

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

- ☒ ☐ 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 No custom software or algorithms were used for data collection.

Data analysis Software used in this study is listed the Methods section as well as in the Supplementary Methods.

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

Datasets associated with this genome project have been registered at NCBI under the BioProject accessions PRJNA494057 (Aurelia aurita Baltic sea strain), PRJNA494062 (Aurelia aurita Roscoff strain), and PRJNA494059 (Morbakka virulenta). Genome assemblies have been deposited at DDBJ/ENA/GenBank under accession numbers REGM000000000 (A. aurita Baltic sea), REGL000000000 (A. aurita Roscoff), RDPX000000000 (M. virulenta). Transcriptome assemblies have been deposited in the NCBI Transcriptome Shotgun Assembly Sequence Database under accession numbers GHAG000000000 (A. aurita Baltic sea), GHAI000000000 (A. aurita Roscoff), GHAS000000000 (A. aurita Kujukushima), GHAK000000000 (A. aurita White sea), GHAF000000000 (M. virulenta), GHAR000000000 (Nemopilema), GHBG000000000 (Copula), GHAQ000000000 (Tripedalia), GHAX000000000 (Chironex), GHBC000000000 (Xenia), GHAW000000000 (Clavularia), GHBA000000000 (Porpita), GHAZ000000000 (Velella), GHBB000000000 (Physalia). Sequencing reads of the genomes and transcriptomes have been deposited in the NCBI Sequence Read Archive under the study accessions SRR7992476, SRR7992477, SRR7992488, SRR7992489, SRR7992486, SRR7992487, SRR7992484, SRR7992485, SRR7992482, SRR7992483, SRR7992480, SRR7992481, SRR7992474, SRR7992469, SRR7992468, SRR7992475, SRR7992472, SRR7992473, SRR7992470, SRR7992471, SRR7992478, SRR7992479 (A. aurita Baltic sea); SRR8040393, SRR8040394, SRR8040410, SRR8040411, SRR8040408, SRR8040409, SRR8040406, SRR8040407,

SRR8040404, SRR8040405, SRR8040402, SRR8040403, SRR8040391, SRR8040401, SRR8040400, SRR8040399, SRR8040398, SRR8040397, SRR8040392, SRR8040389, SRR8040390, SRR8040387, SRR8040388, SRR8040395, SRR8040396 (A. aurita Roscoff); SRR7983773, SRR7983772, SRR7983775, SRR7983774, SRR7983769, SRR7983768, SRR7983771, SRR7983770 (M. virulenta); SRR8089701, SRR8089700, SRR8089699, SRR8089698, SRR8089705, SRR8089704, SRR8089703, SRR8089702 (A. aurita Kujukushima), SRR8090261, SRR8090262, SRR8090257, SRR8090258, SRR8090263, SRR8090264, SRR8090255, SRR8090256, SRR8090259, SRR8090260, SRR8090265, SRR8090266 (A. aurita White sea); SRR8101520, SRR8101519, SRR8101522, SRR8101521, SRR8101524, SRR8101523, SRR8101526, SRR8101525, SRR8101518 (Tripedalia); SRR8101709, SRR8101708, SRR8101707 (Nemopilema); SRR8115525 (Velella); SRR8115524 (Porpita); SRR8116635 (Physalia); SRR8116636 (Copula). Genome browsers, genome assemblies, gene models and transcriptomes, together with the annotation files, are available at MGU web site <http://marinegenomics.oist.jp/gallery/> and OIST BLAST server <http://203.181.243.155/aurelia/>

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	N/A
Data exclusions	N/A
Replication	No replication was applied for genome and transcriptome sequencing experiments.
Randomization	N/A
Blinding	N/A

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Animals and other organisms

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

Laboratory animals	Laboratory strains of Aurelia aurita , Morbakka virulenta, Nemopilema nomurai and Tripedalia cystophora (see Supplementary Note 1)
Wild animals	Mature male medusae of Aurelia aurita were collected in the Bay of Kiel (Kieler Förde, Baltic sea, Germany). Morbakka virulenta male medusae were collected in Ondo Fishing Port, Hiroshima Prefecture, Japan. List of field-collected specimens with corresponding coordinates and complete descriptions is provided in Supplementary Table 1 and Supplementary Table 2.
Field-collected samples	N/A
Ethics oversight	N/A

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