Figure S1

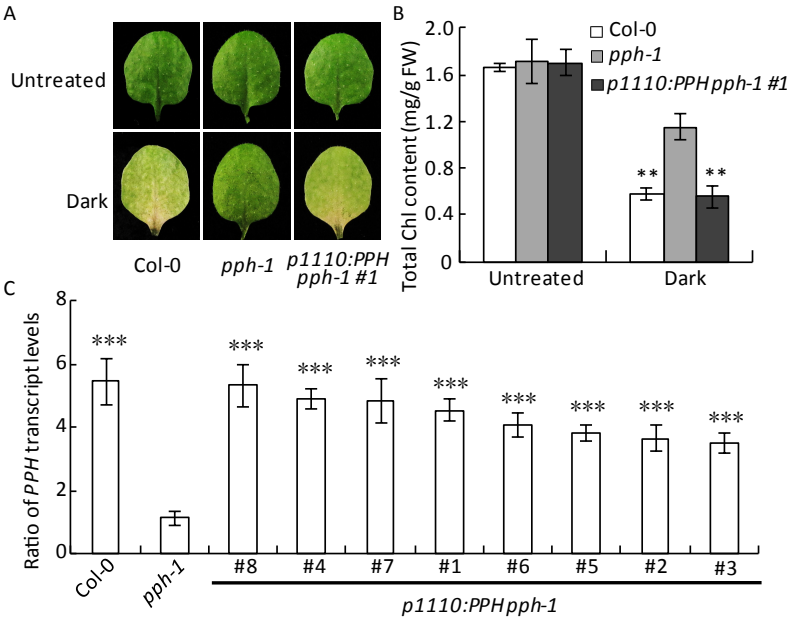

Figure S1 The 1.11-kb fragment upstream of *PPH* start codon contains the core *PPH* promoter

A, Expression of *p1110:PPH* rescued the stay-green phenotype of *pph-1*. Detached 5th and 6th rosette leaves of 3-week-old transgenic plants (T3) were incubated in darkness for 4 days. *p1110*, 1110-bp *PPH* promoter fragment.

B, Chl contents in the detached leaves shown in **A**. *pph-1* was included as the negative control.

C, Ratios of *PPH* transcript levels after dark treatment over those untreated in the leaves of *p1110: PPH pph-1*. *pph-1* was included as the negative control.

In **B** and **C**, data are means ± SD of 2 biological repeats. ** P <0.01, *** P <0.001 (*t*-tests).

Figure S2

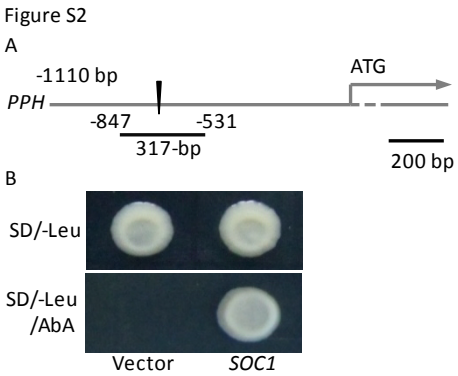

Figure S2 SOC1 protein interacts with *PPH* promoter in an Y1H assay

A, A schematic diagram of the *PPH* promoter showing the positions of CArG-box (black triangle) and the 317-bp bait fragment containing CArG-box, between -847 and -531 bp upstream of the *PPH* start codon.
B, Transformed yeast cells containing both the 317-bp bait and the prey (*SOC1*) constructs were plated on the selective medium (SD/-Leu/AbA). Vector, empty vector control; AbA, Aureobasidin A.

Figure S3

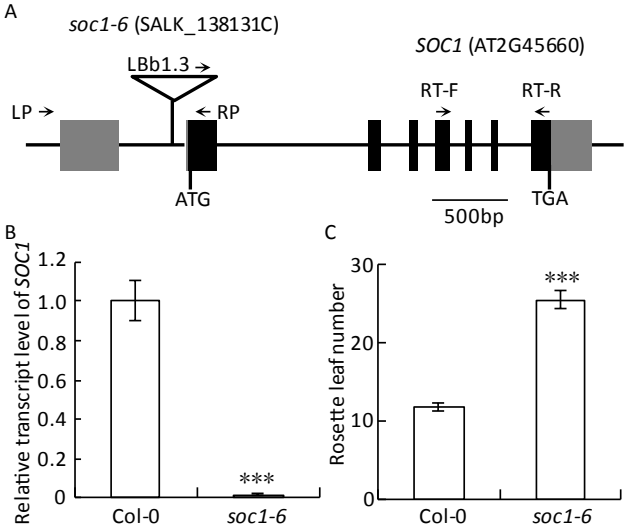

Figure S3 *soc1-6* is a late-flowering mutant

A, A schematic diagram of the *soc1-6* (SALK_138131C) mutant showing the position of T-DNA insertion. Black boxes indicate exons of *SOC1*, and gray boxes represent the UTR of *SOC1.* Genotyping primers (LP, RP and LBb1.3) were used to identify homozygous lines of *soc1-6*, and RT-qPCR primers (RT-F and RT-R) were used to analyze the expression of *SOC1.*

B, Relative transcript levels of *SOC1* in *soc1-6* and Col-0.

