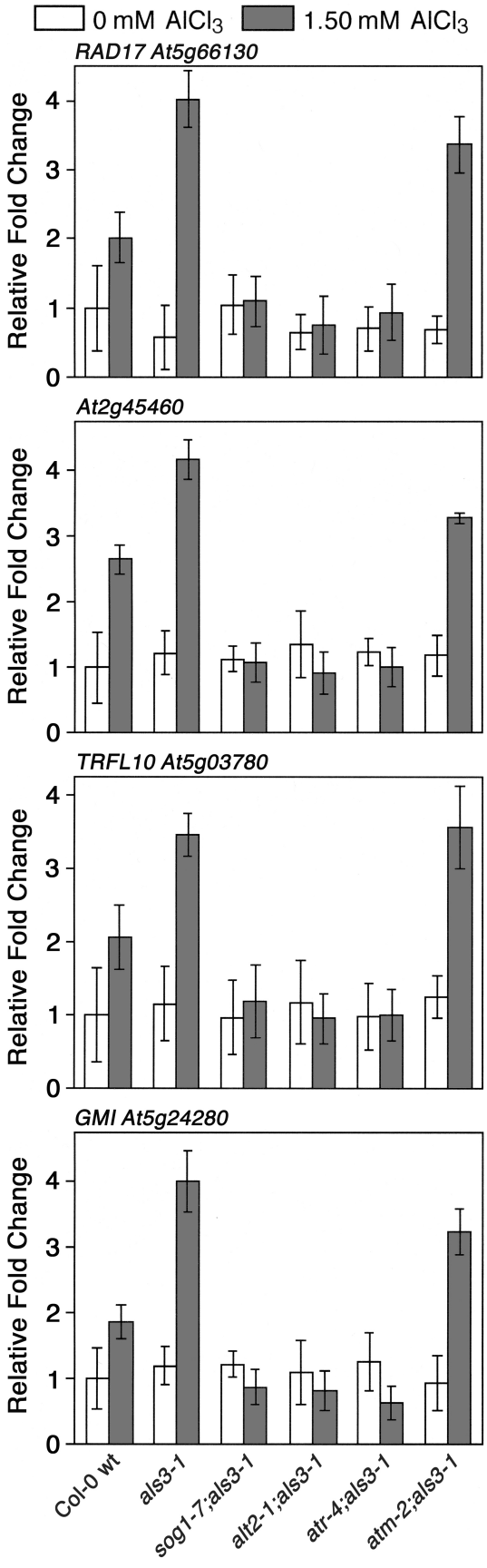
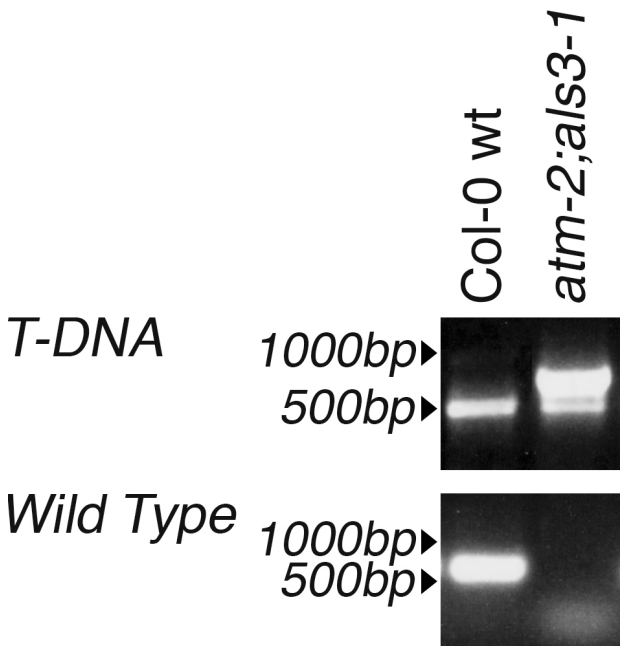


