

Supplementary Material

The absence of the Arabidopsis chaperone complex CAF-1 produces mitotic chromosome abnormalities and changes in the expression profiles of genes involved in DNA repair

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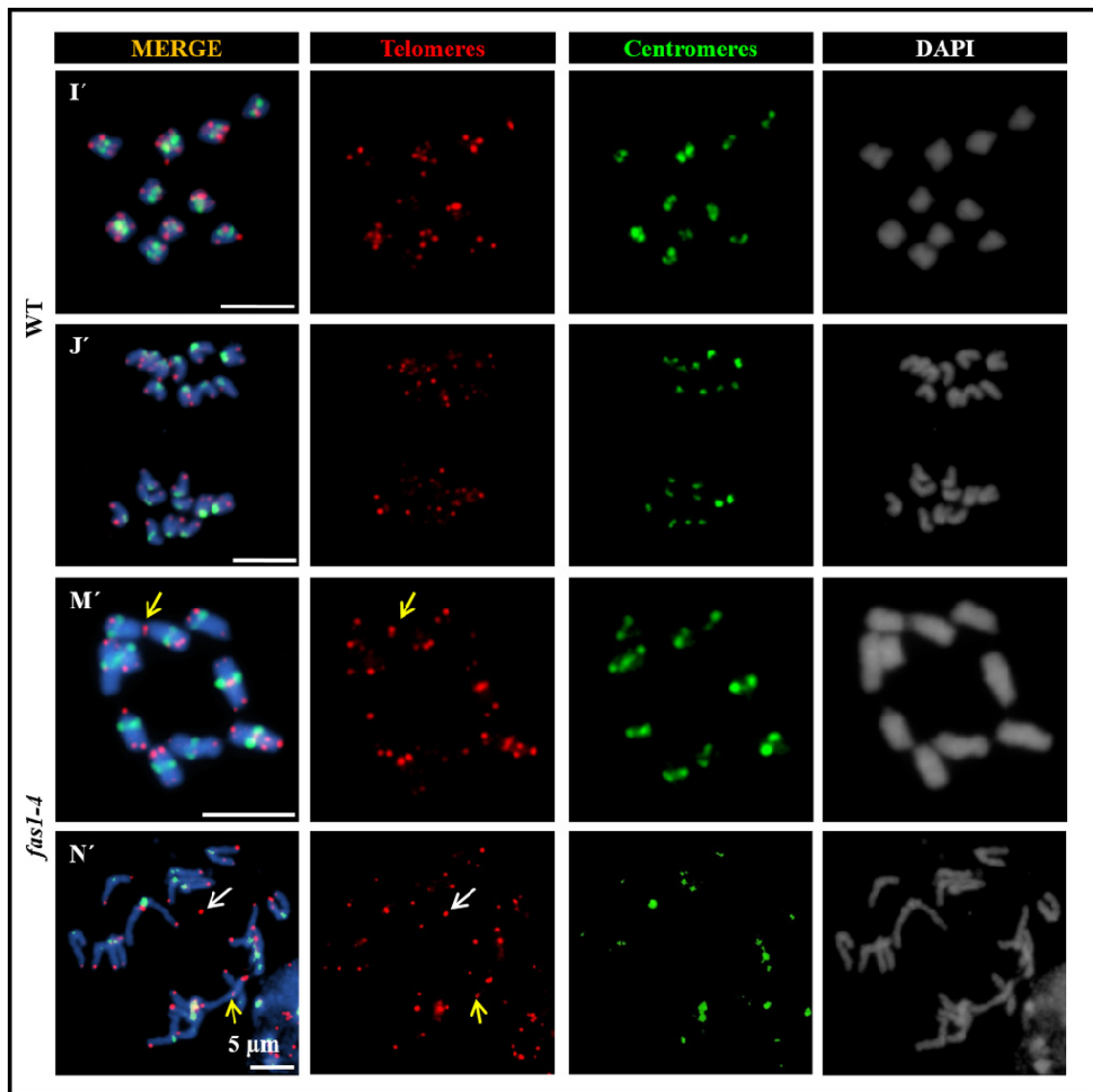
