

Figure S1. Mutation analysis and complementation assays of *rhc4e-3*. (A) Schematic diagrams of the *AtRFC4* gene and T-DNA insertion position. The black boxes and lines indicate exons and introns, respectively; red boxes represent UTRs and red letters represent mutated bases. (B) The relative expression of *RFC4* or *RFC4*^{G54E} of Col-0 or *rhc4e-1*, *rhc4e-2* and *rhc4e-3* seedlings at 12 days. Error bars indicate \pm SD (** $P < 0.01$). (C) Phenotype of wild-type and complementation seedling *rhc4e-3C-1* and *rhc4e-3C-2* at 18 days after germination. Bar = 1 cm.

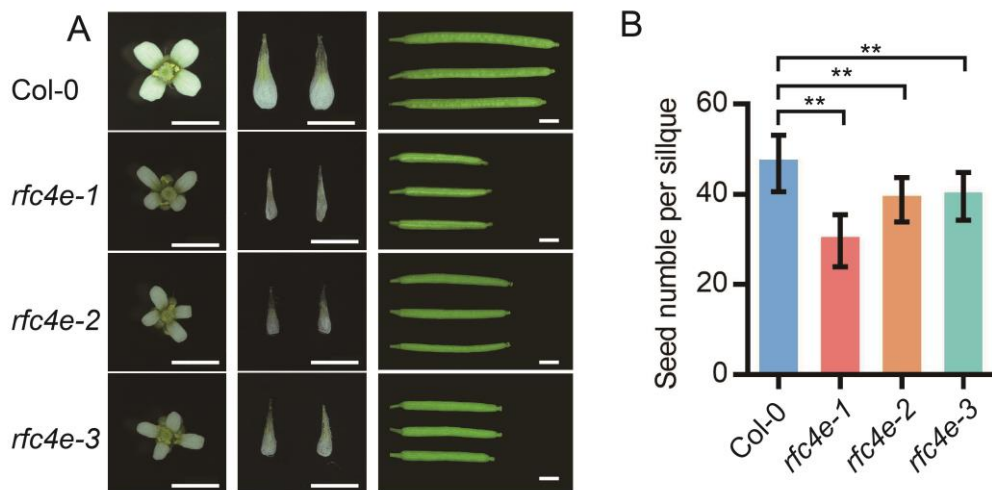


Figure S2. Morphology of representative flowers, petals and siliques for the *rhc4e* mutants. (A) Morphology of representative flowers, petals and siliques of Col-0, *rhc4e-1*, *rhc4e-2* and *rhc4e-3*. Bar = 2 mm. (B) The average number of seeds per silique in Col-0, *rhc4e-1*, *rhc4e-2* and *rhc4e-3*. Error bars indicate \pm SD (** $P < 0.01$).

Table S1 All DEGs ($p < 0.05$) analyzed by Gene Ontology (GO) term enrichment based on the biological process category in *rfc4e-3*. The GO enrichment analysis was based on biological process functional categories of ShinyGo v0.61 software, and the top 20 pathways were showed as follows.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathways
9.2E-12	243	1692	1.6	Response to oxygen-containing compound
6.9E-10	187	1265	1.7	Cellular response to stress
3.1E-08	48	195	2.8	DNA replication
1.2E-07	121	770	1.8	Response to radiation
5.6E-07	38	148	2.9	DNA-dependent DNA replication
1.7E-06	220	1716	1.5	Cellular response to chemical stimulus
1.8E-06	73	411	2	Response to water
3.2E-06	33	127	3	Response to karrikin
3.4E-06	54	273	2.3	Response to extracellular stimulus
3.6E-06	44	202	2.5	Response to starvation
3.8E-06	136	962	1.6	Response to inorganic substance
3.9E-06	237	1914	1.4	Response to external stimulus
3.9E-06	46	219	2.4	Cellular response to extracellular stimulus
3.9E-06	34	137	2.8	Double-strand break repair
4.0E-06	75	442	1.9	Response to acid chemical
4.1E-06	66	371	2	Secondary metabolic proc.
6.7E-06	110	746	1.7	Response to light stimulus
8.8E-06	134	966	1.6	Response to lipid
1.5E-05	68	402	1.9	Response to water deprivation
1.6E-05	46	232	2.3	Response to nutrient levels

