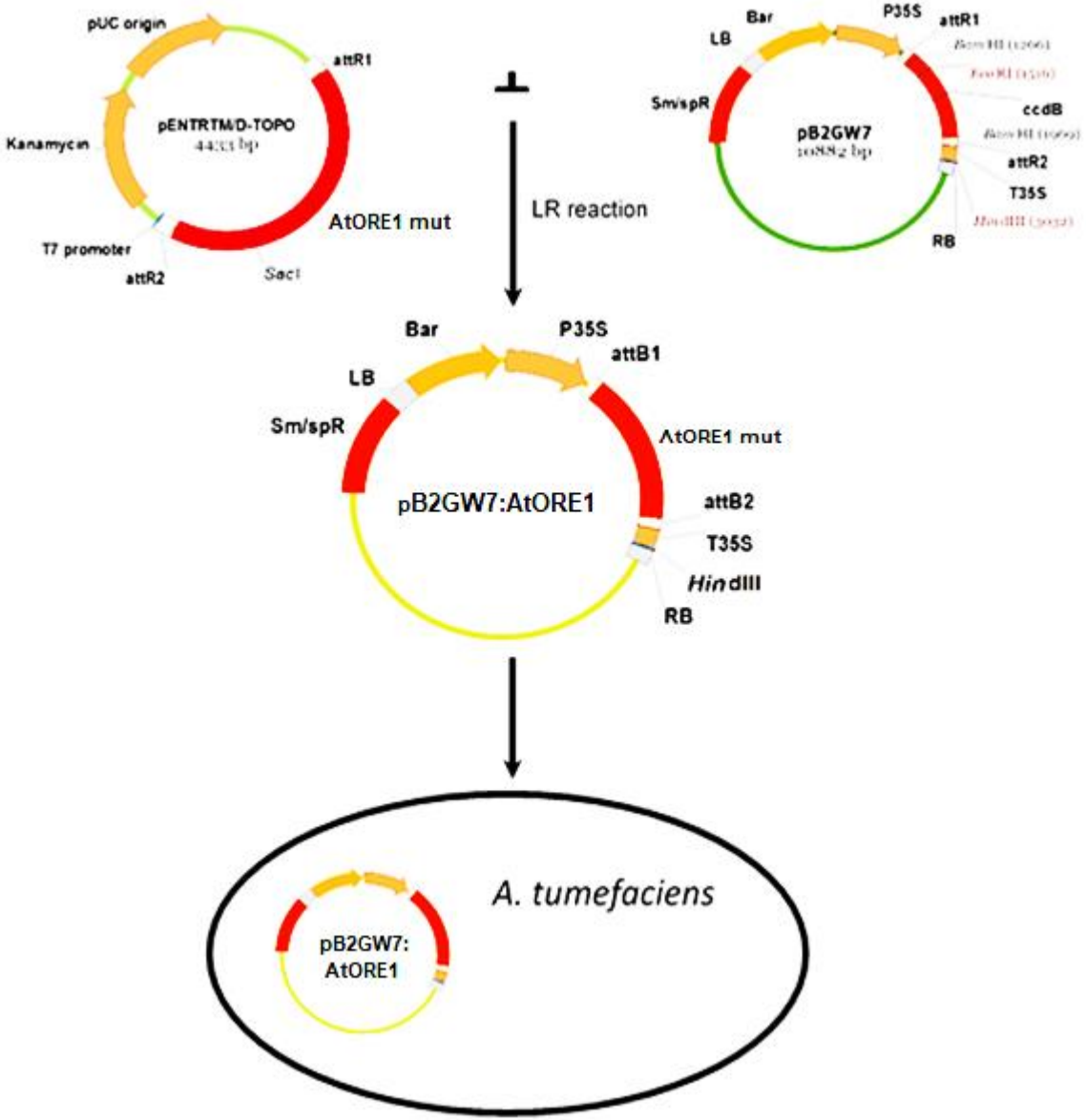

Figure S1. Construction of pB2GW7-Atore1 vector. The *Atore1* gene was transferred from the cloning vector pENTRTM/D-TOPO- Atore1 to the pB2GW7 vector by LR reaction. Plasmid harboring pB2GW7-Atore1 was transferred into *A. tumefaciens* EHA105 by electrical impulse method.

