



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](#)), life science research (see the [BioSharing Information Resource](#)), or the [ARRIVE guidelines](#) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

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:

- Sample sizes can be found in the "Results" section.
- MnPV is spread in the colony via natural infection. While some animals do not seroconvert throughout their life and are considered uninfected, infected animals have unequal infection histories regarding time point, viral load and therefore seroconversion.
- Based on discrepancy rates of 5% for $L1_{SHORT}^+/L1_{LONG}^-$ and 25% for $L1_{SHORT}^-/L1_{LONG}^+$ among usable animals, and a general loss rate of 15% of the animals, the use of 60 animals gives a power of >80% (two-tailed McNemar's test, alpha = 5%) to differentiate between seroconversion against the long and the short L1 variant.

- The used animals originated from the different breeding families available in the colony to represent the whole colony population.

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)

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:



- Regarding the animal experiments, this information is explicitly described in the “Results” section and the respective figure legends.
- GST-ELISAs of all sera and for all antigens tested were performed in technical replicates (analysis of the same serum sample). No outliers were excluded.
- Numbers of biological replicates (analysis of different cells from different passages) of the other experiments are indicated in the respective figure legends in the “Results” section.
- The examination of the different monoclonal antibodies (Figure 7), however, was performed in technical replicates (analysis of the same antibody-containing hybridoma supernatant).

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.

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:

- Statistical tests used for the individual experiments are explained in detail within the “Material & Methods” section and individual information for the experiments are given in the respective figure legends.

(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:

- No grouping was performed.
- However, when stated in the respective figure legend, the shown correlation only included sera with distinct reactivities, thereby excluding others (e.g. L1_{LONG}⁺/L1_{SHORT}⁻ sera in Figure 4C).



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:

- Does not apply.