

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 Sequencing data were collected from Illumina sequencing machines. No additional software were used to collect sequencing data.

Data analysis

R version 3.5.1
 bwa version 0.7.17-r1188
 Sentieon (<http://www.sentieon.com>)
 VCFtools version 0.1.15
 HapScanner (<https://github.com/PlantGeneticsLab/TIGER/wiki/HapScanner>)
 samtools version 0.1.19
 TASSEL version5
 MUMmer4 version 4.0.0.beta2
 RAXML version 8.2.12
 iTOL (<https://itol.embl.de/>)
 sNMF version 1.2
 CLUMPP version 1.1.2
 XP-CLR version 1.0
 PLINK version 1.90b6.7
 ABBABABAWindows.py and popgenWindows.py from https://github.com/simonhmartin/genomics_general
 OrthoMCL Version 2.0
 BLAST version 2.9.0
 agriGO version 2.0
 clusterProfiler version 3.10.0
 kallisto version 0.46.0
 SNP filtering: <https://github.com/YaoZhou89/WGSc>

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

The raw sequence data were deposited in Sequence Read Archive (<https://www.ncbi.nlm.nih.gov/sra>) under accession number PRJNA439156 and PRJNA663409. The raw sequence data were also deposited in Genome Sequence Archive (<https://bigd.big.ac.cn/gsa>) under accession number CRA001951. The genotype data of VMap 1.0 are publicly available at Genome Variation Map (<https://bigd.big.ac.cn/gvm>) under accession number GVM000082.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	We developed a high-density genetic variation map (VMap 1.0) of wheat by whole-genome sequencing of all species of AA, AABB and AABBDD genomes within the genus Triticum, and the progenitor of D subgenome of bread wheat, Ae. tauschii.
Research sample	A total of 414 accessions of 5 species, 25 subspecies from 71 countries were collected, including 91 diploid Triticum accessions (AA taxa), 30 diploid Ae. tauschii accessions (DD taxa), 121 tetraploid accessions (AABB taxa), and 172 hexaploid accessions (AABBDD taxa).
Sampling strategy	This collection consisted of Triticum species from a wide range of taxonomic groups, geographic distribution, and ploidy levels.
Data collection	Seeds of each accession were first sterilized in 30% H2O2 for 10 minutes, then thoroughly washed for five times with distilled water. The sterilized seeds were germinated in water at 25 degree for 2 days. After germination, seeds with endosperm residue were transplanted into soil and grown in greenhouse. After a 15-day to 30-day growth under long-day conditions and a 2-day etiolation processing, the leaves were sampled.
Timing and spatial scale	Not applicable.
Data exclusions	No data excluded.
Reproducibility	Not applicable.
Randomization	Not applicable.

Blinding

Not applicable.

Did the study involve field work? ☐ Yes ☒ No

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