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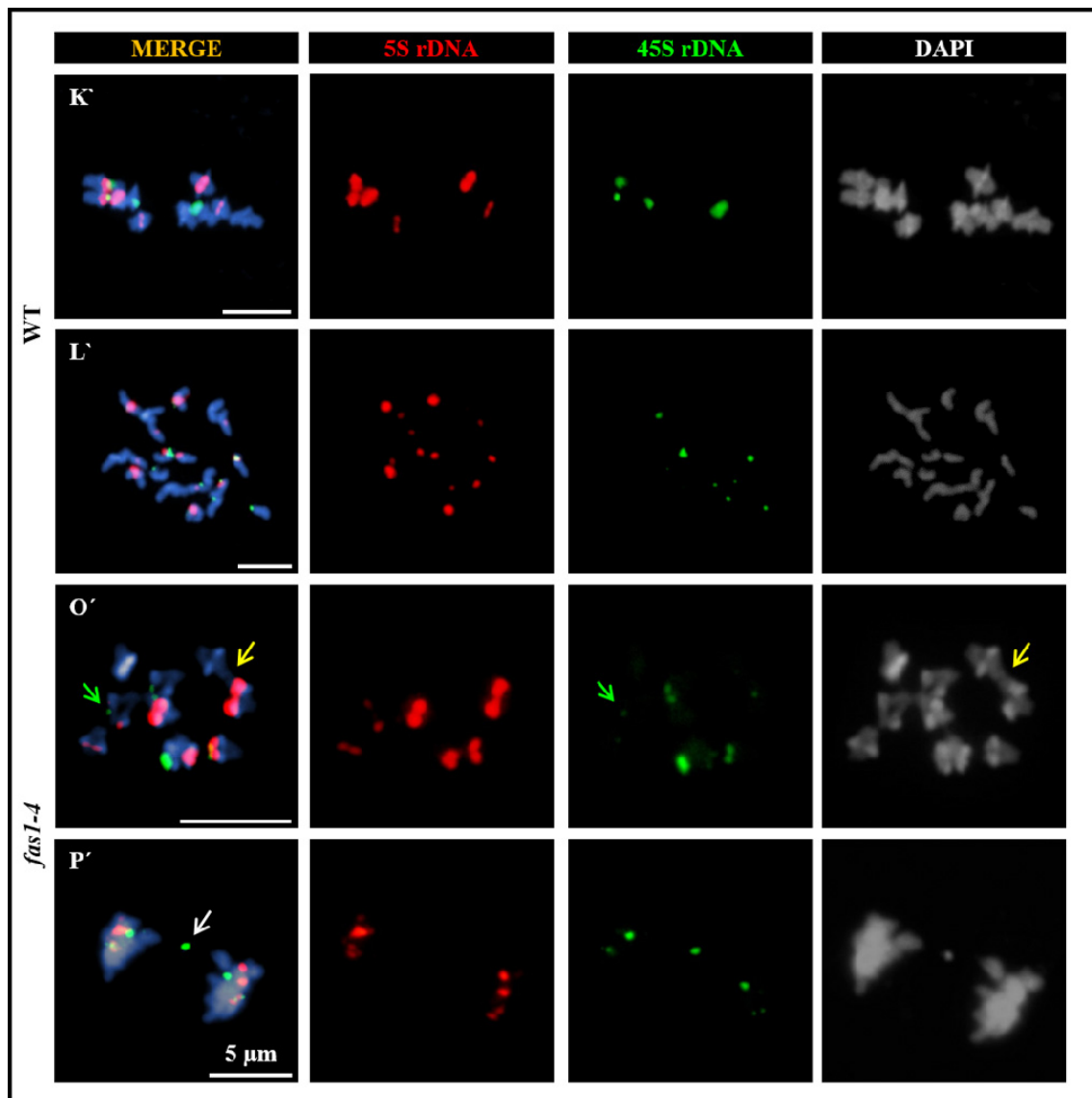
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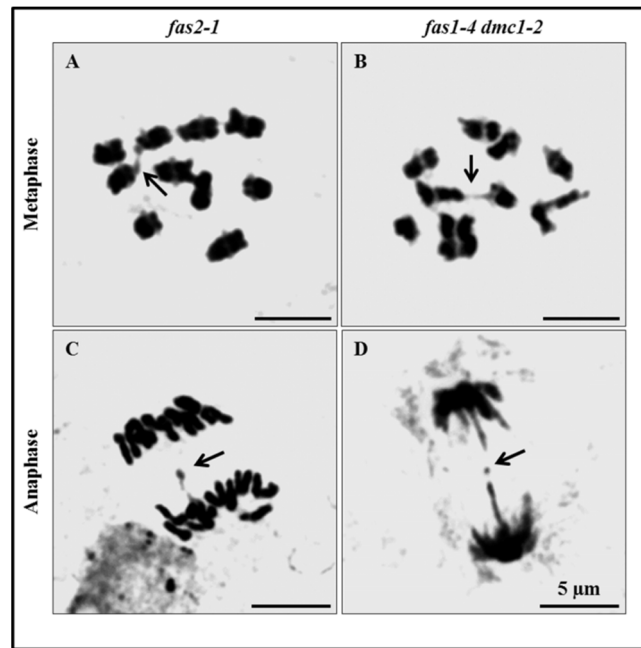
