

## Supplemental information

**Protection from SARS-CoV-2 Delta one year after**

**mRNA-1273 vaccination in rhesus macaques**

**coincides with anamnestic antibody response in the lung**

**Matthew Gagne, Kizzmekia S. Corbett, Barbara J. Flynn, Kathryn E. Foulds, Danielle A. Wagner, Shayne F. Andrew, John-Paul M. Todd, Christopher Cole Honeycutt, Lauren McCormick, Saule T. Nurmukhambetova, Meredith E. Davis-Gardner, Laurent Pessaint, Kevin W. Bock, Bianca M. Nagata, Mahnaz Minai, Anne P. Werner, Juan I. Moliva, Courtney Tucker, Cynthia G. Lorang, Bingchun Zhao, Elizabeth McCarthy, Anthony Cook, Alan Dodson, I-Ting Teng, Prakriti Mudvari, Jesmine Roberts-Torres, Farida Laboune, Lingshu Wang, Adrienne Goode, Swagata Kar, Seyhan Boyoglu-Barnum, Eun Sung Yang, Wei Shi, Aurélie Ploquin, Nicole Doria-Rose, Andrea Carfi, John R. Mascola, Eli A. Boritz, Darin K. Edwards, Hanne Andersen, Mark G. Lewis, Mehul S. Suthar, Barney S. Graham, Mario Roederer, Ian N. Moore, Martha C. Nason, Nancy J. Sullivan, Daniel C. Douek, and Robert A. Seder**

<b>Variant</b>	<b>Mutations in RBD</b>
<b>WA1</b>	None
<b>B.1.617.2</b>	L452R, T478K
<b>B.1.351</b>	K417N, E484K, N501Y

<b>Variant</b>	<b>Mutations in S-2P</b>
<b>WA1</b>	None
<b>B.1.617.2</b>	T19R, G142D, Δ156-158EFRinsG, L452R, T478K, D614G, P681R, D950N

**Table S1. List of mutations in biotinylated probes used in variant-specific MULTI-ARRAY ELISA and B cell assessments, related to Figures 1, 3, and 4**

All variant positions in reference to Wuhan-Hu-1 sequence (Genbank: MN908947.3).

Subdomain	Site	mAb		
RBD			RBD classification (Barnes et al., 2020)	RBD community (Hastie et al., 2021)
A	B1-182	+	CLASS I	RBD-1/RBD-2
B	CB6	+		
C	A20-29.1		CLASS II	RBD-4
E	LY-COV555			
F	A19-61.1	+	CLASS III	RBD-5
G	S309			

**Table S2. SARS-CoV2 S Antigenic Sites, related to Figure 2**

Monoclonal antibodies (mAbs) used to define cross-reactive antigenic sites on SARS-CoV-2 S are defined by non-competing binding on SARS-CoV-2 WA1 S. RBD-targeted mAbs have been grouped based on their RBD classification (Barnes et al., 2020) and community (Hastie et al., 2021). mAbs which have been shown to be neutralizing to B.1.617.2 variant of SARS-CoV-2 are denoted with “+”.

Time Point	Site	Assay	sgRNA_N (Copies / mL or Copies / swab)					
			Day 2 BAL	Day 4 BAL	Day 7 BAL	Day 2 NS	Day 4 NS	Day 7 NS
Week 6	Serum	WA1 S-2P Titers (BAU/mL)	0.19	-0.12	-0.34	-0.05	-0.38	0.21
Week 48	Serum	WA1 S-2P Titers (BAU/mL)	0.05	-0.19	-0.34	-0.48	-0.45	0
Week 6	Serum	B.1.617.2 RBD IgG Titers (AUC)	0.1	-0.1	-0.1	-0.26	-0.36	0
Week 48	Serum	B.1.617.2 RBD IgG Titers (AUC)	-0.1	-0.24	-0.1	-0.43	-0.26	-0.05
Week 6	BAL	B.1.617.2 RBD IgG Titers (AUC)	0.17	0.02	-0.17	-0.38	-0.67	-0.4
Week 42	BAL	B.1.617.2 RBD IgG Titers (AUC)	-0.4	-0.52	-0.37	-0.45	-0.43	-0.57
Week 6	Nasal Wash	B.1.617.2 RBD IgG Titers (AUC)	-0.1	-0.24	-0.22	-0.52	-0.45	-0.21
Week 42	Nasal Wash	B.1.617.2 RBD IgG Titers (AUC)	-0.12	-0.31	-0.22	-0.33	-0.21	0.07
Week 6	BAL	B.1.617.2 RBD IgA Titers (AUC)	0.29	0.1	-0.39	-0.02	-0.07	0.38
Week 42	BAL	B.1.617.2 RBD IgA Titers (AUC)	-0.26	-0.24	-0.05	0.12	0.14	-0.17
Week 6	Nasal Wash	B.1.617.2 RBD IgA Titers (AUC)	-0.21	0	-0.1	-0.55	0.36	-0.02
Week 42	Nasal Wash	B.1.617.2 RBD IgA Titers (AUC)	-0.1	0.12	0.17	-0.64	0.19	-0.14
Week 6	Serum	D614G Pseudovirus NT (ID <sub>50</sub> )	-0.1	-0.12	0.27	-0.31	-0.43	-0.38
Week 48	Serum	D614G Pseudovirus NT (ID <sub>50</sub> )	0.21	0.19	-0.24	<b>-0.81</b>	-0.45	-0.31
Week 6	Serum	B.1.617.2 Pseudovirus NT (ID <sub>50</sub> )	0.33	0.1	-0.51	-0.38	<b>-0.71</b>	-0.21
Week 48	Serum	B.1.617.2 Pseudovirus NT (ID <sub>50</sub> )	0.32	0.31	-0.11	<b>-0.72</b>	-0.35	-0.12

**Table S3. Correlates analyses of antibody responses and virus subgenomic copy numbers, related to Figure 6 and S6**

Correlations between antibody responses in the blood, BAL, and nasal washes at week 6 (peak) or at week 42-48 (memory and time of challenge) to sgRNA\_N copy numbers in the BAL and nose at days 2, 4, and 7 after B.1.617.2 challenge. Values listed are Spearman correlation coefficient (R). R values in red denote correlations that are statistically significant ( $p < 0.05$ ). All analyses are exploratory, and significant associations should be viewed as suggestive.