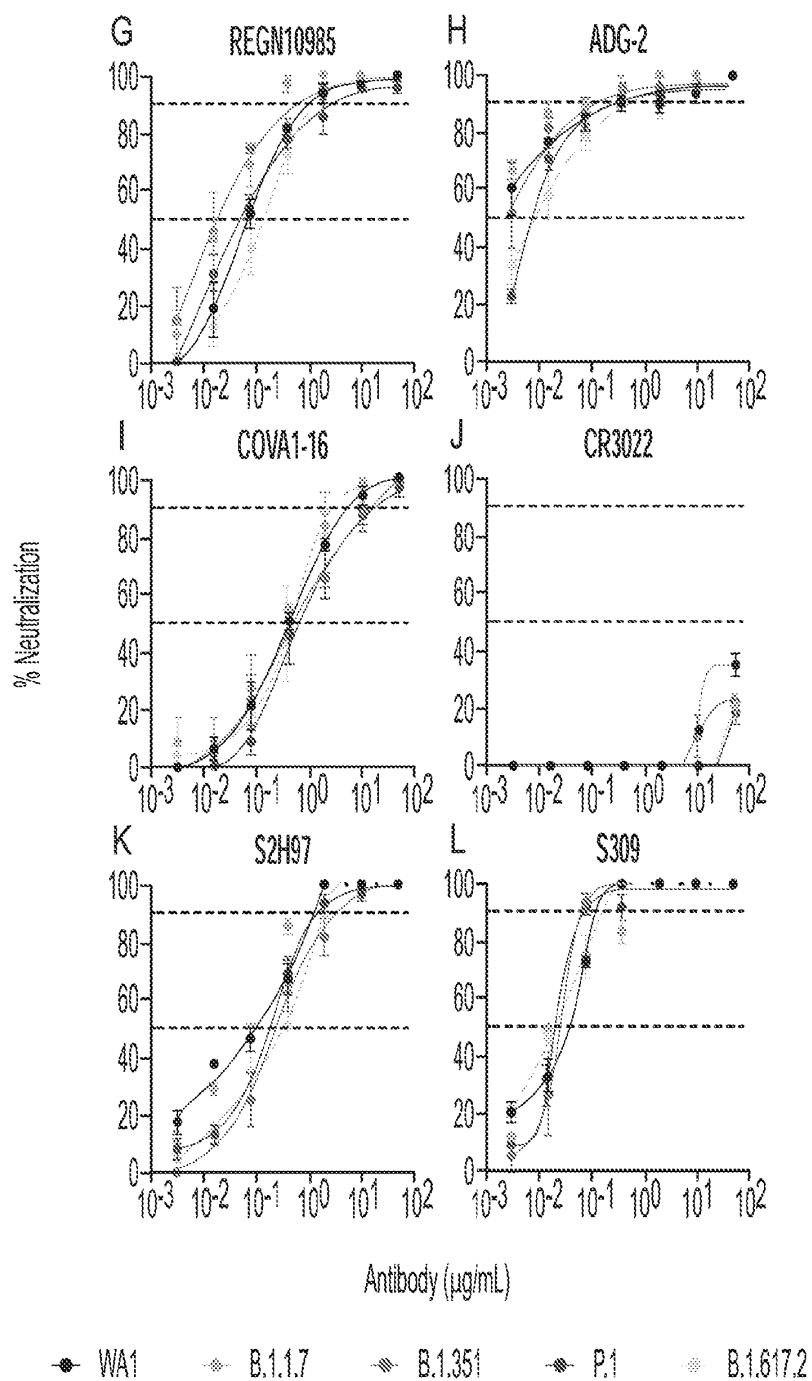
FIGS. 14A-L

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FIGS. 15A-F

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FIGS. 15G-L

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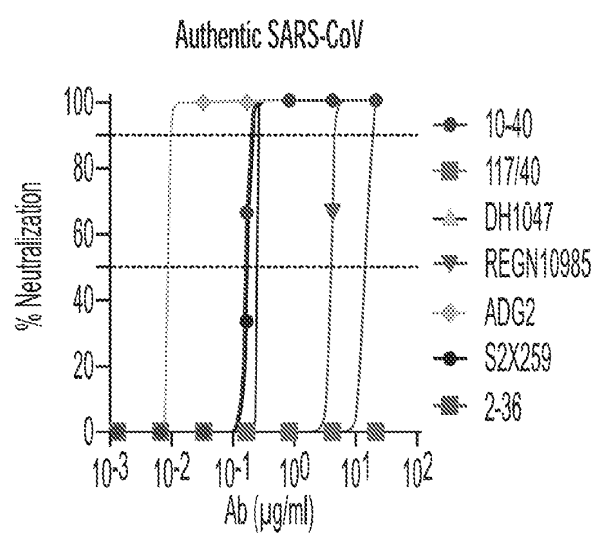
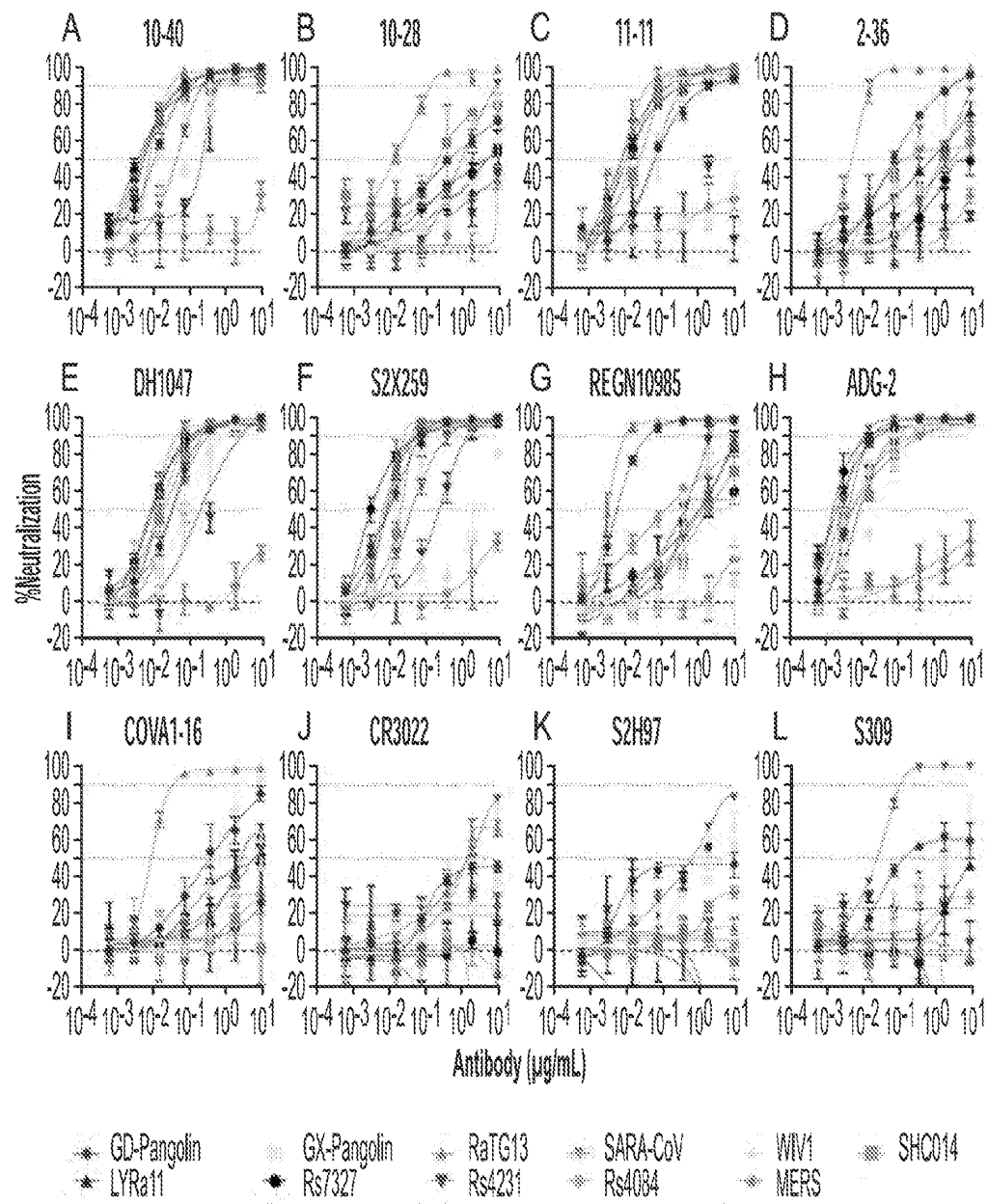
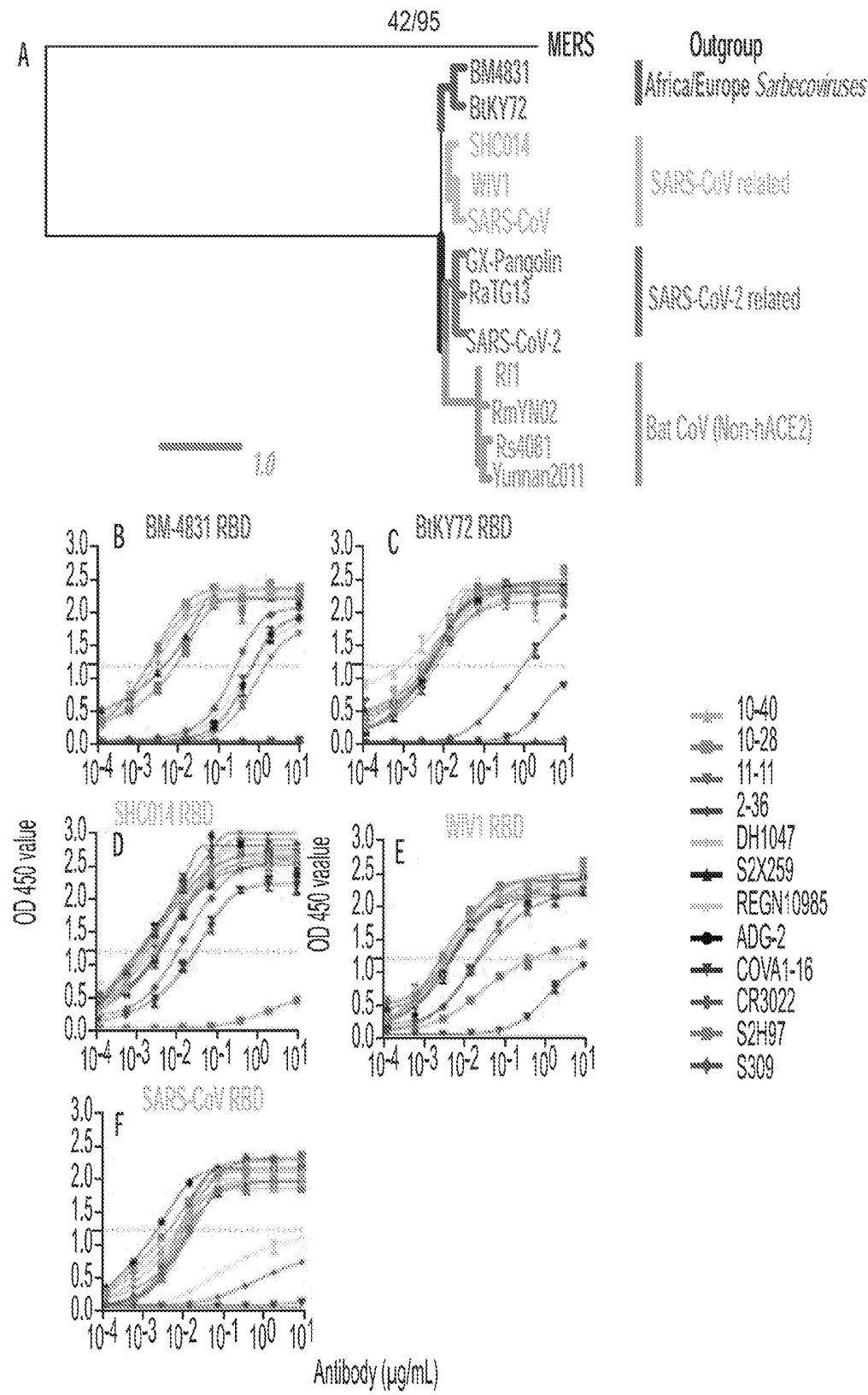


FIG. 15M



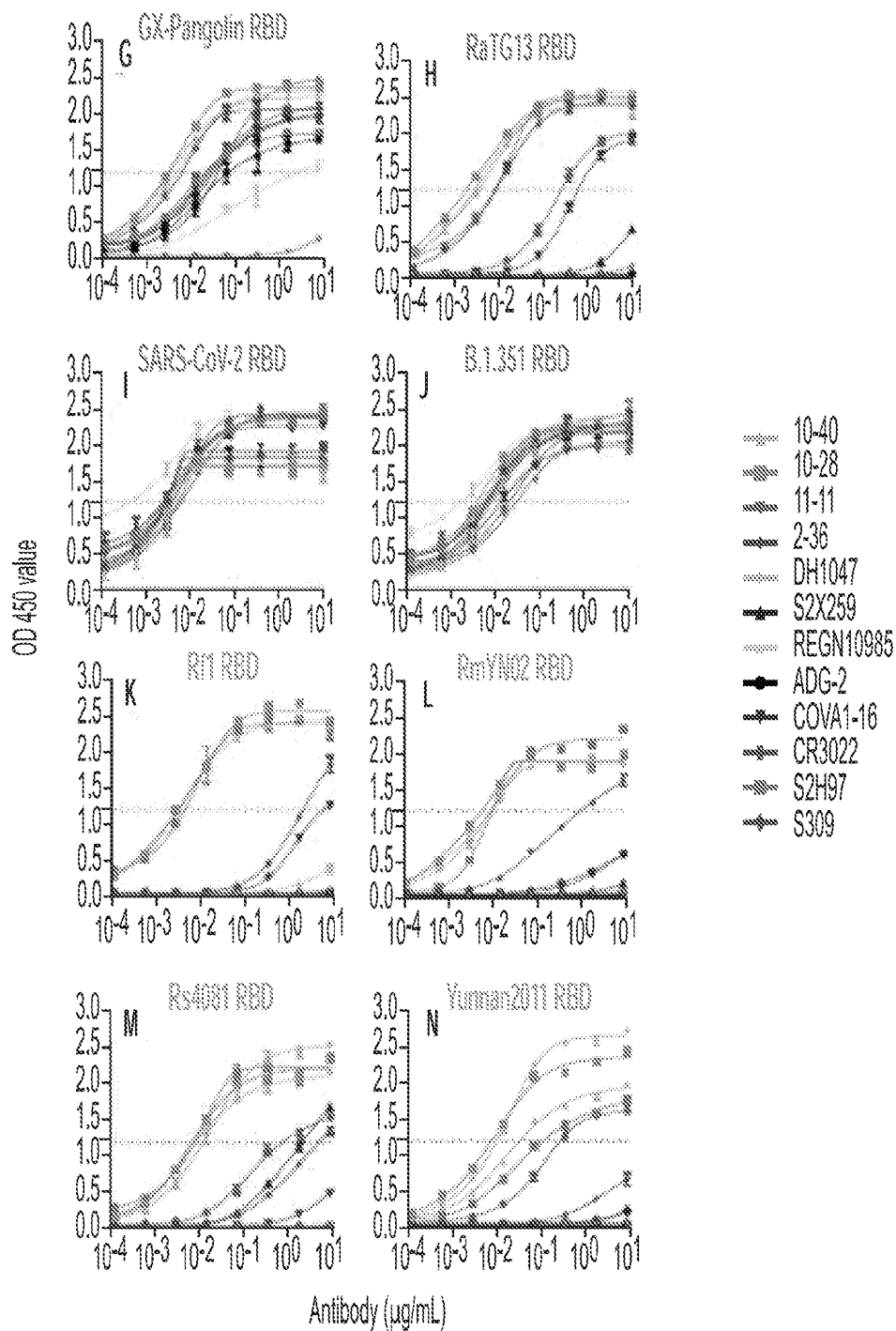
FIGS. 16A-L



FIGS. 17A-F

SUBSTITUTE SHEET (RULE 26)