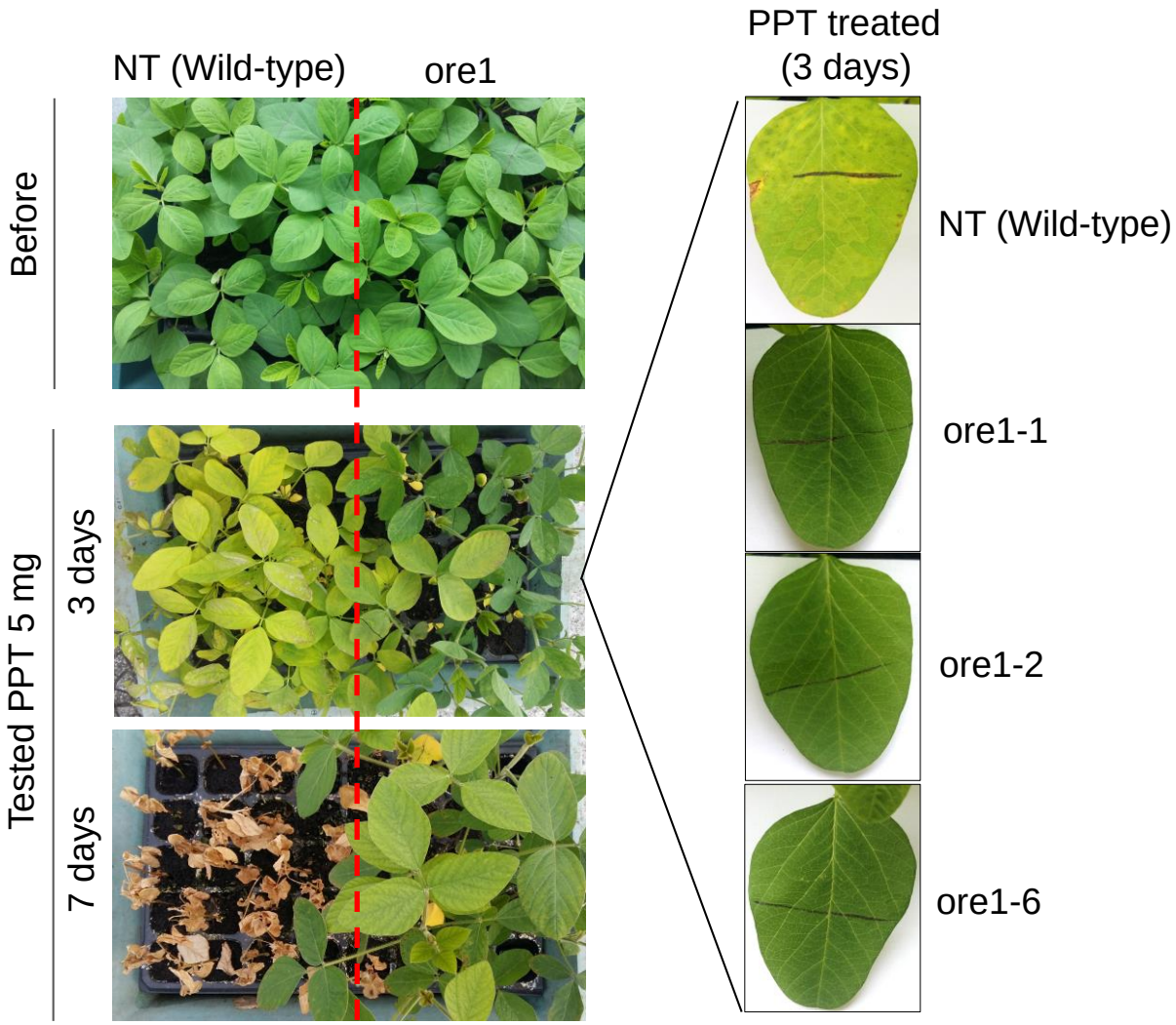

Figure S2. Screening the soybean transgenic plants by painting phosphinothricin (PPT) at 5 mg ml^{-1} after 7 days. The leaf was tested by PPT 0.5 mg mL^{-1} as shown the yellow color in wide-type, but not exhibited in transgenic lines.

