

## 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

Data analysis

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](#)

All data generated or analysed during this study are included in this published article and its supplementary information files. The datasets for the phylogenetic, disparity, and biogeographic analyses are deposited in Figshare: <https://doi.org/10.6084/m9.figshare.22343920>.

## 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	Our investigation considers all available specimens of the studied species and the phylogenetic analyses include the so far most comprehensive sample of Permo-Triassic archosauromorph species (255 operational taxonomic units). Terminals of the phylogenetic data matrices were scored based on the type specimens and all available, unambiguously referred specimens.
Data exclusions	No exclusions were performed because taxonomic and character samples of the phylogenetic investigations were intended to be as broad as possible.
Replication	The parsimony phylogenetic analysis was conducted until 100 optimal results were recovered under the tree search replications. In the morphological disparity analyses, the 95% confidence intervals were generated using the two tails of values recovered from 9,999 bootstrap replicates. All the replications were successful.
Randomization	Not applicable. All available fossil material was included and the random and incomplete nature of the vertebrate fossil record acts as a natural randomization process.
Blinding	Permo-Triassic archosauromorph species are known from a single or a few specimens ( $n < 5$ ) and cases where several specimens are known is scarce ( $n > 4$ ). Thus, in our analyses it was possible to include all the available specimens for the scoring of characters in each sampled species and a blinding was not necessary.

## 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 type="checkbox"/>	<input checked="" type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input 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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

### 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

## Palaeontology and Archaeology

Specimen provenance	The new specimen was excavated from the Buriol site (29°39'34.2" S; 53°25'47.4" W), São João do Polêsine, Rio Grande do Sul, Brazil. The fieldwork and curation was performed by federal servants under the Brazilian legislation.
Specimen deposition	Specimen is deposited in the fossil vertebrate collection of the Centro de Apoio à Pesquisa Paleontológica da Quarta Colônia da Universidade Federal de Santa Maria (CAPP/UFMS), São João do Polêsine, Rio Grande do Sul, Brazil.
Dating methods	No new dates were performed. Dates used for the Bayesian inference analysis are provided in the supplementary file.
<input checked="" type="checkbox"/>	Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.
Ethics oversight	No ethical approval or guidance was required because our study is based on previously collected fossil specimens.

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