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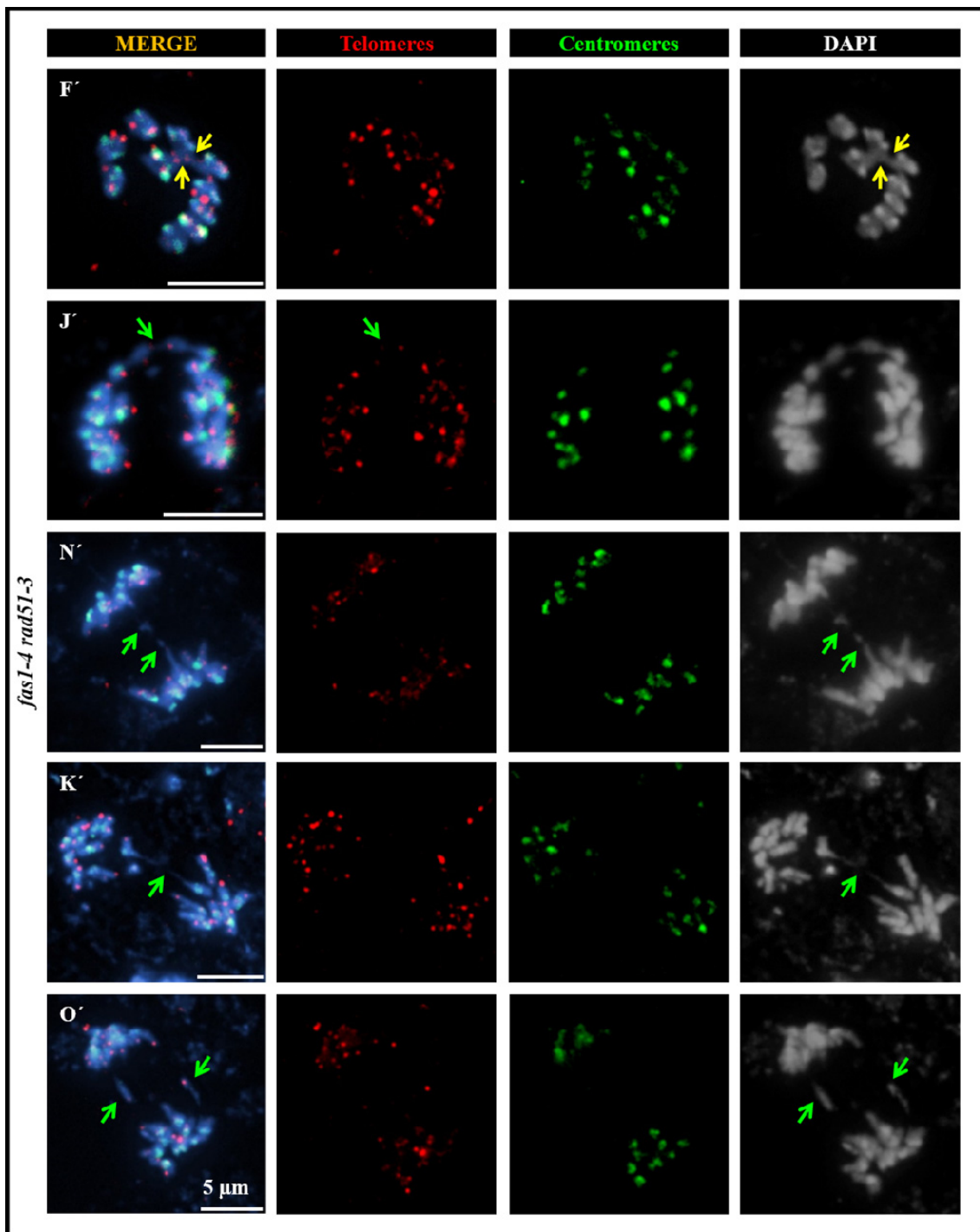
Supplementary Figure S1. Single channel images from WT and *fas1-4* cells after FISH with probes to detect telomeres and centromeres. See Figure 1 for further details. Scale bars represent 5 μm.