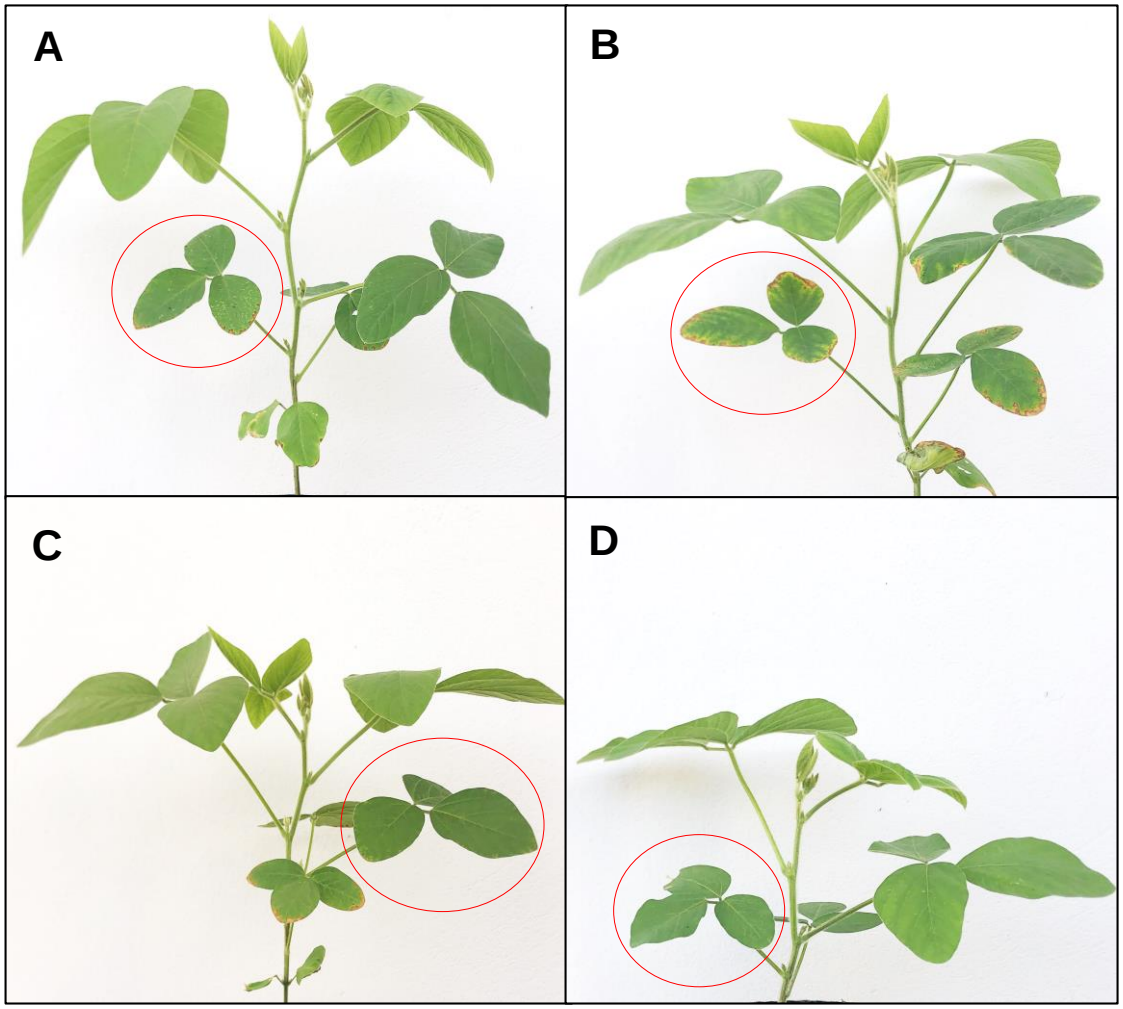

Figure S3. Phenotypic change in specific leaves tissue senescing of wide-type (NT) compared to transgenic lines**.** (A) Wide-type, (B) *ore1-1*, (C) *ore1*-2 and (D) *ore1*-6. The detached leaves No.3 senescent at the V3-vegetative stage. Data are represented as mean ± SE of three biological replicates (n = 3).

