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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 our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on 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 statistical parameters 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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection
GraphPad Prism 8 for windows 64-bit (Version 8.4.3)

Data analysis
GraphPad Prism 8 for windows 64-bit (Version 8.4.3)

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 and reviewers. 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

All data generated or analyzed during this study are included in this article (and its supplementary files). The detailed study design of the phase I clinical trial was published previously. The full trial protocol can be accessed by submitting an enquiry to Merck & Co. via the website: http://engagezone.msd.com/doc/ProcedureAccessClinicalTrialData.pdf.
Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

**Sample size**

It is a sub-study of a previous phase I clinical trial (NCT01986010, registered on November 18th, 2013). The trial was a 2-part, single-blind, randomized, placebo-controlled, dose-escalating study, conducted at 9 clinical sites in the United States. In this sub-study, to characterize the vaccine-induced monoclonal antibodies, we selected, at random, six vaccinated participants from: the 30U intramuscular injection group (n = 3, seronegative, without adjuvant, enrolled in Virginia Commonwealth University), the 30U intradermal injection group (n = 3, seronegative, without adjuvant, enrolled in University of Texas Medical Branch), and the two placebo controls of the intradermal injection group (n = 2, without adjuvant, enrolled in University of Texas Medical Branch).

**Data exclusions**

No data was excluded.

**Replication**

Three replications in each group for the antibody characterization of this study.

**Randomization**

The subjects were randomly picked from the indicated groups.

**Blinding**

The investigators were not blinded in the data collection in this study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

**Materials & experimental systems**

- n/a
- Antibodies
- Eukaryotic cell lines
- Palaeontology and archaeology
- Animals and other organisms
- Human research participants
- Clinical data
- Dual use research of concern

**Methods**

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

Antibodies

**Antibodies used**

All antibodies are generated in-house.

**Validation**

Viral neutralization assay and viral antigen binding assay.

Eukaryotic cell lines

**Policy information about cell lines**

- Cell line source(s)
  - Both ARPE-19 and MRC-5 are purchased from ATCC
- Authentication
  - None of the cell lines used were authenticated
- Mycoplasma contamination
  - All cell lines are negative for mycoplasma contamination
- Commonly misidentified lines
  - See ICLAC register
  - n/a
Palaeontology and Archaeology

Specimen provenance
Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).

Specimen deposition
Indicate where the specimens have been deposited to permit free access by other researchers.

Dating methods
If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

 Ethics oversight
Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Animals and other organisms

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

Laboratory animals
For laboratory animals, report species, strain, sex and age OR state that the study did not involve laboratory animals.

Wild animals
Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.

Field-collected samples
For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.

Ethics oversight
Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Human research participants

Policy information about studies involving human research participants

Population characteristics
The informations were listed in supplementary Table 1. Age range 20s-40s; include both male and female, are HCMV seronegative at the time of enrollment of this study.

Recruitment
The subjects in this study are recruited by two separate clinical sites, and are HCMV seronegative subjects. Healthy subjects eligible for inclusion in this sub-study were over 18 years of age with bodyweight more than 50 kg and body mass index 19 - 32 kg/m2.

Ethics oversight
Western Institutional Review Board, Inc.; Institutional Review Board of UTMB

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration
NCT01986010, registered on November 18th, 2013

Study protocol
The full trial protocol can be accessed by submitting an enquiry to Merck & Co. via the website: http://engagezone.msd.com/doc/ProcedureAccessClinicalTrialData.pdf.

Data collection
We selected, at random, six vaccinated participants from: the 30U intramuscular injection group (n = 3, seronegative, without adjuvant, enrolled in Virginia Commonwealth University), the 30U intradermal injection group (n = 3, seronegative, without adjuvant, enrolled in University of Texas Medical Branch), and the two placebo controls of the intradermal injection group (n = 2, without adjuvant, enrolled in University of Texas Medical Branch). Human memory B cells were isolated from these subjects, the cells culture and screening of HCMV specific antibodies were performed. We characterized the antibodies for the binding the neutralizing to HCMV.

Outcomes
Primary outcome: The serum neutralizing titer of the subject after vaccination.
Secondary outcome: The binding specificity the neutralizing activity of vaccine induced monoclonal antibodies from the subjects
Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No  Yes

-公共健康
-国家安全
-农作物和/或家畜
-生态系统
-其他重要的领域

Experiments of concern

Does the work involve any of these experiments of concern:

No  Yes

-示证如何使疫苗无效
-使抗微生物或抗病毒药物无效
-增强病原体的毒性或使非病原体成为病原体
-增加病原体的传播性
-改变病原体的宿主范围
-使诊断/检测工具失效
-使生物武器或毒素成为武器
-任何其他可能有害的组合实验和病原体

ChIP-seq

Data deposition

-确认原始和最终处理的数据已被存入公共数据库，如GEO。
-确认您已存入或提供图文件（如BED文件）作为已调用的峰。

Methodology

-重复实验：说明实验的重复方式，包括数量、类型和重复一致。
-测序深度：描述每个实验的测序深度，包括总的读数数量、唯一映射的读数长度和读数是配对还是单端。
-抗体：描述ChIP-seq实验使用的抗体，如适用，则提供供应商名称、目录号、克隆号和批号。
-峰调用参数：指定读取映射和峰调用的命令行程序和参数，包括Chip、控制和索引文件。
-数据质量：描述确保数据质量的全方法，包括峰的个数。
-软件：描述用于收集和分析ChIP-seq数据的软件。对于已存入社区存储库的自定义代码，提供访问细节。
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
Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

Instrument
Identify the instrument used for data collection, specifying make and model number.

Software
Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.

Cell population abundance
Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.

Gating strategy
Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between “positive” and “negative” staining cell populations are defined.

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

Magnetic resonance imaging

Experimental design

Design type
Indicate task or resting state, event-related or block design.

Design specifications
Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures
State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)
Specify: functional, structural, diffusion, perfusion.

Field strength
Specify in Tesla

Sequence & imaging parameters
Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.

Area of acquisition
State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.

Diffusion MRI
- Used
- Not used

Preprocessing

Preprocessing software
Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization
If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template
Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal
Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).
**Volume censoring**

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

**Statistical modeling & inference**

**Model type and settings**

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

**Effect(s) tested**

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

**Specify type of analysis:**

- [ ] Whole brain
- [ ] ROI-based
- [ ] Both

**Statistic type for inference**

(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

**Correction**

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

**Models & analysis**

| n/a | Involved in the study |
|-----|-----------------------|
|     | Functional and/or effective connectivity |
|     | Graph analysis |
|     | Multivariate modeling or predictive analysis |

**Functional and/or effective connectivity**

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

**Graph analysis**

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

**Multivariate modeling and predictive analysis**

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.