

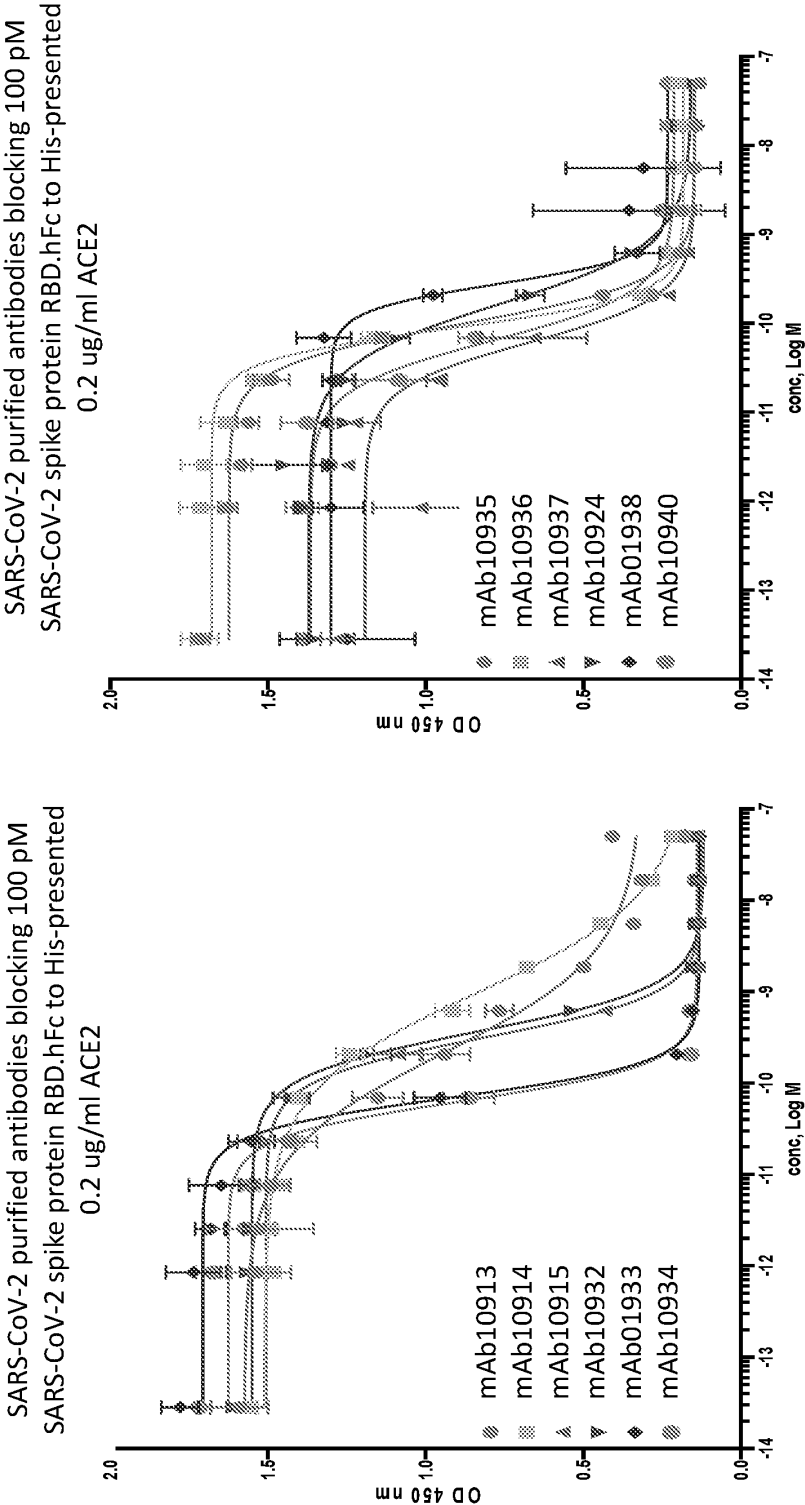


Figure 1

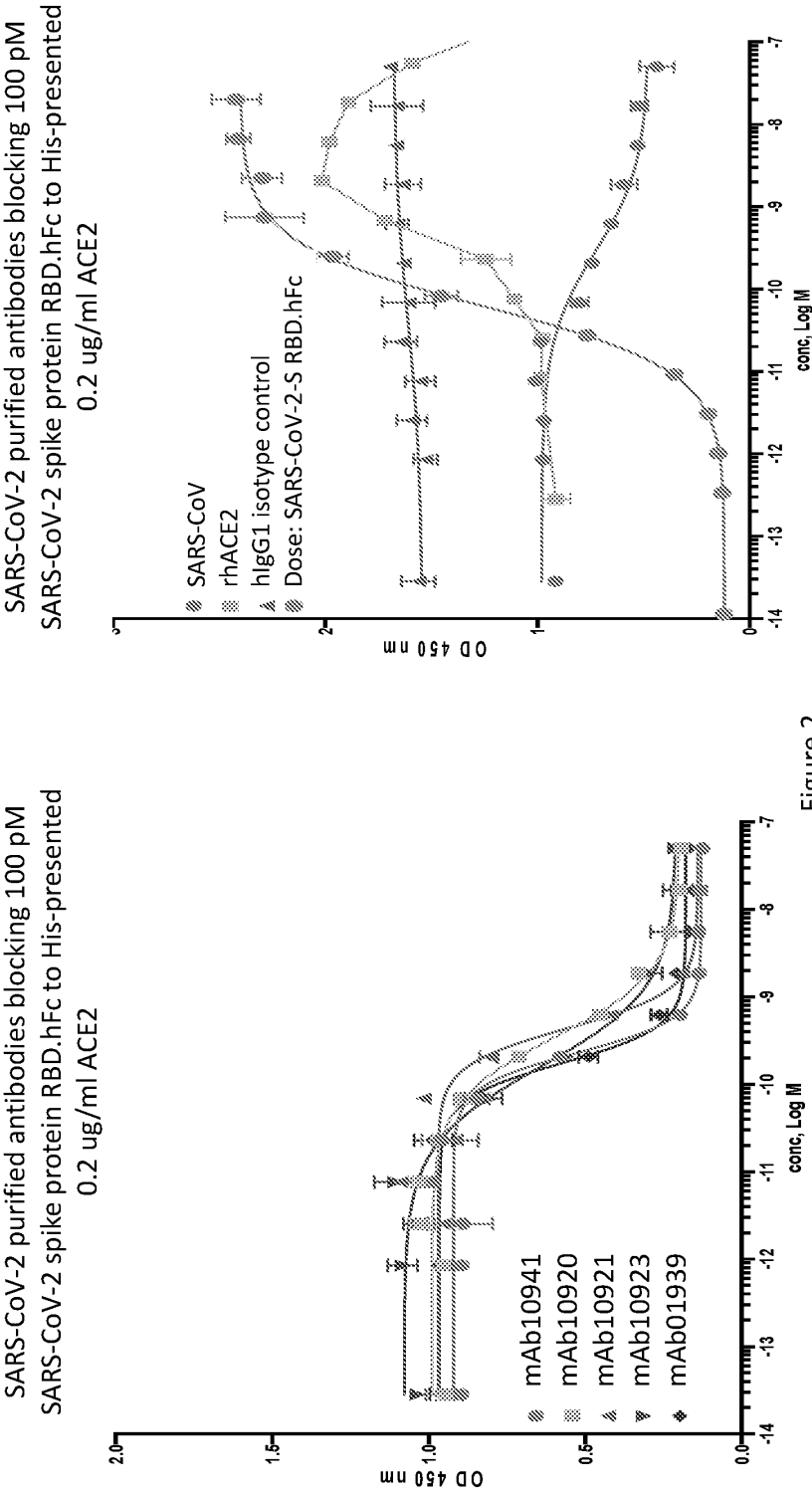


