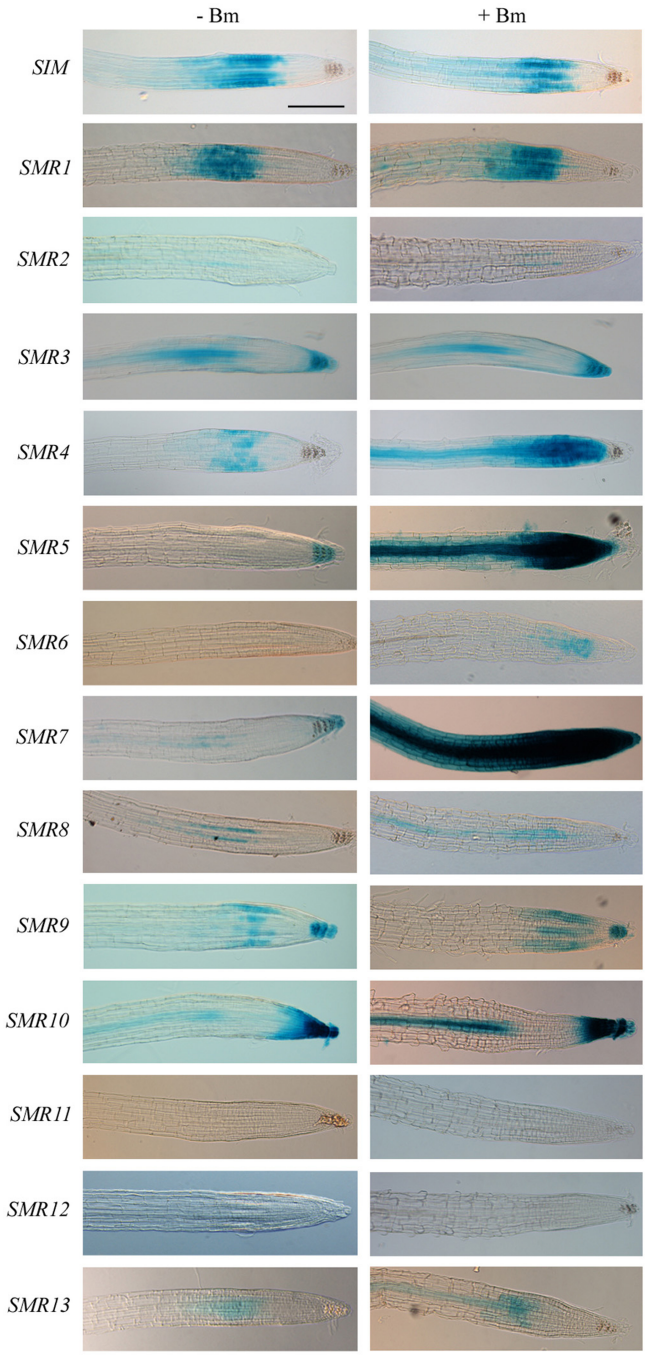
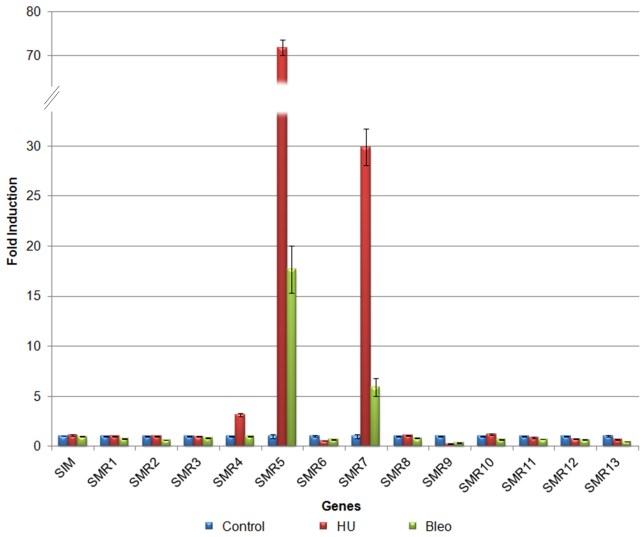
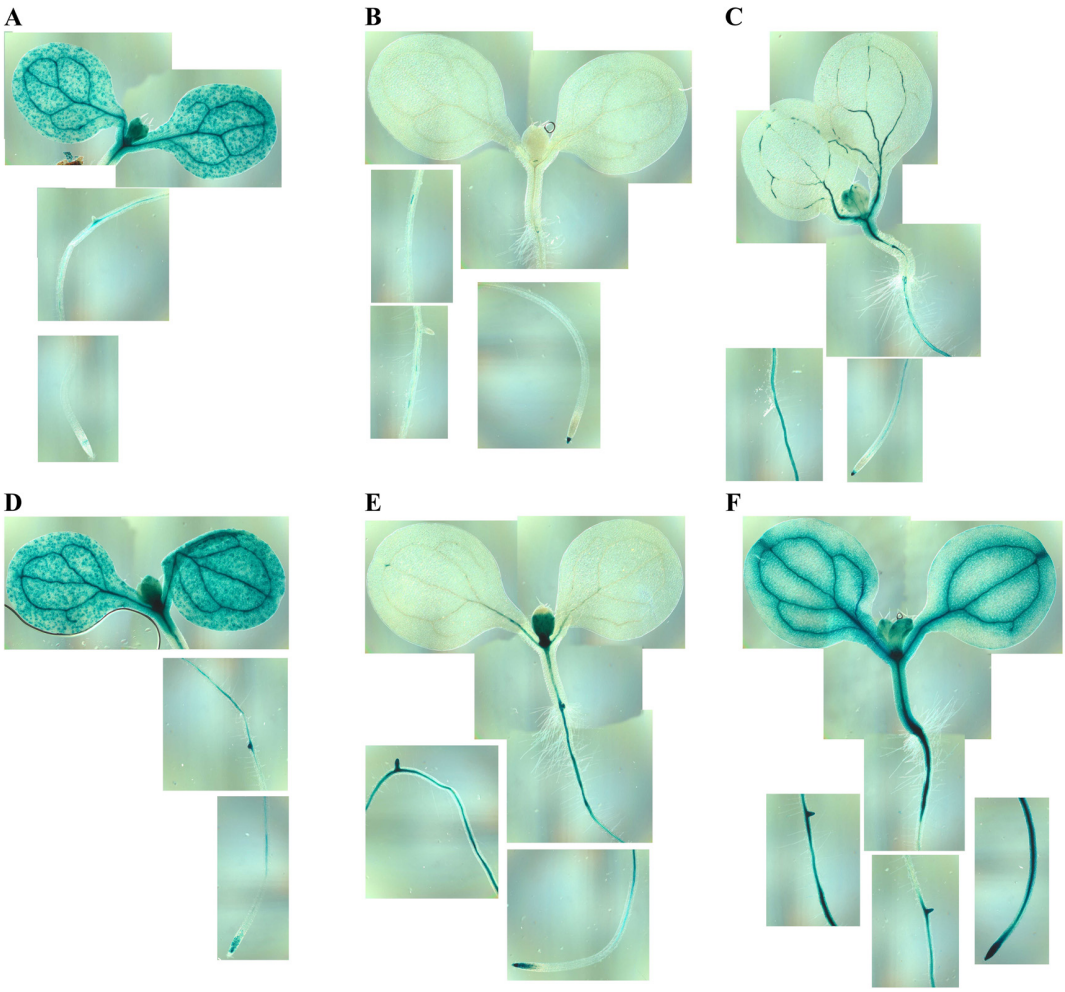


