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Corresponding author(s): Baoan Song, Chuan He, Guifang Jia and NBT-RA48858C

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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	Images of agarose gel were collected by Bio-Rad Image Lab™ software or MP1600 Tanon imaging software. The qPCR data was acquired by QuantStudio™ Software V1.3 on Applied Biosystems ViiATM7 Real-Time PCR System (Applied Biosystems, USA). The western blot data was acquired by MP-5200 Tanon imaging software on a 5200 chemiluminescence imaging machine (Tanon, China). The sections stained with Safranin O (Coolaber, China) and Fast Green (Coolaber, China) was imaged by cellSens Standard 1.9 Olympus imaging software under bright-field through a microscope (Olympus, IX73, Japan). Tiller buds at shoot basal regions of 4-leaf stage seedlings were imaged by NIS Elements 4.60 Nikon imaging software under bright-field through a microscope (Nikon, SMZ 18, Japan). Root morphological parameters were collected by EPSON scanner (Epson Expression 1600pro, Japan) and Win-RHZIO software (Regent Instruments Inc., Canada). Photosynthesis datas were collected by LI-6800 (LI-COR Inc., USA). The fluorescence images were taken immediately using ZEN lite from a Zeiss LSM 700 laser scanning confocal microscope (Germany). Mass spectrometry data was collected by Agilent MassHunter Workstation Software in a Triple Quad 5500 mass spectrometer (AB SCIEX, USA). Poly(A) RNA quantification data was collected by Agilent bioanalyzer 2100 (USA). Ploidy data was acquired by BD LSRFortessa cell analyzer (USA) High through-put sequencing data was collected by illumina HiSeq Control Software v3.4.0 for HiSeq 4000 Systems.
Data analysis	Cutadapt v1.15 was used to trim adapters of raw reads. HISAT2 v2.1.0 was used to map reads to the rice genome. MeTPeak was used to identify m6A peaks. HOMER v4.9 was used for motif enrichment analysis. featureCounts from Subread v1.6.4 was used for counting reads. The R package affy was used for normalizing gene expression. agriGO v2.0 was used to perform GO analysis.

Flow cytometry data was collected with BD FACSDiva 7.0, analyzed and exported by flowJo10.5.3.
The GSEA software was used for gene set enrichment analysis.
EnrichmentMap was used to show the GSEA network.

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

The m6A-seq and quantitative RNA-seq data generated by this study have been deposited in NCBI Gene Expression Omnibus (GEO) under the accession number GSE135549. All other data supporting the findings of this study are available from the corresponding authors on 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	Sample sizes were determined based on the Authors' experience of what is necessary to generate a convincing and compelling result. The sample size (n) of each experiment is provided in the figure/table legends in the main manuscript and supplementary information files. For laboratory and greenhouse experiments: in our laboratory, we regularly use at least 3 biological replicates (with exceptions for the seq data) which results in reproducible data and the detection of significant changes that support meaningful conclusions. For the field trial: there were 32 plants for each rice genotype in one plot and each genotype was arranged in 3 random plots, as this amount of replication is adequate to detect meaningful (biologically and practically) phenotypic changes in rice; there were more than 100 plants for each genotype of potato in one plots and each genotype was grown in 3 random plots.
Data exclusions	No data points were excluded from analysis in any experiment depicted in this manuscript.
Replication	The findings in this paper were remarkably reproducible. Every experiment was performed multiple times.
Randomization	All crops included in this paper were grown in the fields in a random arrangement.
Blinding	The investigators were blinded to genotypes during phenotype associated data collection, especially yield 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
☒	☐ 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	The primary antibodies used were commercially available: mouse anti-FTO antibody (ab92821, Abcam, USA), rabbit anti-Histone

	H3 antibody (ab1791, Abcam, USA), mouse anti-H3K9me2 antibody (ab1220, Abcam, USA), and anti-H3K27me3 antibody (61017, Active motif, USA), and mouse anti-β-actin (HX1843, Huaxingbio Biotechnology, China).
Validation	Further information on these antibodies is available at https://www.abcam.com/, https://www.activemotif.com/, and http://www.huaxingbio.com/.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	To examine the ploidy level of FTO plants in this analysis, fresh leaves were chopped with a sharp razor in precooled extraction buffer (0.1M citric acid, 0.5% Tween 20, pH 2.3). After filtered through 30 μm cell strainer, the DNA content per nucleus stained with DAPI were measured by using the BD LSRFortessaTM cell analyzer (USA).
Instrument	BD LSRFortessa cell analyzer (USA)
Software	Flow cytometry data was collected with BD FACSDiva 7.0， analyzed and exported by flowJo10.5.3
Cell population abundance	No sorting was done, just analysis the data according to gating strategy.
Gating strategy	Nuclei for analysis was gated according to the FSC and SSC channel.To reduce interference from debris and other cellular particles, events were gated on SSC and DAPI fluorescence to distinguish between noise and fluorescence signals from the nucleus.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.