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FIGS. 17G-N

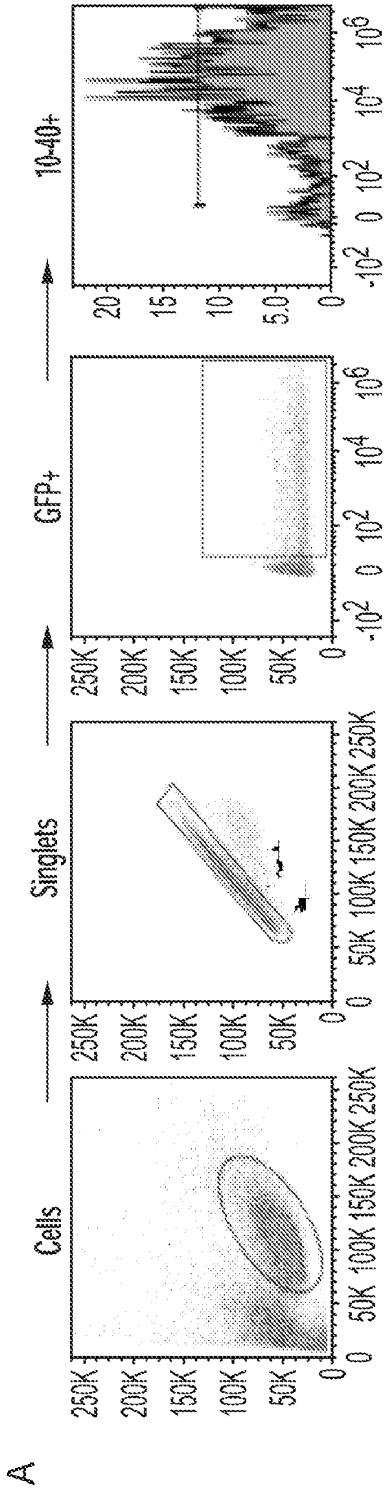


FIG. 18A

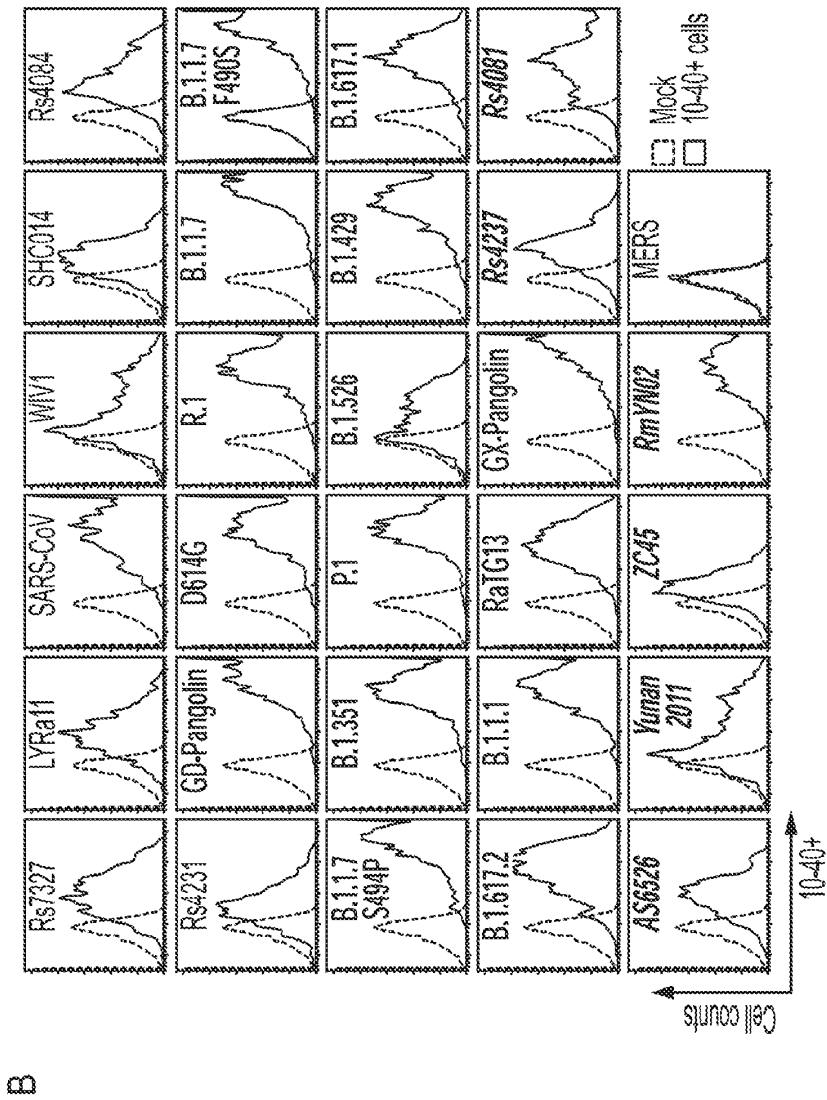
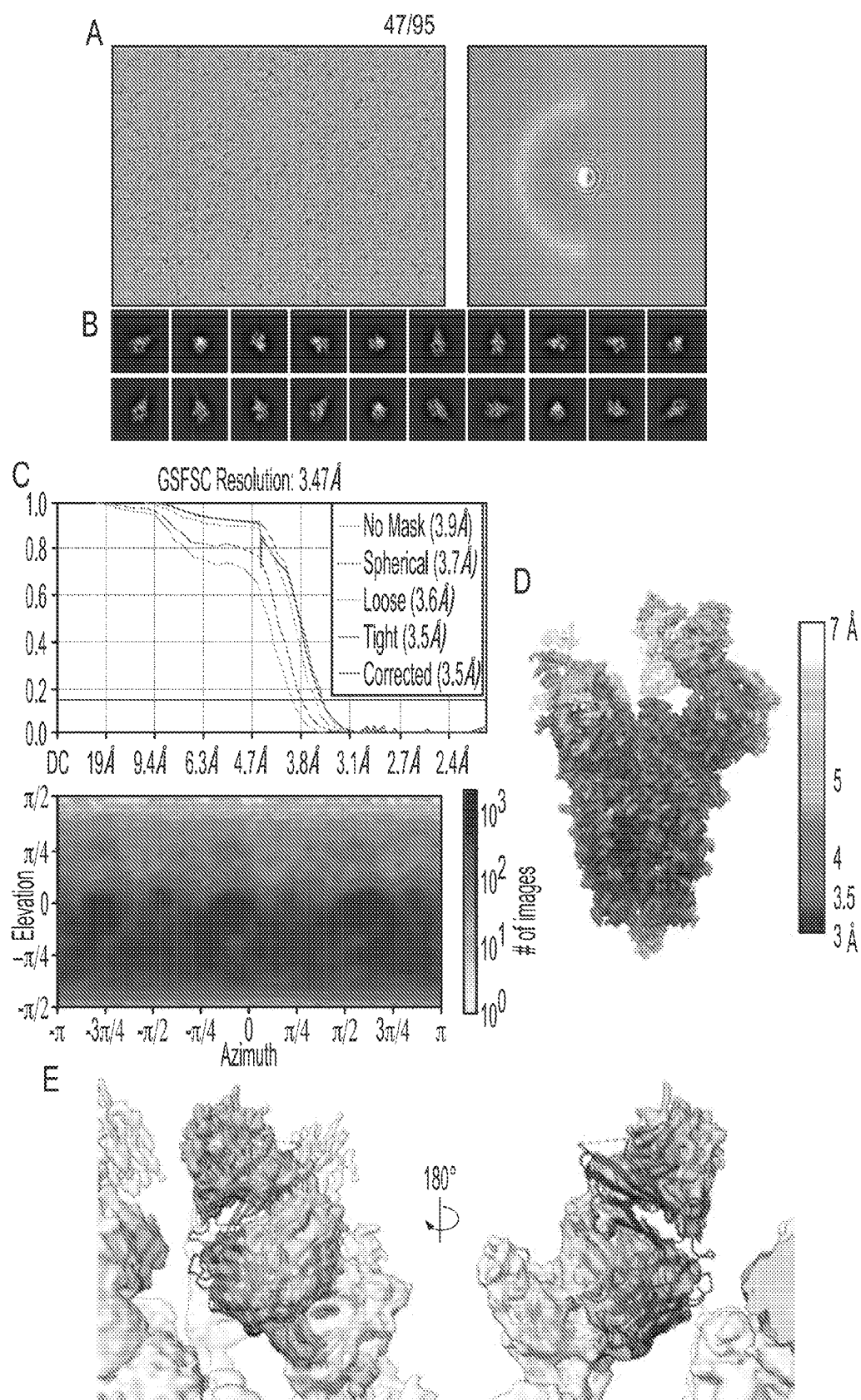


FIG. 18B

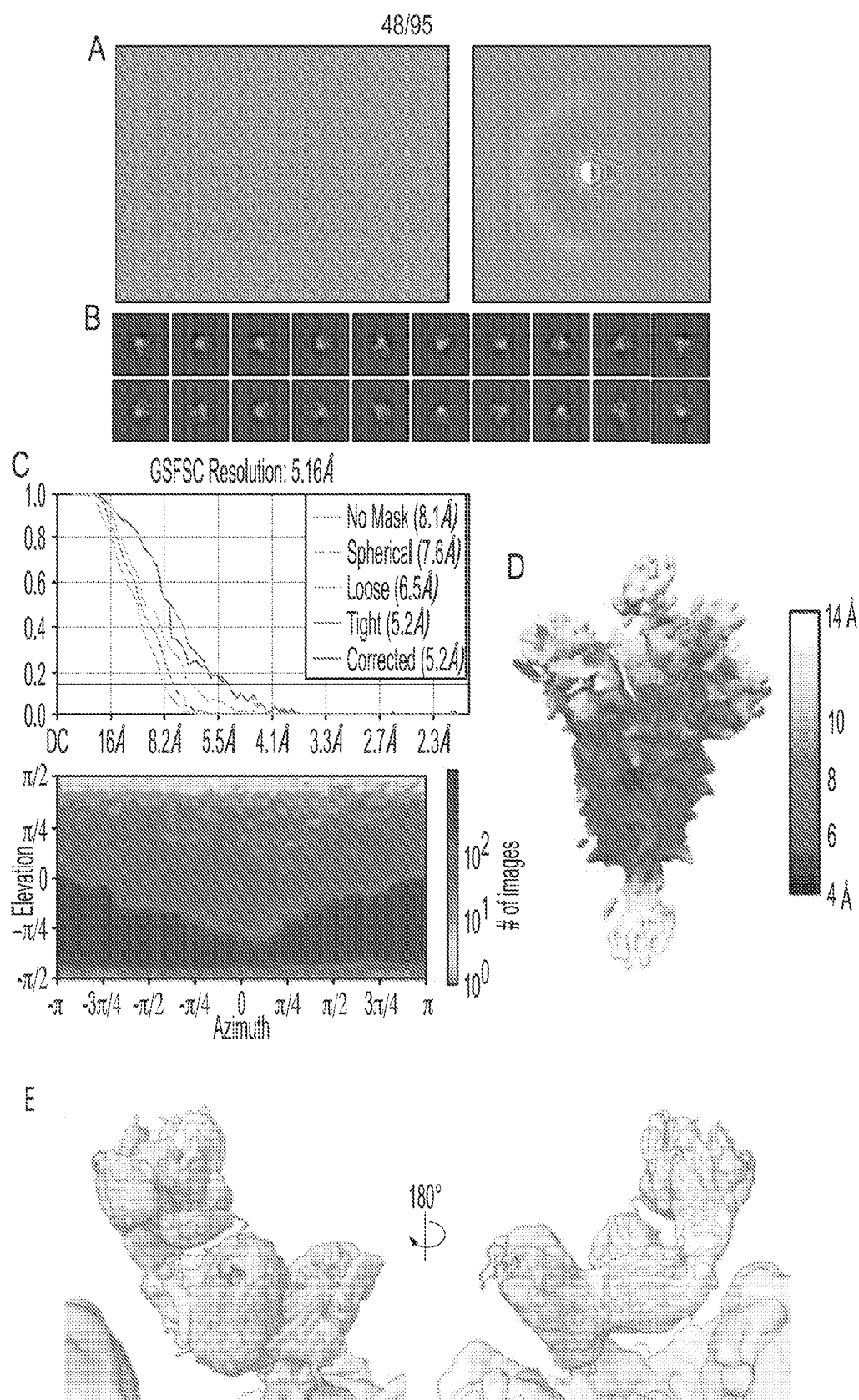
Cell surface staining MFI	10-40	10-28	11-11	2-36	DH1047	S2X259	REGN 10985	ADG-2	COVA 1-16	CR3022	S2H97	S309
GX-Pangolin	101976	56406	1518	91039	102043	5601	13551	5754	3138	664	6988	99701
RaTG13	9196	9209	5715	7972	10024	169	5296	208	238	52	63	101331
GD-Pangolin	91625	81502	85609	81271	87609	1856	84923	2810	558	2853	1989	114632
RmYN02	13124	14431	86	8349	11765	144	34	401	45	46	37	45
ZC45	244	176	71	108	233	31	47	31	32	30	31	221
Yunnan2011	1480	1498	830	1033	1518	34	630	46	34	31	47	8251
As6526	1633	1695	39	488	1786	41	33	38	31	29	32	105
Rs4237	1114	1131	93	415	1108	38	40	39	34	33	36	90
Rs4081	10305	11806	99	4113	11534	145	40	225	31	33	32	91

FIG. 19



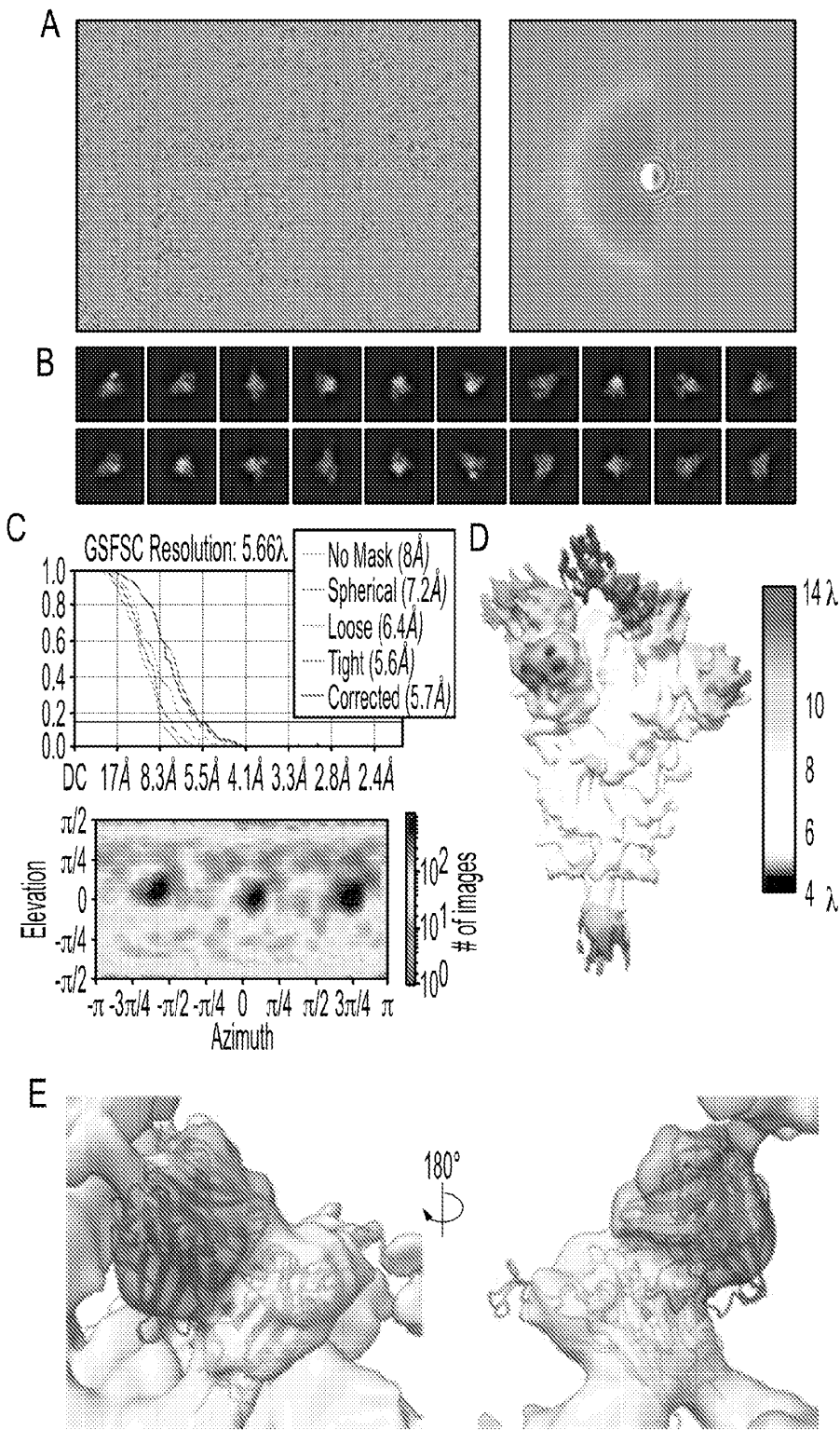
FIGS. 20A-E

SUBSTITUTE SHEET (RULE 26)



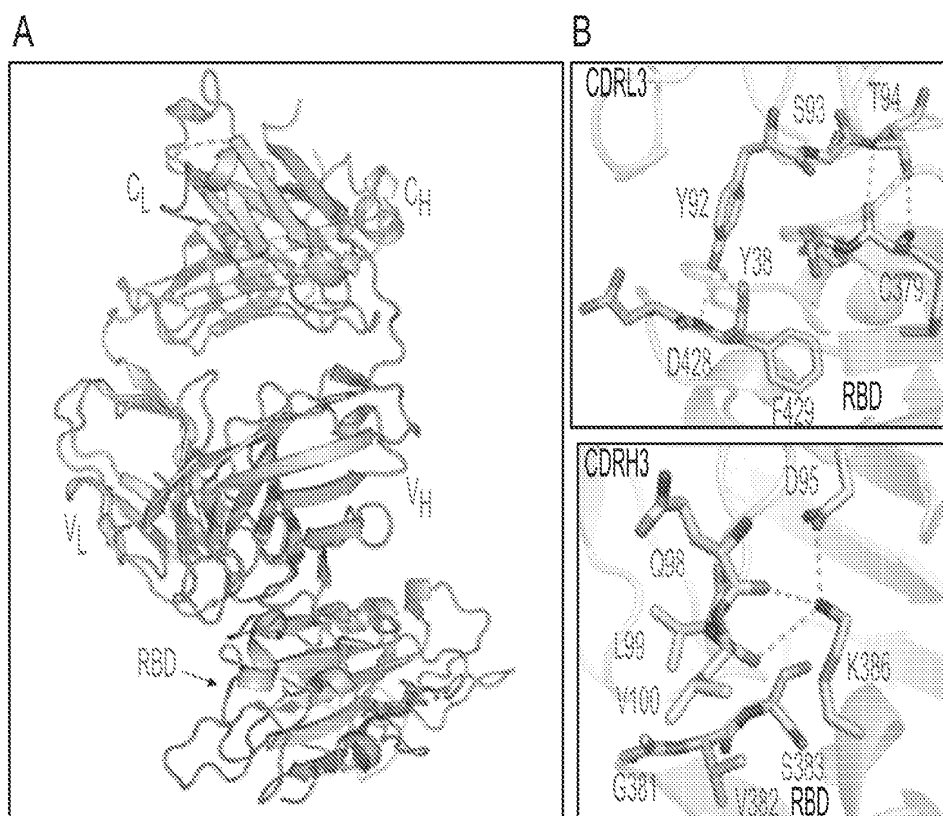
FIGS. 21A-E

SUBSTITUTE SHEET (RULE 26)