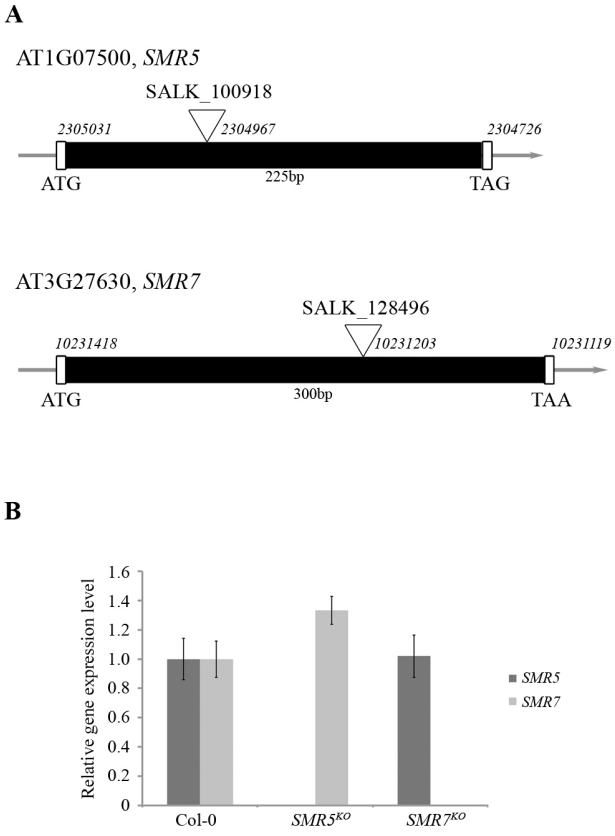
Supplemental Figure 1. *SIM/SMR* induction in response to bleomycin. One-week-old *SMR* reporter seedlings (names indicated on the left) were transferred to control (-Bm) medium or medium supplemented with 0.3 μg/mL bleomycin (+Bm). GUS assays were performed 24 h after transfer. Scale bar = 200 μm. All pictures at same magnification.



