

## 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.

- |                                     |  |
|-------------------------------------|--|
| n/a                                 | Confirmed  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The exact sample size ( <i>n</i> ) for each experimental group/condition, given as a discrete number and unit of measurement   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> 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<br><i>Give P values as exact values whenever suitable.</i>                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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 | No data collection software were used in this manuscript.  |
| Data analysis   | <p>Bioconductor DESeq2 R package v3.5.1 Love et al., 2014 <a href="https://anaconda.org">https://anaconda.org</a><br/>         HISAT v2.1.0 Kim et al., 2015 <a href="https://anaconda.org">https://anaconda.org</a><br/>         samtools v1.9 Li et al., 2009 <a href="https://anaconda.org">https://anaconda.org</a><br/>         FeatureCounts v1.6.3 Liao et al., 2014 <a href="https://anaconda.org">https://anaconda.org</a><br/>         cutadapt v1.18 Marcel Martic 2011 <a href="https://anaconda.org">https://anaconda.org</a><br/>         MUMmer v3.0 and MUMmer-plot Kurtz et al., 2004 <a href="https://mummer4.github.io/manual/manual.html">https://mummer4.github.io/manual/manual.html</a><br/>         NUCmer v3.23 (from MUMmer package) Kurtz et al., 2004 <a href="https://mummer4.github.io/manual/manual.html">https://mummer4.github.io/manual/manual.html</a><br/>         dnadiff v3.23 (from MUMmer package) Kurtz et al., 2004 <a href="https://mummer4.github.io/manual/manual.html">https://mummer4.github.io/manual/manual.html</a><br/>         SMRT Link v8.0 <a href="https://www.pacb.com/wp-content/uploads/SMRT-Link-User-Guide-v8.0.pdf">https://www.pacb.com/wp-content/uploads/SMRT-Link-User-Guide-v8.0.pdf</a></p> <p>A snakemake workflow (CITE snakemake (Köster and Rahmann, 2018)) was created for the RNA-seq analysis and can it be found at <a href="https://github.com/cristianriccio/celegans-pathogen-adaptation">https://github.com/cristianriccio/celegans-pathogen-adaptation</a>.</p> |

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

Genomic DNA and RNA-seq data that support the findings of this study have been deposited at the European Nucleotide Archive under the accession code PRJEB32993. The raw data related to metabolomics is available on Metabolomics Workbench using the DataTrack ID 1891.

## 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](https://www.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 chosen to compare to the literature in the field -- Burton et al., 2017, Burton et al., 2018, and Moore et al., 2019.             |
| Data exclusions | No data was excluded.   |
| Replication     | All experiments were repeated at least 3 times and replication was successful on all occasions.   |
| Randomization   | Embryos from all animals/genotypes were collected and randomly allocated to different experimental plates.  |
| Blinding        | Experimenters were not blinded during this study as all animals were quantified and all quantifications were fully reported without any exclusions. |

## 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                                 | Involvement in the study  |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                             |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines                  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology                          |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                          |

### Methods

| n/a                                 | Involvement in the study                        |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

|                         |   |
|-------------------------|---|
| Laboratory animals      | C. elegans (nematode) all larval stages and adult hermaphrodites of the N2 genetic background unless specific mutation noted in methods; P. vranovensis, P. luminescens, P. aeruginosa (bacteria) |
| Wild animals            | This study did not involve wild animals.  |
| Field-collected samples | This study did not involve animals collected from the field.  |
| Ethics oversight        | No ethical approval was required as this study did not use any vertebrates or controlled animal species.  |

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