Supplemental information

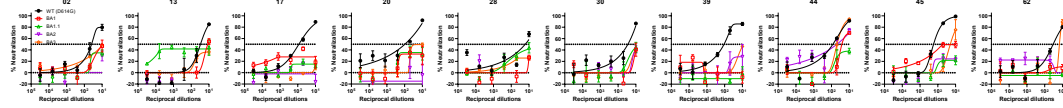## Antibody evasion of SARS-CoV-2 Omicron
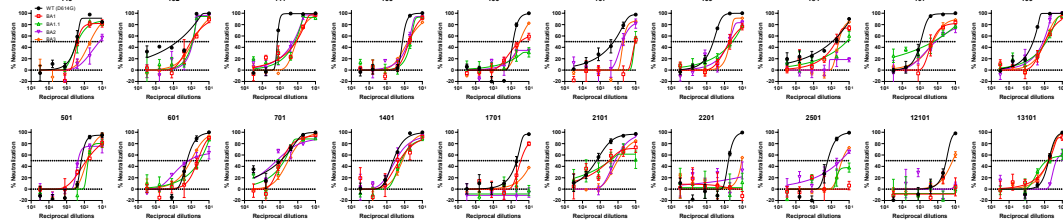
BA.1, BA.1.1, BA.2, and BA.3 sub-lineages

Jingwen Ai, Xun Wang, Xinyi He, Xiaoyu Zhao, Yi Zhang, Yuchao Jiang, Minghui Li, Yuchen Cui, Yanjia Chen, Rui Qiao, Lin Li, Lulu Yang, Yi Li, Zixin Hu, Wenhong Zhang, and Pengfei Wang
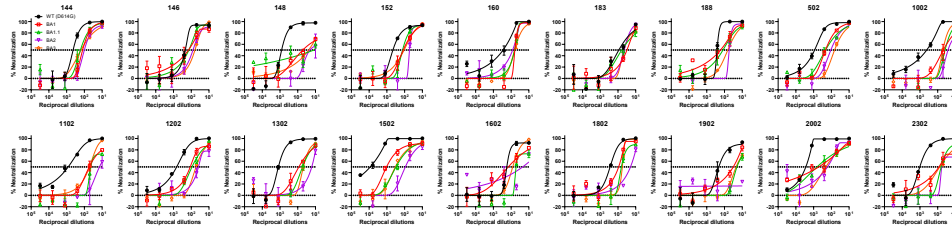
Supplementary Figures
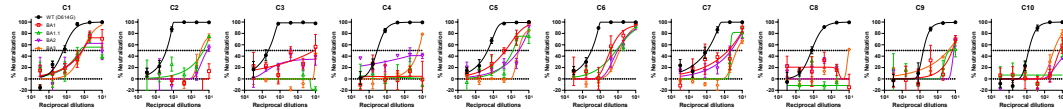
Figure S1. Neutralization curves for sera collected from individuals vaccinated with 2-dose BBIBP-CorV only (**A**), with a BBIBP-CorV homologous booster (**B**) or with a ZF001 heterologous booster dose (**C**) following two doses of BBIBP-CorV, or from individuals infected by Delta virus after vaccination (**D**).

Related to Figure 1
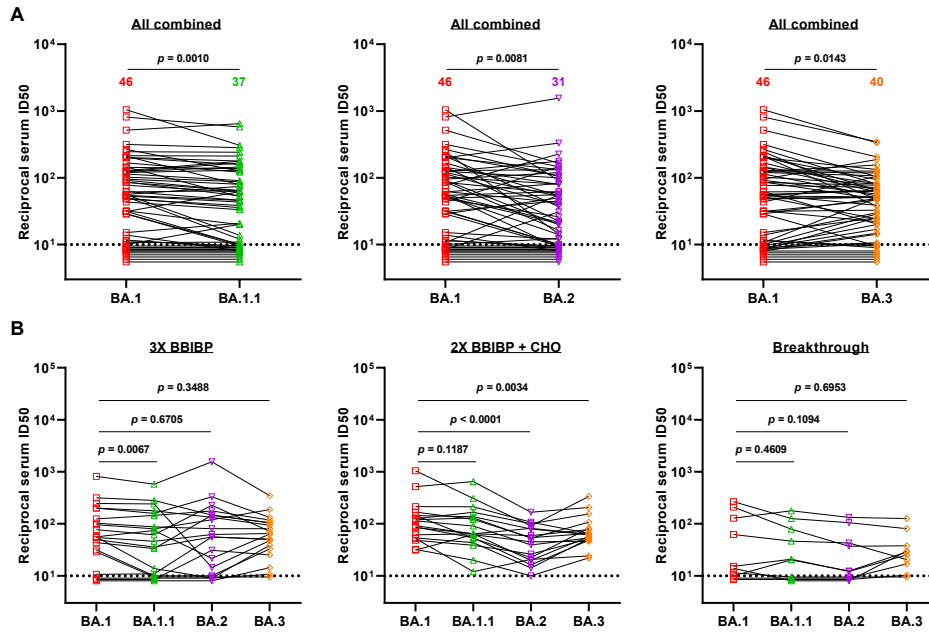
Figure S2. Comparison between BA.1 and the other Omicron sub-lineages with all the sera neutralization data combined (**A**) or within the different immunization groups (**B**). *P* values were determined by using a Wilcoxon matched-pairs signed-rank test (two-tailed).