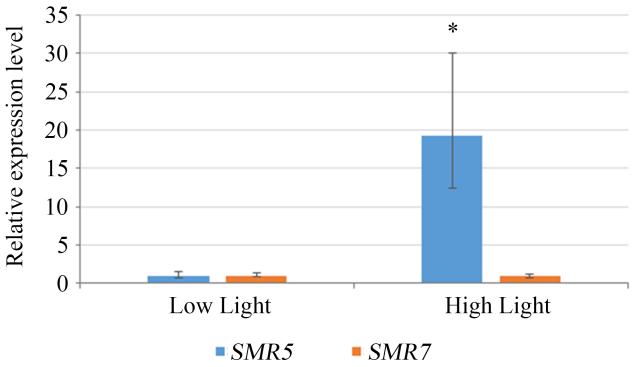
Supplemental Figure 2. Transcriptional induction of *SIM/SMR* genes upon HU and bleomycin treatment. One-week-old wild-type Arabidopsis seedlings were transferred to control medium (blue), or medium supplemented with 1 mM HU (red) or 0.3 µg/mL bleomycin (green). Root tips were harvested after 24 h for qRT-PCR analysis. Expression levels in the control condition were arbitrarily set to one. Data represent mean ± SE (n = 3).



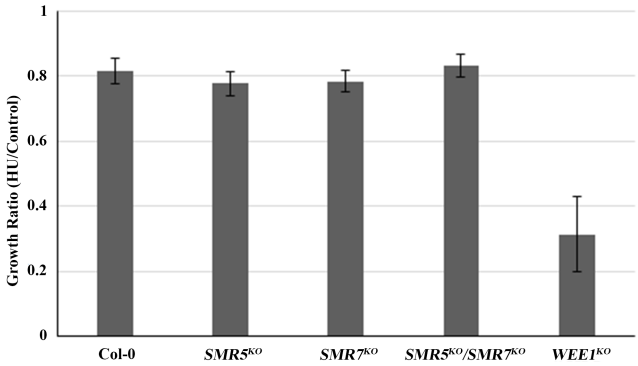
Supplemental Figure 3. Transcriptional induction of *SIM/SMR* genes upon γ-irradiation. **(A-F)** *PSMR4:GUS* (A and D), *PSMR5:GUS* (B and E) and *PSMR7:GUS* (C and D) either control-treated (A-C) or irradiated with 20 Gy of γ-rays (D-F). GUS assays were performed 1.5 h after irradiation.



Supplemental Figure 4. Graphical representation of the *SMR5* and *SMR7* T-DNA insertion lines. **(A)**, Intron-exon organization of the *Arabidopsis SMR5* and *SMR7* genes. Black and white boxes represent coding and non-coding regions, respectively. The white triangles indicate the T-DNA insertion sites. **(B)**, qRT-PCR analysis of wild-type, $SMR5^{KO}$, and $SMR7^{KO}$ seedlings using primers specific to either *SMR5* (dark grey) or *SMR7* (light grey). Expression levels in the wild type were arbitrarily set to one. Data represent mean ± SE (n = 3).



Supplemental Figure 5. *SMR5* and *SMR7* expression levels in response to high light treatment. One-week old wild type Col-0 plants were either control treated or exposed for 48 h to high light. Complete seedlings were harvested for RT-PCR analysis. Data represent mean ± SE (n = 3), *, P-value < 0.01 (two-tailed Student's *t*-test).



Supplemental Figure 6. Relative root growth of *SMR5*^{KO}, *SMR7*^{KO}, and *SMR5*^{KO} *SMR7*^{KO} plants upon HU treatment. Five-day-old seedlings were transferred to control medium or medium supplemented with 1 mM HU. Data plot the root growth ratio on HU versus control plates over 4 days after transfer. HU-hypersensitive *WEE1*^{KO} plants were included as q positive control. Data represent mean ± SE (n > 15).

