

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 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☐ | ☒ 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

Base calling: Oxford Nanopore Technology provided Guppy basecaller v4.2.2 (commercial product)
 PEPPER v0.4: <https://github.com/kishwarshafin/pepper> (MIT License)
 Margin v2.0: <https://github.com/UCSC-nanopore-cgl/margin> (MIT License)
 DeepVariant v1.1.0: <https://github.com/google/deepvariant> (BSD-3-Clause License)
 Minimap2 2.17-r941: <https://github.com/lh3/minimap2> (MIT License)
 Pbbmm2 1.4.0: <https://github.com/PacificBiosciences/pbbmm2> (BSD-3-Clause-Clear License)
 Samtools 1.10: <https://github.com/samtools/samtools> (MIT/Expat License)
 Medaka v1.2.1: <https://github.com/nanoporetech/medaka> (MPL-2.0 License)
 Clair v2.1.1: <https://github.com/HKU-BAL/Clair> (BSD-3-Clause License)
 Longshot v0.4.2: <https://github.com/pjedge/longshot> (MIT License)
 Hap.py v0.3.12: <https://github.com/illumina/hap.py> (simplified BSD license)
 WhatsHap v1.0: <https://github.com/whatshap/whatshap> (MIT License)
 Canu (Trio-binning) v2.1.1: <https://github.com/marbl/canu> (GNU General Public License, version 2)
 Natural switch error visualization: https://github.com/tpesout/genomics_scripts (MIT License)
 Local Phasing Correctness visualization: https://github.com/tpesout/genomics_scripts (MIT License)
 hifiasm 0.14: <https://github.com/chenh123/hifiasm> (MIT License)
 Shasta 0.7.0: <https://github.com/chanzuckerberg/shasta> (MIT License)
 Flye 2.8.2: <https://github.com/fenderglass/Flye> (BSD-3-Clause License)
 K-mer analysis with YAK 0.1: <https://github.com/lh3/yak> (MIT License)
 dipcall v0.2: <https://github.com/lh3/dipcall> (No License/CC0)
 RTG 3.12: <https://github.com/RealTimeGenomics/rtg-tools> (BSD 2-Clause)

svim-asm 1.0.2: <https://github.com/eldariont/svim-asm> (GNU General Public Licence, v3.0)
 SAnalyzer v0.36: <https://github.com/nhansen/SAnalyzer> (Public Domain)

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 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

We have made the analysis data that we used to generate the figures available publicly (variant calling outputs, runtime, genome assemblies etc.) in: https://console.cloud.google.com/storage/browser/pepper-deepvariant-public/analysis_data.

Sequencing data availability:

Genome-In-a-Bottle consortium: <https://ftp-trace.ncbi.nlm.nih.gov/giab/ftp/data/>

Human Pangenome Reference Consortium (HPRC): <https://s3-us-west-2.amazonaws.com/human-pangenomics/index.html>

Telomere-to-telomere consortium: <https://github.com/nanopore-wgs-consortium/CHM13>

In the supplementary data section, we have listed the URLs of the FASTQ files used for each sample that are publicly available via different consortium.

There are no restrictions on any of the data we presented in our study.

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	No sample size calculation was performed as we used all available sample data for which GIAB has truth variants (training on HG002, evaluating on HG001, HG003-HG007).
Data exclusions	No data was excluded from the study.
Replication	Each sample was sequenced using a consistent sequencing protocol. We evaluated on all available data for which GIAB has truth variants.
Randomization	Randomization was not relevant to our study.
Blinding	Investigators were not blind to group, as all data was pooled together and publicly available.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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