***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
* 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:

Section "Supplementary Exploratory Analysis" in "Appendix 1.

Section "Stochastic model fitted for 3B super resolution microscopy" in Appendix 1.

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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)

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:

Main Text: Section “Qualitative analysis of VP morphology and structure through SRM”.

Appendix 1: “Supplementary Exploratory Analysis”

Appendix 1: “Stochastic model fitted for 3B super resolution microscopy”

Initially, a set of three independent experiments to analyze the NSP2-NSP4, NSP2-NSP5, NSP2, VP4, NSP2-VP7Mon, and NSP2-VP7Tri combinations was carried out. For each experiment, enough images were collected to obtain 60 viroplasms per combination. The experiments were performed around two to three weeks apart. Six months after these experiments, a second set of two independent experiments to analyze the NSP2-VP1, NSP2-VP2, NSP5-VP4, NSP5-VP6, and NSP4-VP6 combinations was carried out. As above, 60 viroplasms per pairwise combination were collected. The experiments were done around two weeks apart.

**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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Appendix 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
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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:

**NSP2.scv**: - All the graphics in the main text.

- Section “Model Considerations” in Appendix 1 (all figures and tables).

- Section “Supplementary Exploratory Analysis” in Appendix 1 (all figures and tables).

- Section “Linear dependency between the viral components” in Appendix 1 (all figures and tables).

**NSP4.scv and NSP5.scv**: Section “NSP5 and NSP4 as reference proteins” in Appendix 1 (all figures and tables).

**Validation\_Circle\_Hypothesis.csv:** Section “Model Considerations” in Appendix 1 (all figures and tables).

**Algorithm\_Validation.csv**: Section “Algorithm Validation” in Appendix 1 (all figures and tables).