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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.

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* Statistical analysis methods should be described and justified
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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.