Figure 2

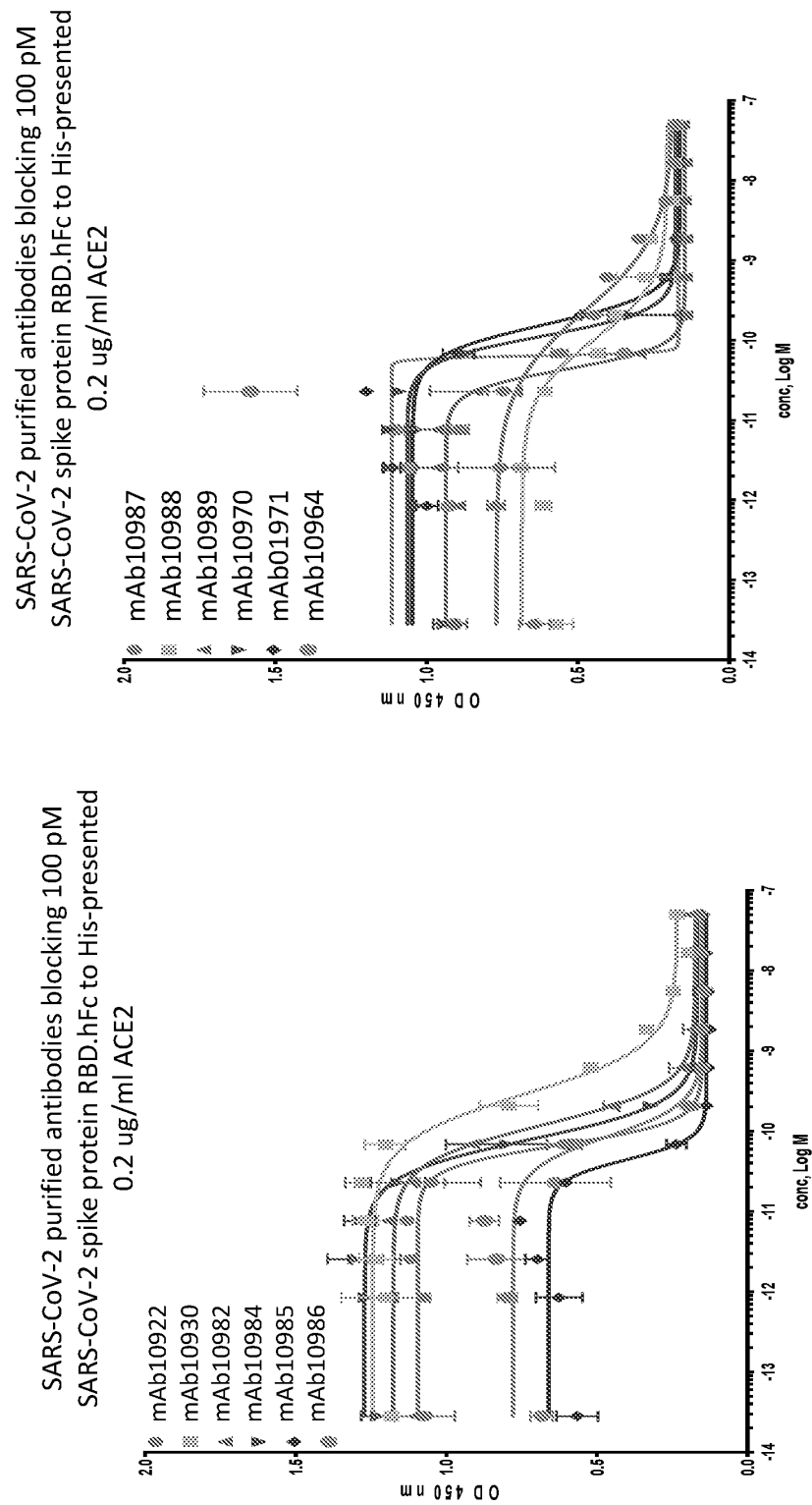


Figure 3

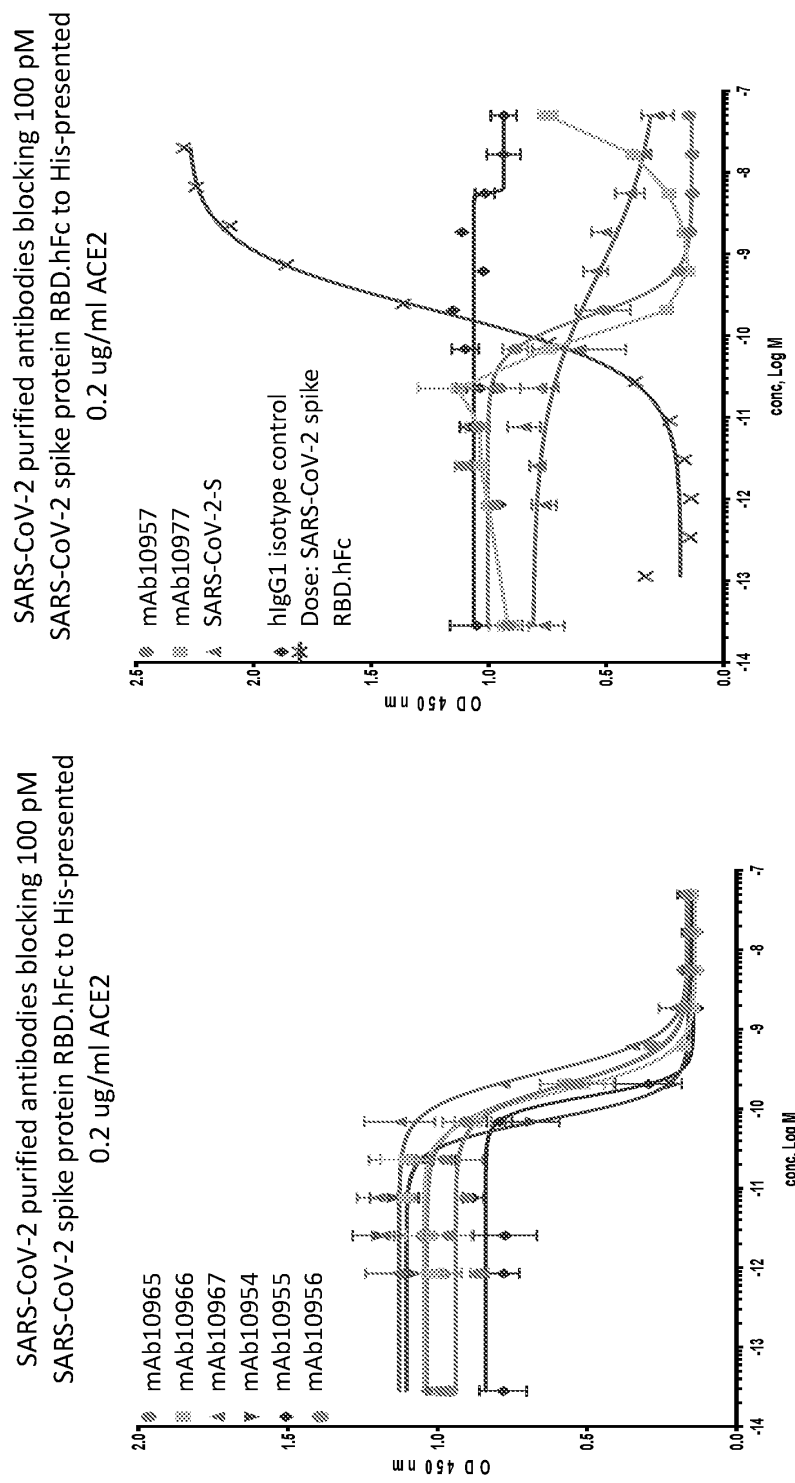


