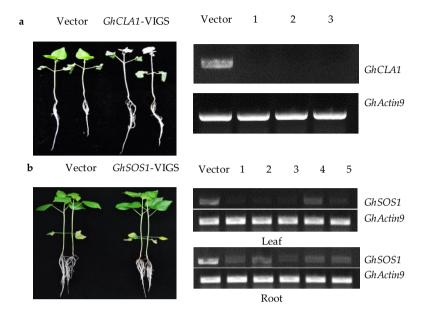
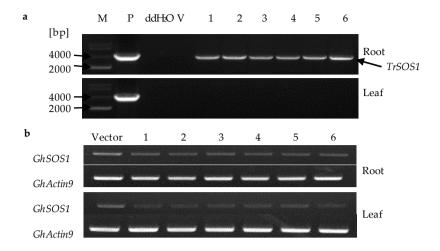
## **Supplementary Materials:**



**Figure S1.** Construction and identification of *GhCLA1*-VIGS or *GhSOS1*-VIGS cotton plants. (a) *GhCLA1*-VIGS cotton plants infected with *Agrobacterium tumefaciens* GV3101 containing pTRV1 and pTRV2-*GhCLA1* showed photobleaching phenotypes, and the empty-vector-transformed plants infected with *A. tumefaciens* GV3101 containing pTRV1 and pTRV2 was as a control (**left**); after 10 days of infection, the gene expression patterns of *GhCLA1* in the leaves of Vector and *GhCLA1*-VIGS plants was analyzed by semi-quantitative RT-PCR, and the housekeeping gene *GhActin9* was used as an internal control (right). (b) *GhSOS1*-VIGS cotton plants infected with *A. tumefaciens* GV3101 containing pTRV1 and pTRV2-*GhSOS1* and empty-vector-transformed plants was cultured with 1/2 Hoagland solution (**left**), the gene expression patterns of *GhSOS1* in the roots and leaves of Vector and *GhSOS1*-VIGS plants was analyzed by semi-quantitative RT-PCR (right).



**Figure S2.** Construction and identification of hairy root composite cotton plants of *hrGhSOS1*-VIGS or *hrTrSOS1*-OE/*GhSOS1*-VIGS. (a) The plants were firstly infected with pSuper\*1300-*TrSOS1*-containing *Agrobacterium rhizogenes* strain K599 to obtain *TrSOS1*-overexpressed hairy root composite cotton plants (*hrTrSOS1*-OE), the gene expression patterns of *TrSOS1* in the roots and leaves was analyzed using DNA as the template by PCR. M: DNA marker; P: Positive control; V: Empty vector, represented as the negative control; ddH<sub>2</sub>O: Distilled deionized water, also represented as the negative control; (b) The abovementioned empty-vector- or *TrSOS1*-transformed cotton plants were infected with *A. tumefaciens* GV3101 containing pTRV1 and pTRV2-*GhSOS1*-VIGS plants. The plants infected with *A. tumefaciens* GV3101 containing pTRV1 and pTRV2 was used as a control (Vector), the gene expression patterns of *GhSOS1* in the roots and leaves of *hrGhSOS1*-VIGS or *hrTrSOS1*-OE/*GhSOS1*-VIGS plants were analyzed by semi-quantitative RT-PCR.