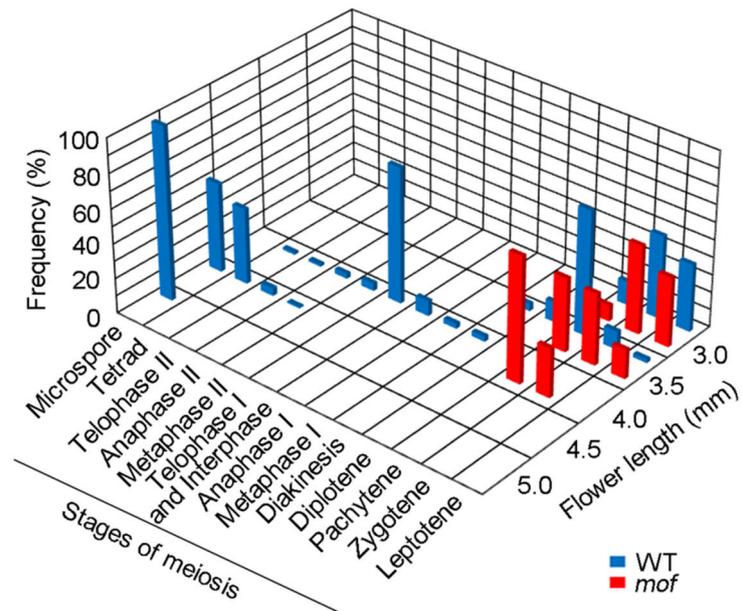


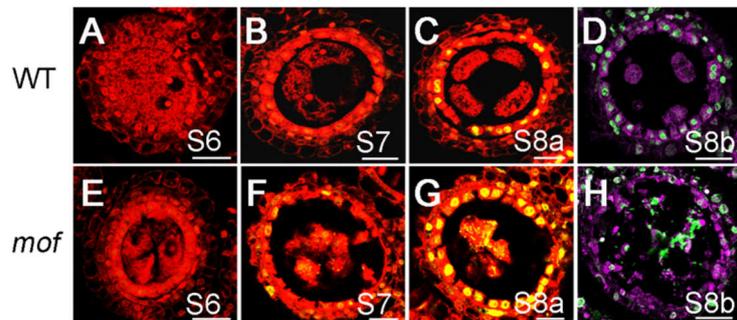
Supplemental Figure 1. TEM of Wild-Type and *mof* Anthers.

Anthers from wild-type (A-H) and *mof* (I-P) plants from stage 7 to stage 9 are shown. (A) and (I) Stage 7; (B) and (J) Higher magnification of the wild-type and *mof* meiocytes in (A and I). (C) and (K) Stage 8a; (D) and (L) Higher magnification of the wild-type and *mof* meiocytes in (C and K) showing abnormal degradation of meiocytes in *mof* mutants (L). (E) and (M) Stage 8b; (F) and (N) Higher magnification of the wild-type and *mof* meiocytes in (E and M) showing residues of meiocytes in the anther locule in *mof* (N). (G) and (O) Stage 9; (H) and (P) Higher magnification of the wild-type and *mof* anther in (G and O) showing materials released from the tapetum (arrow) in *mof* (P). Cr, chromatin or chromosome; E, epidermis; En, endothecium; MC, meiocyte cell; ML, middle layer; Ms, microspores; Mt, mitochondrion; N, nucleus; T, tapetum; Tds, tetrads; V, vacuole. Bars = 5 μ m (A-D) and (G-J), 2 μ m (C-F) and (K-N).



Supplemental Figure 2. Distribution of Prophase I Cells in Wild-Type and *mof* Anthers.

Histogram showing the number of meiocytes in each meiotic stage, counted in flowers from 3.0 to 5.0 mm long from wild-type and *mof* plants.



Supplemental Figure 3. DNA Fragmentation Assay Analysis of Wild-Type and *mof* Anthers.