Figure 4

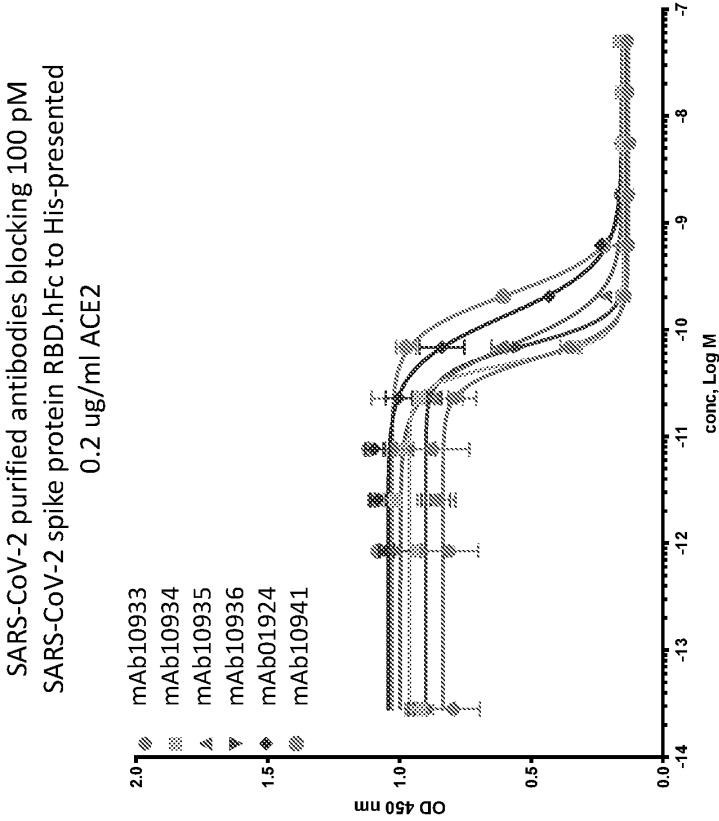


Figure 5

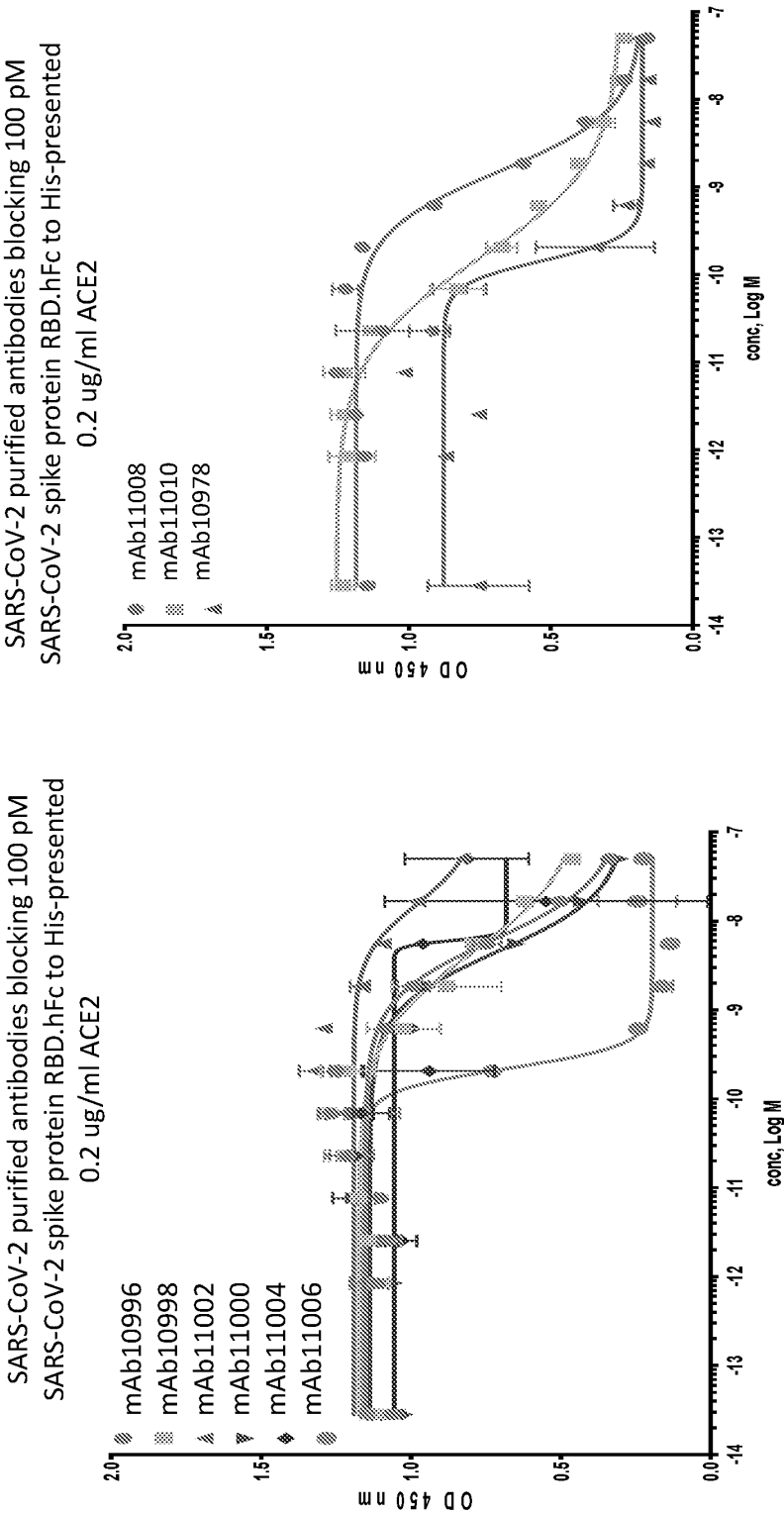


