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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 *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 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 *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

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	Prunus persica Whole Genome Assembly v2.0 & Annotation v2.1 (https://phytozome.jgi.doe.gov/pz/portal.html) and the BLASTP program were used to identify peach SWEET genes. The Arabidopsis SWEETs were retrieved from the TAIR (http://www.arabidopsis.org/) database. Nikon Elements (NIS ElementsAR ver. 4.6.0.) and Zeiss Zen software (2012 S4) were used to acquire images.
Data analysis	Multiple alignments were performed with amino acid sequences using the DNAMAN software, and a phylogenetic analysis was conducted with the MEGA 5.0 program. The chromosomal location of SWEET genes was obtained from the peach genome annotation GFF file using TBtools (Chen et al., 2020). The gene structure, i.e., exon and intron composition, of SWEET genes in peach was performed using GSDS 2.0 (http://gsds.gao-lab.org/). The 2000 bp sequences upstream of the initiation codon were used to predict the cis-elements using PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/). Gene synteny and collinearity was determined using Quick MCScanX Wrapper software (Wang et al., 2012). The returned results were collated and visualized using TBtools (Chen et al., 2020). The relative expression level was calculated according to the 2−ΔΔCT method. Data were subjected to one-way ANOVA for statistical analysis using SPSS software (17.0).

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

All raw and processed data will be made available 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	Our research did not involve human participants,and this information has not been collected.
Reporting on race, ethnicity, or other socially relevant groupings	Our research did not involve human participants,and this information has not been collected.
Population characteristics	Our research did not involve human participants,and this information has not been collected.
Recruitment	Our research did not involve human participants,and this information has not been collected.
Ethics oversight	Our research did not involve human participants,and this information has not been collected.

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

Life sciences study design

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

Sample size	For each Arabidopsis tissue type, each replication included at least five samples. For light-responsiveness analysis, after a 24-dark treatment with blacking bagging, the mature leaves were collected on 0, 0.5, and 1 h of light exposure on a sunny day. Peach fruit with one branch and several leaves were collected at the red mature stage, and the branch was immediately placed in ddH2O (double distilled H2O) for culture.The fruit showing overexpressed or silenced target genes in their adjacent leaves were collected for starch and soluble sugar analysis. Fifteen fruits were included in each transgenic analysis.
Data exclusions	Data was not excluded from analysis.
Replication	For each tissue type, three biological replicates were collected, and each replication included at least five samples. All samples were immediately frozen in liquid nitrogen and stored at -80℃ for analysis. In reverse transcription-quantitative PCR (RT–qPCR) analyses,three biological replicates were analyzed for each sample.
Randomization	'Pink fruit' peach juvenile leaves, mature leaves, branches, and mature fruits from the same branch were collected for gene expression analysis on the same date and time. To ensure an equal copy number of transgene, the total volume of injected solution was controlled at 1 mL per mature leaf for all transient analyses.
Blinding	Our research did not involve human participants,so it is not relevant to our 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 & 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

Plants

Seed stocks	P. persica cv. Baifeng grown at Chongqing Yunduo Agricultural Development Co., Ltd. was used in this study. Arabidopsis atsweet11 atsweet12 double mutant seeds were from the Arabidopsis Biological Resource Center (ABRC). Arabidopsis seeds from wild-type (WT) 'Columbia-0' (Col-0) were bought from The Arabidopsis Information Resource(TAIR).
Novel plant genotypes	We overexpressed PpSWEET9a or PpSWEET14 individually in the atsweet11 atsweet12 double mutant. To obtain transgenic lines overexpressing PpSWEET9a or PpSWEET14 in at sweet11 atsweet12 mutant,the PHB-X-YFP mediated constructs overexpressing PpSWEET9a or PpSWEET14 were individually transformed into Arabidopsis atsweet11 atsweet12 double mutant by the floral dip method (Clough and Bent, 1998). The rosette leaves from T3 homozygous 35S:PpSWEET9a-YFP or 35S:PpSWEET14-YFP/atsweet11 atsweet12, atsweet11 atsweet12, and Col-0 plants were collected for starch measurement after being subjected to 7h-treatment of darkness.
Authentication	The relative expression level of transgenic lines is shown in Figure 4b.