Table S2 Down-regulated genes ($P < 0.05$, foldchange ≤ 0.67) analyzed by Gene Ontology (GO) term enrichment based on the biological process category in *rfc4e-3*. The GO enrichment analysis was based on biological process functional categories of ShinyGo v0.61 software, and the top 10 pathways were showed as follows.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway
9.77E-10	22	80	6.826325	Cellular response to phosphate starvation
4.72E-08	26	148	4.360797	Inorganic anion transport
2.78E-08	28	164	4.238073	Cellular response to starvation
1.69E-08	30	179	4.160279	Cellular response to nutrient levels
3.58E-08	31	202	3.80947	Response to starvation
2.74E-08	33	219	3.740452	Cellular response to extracellular stimulus
1.37E-08	71	746	2.362511	Response to light stimulus
2.78E-08	71	770	2.288874	Response to radiation
9.31E-09	128	1716	1.851599	Cellular response to chemical stimulus

Table S3. Up-regulated genes ($P < 0.05$, foldChange ≥ 1.5) analyzed by KEGG term enrichment based on the biological process category in *rfc4e-3*. The KEGG enrichment was analyzed by ShinyGo v0.61 software.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway
3.88E-08	18	63	6.048823	Homologous recombination
1.05E-05	13	48	5.73378	DNA replication
0.000179	10	37	5.72186	Mismatch repair
0.002875	9	42	4.536617	Base excision repair
0.005244	11	67	3.475816	Nucleotide excision repair

Table S4. Primers used in this study.

Name	Sequence (5'-3')	Description
<i>FP1</i>	aacaagtaccctacactaaaaggccg	Amplify upstream sequences for <i>RFC4(G54E)</i> mutagenesis
<i>At4eMR1</i>	gcagtagtggttttctcagtcctgggtgg	
<i>At4eMF2</i>	ccaccaggcactgagaaaaaccactactgc	Amplify downstream sequences for <i>RFC4(G54E)</i> mutagenesis
<i>At4R2</i>	gcaatgtccatcaagctatctggtc	
<i>At4F</i>	gaccatgattacgaattcgagctctacagtttgtatccagc	Amplified full-length sequence of <i>AtRFC4</i>
<i>AT4R</i>	caggctcgactctagaggatccctacactatgatagtctcataag	
<i>RP1</i>	ctgtctagctacctaattggg	<i>rfc4-1</i> T-DNA insert identification
<i>LBa1</i>	tggttcacgtagtgggccatcg	
<i>FP1</i>	aacaagtaccctacactaaaaggccg	<i>AtRFC4</i> in situ identification
<i>RP1</i>	ctgtctagctacctaattggg	
<i>FLAG-R</i>	aacgatcggggaaattcgag	Site-directed mutagenesis plasmid transfer validation
<i>FP2</i>	agtgacataacagacatgc	
<i>GFP-R</i>	ttcacctctccactgacag	Complementary plasmid transfer verification
<i>FP2</i>	agtgacataacagacatgc	
<i>AtBRCA1-F</i>	ccatgtattttgcaatgcgtg	At4g21070, for RT-qPCR
<i>AtBRCA1-R</i>	tgtggagcacctcgaatctct	
<i>AtRAD51-F</i>	cgaggaaggatctcttcgag	At5g20850, for RT-qPCR
<i>AtRAD51-R</i>	gcactagtgaacccagagg	
<i>AtRAD54-F</i>	cagcaggtgacgaggtgac	At3g19210, for RT-qPCR
<i>AtRAD54-R</i>	cgcttatttacaggttggtcc	
<i>AtPARP1-F</i>	acccatcagaggctcaaaca	At2g31320, for RT-qPCR
<i>AtPARP1-R</i>	acgcatcttgattgttcaca	
<i>AtPARP2-F</i>	tatgccaaactggcgctaa	At4g02390, for RT-qPCR
<i>AtPARP2-R</i>	tcattgtctccaaagcaacctc	
<i>AtRPA1E-F</i>	tggagaagtgcgactgaagc	At4g19130, for RT-qPCR
<i>AtRPA1E-R</i>	acctccagttgcggaacaat	
<i>AtPCNA1-F</i>	attggaaccgctaaca	At1g07370, for RT-qPCR
<i>AtPCNA1-R</i>	caactccgacgataag	
<i>AtKU80-F</i>	tcgtaaaggctgcgtcttgg	At1g48050, for RT-qPCR

