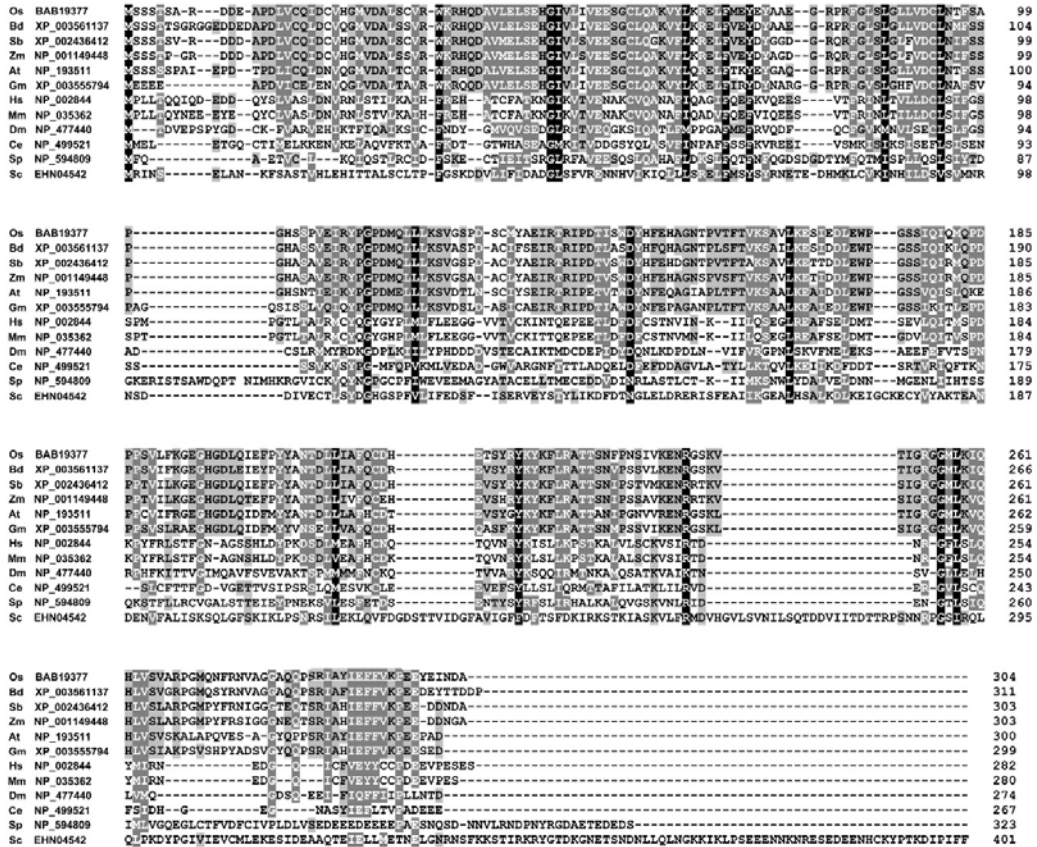# Supplemental Data

Supplemental Figure S1.

