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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Cor	nfirmed
\boxtimes		The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
\boxtimes		An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
\boxtimes		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.
\boxtimes		A description of all covariates tested
\boxtimes		A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
\boxtimes		A full description of the statistics including <u>central tendency</u> (e.g. means) or other basic estimates (e.g. regression coefficient) AND <u>variation</u> (e.g. standard deviation) or associated <u>estimates of uncertainty</u> (e.g. confidence intervals)
\boxtimes		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>
\boxtimes		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes		Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
\boxtimes		Clearly defined error bars State explicitly what error bars represent (e.g. SD, SE, CI)
		Our web collection on <u>statistics for biologists</u> may be useful.

Software and code

Policy information about availability of computer code

oney information about <u>availability of computer code</u>							
Data collection	No software was used						
Data analysis	No software was used						

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 upon request. 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

There are no formal restrictions on data availability.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

For a reference copy of the document with all sections, see <u>nature.com/authors/policies/ReportingSummary-flat.pdf</u>

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Revealing the preservation mechanism of the Ediacara biota: description of fossils, study of thin sections, Scanning Electron Microscopy and laboratory simulations with sand and clay.					
Research sample	Ediacaran fossils from the Lyamtsa and Zimnie Gory localities of the Ediacara biota in the White Sea region (Russia) and from South Australia.					
Sampling strategy	No sample-size calculation was performed					
Data collection	Some fossils were collected by Ilya Bobrovskiy during field work 2015 to 2018. The rest were studied at the collections of Ediacaran macrofossils of the Borissiak Paleontological Institute RAS (Moscow, Russia). Ediacaran fossils from South Australia were studied at the South Australian Museum (Adelaide, Australia).					
Timing and spatial scale	Samples stored in museum collections were collected from 1942 to 2018.					
Data exclusions	Weathered samples were not studied for early diagenetic history.					
Reproducibility	All attempts to repeat the experiment were successful.					
Randomization	Samples were not allocated into groups.					
Blinding	No statistical analyses were performed.					
Did the study involve field work? 🛛 Yes 🗌 No						

Field work, collection and transport

Field conditions	Rock outcrops in the cliffs of the White Sea.
Location	Lyamtsa Village and Zimnie Gory in the Arkhangelsk Region (Russia)
Access and import/export	Samples were collected under the license ARKH 01562 PD given to the Borissiak Paleontological Institute RAS for collecting palaeontological samples in the Arkhangelsk Region, Russia; no samples were imported/exported.
Disturbance	Only rock outcrops with no vegetation were explored.

Reporting for specific materials, systems and methods

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

Palaeontology

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Specimen provenance	Samples were collected under the license ARKH 01562 PD from 12.07.2016 given by Rosnedra to the Borissiak Paleontological Institute RAS for collecting palaeontological samples in the Arkhangelsk Region, Russia				
Specimen deposition	All specimens are located at the Borissiak Paleontological Institute RAS (Moscow, Russia) and the South Australian Museum (Adelaide, Australia).				
Dating methods	No new dates are provided.				

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.