Gene	Relative expression level					
	G2 *ddm1*		G5 *ddm1*		G6 *ddm1*	
	Average	SD	Average	SD	Average	SD
CTC1	1.69	±1.02	1.87	±0.15	0.89	±0.15
STN1	1.92	±0.50	1.66	±0.09	1.38	±0.34
TEN1	1.03	±0.57	1.12	±0.51	1.03	±0.32
POT1a	1.84	±0.07	2.14	±0.03	1.63	±0.27
TER1	1.94	±0.77	1.89	±0.86	1.11	±0.20
TER2	2.32	±1.55	1.85	±0.42	0.94	±0.36
Ku70	1.53	±0.45	1.57	±0.45	1.33	±0.24

Table S1. Steady state transcript levels of telomere and telomerase-related genes in *ddm1-2* mutants. The average WT levels of specific mRNA were set to 1, and transcript levels in *ddm1-2* mutants were converted to these values. Data are presented as mean ± standard deviation (n >=3). No significant differences (p-value >0.05, *t*-test) were observed among all transcripts tested.

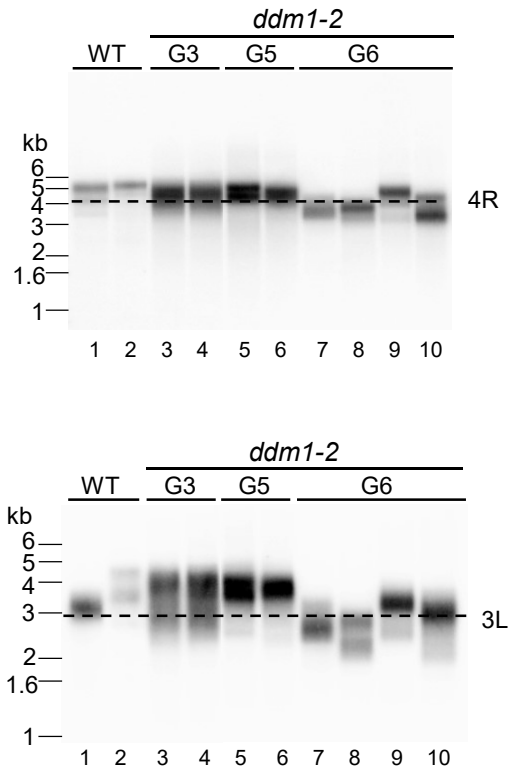

Figure S1. Telomere length analysis for individual chromosome arms in WT and *ddm1* mutant plants. Telomere length was assessed on individual chromosome arms by primer extension telomere repeat amplification (PETRA). Data are shown for two independent plants monitoring telomere length on the right arm of chromosome 4 (4R) (top) and the left arm of chromosome 3 (3L) (bottom). Dashed line indicates the minimal telomere length in WT samples.