C, The rosette leaf number of *soc1-6* at the bolting stage compared to that of WT under long-day conditions.

In **B** and **C**, data are means ± SD of 2 biological repeats. *** P <0.001 (*t*-tests).

Figure S4

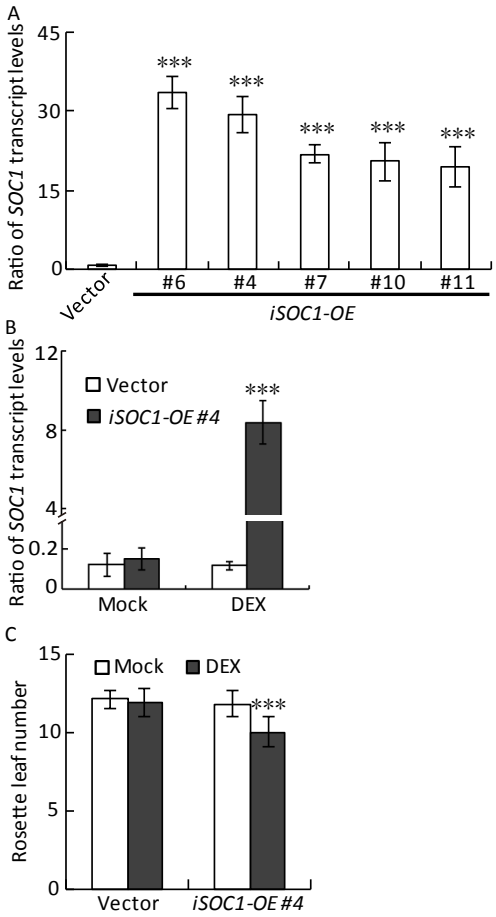

Figure S4 DEX treatment could induce the transcription of *SOC1* in *iSOC1-OE* transgenic lines (T3)

A, Ratios of *SOC1* transcript levels after DEX treatment over those treated by Mock in *iSOC1-OE* transgenic plants. Detached 5th and 6th rosette leaves of 3-week-old plants were treated with DEX and *SOC1* mRNA levels were quantified by RT-qPCR after 6 hours.
B, Ratios (Dark/Untreated) of *SOC1* transcript levels in the leaves shown in Figure **1G**.
C, Induced overexpression of *SOC1* caused early flowering phenotype. Five-day-old (after germination) plants were sprayed with DEX every other day. Mock, water; DEX, 30 μM dexamethasone water solution; vector, empty vector control.
Data are means ± SD of 2 biological repeats. *** P <0.001 (*t*-tests).

Figure S5

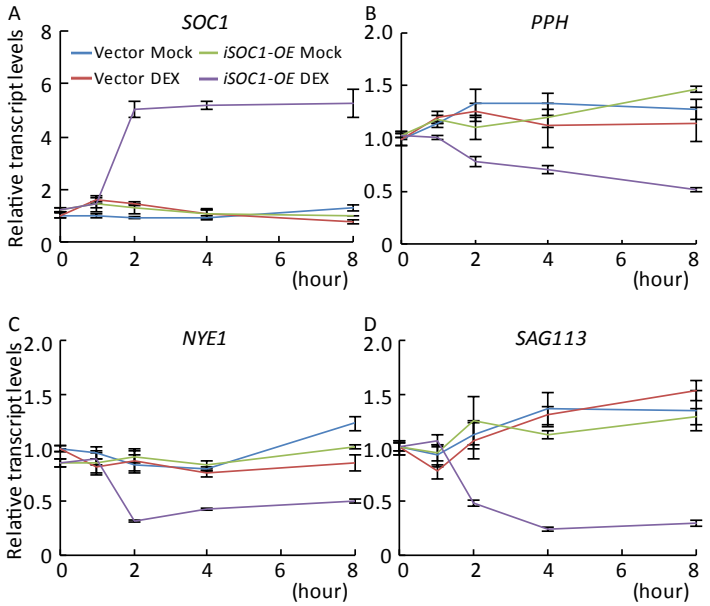

Figure S5 An induced *SOC1* (A) inhibits *PPH* (B), *NYE1* (C) and *SAG113* (D) transcriptions in a short time window during dark treatment

Detached 5th and 6th rosette leaves of 3-week-old plants were incubated in darkness for 2 days before Mock or DEX treatment. Transcript levels of respective genes in Col-0 at hour 0 were set to 1. Mock, water; DEX, 30 μM dexamethasone water solution; vector, empty vector control. Data are means ± SD of 2 biological repeats.