Supplemental Figure S1. Multiple sequence alignment of OsRAD1 homologs. Os, *Oryza sativa*; Bd, *Brachypodium distachyon*; Sb, *S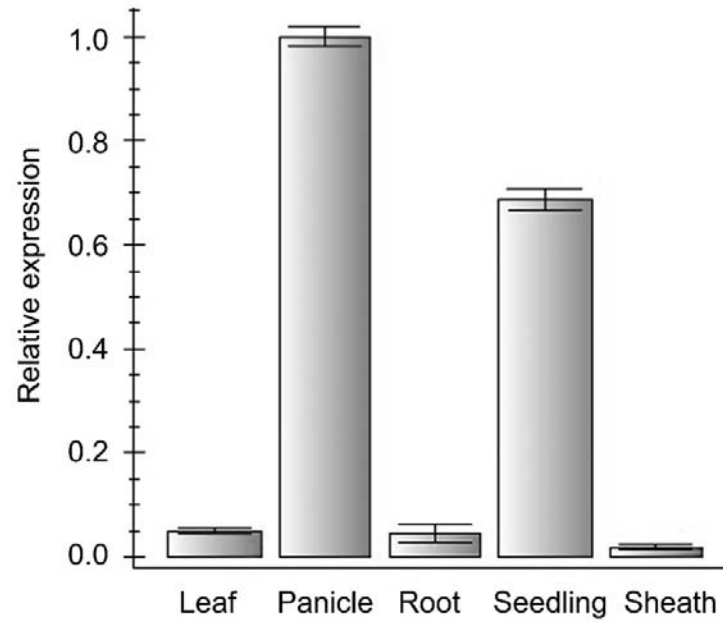orghum bicolor*; Zm, *Zea mays*; At, *Arabidopsis thaliana*; Gm, *Glycine max*; Hs, *Homo sapiens*; Mm, *Mus musculus*; Dm, *Drosophila melanogaster*; Ce, *Caenorhabditis elegans*; Sp, *Schizosaccharomyces pombe*; Sc, *Saccharomyces cerevisiae*. Identical amino acids are shaded in black. Similar amino acids are shaded in gray.

10 **Supplemental Figure S2.**

11 **Supplemental Figure S2.** Expression analysis of *OsRAD1* in leaf, young panicle, sheath, root and

12 seeding by Real-Time QPCR. The error bar represents the SE of mean values in three biological
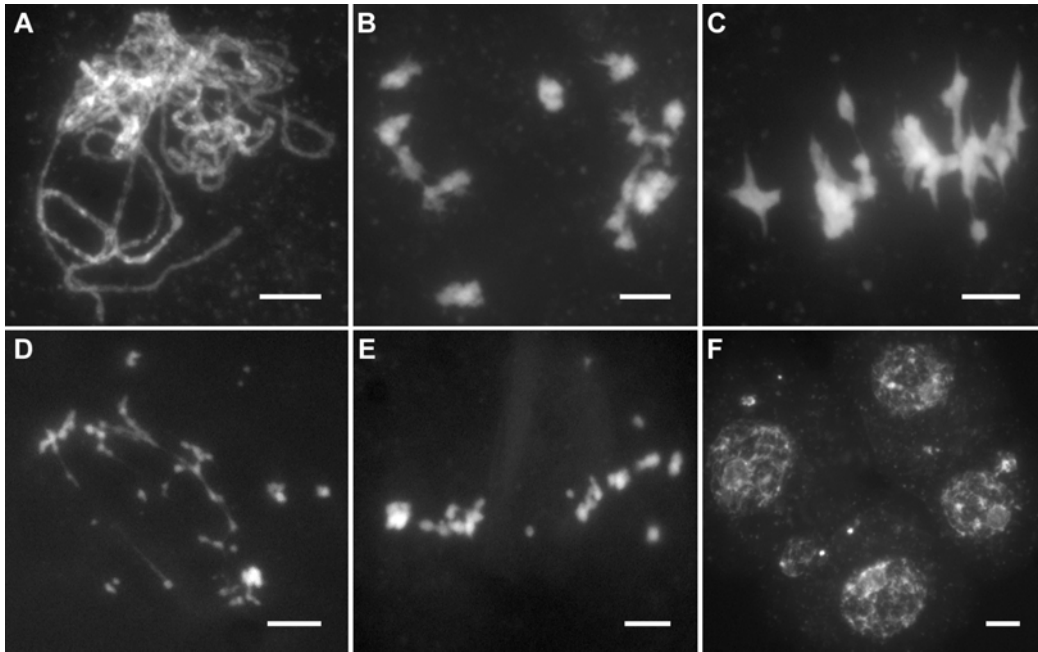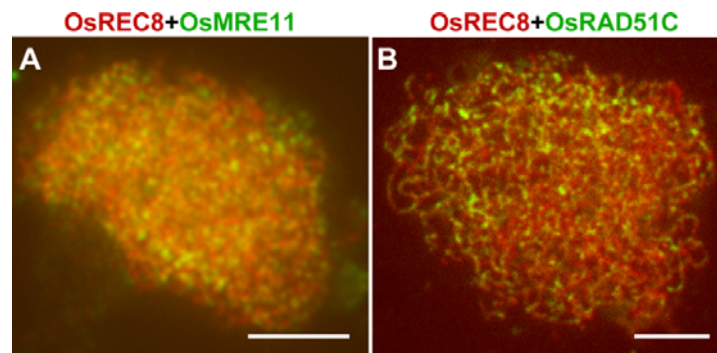
13 replicates.

