

Supplemental information

**Neutralizing and protective human monoclonal
antibodies recognizing the N-terminal
domain of the SARS-CoV-2 spike protein**

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Supplementary Table 1. Sequence and functional features of NTD-reactive human monoclonal antibodies (mAbs), Related to Figure 1 and Figure S2.

MAb	Antibody variable gene sequence features						Neutralization IC ₅₀ value (ng/mL)		Reference
	Heavy chain			Light chain			Pseudovirus or VSV	Authentic virus	
	V _H gene	CDR3 (amino acids)	GenBank number	V gene	CDR3 (amino acids)	GenBank number			
COV2-2489	<i>IGHV4-39</i>	ARQWKWFGAEAWYFDL	MT665457	<i>IGKV3-20</i>	QQYGSSPFT	MT665070	56	199	Zost <i>et al.</i> , 2020
COV2-2676	<i>IGHV1-69</i>	ARSCGDCYSADLDF	MT665456	<i>IGKV3-11</i>	QRRSNWPPFT	MT665069	38	501	Zost <i>et al.</i> , 2020
4A8	<i>IGHV1-24</i>	ATSTAVAGTPDLFDYYYGMDV	MT622683	<i>IGKV2-24</i>	TQATQFPYT	MT622682	49,000	610	Chi <i>et al.</i> , 2020
4-8	<i>IGHV1-69</i>	ASLQTVDTAIEKYYGMDV	MT712311	<i>IGLV3-1</i>	QAWDSSTAV	MT712278	32	9	Liu <i>et al.</i> , 2020

Supplementary Table 2. Summary of electron microscopy data collection and statistics SARS-CoV-2_{ecto} protein in complex with human Fabs, Related to Figure 2.

		Structure of SARS-CoV-2 S6P _{ecto} protein in complex with indicated Fab	
		Fab COV2-2489	Fab COV2-2676
	EMDB #:	EMD-23154	EMD-23155
Microscope setting	Microscope	TF-20	TF-20
	Voltage (kV)	200	200
	Detector	US-4000 CCD	US-4000 CCD
	Magnification	50,000 \times	50,000 \times
	Pixel size	2.18	2.18
	Exposure (e-/Å ²)	30	30
	Defocus range (μ m)	1.5 to 1.8	1.5 to 1.8
Data	Micrographs, #	221	376
	Particles, #	39,108	44,443
	Particles #, after 2D	36,081	16,960
	Final particles, #	2,591	4,859
	Symmetry	C1	C1
Model docking	CoV-2-S CC	PDB: 7JJI 0.815	PDB: 7JJI 0.939
	Fab (PDB: 12E8) CC	0.908	0.91