nature portfolio

Corresponding author(s): Jian Ye

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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	Confocal microscopy: Leica SP8 STED. qPCR: Bio-Rad (CFX96). Photographing of plant: Nikon camera (D750). Imaging leaf hydrogen peroxide levels: OLYMPUS SZ61. Ion leakage measurement: Five Easy Plus.
Data analysis	Confocal images: Leica LAS X. Graphics: GraphPad Prism software (version 8.0). Image analysis: ImageJ (v1.52). Phylogenetic tree: MEGA 11. Sequence alignment: Snapgene (v6.0.2). Protein structure prediction: AlphaFold 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 data are available in the main text and the supplementary materials. Sequence data described in this article can be accessed at National Center for Biotechnology Information (NCBI) (https://www.ncbi.nlm.nih.gov) , the Arabidopsis Information Resource (https://www.arabidopsis.org) and the Sol Genomics Network (https://solgenomics.net) under the following accession numbers: AtBAG3 (AT5G07220), MC4 (AT1G79340), SlBAG1 (Solyc03g026220.3.1), SlBAG3 (Solyc06g035720.3.1), SlBAG3-like (Solyc08g080320.3.1), OsBAG3 (LOC4339971), ZmBAG3 (LOC103647604), MpBAG3 (Mapoly0056s0101), PpBAG3 (LOC112281472), NbNRC2 (KT936525.1 and KT936526.1), NbNRC3 (MK692736.1), NbBAG1 (Niben101Scf17538g00008.1), NbBAG3 (Niben101Scf01957g02003.1), NbBAG3-like (Niben101Scf10753g01015.1) and TYLCV Rep (AM282874). RNA-seq data sets are accessible under accession number PRJNA1214420.

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

Life sciences study design

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

Sample size	The sample size and the results of statistical analyses are described in the relevant figures or method section. Sample size was determined based on experimental trials and previous publications on similar experiments (Zhao et al., Science, 2025; Zhang et al., Plant Communications, 2023; Zhao et al., Science Advances, 2019; Li et al., The Plant Cell, 2014).
Data exclusions	No data were excluded from analyses in the experiments.
Replication	All experiments were duplicable and repeated more than three times.
Randomization	All samples were arranged randomly into experimental groups.
Blinding	Blinding was not used in 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

Antibodies

Antibodies used

Anti-GFP (Transgen Cat# HT801-01; 1:5000);
Anti-GFP (ABclonal Cat# AE011; 1:5000);
Anti-Flag (Transgen Cat# HT201-01; 1:5000);
Anti-His (Transgen Cat# HT501-01; 1:5000);
Anti-GST (Transgen Cat# HT601-01; 1:5000);
Anti-H+-ATPase (Agrisera Cat# AS07 260; 1:5000);
Anti-BAG3 (1:5000);
Anti-c-Myc (Transgen Cat# HT101-01; 1:5000);
Goat anti-mouse IgG-HRP (Transgen Cat# HS002-01; 1:10000);
Goat anti-rabbit IgG-HRP (Transgen Cat# HS101-01; 1:10000).

Validation

Antibody against BAG3 (1:5000) protein was generated in rabbit.The DNA fragment of AtBAG3 was cloned into pET-30a vector to generate His-tagged constructs. His-tagged protein was purified using Ni-NTA agarose (Qiagen, R90101) according to the manufacturer's instructions. The purified protein was used as an antigen to immunize rabbits for the production of polyclonal antibodies by BGI (Beijing, China).
The antibodies are commercial available: anti-GFP , anti-Flag, anti-His, anti-GST, anti-c-Myc , goat anti-mouse IgG-HRP and goat Anti-rabbit IgG-HRP (https://www.transgen.com/index.html); Anti-GFP (https://abclonal.com.cn/); Anti-H+-ATPase (https://www.agrisera.com/)

Plants

Seed stocks

Arabidopsis Col-0, mc4, PROPEP1-YFP and PROPEP1-YFP/mc4; Nicotiana benthamiana WT, Nbeds1, Nbnrc2/3, Nbnrc4 and Nbnrc2/3/4; Solanum lycopersicum cv. MicroTom WT.

Novel plant genotypes

Arabidopsis YFP-BAG3 transgenic plants; Arabidopsis bag3 mutant plants; Solanum lycopersicum Slbag1/3/3l mutant plants.

Authentication

Arabidopsis mc4, PROPEP1-YFP and PROPEP1-YFP/mc4 were described previously (Hander et al., Science, 2019).
Nicotiana benthamiana Nbeds1 mutant plants was described previously (Schultink et al., Plant Journal, 2017).
Nicotiana benthamiana Nbnrc2/3 mutant plants was described previously (Witek et al., Nature Plants, 2021).
Nicotiana benthamiana Nbnrc4 mutant plants was described previously (Wu et al., Plant Physiol, 2020).
Nicotiana benthamiana Nbnrc2/3/4 mutant plants was described previously (Adachi et al., Elife, 2019).
Arabidopsis YFP-BAG3 transgenic plantswere verified by immunoblot.
Arabidopsis bag3 mutant plants and Solanum lycopersicum Slbag1/3/3l mutant plants were verified by PCR and sequencing.