Figure S6

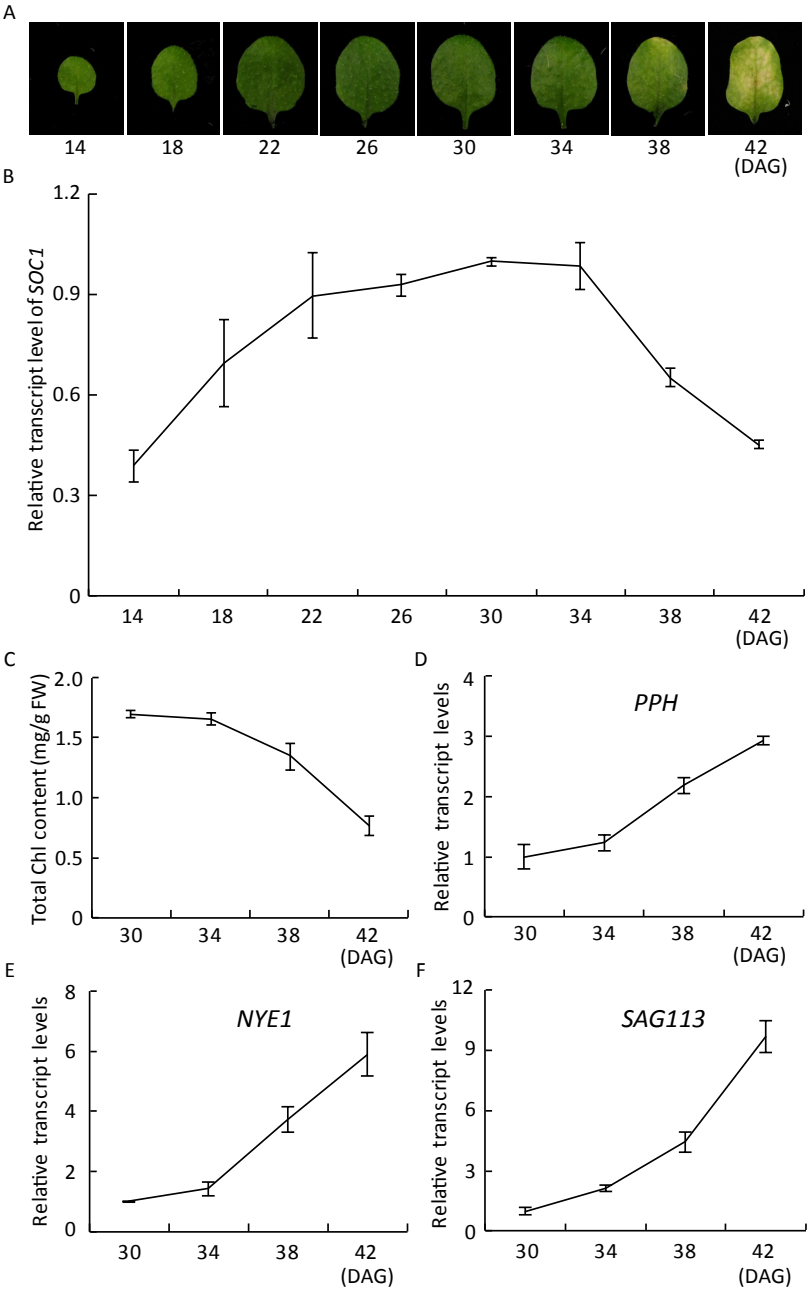

Figure S6 Developmental senescence phenotype of the wild-type *Arabidopsis* leaves

A, The 5th and 6th rosette leaves from 14, 18, 22, 26, 30, 34, 38, 42-day-old (after germination) Col-0 plants. DAG, days after germination.
B, Relative transcript levels of *SOC1* at each time point shown in **A**. To facilitate the comparison between *SOC1* expression and some *SAGs*' expressions during the late developmental stage, the relative transcript level of *SOC1* in 30-day-old leaves was set to 1.
C, Chl contents in the leaves shown in **A** from 30 DAG to 42 DAG.
D-F, Relative transcript levels of *PPH*, *NYE1*, and *SAG113* from 30 DAG to 42 DAG in the leaves shown in **A**. The transcript level of each gene at day 30 was set to 1.
In **B-F**, data are means ± SD of 2 biological repeats.

