SUPPLEMENTARY DATA

TABLE S1. Gene-specific oligo-DNA primers used in the RT-PCR analysis. Accession numbers are for Phytozome v. 10, *Glycine max* (http://www.phytozome.net/soybean)

Gene name	Nucleotide sequences
GmACS2e	F: CAAGGCATAGCCACTTCACAAAAGG
(Glyma18g47280)	R: TCCACATATACAGGACAACAGTTCAA
GmACS6a	F: GTCATTGTGCACGCAAAATGTCAAGC
(Glyma05g37410)	R: GCGAGCTCAATTGTGGCTTTAACCAGAGGTGACTG
GmACS9b	F: CGACGTCAGAGAAACCTCGTTTCAG
(Glyma01g40400)	R: TAACTTGTAACTCCACCAAAAATATTCGG
GmERF	F: CTCGGATCCATGGATTCACCTTCCTCCTTCTTCAAC
(Glyma08g15480)	R: TTCCCCGGGCTAATTTCCTTCTCAAGGAGTGTTTC
Actin	F: GCGTGATCTCACTGATGCCCTCAT
(Glyma19g32990)	R: AGCCTTCGCAATCCACATCTGTTG

Accession numbers are for Phytozome v. 10, *Glycine max* (http://www.phytozome.net/soybean).

FIG. S1. Morphology of the embryonic axis (root tip + elongation zone) of seeds treated with (A) distilled water (control); (B) 25 mM *N*-acetylcysteine (NAC); (C) 25 mM NAC + 300 ppm ethephon; or (D) 25 mM NAC + 100 mM H_2O_2 for 24 h. Sections of the embryonic axis were stained with 0.1% toluidine blue. Scale bars = 100 μm.

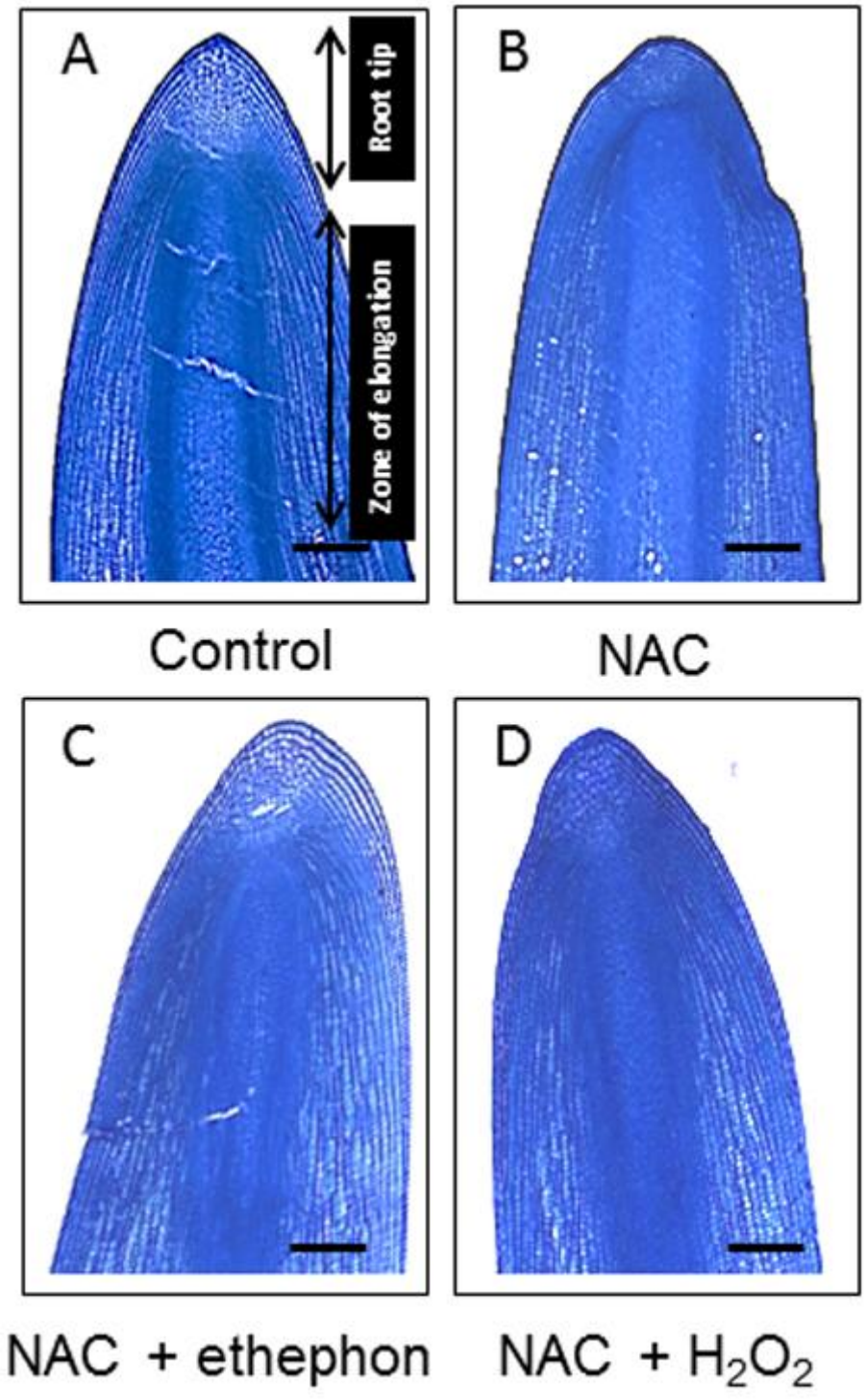

FIG. S2. Hydrogen peroxide (H_2O_2) promotes expression of genes for ethylene biosynthesis in embryonic axis during soybean seed germination. Soybean seeds were treated with distilled water (control), H_2O_2 (100 mM), *N*-acetylcysteine (NAC; 25 mM) and 25 mM NAC + 100 mM H_2O_2 for 24 h.

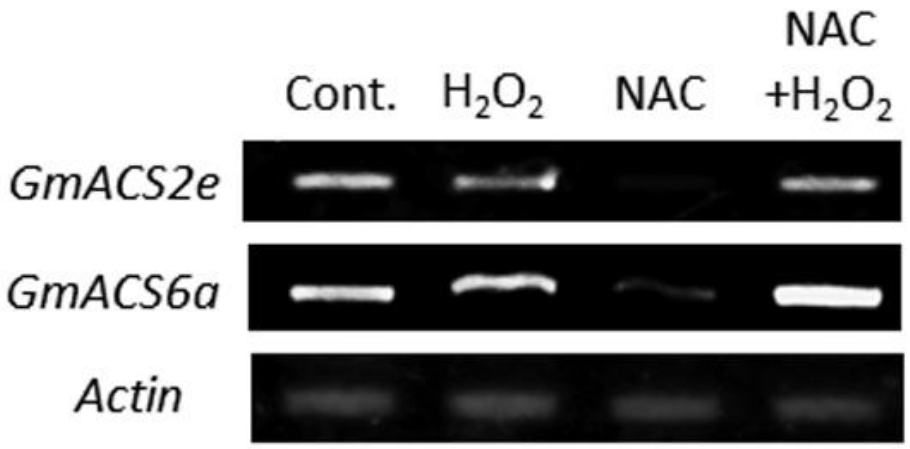

FIG. S3. Number and area of cells in the zone of elongation in the root of seeds treated with distilled water (control) or *N*-acetylcysteine (NAC). (A) The number of cells and (B) the cell area in the elongation zone were traced and then measured using ImageJ software. Values are means ± s.d. (n = 5).