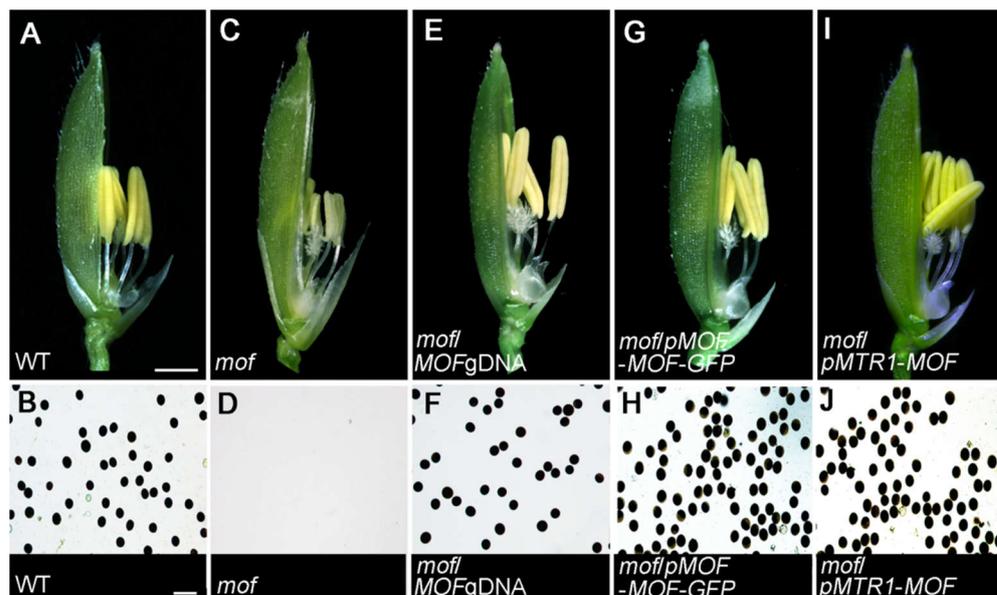
Anthers from the wild type (A-D) and *mof* (E-H) from stage 6 to stage 8 are shown. Nuclei have been stained with propidium iodide indicated by red fluorescence, while yellow to green fluorescence results from staining of TUNEL-positive nuclei.

(A) and (E) Stage 6. (B) and (F) Stage 7. (C) and (G) Stage 8a. (D) and (H) Stage 8b. Bars = 2 μ m.

Supplemental Data. He et al. (2016). Plant Cell 10.1105/tpc.16.00108.

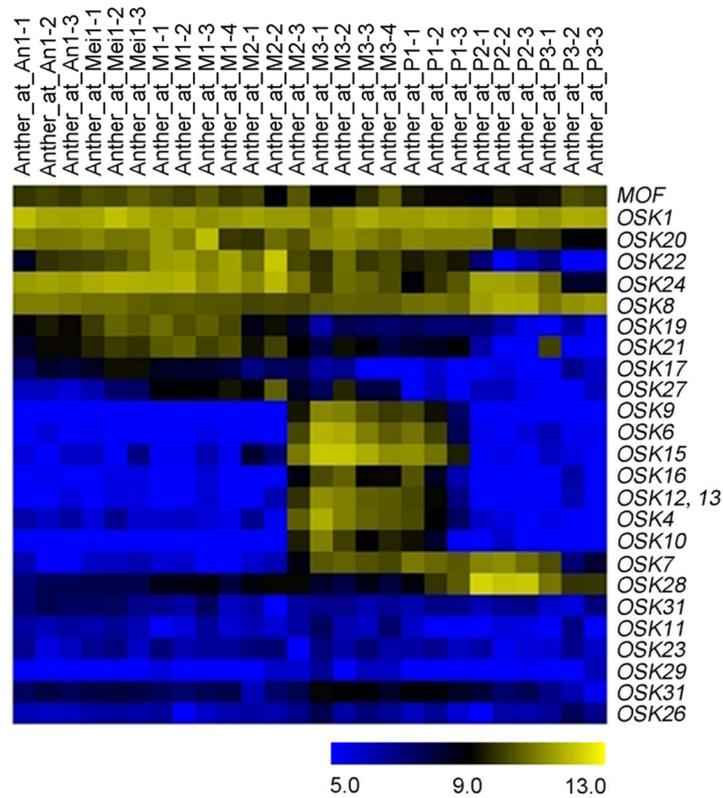
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Supplemental Figure 4. Nucleotide and Amino Acid Sequences of MOF. The F-box domain in MOF is underlined in blue. The box in red indicates the position of the two-nucleotide deletion mutation, and this mutation leads to a frameshift and premature translational termination of MOF. The asterisks indicate the position of the stop codon.



