

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

MinKnowv1.4.2 and v2.0 and albacorev1.1.2 - nanopore sequencing

Data analysis

Trimmomatic v0.32 - sequence clean up; RSEM v1.2.31 - expression analyses; Jellyfish v2.2.6 - kmer frequency; CANU v1.6 - error correction; SmartDenovo v1.0 - genome assembly; Pilon1.22 - error correction; BUSCO v3.0.2 - quality assessment; Bowtie2 - read mapping; STAR v2.7 - RNASeq read mapping; Trinity v2.8.4 - transcript assembly; MAKER-P v2.31.10 - annotation; PASAv2.3.3 - annotation; RepeatModelerv1.0.11 - repeat annotation; OrthoFinder v2.2.7 - identify gene orthologues; CAFEv4.3.1 - gene family analyses; McScanX (version n/a) - synteny analyses; ClustalW v2.1 - sequence alignment; RAxMLv8.2.12 - phylogeny; RGAuguryv2017.10.21 - resistance gene annotation; BSMAPv2.9 - cytosine methylation; Nanopolish v0.10.1 - methylation analyses; EMBOSS v6.6.0.0 - CpG islands.

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

Genome assembly and annotation, DNA-seq data, RNA-seq data and WGBS-seq data has been deposited to NCBI under BioProject ID PRJNA516907. A Jbrowse instance for each genome can be accessed at <http://cruciferseq.ca>. The YZ12151 B. nigra and B. rapa version 3 genome files were downloaded from <http://brassicadb.org/brad/datasets/pub/Genomes>. UniProt Release 2016_03 and Pfam32.0 were used in gene annotation and classification.

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 | Sample size is not relevant, since reference genome sequences were being generated from representative samples of a specific species. |
| Data exclusions | No data was excluded from the analyses |
| Replication | Replication was limited but used where necessary to ensure the relevance of any analyses, for example bootstrapping in phylogenetic analyses, where at least 100 replications were used. |
| Randomization | Randomization was not relevant in the context of the types of statistical analyses performed, where predominantly genomic features or expression data was being analysed. There were no field or lab based experiment that might require randomization. |
| Blinding | There were no group comparisons performed, so blinding is not relevant. |

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 checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology |
| <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 |

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 |