Supplementary information:

Behavioral factors and SARS-CoV-2 transmission heterogeneity within a household cohort in Costa Rica

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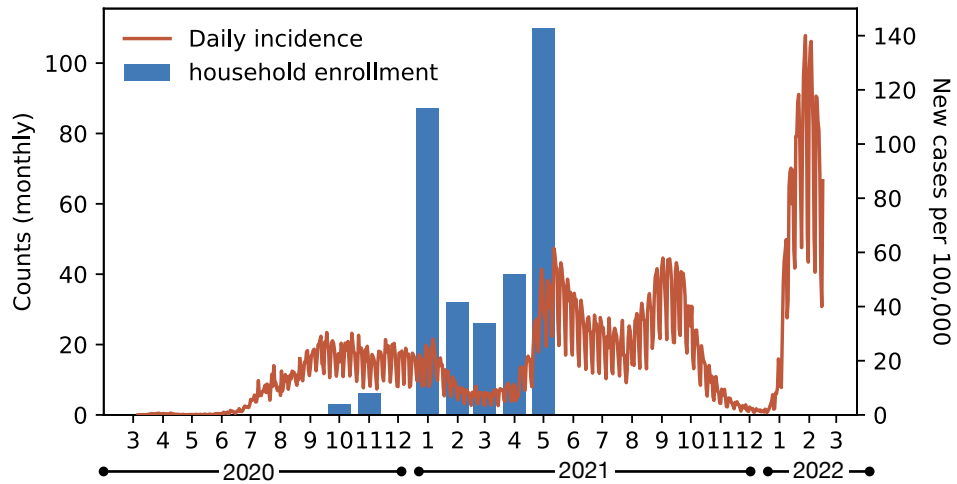
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**Table S1:** Model selection on the risk factors for household chain-binomial transmission model.

| Model	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Log Likelihood	477	476	475	467	467	465	463	462	437	429	420	418	416	415	413	412
Akaike Information Criterion (AIC)	959	955	965	957	957	957	955	954	907	891	876	876	876	877	878	880
ΔAIC	0	-4	+6	-2	-2	-2	-4	-5	-52	-68	-83	-83	-83	-82	-81	-79
Baseline — Baseline community risk	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Index case & seropositive household members	*															
Index case		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Seropositive household members		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Risk factors — Cumulative incidence rate (relative community risk)		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Age, transmissibility			*	*	*	*	*	*	*	*	*	*	*	*	*	*
Age, susceptibility				*	*	*	*	*	*	*	*	*	*	*	*	*
Sex, transmissibility					*	*	*	*	*	*	*	*	*	*	*	*
Sex, susceptibility						*	*	*	*	*	*	*	*	*	*	*
Obesity, transmissibility							*	*	*	*	*	*	*	*	*	*
Obesity, susceptibility								*	*	*	*	*	*	*	*	*
Household size									*							
Log2 (No. of household contacts)										*	*	*	*	*	*	*
Shared bedroom with index (Y/N)											*	*	*	*	*	*
Cared for index (Y/N)												*	*	*	*	*
If wore mask > half of the time (index case)													*	*	*	*
If wore mask > half of the time (household member)														*	*	*
Hours with index outside bedroom															*	*
If symptomatic																*