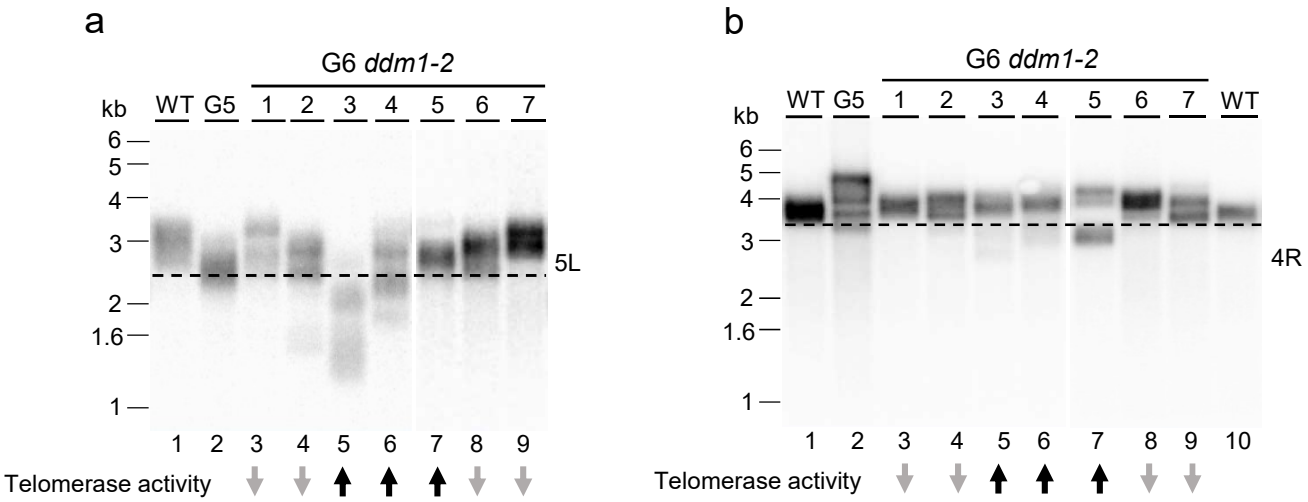

Figure S2. Comparison of telomere length and relative telomerase activity in individual *ddm1-2* mutants. Telomere length was assessed by PETRA using a subtelomeric primer for the left arm of chromosome 5 (5L) (left) or right arm of chromosome 4 (4R) (right). The relative change in telomerase activity for each mutant plant is shown below the lane. Upward black arrows indicate an increase in telomerase activity; downward grey arrows indicate a decrease in telomerase activity for these specific samples. Dashed line indicates the minimal telomere length in WT samples.

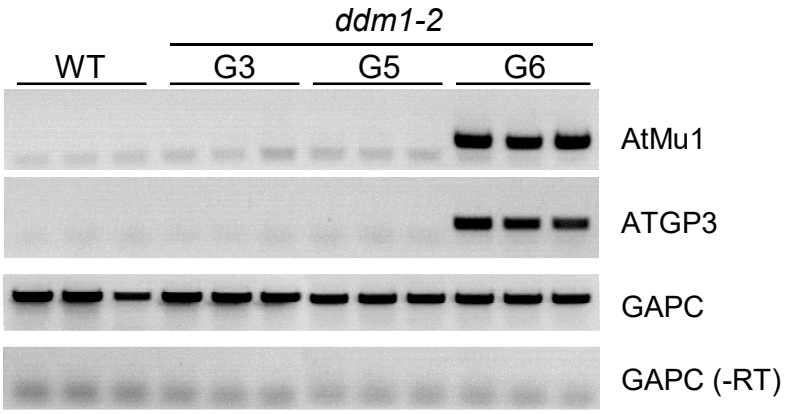

Figure S3. Increased transcription of retrotransposons in G6 *ddm1-2* mutants. Total RNA from leaves of three biological replicates was reverse transcribed and amplified by PCR. RT-PCR results for transcripts from mutator-like elements (AtMu1) and a *gypsy* family retrotransposon (ATGP3) are shown. RT-PCR analysis of GAPC transcripts serves as an input control. The GAPC (-RT) panel is a PCR control using total RNA without reserve transcription, showing no genomic DNA contamination.