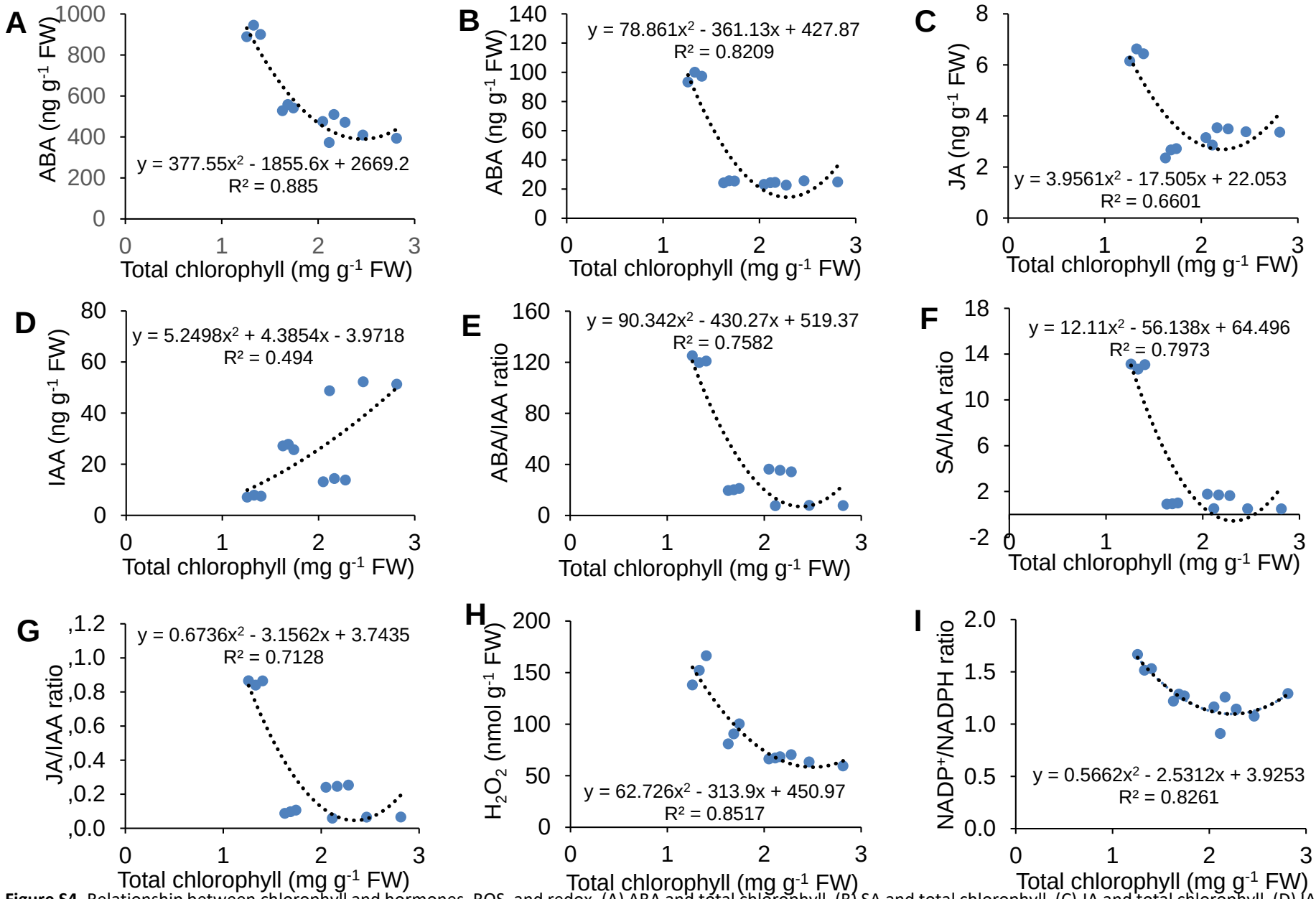

Figure S4. Relationship between chlorophyll and hormones, ROS, and redox. (A) ABA and total chlorophyll, (B) SA and total chlorophyll, (C) JA and total chlorophyll, (D) IAA and total chlorophyll, (E) ABA/IAA ratio and total chlorophyll, (F) SA/IAA ratio and total chlorophyll, (G) JA/IAA ratio and total chlorophyll, (H) H_2O_2 and total chlorophyll, (I) $NADP^+$/NADPH ratio and total chlorophyll. Among these, auxin is a positive relationship to chlorophyll in wide-type and transgenicc lines. Data are represented as mean ± SE of three biological replicates (n = 3).

