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432 **Supplemental Figure 1. Additional viral load curves and transmission plots by household in**

433 **the primary analysis set.** Households are shown where either a shared exposure exists or

434 possible transmission has occurred, as all cases are genetically linked to the index case.

435 Households are shown where two separate infection clusters were identified.

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SUPPLEMENTAL TABLES

Supplemental Table 1. Additional Baseline Data

Characteristic	All Participants (N=99)	Index Cases (N=33)	Contacts (N=66)
Currently Working / Employment (N, %) – <i>missing 13</i>			
Yes	57 (66.3)	18 (69.2)	39 (65.0)
No	29 (33.7)	8 (30.8)	21 (35.0)
Missing	13	7	6
Student (N, %) – <i>missing 9</i>			
Yes	32 (35.6)	13 (43.3)	19 (31.7)
No	58 (64.4)	17 (56.7)	41 (68.3)
Missing	9	3	6
If yes (N=32), level (N, %)			
Elementary	11 (34.4)	5 (38.5)	6 (31.6)
Middle School	12 (37.5)	5 (38.5)	7 (36.8)
High School	5 (15.6)	2 (15.4)	3 (15.8)
Community College	0	0	0
College or University	4 (12.5)	1 (7.7)	3 (15.8)
Currently Uses eCigarettes/Vape (N, %) – <i>missing 9</i>	1 (1.1)	0	1 (1.6)
Currently Smokes Cigarettes (N, %) – <i>missing 9</i>	1 (1.1)	0	1 (1.6)

History of Smoking Cigarettes (N, %) – missing 10	11 (12.4)	3 (10.3)	8 (13.3)
If yes, packs per day (N, %)			
0.5	7 (63.6)	1 (33.3)	6 (75.0)
1.0	4 (36.4)	2 (66.7)	2 (25.0)
1.5	0	0	0
2.0	0	0	0
2.5	0	0	0
3 or more	0	0	0
If yes, how many years (N, %)			
1-5	8 (72.7)	2 (66.7)	6 (75.0)
5-10	0	0	0
10-15	1 (9.1)	0	1 (12.5)
15-20	0	0	0
20 or more	2 (18.2)	1 (33.3)	1 (12.5)
Concurrent Use of Steroids or Immune Suppressing Medications (N, %) – missing 12	6 (6.9)	1 (3.6)	5 (8.5)
Concurrent use of NSAIDs – missing 13	38 (44.2)	10 (37.0)	28 (47.5)

Supplemental Table 2. Baseline Characteristics of Study Households in Primary Analysis Set

Characteristic	Total Households (N=33)
Number of persons in household (Median, Min-Max)	3.5 (2-5)
House size (in square feet) as reported by index (Median, Min-Max)	1400 (740-3300)
Missing or unknown data from 11 households	

Supplemental Table 3. SARS-CoV-2 Viral Kinetics in Primary Analysis Set, Excluding 2 Cases of Outside Introduction

Outcome	Index Cases (N=30)^a	Infected Contacts (N=26)
Lowest Ct (median, min-max)	25.65 (15.9-35)	23 (8.1-36.2)
Duration of viral shedding ^b (median, min-max)	6.5 days (1-19)	8 days (1-20)
Time to first positive SARS-CoV-2 from index diagnosis date	N/A	3 days (0-10)

a. Excluding 3 index cases who were PCR negative at baseline.

b. From first positive SARS-CoV-2 test.

Supplemental Table 4. Sequencing Performance

Household	Participant	Samples	Samples Producing Genome with Minimum Unambiguous Genome Length of 15 kbp
AXB	1	1	0
	2	6	5
JRP	1	5	5
	2	6	6
ODK	1	1	1
EGI	1	6	6
	4	5	4
CWA	1	4	3
	2	4	3
VBL	1	1	1
TSE	1	1	1
	2	6	5
KQX	1	1	1
DUC	1	2	1
	2	8	7
MPO	2	5	4
	3	9	7
	4	4	3
HXJ	1	4	1
	3	5	5
BQE	1	7	5
	2	5	5
SVW	1	1	1

IRG	1	2	2
	2	6	6
	3	4	3
	4	8	5
LCT	1	7	5
	4	11	9
	5	9	9
PFK	1	1	1
	4	2	1
JDU	1	1	1
XOA	1	6	1
	2	4	4
REZ	1	1	0
WMD	1	2	1
	3	4	3
HSA	1	1	1
	2	5	3
YVB	1	1	0
NKF	1	1	1
	2	1	0
QEC	1	1	1
OXS	1	2	2
	2	1	1
	4	2	2
LME	1	1	1

Supplemental Table 5. Household Transmission Analysis

Household	Transmission Direction	SNV Distance	Difference in Dates of Diagnosis (Days)	iSNV Information	Transmission Pair Categorization	Household Transmission Categorization
JRP	1>2	1	4		Highly probable	Highly probable
EGI	1>4	1	4		Highly probable	Highly probable
CWA	1>2	0	2	C21721T; T22917A; C23673T present at mixed sites in 1 (possible BA.2.12.1 & BA.2.10 co-infection) and fixed in 2	Possible	Possible
	2>1	0	-2		Possible	
TSE	1>2	3	5		Unlikely	Unlikely
	2>1	3	-5		Unlikely	
DUC	1>2	0	2		Possible	Possible
	2>1	0	-2		Possible	
MPO	4>2	0	3		Possible	Possible
	4>3	0	6		Possible	
	2>4	0	-3		Possible	
	2>3	0	3		Possible	
HXJ	1>3	0	1	share C23393T at < 10% frequency	Possible	Possible
	3>1	0	-1		Possible	
BQE	2>1	0	2		Possible	Possible
	1>2	0	-2		Possible	
IRG	1>4	3	2		Unlikely	Mixed household
	4>1	3	-2		Unlikely	
	4>2	0	3		Possible	
	4>3	0	5		Possible	
	2>3	0	2		Possible	
LCT	4>1	4	1		Unlikely	Mixed household

SUPPLEMENTAL FIGURE 1