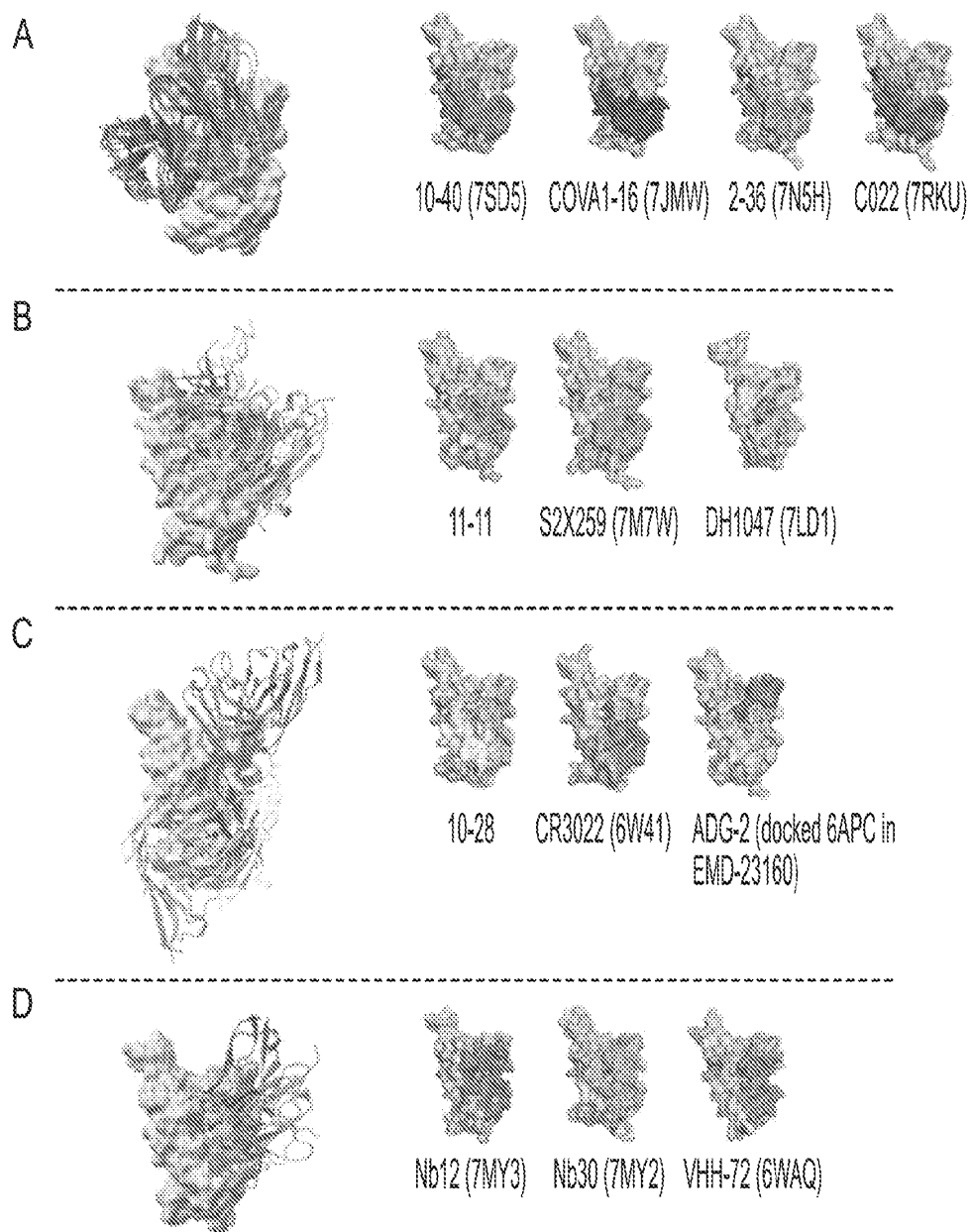
FIGS. 22A-E

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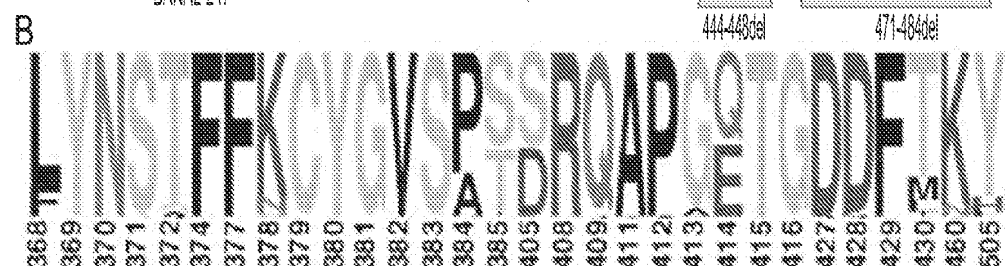
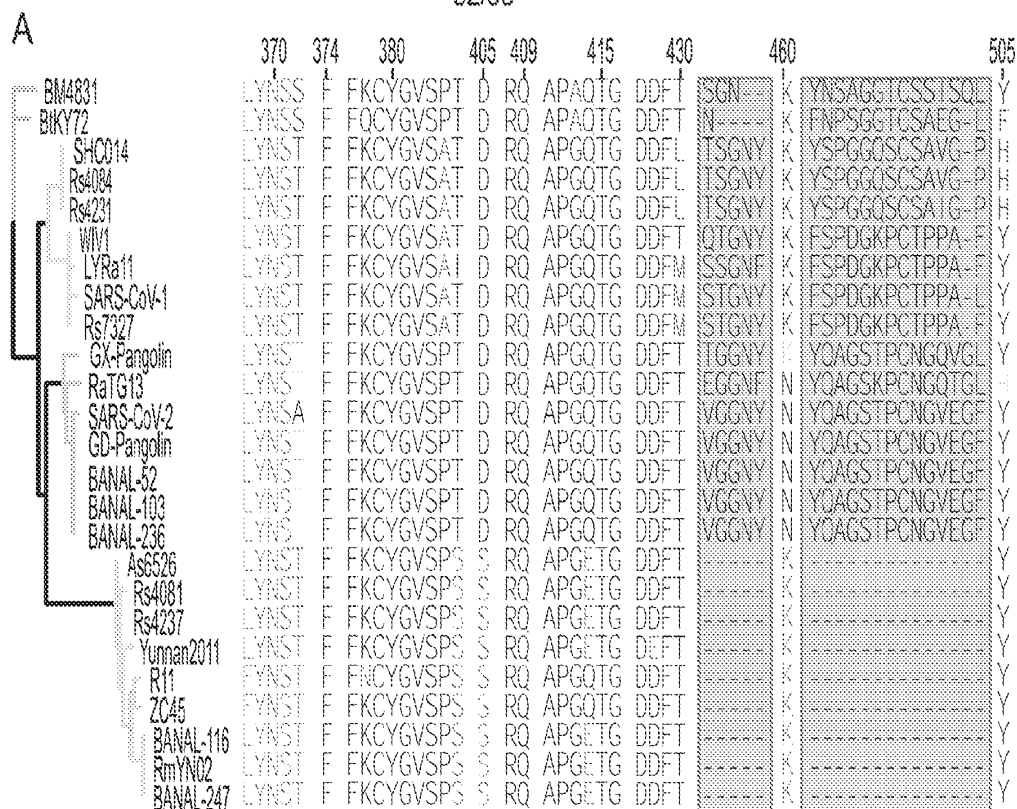
FIGS. 23A-B

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FIGS. 24A-D

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FIGS. 25A-C

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Region	Signature motifs	Compatible genes	Critical
CDRH1	GGS[IV]SSS[NR][FY]Y	IGHV4-39, IGHV4-61, IGHV4-31, IGHV4-30-2/4	No
	GYTFTSY	IGHV1-46, IGHV1-2	No
CDRH3	ARx{4-5}YYDRSGYx{8-9}	IGHD3-22*01	Yes
Light Chain	NA	IGLV6-57, IGKV3-20, IGKV1-33, IGKV1-9	No

FIG. 26

	SARS-CoV-2 B.1.351 S2P +10-40 Fab	SARS-CoV-2 B.1.351 S2P +10-28 Fab	SARS-CoV-2 B.1.351 S2P +11-11 Fab
EMDB ID	EMD-25146	EMD-25166	EMD-25167
Data Collection			
Microscope	FEI Titan Krios	FEI Titan Krios	FEI Titan Krios
Voltage (keV)	300	300	300
Magnification	81,000	81,000	81,000
Defocus Range (μm)	-0.8/-2.0	-0.8/-2.0	-0.8/-2.0
Camera	Gatan K3 BioQuantum	Gatan K3 BioQuantum	Gatan K3 BioQuantum
Pixel Size (Å/pix)	1.07	1.07	1.07
Recording Mode	counting	counting	counting
Total Dose (e-/Å ²)	42	42	42
Dose Rate (e-/pixel/s)	20	20	20
Exposure Time(s)	2.4	2.4	2.4
Frame Time(ms)	50	50	50
Software	SerialEM	SerialEM	SerialEM
Data Processing			
Software	cryoSPARC v3.2.0	cryoSPARC v3.2.0	cryoSPARC v3.2.0
Micrographs used	9,881	2,542	2,565
Number of Particles	799,933	251,871	281,235
Particles/Micrograph	81.0	99.1	109.6
Symmetry	C1	C1	C1
Box Size (pix)	440	384	384
Global Map FSC _{Q143} (Å)	3.5/3.6	5.2/6.5	5.6/6.4

FIG. 27

SUBSTITUTE SHEET (RULE 26)

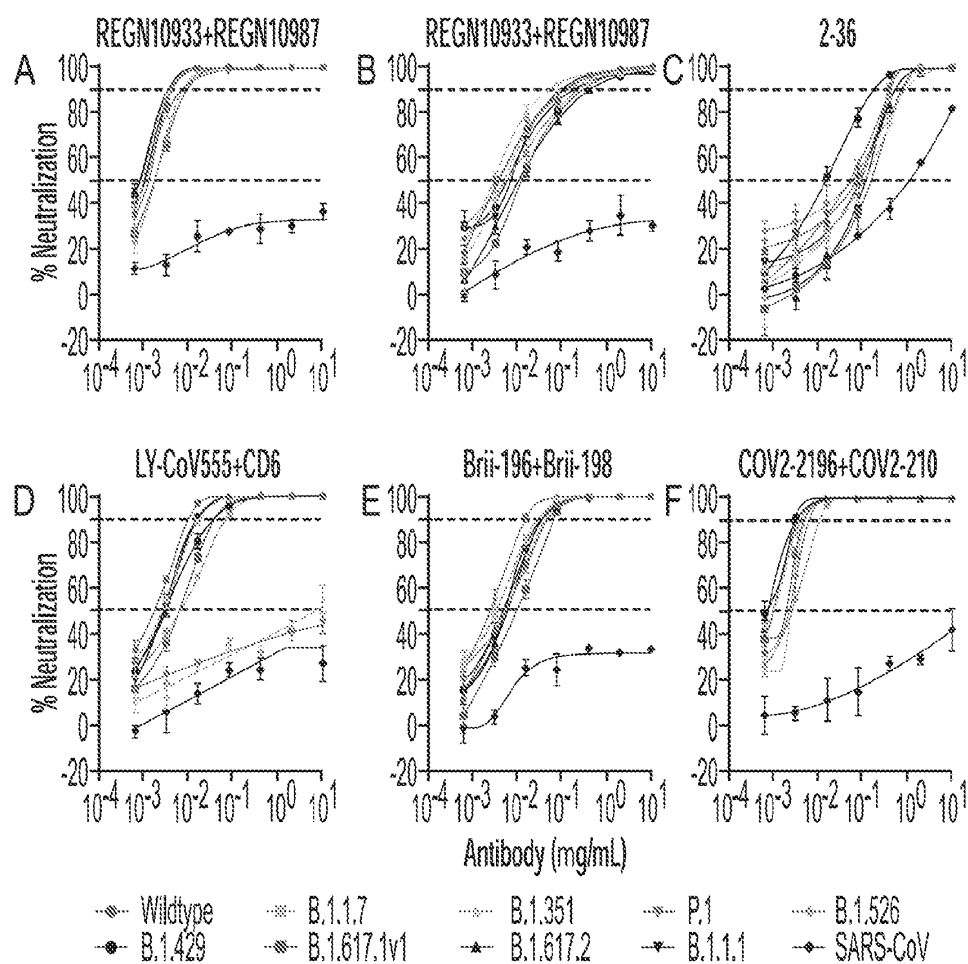
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	SARS-CoV-2 RBD in complex with 10-40 Fab	SARS-CoV-2 RBD in complex with 10-28 Fab
PDB ID	7SD5	XXXX
Data Collection		
Space group	P2 ₁ 2 ₁ 2 ₁	C222 ₁
Unit cell dimensions		
<i>a,b,c</i> , (Å)	75.7, 79.8, 118.8	123.7, 226.6, 186.2
α,β,γ , (°)	90.0, 100.0, 90.0	90.0, 90.0, 90.0
Resolution range (Å)	47.67 - 1.50 (1.7-1.5)*	108.6 - 3.0 (3.12-3.00)*
Total reflections	221728 (17750)	86848 (8516)
Unique reflections	111815 (9153)	43474 (4062)
Completeness (%)	99.20 (98.96)	97.74 (94.91)
Redundancy	2.0 (1.9)	2.0 (2.0)
<i>I</i> / σ (<i>I</i>)	17.99 (0.89)	6.22 (1.29)
Rmerge	0.016 (0.83)	0.085 (0.67)
CC1/2	1 (0.35)	0.690 (0.40)
Refinement		
Resolution range (Å)	47.67 - 1.50	88.03 - 3.20
Number of complexes per Asymmetric unit	1	3
Rwork/Rfree	0.17/0.19	0.23/0.28
Number of atoms		
Protein	4905	14340
Ligands	28	109
Water	627	0
B-factors (Å ²)		
Protein	30.7	81.4
Ligands	74.3	81.1
Water	38.3	
R.m.s. deviations		
Bond lengths (Å)	0.013	0.014
Bond angles (°)	1.33	1.97
Ramachandran statistics		
Favored (%)	97.60	96.24
Allowed (%)	2.40	3.76
Outliers (%)	0	0

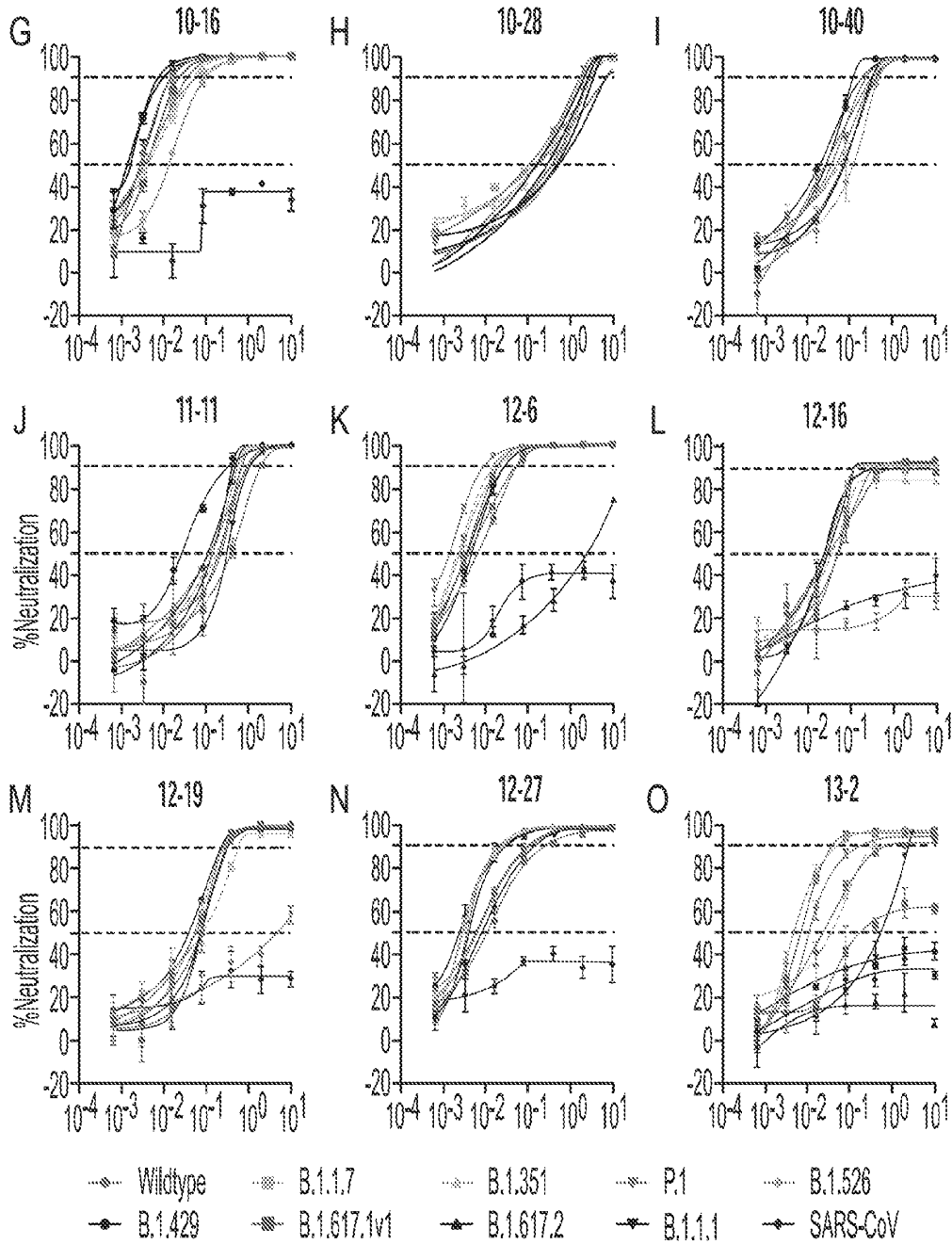
Statistics for the highest-resolution shell are shown in the parentheses.