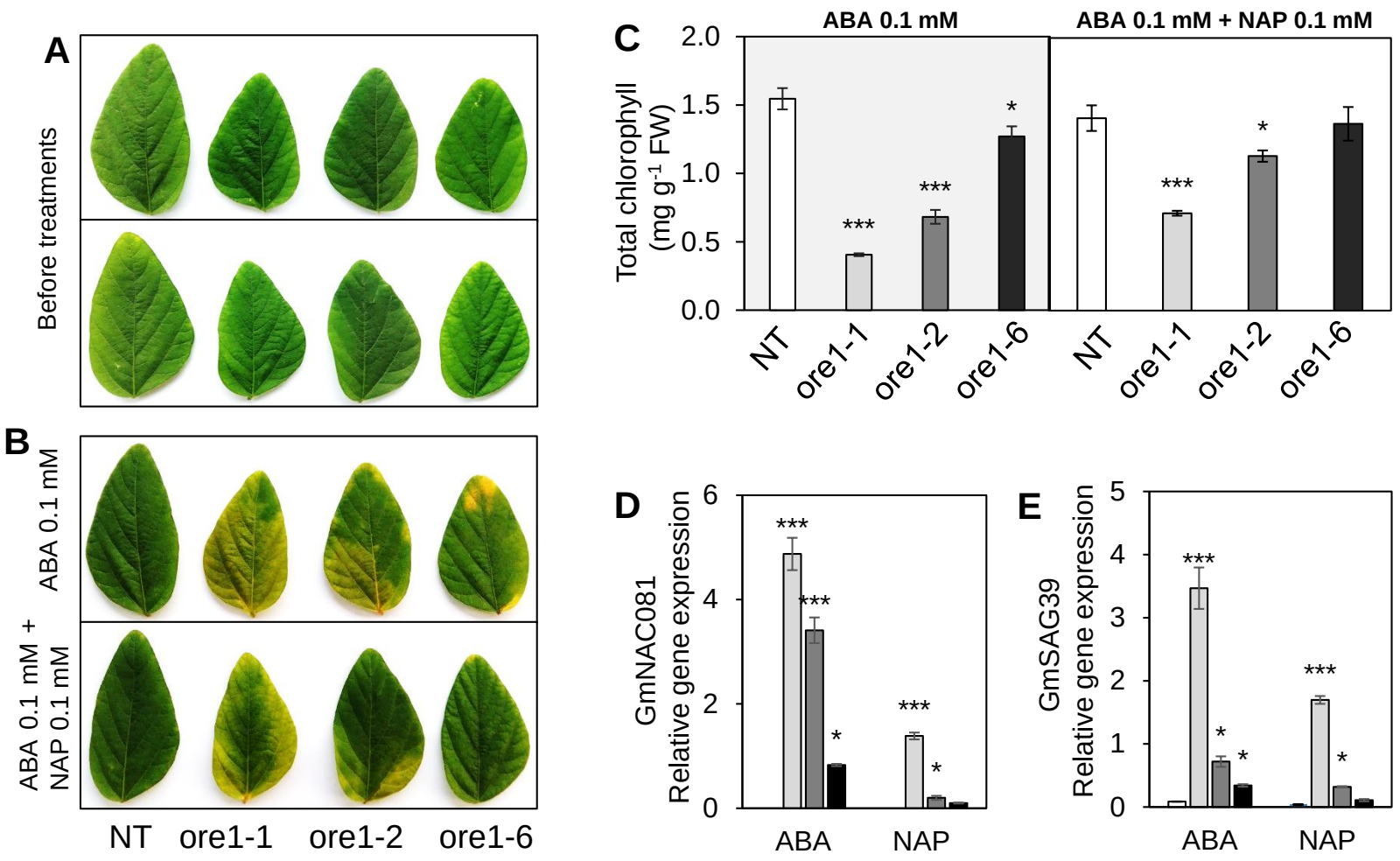

Figure S5. Effect of ABA in soybean transgenic plants under leaf disc condition. (A) The detached 3rd fully expanded leaves of 6-week-old plants before treatment. (B) Shown are wide-type and transgenic lines inoculated with ABA 0.1 mM and NAP 0.1 mM (Naproxen, ABA inhibitor). (C) Total chlorophyll content measurement after 72 hours. (C) and (D) Transcript expression levels of *GmNAC081* and *GmSAG39* was expressed in ore1 lines compared to the wide-type under ABA and NAP treatments. Data are represented as mean ± SE of three biological replicates (n = 3). Asterisks indicate significant differences from wide-type (NT) and transgenic lines as determined by Turkey's t-test; $^{*}P < 0.05$, $^{***}P < 0.001$.

