

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 for data collection

Data analysis

BWA MEM (v 0.7.10-r789), samtools (v0.1.19-44428cd), blastn (v2.2.29+), bedtools (v2.17.0), R (v3.4.3), RStudio (v1.1.383), Microsoft Excel (v14.4.1), Bcftools (v1.7), GATK (v3.7-0), Trimmomatic (v0.32), Tophat2 (v2.0.12), HTSeq count (v0.9.1), edgeR (v3.20.9), PicardTools (v2.9.4).

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 upon request. 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

Figure 1, Figure 3, Supplementary Figure 1, Supplementary Figure 2, Supplementary Figure 3. No restrictions on data availability. All raw data is made available in a Supplementary File "Soyk-et al-SourceData".

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 ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see 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	Sample sizes were defined based on previous work that found to be sufficient for determining statistically significant results. At least 3 independent replicates analyzed in each experiment. n values and statistical tests are presented
Data exclusions	Mechanically damaged and diseased plants were excluded from the analyses to minimize environmental effects and focus on the genetic control of the observed developmental phenotypes.
Replication	All presented in figure legends and methods. Individual replicates (e.g. tissue samples, plants, shoots, flowers and fruits) are indicated and at least 3 independent replicates analyzed for each experiment
Randomization	For the QTL-sequencing experiment, a segregating F2 mapping population of 1536 individual plants was randomly sown and transplanted in an agricultural field. This randomized and blinded experiment allowed the identification of the suppressor loci sb1 and sb3, which were confirmed in two field-grown experiment that were grouped and labelled by genotype.
Blinding	For the QTL-sequencing experiment, we selected phenotypic extremes from a randomized F2 mapping population of 1536 individual plants and phenotyped these individuals for inflorescence branching. This randomized and blinded experiment allowed the identification of the suppressor loci sb1 and sb3, which were confirmed in two field-grown experiment that were grouped and labelled by genotype.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Animals and other organisms

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

Laboratory animals	this study did not involve laboratory animals
Wild animals	this study did not involve wild animals

Phenotypic data and tissue samples for QTL-sequencing were collected between 11 am and 1 pm on July 8, 2017 in the fields of the Cornell Long Island Horticultural Experiment Station in Riverhead, New York.