FIG. 28

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FIGS. 29A-F



FIGS. 29G-O

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IC50(μg/ml)	D614G	B.1.1.7	B.1.351	P.1	B.1.526	B.1.429	B.1.617.1	B.1.617.2	C.37	SARS-CoV
REGN10933+REGN10987	0.001	0.001	0.001	0.001	0.002	0.001	0.002	0.001	0.001	>10
2-7	0.003	0.005	0.003	0.004	0.005	0.005	0.012	0.011	0.007	>10
2-36	0.07	0.034	0.106	0.05	0.055	0.015	0.149	0.117	0.091	1.106
LY-CoV555+CB6	0.002	0.003	7.024	>10	0.006	0.003	0.006	0.003	0.003	>10
Brii196+Brii198	0.005	0.003	0.004	0.003	0.006	0.005	0.01	0.006	0.005	>10
COV2-2196+COV2-2130	0.001	0.001	0.002	0.002	0.002	0.001	0.002	0.001	0.001	>10
10-16	0.003	0.004	0.004	0.003	0.003	0.001	0.004	0.003	0.002	>10
10-28	0.161	0.132	0.167	0.103	0.447	0.165	0.336	0.271	0.432	0.534
10-40	0.026	0.035	0.053	0.045	0.117	0.027	0.069	0.053	0.059	0.019
11-11	0.207	0.372	0.17	0.111	0.14	0.155	0.176	0.128	0.284	0.025
12-6	0.007	0.004	0.002	0.001	0.002	0.004	0.003	2.476	0.005	>10
12-16	0.051	0.051	0.039	>10	0.025	0.023	0.05	0.03	0.023	>10
12-19	0.059	0.05	0.063	4.658	0.056	0.04	0.074	0.077	0.07	>10
12-27	0.006	0.011	0.003	0.006	0.003	0.002	0.003	0.004	0.003	>10
13-2	0.022	0.172	0.036	0.011	0.005	>10	0.007	>10	0.539	>10

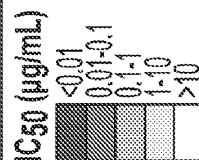
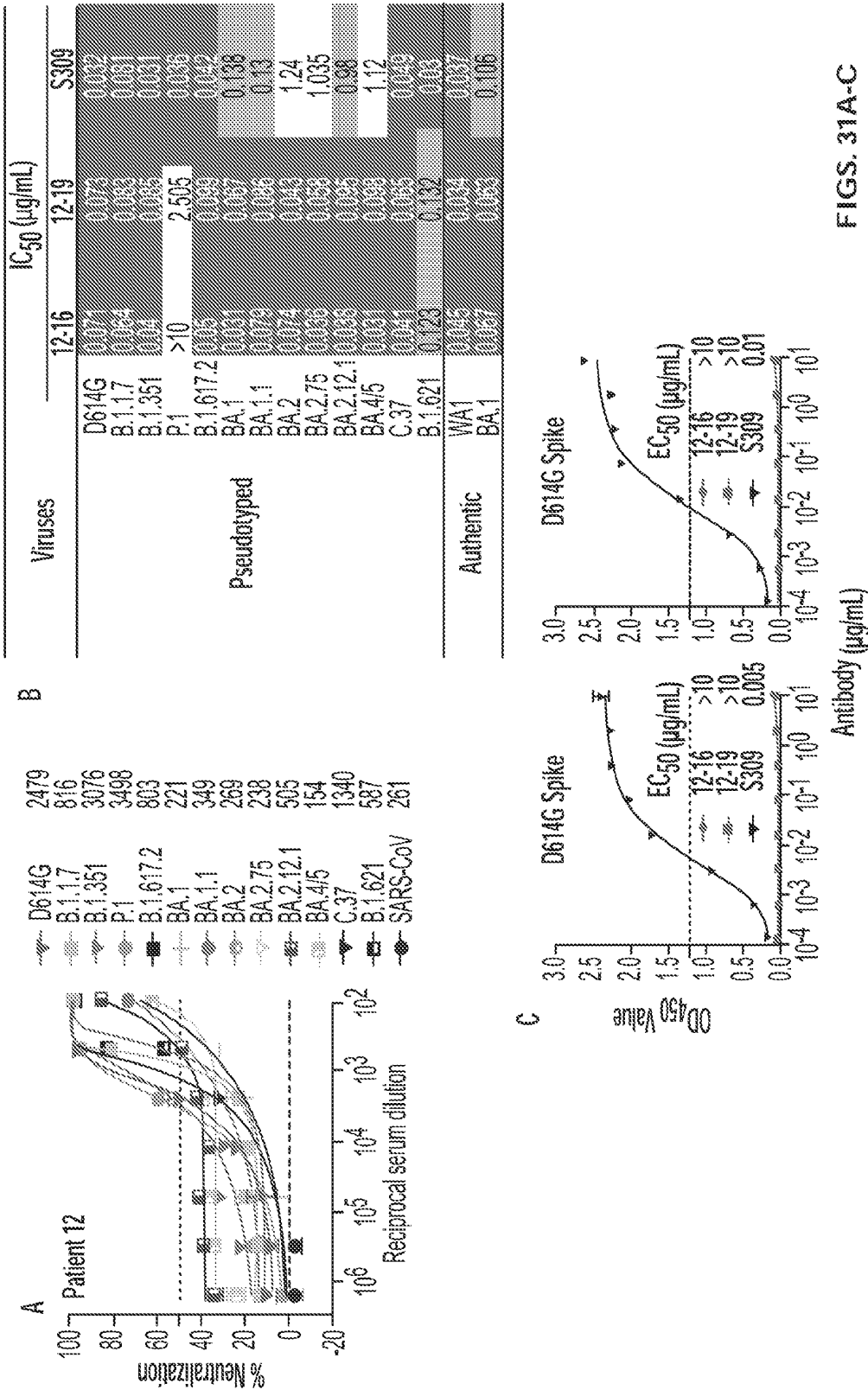
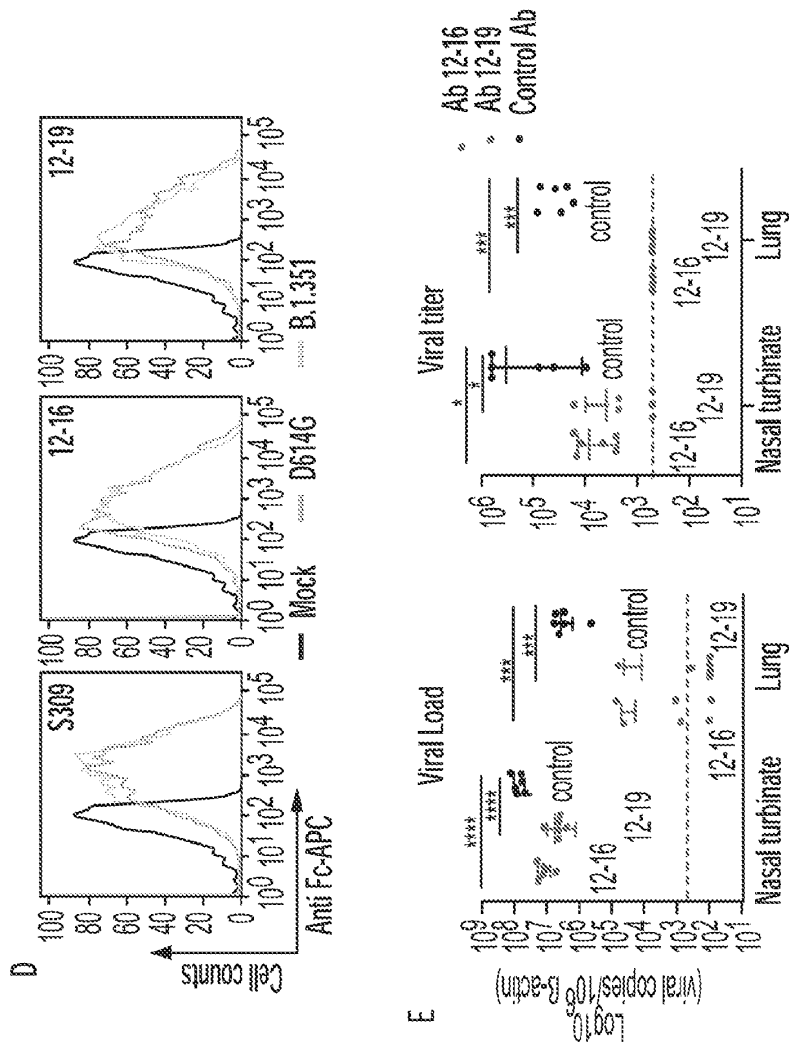