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23   **Supplemental Figure S3**

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25   **Supplemental Figure S3.** Meiotic defects in *Osrad1-2*. **(A)** Pachytene. **(B)**Diakinesis. **(C)**

26   Metaphase I. **(D)** Anaphase I. **(E)** Metaphase II. **(F)** Tetrad. Bars = 5µm.
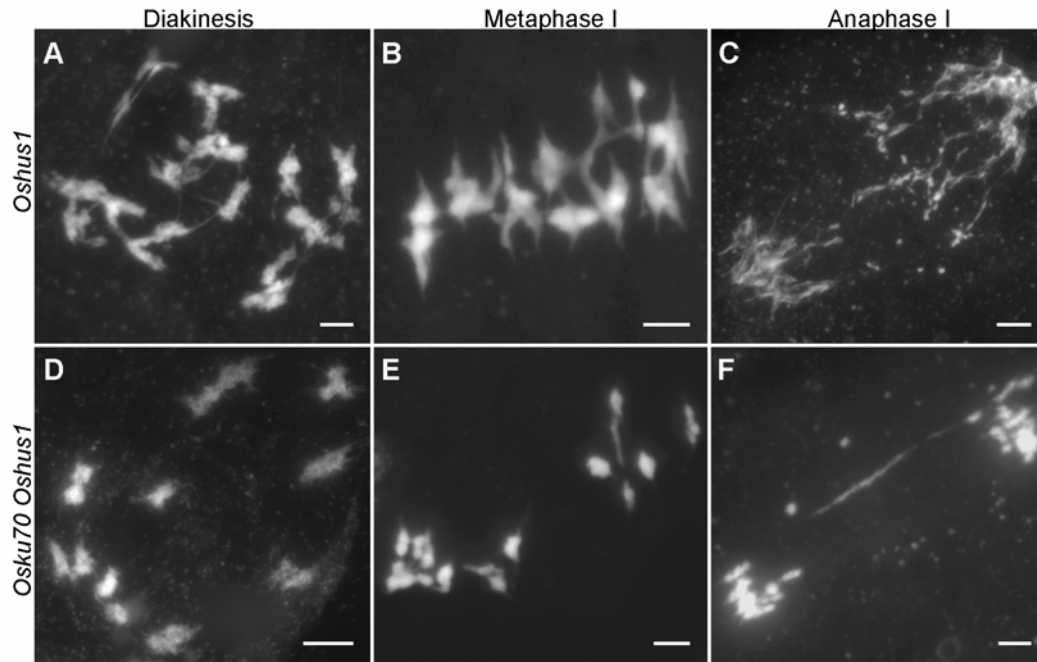
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28   **Supplemental Figure S4**

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30   **Supplemental Figure S4.** Localization of OsMRE11 and OsRAD51C in *Osrad1*. **(A)**

31   Immunostaining of the *Osrad1* mutant for OsREC8 and OsMRE11. **(B)** Immunostaining of the

32   *Osrad1* mutant for OsREC8 and OsRAD51C. Bars = 5µm.