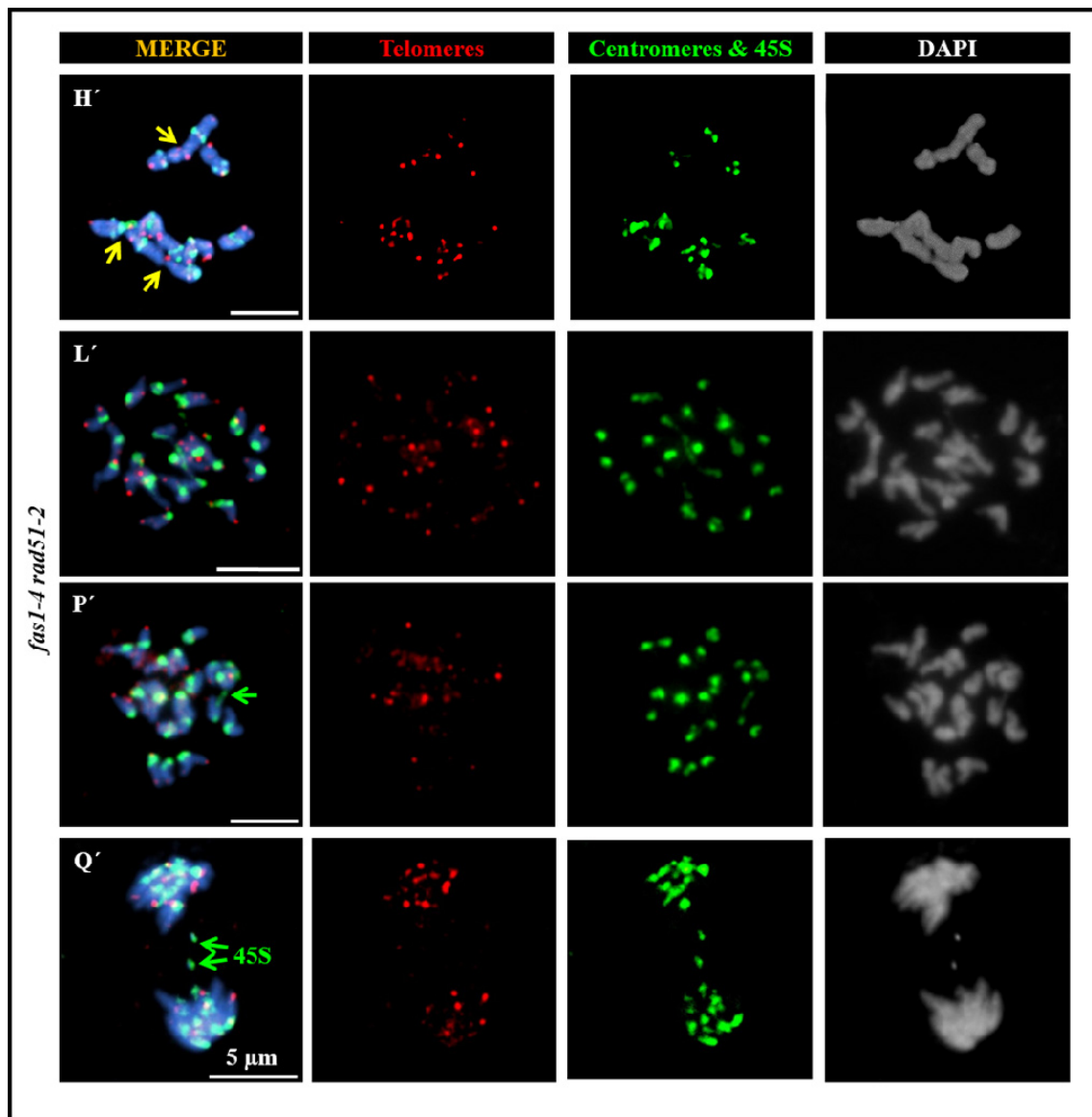
Supplementary Figure S2. Single channel images from WT and *fas1-4* cells after FISH with probes to detect 5S and 45S rDNA regions. See Figure 1 for further details. Scale bars represent 5 μ m.