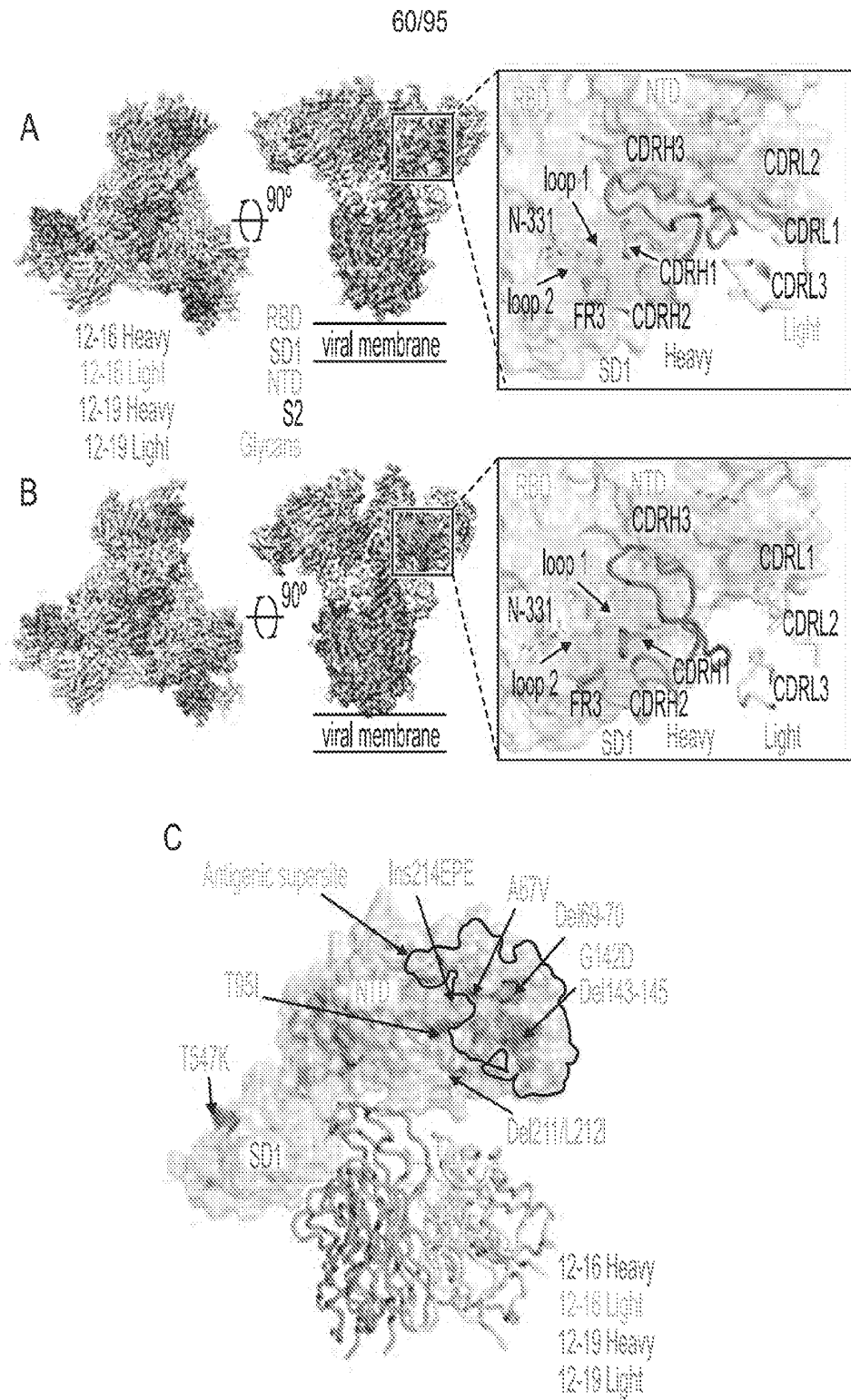
FIG. 30



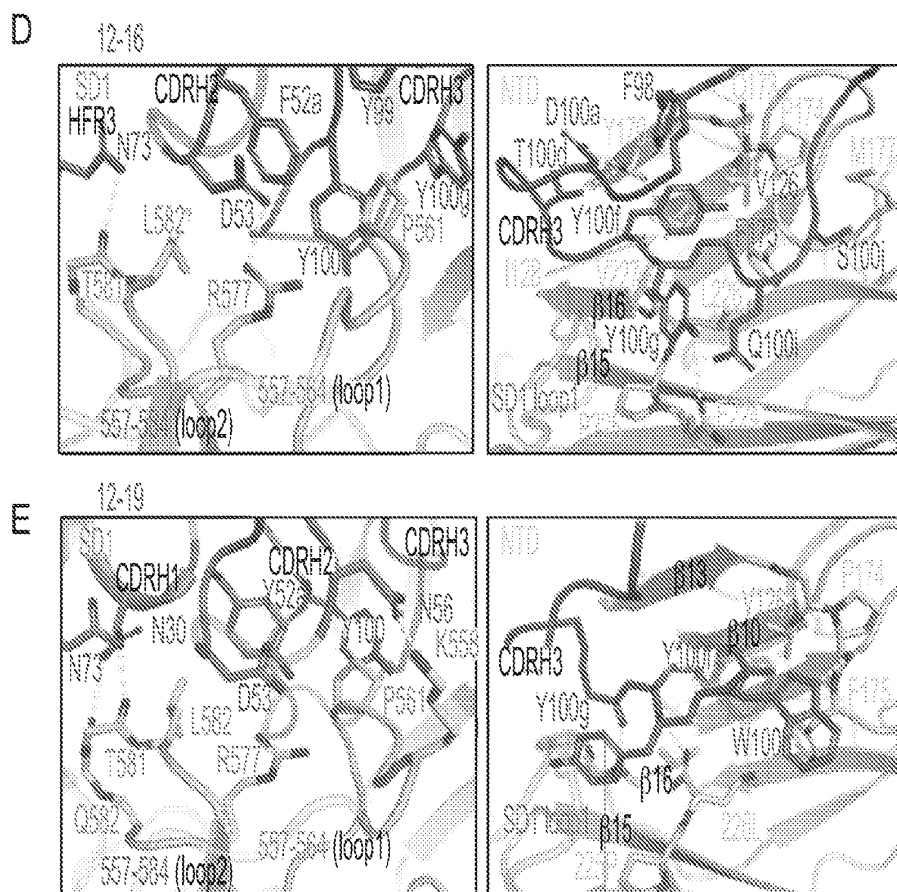
FIGS. 31A-C



FIGS. 31D-E

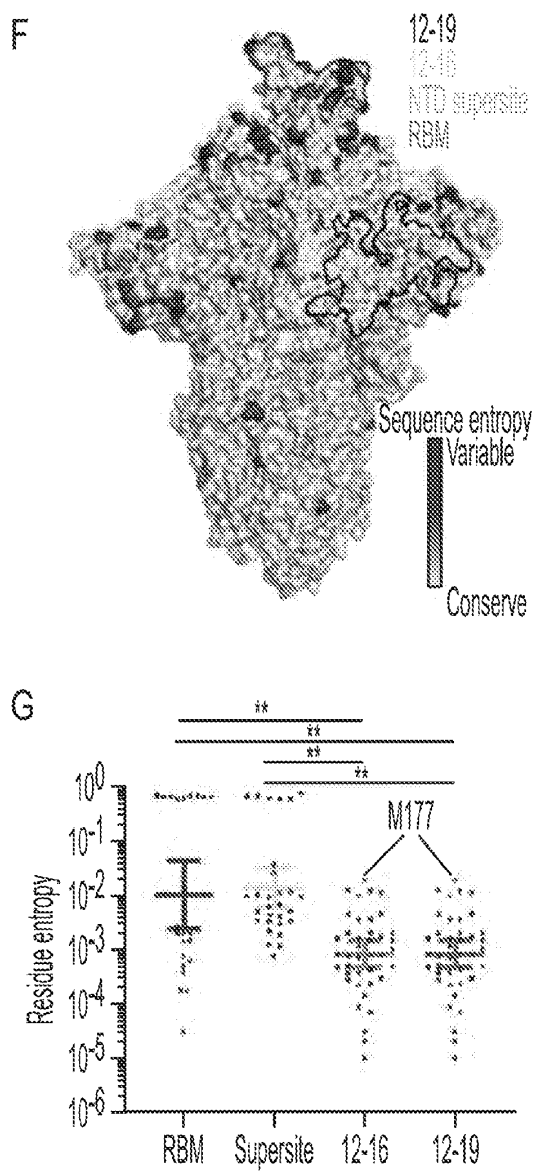


FIGS. 32A-C

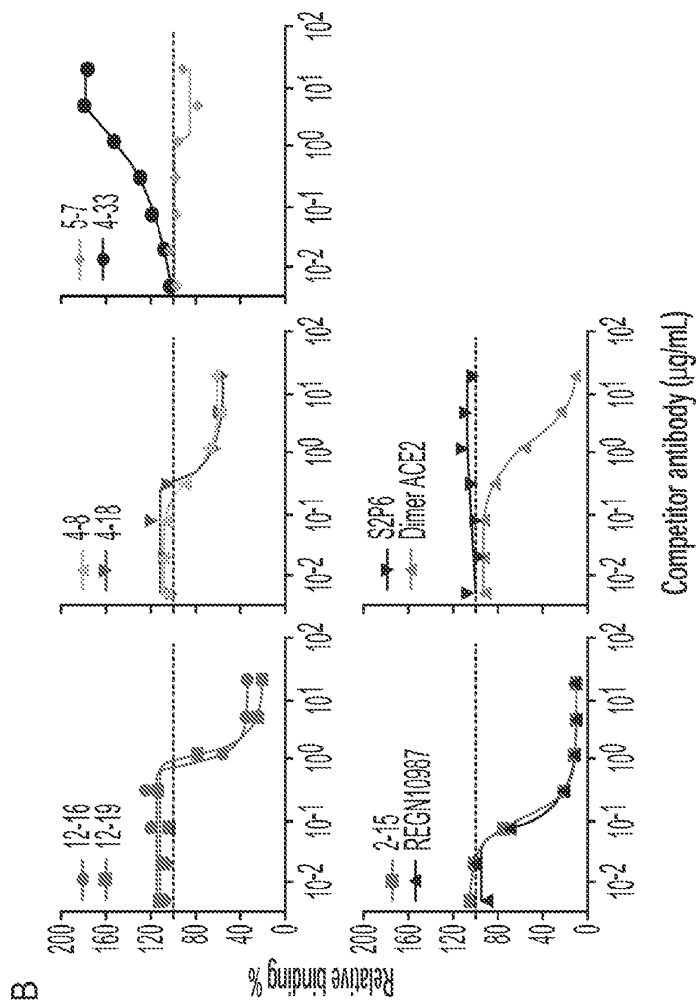


FIGS. 32D-E

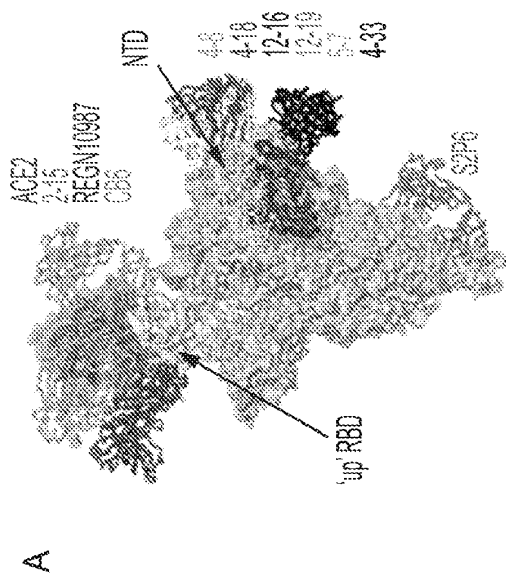
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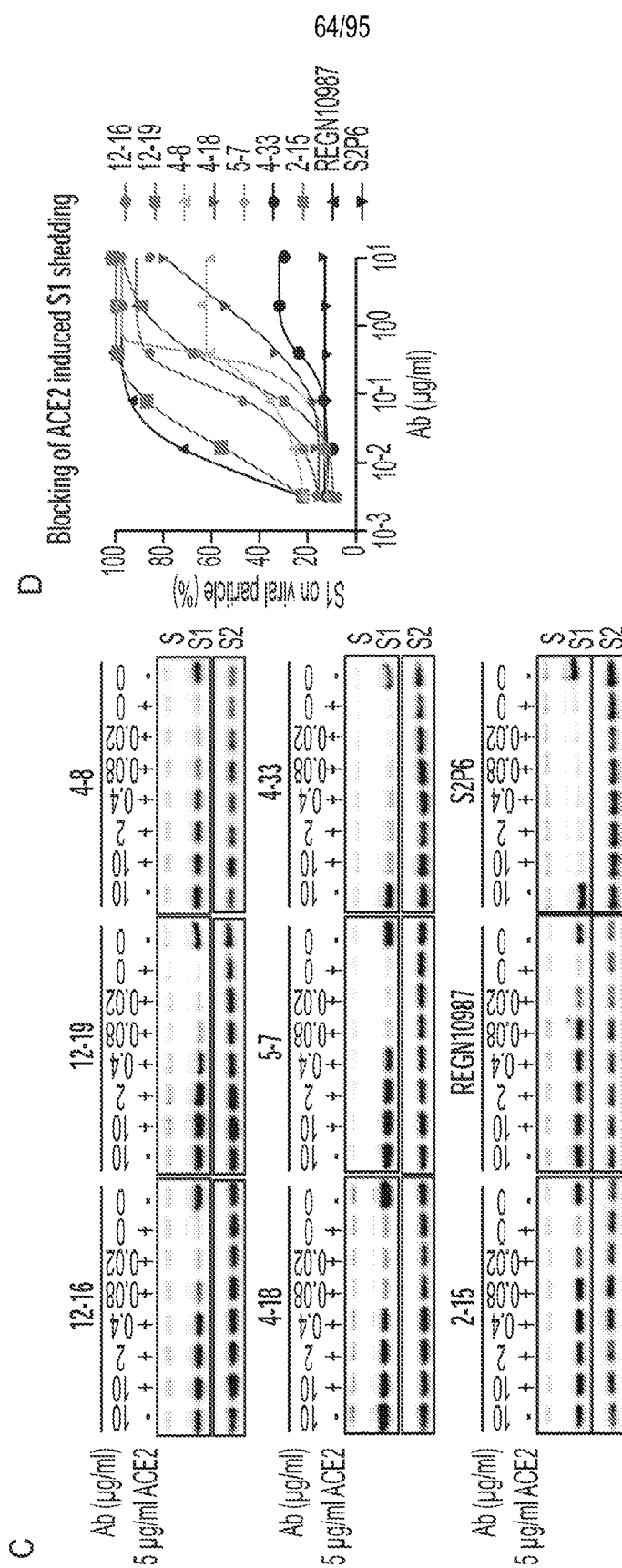


FIGS. 32F-G



FIGS. 33A-33B





3

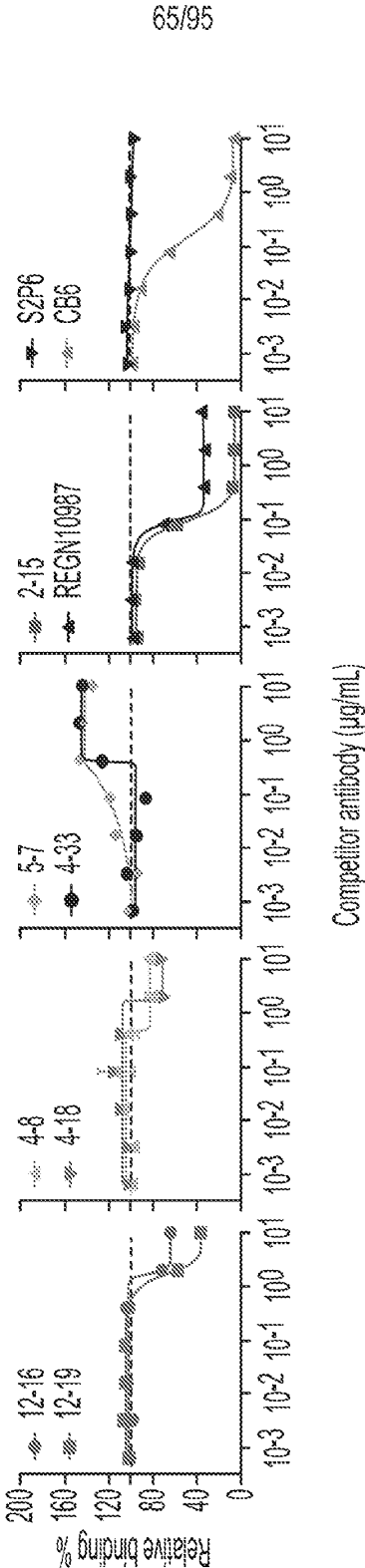


FIG. 33E

F

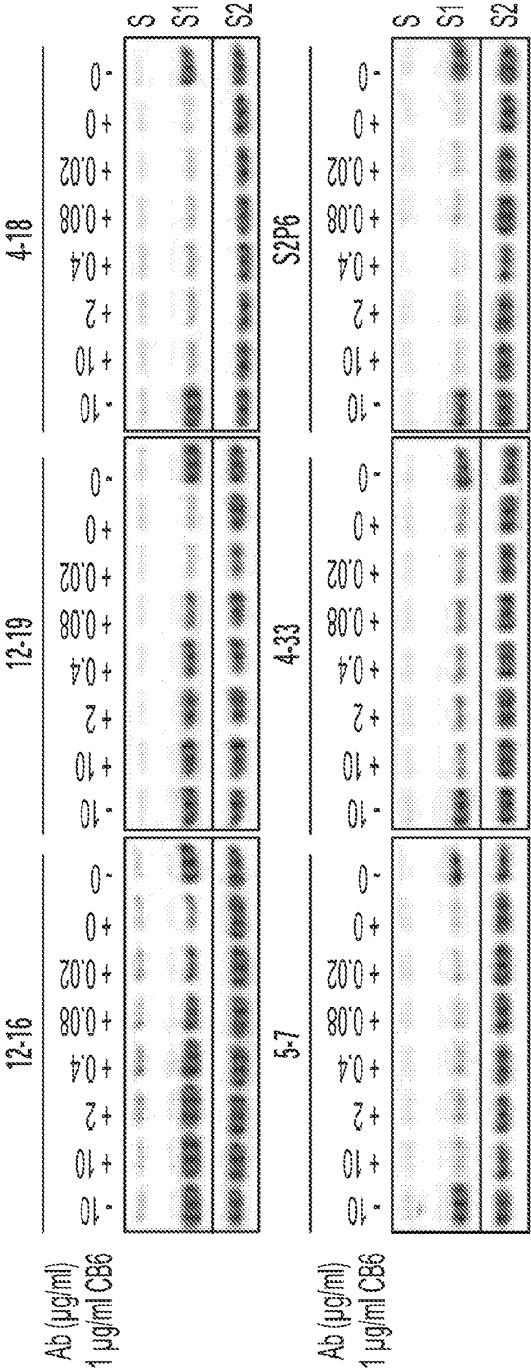


FIG. 33F

G

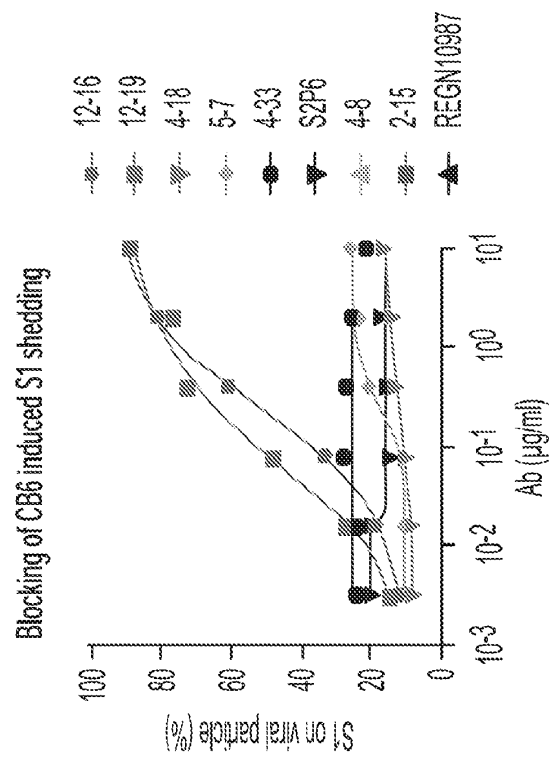
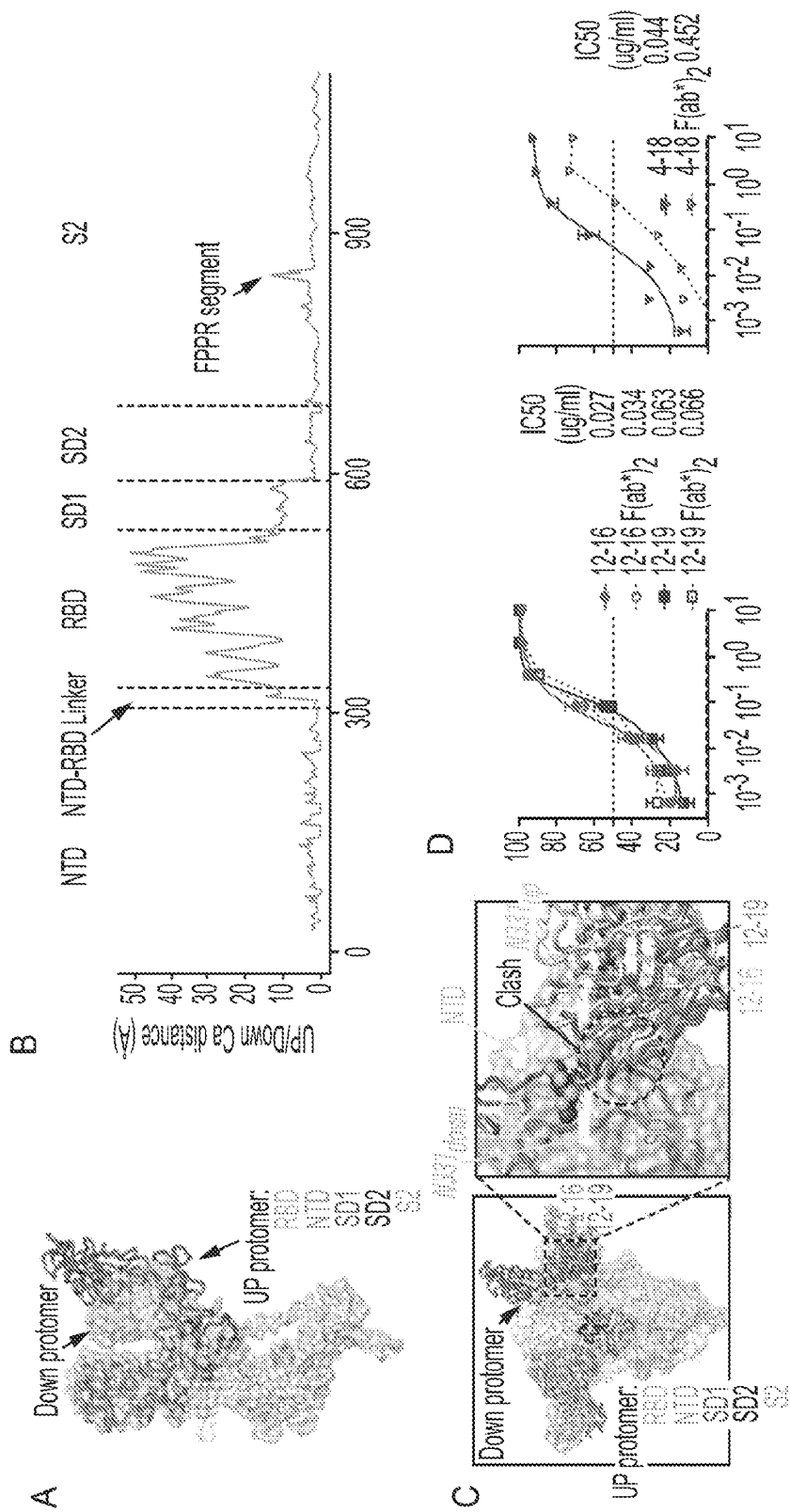


FIG. 33G



FIGS. 34A-D

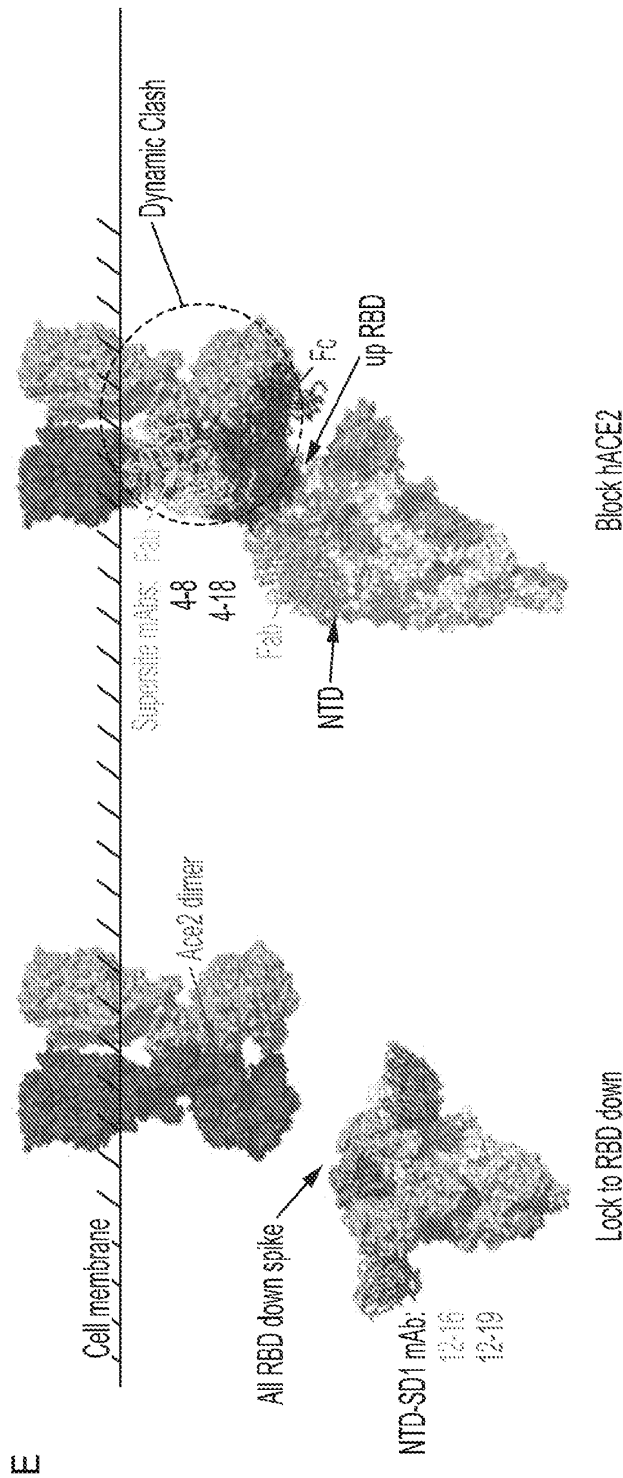


FIG. 34E

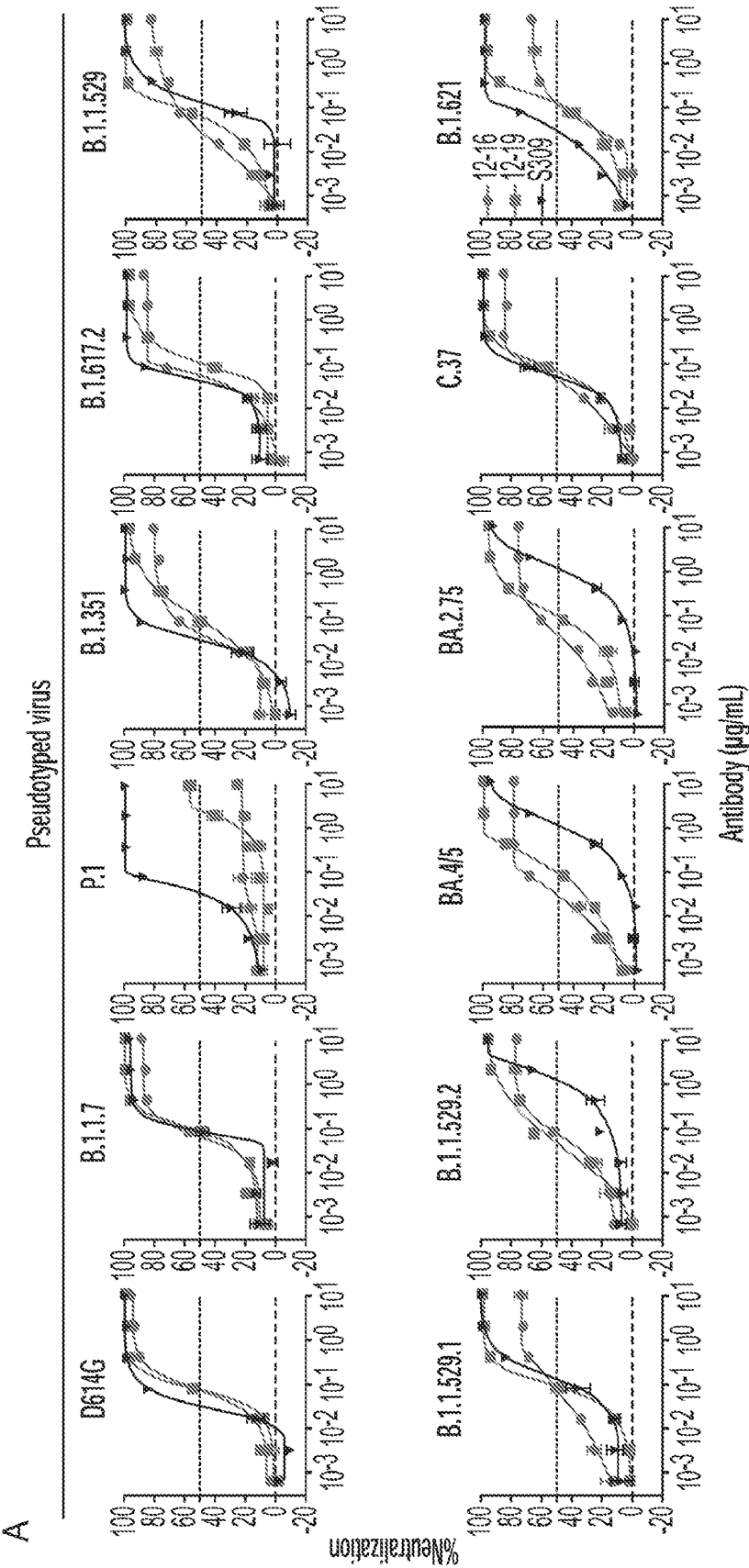


FIG. 35A

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B

Authentic virus

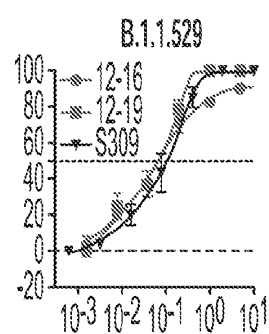
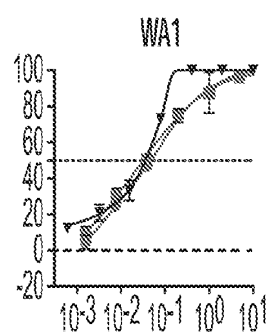