Table S1: Annotated Arabidopsis *SIM/SMR* genes

AGI locus	Annotation
At5g04470	SIM
At3g10525	SMR1
At1g08180	SMR2
At5g02420	SMR3
At5g02220	SMR4
At1g07500	SMR5
At5g40460	SMR6
At3g27630	SMR7
At1g10690	SMR8
At1g51355	SMR9
At2g28870	SMR10
At2g28330	SMR11
At2g37610	SMR12
At5g59360	SMR13

Table S2: DNA ploidy level distribution in transgenic plants overexpressing *SMR4, SMR5, or SMR7*

Ploidy (%)	Col-0	*SMR4* ^{OE}	*SMR5* ^{OE}	*SMR7* ^{OE}
2C	19.6 ± 0.2	17.1 ± 0.1	23.6 ± 0.9	24.2 ± 1.3
4C	26.3 ± 1.2	19.4 ± 0.5	21.3 ± 0.8	29.2 ± 0.7
8C	49.2 ± 0.5	34.9 ± 3.4	34.8 ± 0.5	36.1 ± 0.2
16C	4.6 ± 0.7	27.1 ± 3.1	19.6 ± 0.2	9.5 ± 0.9
32C	0.2 ± 0	1.5 ± 0.6	0.7 ± 0.1	1.1 ± 0.1

Table S3: List of primers used for cloning, genotyping, and RT-PCR

Promoter cloning primers

SIAMESE	Fw	ATAGAAAAGTTGGTATTGTAATTATATATGAAAAAATAGTAAT
	Rev	GTACAAACTTGTTCTTTTTTGTTTATATAAATATTAAATGT
SMR1	Fw	ATAGAAAAGTTGTCACAAGTGCATTTTTAATTTGTAGGA
	Rev	GTACAAACTTGCATCTAAACTTGTGTATGTTTTTGTTTTTTGG
SMR2	Fw	ATAGAAAAGTTGGTAACTCCTTCGGCATCTTTGT
	Rev	GTACAAACTTGTGGTCACATGGATGTGAAAGTTT
SMR3	Fw	ATAGAAAAGTTGGTATTTTAAATTACGATTTCAAAATCTTGA
	Rev	GTACAAACTTGTTAGACAAGTTTTACAGAGAGAAAGAAGAG
SMR4	Fw	ATAGAAAAGTTGGTGAAACACAAAGCATCTTCG
	Rev	GTACAAACTTGTTCTTCTCTCTCGAACTCG
SMR5	Fw	ATAGAAAAGTTGGTCAGAACGAACAAAAG
	Rev	GTACAAACTTGTTTTTGTCCGCTCTCTCG
SMR6	Fw	ATAGAAAAGTTGGTCAGTGTGTCAAAACCGACG
	Rev	GTACAAACTTGTCTCTCTTTAACTAACTCAAAACCAAGA
SMR7	Fw	AGAAAAGTTGCGTTGACGCGGGAAAATTAA
	Rev	GTACAAACTTGCTTAAAACAGTTGGAGATTGAG
SMR8	Fw	ATAGAAAAGTTGGTAGATCCCACATTACTTAAGAAATTGG
	Rev	GTACAAACTTGTGACTTCTCTCGAATGTGAATGAAGA
SMR9	Fw	ATAGAAAAGTTGGTACATATAAAGGTGTTATACACACCCTT
	Rev	GTACAAACTTGTTTTTGAGACCAGAATAAGAGAGAAG
SMR10	Fw	ATAGAAAAGTTGGTTTTAAAAAACCGTTTCAAACTAGTGC
	Rev	GTACAAACTTGTCTTTGAGAAGAAACGTCGCTC
SMR11	Fw	ATAGAAAAGTTGGTTGTGGTAATCTACATGGAATTTGC
	Rev	GTACAAACTTGTTTGGATTCACGAGATCTAAGCA
SMR12	Fw	ATAGAAAAGTTGGTTCGGCTCACCTTGTTTTCC
	Rev	GTACAAACTTGTGTGCGCTTTTTTTTCTTCTCAG
SMR13	Fw	ATAGAAAAGTTGGTAAAACTCAAGACACTTCTTTTTTTGG
	Rev	GTACAAACTTGTCTTATCACAAACAGGAAAAGAGAGAGT

ORF cloning primers

SMR4	Fw	AAAAAGCAGGCTTCATGGAGGTGG TGGAGAGGAA G
	Rev + stop code	AGAAAGCTGGGTCCTAAGCGCAAGCTTCTCTTC
	Rev - stop code	AGAAAGCTGGGTCAGCGCAAGCTTCTCTTC
SMR5	Fw	AAAAAGCAGGCTTCATGGAGGAGAAAAACTACGACG
	Rev + stop code	AGAAAGCTGGGTCCTAGGTTGCCGCTTGGG
	Rev - stop code	AGAAAGCTGGGTCGGTTGCCGCTTGGGA
SMR7	Fw	AAAAAGCAGGCTTCATGGGAATTTCGAAAAAATCTC
	Rev + stop code	AGAAAGCTGGGTCTTAACGGCGTTGTATAAACACC
	Rev - stop code	AGAAAGCTGGGTCACGGCGTTGTATAAACACCA