Figure 6

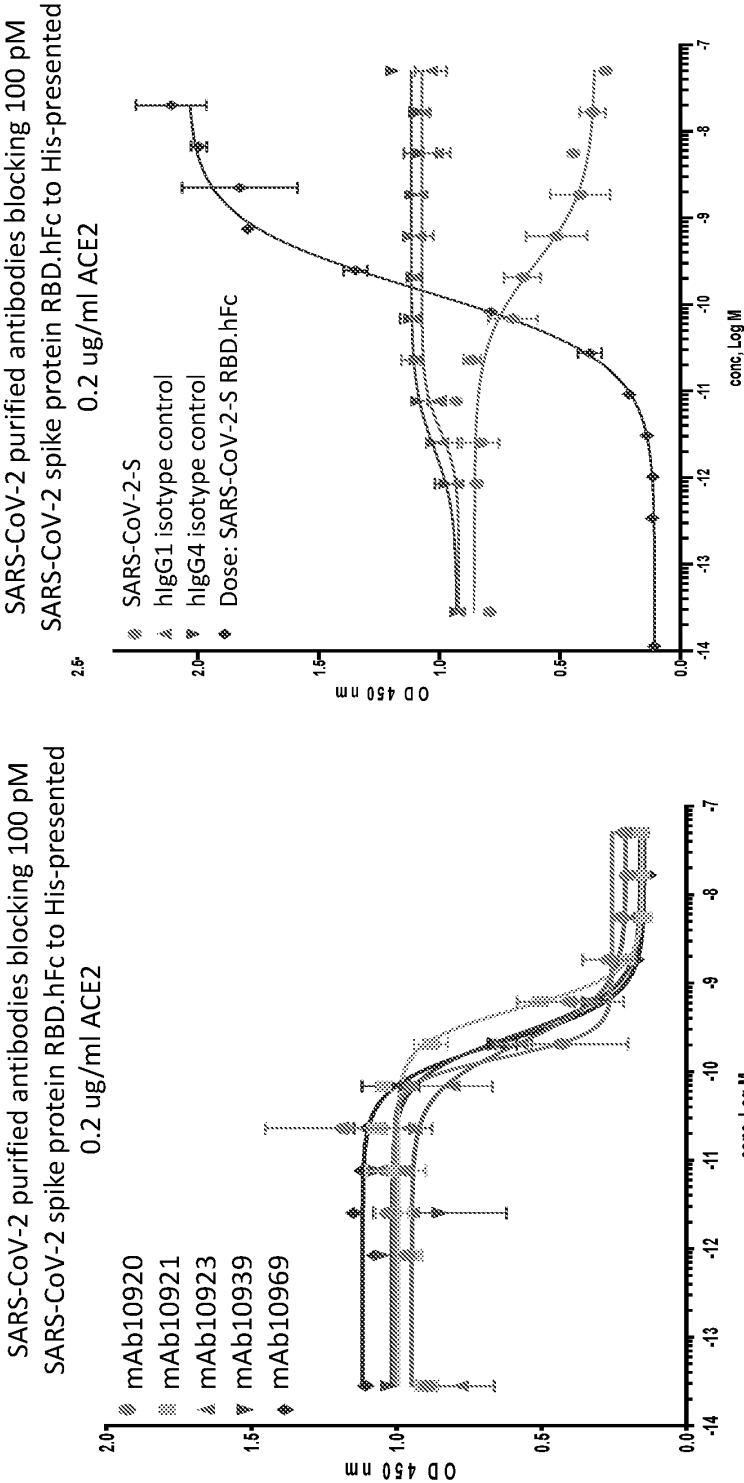


Figure 7

SARS-CoV-2 purified antibodies blocking 100 pM
SARS-CoV-2 spike protein RBD.hFc to His-presented
0.2 ug/ml ACE2

