

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 software was used for data collection.

Data analysis

Bionano IrysSolve assembler version 5134, 10x Genomics Supernova assembler v1.0, SSPACe-LongRead, dopseq, cupadapt v1.13, pybedtools v0.7.10, LAST, RepeatMasker, STAR version 2.6.0, Trinity version 2.4.0, exonerate version 2.2.0, MAKER version 3.01.02, SNAP, Augustus version 3.1.1, InterProScan version 5.31.70, OrthoFinder version 2.0.0, tRNAscan-SE version 1.3.1, Infernal software suite, PRANK v.170427, IQ-TREE version 1.6.7.1, CAFE v4.2, Protein-Protein BLAST 2.6.0+, TMHMM v2.0, MAFFT v7.310, trimAL, PAL2NAL, HYPHY, aBSREL, EMBOSS needle version 6.6.0.0

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

The assembled Komodo dragon genome is available in NCBI under the accession SJP000000000. All DNA sequencing used to generate the assembly is available in the NCBI SRA database under accession PRJNA523222. Illumina sequencing data from chromosome pools is available in the NCBI SRA under accession PRJNA529483. RNA-seq data of heart tissue is available in the NCBI SRA under accession PRJNA527313. Original protein annotations, noncoding RNA annotations, all alignments for phylogenetic analyses and selection analyses, and newick files of phylogenetic trees are available in the following Figshare repositories: doi:10.6084/m9.figshare.7961135.v1, doi:10.6084/m9.figshare.7955891.v1, doi:10.6084/m9.figshare.7955879.v1, doi:10.6084/m9.figshare.7949483.v1, doi:10.6084/m9.figshare.7759496.v1, doi:10.6084/m9.figshare.7967300. The project folder for all Figshare data is available at <https://figshare.com/projects/>

Data_for_Komodo_dragon_genome_paper/61271.

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	The comparative genomics work in this study was performed using single genomes from individual species, so no sample size calculations were performed.
Data exclusions	No data were excluded.
Replication	No biological experiments were performed in this work that could be replicated.
Randomization	Randomization is not relevant to this paper, as the main hypotheses in this work refer to individual species.
Blinding	No blinding was possible for analyses carried out in this study as hypotheses were tested on single genomic sequences.

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	Varanus Komodoensis, ages 20 and 6, house at Zoo Atlanta, one individual at Reptilandia zoo in Gran Canaria in the Canary Islands, and one deceased individual (tissue previously collected) and San Diego Zoo. All maintained under ambient conditions.
Wild animals	No wild animals
Field-collected samples	No field collected samples
Ethics oversight	Zoo Atlanata IACUC

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