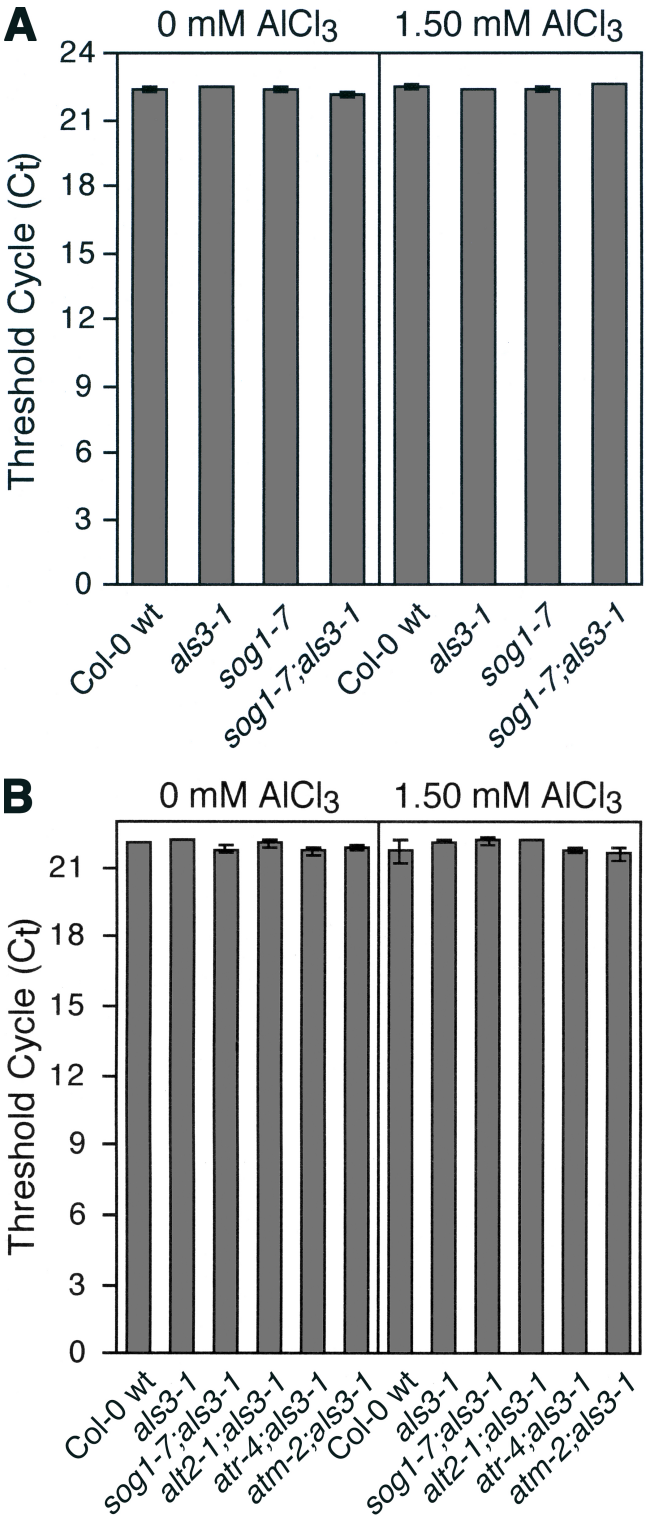
Supplemental Figure 1. Al-responsive expression of DNA damage response genes is largely independent of ATM.

Seedlings of Col-0 wt, *als3-1*, *sog1-7;als3-1*, *alt2-1;als3-1*, *atr-4;als3-1*, and *atm-2;als3-1* were grown in the absence or presence of 1.50 mM $AlCl_3$ (pH 4.2) in a soaked gel environment for 3 d after which tissue was collected for RNA isolation. Following cDNA synthesis, real-time PCR was performed to examine expression patterns for a group of previously documented SOG1-regulated genes (Yoshiyama et al., 2009). Mean ±SD values were determined from three technical replicates.