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35 **Supplemental Figure S5**

	Diakinesis	Metaphase I	Anaphase I
Oshus1	A	B	C
Osku70 Oshus1	D	E	F

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37 **Supplemental Figure S5.** Genetic analysis of *OsHUS1* with *OsKU70*. **(A)** to **(C)** *Oshus1*

38 mutation leads to ectopic chromosome associations during meiosis. **(D)** to **(F)** Loss of *OsKU70*

39 partially rescues the meiotic defects of *Oshus1*. Bars = 5µm.

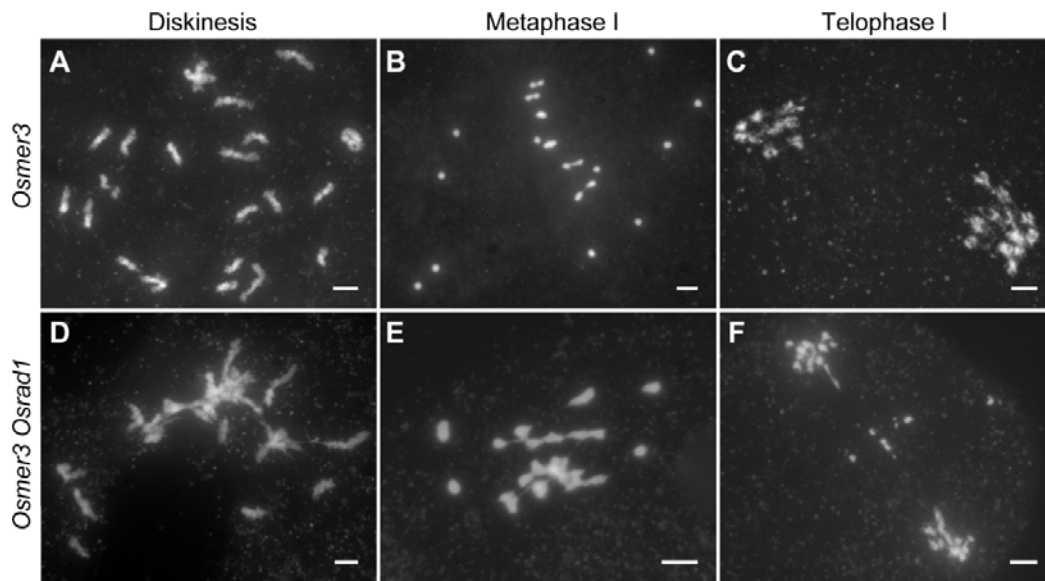40

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Supplemental Figure S6

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52   **Supplemental Figure S6.** Chromosome behaviors in *Osmer3* and *Osmer3 Osrad1*. **(A)** to **(C)**

53   Meiotic chromosomes in *Osmer3*. **(D)** to **(F)** Ectopic chromosome associations occur in the

54   *Osmer3 Osrad1* double mutant. Bars = 5μm.

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57 **Supplemental Table S1. Markers used in Map-based Cloning**

Name	Primer	Sequence(5'-3')
M1	F	GTGTGGCTTGGCTACTGATT
	R	CGGGGCACGCTTTGAGTTGT
P1	F	GGCCTAGGGGCCTAAAGAAAAC
	R	GTCCACCTGTCCGTGCGTATCA
P2	F	CATTTATTCTAGATATTGTG
	R	GTGATTCTCTCTTGATCATC

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59 **Supplemental Table S2. Primers for RACE, RT -PCR, and Plasmid Construction**

Name	Sequence(5'-3')
Adaptor-T(18)	CTGATCTAGAGGTACCGGATCCTTTTTTTTTTTTTTTTTT
R3-1	TCTTCGTGCAACAACTTCG
R3-2	CCCAAACAGTATTGTGAAGG
RO-F	ATGAGCTCGTCGACGTCCGC
RO-R	CTACGCATCATTTATCTCAT
RAD1RT-F	CAGGTTCCAGCATTCAGATTC
RAD1RT-R	TGTTTCATGGTCACATTGGAATG
Actin-F	CTGACAGGATGAGCAAGGAG
Actin-R	GGCAATCCACATCTGCTGGA

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