

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
☐	☒ The exact sample size (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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 recorded as fastq files (see Methods), quantitative phenotypic data were collected manually in fields and greenhouses and recorded in Microsoft Excel version 16.94, Promega Glomax Microplate Reader (default parameters), BioRad Image Lab (v6.1, default parameters) (see Methods).
Data analysis	Geneious Prime (v2025.0.2), BioRad ImageLab (v6.1, default parameters), MAFFT (v7.505), HMMER (v3.3.2), IQ-TREE (v2.2.2), FastQC (v0.11.9), trimmomatic (v0.39), STAR (v 2.6.1), MEME (v4.11.2). R packages: tidyverse (v2.0.0), ggplot2 (v3.4.3), ggpubr (v0.6.0), plyr (v1.8.9), reshape2 (v1.4.4), dplyr (v1.1.3), DESeq2 (v1.38.), ape (v5.8-1), DescTools(0.99.54). Python packages: Figures 1-3 and associated Supplementary Data: matplotlib (v3.7.0), pandas (v1.5.3), plotly (v5.9.0), scikit-learn (v1.2.1), scipy (v1.10.0), sklearn (v0.0.post5). Figure 4 and associated Supplementary Data: matplotlib (v3.7.5), numpy (v1.24.4), pandas (v2.0.3), scipy (v1.10.1), seaborn (v0.11.1), statsmodels (v0.14.1), torch (v2.4.1). Code availability: https://github.com/cmarti/tomato_branching/tree/master , DOI: 10.5281/zenodo.15552524.

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](#)

All data are available within this Article and its Supplementary Information. RNA sequencing data generated in this study is available at the Gene Expression Omnibus (<https://www.ncbi.nlm.nih.gov/geo/>) under accession GSE289537, and previously published RNA sequencing is available at Sequence Read Archive (SRA, <https://ncbi.nlm.nih.gov/sra>) under BioProjects PRJNA376115 and PRJNA343677. The tomato pangenome is available at SRA under BioProject PRJNA557253. The Arabidopsis thaliana non-redundant motif database used is available at <https://plantfdb.gao-lab.org/index.php?sp=Ath>. The raw data with the number of branching events for each plant and inflorescence is provided in Supplementary Tables. All unique biological materials used in this manuscript are available for distribution upon request.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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	Sample size for RNA-Seq was based on four independent samples, as done previously (Alonge, Wang et al., 2020). No statistic methods were used to predetermine sample size for quantitative phenotypic analyses. Required experimental sample size was estimated based on our past experience performing similar experiments including greenhouse and field tests (see for example Kwon et al., 2022, Alonge, Wang et al., 2020, Rodríguez-Leal et al., 2017).
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 relevant information is presented in figure legends, methods, and supplementary data files. Individual replicates (e. g. tissue samples, plants, shoots, flowers and fruits) are indicated and at least four independent replicates were analyzed for each experiment. Raw phenotypic data are provided in supplementary data files.
Randomization	For the segregating population experiments, F2 population plants were randomly sown and transplanted in an agricultural field and genotyping was completed after phenotypic analysis. These randomized and blinded experiments formed the basis of the model.
Blinding	For the segregating population experiments, F2 population plants were randomly sown and transplanted in an agricultural field and genotyping was completed after phenotypic analysis. These randomized and blinded experiments formed the basis of the model.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

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

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
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	Solanum lycopersicum (cultivar M82, LA3475), Solanum habrochaites (LA1777), and Solanum pennellii (LA0716) were from our stocks. Introgression line IL3-4 (Solanum pennellii chromosome 3 introgressed into M82, LA4046) and two overlapping Solanum habrochaites chromosome 3 introgression lines LA3925 and LA3926, introgressed into tomato cultivar TA209, were obtained from the USDA core germplasm collection (Department of Plant Science, University of California, Davis).
Novel plant genotypes	Novel coding alleles of PLT3 and PLT7 were obtained by CRISPR-Cas9 editing. Novel coding alleles of PLT3 and PLT7 were obtained by CRISPR-Cas9 editing.
Authentication	All variants were validated by PCR amplification and Sanger sequencing.