FIG. 35B

A

mAbs	HV	HD	HJ	Isotype	H_SHM	CDRH3_len	HCDR3	LV	LJ	L_SHM	CDRL3_len	LCDR3
12-16	IGHV3-30*18	IGHD3-9*01	IGHJ6*02	IGHG3*04	1.7%	25	AKDLSFYVDISTGYYPQSYNSGTDV	IGLV3-1*01	IGLJ1*01	1.4%	11	QGWDPRSTGYVY
12-19	IGHV3-33*01	IGHD3-9*01	IGHJ6*02	IGHG1*04	2.7%	26	ARDRTPYDILIGYYWPPRVDGMDV	IGKV2-29*02	IGKJ2*02	2.3%	9	MQSIQLPFT

FIG. 36A

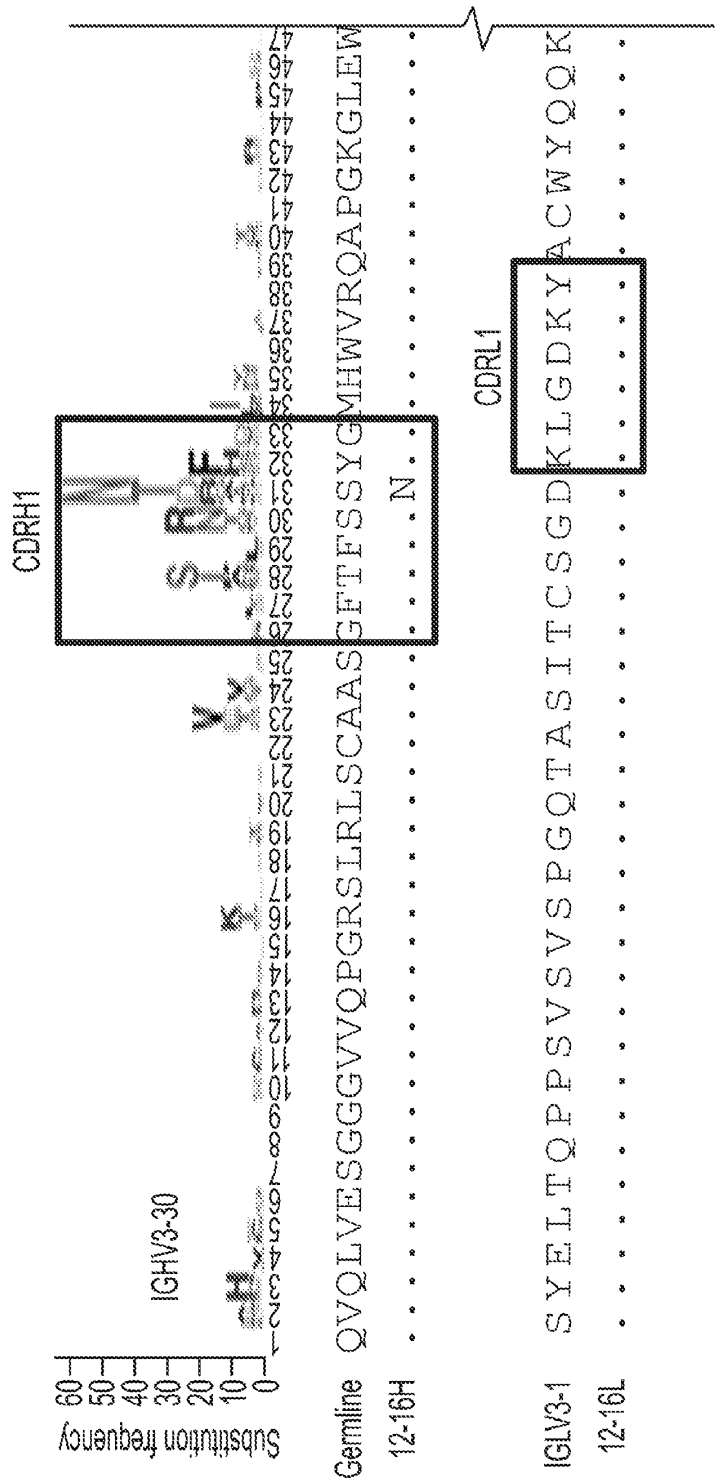


FIG. 36B

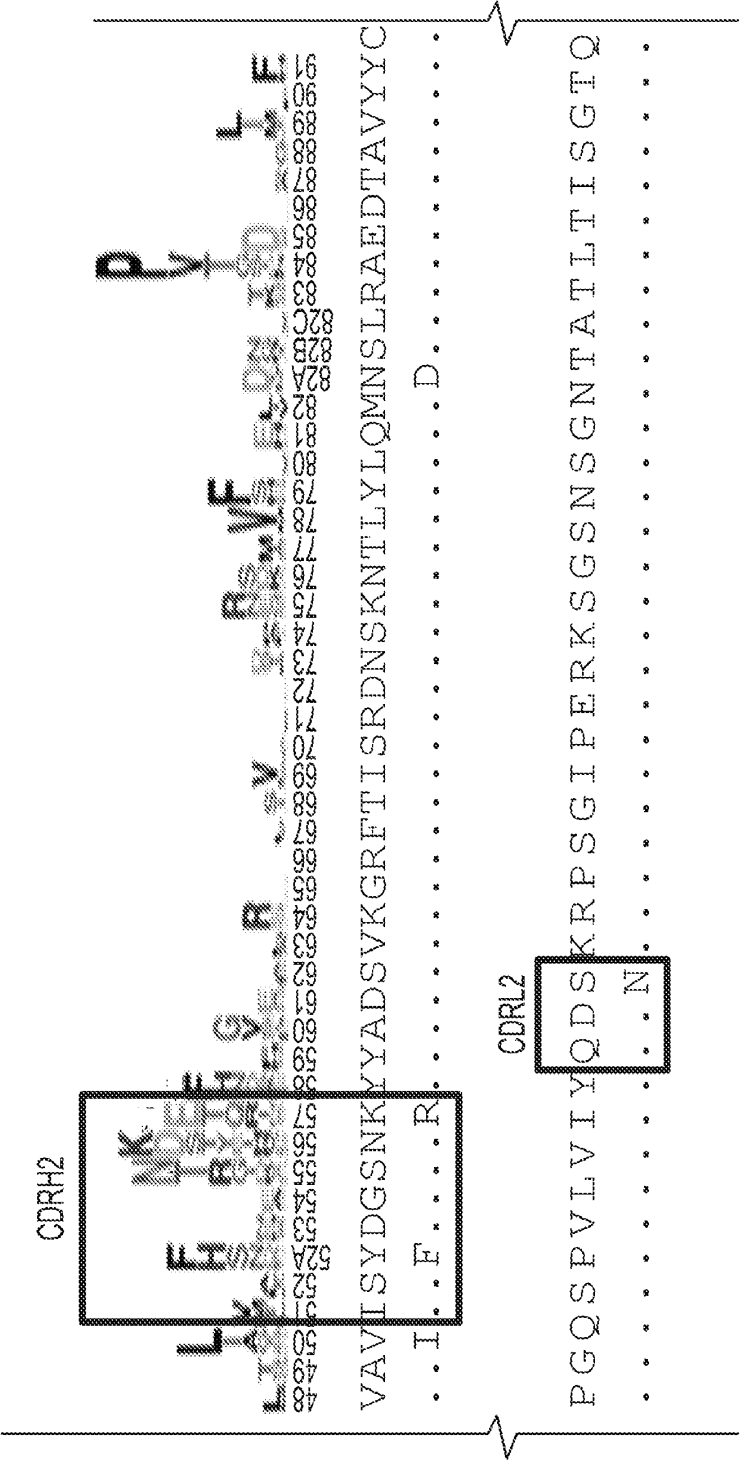


FIG. 36B
CONTINUED

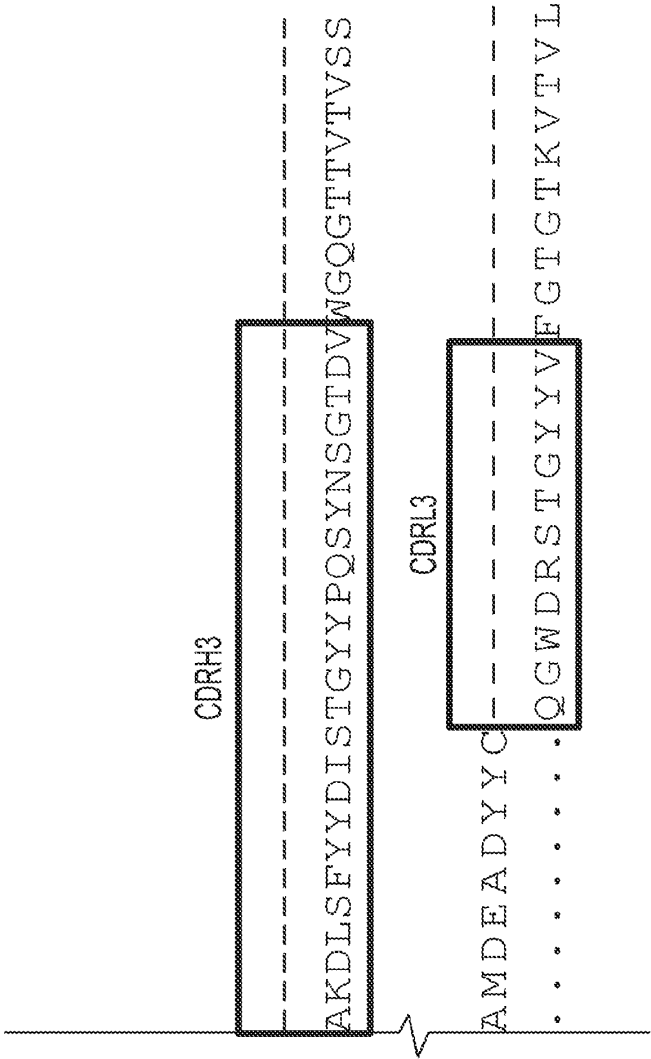


FIG. 36B
CONTINUED

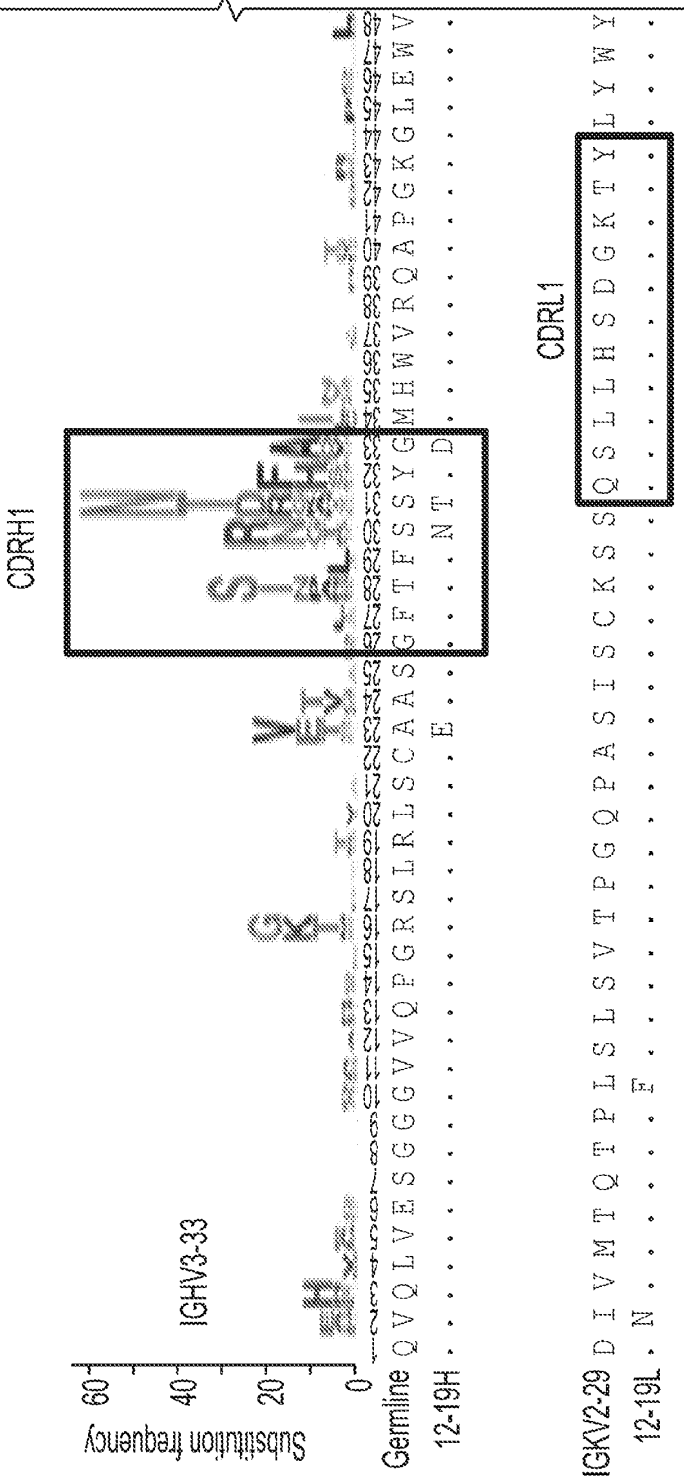


FIG. 36C

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CDRH2

[illegible]

CORL2

LQKPGQSPQLLIYEVS SRFSGVPPDRFSGSGTFTLKIS

FIG. 36C
CONTINUED

CDRH3

ARDRTPVYDILITGYYWPPPRVDGMDVWGGTTVTVSS

CDRL3

RVEAEDVG VY C
.....MQSIQLPEFTFGQGTKLEIK

FIG. 36C
CONTINUED

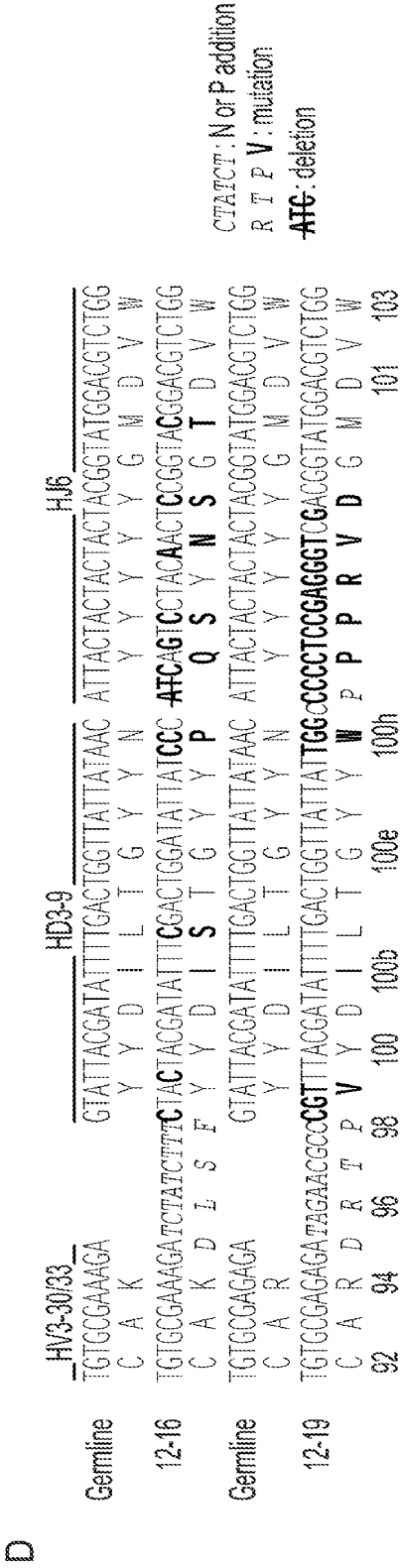
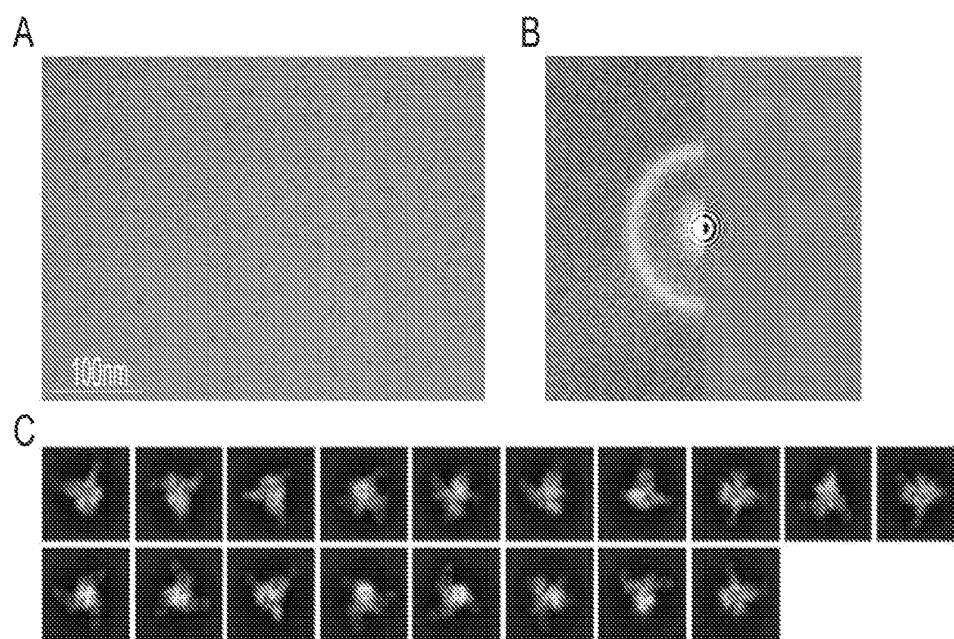


