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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	For the DNAseq, RNAseq and sRNAseq: - Illumina NextSeq 500 instrument For the gene expression (qRT-PCR): - LightCycler® 480 Instrument II For the RNA and Protein blot: - Image Lab 6.0 For the GUS quantification : - BMG FLUOstar OPTIMA
Data analysis	For the DNAseq analysis: - SHORE and SHOREmap For the gene expression analysis (qRT-PCR): - LightCycler® 480 Instrument II - Microsoft excel 2010 - GraphPad Prism 8

For the sRNAseq analysis:
- Bowtie
- Mirdeep2
- FeatureCounts
- psRNATarget

For the RNAseq analysis:
- Galaxy
- R (edgeR)

For polyadenylation and uridylation analysis:
- CLC Main Workbench 7

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 upon request. 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

The data that support the findings of this study are available from the corresponding author upon request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	No sample-size calculation was performed. In this study, for gene expression analysis (qPCR analysis and NGS data) 12 plants of 12 days old or 6 plants of 17 days old were harvested per sample. The reasons for this are: 1) This amount of plants is enough to obtain good RNA quality; 2) it provides a sufficiently large pool to reflect the average of gene expression in the respective lines
Data exclusions	No data were excluded from analysis in any experiment depicted in this manuscript.
Replication	All experimental findings were reliably reproduced at least three times for each described experiment. To reproduce the experiments, all the experiments were performed during same period, independently, with several days between different biological replicates. For each repeat, plants were grown in the same growth chamber with similar humility and temperature to ensure similar growth rates. After harvesting 3 all repeats, RNA or protein samples were processed at the same time, with same protocol and kits to reduce technical errors. For each experiment, the number of biological replicates is indicated in the figure legend.
Randomization	Samples were grown on the same condition and sorted based on their genotype. Within each genotype, healthy samples were randomly harvested for the experiments.
Blinding	The investigators were not blinded to group allocation during data collection and analysis, as multiple plants of the same genotype needed to be pooled. It would thus have been impossible to trace back the genotype of each plant after sample processing. For the phenotypic analysis of mutant crosses, the investigators were blind as the phenotypes were recorded first, followed by genotype determination.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	All unique materials are readily available from the authors.

Antibodies

Antibodies used	GR antibody, 1:10, Santa Cruz, GR P-20; AGO1 antibody, 1:5000, Agrisera, AS09527. We also include this information in the manuscript.
Validation	Both antibodies were used in Arabidopsis. The GR antibody is not as efficient as indicated on the website, we needed to increase the concentration to 1:10 for successful western blot detection. However, at this concentration the negative control sample was still negative. The AGO1 protein was detected with anti-AGO1 antibody with1:5000 dilution (same as described in website).