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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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	For bioinfomatic analysis, BLAST search of OsDAF1 was conducted on NCBI website (http://www.ncbi.nlm.nih.gov/). For confocal imaging, LAS X software was used to obtain figures.
Data analysis	The percent of identity of OsDAF1 homologs were based on BLAST results from NCBI. Box plot and histogram was produce using Origin9 software.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data supporting the findings of this study are available within the article and its Supplementary Information files or from the corresponding author upon reasonable request.

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 qRT experiment, 50 μg anther samples of each stage was used to extract RNA. For co-ip and western blot assay, 500 μg of tobacco powder was used to extract total protein.
Data exclusions	No data was excluded
Replication	Every experiment was repeated for at least three times, and similar results were obtained.
Randomization	Sample allocation is not relevant to our study. Comparison of phenotypes was based on different genotypes. Blinding
Blinding	All the experiments were performed without prior knowledge of the final outcome, and therefore blinding was not applied.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Commercial antibodies used: α-GFP (G1544, Rabbit polyclonal antibody, Sigma, 1:5000 dilution), α-HA (M20003, Mouse monoclonal antibody, Abmart, 1:2000 dilution), α-actin (M20009, Mouse monoclonal antibody, Abmart, 1:2000 dilution), Goat Anti-Mouse IgG HRP (M21001, Abmart, 1:5000 dilution), Goat Anti-Rabbit IgG HRP (M21002, Abmart, 1:5000 dilution).
Validation	Anti-GFP, anti-HA, anti-actin, goat anti-mouse IgG-HRP and goat anti-rabbit IgG-HRP antibodies are commercially available and validated by Western blotting and/or in prior publications on the following websites. Anti-GFP: https://www.sigmaaldrich.com/catalog/product/sigma/g1544?lang=zh&region=CN; Anti-HA: http://www.ab-mart.com.cn/page.aspx?node=60&id=963 Anti-Actin: http://www.ab-mart.com.cn/page.aspx?node=59&id=985 Goat anti-mouse IgG-HRP: http://www.ab-mart.com.cn/page.aspx?node=62&id=960 Goat anti-rabbit IgG-HRP: http://www.ab-mart.com.cn/page.aspx?node=62&id=980