T-DNA genotyping primers

SMR5	SALK_100918	LB	GAACGAACAAAAGTGAGCTCG
		RB	TTTCCCAACCTGACAGAAAAC
SMR7	SALK_128496	LB	AAAATCGATAACTAAAACGAACCG
			RB

RT-PCR primers

SIAMESE	Fw	CACAAGATTCCTCCCACCACAG
	Rev	CAGAGGAGAAGAACCGCTCGAT
SMR1	Fw	CACCCACATCCCAAGAACACAAG
	Rev	GACGGAGGAGAAGAAACGGTCAA
SMR2	Fw	AGAGCAGAAACCCAGAAGCCAAG
	Rev	GAAATCTCACGCGGTCGCTTTCTT
SMR3	Fw	CGATCACAAGATTCCGGAGGTG
	Rev	CGGCTCAGATCAATCGGTATGC
SMR4	Fw	GCCGAGAAGCACGATGTATAG
	Rev	AGATCTGGTGGCTGAAAGTACC
SMR5	Fw	AAACTACGACGACGGAGATACG
	Rev	GCTACCACCGAGAAGAACAAGT
SMR6	Fw	GGGCTTCGTTGAAACCAGTCAAG
	Rev	TTTCTCGGTGCTGGTGGACATTC
SMR7	Fw	GCCAAAACATCGATTCGGGCTTC
	Rev	TCGCCGTGGGAGTGATACAAAT
SMR8	Fw	TAACCTATCTCCCGGCGTCACA
	Rev	GCACTTCAACGACGGTTTACGC
SMR9	Fw	GCCACTTCAAGAACCCATCTCC
	Rev	TCCGGAGTACAACATCCACTCTCT
SMR10	Fw	GCAAAGAAGGAGCAACCGTCAAG
	Rev	CGGTGGACAAATTCTTGGCATCG
SMR11	Fw	CTGCTTCGATCTCGGATTGTGTT
	Rev	GACGAAGGAGGCGGTGTTTTAC
SMR12	Fw	GGTATGTCGGAGACGAGCTTGA
	Rev	GAGTCGGTGTCTTGAACCCATCA
SMR13	Fw	GAACCACCAACACCGACAACAAG
	Rev	GTTCGAGTTTCTCGGCGTCTCT
Actin2	Fw	GGCTCCTCTTAACCCAAAGGC
	Rev	CACACCATCACCAGAATCCAGC
EMB2386	Fw	CTCTCGTTCCAGAGCTCGCAAAA
	Rev	AAGAACACGCATCCTACGCATCC
PAC1	Fw	TCTCTTTGCAGGATGGGACAAGC
	Rev	AGACTGAGCCGCCTGATTGTTTG
RPS26C	Fw	GACTTTCAAGCGCAGGAATGGTG
	Rev	CCTTGTCCTTGGGGCAACACTTT

Primers used for ChIP experiments

SMR5-ChIP-F1	GGAACAAAGTCATGAGAATTAACGC
SMR5-ChIP-R1	TTCCTGCTAAAGGACGTGGTG
SMR5-ChIP-F2	GTTGTCAACAATCCTACAATTGTGTG
SMR5-ChIP-R2	GATGTCGAATCCATTTGGTACTATG
SMR5-ChIP-F3	ATCACAACGAAACGAACCTTAGAAC
SMR5-ChIP-R3	TGGGTTTCTATATATTATGCGAGCTC
SMR5-ChIP-F4	ACGTGGCAGTACGTTCCTCC
SMR5-ChIP-R4	GTCCGCTCTCTCGCACTTTC
SMR7-ChIP-F1	ATCACCAGAAGCAGTCAGAAGAC
SMR7-ChIP-R1	ACATTTCTTGGATCAAGGTGTG
SMR7-ChIP-F2	TAAACCTAAATCACAAACGACCA
SMR7-ChIP-R2	GTTCTGTTGATTACTCAATGTAGCTAG
SMR7-ChIP-F3	GGTGTGGTCTCTCATTTGACGC
SMR7-ChIP-R3	GGCCATCATATATGGGCCTTAC
SMR7-ChIP-F4	TAGTCTCAAAACCATGGCGC
SMR7-ChIP-R4	GAAGCTTTCAGAGGAAGATTATTAGG