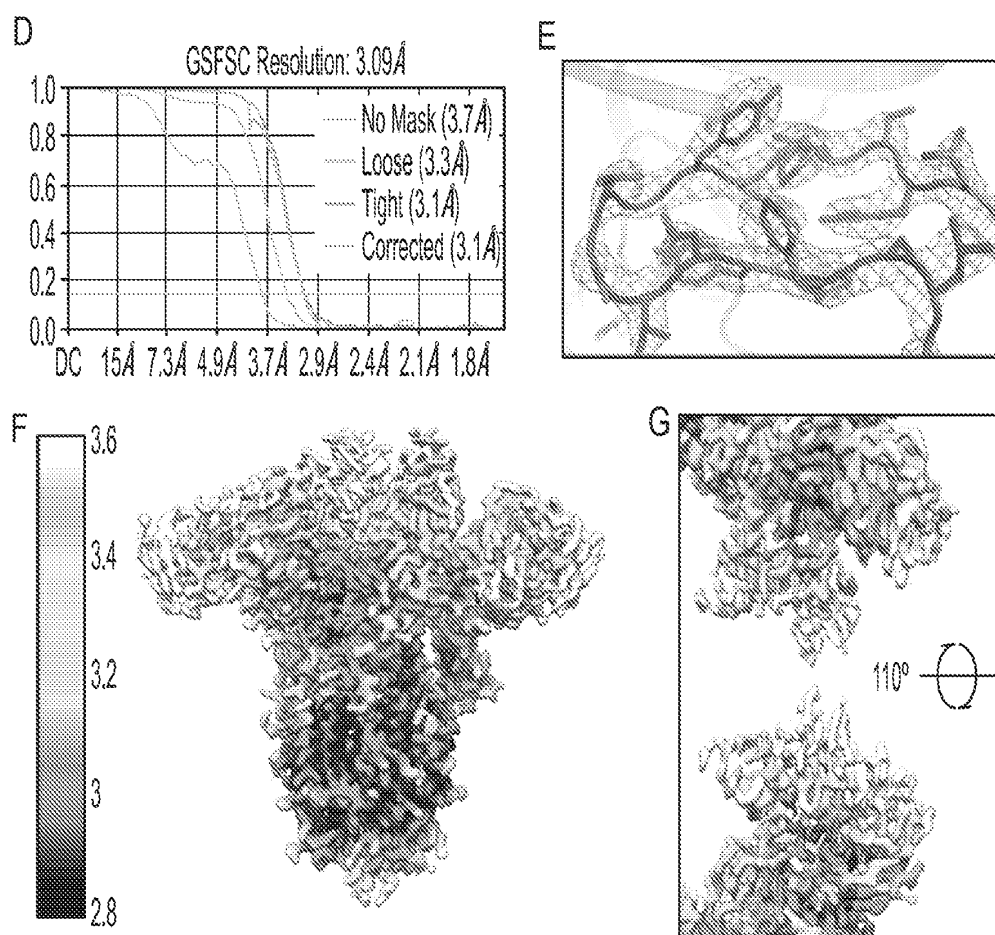
FIG. 36D

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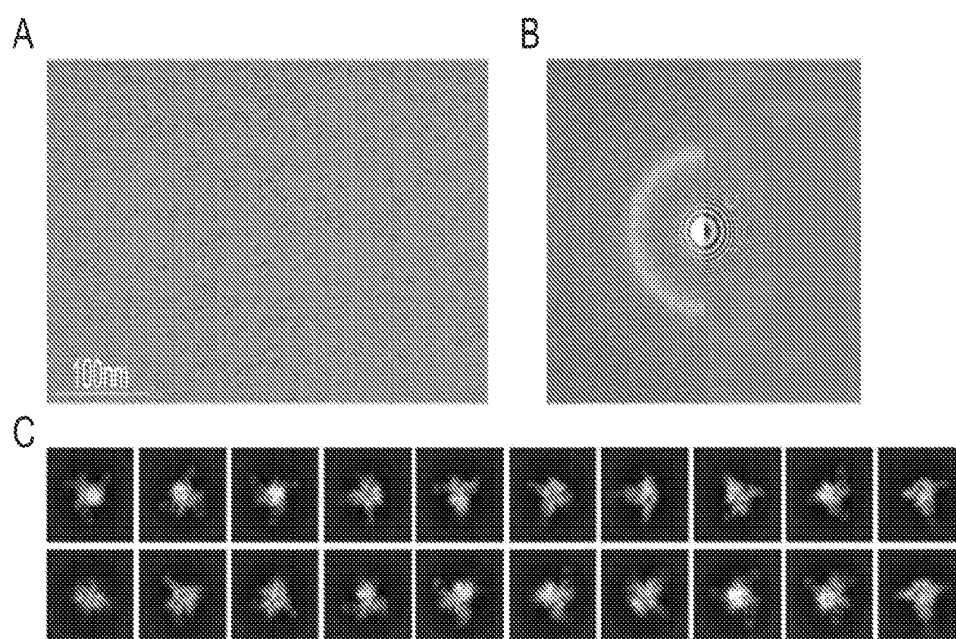
FIGS. 37A-C

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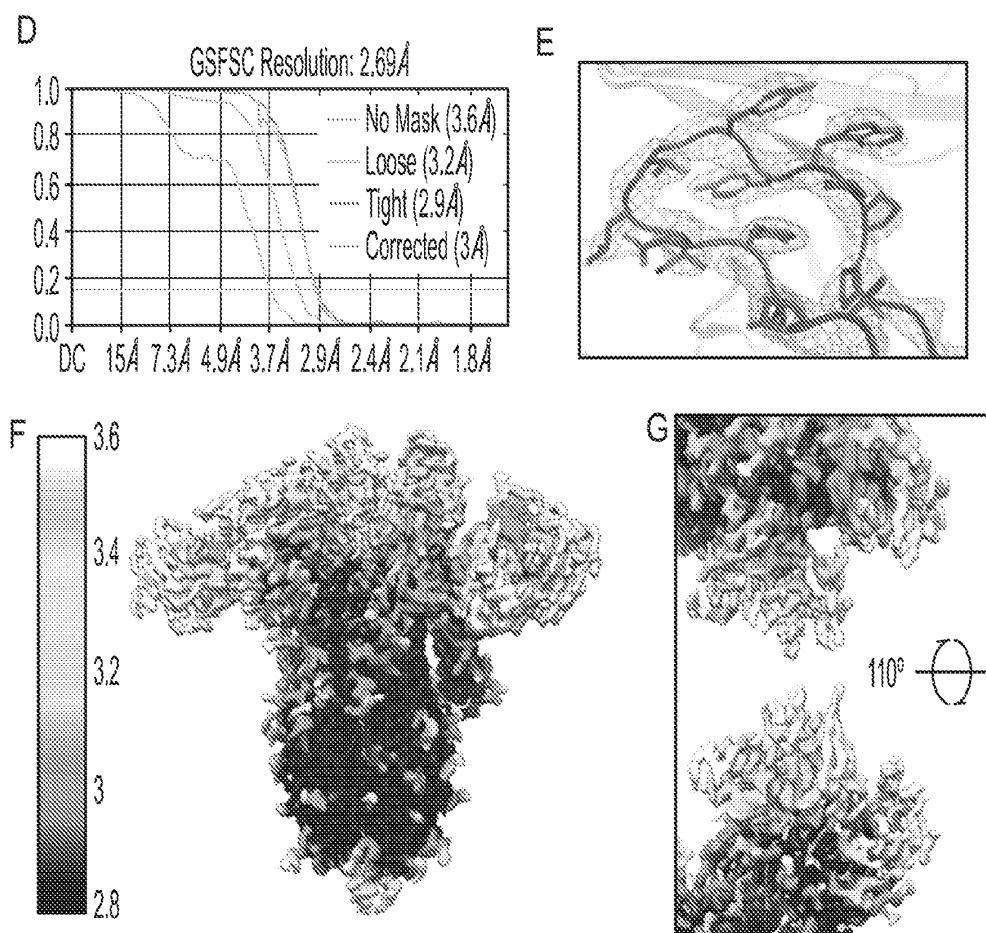
FIGS. 37D-G

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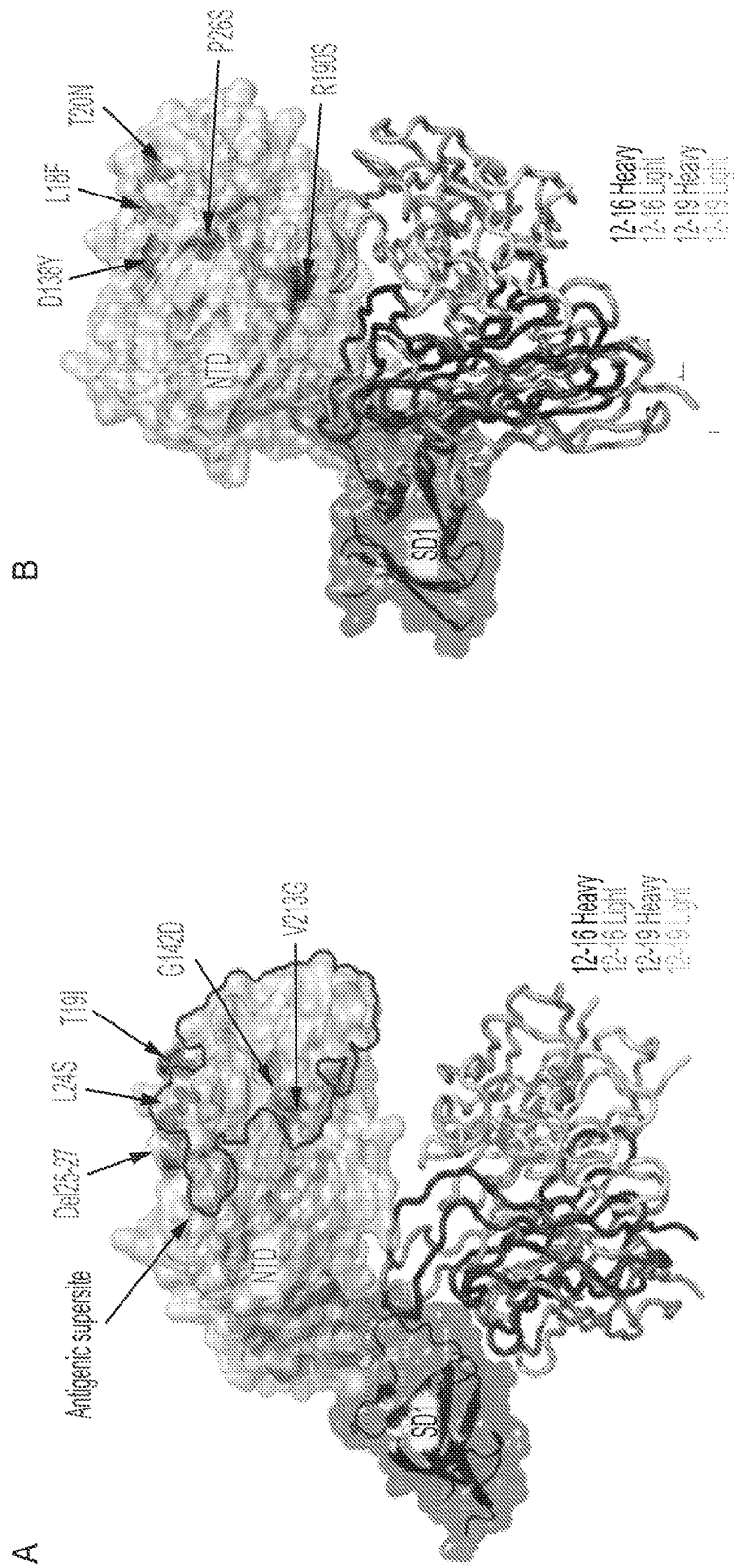
FIGS. 38A-C

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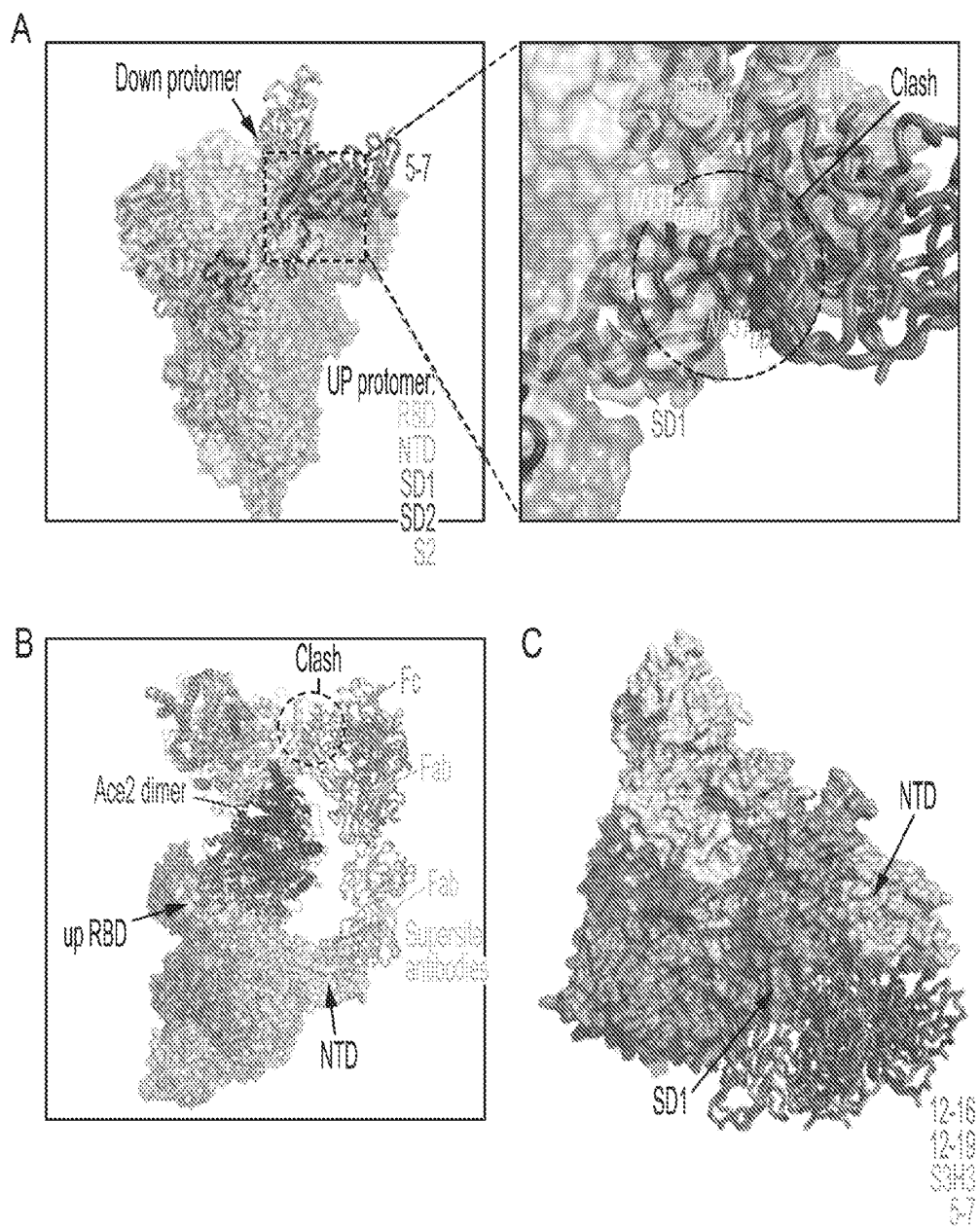
FIGS. 38D-G