Supplementary Figure S3. Mitosis in *fas2-1* and in the double mutant *fas1-4 dmc1-2*. DAPI stained chromosomes at metaphase and anaphase. Arrows indicate interchromosomal connections and chromosome bridges. Scale bars represent 5 μm .



Supplementary Figure S4. Single channel images from *fas1-4 rad51-3* cells after FISH with probes to detect telomeres and centromeres. See Figure 3 for further details. Scale bars represent 5 μ m.



Supplementary Figure S5. Single channel images from *fas1-4 rad51-2* cells after FISH with probes to detect telomeres, centromeres and NORs (45S rDNA). See Figure 3 for further details. Scale bars represent 5 μ m.

SUPPLEMENTARY TABLES

Supplementary Table S1. Primers used for genotyping.

Mutant	Sequence 5'- 3'	Collection
Line specific primers		
<i>fas1-4</i>	AAGGAACAAGCCGAGCTAAAG CAAGTTGTAAAGCCACGTCGT	SAIL
<i>rad51-3</i>	TCTCAAGAACTTTGCAAGATGC ATGCCAAGGTTGACAAGATTG	SALK
<i>rad51-2</i>	AAGCATCACCATCTCCAATG GCCCCAGAAAAATCTTCCAG	JP (Spanish collection)
<i>dmc1-2</i>	GACTCATTGTTGCTTGATCCC TCCACTCGGAATAAAGCAATG	SAIL
T-DNA specific primers		
LBb1.3	ATTTTGCCGATTTCGGAAC	SALK
LB2-SAIL	GCTTCCTATTATATCTTCCCAAATTACCAATACA	SAIL
LB2	TGCCAGGTGCCACGGAATAG	JP

Supplementary Table S2. Primers and probes used in the RTqPCR to analyze the expression of genes involved in DSB repair.