Supplemental Figure 2. *atm-2* genotype analysis for generation of an *atm-2;als3-1* double mutant.

DNA was isolated from the leaves of the F_2 progeny of *als3-1* x *atm-2* and then analyzed by PCR as follows: one repeat of 30 sec at 94°C, and then 40 repeats of 30 sec at 94°C, 30 sec at 55°C, and 30 sec at 72°C. Amplicons were subsequently analyzed by running out on a 1% agarose gel visualized with ethidium bromide under UV light. The T-DNA band amplified with *At3g48190* 3' reverse and T-DNA primers is predicted to result in an amplicon of 680 bp whereas the band resulting from amplification with the *At3g48190* 5' forward and 3' reverse primers is expected to result in a product that is 598 bp (see Supplemental Table 1 for WT and T-DNA primer sequences).



Supplemental Figure 3.
Expression analysis of reference gene, *EF1a*. **A)** Seedlings of Col-0 wt, *als3-1*, *sog1-7* and *sog1-7;als3-1* were grown for 3 d with 0 or 1.50 mM $AlCl_3$ (pH 4.2), after which tissue was harvested for RNA isolation. Following cDNA synthesis, real-time PCR was performed and Ct values were compared to check for equivalent expression across all genotypes in the presence and absence of Al. **B)** Seedlings of Col-0 wt, *als3-1*, *sog1-7;als3-1*, *alt2-1;als3-1*, *atr-4;als3-1*, and *atm-2;als3-1* were grown in the absence or presence of 1.50mM $AlCl_3$ (pH 4.2) in a soaked gel environment for 3d after which tissue was collected for RNA isolation. Following cDNA synthesis, real-time PCR was performed and Ct values were compared to check for equivalent expression across all genotypes in the presence and absence of Al. For both analyses, mean ±SD values were determined from three technical replicates.

Supplemental Table 1. Primer Sequences.

TAIR #	Gene Name	Direction	Sequence (5' to 3')	Purpose
AT5G60390	*EF-1A*	5' FORWARD	TGAGCACGCTCTTCTTGCTTTCA	RT-PCR
AT5G60390	*EF-1A*	3' REVERSE	GGTGGTGGCATCCATCTTGTTACA	RT-PCR
AT1G25580	*SOG1*	5' FORWARD	TCTCTTGGGATCACAGGACAG	RT-PCR
AT1G25580	*SOG1*	3' REVERSE	CAAGGTCTTAAGCTCGTGGTAG	RT-PCR
AT4G21070	*BRCA1*	5' FORWARD	GAGCCATATGAGATCACTATG	RT-PCR
AT4G21070	*BRCA1*	3' REVERSE	ATCCTACAAACAAGTAACAAC	RT-PCR
AT2G18600		5' FORWARD	ATCTAGAAGGAAACGTCTGTC	RT-PCR
AT2G18600		3' REVERSE	TCTCAATGTACAAGAGTAGAC	RT-PCR
AT5G24280	*GMI1*	5' FORWARD	TTGGTGTGCAAATCATCACAG	RT-PCR
AT5G24280	*GMI1*	3' REVERSE	CACCAACCTGCGCAACGAACG	RT-PCR
AT5G20850	*RAD51*	5' FORWARD	CTACCGCTCTCTACAGAACAG	RT-PCR
AT5G20850	*RAD51*	3' REVERSE	GCAGAGAGAAGCAAGGCATTG	RT-PCR
AT5G03780	*TRFL10*	5' FORWARD	CAGGTAACTTCATCGGTTCAAG	RT-PCR
AT5G03780	*TRFL10*	3' REVERSE	GTTCACCAAGTCTGGCTTCATC	RT-PCR
AT2G45460		5' FORWARD	GATAAAACATGGTACTCGTTC	RT-PCR
AT2G45460		3' REVERSE	GTGTGCGAATACAAAACAAAG	RT-PCR
AT2G30250	*WRKY25*	5' FORWARD	GTATGGTGAGATAGATGAAGAG	RT-PCR
AT2G30250	*WRKY25*	3' REVERSE	CATATTACTAGTGACTAAGTC	RT-PCR
AT1G17460	*TRFL3*	5'	CTTGGACTATCTCTGAAGTTG	RT-PCR