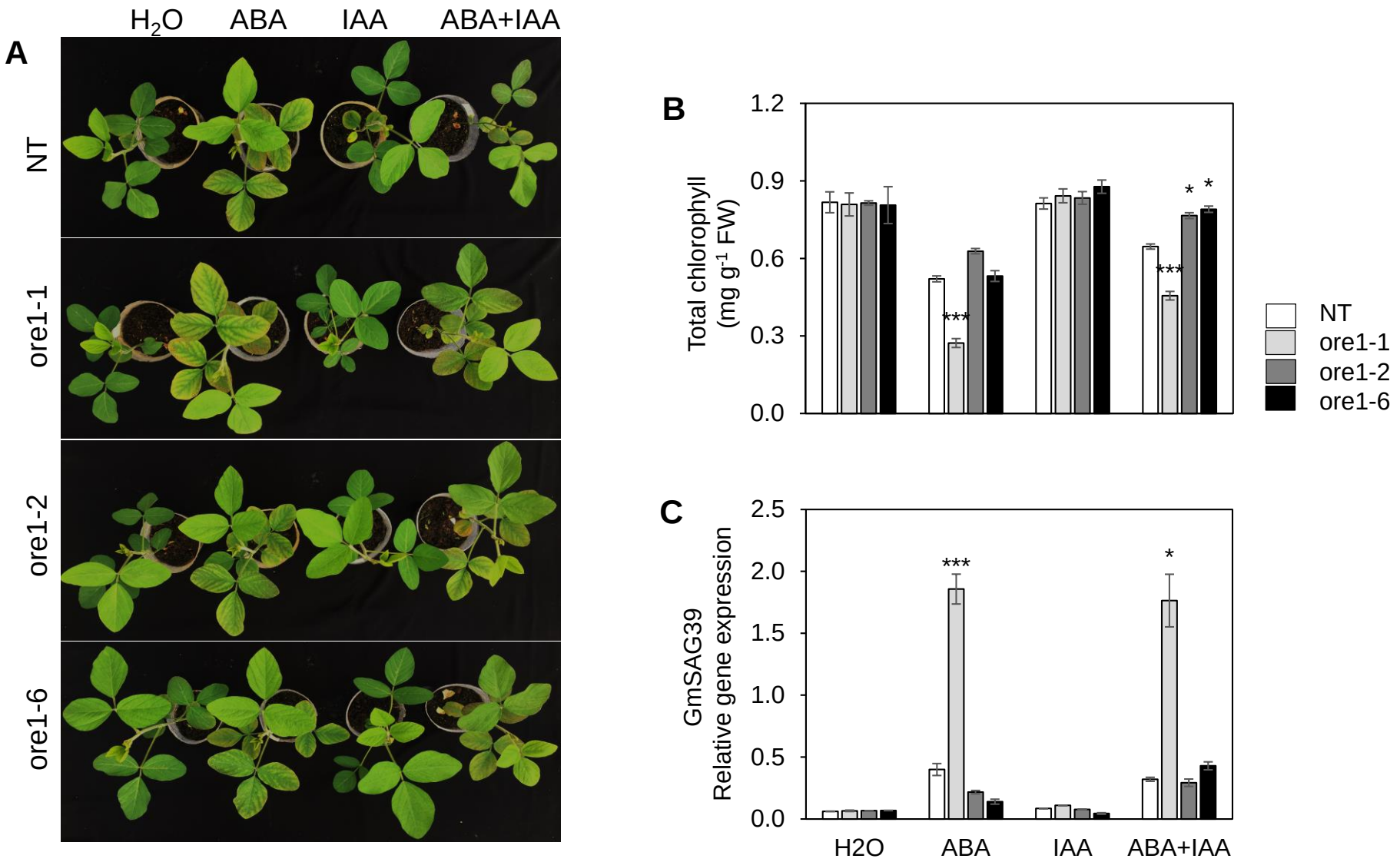

Figure S6. Effect of ABA and IAA on wide-type and soybean transgenic lines. (A) Whole leaf of plants 5-week-old genotypes. The rosette leaf No.3 was highlighted in yellow color visualization. (B) Total chlorophyll content was detected in leaf No.3 measurement after 72 hours. (C) Transcript levels of *GmSAG39* expressed under ABA and IAA treatments, which was determined by quantitative real-time PCR. Data are represented as mean ± SE of three biological replicates (n = 3). Asterisks indicate significant differences from wide-type (NT) and *ore1* mutants as determined by Turkey's t-test; $^{*}P < 0.05$, $^{***}P < 0.001$. **Figure S6.** Effect of ABA and IAA on wide-type and soybean transgenic lines. (A) Whole leaf of plants 5-week-old genotypes. The rosette leaf No.3 was highlighted in yellow color visualization. (B) Total chlorophyll content was detected in leaf No.3 measurement after 72 hours. (C) Transcript levels of *GmSAG39* expressed under ABA and IAA treatments, which was determined by quantitative real-time PCR. Data are represented as mean ± SE of three biological replicates (n = 3). Asterisks indicate significant differences from wide-type (NT) and *ore1* mutants as determined by Turkey's t-test; $^{*}P < 0.05$, $^{***}P < 0.001$.