Figure S7

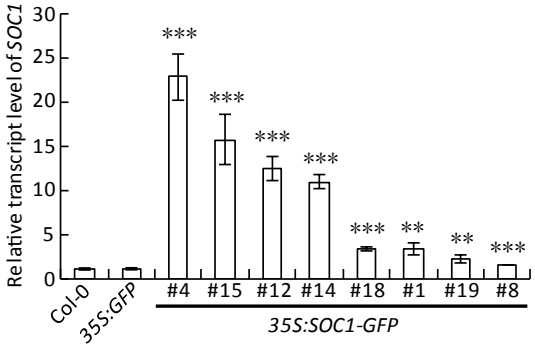

Figure S7 Relative transcript levels of *SOC1* in *35S:SOC1-GFP* transgenic lines (T3)

SOC1 transcript levels in Col-0 and *35S:GFP* plants were used as controls. Data are means ± SD of 2 biological repeats. ** P <0.01, *** P <0.001 (*t*-tests).

Figure S8

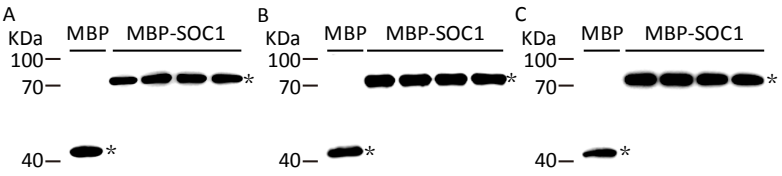

Figure S8 Western immunoblot analysis of the purified MBP and MBP-SOC1 proteins

The proteins were detected with anti-MBP antibodies, and the amounts of each protein loaded for the EMSA shown in Figure **2D** (**A**, *PPH*) and Figure **5D** (**B**, *NYE1*; **C**, *SAG113*) were the same as those for Western blot assay.

Figure S9

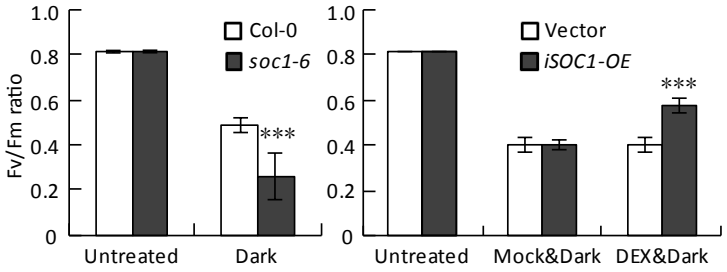

Figure S9 Fv/Fm ratios of the detached 5th and 6th rosette leaves of 3-week-old *soc1-6* and *iSOC1-OE* plants during dark treatment

Detached 5th and 6th rosette leaves of *soc1-6* and WT plants were treated in darkness for 5 days, whereas those of *iSOC1-OE* and the vector control plants treated for 6 days. Mock, water; DEX, 30 μM dexamethasone water solution; vector, empty vector control.
Data are means ± SD of 3 biological repeats. *** P <0.001 (*t*-tests).

Figure S10

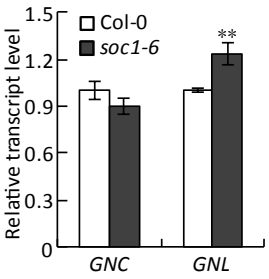

Figure S10 Relative transcript levels of *GNC* and *GNL* in the 5th and 6th rosette leaves of 3-week-old *soc1-6* plants

Data are means ± SD of 2 biological repeats. ** P <0.01 (t-tests).