Related to Figure 1
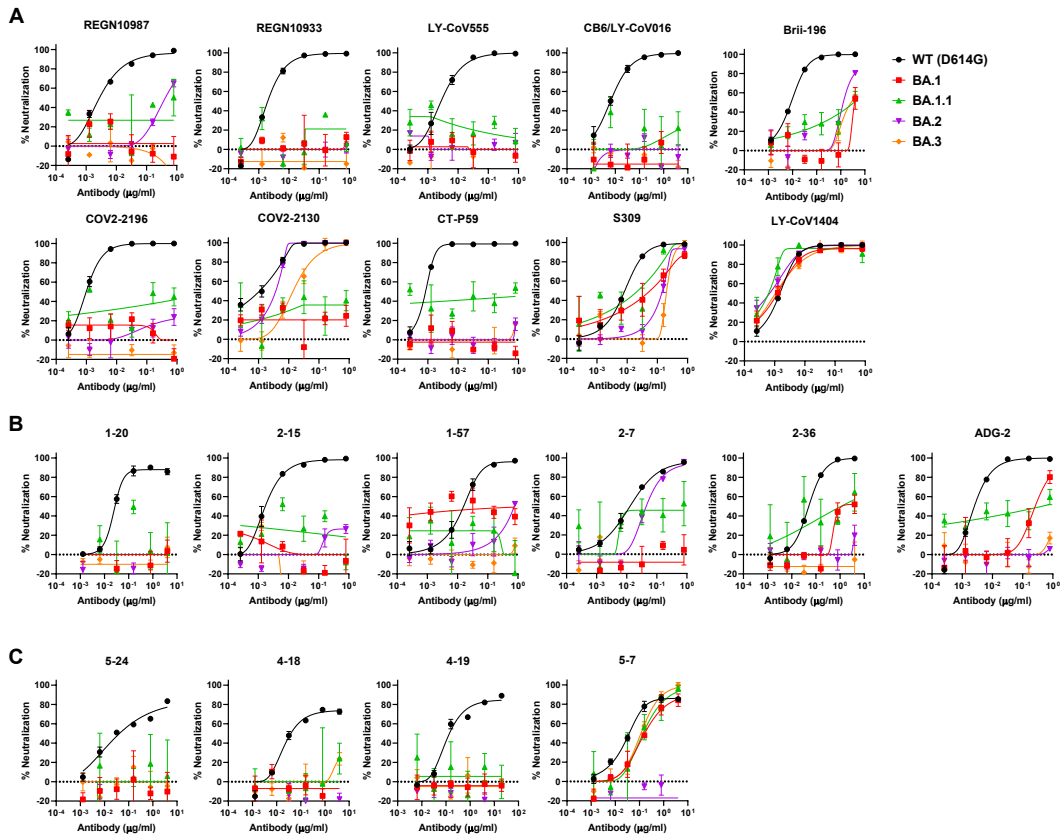
Figure S3. Neutralization curves for mAbs against WT (D614G) and Omicron sub-lineage viruses.