	Gene	AGI code	Sequence 5'-3'	UPL probe	Length (bp)
HR	<i>MRE11</i>	At5g54260	GTTTCCGCCAGTCTCAAAGA TTCTCCAATGGTGGAAAGCA	8	74
	<i>RAD50</i>	At2g31970	GCAGTGCAGGTCAAAAAGGTT GGCCCATCCAGGTTTGTAG	136	118
	<i>NBS1</i>	At3g02680	TGCGAAGGATCCATACAAAGA AAGTCCTCTGCAATGGCTTC	38	99
	<i>COM1</i>	At3g52115	CAGCATGAGAAATCAGCAATCT CGAGCCAGTACCAATTCTCAC	68	93
	<i>ATM</i>	At3g48190	AGGGTGGTGAGATGAGAAGC TCTGTGTCAATTGCGTCTTGT	98	67
	<i>ATR</i>	At5g40820	TTCAGCGCCCAAAGAAGA GGCTTGCAGAGGAATGGATA	3	67
	<i>BRCA1</i>	At4g21070	CCAAGAAATTGGTCTTATCTTGC AGTTCCGCAAATTCTGCAAT	100	73
	<i>BRCA2B</i>	At5g01630	CACCTTAAAACCCGCAGTG AGGTGATTTACAAGCACCGATT	140	117
	<i>RAD51C</i>	At2g45280	TCAACTAGCGCTTGCTTTAGG AATACAGAATGACTCGGTTGGTG	54	65
	<i>RAD51</i>	At5g20850	CATGCCACCACAACAAGG ACATGGCGAGCTTATCACTTTAC	91	78
	<i>MND1</i>	At4g29170	TGCGAAAGACAAGATTGGAA AAGTTTCTGGCGAACACTCC	33	88
	<i>AHP2</i>	At1g13330	GAACATTACGTTGCGTTGTT GGCTGCGTCAACCAATAGTC	53	60
	<i>SMC6A</i>	At5g07660	TGCCTCAAGATGCAACAAAC AAAGTCGAGAAAGACCGTTCC	150	76
	<i>SMC6B</i>	At5g61460	TCGCACGAGAGGATAAAGAAA TGACTCAAAGCCGAGGATG	68	106
cNHEJ	<i>KU70</i>	At1G16970	TTGCAAAAACCGGAAAGC ACGAGGAGATTGTTGGCAGT	114	76
	<i>KU80</i>	At1g48050	GGAATGTGTACTCGCTCTTCG GGCATAACTTGAATAGATGGTTCA	125	92
	<i>SNM1</i>	At3g26680	CGGAGATTTCAAGGCTTCTA AACACATCTTCTTTAGAAGGGAATT	55	129
	<i>POLλ</i>	At1g10520	CGTGTTGAACAGAAGGCTGA CAGACTTGCAGTTCTCTAGCA	33	124
	<i>TDP1</i>	At5g15170	AGACCGAGATTTGCCTGAGA GTAGCCTCGGTCCCATGAC	154	101
	<i>LIG4</i>	At5g57160	TCGCACCTTGTAGTTCTTGC ACGTTTCTCCATTTTCGCTGA	29	84
	<i>XRCC4</i>	At3g23100	AGTTTGAGAGTGCAACTTATGCAA TCCTCCTCAACTACTCTCACTGAA	155	109
aNHEJ	<i>PARP1</i>	At2g31320	TCAAAGGTCAAGGCTTCTGAG CCTTACTTTCAACAAGAACTGCAA	26	90
	<i>PARP2</i>	At4g02390	GTTCCACTTGGCAAACCAG CGCATCTTGATTTGTTCCAC	125	95
	<i>XRCC1</i>	At1g80420	GGCTTGAGAGTCAGGAGGAA ACTGATCCAATGTCCTGCTTC	12	124
	<i>LIG6</i>	At1g66730	TTGTGAAGGAATCATGGTCAAG TCGCCAATCCATCTACATAA	43	111
MMEJ	<i>RAD1</i>	At5g41150	TCACAAACAATCCACAGAAGGTA CATACTGCGGAGCTCAATTTT	62	77
	<i>ERCC1</i>	At3g05210	GATTGGCGAACGTAAGGTG ACATCCTTCTCAACTGGAGCTT	119	123

