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Life Sciences Reporting Summary

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Experimental design

1. Sample size

   Describe how sample size was determined.

   No sample size calculation was performed. Sample size was based on previous literature and experimental logistic. The data is consistent within and between independent experiments.

2. Data exclusions

   Describe any data exclusions.

   No data were excluded.

3. Replication

   Describe the measures taken to verify the reproducibility of the experimental findings.

   SPR kinetic curves were measured at least 3 times using aliquots from at least 2 different protein preps, with comparable results.
   For the cell death assay in Nicotiana benthamiana 3 biological replicas with 30 repeats each were performed. In the case of data shown in supplemental Fig.2 (repetition of previously published data with a different vector), one of the biological replicas included only 20 repeats. All attempt at replication were successful.
   Co-IP and Yeast-2-Hybrid experiments were repeated at least 3 times with similar results.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   No experimental group was used in this study. In the cell death assay, to avoid possible positional and developmental effect, each combination to be tested was spotted in a different position on the leaf, and on younger and older leaves, for each replica.

5. Blinding

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   No blinding has been used. High resolution images of all samples have been stored and could be scored again at any time.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☒	☐ 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 any assumptions or corrections, such as an adjustment for multiple comparisons
☒	☐ Test values indicating whether an effect is present *Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.*
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation)

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

All crystallography data were processed using the CCP4 Program Suite v. 7.0.051 (including xia2, AIMLESS, COOT and REFMAC5) with user interface CCP4i2 v. 0.0.5 (http://www.ccp4.ac.uk).
The final models were evaluated using MOLPROBITY 4.4 (http://molprobity.biochem.duke.edu)
The boxplot were generated using R v. 3.4.3 (https://www.r-project.org/) and the graphic package ggplot2 (H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2009).
All other graphs have been generated using Microsoft Excel for Mac v. 16.9 (Microsoft Corporation, USA)
The Surface Plasmon Resonance data were processed using the Biacore T200 Evaluation Software v. 2.0 from GE Healthcare Bio-Science AB, Sweeden.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

All unique materials used in this study are readily available from the authors.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Anti c-Myc monoclonal antibody produced in mouse from Santa Cruz Biotechnology, Cat. n. c-Myc Antibody (9E10): sc-40 HRP, Lot n. A0716. Used diluted 1:3000.
Monoclonal ANTI-FLAG® M2 antibody produced in mouse from SIGMA, Cat. n. F1804, Lot n. SLBT7654. Used diluted 1:3000.
Monoclonal anti-HA high affinity antibody 3F10 produced in rat from Roche, Cat. n.11867423001, Lot.n. 14553800. Used diluted 1:3000.
SIGMA Anti-GAL4 DNA-BD antibody produced in rabbit, Cat no. G3042. Used diluted 1:3000.
SIGMA Anti-GAL4 Activation domain antibody produced in rabbit, Cat no. G9293. Used diluted 1:3000.
Sigma Anti-Rat IgG-Peroxidase antibody produced in goat, Cat. no. A9307. Used diluted 1:10000
SIGMA Anti-Rabbit IgG–Peroxidase antibody produced in goat, Cat. no. A0545. Used diluted 1:10000
Promega Anti-Mouse IgG, HRP Conjugate, Cat. no. W4021. Used diluted 1:10000
All the antibodies used in this study were commercial antibodies to standard epitope tags, validated by manufacturers.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines have been used in this study.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines have been used in this study.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines have been used in this study.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No eukaryotic cell lines have been used in this study.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.

No animals were used in this study.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

This study did not involved human research participants.