Supplemental Table 1. Workflows used to isolate SARS-CoV-2 specific human mAbs from single B cells

Single B cell technique	Ag used for cell sorting	Feeder layer stimulation	Functional screen on instrument	Sequencing technique (cDNA used)	Screening, sequencing, cloning information
Beacon	$S2P_{ecto\ +/-}$ S_{RBD}	+	$S2P_{ecto}$ binding	PacBio SMRT or Sanger (PCR amplicon)	Cells loaded to instrument: ~14,000 Cells in pens for screen: ~4,000 % Ag-reactive: ~55% Cells exported: 288 V_H:V_L paired sequences recovered: 156 mAbs cloned and expressed: 96 Ag-reactive mAbs: 78 Directly cloned cDNA in pMCis_G1 vector
			RBD-mFc binding		
			RBD-mFc binding + ACE2 blocking		
Chromium	$S2P_{ecto}$	+	na	Illumina Novaseq (Chromium libraries)	Cells sequenced: ~4,500 unstimulated ~40,000 stimulated Number of mAbs synthesized: 761 Ag-reactive mAbs: 311 % Ag-reactive synthesized mAbs: ~41% Synthesized cDNA in pTwist-mCis_G1 vector
		-			
	S_{RBD}	+			
		-			

Supplemental Table 2. Summary of electron microscopy data collection and statistics SARS-CoV-2 S2P$_{ecto}$ protein		
Microscope setting	Microscope	TF-20
	Voltage (kV)	200
	Detector	US-4000 CCD
	Magnification	50,000×
	Pixel size	2.18
	Exposure (e-/Å2)	25
	Defocus range (μm)	1.5 to 1.8
Data	Micrographs, #	122
	Particles, #	3,836
	Particles, # after 2D	2,718
	Final particles, #	2,188
	Symmetry	C1

Supplemental Table 3. Human subjects studied in this paper

Subject type	**Subject**	**Age** (years)	**Sex**	**City where infected**	**Date of symptom onset**	**Date of blood sample collection** (days after symptom onset)
COVID-19	1	35	M	Wuhan	Jan. 15, 2020	February 19, 2020 (35 days)
	2	52	F	Beijing	Feb. 1, 2020	March 8, 2020 (36 days)
	3	56	M	Wuhan	Jan. 20, 2020	March 10, 2020 (50 days)
	4	56	F	Wuhan	Jan. 20, 2020	March 10, 2020 (50 days)
Healthy donors	5	58	M	na	na	March 12, 2020 (na)
	6	Unknown	Unknown	na	na	Unknown, commercially sourced healthy donor sample

na: indicates not applicable