Related to Figure 2

Table S1. Baseline characteristics of enrolled participants, including Breakthrough infection group, BBIBP-CorV two doses group, BBIBP-CorV homologous booster group and BBIBP-CorV/ZF2001 heterologous booster group. Related to Figure 1

	Breakthrough infection (n=10)	BBIBP-CorV two doses (n=10)	BBIBP-CorV homologous booster (n=20)	BBIBP-CorV/ ZF2001 heterologous booster (n=18)	P value
Age (years), median(range)	46 (34-54)	31.5 (23-51)	28 (21-59)	29.5 (23-53)	< 0.001
Male, n (%)	3 (30.00%)	2 (20.00%)	8 (40.00%)	4 (22.22%)	0.581
BMI (kg/m^2), mean (SD)	24.45(5.64)	23.35 (3/16)	22.25 (2.96)	20.56 (2.01)	0.028
Comorbidities (%)					
Any, n (%)	4 (40.00%)	0 (0.00%)	2 (10.00%)	0 (0.00%)	0.008
Cardiovascular diseases, n (%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	/
Hypertension, n (%)	3 (30.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0.008
Diabetes, n (%)	1 (10.00%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	0.345
Interval between the first two doses (median, days)	25	14	21	16	0.010

Table S2. Calculated synergistic effects for spike mutation combinations. Related to Figure 2

	mAbs	Joint Effect	Expected Effect If Independent	Synergy Effect[a]	P value[b]
S371L+S373P+S375F	REGN10987	-16.5	-9.2	1.8	>0.9999
	REGN10933	-81.3	-5.8	**14.0**	**<0.0001**
	LY-CoV555	3.5	1.4	0.4	>0.9999
	CB6/LY-CoV016	<-630	-2.4	**1191.3**	**<0.0001**
	S309	-2.5	-2.1	1.2	>0.9999
	COV2-2130	1.5	3.1	2.1	>0.9999
	COV2-2196	1.9	3.2	1.7	>0.9999
	CT-P59	3.4	2.4	0.7	>0.9999
	Brii-196	-14.4	-12.7	1.1	>0.9999
	LY-CoV1404	1.6	-2.7	0.2	>0.9999
	1-20	-81.7	-2.4	**34.4**	**<0.0001**
	2-15	-1.5	-1.2	1.2	>0.9999
	1-57	-3.3	-6.2	0.5	>0.9999
	2-7	5.4	-1.9	0.1	>0.9999
	2-36	-11.2	-1.8	6.2	0.2371
	ADG-2	-14.4	-8.1	1.8	>0.9999
	5-24	-1.1	-22.0	0.1	>0.9999
	4-18	1.4	2.1	1.5	>0.9999
	4-19	-2.7	3.8	10.0	0.0013
	5-7	1.7	-4.7	0.1	>0.9999
Q493R+G496S+Q498R	REGN10987	-102.5	-204.9	0.5	>0.9999
	REGN10933	-180.0	-42.0	4.3	0.9339
	LY-CoV555	<-291	<-291	0.4	>0.9999
	CB6/LY-CoV016	<-630	-121.6	**15.4**	**<0.0001**
	S309	-1.4	2.1	2.9	>0.9999
	COV2-2130	-5.3	-3.2	1.7	>0.9999
	COV2-2196	-31.8	-3.0	**10.7**	**0.0008**
	CT-P59	<-949	<-949	5.4	0.4020
	Brii-196	-42.1	-424.5	0.1	>0.9999
	LY-CoV1404	-1.1	-7.1	0.2	>0.9999
	1-20	-51.8	-6.3	8.3	0.0071
	2-15	<-468	<-468	0.0	>0.9999
	1-57	<-50	<-50	0.0	>0.9999
	2-7	-1.6	-2.9	0.6	>0.9999
	2-36	-2.8	-1.5	1.8	>0.9999
	ADG-2	1.2	-5.0	0.2	>0.9999
	5-24	1.3	4.6	3.5	0.9996
	4-18	1.2	-1.4	0.6	>0.9999
	4-19	-12.5	-4.3	2.9	>0.9999
	5-7	-1.7	-2.6	0.7	>0.9999

[a]The synergy effect was calculated by comparing the joint effect (tested fold change of IC$_{50}$ compared to WT) to the expected effect of independence (calculated fold change assuming stochastical independence) with the following equation:

$$Synergy\ Effect = \frac{Joint\ Effect}{Expected\ Effect\ of\ Idenpendency} = \frac{Y|A,B,C}{Y|A \cdot Y|B \cdot Y|C}$$

[b]Outlier analysis was performed to evaluate the statistical significance of these synergy effect. The distribution of outlier boundary was estimated by bootstrapping method. We resampled all the synergy results with replacement for 10000 times. For each sampling, the outlier boundary was calculated as sum of the third quartile and 1.5 times the interquartile range. P value of each synergy effect represents the probability that this value is lower than the upper outlier boundary in the bootstrapping test.