

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 (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 no software was used for data collection

Data analysis bwa (v.0.7.15), samtools (v.0.1.19), Cytospace (v.3.8.0), R (v.4.1.1) (prcomp, cor.test, hclust, t.test, ggplot2(v.3.3.5), ComplexHeatmap(v.2.8.0), edgeR (v.3.28.1), WGCNA(v.1.70.3)

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 Illumina sequencing data have been deposited to the DDBJ database: Short Read Archives (SRA) database (SRA submission ID: DRA013154, Run ID DRR332477-DRR332618), which have been already released.

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	No sample size calculation was performed. For gene expression and co-expression network analysis, total 117 samples constituted of 4-type of the sexuality (male, female, and two-types of hermaphroditism) in 23 cultivars of Diospyros kaki (D. kaki), in 2 developmental stages, were tested. For detection of plant hormone concentrations, total 6 and 9 flowers in D.kaki and in Nicotiana tabacum (N. tabacum), respectively, were collected. For transformation, independent 12 and 7 transgenic lines in Arabidopsis thaliana (A. thaliana) and N. tabacum, respectively, were examined. For gene expression analysis with A. thaliana developing flowers (stage 8) were conducted with 3 independent DkRAD-overexpressed and control Col-0 lines were examined. For transient over-expression analysis in D. kaki, mRNA-seq analysis was conducted with 3 leaves in transiently overexpressed DkRAD and 3 control leaves.
Data exclusions	No data was excluded from the analyses.
Replication	For expression analysis, each cultivar was used as a biological replicate (N = 10-23 for the biological replicates). For plant hormone analysis, almost same results were confirmed from the samples in different year. For transformation analysis, over-growth of gynoeceum in 6 independent T2 overexpression lines of DkRAD was confirmed.
Randomization	We randomly sampled 5 flowers for each sexuality per cultivar in a single orchard (Experimental orchard in Kyoto University). The selected persimmon cultivars, which often produce male and hermaphrodite flowers, were randomly planted in the orchard.
Blinding	Blinding was not possible for the grouping of flower sexuality. Female and male were discriminated by the inflorescence morphology according to previous reports. Discrimination of hermaphroditism was dependent on the carpel length, and the flowers with > 0.5 cm carpels were randomly sampled.

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

Methods

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

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