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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	The whole genome sequencing data for 423 BC1 individuals were sequenced on the NovaSeq PE150 platform at Novogene and have been deposited in the National Center for Biotechnology Information Sequence Read Archive under the associate code PRJNA1198964. The RNA-seq data for immature anthers from mop1 mutants and their WT siblings are available in the NCBI Gene Expression Omnibus under the accession number GSE304481. Whole genome bisulfite sequencing data analyzed in this study were downloaded using fastq-dump from SRA toolkit (version 3.0.5). ChIP-seq data, including the peak information for different histone modifications, were collected from a previously published source.
Data analysis	Raw reads of the 423 BC1s were quality controlled by FastQC (version 0.11.4) and trimmed using Trimmomatic (version 0.39) to remove adapters and low-quality reads. Clean reads were mapped to the maize B73 reference genome version 5 using Bowtie 2 (version 2.2.9). Duplicate reads were removed with PicardTools (version 1.98), and SNP calling was performed using the Genome Analysis Toolkit (GATK, version 4.4.0.0). Genetic maps and recombination rates were developed using TASSEL (version 5.0, https://www.maizegenetics.net/tassel), R/qtl (version 1.70, https://rqtl.org/), ASMap (version 1.0-8, https://cran.r-project.org/web/packages/ASMap/index.html), and MareyMap (version 1.3.7, https://cran.r-project.org/web/packages/MareyMap/index.html). Crossover motifs were identified using STREME.

WGBS raw reads were trimmed with Trimmomatic (version 0.39) and mapped to the B73 reference genome v5 using Bismark (version 0.24.2) with the following parameters (-l 50, -N 1). PCR duplicates between WT and mop1 were removed using PicardTools (version 1.98).

DMR calling was performed using metilene (http://legacy.bioinf.uni-leipzig.de/Software/metilene/).

Raw RNA-seq reads were quality controlled by FastQC v0.11.7 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and trimmed using Trimmomatic v0.39 to remove adapters and low-quality reads. The trimmed reads were then aligned to the B73 reference genome version 5, using HISAT v2.2.1. Only uniquely mapped reads were retained. The number of reads per gene for each sample was quantified using HTSeq v0.11.298 (ref). Differentially expressed genes (DEGs) were identified using the R package DESeq2 v1.12.3.

Bedtools (version 2.30.0) was used for the comparisons of crossovers with genes, TEs, and DMRs.

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

The whole genome sequencing data for 423 BC1 individuals, derived from female and male mop1 mutants and their wild-type controls, have been deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive under the associate code PRJNA1198964. The RNA-seq data for immature anthers from mop1 mutants and their WT siblings are available in the NCBI Gene Expression Omnibus under the accession number GSE304481.

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

Life sciences study design

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

Sample size	In total, 110, 97, 94, and 122 BC1 individuals derived from female WT, female mop1, male WT, and male mop1, respectively, were used for whole genome re-sequencing to construct high-resolution crossover maps. Based on published research and our experience, a population size of 100 is sufficient for determining recombinants. We generated high-resolution crossover maps, with 60% mapped to less than 5 kb and 45% mapped to less than 2 kb of two SNP markers.
Data exclusions	No data were excluded.
Replication	Our previously published research (Zhao et al., 2021, PNAS) has already served as a biological replicate. In this study, we aimed to construct high-resolution crossover maps by sequencing 423 BC1 individuals derived from female WT, female mop1, and male WT, to determine the genomic and epigenomic features underlying the recombination changes in mop1. Our RNA-seq experiment has three biological replicates for both WT and mop1.

Randomization	Randomization is not relevant to our study, as we included all samples in the analysis. All plants were grown under the same environmental conditions, and tissues were collected at the same time.
Blinding	Blinding is not relevant to our study as there was no group allocation during data collection.

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

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	The mop1 mutants in the B73 and Mo17 backgrounds are available in MaizeGDB. The BC1 populations are available upon request.
Novel plant genotypes	The genetic strategy used to construct BC1 populations was described in Fig. 1a and methods. Heterozygous mop1 plants in the Mo17 background were crossed with heterozygous mop1 plants in the B73 background (Mo17;mop1/+ × B73;mop1/+) to generate F1 hybrid mop1 mutants (Mo17/B73;mop1/mop1) and their hybrid wild-type siblings (Mo17/B73;+/+). These F1 hybrid mop1 mutants and wild-type plants were reciprocally backcrossed with B73 to produce four BC1 populations derived from male mop1, female mop1, male WT, and female WT.
Authentication	The mop1-1 (mediator of paramutation1) mutation is a Mutator (Mu) transposon insertion. Mu transposons have two terminal inverted repeats (TIRs). The primer TUSC (AGAGAAGCCAACGCCAWCGC) targets the two TIRs. Because the Mu insertion is large, using primers RDR2-F (TCTCCACCGCCCACTTGAT) and RDR2-R (ATGGCCAGCAGGGTGTCGCAGAT), which produce a PCR band, indicates the absence of a Mu insertion, suggesting the allele is wild-type (WT). Combining the primer TUSC with either RDR2-F or RDR2-R to amplify a band indicates the mop1 allele.