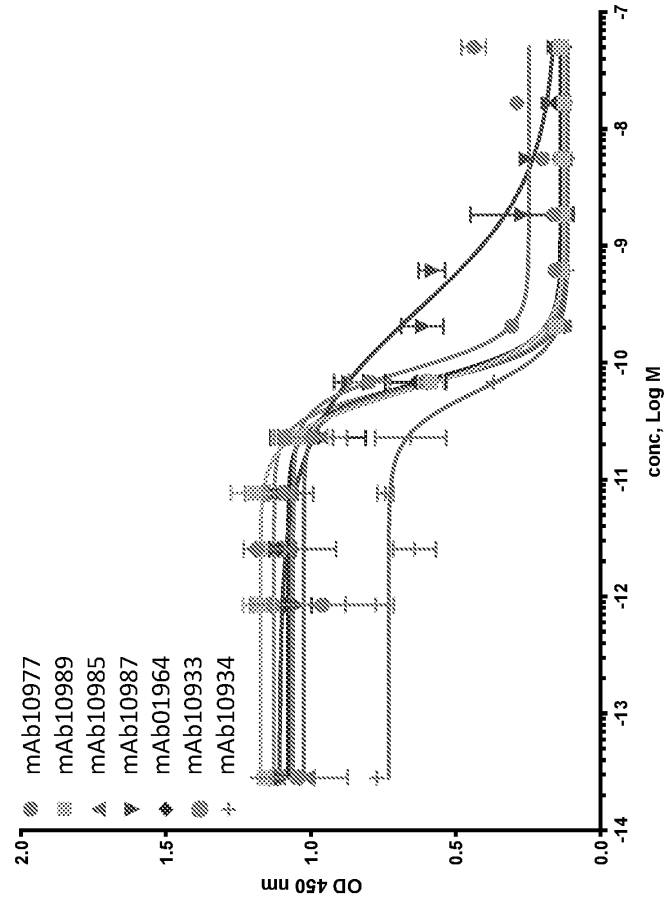


Figure 8

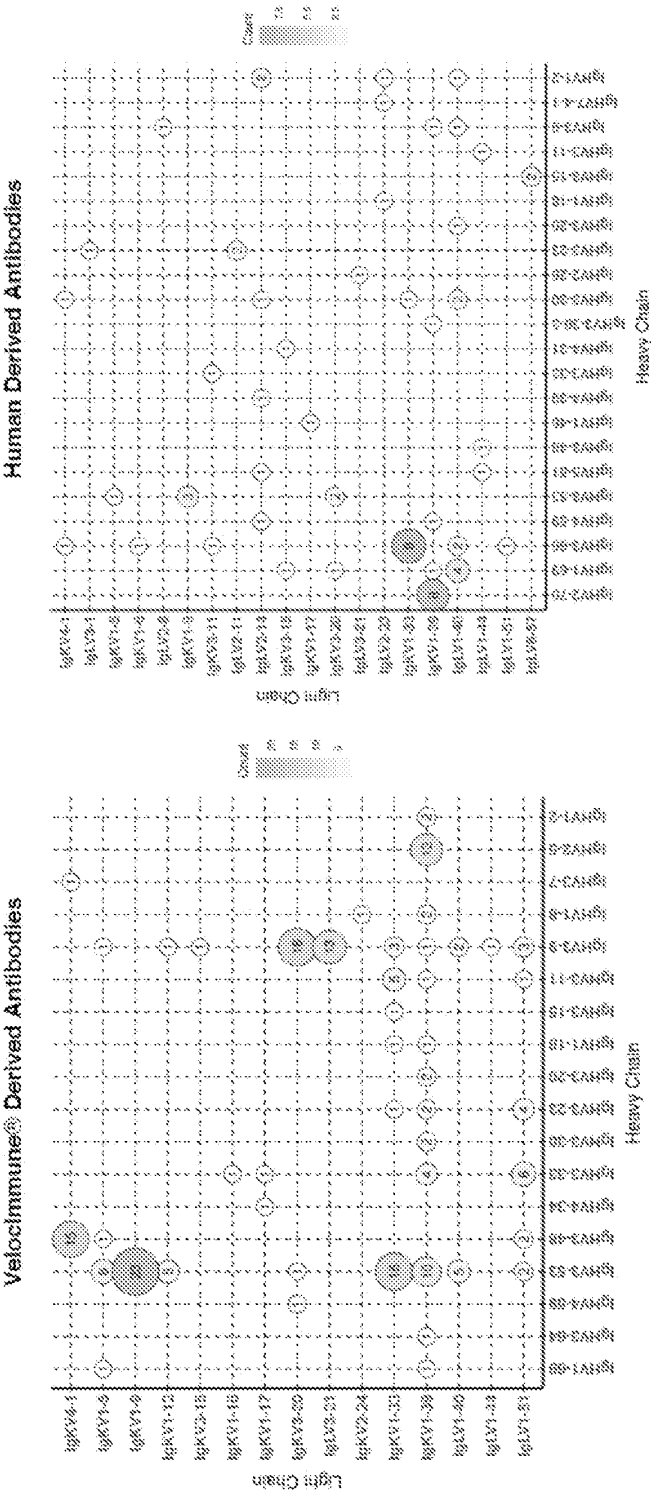


Figure 9B

Figure 9A

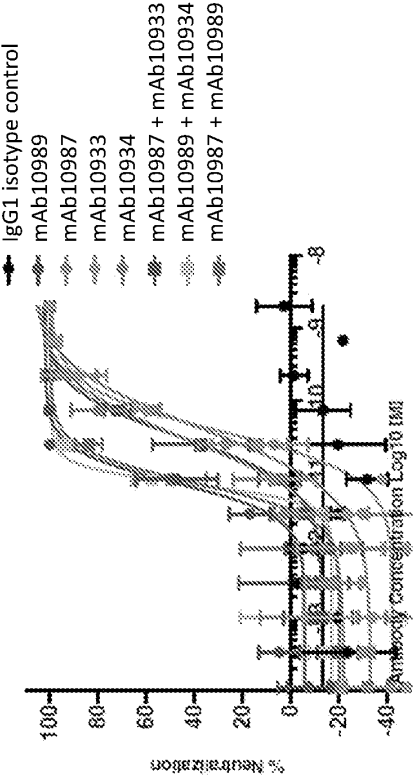


Figure 10B

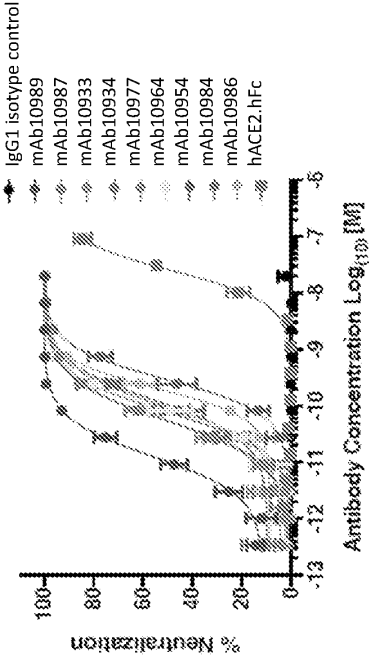


Figure 10A

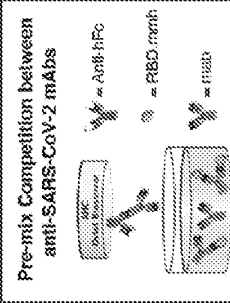
Pre-mix Competition between anti-SARS-CoV-2 mAbs		Phase I		Measure mAb1 captured	Phase II measure IgG blocking mAb (nm)	Phase III, Response of 100 nM SARS CoV-2 RBD-MMH complexed 600 nM of mAb2 binding site (nm)									
		mAb1		nm captured mAb1	nm mAb bound	Pre-mix Competition									
Bi-directional Competition		mAb10977	mAb10987	1.69 ± 0.05	0.00	mAb10977	mAb10989	mAb10933	mAb10964	mAb10984	mAb10986	mAb10954	mAb10934	mAb10987	
