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.

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
- BD LSR Fortessa SORP
- BD FACS Aria SORP
- Olympus IX83 FV1200
- Thermo ARRAYSCAN VTI HCS Reader
- Bio-Rad CFX96 Real-Time System
- FluorChem FC3

Data analysis
- GraphPad Prism 6.0
- ImagJ 1.5
- FlowJo2
- Imaris9
- Bio-Rad CFX Maestro

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. 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 analysed during this study are included in this published article and supplementary information file.
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.

- [x] 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.

<table>
<thead>
<tr>
<th>Sample size</th>
<th>Each QPCRs and FACs experiment has been performed at least 3 times (n ≥ 3) and each n has at least 2 technical repeats. Blot analyses were performed at least twice.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data exclusions</td>
<td>No data were excluded.</td>
</tr>
<tr>
<td>Replication</td>
<td>Each QPCRs and FACs experiment has been performed at least 3 times (n ≥ 3) and each n has at least 2 technical repeats. Blot analyses were performed at least twice.</td>
</tr>
<tr>
<td>Randomization</td>
<td>No randomization was performed.</td>
</tr>
<tr>
<td>Blinding</td>
<td>No blinding was performed.</td>
</tr>
</tbody>
</table>

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**

<table>
<thead>
<tr>
<th>Materials &amp; experimental systems</th>
<th>n/a</th>
<th>Involved in the study</th>
</tr>
</thead>
<tbody>
<tr>
<td>Antibodies</td>
<td>[x]</td>
<td>[x]</td>
</tr>
<tr>
<td>Eukaryotic cell lines</td>
<td>[x]</td>
<td>[x]</td>
</tr>
<tr>
<td>Palaeontology</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Animals and other organisms</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Human research participants</td>
<td>[x]</td>
<td>[x]</td>
</tr>
<tr>
<td>Clinical data</td>
<td>[x]</td>
<td>[x]</td>
</tr>
</tbody>
</table>

**Methods**

<table>
<thead>
<tr>
<th>Methods</th>
<th>n/a</th>
<th>Involved in the study</th>
</tr>
</thead>
<tbody>
<tr>
<td>ChIP-seq</td>
<td>[x]</td>
<td>[x]</td>
</tr>
<tr>
<td>Flow cytometry</td>
<td>[x]</td>
<td>[x]</td>
</tr>
<tr>
<td>MRI-based neuroimaging</td>
<td>[x]</td>
<td>[x]</td>
</tr>
</tbody>
</table>

**Antibodies**

<table>
<thead>
<tr>
<th>Antibodies used</th>
<th>The information of all antibodies used are described in the manuscript.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Validation</td>
<td>All antibodies used have been validated.</td>
</tr>
</tbody>
</table>

**Eukaryotic cell lines**

<table>
<thead>
<tr>
<th>Policy information about cell lines</th>
<th>Jurkat cells E6.1 clone, MAGI-CCR5 cells, TZM-bi cells were from NIH HEK293T cells were from ATCC Rev-A3RS-GFP cells were from Virongy.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Authentication</td>
<td>Cells were checked permanently according to morphology and function features or resistant to certain antibiotics.</td>
</tr>
<tr>
<td>Mycoplasma contamination</td>
<td>Cell lines have been regularly test for mycoplasma contamination using a commercial kit (Vazyme). If contaminated, cells would be discarded.</td>
</tr>
<tr>
<td>Commonly misidentified lines (See ICLAC register)</td>
<td>No commonly misidentified cell lines were used.</td>
</tr>
</tbody>
</table>
Human research participants

Policy information about studies involving human research participants

Population characteristics The healthy participants were in the age range 16-40.

Recruitment Volunteer participants were selected based on two criteria: (1) they are HIV negative; (2) they are in good health condition.

Ethics oversight The study has been approved by the Institutional Review Board of Beijing You’An Hospital.

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

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 The preparation processes of cell fixation and staining are described in manuscript.

Instrument Data were collected on BD LSR Fortessa SORP and different cell population were separated by BD FACS Aria SORP.

Software FlowJo2

Cell population abundance The abundance were identified by using control groups like isotope staining or uninfected cell group.

Gating strategy Gated only high forward/side scatter cells to ensure exclusion of cell debris.

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