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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	No software was used to collect data
Data analysis	Modeling code:https://github.com/HayLab/Pigss Plots were generated in R (version 4.2.3) with the ggplot2 package Nanopore reads were mapped to the ykt61 reference locus with minimap2 (version 2.17). Illumina NextSeq2000 reads were analyzed with the DRAGEN Germline pipeline (version 3.10.12) against the Arabidopsis TAIR 10 genome

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 is available in the main text and the supplementary information files. Illumina sequencing reads were deposited to SRA (bioproject: PRJNA1074841). The Arabidopsis TAIR 10 genome assembly was used in this study.

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

Ecological, evolutionary & environmental sciences study design

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

Study description	In this study we performed manual outcrosses of different plant genotypes. Details about the number of replicates are in the main text. In general we set up 4 crosses per plant for 3-4 individual plants per line.
Research sample	Samples were Arabidopsis thaliana Col-0
Sampling strategy	No sample size calculation was performed. Sample sizes were based on previously published gene drive papers.
Data collection	Georg Oberhofer recorded the data by scoring siliques under a fluorescent microscope.
Timing and spatial scale	NA
Data exclusions	As described in the main text, certain lines were not further characterized due to poor drive performance in a self cross. Despite repeated efforts we have not been able to identify a single unambiguous location for the Ubq6 element, which is featured in data in Figure 3 and 4. Based on this, and to avoid uncertainty if others want to repeat these experiments with our stocks, we have removed data for this line from the paper for experiments shown in Figures 3 and 4 and in the supplementary materials.
Reproducibility	Outcrosses to determine drive activity were repeated for 2 consecutive generations (T3 and T4)
Randomization	We did not randomize samples because we were interested in the cross outcomes of specific genotypes.
Blinding	Blinding was not performed because only a single person was working on the crossing of plants.

Did the study involve field work? ☐ Yes ☒ No

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

Plants

Seed stocks	The Arabidopsis wildtype strain used to create transgenics was Col-0
Novel plant genotypes	We used the floral dip method with agrobacteria as described previously (ref 81) ClvR plasmids were transformed into GV3101 ElectroCompetent Agrobacterium strain from Intact Genomics.
Authentication	To determine the T-DNA insertion site of line ClvRubq7 we extracted genomic DNA from two different plants and constructed sequencing libraries using NEBNext® Ultra™ II FS DNA Library Prep Kit for Illumina (NEB #E7805) following manufacturer's instructions. The libraries were sequenced on Illumina NextSeq2000 in paired end mode with read length of 150 nt to the sequencing depth of 35 million paired end reads per sample. Base calls were performed with DRAGEN BCL Converter and structural variant analysis was performed with the DRAGEN Germline pipeline v3.10.12 against the Arabidopsis TAIR 10 genome. The resulting VCF files contained information on large structural variants (insertions).. Potential insertion sites were verified with custom primers amplifying the insertion sites followed by sequencing.