Figure S1: Daily incidence of reported SARS-CoV-2 cases in Costa Rica (red line) and the monthly number of enrolled households based on the index cases' diagnosis time (blue bar).
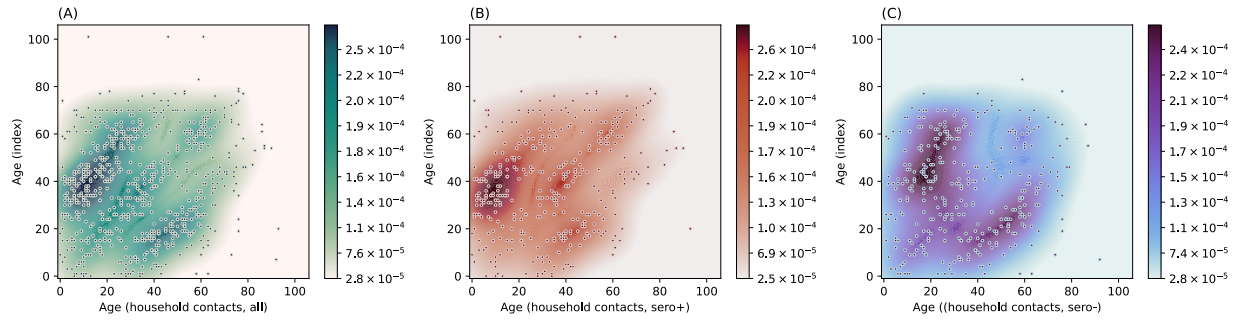
Figure S2: (A) Contact patterns between index cases and household members. Each dot represents the age pairs between index and household member and heatmap represents the frequency. (B) Same as (A) but only for seropositive household members only. (C) Same as (A) but for seronegative household members only. Colorbars indicate probability density.