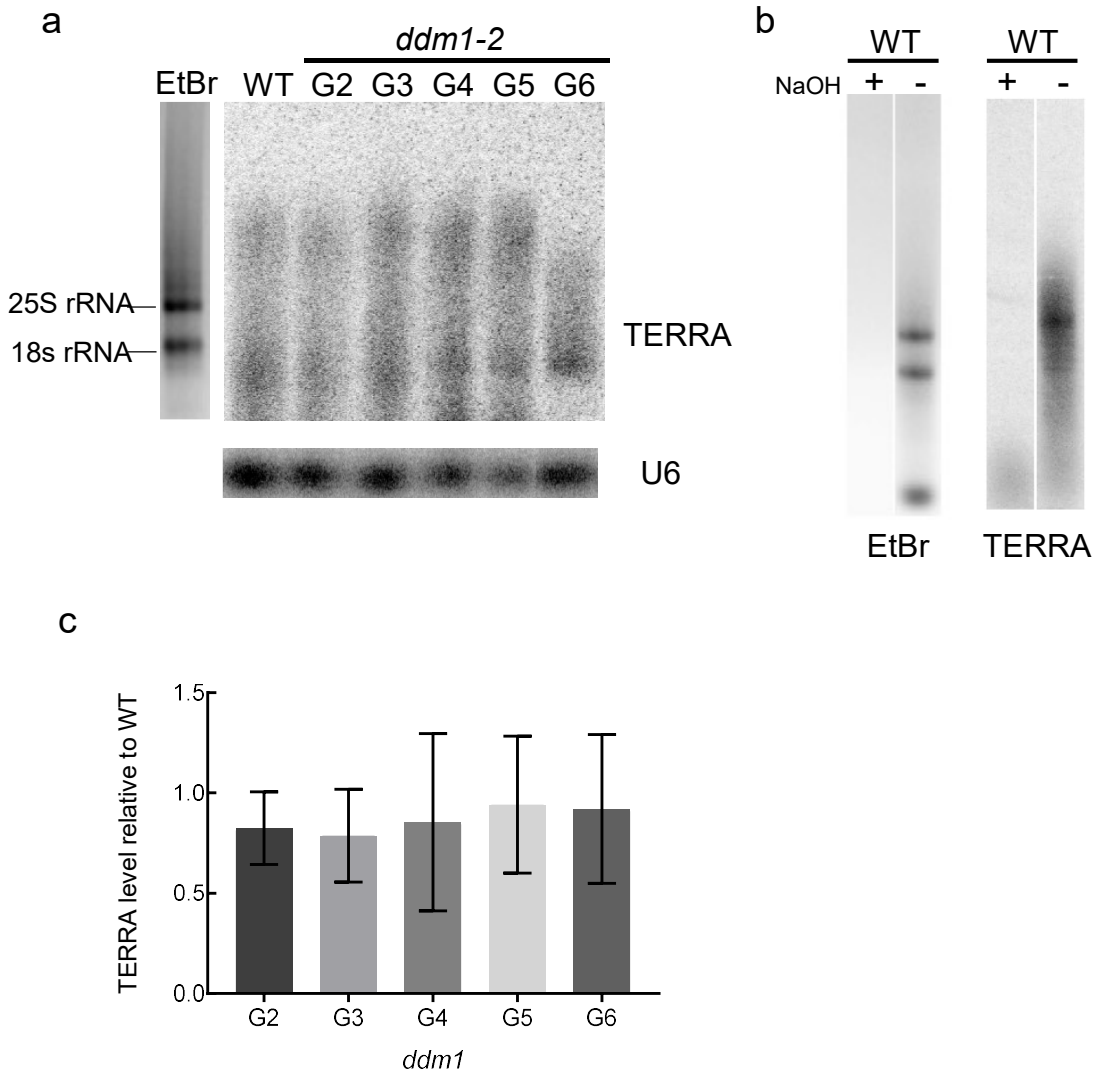

Figure S4. The abundance of the telomere transcript TERRA is unchanged in *ddm1*-2 mutants. (a) Northern blot analysis of TERRA was carried out using total RNA from 2-week-old seedlings. EtBr gel image (left) indicates the molecular weight makers of 25S (3374 nt) and 18S (1804 nt) rRNA for the blot on the right. U6 snRNA serves as a loading control (bottom right). (b) Sensitivity of TERRA signal to alkaline. Total RNA was treated with (+) or without (-) 0.1 N NaOH for 10 min at 97˚C and northern blotting was carried out with a probe for TERRA. The EtBr gel image (left) shows complete RNA hydrolysis in the presence of NaOH. The TERRA signal (right) was depleted in the alkaline treated sample, indicating the signal is derived from RNA. (c) Quantification of the TERRA signal for G2, G5 and G6 *ddm1* mutants. Signals were normalized to WT, and three biological replicates were analyzed. Error bars represent the standard deviation.

