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* You should state whether an appropriate sample size was computed when the study was being designed
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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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Participant inclusion and experiments carried out were explained in detail in Methods sections Human Subjects, Neutralization Assay, Single-cell flow cytometry sorting. Sequence generation and processing can be found in Methods section B-cell receptor sequencing. Sequence repertoire, along with the annotations used to present results are available as part of the publication in Supplementary file 2.

**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)
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Statistical methods used are described in Methods B-cell receptor sequencing and Analysis sections. Statistical tests and significance measures can also be found in legends and in Results section where necessary.

(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.)

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* 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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All BCR sequences analysed in this manuscript are provided as Supplementary file 2 with all necessary annotations that are found as part of the analysis carried out in this manuscript.