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FIGS. 39A-B

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FIGS. 40A-C

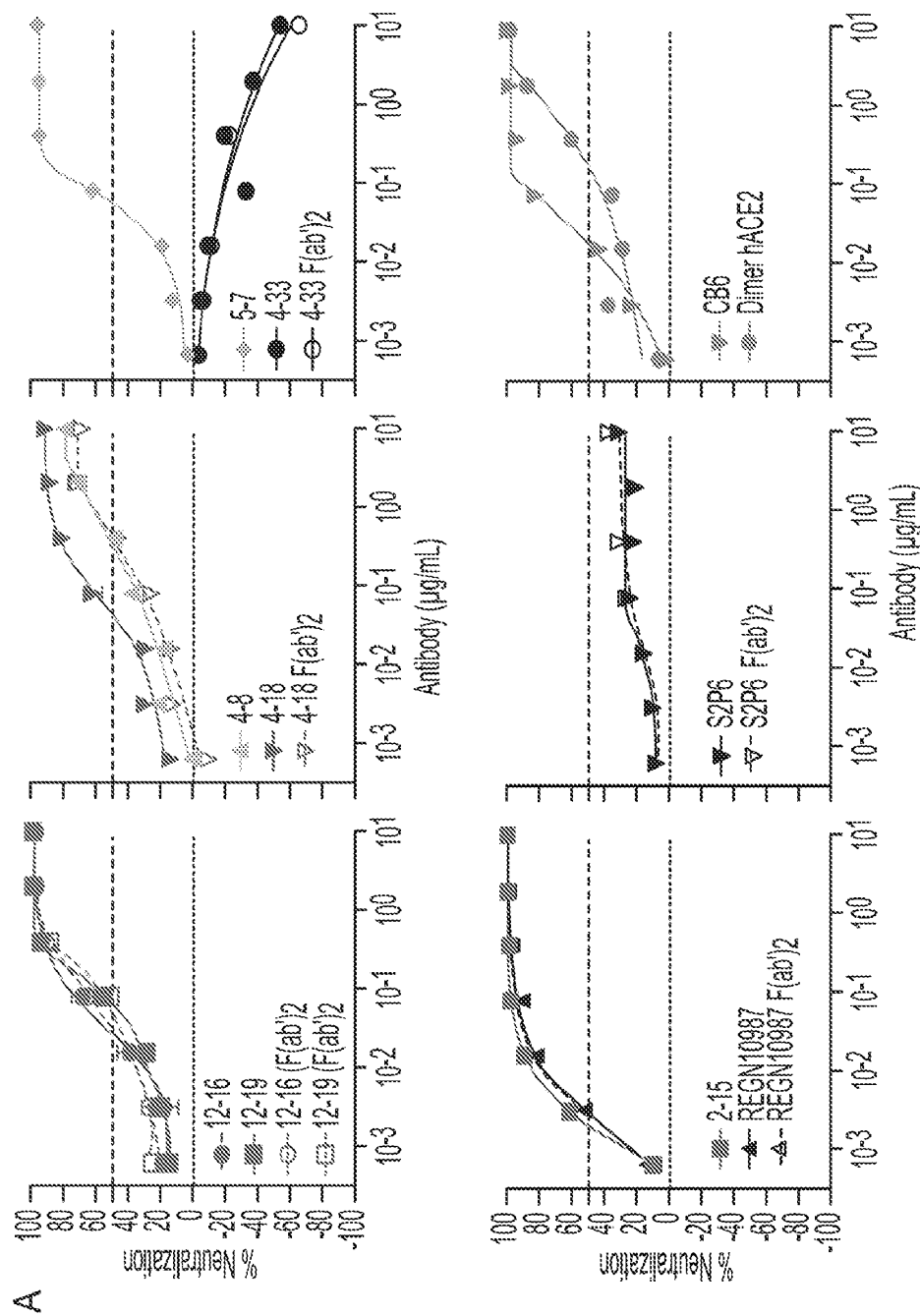


FIG. 41A

B

mAb	12-16	12-19	4-18	4-33	S2P6	REGN10987	5-7	2-16	CB6	hACE2-Fc
Format	WT	F(ab') ₂	WT	F(ab') ₂	WT	F(ab') ₂	WT	F(ab') ₂	WT	F(ab') ₂
IC50 (μg/ml)	0.027	0.034	0.053	0.068	0.044	0.452	>10	>10	>10	>10
							0.003	0.003	0.338	0.056
							0.002	0.002	0.002	0.172

FIG. 41B

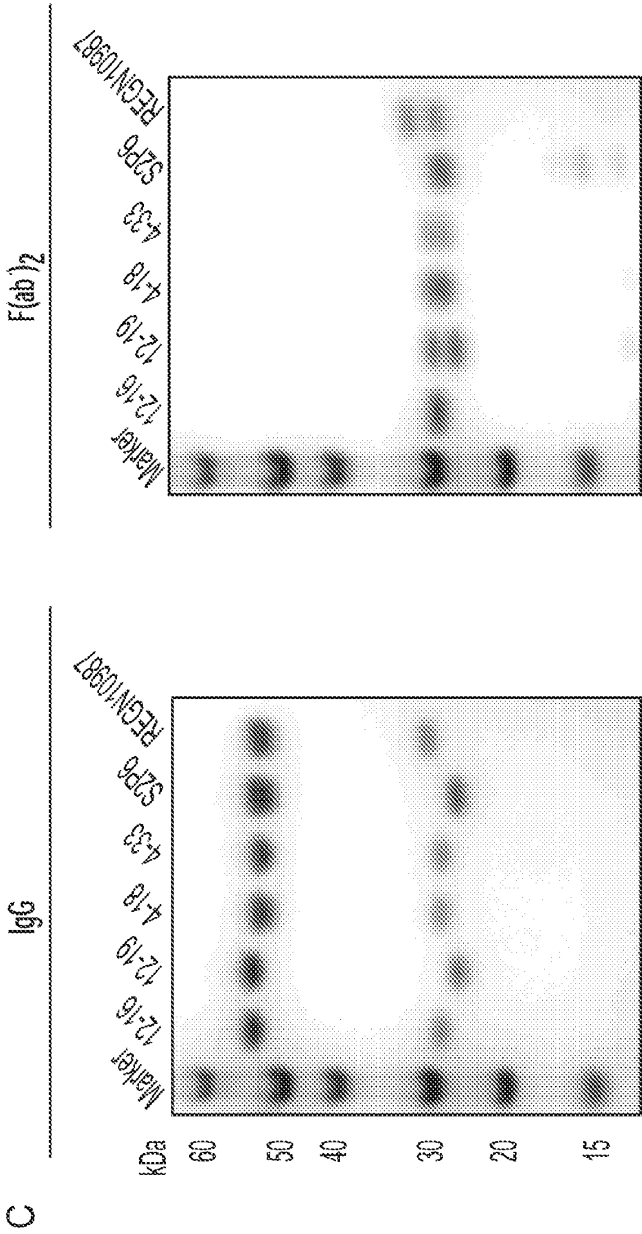
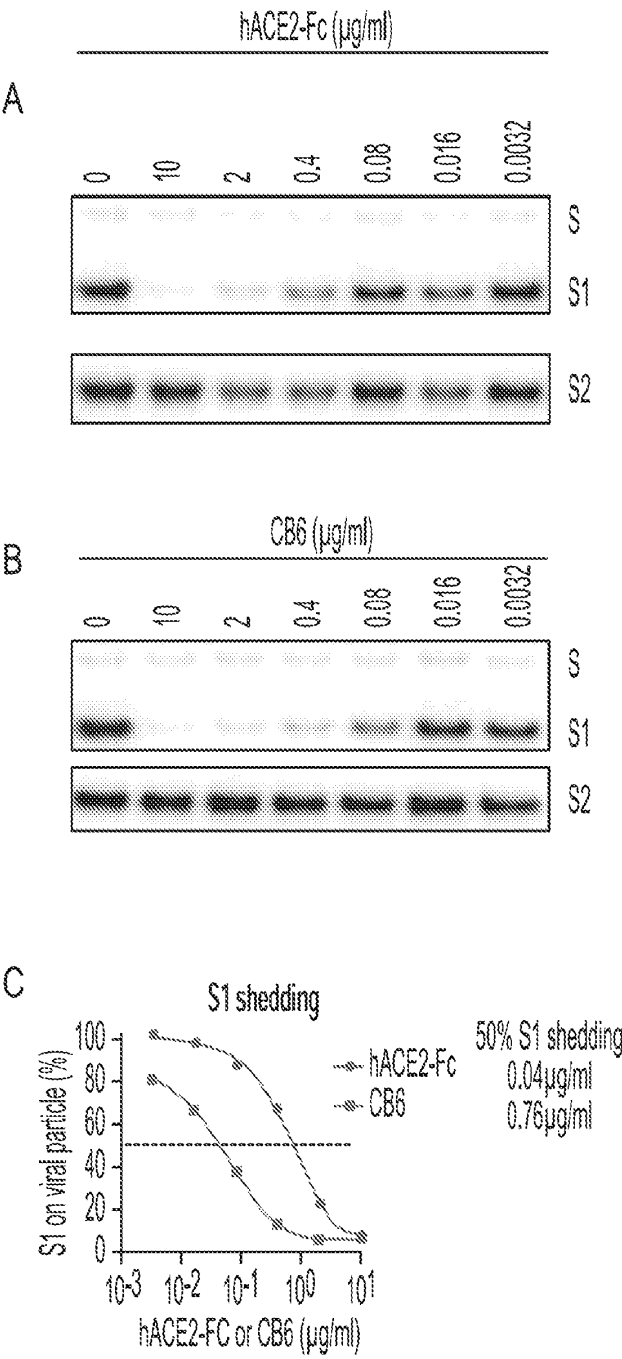


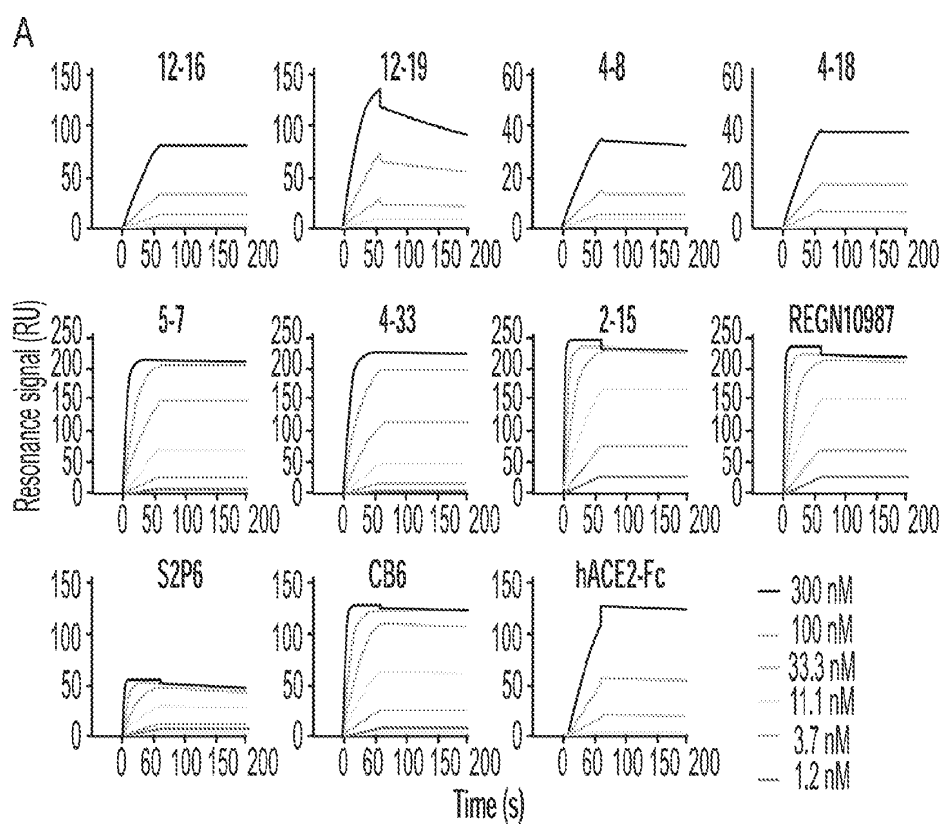
FIG. 41C

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FIGS. 42A-C

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**B**

mAb	SARS-CoV-2 Spike		
	k_a (1/Ms)	k_d (1/s)	K_D (M)
12-16	4.14E+04	6.62E-05	1.60E-09
12-19	2.35E+05	2.20E-03	9.35E-09
4-8	3.90E+04	4.94E-04	1.26E-08
4-18	6.17E+04	6.24E-07	1.01E-11
5-7	6.16E+05	5.60E-05	9.09E-11
4-33	3.61E+05	3.45E-05	9.57E-11
2-15	2.03E+06	1.57E-04	7.74E-11
REGN10987	1.73E+06	1.75E-04	1.01E-10
S2P6	1.41E+06	8.89E-04	6.30E-10
CB6	1.05E+06	1.92E-04	1.83E-10
hACE2-Fc	5.69E+04	2.97E-04	5.21E-09

FIGS. 43A-B

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	SARS-CoV-2 S2P + 12-16 Fab	SARS-CoV-2 S2P + 12-19 Fab
EMDB ID		
PDB ID		
Data Collection		
Microscope	FEI Titan Krios	FEI Titan Krios
Voltage (keV)	300	300
Magnification	105k	105k
Defocus Range (μm)	-0.8/-2.0	-0.8/-2.0
Camera	Gatan K3 BioQuantum	Gatan K3 BioQuantum
Pixel Size ($\text{\AA}/\text{pix}$)	0.83	0.83
Recording Mode	counting	counting
Dose Rate ($\text{e}^-/\text{pixel}/\text{s}$)	16	16
Electron Dose ($\text{e}^-/\text{\AA}^2$)	58	58
Data Processing		
Software	cryoSPARC v3.3	cryoSPARC v3.3
Micrographs used	3,691	4,042
Number of Particles	463,850	475,759
Symmetry	C1	C1
Box Size (pix)	440	440
Global Map FSC _{0.143} ($\text{\AA}$)	3.09	2.96
Refinement and Validation		
Software	Phenix, ISOLDE, Rosetta	Phenix, ISOLDE, Rosetta
Initial Model Used	6XM5(Spike), Alphafold(Fab)	6XM5(Spike), Alphafold(Fab)
Number of Atoms	30,246	28,230
Protein Residues	3,795	3,526
Ligands	NAG: 48	NAG: 47
Model vs. Data CC (mask)	0.83	0.76
RMS deviations		
Bond lengths ($\text{\AA}$) (# >4 σ)	1	4
Bond angles ($^\circ$) (# >4 σ)	25	17
MolProbity Score	1.25	1.26
Clashscore (all atom)	2.52	2.57
Poor rotamers (%)	0	0
Ramachandran plot		
Favored (%)	96.63	96.59
Allowed (%)	3.37	3.41
Outliers (%)	0	0

FIG. 44

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A

The multiple sequence alignment of the light chain variable domains

mAbs	10-16	10-28	10-40	11-11	12-6	12-27	13-2	12-16	12-19
10-16	100	71	48	55	70	61	53	50	61
10-28	71	100	48	53	94	81	50	49	56
10-40	50	50	100	66	50	46	59	58	43
11-11	55	53	64	100	54	52	62	60	48
12-6	70	94	48	54	100	80	51	47	56
12-27	61	81	44	52	80	100	46	43	52
13-2	53	50	57	62	51	46	100	76	54
12-16	50	49	55	60	47	43	76	100	48
12-19	61	56	41	48	56	52	54	48	100

B

The multiple sequence alignment of the heavy chain variable domains

mAbs	10-16	10-28	10-40	11-11	12-6	12-27	13-2	12-16	12-19
10-16	100	49	42	41	68	50	50	49	47
10-28	49	100	47	50	52	52	84	75	75
10-40	42	47	100	81	41	47	54	52	52
11-11	41	50	81	100	44	47	54	54	50
12-6	68	52	46	47	100	59	56	55	51
12-27	50	52	47	47	59	100	52	47	47
13-2	50	84	54	54	53	52	100	83	81
12-16	49	75	52	54	52	47	83	100	82
12-19	47	75	52	49	48	47	81	82	100

The similarities among antibody sequences were calculated by blastp in BLAST+ 2.8.1

FIGS. 45A-B

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A

The multiple amino acid sequence alignment of the complementarity determining regions (CDRs) in the light chain variable domains

mAbs	10-16	10-28	10-40	11-11	12-6	12-27	13-2	12-16	12-19
10-16	100	46	39	<10	60	40	<10	<10	<10
10-28	46	100	<10	<10	93	<10	<10	<10	<10
10-40	39	<10	100	57	33	<10	45	38	<10
11-11	<10	<10	57	100	<10	<10	75	<10	<10
12-6	60	93	33	<10	100	<10	<10	<10	<10
12-27	40	<10	<10	<10	<10	100	<10	<10	<10
13-2	<10	<10	45	75	<10	<10	100	42	<10
12-16	<10	<10	38	<10	<10	<10	42	100	<10
12-19	<10	<10	<10	<10	<10	<10	<10	<10	100

B

The multiple amino acid sequence alignment of the complementarity determining regions (CDRs) in the heavy chain variable domains

mAbs	10-16	10-28	10-40	11-11	12-6	12-27	13-2	12-16	12-19
10-16	100	<10	<10	47	<10	<10	<10	<10	<10
10-28	<10	100	<10	<10	<10	25	50	68	54
10-40	<10	<10	100	63	0	54	38	38	38
11-11	47	<10	63	100	0	<10	50	<10	<10
12-6	<10	<10	40	36	100	<10	39	45	46
12-27	<10	25	54	<10	<10	100	<10	<10	<10
13-2	<10	50	38	50	<10	<10	100	56	59
12-16	<10	68	38	<10	<10	<10	56	100	55
12-19	<10	54	38	<10	<10	<10	59	55	100

The similarities among antibody sequences were calculated by blastp in BLAST+ 2.8.1

FIGS. 46A-B

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	CDRH1	CDRH2	CDRH3
>10-16	GFTFISSA	IVVGSNT	AAPYCNSTNCYDAFNI
>10-28	GFTFSSYD	ISYDGSSK	VKDGEQLVPLFDY
>10-40	GCSSSSNFY	ITYSGRT	ARTFPSYDRSGYHYLNYGMDV
>11-11	GCSSSSGGYY	IYVSGST	ASSNYDGGSYNLLLESYGMDV
>12-6	GGTFSSNYA	FIRIFDTA	ARSPYYDKSGYYVFDH
>12-27	GYNFTFYW	IYPGDSE	TARLSGVQTALEYFDF
>13-2	GFIFSDFG	ISYDGSN	KARDYYDISGFYHPPNFDY
>12-16	GFTFSNYG	ISFDGSNR	AKDLSFYDIDTGYYPQSYNSGTDV
>12-19	GFTFNTYD	IWYDGSNK	ARDRTPVYDILTYGYWPPPRVDGMDV

FIG. 47

	CDRL1	CDRL2	CDRL3
>10-16	QSVSSY	GAS	QQYGRSPWT
>10-28	QSISSY	AAS	QQSYSTPGVT
>10-40	SGSIASNY	EDN	QSYDSSSW
>11-11	SSNIGAGYD	GNS	QSYDSSLGSW
>12-6	QNISSY	AAS	QQSYSPQWT
>12-27	QDITNH	DAS	QQYDNLILT
>13-2	TLPKQY	KDS	QSADSSGTYW
>12-16	KLGDY	QDN	QGWDRSTGYW
>12-19	QSLHSDGKTY	EVS	MQSIQLPFT

FIG. 48