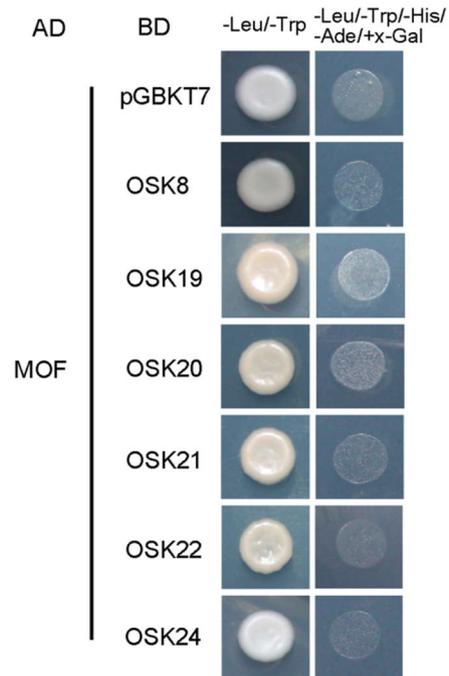
Supplemental Figure 5. Complementation Analysis of *mof*.

(A) and (B) Phenotypes of the flower (A) and pollen grain staining by I₂-KI (B) in the wild type at stage 13. (C) and (D) Phenotypes of the flower (C) and pollen grain staining by I₂-KI (D) in *mof* mutants at stage 13. (E) and (F) Phenotypes of the flower (E) and pollen grain staining by I₂-KI (F) in the *mof*/MOFgDNA complemented line at stage 13. (G) and (H) Phenotypes of the flower (G) and pollen grain staining by I₂-KI (H) in the *mof*/pMOF:MOF:eGFP line at stage 13. (I) and (J) Phenotypes of the flower (I) and pollen grain staining by I₂-KI (J) in the *mof*/pMTR1-MOF line at stage 13.



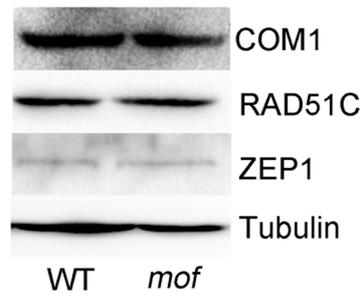
Supplemental Figure 6. Expression Pattern of OSK Genes in Rice.

Microarray analysis data of rice OSK genes from the Rice Oligonucleotide Array Database (<http://www.ricearray.org/>).



