***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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No sample size calculation was performed since this study did not include the collection of novel data.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Biological replication: this does not apply since this study did not include the collection of novel data.

Technical replication: the number of steps used in our Markov chain Monte Carlo model fitting procedure is given in the Materials and Methods (“Likelihood and model fitting”). This fitting procedure was also tested using simulated data to ensure convergence in these test cases.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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No statistical analyses were performed on raw data. Bayesian (Markov chain Monte Carlo) methods were used to fit the models. The fitting procedure is described in the Materials and Methods (“Likelihood and model fitting”), and full details including choices of priors are provided in the Appendix (“Details of model fitting procedure”). ΔAIC values, indicating the relative goodness of fit of the different models, are given in the Results. Central estimates and credible intervals for fitted parameters are given in Supplementary File 1.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

A source data file has been provided for Figure 2, containing the SARS-CoV-2 transmission pair data used in our analyses. Code for reproducing our results is available at https://github.com/will-s-hart/COVID-19-Infectiousness-Profile.