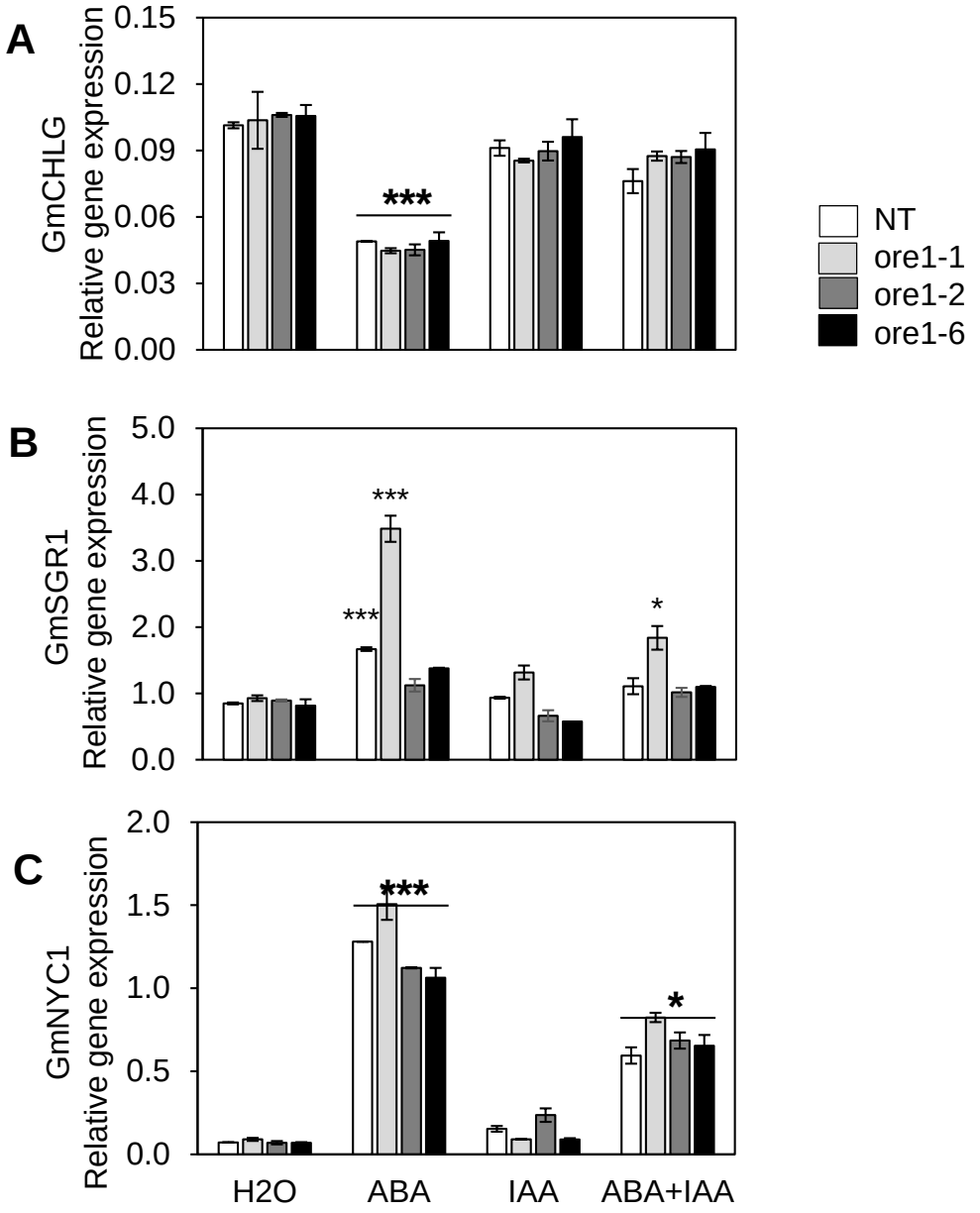

Figure S7. Effect of ABA and IAA on chlorophyll synthesis and its degradation related genes in wide-type and transgenic lines. (A) Relative expression of chlorophyll synthase (CHLG)-related chlorophyll synthesis. (B) Soybean chlorophyll catabolic genes (CCGs) including STAYGREEN1 (*GmSGR1*) and NON-YELLOWING COLORING 1 (*GmNYC1*) expression under ABA and IAA treatments, which was determined by quantitative real-time PCR. Four-week-old detached leaf (upper) or whole plants (lower) grown in same condition. Data are represented as mean ± SE of three biological replicates (n = 3). Asterisks indicate significant differences from wide-type (NT) and transgenic plants as determined by Turkey's t-test; $^{*}P < 0.05$, $^{***}P < 0.001$.