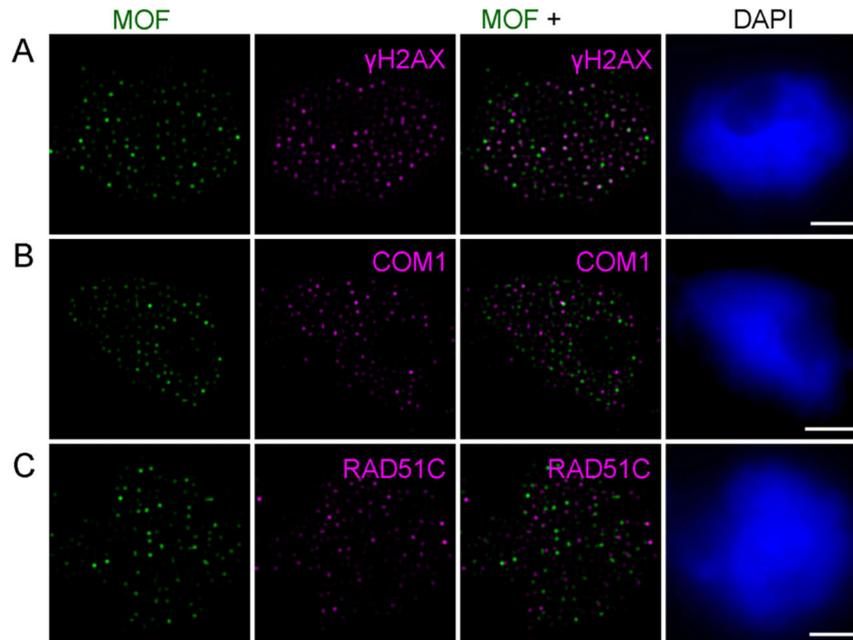
Supplemental Figure 7. Yeast Two-hybrid Assay for Interaction of MOF with Selected OSK Proteins.

Yeast two-hybrid assay for interaction of MOF with OSK8, OSK19, OSK20, OSK21, OSK22, and OSK24. The interactions were verified by the growth of yeast strains on -Leu-Trp-His-Ade+x-Gal selection medium.



Supplemental Figure 8. Protein Levels of Meiosis-related Components in Wild Type and *mof* plants.

Protein levels of the meiosis-related proteins were determined by immunoblot analysis using COM1, RAD51C, and ZEP1 antibodies, with α -tubulin as the loading control. Flowers at the meiosis stage from wild type and *mof* mutants were used.



Supplemental Figure 9. Dual Immunolocalization of MOF and γ H2AX, COM1, RAD51C in Male Meiocytes of the Complemented Transgenic Line.

(A) Dual immunolocalization of MOF (GFP, green) and γ H2AX (magenta) at zygotene stage. In these cells, $57.2 \pm 11.5\%$ ($n=18$) of the MOF foci overlapped with those of the γ H2AX signal.

(B) Dual immunolocalization of MOF (GFP, green) and COM1 (magenta) at zygotene stage. In these cells, $36.7 \pm 7.9\%$ ($n=12$) of the MOF foci overlapped with those of the COM1 signal.

(C) Dual immunolocalization of MOF (GFP) and RAD51C (magenta) at zygotene stage. In these cells, $37.7 \pm 7.2\%$ ($n=14$) of the MOF foci overlapped with those of the RAD51C signal. Bars = 5 μ m.

Supplemental Table 1. Primers Used in This Study.

