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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	Lipidomic data were acquired using the Q Exactive UHMR mass spectrometer controlled by Xcalibur software (v4.2.47, Thermo Fisher Scientific). Data for the quantification of 20E were acquired and processed using Analyst 1.6.3 software (Sciex) on the QTRAP 6500+ LC-MS/MS system. Lengths of ovarian follicles was measured using ImageJ software.
Data analysis	Statistical analyses were conducted using GraphPad Prism version 5.00 for Windows (GraphPad Software).The statistical significance of the survival data was analyzed with a log-rank (Mantel–Cox) test. The statistical significance of multiple groups comparisons was analyzed using one-way ANOVA test. Tukey's HSD tests were applied as follow-up analyses only when the ANOVA reached significance ($p < 0.05$). The statistical significance of egg numbers was analyzed using a two-tailed Mann–Whitney test. Other comparisons were calculated using a two-tailed Student's t test for unpaired comparisons between two groups. A value of $P < 0.05$ was considered to be statistically significant. Lipidomic data were normalized by total lipid content. Molecular lipid species were analyzed in univariate model and p-values were corrected for false discovery rate (FDR) with the Benjamini–Hochberg method. Significant lipids were defined as FDR < 0.05. Lipidomic data were processed using MS-DIAL (version 4.7.0) and further analyzed with Heatmapper (http://www.heatmapper.ca/) for visualizing clustering of data. Data for the measurement of 20E were quantified using MultiQuant 3.0.2 software (AB Sciex).

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 data supporting the findings of this study are available in the article and the Supplementary Materials. Mass spectrometry lipidomics data provided in the Supplementary Data and the raw data are available on the MetaboLights repository (https://www.ebi.ac.uk/metabolights/MTBLS12928). 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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	To evaluate the survival rates, 30-40 mosquitoes were used in each group. To evaluate the genes expression by qPCR , at least 20 mosquitoes were used in each group. To evaluate the fecundity and fertility of dsRNA-treated mosquitoes, 15-25 mosquitoes were used in each group. For lipid extraction and lipidome analysis by UPLC-MS/MS, 30 mosquitoes were used in each group. To measure the enzyme activity (like caspase activity or trypsin activity), 30 mosquitoes were used in each group. To measure hydrogen peroxide production, 20 mosquitoes were used in each group. To measure 20E concentration by UHPLC-MS/MS, 30 mosquitoes were used in each group.
Data exclusions	No data were excluded.
Replication	All replications showed similar results.
Randomization	The same batch of adult mosquitoes were separated in to different groups randomly in each test.
Blinding	Blinding was not relevant to 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	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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Six-week-old male SPF (specific pathogen free) grade ICR (Institute of Cancer Research) mice were used for mosquito blood feeding in this study.
Wild animals	N/A
Reporting on sex	Animal sex is not relevant to this study.
Field-collected samples	N/A
Ethics oversight	This study was conducted in accordance with the guidelines of the CAS Center for Excellence in Molecular Plant Sciences (Shanghai Institute of Plant Physiology and Ecology) Animal Care and Use Committee (A01MP2001)

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

Plants

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