Materials Design Analysis Reporting (MDAR)
Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: doi:10.31222/osf.io/9sm4x.). The MDAR checklist is a tool for authors, editors and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

Materials

Antibodies	Yes (indicate where provided: page no/section/legend)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.		x

Cell materials	Yes (indicate where provided: page no/section/legend)	n/a
Cell lines: Provide species information, strain. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID		x
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		x

Experimental animals	Yes (indicate where provided: page no/section/legend)	n/a
Laboratory animals: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID		x
Animal observed in or captured from the field: Provide species, sex and age where possible		x
Model organisms: Provide Accession number in repository (where relevant) **OR** RRID		x

Plants and microbes	Yes (indicate where provided: page no/section/legend)	n/a
Plants: provide species and strain, unique accession number if available, and source (including location for collected wild specimens)	Different *Arabidopsis thaliana ap1-1 cal-1 clv3* mutants were obtained through a CRISPR-Cas9 strategy in this study (Figure 4, see Materials and methods page S5 for numbers). *Arabidopsis thaliana* triple mutant *ap1-7 cal-1 lfy-12* (Columbia-0 background) was obtained by crosses in this study (Figure S3).	
Microbes: provide species and strain, unique accession number if available, and source		x

Human research participants	Yes (indicate where provided: page no/section/legend)	n/a
Identify authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		x
Provide statement confirming informed consent obtained from study participants.		x
Report on age and sex for all study participants.		x

Design

Study protocol	Yes (indicate where provided: page no/section/legend)	n/a
For clinical trials, provide the trial registration number **OR** cite DOI in manuscript.		x

Laboratory protocol	Yes (indicate where provided: page no/section/legend)	n/a
Provide DOI or other citation details if detailed step-by-step protocols are available.	All methods are described in details in Supplementary informations	x

Experimental study design (statistics details)	Yes (indicate where provided: page no/section/legend)	n/a
State whether and how the following have been done**, or** if they were not carried out.		
Sample size determination		x
Randomisation		x
Blinding		x
Inclusion/exclusion criteria		x

Sample definition and in-laboratory replication	Yes (indicate where provided: page no/section/legend)	n/a
State number of times the experiment was replicated in laboratory	Different *Arabidopsis thaliana ap1-1 cal-1 clv3* mutants were obtained through a CRISPR-Cas9 strategy in this study (Figure 4, see Materials and methods page S5 for numbers). RNA-seq :for both Cauliflower and Romanesco, 3 replicates were done. For Cauliflowers from OBS, only one replication was done. (Supplementary information, page S8, section cauliflower curd sequencing)	
Define whether data describe technical or biological replicates	Both for RNA-seq. For Cauliflower and Romanesco RNA-seq, two samples were sequenced, one of them in two technical replicates (Supplementary information, page S8, section cauliflower curd sequencing)	

Ethics	Yes (indicate where provided: page no/section/legend)	n/a
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		x
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		x
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		x

Dual Use Research of Concern (DURC)	Yes (indicate where provided: page no/section/legend)	n/a

If study is subject to dual use research of concern, state the authority granting approval and reference number for the regulatory approval		x

Analysis

Attrition	Yes (indicate where provided: page no/section/legend)	n/a
State if sample or data point from the analysis is excluded, and whether the criteria for exclusion were determined and specified in advance.		x

Statistics	Yes (indicate where provided: page no/section/legend)	n/a
Describe statistical tests used and justify choice of tests.	ChIP-qPCR analysis with fragments of the *TFL1* promoter was assayed in triplicate, with each biological replicate including three technical replicates (Legend figure 2; Materials and methods, chromatin immunoprecipitation assay). Relative enrichments, with associated relative errors, were calculated as described in Dorca-Fornell et al., 2011 (supplementary reference 62). The biological replicate closest to the mean of the 3 independent assays was selected to show in figure 2k-l (legend figure 2). For luciferase transient expression assays with fragments of the *TFL1* promoter, a Student's t-test was applied to detect differences between groups (legend figure 2). For global RNA-seq analysis, negative binomial was used to search for differentially expressed genes, following the EdgeR methodology (Supplementary information, page S8, section cauliflower curd sequencing) For the differential expression of 8 selected genes between Cauliflowers and Romanesco samples, a Mann & Whitney test was performed as the number of observations per genes did not allow for a parametric test (legend figure S6). Genetic segregation was tested by a chi-square test, comparing an observed distribution to a theoretical one (Materials and methods, Molecular characterization of *clv3* CRISPR-Cas9 lines). A nonparametric Wilcoxon test was used to compare phenotypes (axes countings) on plants from different genotypes (small sample size) in Figure S3.	

Data Availability	Yes (indicate where provided: page no/section/legend)	n/a
State whether newly created datasets are available, including protocols for access or restriction on access.	Genomic datasets publicly available	
If data are publicly available, provide accession number in repository or DOI or URL.	RNA-seq datasets are publicly available on Gene Expression Omnibus (GEO) under the accession: GSE150627 (Supplementary information, page S8, section cauliflower curd sequencing)	
If publicly available data are reused, provide accession number in repository or DOI or URL, where possible.	Datasets for expression in multiple tissues can be found on GEO under the accession: GSE42891 (Supplementary information, page S8, section cauliflower curd sequencing) Datasets for D-134 genome can be found under the accession CNP0000469 at the china national genebank database. (Supplementary information, page S9, section BoAP1 promoter analysis)	

Code Availability	Yes (indicate where provided: page no/section/legend)	n/a
For all newly generated code and software essential for replicating the main findings of the study:	Yes, provided as a supplementary archive file containing all the files necessary to run the models	
State whether the code or software is available.	Yes, provided as a supplementary archive file containing all the files necessary to run the models	

If code is publicly available, provide accession number in repository, or DOI or URL.	Yes, provided as a supplementary archive file containing all the files necessary to run the models. Open software LGPL license	

Reporting

Adherence to community standards	**Yes (indicate where provided: page no/section/legend)**	**n/a**
MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR.		x
State if relevant guidelines (eg., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (eg., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.		x