		mAb10989	mAb10987	1.95 ± 0.03	0.07	mAb10989	0.00	-0.04	-0.04	-0.04	0.46	0.33	0.00	0.96	
		mAb10933	mAb10987	1.73 ± 0.06	0.10	mAb10933	0.04	0.00	-0.01	-0.01	0.04	0.00	0.25	1.92	
		mAb10964	mAb10987	1.90 ± 0.03	0.04	mAb10964	0.02	0.04	0.00	0.01	0.05	0.04	0.38	1.37	
		mAb10984	mAb10987	1.83 ± 0.04	0.11	mAb10984	0.03	0.15	0.02	0.00	0.09	0.06	0.55	1.13	
Partial competition		mAb10986	mAb10987	1.73 ± 0.04	1.09	mAb10986	0.14	0.32	-0.03	-0.06	0.00	-0.04	0.86	1.21	
		mAb10954	mAb10987	1.83 ± 0.04	0.85	mAb10954	0.03	0.53	-0.01	-0.04	0.02	0.00	1.12	1.16	
		mAb10934	mAb10987	1.79 ± 0.06	0.97	mAb10934	0.05	0.03	-0.03	0.65	1.23	1.60	0.00	0.31	
No competition															
Self-self competition		mAb10987		1.83 ± 0.04	1.29	mAb10987	0.06	0.76	0.86	1.03	1.05	1.07	-0.08	0.00	

