***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:

not applicable. We have investigated 4 different Spike genes: the original Wuhan SARS-CoV-2 Spike gene, and 3 different codon-optimized Spike open reading frames cloned into 3 different adenoviral vector systems

**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
* If you encountered any outliers, you should describe how these were handled
* 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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Luciferase assays have been performed with 6 technical replicates when analyzing intracellular Luciferase activity. Supernatant Luciferase activity has been measured once only.

DNA Sequencing analyses of splice sites have been done after performing by RT-PCR experiments, cutting out gel slices and cloning the extracted DNA into into Topo TA 2.1 vectors, Subsequently, clones were picked, minilysates have been prepared and isolated DNA was sequenced. We have sequences about 300 clones to obtain the presented spectrum of splice sites. All relevant data is already given in the Figure 4-8 and 11 of the current manuscript-

Western blot experiments have been performed twice (9 different cell lines,2 different antibodies, 1x supernatant and 1x intracellular).

**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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(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:

The original WUHAN SARS-CoV-2 sequence is available by the NCBI database (NCBI Reference Sequence: NC\_045512.2); the adenoviral and codon-optimized Spike sequence data have a protected intellectual property by the companies. The primary sequence of Ad5.S, designed and used by the colleagues in Ulm, can be retrieved upon request (please contact Prof. Stefan Kochanek).