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Corresponding author(s): Hendrik Dietz

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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.

n/a	Confirmed	
☐	☒	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	EPU 1.2 up to 2.6 (Thermo Fisher Scientific), SerialEM 3.5.6, Attune Nxt Software v3.1, NIS-Elements AR Ver5.02.01
Data analysis	RELION-2, RELION-3, CrYOLO v1, MotionCor 2, CTFFIND 4.1, UCSF Chimera 1.11.2, UCSF ChimeraX v0.1, Etomo 4.9.0 (Imod), Graphpad Prism v6.01, Attune Nxt Software v3.1, ImageJ v2.1.0/1.53c, caDNAno 2

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

The data supporting the findings of this study are available within the paper and its supplementary information files and are available from the corresponding author upon reasonalbe request. Cryo-EM data of this study have been deposited in the Electron Microscopy Data Bank (EMDB) with accession codes: EMD-12007, EMD-12008, EMD-12009, EMD-12010, EMD-12011, EMD-12012, EMD-12013, EMD-12014, EMD-12015, EMD-12016, EMD-12019, EMD-12020, EMD-12021, EMD-12022, EMD-12023, EMD-12024, EMD-12044, EMD-12045, EMD-12046, EMD-12049

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	A sample size of 3 biological replicates was used to detect a significant difference ($p<0.05$) between groups with a signal to noise ratio of 3.0 with 80% power. For cryo-EM reconstructions, the sample size is dependent on the particle density per micrograph and the number of acquired micrographs which is limited by beam time. The number of particles was sufficient to reconstruct all acquired DNA-origami structures.
Data exclusions	No data was excluded. For cryo-EM reconstructions we manually sorted out damaged particles by 2D and 3D classification for the final refinement.
Replication	Experiments were performed multiple times to confirm the observations, the number of biological replicates is provided in the caption of the relevant figures. All attempts at replication were successful.
Randomization	Cells used for test experiments were randomly assigned to experimental groups in the process of sample preparation. For cryo-EM reconstructions all particles are randomly assigned to two groups which are reconstructed separately and merged after convergence in the final refinement.
Blinding	This is not relevant for the underlying study. Blinding was not used for cell experiments due to the use of automated collection and analysis systems, where the entire set of cytometry data was acquired and analyzed using identical parameters. Blinding was not performed for EM-micrographs and fluorescent microscopy experiments as they were not used for direct measurements or statistical analysis to justify blinding. The ELISA assay was essentially blinded as the samples were prepared and measured by different individuals.

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	Involved in the study
☐	☒ 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	1) Anti-HBc , 17H7 Isotype IgG-2b, produced by MAB Monoclonal Antibody Core Facility of the Helmholtz Zentrum München - German Research Center for Environmental Health 2) Anti-IFA-HepBcore provided by Centro De Ingenieria Genetica y Biotecnologia de sancti spiritus in Cuba, Lot 161 3) Anti-HepBcore-HRP provided by Centro De Ingenieria Genetica y Biotecnologia de sancti spiritus in Cuba, Lot 171 4) Anti-AAV2 mouse recombinant, Progen Cat. No.: 610298, A20R, Lot: 810021-03
Validation	1) Anti-HBc (17H7 Isotype IgG-2b): Validated with immunostaining, precipitation reactions, ELISA experiments and Wesern Blot analysis (see Methods: Production of anti-HBc) 2) Anti-IFA-HepBcore: Validated with ELISA 3) Anti-HepBcore-HRP: Validated with ELISA 4) Anti-AAV2: "Validation: application confirmed" as provided by the supplier Progen (https://www.progen.com/anti-aav2-intact-particle-mouse-recombinant-a20r-lyophilized-purified.html)

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293T cells were purchased from Leibniz Institute, DSMZ-German Collection of Microorganisms and Cull Cultures GmbH.
Authentication	Cell lines were kept at low passage and were not further authenticated.
Mycoplasma contamination	Cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

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	HEK293T cells were washed with PBS and trypsinized. Cells were then collected and fixed with 2% formaldehyde before being run on the flow cytometer.
Instrument	Attune NxT Flow Cytometer
Software	Attune NxT Flow Cytometer Software
Cell population abundance	20,000 single cells were analyzed for each condition.
Gating strategy	Cells were gated first by FSC/SSC, and then single cells were gated on SSC-A/SSC-H. Untreated cells were used as a negative control.

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