Figure 11

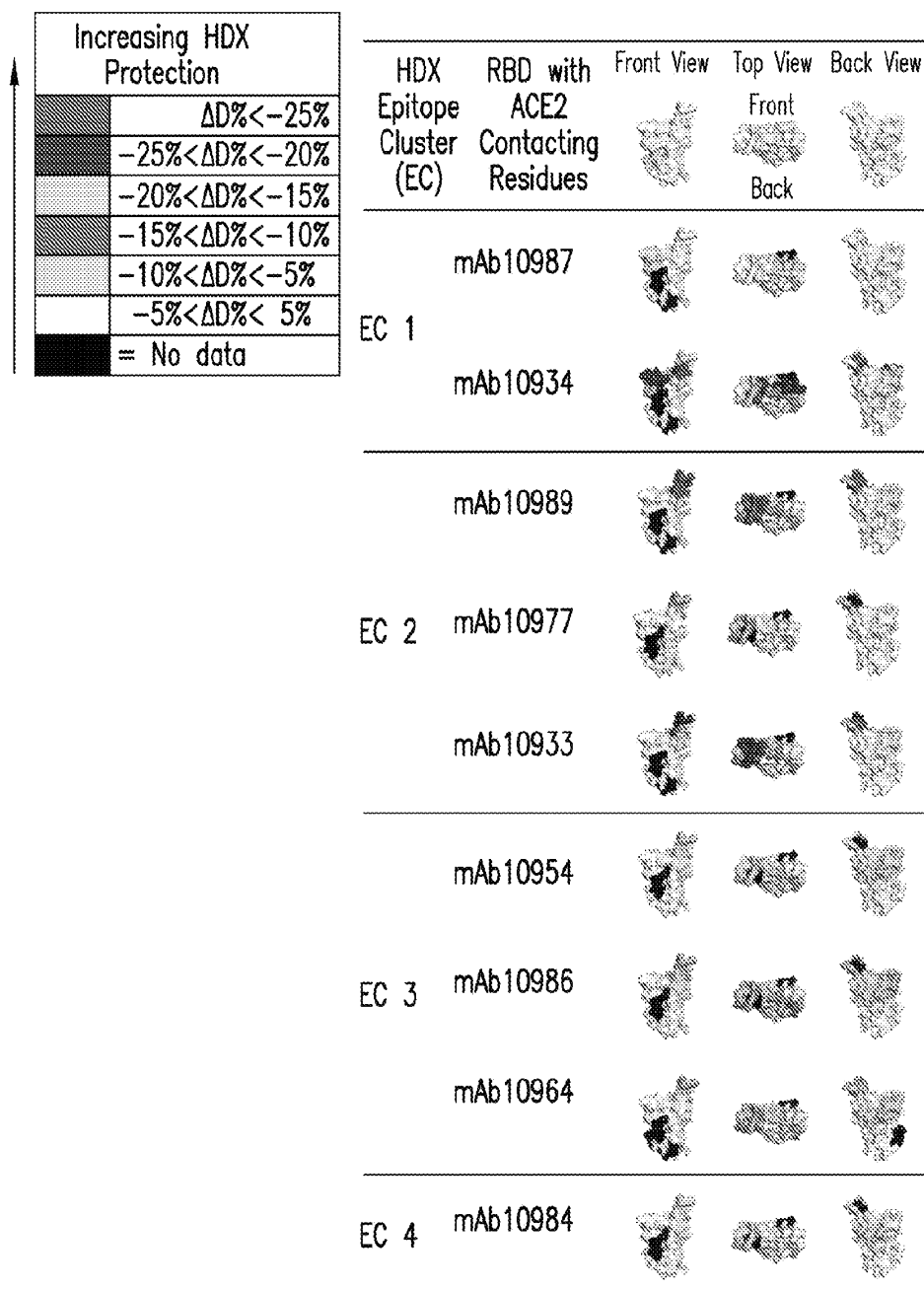


FIG. 12

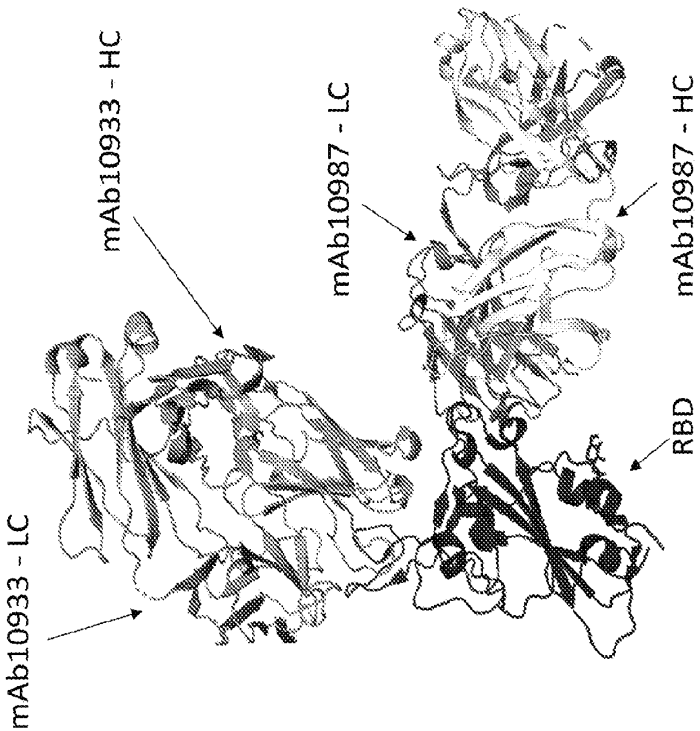


FIG.13B

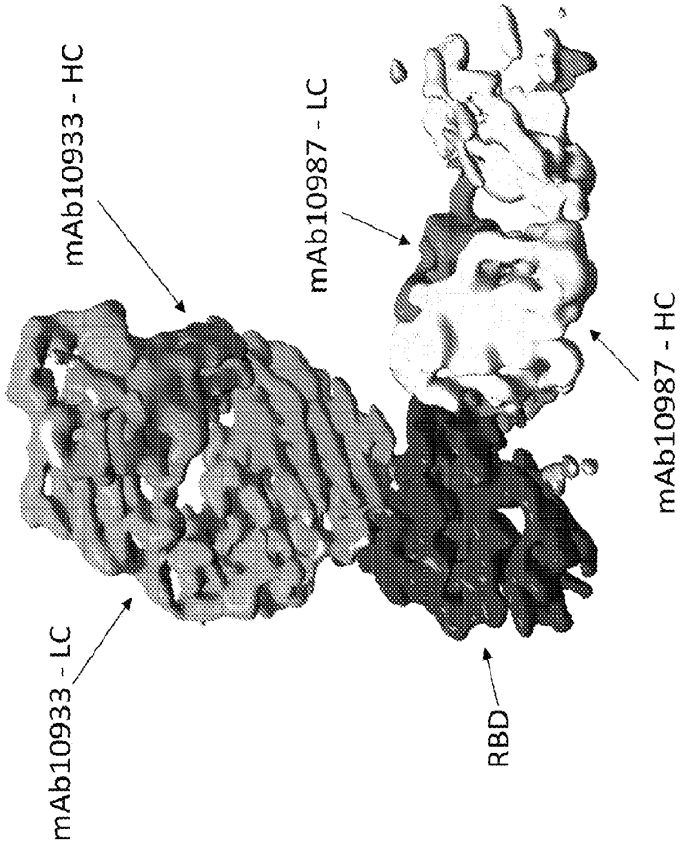


FIG.13A

SARS-CoV-2 RBD: mAb10933 : mAb10987 complex	
Data collection and processing	
Magnification	105,000
Voltage (kV)	300
Electron exposure (e ⁻ /Å ²)	40
Defocus range (μm)	1.6–3.0
Pixel size (Å)	0.85
Symmetry imposed	C1
Initial number of particles	989,553
Final selected particles	61,707
Map resolution (Å)	3.9
FSC threshold	0.143
Refinement	
Map sharpening B factor (Å ²)	–122
Model composition (# of atoms)	7979
Model vs. map correlation coefficient	0.64
R.m.s. deviations	
Bond lengths (Å)	0.02
Bond angles (°)	1.12
Validation	
MolProbity score	2.7
Rotameric outliers (%)	1.0
Ramachandran plot	
Favored (%)	83.0
Allowed (%)	16.3
Disallowed (%)	0.7

FIG.14

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