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Corresponding author(s): George Fu Gao

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☒	☐	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Not applicable to this study, no algorithms or software not previously described was used.
Data analysis	Not applicable to this study.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

There are no restrictions on data availability.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	For mice experiments, the study is powered to confirm a difference in survival of at least 100% at the 95% confidence interval with 80% power, as calculated with the following website from the UCSF Clinical & Translational Science Institute: http://www.sample-size.net/sample-size-proportions/. For the samples in flow cytometry, experiments were performed in duplicate or triplicate, as indicated in the Materials and Methods, and Figure legends.
Data exclusions	No data were excluded.
Replication	The mice experiment was not repeated due to robust findings in the animal experiments (with different antibodies) and supporting structural data. Cell staining assays were performed in duplicate or triplicate, as indicated in the Materials and Methods, and Figure legends.
Randomization	The animals used in this study were allocated by random individual numbering into experimental groups (i.e. A1, A2, B1, B2...etc.)
Blinding	The investigators were not blinded to the study.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	anti-His/PE: Miltenyi Biotec, Cat No: 130-092-691; anti-hCD3/PE-Cy™5: BD Pharmingen™, Material Number: 555334; anti-hCD16/PE-Cy™5: BD Pharmingen™, Material Number: 555408 anti-hCD19/APC-Cy™7: BD Pharmingen™, Material Number: 557791 anti-hCD27/Pacific Blue™: BioLegend, Catalog # 302821 anti-hCD38/APC: BD Pharmingen™, Material Number: 555462 anti-CD235a/PE-Cy™5: BD Pharmingen™, Material Number: 559944 anti-hIgG/FITC: BD Pharmingen™, Material Number: 555786 anti-hIgG/APC: BioLegend, Catalog # 409306 Streptavidin-PE: BD Pharmingen™, Catalog # 554061
Validation	We follow the manufactures' instruction to use the above listed antibodies to stain human PBMCs. All antibodies work well.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	ATCC
Authentication	The cell lines were not authenticated since they were purchased commercially and are not commonly misidentified.

Mycoplasma contamination	The cells were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	The cell lines used in this study do not appear on the ICLAC register.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	BALB/c, female, 6-8 weeks old
Wild animals	Not applicable to this study.
Field-collected samples	Not applicable to this study.

Human research participants

Policy information about studies involving human research participants

Population characteristics	We used the blood of the first imported Rift Valley fever case in China. The patient was 45-year-old man when the biospecimen was collected.
Recruitment	On Day 7 of the disease onset, the patient returned from Angola to Beijing and was admitted to Beijing Ditan Hospital. Upon admission to the hospital, the patient agreed to provide the biospecimen for detection, further diagnostic and scientific research.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Sample preparation listed in Methods
Instrument	BD FACSAria II, BD FACSCalibur and BD FACSCanto II.
Software	FlowJo
Cell population abundance	After cell sorting, the collected cells were subjected for RT-PCR to determine the genes of the IgG. Thus, we did not test the relevant cell populations within post-sort fractions.
Gating strategy	For the isolation of antigen-specific memory B cells, we used the unstained PBMCs as control to gate cells. In order to evaluate the binding of indicated MAbs to the specific antigen, cells that expressed M genes and were stained with anti-hIgG/APC, were used as the control for gating. In order to evaluate the effectiveness of the indicated MAb on preventing the binding of Gn tetramers to Huh7, Huh7 cells that were sequentially incubated with MHC-tetramer and streptavidin-PE were used as the control to gate cells. To investigate the interaction of Gn MAbs with RVFV, Vero or Huh 7 cells incubated with RVFV and then sequentially fixed with PFA, stained with Z3L1 (MAb against Zika, used as negative control) and anti-hIgG/APC were used as control to gate cells. To test the blocking effect of RVFV MAb on viral attachment, cells stained with indicated MAb and anti-hIgG/APC used as control to gate the cell. To evaluate the interaction between Gn MAbs and Gn mutants, HEK293T cells, which transiently expressed GFP-tagged Gn mutants, stained with Z3L1 used as control to gate cells. To map the critical patch for indicated MAbs binding, HEK293T cells, which transiently expressed RVFV-Gc-eGFP and stained with indicated MAb as control to gate the cell.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.