		FORWARD		
AT1G17460	*TRFL3*	3' REVERSE	ACAGAGAAGTTAACCTCACAG	RT-PCR
AT5G66130	*RAD17*	5' FORWARD	AGAGGATGTTCCACAGTCAG	RT-PCR
AT5G66130	*RAD17*	3' REVERSE	GTTGTTAACTATCATACCAG	RT-PCR
AT5G64060	*ANAC103*	5' FORWARD	CTCAAGTATCTCTCGATGGTG	RT-PCR
AT5G64060	*ANAC103*	3' REVERSE	CCAAAGCAAGAAAGAGCATAAG	RT-PCR
AT5G48720	*XRI1*	5' FORWARD	GAATGTGCCACCAGAAACAGAG	RT-PCR
AT5G48720	*XRI1*	3' REVERSE	CTATCAGCTTATTACTACTTAC	RT-PCR
AT5G60250		5' FORWARD	GAATGATCGTAATCCTGAAGAG	RT-PCR
AT5G60250		3' REVERSE	CAGTCTTATATAGAACAATAC	RT-PCR
AT3G07800	*TK1A*	5' FORWARD	CCAATAGCTGATTCTGTGAC	RT-PCR
AT3G07800	*TK1A*	3' REVERSE	GACCAGAGGCTGTAGAGAAAG	RT-PCR
AT4G02390	*PARP2*	5' FORWARD	GTTCCACTTGGCAAACCAGTG	RT-PCR
AT4G02390	*PARP2*	3' REVERSE	GAAGGAGTTTGAAAGAAATAC	RT-PCR
AT4G37490	*CYCB1;1*	5' FORWARD	CAGCACTCTCAAGCATCACAC	RT-PCR
AT4G37490	*CYCB1;1*	3' REVERSE	CTAGGCTTGGTTCTTCAGCTTC	RT-PCR
AT5G40840	*SYN2*	5' FORWARD	TCAAGATTCTGCTGCTTTGAC	RT-PCR
AT5G40840	*SYN2*	3' REVERSE	ACTACTTCCTCGTCTAGCTTC	RT-PCR
AT5G60390		5' FORWARD	TGAGCACGCTCTTCTTGCTTTCA	RT-PCR
AT5G60390		3' REVERSE	GGTGGTGGCATCCATCTTGTTACA	RT-PCR
AT1G25580	*sog1-7*	5' FORWARD	CAGAGACTTCCTGTTCAG	CAPS Genotyping
AT1G25580	*sog1-7*	3' REVERSE	CAATCAAAGCTTATAGCACAG	CAPS Genotyping

