nature portfolio

Corresponding author(s): Cyrille Boyer, Megan D. Lenardon, Sascha Brunke

Last updated by author(s): Jun 26, 2024

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 (*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	Array scan & data extraction - GenePix Pro 6.1 (Molecular Devices); Fluorescence micrograph acquistion - ZEN Blue 3.3 (Zeiss)
Data analysis	Statistics - Prism 10.1 (GraphPad); Transcriptome data - GeneSpring 14.8 (Agilent); Clustering, KEGG pathway analysis - R 4.3.2 with packages clusterProfiler 4.10.1 and factoextra 1.0.7; GO term enrichment analysis Candida Genome Database online tool "GO term finder" (www.candidagenome.org; accessed on 18/01/2023); Sequence analysis - Trimmomatic 0.40, bowtie2 2.4, SnpEff 5.1, samtools 1.15.1, IGV 2.8.7; Image analysis - ImageJ 1.51; Structures - ChemDraw 19.0 (PerkinElmer); Data tabulation - Office 2016 (Microsoft)

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

The whole genome sequencing data generated in this study have been deposited in the European Nucleotide Archive database under accession code PRJEB65085 [https://www.ebi.ac.uk/ena/browser/view/PRJEB65085]. The microarray data generated in this study have been deposited in the ArrayExpress database under

accession code E-MTAB-13294 [https://www.ebi.ac.uk/biostudies/arrayexpress/studies/E-MTAB-13294]. 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	Age, sex or gender of the donors was not taken into account.
Reporting on race, ethnicity, or other socially relevant groupings	No grouping, social or otherwise, was taken into account
Population characteristics	No specific treatment or disease states were considered or checked for blood taking. All donors were generally healthy persons of 20-50 years of age.
Recruitment	Volunteers were recruited from workers at the research institute where the study was performed.
Ethics oversight	The blood donation procedure was approved by the Jena institutional ethics committee (Ethik-Kommission des Universitätsklinikums Jena, Permission No 2207–01/08). All donors gave written informed consent and did not receive any compensation.

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	Sample sizes were based on the expected, large effect sizes, and for most designs three biologically independent replicates (n=3) were used. The sample size is indicated in each figure legend.
Data exclusions	No data were excluded from the analysis
Replication	For each experiment, the biological replicates were performed on different days from different pre-cultures or with freshly grown cell lines (where applicabe) three times unless stated specifically otherwise (the n is given in each figure legend as number of biological replicates). All replicates were successful and included in the paper. Technical replicates, where applicable and mentioned, were performed in parallel.
Randomization	Wherever possible, treatments and measurements were assigned randomly (e.g. Galleria larvae, fields of view for GFP determination...); for experiments with donated blood (macrophages), all experimental conditions were applied to each of all donated samples
Blinding	Blinding was not relevant in most of these studies, as defined parameter were determined (like automatically determined OD, GFP signal from randomized fields of view, transcript levels...). For the electron micrographs, the experimentator was unaware of the expected outcome.

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

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	A 431 vaginal epithelial cells obtained from DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen in May 2021
Authentication	Identity is regularly checked by STR analysis, most recently 17. February 2023
Mycoplasma contamination	Mycoplasma contamination tests are regularly performed, before and after experiment; last test on 16. August 2023 with expected negative result.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified line was used

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*