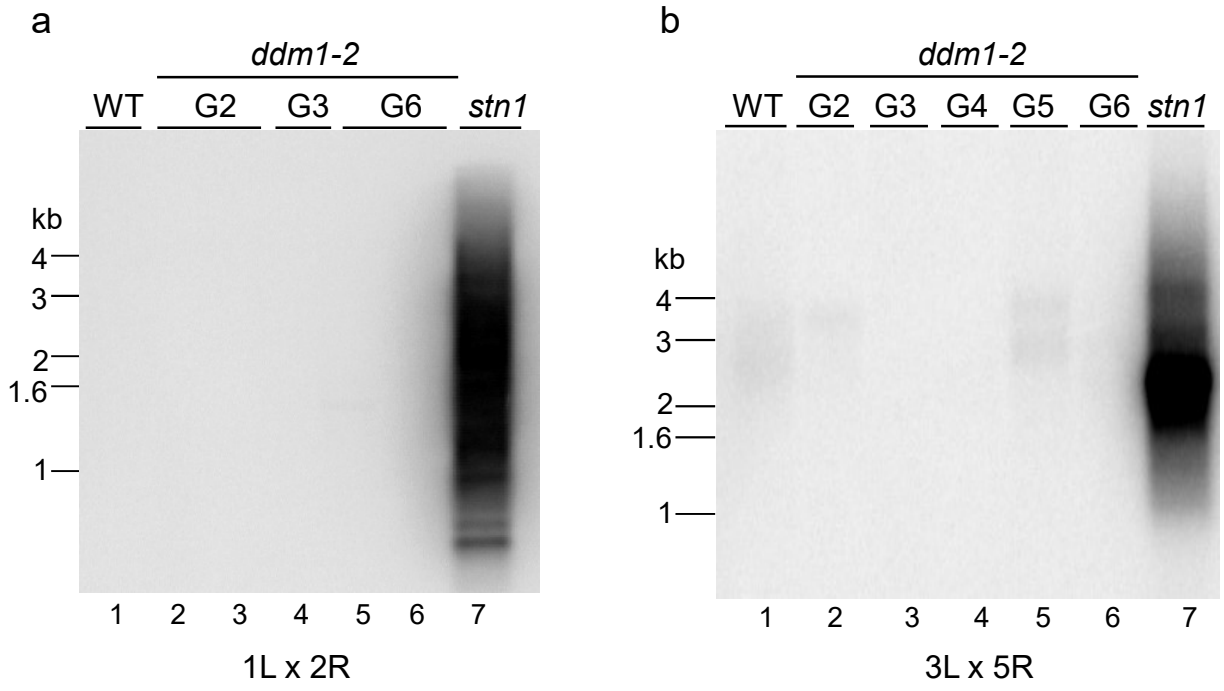

Figure S5. No evidence of end-to-end chromosome fusions in *ddm1-2* mutants. Representative data for telomere fusion PCR using subtelomeric primers 1L and 2R (a) and 3L and 5R (b) are shown. DNA from a *stn1* mutant served as a positive control. PCR products were resolved in a 0.8% agarose gel. Hybridization was conducted with a [^{32}P] 5' labeled $(T_3AG_3)_4$ oligonucleotide probe. Representative results from at least three independent experiments are shown.

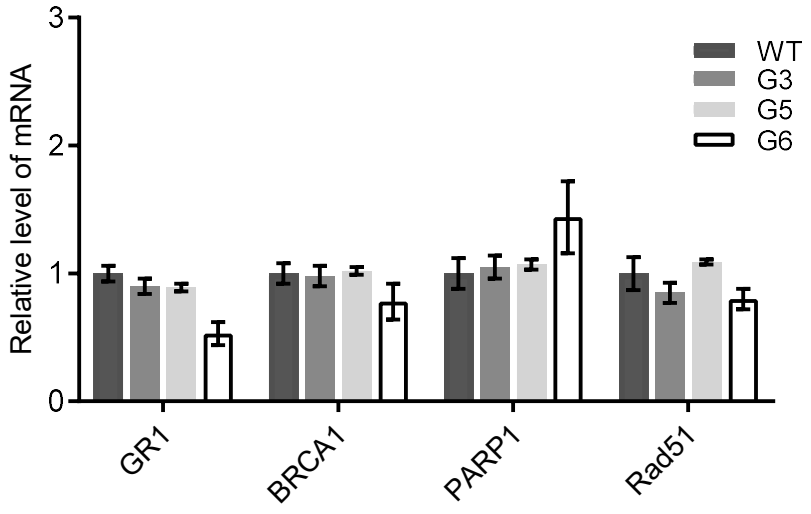

Figure S6. Steady state transcript levels of DNA damage response genes in *ddm1-2* mutants. The average WT levels of specific mRNA were set to 1, and transcript levels in *ddm1-2* mutants as measured by qPCR were plotted. Data are presented as mean ± standard deviation (n >=3).