Name	Sequence (5'-3')	Description
<i>AtKU80-R</i>	ttggcataacttgaatagatggttca	
<i>AtKU70-F</i>	cgagcttcgtgaaaccagagatg	At1g16970, for RT-qPCR
<i>AtKU70-R</i>	ctttctcatcagggtcatcgcc	
<i>AtPol λ-F</i>	acgacgtgttgaacagaaggc	At1g10520, for RT-qPCR
<i>AtPol λ-R</i>	agctgggaatagtcagtgctg	
<i>AtLIG4-F</i>	ttggcttcaagtgagaacagagc	At5g57160, for RT-qPCR
<i>AtLIG4-R</i>	tgaccacttcatctcctgagc	
<i>AtNAC053-F</i>	caacagagtttgagccag	At3g10500, for RT-qPCR
<i>AtNAC053-R</i>	ttgccgtatgaccagccca	
<i>AtNAC103-F</i>	gtcactgggaagataagaa	At5g64060, for RT-qPCR
<i>AtNAC103-R</i>	gagaacgcaaagcacataa	
<i>AtGR1-F</i>	gaaggagcagacaaagtgag	At3g24170, for RT-qPCR
<i>AtGR1-R</i>	ggtgagatggaagtgatagg	
<i>AtRAD17-F</i>	ctctggcaagtggagcaatc	At5g66130, for RT-qPCR
<i>AtRAD17-R</i>	tcctcatctgtctcttcgcc	
<i>AtCYCB1;1-F</i>	gatcaatcatcgtctctgtacacg	At4g37490, for RT-qPCR
<i>AtCYCB1;1-R</i>	caegtctactaccttgggttccc	
<i>AtSMR4-F</i>	gccgagaagcacgatgtatag	At5g02220, for RT-qPCR
<i>AtSMR4-R</i>	agatctgggtggctgaaagtacc	
<i>AtSMR5-F</i>	aaactacgacgacggagatagc	At1g07500, for RT-qPCR
<i>AtSMR5-R</i>	gctaccaccgagaagaacaagt	
<i>AtSMR7-F</i>	gccaaaacatcgattcgggcttc	At3g27630, for RT-qPCR
<i>AtSMR7-R</i>	tcgccgtgggagtgatacaaat	
<i>AtWEE1-F</i>	tattactcctcgtgggt	At1g02970, for RT-qPCR
<i>AtWEE1-R</i>	atgcctttgctatctg	
<i>AtFT-F</i>	gaacaacctttggcaatgagatt	At1g65480, for RT-qPCR
<i>AtFT-R</i>	caccctgggtgcatacactgtt	
<i>AtFLC-F</i>	atccgtcgtcttctcgtc	At5g10140, for RT-qPCR
<i>AtFLC-R</i>	cggctcttctggctctagtca	
<i>AtAP1-F</i>	ccatacaggagcaaacagc	At1g69120, for RT-qPCR
<i>AtAP1-R</i>	tcttcttgatacagaccacc	
<i>AtACTIN1-F</i>	cgatgaagctcaatccaaacga	At2g37620, for RT-qPCR
<i>AtACTIN1-R</i>	cagagtcgagcacaataaccg	