

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

We generated multi-platform sequencing data of a male Chinese rhesus, involving tools including PacBio: Sequel (<https://www.pacb.com/products-and-services/sequel-system/>); Bionano: saphyr (<https://bionanogenomics.com/products/saphyr/>); Hi-C: Illumina X10; Iso-seq: Sequel; RNA-seq: Illumina X10.

Data analysis

FALCON (v1.8.7): <https://github.com/falconry/falcon>
 Solve (v3.1): <https://bionanogenomics.com/support-page/bionano-solve>
 Arrow(v2.3.0):<https://github.com/PacificBiosciences/GenomicConsensus>
 Jellyfish (v1.1.11): <https://github.com/gmarcais/Jellyfish>
 HiC-Pro (v2.8.1): <https://github.com/nservant/HiC-Pro>
 LACHESIS (v1.0): <https://github.com/shendurelab/LACHESIS>
 MUMmer (v.4.0): <https://github.com/mummer4/mummer>
 BWA (v0.7.12): <http://bio-bwa.sourceforge.net/>
 GATK (v3.6): <https://software.broadinstitute.org/gatk/>
 SAMtools (v1.3.1): <http://samtools.sourceforge.net/>
 FastQC (v0.11.6): <https://github.com/s-andrews/FastQC>
 Delly (v0.7.7): <https://github.com/dellytools/delly>
 MAKER (v2.31.8): <http://www.yandell-lab.org/software/maker.html>
 Augustus (v3.2.2): <https://github.com/opendatagroup/augustus>
 SNAP (v1.0): <https://github.com/lcoghill/snap>
 BUSCO (v3.0.1): <https://gitlab.com/eizlab/busco>
 tRNAscan-SE (v1.0): https://github.com/yookuda/docker_trnscan_se
 RNAmmer (v1.2): <http://www.cbs.dtu.dk/services/RNAmmer>
 LoRDEC (v1.0): <https://github.com/kamimrcht/ELECTOR>
 GMAP (v1.0): <https://github.com/juliangehring/GMAP-GSNAP>
 Bowtie2 (v2.3.4.3): <https://github.com/BenLangmead/bowtie2>

HISAT2 (v2.1.0): <https://github.com/infp/hisat2/releases>
 Tandem Repeats Finder (TRF, v4.07b): <http://tandem.bu.edu/trf/trf.html>
 RepeatMasker (v4.0.6): <https://github.com/rmhubble/RepeatMasker>
 IGV (Integrative Genomics Viewer) <http://software.broadinstitute.org/software/igv>
 LiftOver (<https://genome.ucsc.edu/cgi-bin/hgLiftOver>)
 SVTyper (v0.7): <https://github.com/hall-lab/svtyper>
 smartie-sv (v1.0): <https://github.com/zeeev/smartie-sv>
 VEP (Variant Effect Predictor): <http://asia.ensembl.org/info/docs/tools/vep/index.html>
 DAVID (v6.8): <https://david.ncifcrf.gov>
 LASTZ (v1.04): <https://github.com/lastz/lastz>
 MEGA-X (v10.0.5): <https://www.megasoftware.net>
 Primer Premier5 (v5.0): <https://primer-premier-5.software.informer.com/>

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 PacBio sequence data, Illumina sequencing reads, rheMacS assembly and its annotation files have been deposited in NCBI and GSA (Genome Sequence Archive) under the project accession numbers of PRJNA514196 and PRJCA001197, respectively.

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

Life sciences study design

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

- Sample size: An adult Chinese rhesus macaque (*Macaca mulatta*) (male, five-year-old) and five Chinese rhesus macaques for variant genotyping.
- Data exclusions: No data were excluded.
- Replication: No replication is need in this study.
- Randomization: The all macaques used in this study are chose randomly.
- Blinding: The investigators were not blinding to group allocations.

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 |
| <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 | Involved 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	An adult Chinese rhesus macaque (<i>Macaca mulatta</i>) (male, five-year-old) and five unrelated Chinese rhesus macaques.
Wild animals	<i>Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.</i>
Field-collected samples	<i>For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.</i>
Ethics oversight	All animal protocols were approved in advance by the Institutional Animal Care and Use Committee of Kunming Institute of Zoology (Approval No: SYDW-2010002).

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