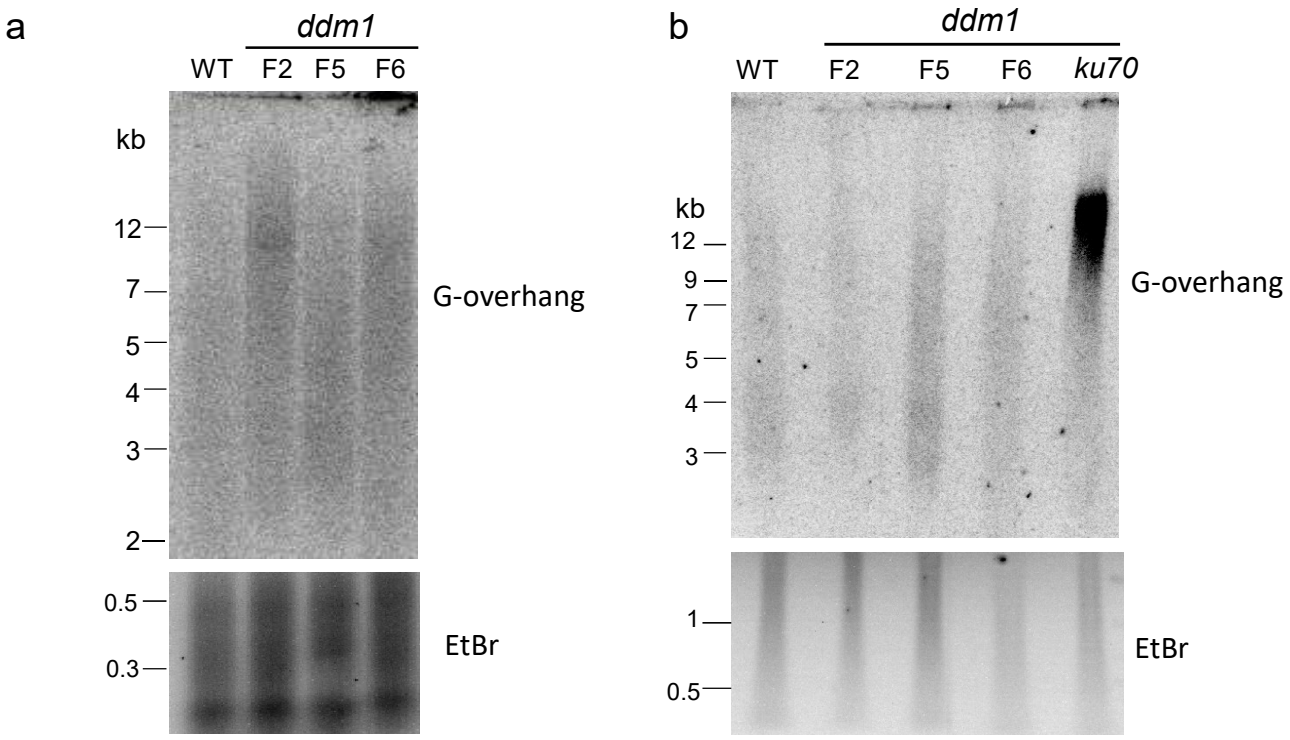

Figure S7. Increased G-overhang signal in late generation *ddm1-2* mutants and *ku70* mutant. Representative data for in-gel hybridization assays are shown. Digested genomic DNA was resolved in a 0.8% agarose gel. Top panels, in-gel hybridization was conducted with a [^{32}P] 5' end labeled $(C_3TA_3)_4$ oligonucleotide probe. Bottom panels, prior to in-gel hybridization, EtBr staining was performed to serve as a loading control.

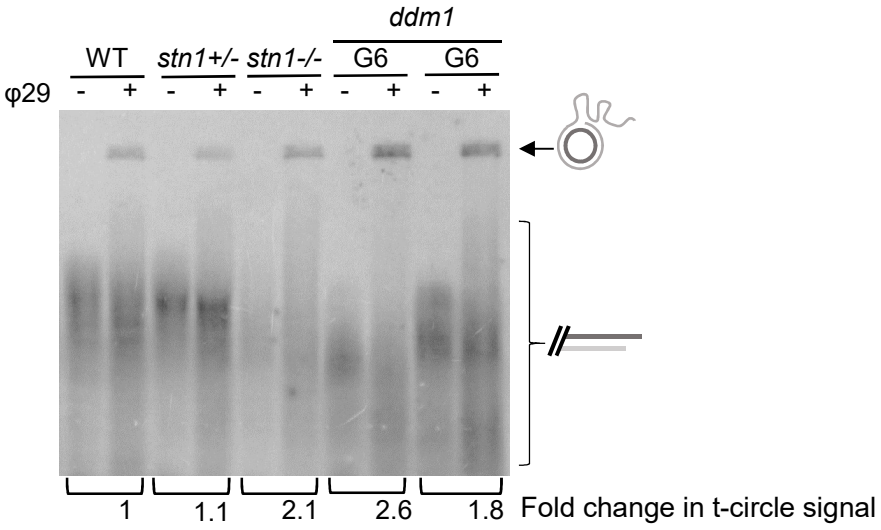

Figure S8. Increased ECTC production in *stn1* and G6 *ddm1-2* mutants. The telomeric circle amplification (TCA) was carried out with DNA from WT, *stn1* heterozygotes (+/-), *stn1* homozygotes (-/-), and G6 *ddm1-2* mutant plants. Circular and linear telomere repeats are indicated.