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

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

To assess sample size in a study in our critical appraisal tool, we used the following calculation:

where is the sample size threshold, is the z-score for the level of confidence (95%), is the standard deviation (assumed to be 3 log10 copies/ml, one quarter of the full range of rVLs) and is the marginal error (assumed to be 1 log10 copies/ml, based on the minimum detection limit for qRT-PCR across studies) (Johnston, Lakzadeh, Donato, & Szabo, 2019). This is described in the Methods section/

**Replicates**

* 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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* Criteria for exclusion/inclusion of data should be clearly stated
* 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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The number of studies, specimen numbers or case numbers are shown in each figure, its caption or each table in our study.

**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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The statistical tests used in each figure are described in the caption. Greater detail on these statistical tests is described in the Methods section. Exact P-values above 0.001 are reported. Raw data in the meta-regression was presented in Fig. 2 (see the circles). Raw data in the kinetic analysis was presented in Fig. 4D (see the circles). 95% CIs are specified throughout the results section, in figures or in figure supplements. Sample numbers are described throughout the results section, in figures or in figure supplements.

(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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Definitions of symptomatology or age subgroups were defined in the Methods section. As our study was based on a systematic review and meta-analyses, there was no experimental groups or randomization.

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

This manuscript includes a Data Availability statement, which reads “The systematic dataset and model outputs from this study are uploaded to Zenodo (https://zenodo.org/record/4658971). The code generated during this study is available at GitHub (https://github.com/paulzchen/sars2-heterogeneity). The systematic review protocol was prospectively registered on PROSPERO (registration number, CRD42020204637).”