Primer name	Sequence (5'-->3')	Objective
HY407-002F	GTGAATCCATCGTGAGTGTG	Fine mapping
HY407-002R	TATTCCTCGATAAGCGAAA	Fine mapping
407-05-1F	TGGTCATCTACCAGAGCAAA	Fine mapping
407-05-1R	CAGGGAAGCAAAAGTCAAAT	Fine mapping
MOF-EYFP-F	GAAGATCTATGCGACGCGAGCGCGACGC	Bi-FC
MOF-EYFP-R	GGGGTACCCTACTTTCTATTGAGCTCGA	Bi-FC
OSK1-EYFP-F	GAAGATCTATGGCGGCTGAGGGAGAGAA	Bi-FC
OSK1-EYFP-R	GGGGTACCCTACTCAAAGCCCACTGGT	Bi-FC
MOF-CoIP-F	AGCTACGCGTCTCGAGATGCGACGCGAGCGCGACGCGA	Co-IP
MOF-CoIP-R	TACCGTCGACCTCGAGCTTTCTATTGAGCTCGATTGAT	Co-IP
OSK1-CoIP-F	AGCTACGCGTCTCGAGATGGCGGCTGAGGGAGAGAAGA	Co-IP
OSK1-CoIP-R	TACCGTCGACCTCGAGCTCAAAGCCCACTGGTTCTCC	Co-IP
MOF-infusion-1	CGGTACCCGGGGATCCGTACCGCAATCAACAAACAG	Complementation
MOF-infusion-2	ACCTGTAATTCACACGTGTATTCGTCACCGTATTCGTT	Complementation
MOF(pMTR1-MOF)-F	GCTCTAGAATGCGACGCGAGCGCGACGCGA	Complementation
MOF(pMTR1-MOF)-R	GAAGATCTTCCTTTCTATTGAGCTCGATTG	Complementation
MTR1pro(pMTR1-MOF)-F	GGGGTACCGCATGACATGGTGGCACATA	Complementation
MTR1pro(pMTR1-MOF)-R	GCTCTAGAGGATGCGCGCTTCCCTCGAG	Complementation
MOF(pMOF-MOF-eGFP)-F	GCGCGACGCGCCATGCGACGCGAGCGCGACGC	Complementation
MOF(pMOF-MOF-eGFP)-R	TGCTCACCATACTAGTCTTTCTATTGAGCTCGATTG	Complementation
MOFpro(pMOF-MOF-eGFP)-F	CGGAATTCGTACCGCAATCAACAAACAG	Complementation
MOFpro(pMOF-MOF-eGFP)-R	CATGCCATGGCGCGTCGCGCTATCGTTTTCG	Complementation
OSK1-BK-F	CCCATATGGCGGCTGAGGGAGAGAA	Y2H
OSK1-BK-R	CGGGATCCCTACTCAAAGCCCACTGGT	Y2H

Continued		
Primer name	Sequence (5'-->3')	Objective
OSK8-BKF	CCCATATGCTGCGGAAGGGAGAGGC	Y2H
OSK8-BKR	CGGGATCCTCAGGTGTCCAGATAGTTTG	Y2H
OSK19-BKF	CCCATATGGAGGGAGAGGACGCGGT	Y2H
OSK19-BKR	CGGGATCCTCAGAAGGCCAGGCATCCT	Y2H
OSK20-BKF	CCCATATGGCGGCCGAGGCGGAGAC	Y2H
OSK20-BKR	CGGGATCCTCATTCTGAAGGCCACTGGT	Y2H
OSK21-BKF	CCCATATGGAGGCGGACAAGAGCGG	Y2H
OSK21-BKR	CGGAATTCCTACTCCGGATCCGGGAAGA	Y2H
OSK22-BKF	CCCATATGGCGACGGGGAGCGGAGCA	Y2H
OSK22-BKR	CGGGATCCTCATGCGTGAGTATCCTCCT	Y2H
OSK24-BKF	CCCATATGGCGGCGGCGGCGGGGGC	Y2H
OSK24-BKR	CGGGATCCTTAACGGAGGTAGAGGATGG	Y2H
MOF(-F-BOX)-AD-F	CCCATATGGTGGGGTCGTTCCGCCTCCC	Y2H
MOF-AD-F	CCCATATGCGACGCGAGCGCGACGCGAC	Y2H
MOF-AD-R	CCATCGATCTACTTTCTATTGAGCTCGA	Y2H
MOFyuanwei-T7F	TAATACGACTCACTATAGGGATGCGCCTGGACGAGGACGC	<i>in situ</i>
MOFyuanwei-R	TACGAGCACCTCTCGATGTG	<i>in situ</i>
MOFyuanwei-F	ATGCGCCTGGACGAGGACGC	<i>in situ</i>
MOFyuanwei-T7R	TAATACGACTCACTATAGGGTACGAGCACCTCTCGATGTG	<i>in situ</i>
ACTIN-F	ACCCAAGAATGCTAAGCCAAGAG	qRT-PCR
ACTIN-R	ACTTTGTCCACGCTAATGAAGAAAC	qRT-PCR
MOF-RTF	AAGGTTGACTTCTTGTTGC	qRT-PCR
MOF-RTR	ATCCAATGTCACACTCGTTG	qRT-PCR