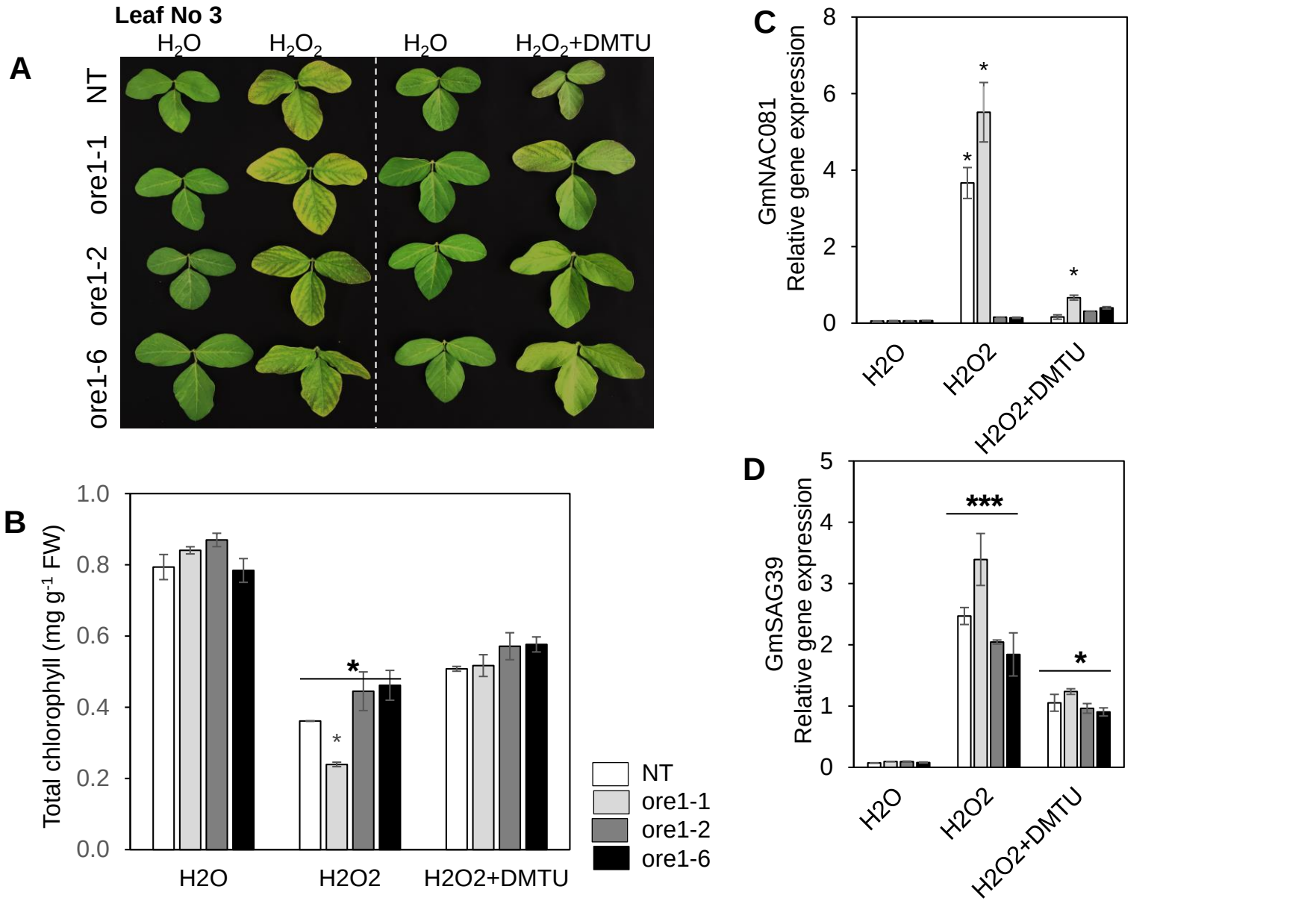

Figure S8. Effect of hydrogen peroxide on soybean-expressed transgenic plants. (A) The detached 3rd fully expanded leaves of 5-week-old plants after treated by H_2O_2 and DMTU (H_2O_2-scavenger). (C) Total chlorophyll content measurement after 3 days. The rosette leaf No.3 of ore1-1 line was highlighted in yellow color visualization. (C) Regulation expression of *GmNAC081*, (D) *GmSAG39* in transgenic plants under H_2O_2 and DMTU treatments, which were determined by quantitative real-time PCR. Data are represented as mean ± SE of three biological replicates (n = 3). Asterisks indicate significant differences from wide-type (NT) and transgenic plants as determined by Turkey's t-test; $^{*}P < 0.05$, $^{***}P < 0.001$.

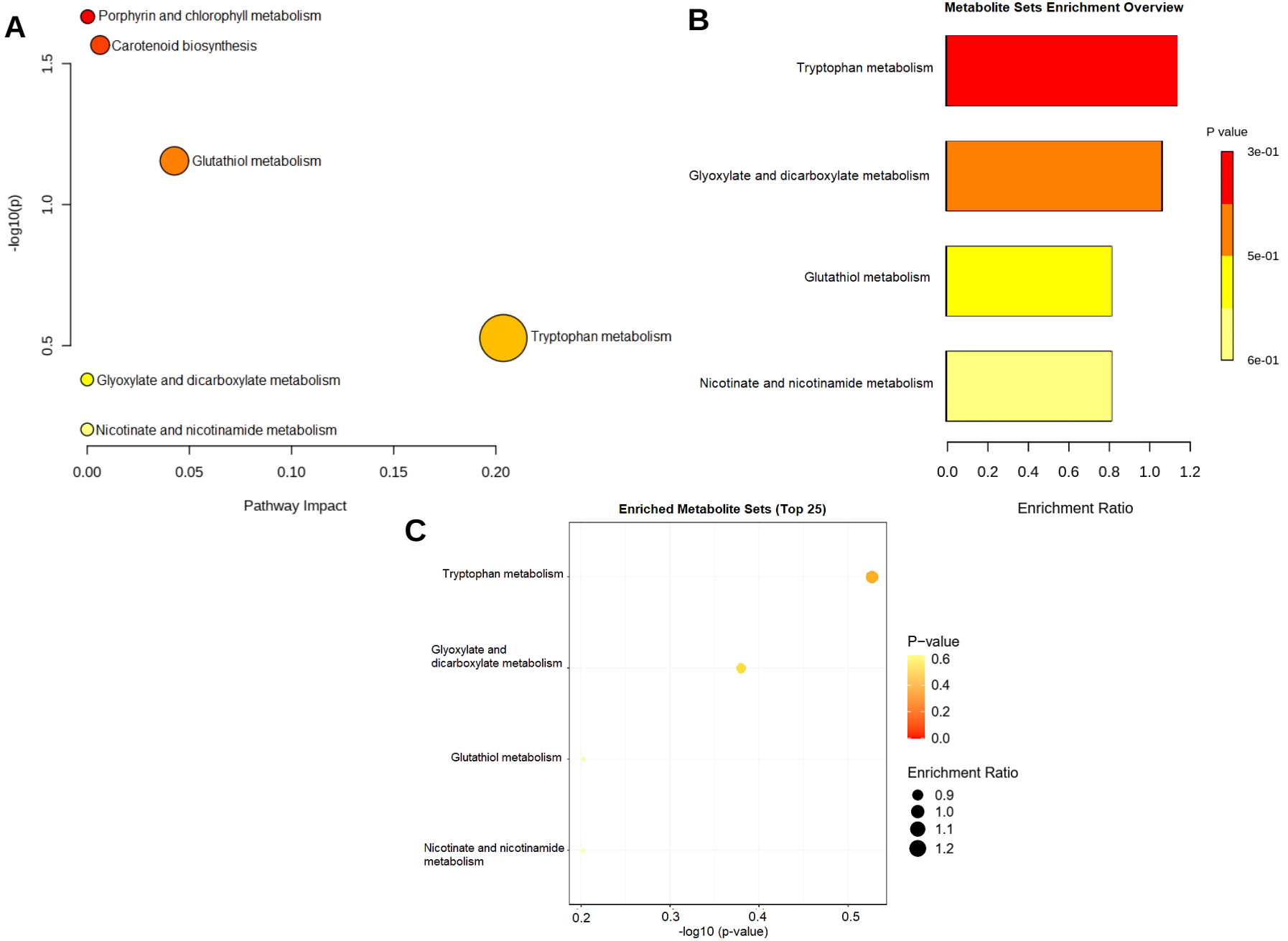

Figure S9. Pathway analysis of *Atore1* gene in soybean transgenic plants. (A) Pathway impact. (B) and (C) Metabolites sets Enrichment for specific metabolites in pathway regulation. Data are represented as mean ± SE of three biological replicates (n = 3).