AGI, Arabidopsis Genome Initiative; UPL, Universal Probe Library; HR, homologous recombination; cNHEJ, classical-NHEJ; aNHEJ, alternative-NHEJ; MMEJ, microhomology end-joining.

Supplementary Table S3. Statistical comparisons of the number of cells with metaphase aberrations between the mutants analyzed.

Genetic background	WT	<i>fas1-4</i>	<i>fas2-4</i>	<i>fas1-4 dmc1-2</i>	<i>fas1-4 rad51-3</i>	<i>fas1-4 rad51-2</i>
WT		***	***	***	***	***
<i>fas1-4</i>			NS	NS	NS	*
<i>fas2-1</i>				NS	NS	*
<i>fas1-4 dmc1-2</i>					NS	*
<i>fas1-4 rad51-3</i>						NS
<i>fas1-4 rad51-2</i>						

Asterisks indicate *P*-values from chi-square test: NS, no significant; ****P*<0.001 and **P*<0.05.

Supplementary Table S4. Statistical comparisons of the number of cells with dicentric chromosomes between the mutants analyzed.

Metaphase	WT	<i>fas1-4</i>	<i>fas2-4</i>	<i>fas1-4</i> <i>dmc1-2</i>	<i>fas1-4</i> <i>rad51-3</i>	<i>fas1-4</i> <i>rad51-2</i>
WT		***	***	***	***	***
<i>fas1-4</i>			NS	NS	NS	NS
<i>fas2-1</i>				NS	NS	NS
<i>fas1-4</i> <i>dmc1-2</i>					NS	NS
<i>fas1-4</i> <i>rad51-3</i>						NS
<i>fas1-4</i> <i>rad51-2</i>						

Asterisks indicate *P*-values from chi-square test: NS, no significant; ****P*<0.001.

Supplementary Table S5. Statistical comparisons of the number of cells with more than three chromosomes fused between the mutants analyzed.

Metaphase	WT	<i>fas1-4</i>	<i>fas2-4</i>	<i>fas1-4</i> <i>dmc1-2</i>	<i>fas1-4</i> <i>rad51-3</i>	<i>fas1-4</i> <i>rad51-2</i>
WT		NS	NS	NS	***	***
<i>fas1-4</i>			NS	NS	*	*
<i>fas2-1</i>				NS	*	*
<i>fas1-4</i> <i>dmc1-2</i>					*	*
<i>fas1-4</i> <i>rad51-3</i>						NS
<i>fas1-4</i> <i>rad51-2</i>						

Asterisks indicate *P*-values from chi-square test: NS, no significant; ****P*<0.001 and **P*<0.05.

Supplementary Table S6. Statistical comparisons of the number of cells with anaphase alterations between the mutants analyzed.

Metaphase	WT	<i>fas1-4</i>	<i>fas2-4</i>	<i>fas1-4</i> <i>dmc1-2</i>	<i>fas1-4</i> <i>rad51-3</i>	<i>fas1-4</i> <i>rad51-2</i>
WT		***	**	**	***	***
<i>fas1-4</i>			NS	NS	*	**
<i>fas2-1</i>				NS	*	**
<i>fas1-4</i> <i>dmc1-2</i>					*	**
<i>fas1-4</i> <i>rad51-3</i>						NS
<i>fas1-4</i> <i>rad51-2</i>						

Asterisks indicate *P*-values from chi-square test: NS, no significant; ****P*<0.001, ***P*<0.01 and **P*<0.05.