***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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This is an epidemiological study of an infectious disease outbreak.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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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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Not applicable, as above.

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* Statistical analysis methods should be described and justified
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Statistical analysis methods are described in full in the supplementary material, measures of uncertainty are reported for all results from statistical analyses and analysis code is provided.

(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
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* 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
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Analysis code is included in the supplementary materials. Datasets analysed and generated during this study are included in the supplementary materials. For estimates of the time-varying effective reproduction number (Figure 2), the complete line listed data within the Australian national COVID-19 database are not publicly available. However, we provide the cases per day by notification date and state (as shown in Figures 1 and S1) which, when supplemented with the estimated distribution of the delay from symptom onset to notification (samples from this distribution are provided as a data file), the same analyses of the time-varying effective reproduction number can be performed and similar results generated.