

## 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](#).

### 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 Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- An indication of 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 statistics 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
- Clearly defined error bars  
*State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on [statistics for biologists](#) may be useful.

### Software and code

Policy information about [availability of computer code](#)

Data collection

No software was used.

Data analysis

All software versions and commands are described in Supplementary Note 1. All software used is freely available.  
 FALCON-Unzip builds 08/24/2017 and 11/02/2017  
 ngmlr 0.2.6  
 sniffles 1.0.8  
 busco 3.0.2  
 bedtools 2.15.0  
 nucmer 3.23.0  
 freebayes v1.1.0-50-g61527c5  
 ArrowGrid github tag 563dcb943160f320fed8bae12cf5b1cf3f586639  
 smrtlink 5.1.0.26412  
 bax2bam 0.0.8  
 pbalign 0.3.1  
 variantCaller 2.2.2  
 dataset 0.1.27  
 canu/meryl github tag c3488e1ab1355da50c60d6ba0b963588def91021  
 canu github tag 78d0188e8186476caadfd93062601a38773a952e

## 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

Sequencing data for the cattle trio is available under NCBI BioProject PRJNA432857. All other sequencing data was obtained from public sources. Data accessions, software versions, and commands used to produce the described results are provided in the Supplementary Note.

## Field-specific reporting

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

Life sciences  Behavioural & social sciences

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://nature.com/authors/policies/ReportingSummary-flat.pdf)

## Life sciences

### Study design

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

Sample size	N/A. The manuscript describes an algorithm for genome assembly, not a statistical test.
Data exclusions	N/A. The manuscript describes an algorithm for genome assembly, not a statistical test.
Replication	The assembly algorithm was tested on reference plant and human genomes to measure its accuracy and effectiveness. Accuracy of the cattle trio assembly was measured using independent data sources such as Illumina sequencing and known SNP chip markers.
Randomization	N/A. The manuscript describes an algorithm for genome assembly, not a statistical test.
Blinding	N/A. The manuscript describes an algorithm for genome assembly, not a statistical test.

## Materials & experimental systems

Policy information about [availability of materials](#)

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique materials
<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"/> Research animals
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

### Research animals

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

Animals/animal-derived materials

As described in the Methods section: "The animals used were part of the Davies Epigenetics and Genetics Resource at the University of Adelaide, Australia, and were established and sampled using procedures approved by the animal ethics committee of the University. A two-year-old cow of the Brahman breed (subspecies *Bos taurus indicus*) was bred by artificial insemination using semen from a five-year-old bull of the Angus breed (*Bos taurus taurus*). The Brahman female had been previously typed for mitochondrial DNA haplotype to verify the maternal lineage as *indicus*-specific. At day 153 post-insemination, the animal was sacrificed and the fetus removed for dissection."

# Method-specific reporting

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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"/> Magnetic resonance imaging