

Statistics of the scRNA and scVDJ sequencing results.

	scRNA-seq					scVDJ-seq				
	Number of cells detected	Mean reads per cell	Mean genes detected per cell	Total reads	Q30 %	Number of cells detected	Mean reads per cell	Number of productive cells	Total reads	Q30 %
Patient 1	32,551	1,484	333	48,308,745	76%	27,859	4,526	17,279	126,083,999	87%
Patient 2	9,880	2,370	515	23,413,679	98%	9,925	6,590	9,484	65,409,208	98%
Patient 3	5,575	3,908	729	21,786,425	98%	5,401	11,734	5,206	63,376,245	98%
Patient 4	7,523	6,100	835	45,891,400	98%	12,105	10,568	11,677	127,928,119	86%
Patient 5	29,029	3,128	615	90,813,480	80%	27,940	2,912	26,030	81,363,174	76%
Patient 6	7,258	2,702	539	19,609,279	75%	7,366	6,059	7,099	44,631,682	78%
Patient 7	6,269	3,138	593	19,673,314	75%	6,400	6,197	6,109	39,658,075	77%
Patient 8	7,738	2,907	489	22,496,801	75%	8,032	9,514	7,406	76,412,687	76%
Patient 9	5,936	16,537	1,242	98,162,900	83%	5,836	6,757	5,563	39,434,213	77%
Patient 10	13,079	14,382	1,332	188,104,614	89%	12,938	9,205	12,536	119,098,397	83%
Patient 11	13,421	1,384	371	18,576,377	90%	13,292	9,572	12,855	127,233,239	86%
Patient 12	10,136	2,042	506	20,701,185	89%	10,367	10,494	9,899	108,794,662	86%
Batch 1	19,311	2,961	618	57,174,894	80%	19,956	4,373	18,911	87,262,694	90%
Batch 2	19,760	2,699	664	53,332,771	90%	8,642	9,971	7,795	86,165,539	83%
Batch 3	16,701	3,336	643	55,708,151	84%	7,154	9,671	6,378	69,185,504	77%
Batch 4	13,123	5,958	1,026	78,191,562	89%	11,914	6,804	11,497	81,065,554	76%
Batch 5	14,812	6,749	917	99,964,928	89%	8,496	9,461	7,664	80,379,542	99%
Batch 6	6,703	5,462	772	36,613,688	91%	3,244	10,458	2,917	33,926,427	92%

Table S3. Statistics of the scRNA and scVDJ sequencing results. Related to STAR METHODS - Single-cell 5' mRNA and VDJ sequencing

Cryo-EM data collection and processing statistics

	Spike/Ab23-Fab complex
Voltage (kV)	300
Microscope	FEI Titan Krios G3
Camera	K2 Summit (Gatan)
Magnification (calibrated)	130,000X
Electron exposure ($e^-/\text{\AA}^2$)	59.8
Exposure rate	$7.1875 e^-/\text{\AA}^2/\text{s}$
Number of frames collected per micrograph	32
Energy filter slit width	20 eV
Automation software	SerialEM
Defocus range (μm)	-1.5 to -2.5
Pixel size (\AA)	1.055
Micrographs used	4,411
Estimated accuracy of translation/rotations	1.682 degrees, 0.886 pixels
Symmetry imposed	C1
Initial particle images (no.)	1,666,415
Final particle images (no.)	56,059
Resolution (\AA)	3.84
FSC threshold	0.143

Table S4. Cryo-EM data collection and processing statistics. Related to Figure 4.

Raw data of BD-368-2 pseudovirus neutralization assay

Control (RLU)		Neutralization (RLU)			
Cell Control	Virus Control		BD-368-2		mAbs dilution-fold
600	1917720	560	80	1040	270
520	1876760	1240	80	1120	810
520	1267320	1440	120	2000	2430
600	1670800	8000	240	59560	7290
880	2013480	8960	26040	70440	21870
1160	1910200	104880	47040	88080	65610
		322040	305960	389240	196830
		1074080	1146920	538920	590490
		1645920	1536720	1393600	1771470
		1927640	1940440	1447000	5314410
		1956080	1962200	2087560	15943230
		2227920	2010520	2269720	47829690

Table S5. Representative raw data of the pseudovirus neutralization assay using BD-368-2. Related to Figure 2.

The cell control indicates the background signal when there is no virus added. No antibody was added to the virus control. mAbs were diluted from 1 µg/mL.