Figure S11

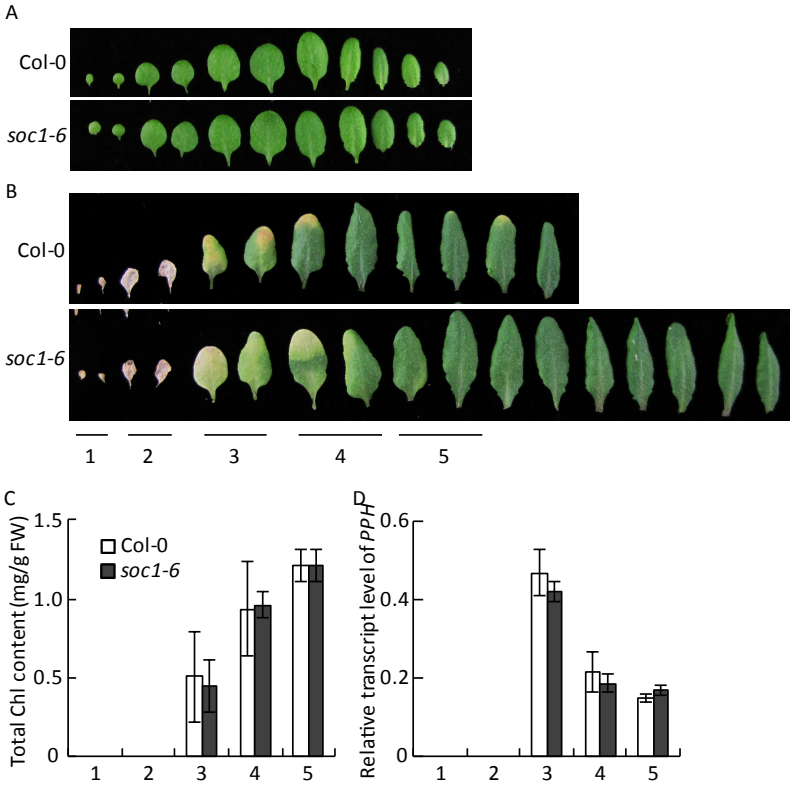

Figure S11 Developmental senescence phenotypes of *soc1-6* leaves

A and **B**, Phenotypes of all the rosette leaves of 3-week-old and 6-week-old plants, respectively.
C, Chl contents of the indicated leaves shown in **B**.
D, Relative transcript levels of *PPH* in the indicated leaves shown in **B**.
In **C** and **D**, data are means ± SD of 2 biological repeats.

Figure S12

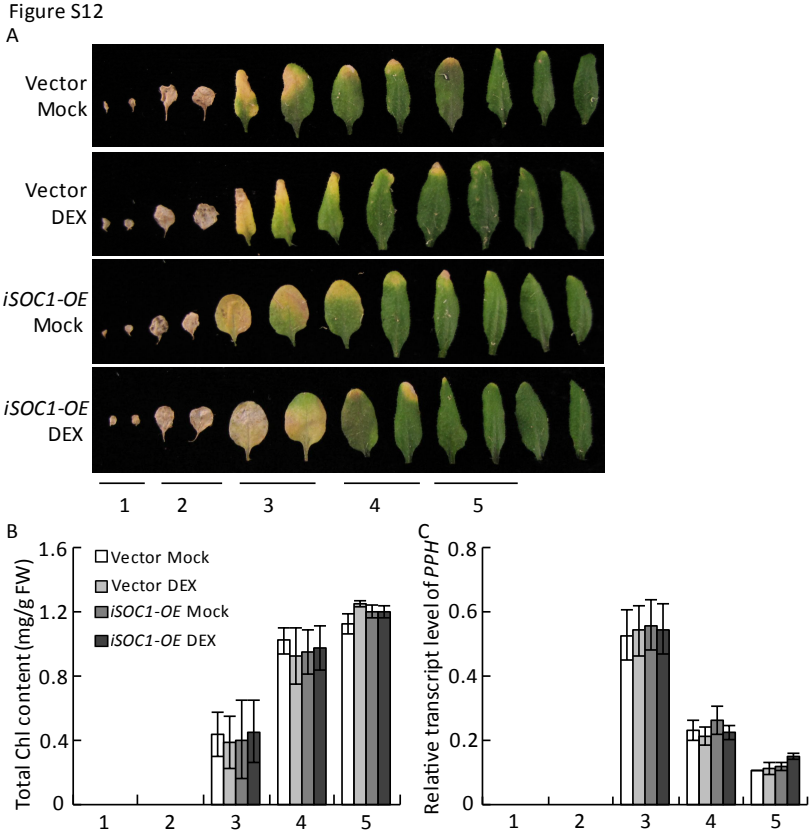

Figure S12 Developmental senescence phenotypes of *iSOC1-OE* leaves

A, Phenotypes of all the rosette leaves of 6-week-old plants. Three-week-old plants were sprayed with DEX every 5 days. Mock, water; DEX, 30 μM dexamethasone water solution; vector, empty vector control.
B, Chl contents in the indicated leaves shown in **A**.
C, Relative transcript levels of *PPH* in the indicated leaves shown in **A**.
In **B** and **C**, data are means ± SD of 2 biological repeats.