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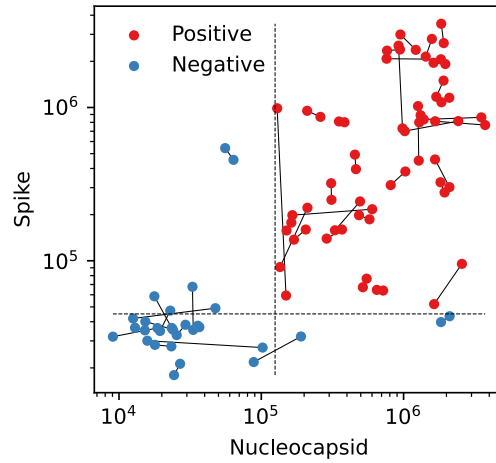
Figure S3: The results of the serologic readout for the quality control samples (including both pre-pandemic samples as negative control and a subset of the study sample). Each sample were tested in duplicate (connected by the solid line). The dashed lines are pre-defined positive cutoff for both the Nucleocapsid and the Spike protein. We require a seropositive sample (red dots) as being positive on both spike and nucleocapsid proteins and seropositive otherwise (blue dots). For the quality control samples, all duplicates give consistent results on seropositivity.
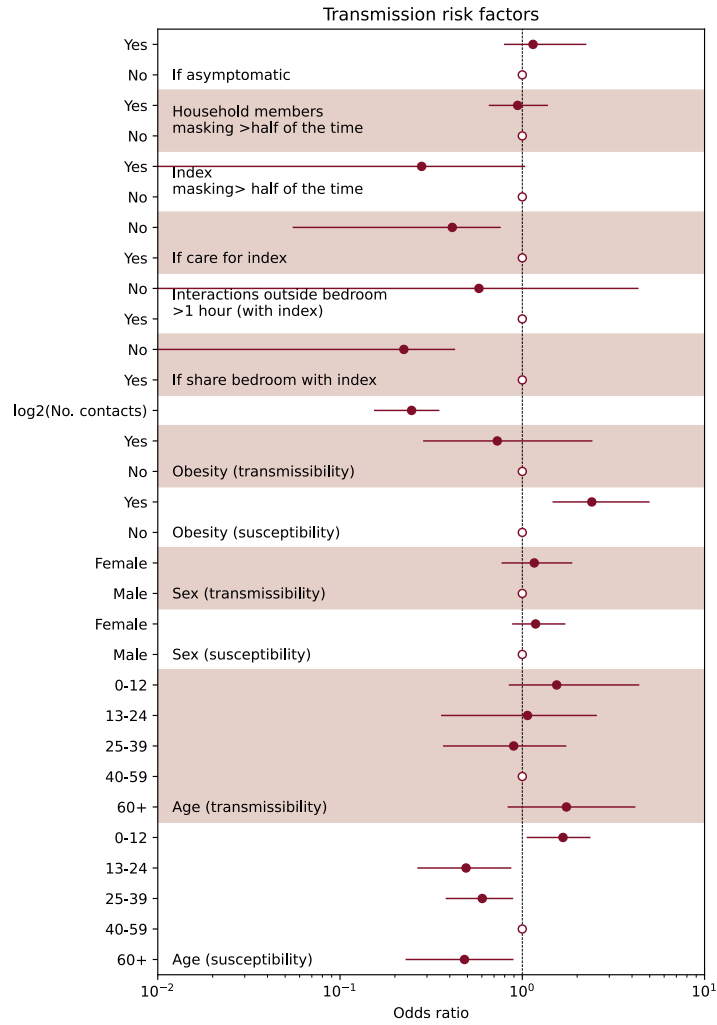
Figure S4: Estimates from the chain-binomial household transmission model with household level bootstrapping. Solid dots and horizontal lines represent point estimates and 95% confidence intervals of the adjusted odds ratios of transmission risk factors. Circles represent the reference class.
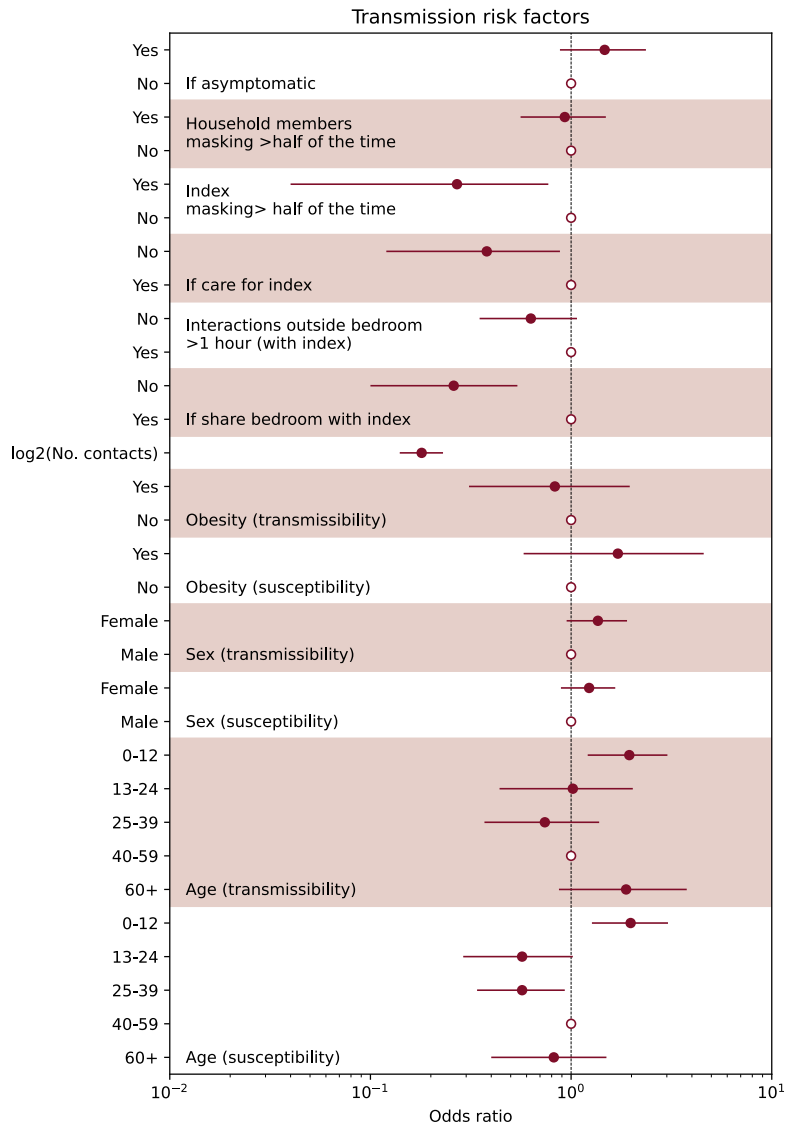
Figure S5: Estimates from the chain-binomial household transmission model excluding households with either index case or household members who had received vaccination prior or during the study period. Solid dots and horizontal lines represent point estimates and 95% confidence intervals of the adjusted odds ratios of transmission risk factors. Circles represent the reference class.