

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Librairies were sequenced on an illumina Novaseq6000 platform and collected in Fastq format. MS data were acquired using Orbitrap astral mass spectrometer (Thermo), and peptides and proteins were identified using DIA-NN library search software.
Data analysis	Integrated Genome Browser - by Nowlan H. Freese, David C. Norris, and Ann E. Loraine, Bioinformatics 2016 Jul 15;32(14):2089-95. GraphPad - Prism 9 R version (4.1.2) , R Development Core Team, (2021-11-01) blastp (version 2.2.31+), Altschul et al., 1990 MEGA X - by Kumar S, Stecher G, Li M, Knyaz C, Tamura K. (2018). Mol Biol Evol 35, 1547-1549. IQ-TREE 2(V2.0.6) TBtools - by Chen, C., Chen, H., Zhang, Y., Thomas, H. R., Frank, M. H., He, Y., & Xia, R. (2020). Molecular plant, 13(8), 1194–1202 fastp (V 0.22.0) BOWTIE2 (V 2.1.0) Hisat2 (V 2.2.1) featureCounts (V 2.0.3) DESeq2 - by Michael Love, Wolfgang Huber, Simon Anders. (2014). Genome Biology, 15:550. DiffBind (V3.2) ChIPseeker (v1.28.3) ChIPpeakAnno (V3.0.0) Samtools (V1.13) deeptools (v3.5.1) MACS2(V2.2.7.1)

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Raw sequencing data and processed data for RNA-seq, CUT&Tag experiments and ATAC-seq are available in the NCBI GEO database under the accession number GSE287537 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE287537>). The mass spectrometry proteomics data of the interactomes have been uploaded to ProteomeXchange under an accession number of PXD060237 (<https://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD060237>) and PXD064041 (<https://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD064041>). Other RNA-Seq data analyzed in this study are publicly available from ToxODB, as indicated in figure legends. All data are included in the article or the Supplementary Information. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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

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

Data exclusions

Replication

Randomization

Blinding

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used

The following primary antibodies were used in the immunofluorescence, immunoblotting and/or ChIP assays: mouse anti-HA (ABMART, China, Shanghai; RRID: AB_2864345), rabbit anti-FLAG (huaxingbio, Beijing, China; RRID:AB_3711191), mouse anti-Ty (BB2, gifts from Professor Qun Liu in China Agricultural University), rabbit anti-TgGAP45 (RRID: AB_2943452), rabbit anti-TgIMC1 (RRID:AB_2943453), mouse anti-TgACP (gifts from Professor Qun Liu in China Agricultural University), rabbit anti-H3K4me3 (PTM Bio, China; RRID:AB_2501543) and rabbit anti-TgCentrin 1 antibody (gifts from Professor Shaojun Long in China Agricultural University), mouse and rabbit anti-TgActin(gifts from Professor Qun Liu in China Agricultural University)

The following secondary immunofluorescent antibodies were used in the immunofluorescence and/or immunoblotting: Secondary immunofluorescent antibodies were conjugated with FITC- or Cy3 for immunofluorescence, and were conjugated to horseradish peroxidase for westernblot.

Validation

No unpublished antibodies were used in this study. No antibodies were generated for this study. All antibodies were validated in previous publications or by the manufacturer:

-Rabbit anti-TgGAP45: K. Frénal, et al. "Functional dissection of the apicomplexan glideosome molecular architecture. Cell Host Microbe. 2010 Oct 21;8(4):343-57. "

-Rabbit anti-TgIMC1: K. Hu, et al. "Daughter cell assembly in the protozoan parasite Toxoplasma gondii. Mol Biol Cell. 2002 Feb;13(2):593-606. "

-Mouse anti-TgACP: R. F. Waller, et al. "Nuclear-encoded proteins target to the plastid in Toxoplasma gondii and Plasmodium falciparum. Proc Natl Acad Sci U S A. 1998 Oct 13;95(21):12352-7. "

-Rabbit anti-H3K4me3: C. F. Brooks, et al. "Toxoplasma gondii sequesters centromeres to a specific nuclear region throughout the cell cycle. Proc Natl Acad Sci U S A. 2011 Mar 1;108(9):3767-3772. "

-Rabbit anti-TgCentrin 1: B. Mahajan, et al. "Centrins, cell cycle regulation proteins in human malaria parasite Plasmodium falciparum. J Biol Chem. 2008 Nov 14;283(46):31871-31883. "

-Mouse anti-Actin: Herm-Götz, et al. "Toxoplasma gondii myosin A and its light chain: a fast, single-headed, plus-end-directed motor. EMBO J 21, 2149-2158 (2002). "

-Mouse anti-Ty (clone BB2): Bastin, P et al. "A novel epitope tag system to study protein targeting and organelle biogenesis in Trypanosoma brucei." Molecular and biochemical parasitology vol. 77,2 (1996): 235-9. doi:10.1016/0166-6851(96)02598-4

-Mouse anti-HA (ABMART, RRID: AB_2864345): validated for IFA, WB, IP and CUT&Tag by the manufacturer.

-Rabbit anti-FLAG (huaxingbio, RRID: AB_3711191), validated for IFA, IP and WB by the manufacturer.

-Cy3/FITC-goat anti-mouse IgG(H+L) (HX2103/HX2028) or Cy3/FITC-goat anti-rabbit IgG(H+L) (HX2102/HX2027), validated for IFA and WB

-HRP-goat anti-mouse/rabbit IgG (HX2031), validated for WB

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

Human foreskin fibroblast HFF — ATCC SCRC-1041; RRID:CVCL_3285. African green monkey kidney Vero — ATCC CCL-81; RRID:CVCL_0059.

Authentication

HFF and Vero cells were obtained directly from ATCC (authenticated source) and used with provided certificates

Mycoplasma contamination

All T. gondii parental lines and host cells were tested negative for Mycoplasma infection by IFA.

Commonly misidentified lines (See [ICLAC](#) register)

N/A

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A