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Last updated by author(s): Aug 16, 2026

## Reporting Summary

Nature Portfolio 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 Portfolio 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

- |                                     |                                     |                                                                                                                                                                                                                                                            |
|-------------------------------------|-------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement                                                                                                                                    |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly                                                                                                                                    |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of all covariates tested                                                                                                                                                                                                                     |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons                                                                                                                                        |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings                                                                                                                                                           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes                                                                                                                                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | 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 FastQC v0.11.9; Trimmomatic v0.39; BWA v0.7.19-r1273, HISAT2 v2.2.1, SAMtools v1.22.1; OrthoFinder v3.

Data analysis BCFtools v1.22; SnpEff v5.0e; VCFtools v0.1.16; PLINK v1.9.0-b.8; GAPIT v3; SNPhylo v20180901; PopLDdecay v3.41; PopART v1.7; DESeq2 v1.34.0; MEME Suit v5.3.3; CHIPseeker v1.30.3; DeepGOPlus; R v4.1.2; XP-CLR v1.1; vcf2phylip v2.0; SPSS v23.0.

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The raw sequencing data generated in this study, including whole-genome sequencing, RNA-seq, and DAP-seq data, have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA1114037 (<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1114037>). The Glycine max Wm82.a2.v1 reference genome was obtained from Phytozome ([https://phytozome-next.jgi.doe.gov/info/Gmax\\_Wm82\\_a2\\_v1](https://phytozome-next.jgi.doe.gov/info/Gmax_Wm82_a2_v1)). All other data supporting the findings of this study are available within the article and its supplementary information files. Source data are provided with this paper.

## Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

|                                                                    |                |
|--------------------------------------------------------------------|----------------|
| Reporting on sex and gender                                        | Not applicable |
| Reporting on race, ethnicity, or other socially relevant groupings | Not applicable |
| Population characteristics                                         | Not applicable |
| Recruitment                                                        | Not applicable |
| Ethics oversight                                                   | Not applicable |

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

## 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     | In this study, 257 soybean accessions belonging to 14 maturity groups, including wild soybeans ( <i>Glycine soja</i> ), landraces and cultivated soybeans ( <i>Glycine max</i> ), were used as plant materials, which exhibit high levels of phenotypic and genetic diversity and simultaneously meet the sample size requirements for genome-wide association studies (GWAS).                                                                                                                                                                                                                                                                                                                        |
| Data exclusions | No data were excluded from the analyses unless they failed predefined quality-control criteria. For sequencing data, adapter sequences and low-quality reads were removed using Trimmomatic v0.39 before downstream analyses. For SNP data used in GWAS, variants with low quality, high missing rate or low minor allele frequency were excluded according to the filtering criteria described in the Methods section. For phenotypic data, accessions with missing records or abnormal values caused by failed germination, severe disease, lodging, pest damage, failure to reach physiological maturity or other obvious environmental damage were excluded before statistical analysis and GWAS. |
| Replication     | Soybean flowering time and maturity were evaluated in multiple field environments. Functional validation of the candidate gene controlling soybean flowering and maturity was performed using independent genetic materials, including overexpression and CRISPR-Cas9 lines. Molecular assays used to investigate the underlying mechanism were performed with at least three independent biological replicates unless otherwise stated. Key phenotypic and molecular results were independently repeated and showed consistent results. All replication attempts were successful.                                                                                                                    |
| Randomization   | Soybean accessions were randomly arranged in field plots using a randomized complete block design where applicable. For controlled-environment and molecular experiments, plants or samples were randomly selected from independently grown individuals. Complete randomization of genotype identity was not applicable because the genotypes were defined by the soybean diversity panel or by the generated functional validation lines. Environmental and positional effects were minimized by using multiple environments, biological replicates and standardized management practices.                                                                                                           |
| Blinding        | Investigators were not blinded to accession or genotype identity during field phenotyping and functional validation because genotype information was required for planting, sampling, transformation and downstream molecular analyses. To minimize potential bias, phenotypic measurements were conducted according to predefined standardized criteria, and sequencing and molecular data were analyzed using fixed computational pipelines and statistical thresholds. Blinding was therefore not applicable to most parts of this plant genetics study.                                                                                                                                           |

## 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 &amp; experimental systems

| n/a                                 | Involved in the study                                  |
|-------------------------------------|--------------------------------------------------------|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Antibodies         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Plants             |

## 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 |

## Antibodies

|                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|-----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Antibodies used | Soluble chromatin was immunoprecipitated using an anti-GFP antibody from Proteintech, catalog number 50430-2-AP. The antibody is a rabbit polyclonal antibody against the GFP epitope and was used for ChIP assays to immunoprecipitate GmRVE4d-GFP-associated chromatin complexes. The clone number is not applicable because this is a polyclonal antibody. The lot number was 20250801.                                                                                                                       |
| Validation      | The anti-GFP antibody, Proteintech 50430-2-AP, is reported by the manufacturer as validated for detection and immunoprecipitation of GFP-tagged proteins. In this study, the antibody was used to immunoprecipitate GmRVE4d-GFP-associated chromatin complexes. Antibody specificity and ChIP performance were evaluated using wild-type promoter regions in GmRVE4d-GFP samples but not in wild-type controls. Expression of the GmRVE4d-GFP fusion protein was confirmed by western blot before ChIP analysis. |

## Dual use research of concern

Policy information about [dual use research of concern](#)

## Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

| No                                  | Yes                                                 |
|-------------------------------------|-----------------------------------------------------|
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| <input checked="" type="checkbox"/> | <input type="checkbox"/> National security          |
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## Experiments of concern

Does the work involve any of these experiments of concern:

| No                                  | Yes                                                                                                  |
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| <input checked="" type="checkbox"/> | <input type="checkbox"/> Enable evasion of diagnostic/detection modalities                           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Enable the weaponization of a biological agent or toxin                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Any other potentially harmful combination of experiments and agents         |

|                       |                                                                                                                                                                                                                                                                                                                                                                                                   |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Seed stocks           | Provided by the Key Laboratory of Soybean Biology, CAAS, Beijing, China. No wild specimens collected; no seed bank numbers assigned.                                                                                                                                                                                                                                                              |
| Novel plant genotypes | Gmrve4d mutants (1-bp, 5-bp, 33-bp deletions) in Jack by CRISPR-Cas9; confirmed by PCR/Sanger sequencing. GmRVE4d-OE lines: GmRVE4dH3 CDS in PTF101.1/CaMV35S, Jack background; three independent T3 lines used.                                                                                                                                                                                  |
| Authentication        | Soybean material identity was based on institutional germplasm records. CRISPR mutants were authenticated by PCR amplification and Sanger sequencing of the target region. GmRVE4d-OE lines were authenticated by qRT-PCR for increased GmRVE4d transcript levels and by western blotting for detection of the GmRVE4d-GFP fusion protein. Homozygous T3 lines were used for downstream analyses. |