AT5G40820	*atr-4*	5' FORWARD	CCTTCCTTCTCTTTCTCTAAGAAG	CAPS Genotyping
AT5G40820	*atr-4*	3' REVERSE	TTCTTCGGTTCAGTTGTATCTG	CAPS Genotyping
AT2G37330	*als3-1*	5' FORWARD	CTCTCGTTATCGGATTTGTTC	CAPS Genotyping
AT2G37330	*als3-1*	3' REVERSE	GACAGAGAGATCACTAGTGC	CAPS Genotyping
TDNA	SALK LB	Left Border	TGGTTCACGTAGTGGGCCATCG	T-DNA Genotyping
AT3G48190	*atm-2*	5' FORWARD	TGCATTGGTTTCGCTTATCA	WT Genotyping
AT3G48190	*atm-2*	3' REVERSE	CAAGCTTGATGTAGATATCTAC	WT Genotyping
AT1G25580	*SOG1*	5' FORWARD	GGAAGGATTTCAATGGCTGGGCGATCATGGCTG	WT MBP fusion
AT1G25580	*SOG1*	3' REVERSE	ATCTAGATCAGTCTTTCCAGTCCC	WT MBP fusion
AT1G25580	*SOG1*	5' FORWARD	GTGCGCTGGCATAAGACAAGAAGAACGAAACCGGTTG	*sog1-1* MBP fusion
AT1G25580	*SOG1*	3' REVERSE	CAACCGGTTTCGTTCTTCTTGTCTTATGCCAGCGCAC	*sog1-1* MBP fusion
AT1G25580	*SOG1*	5' FORWARD	AAGGAAGGTGATTATGTTGTTTTTAAGATTTTCTACCAGCAGCCA	*sog1-7* MBP fusion
AT1G25580	*SOG1*	3' REVERSE	TGGCTGCTGGTAGAAAATCTTAAAAACAACATAATCACCTTCCTT	*sog1-7* MBP fusion
AT4G21070	*BRCA1*	5' FORWARD	AAAGATTGGTGCTTTGACATTG	*BRCA1* promoter
AT4G21070	*BRCA1*	3' REVERSE	TTTCGATCTTCACTCAGAGAAAAC	*BRCA1* promoter
AT5G40820	*ATR*	5' FORWARD	GCGGCCGCATGGCGAAGGACGACAATAATC	ATR GST fusion
AT5G40820	*ATR*	3' REVERSE	GCGGCCGCTCAGAACCAGGGCATCCACCAG	ATR GST fusion

Supplemental Table 2. Mutant genotyping methods and sources.

Mutation Name	Method for Genotyping	Source
als3-1	CAPS PCR followed by ClaI restriction enzyme digest	Larsen et al. 2005
sog1-7	CAPS PCR followed by DdeI restriction enzyme digest	This paper
atr-4	CAPS PCR followed by BstXI restriction enzyme digest	Rounds et al. 2008
alt2-1	Sanger sequence confirmation	Nezames et al. 2012
atm-2	TDNA and WT PCR	ARBC seed stock/ this paper
brca1-1	Refer to source	Dr. Holger Puchta
brca1-3	Refer to source	Dr. Holger Puchta
parp1 *parp2*	Refer to source	Dr. Sylvia de Pater/Jia et al. 2013
parp1 *parp2* *KU80*	Refer to source	Dr. Sylvia de Pater/Jia et al. 2013

Supplemental Table 2. Amplication efficiencies of RT PCR primers.

Gene Name	TAIR #	PCR Efficiency (E)	% Efficiency	Standard Curve R^2
	AT2G18600	2.030607799	103.0607799	0.99786
	AT2G45460	2.031139033	103.1139033	0.99811
	AT5G60250	1.992759976	99.27599759	0.98949
ANAC103	*AT5G64060*	2.043687098	104.3687098	0.9944
BRCA1	*AT4G21070*	2.017022902	101.7022902	0.99171
CYCB1;1	*AT4G37490*	2.028091671	102.8091671	0.99937
EF-1A	*AT5G60390*	2.019313383	101.9313383	0.99802
GMI1	*AT5G24280*	2.006901663	100.6901663	0.9969
PARP2	*AT4G02390*	1.977080681	97.70806809	0.99721
RAD17	*AT5G66130*	1.995358804	99.53588035	0.999
RAD51	*AT5G20850*	2.016376466	101.6376466	0.99757
SOG1	*AT1G25580*	2.000721667	100.0721667	0.99479
SYN2	*AT5G40840*	2.013113414	101.3113414	0.99618
TK1A	*AT3G07800*	1.967949173	96.79491726	0.99398
TRFL10	*AT5G03780*	1.99214315	99.21431497	0.99875
TRFL3	*AT1G17460*	2.016075069	101.6075069	0.99957
WRKY25	*AT2G30250*	1.995152065	99.51520646	0.99486
XRI1	*AT5G48720*	1.987031752	98.70317522	0.99806