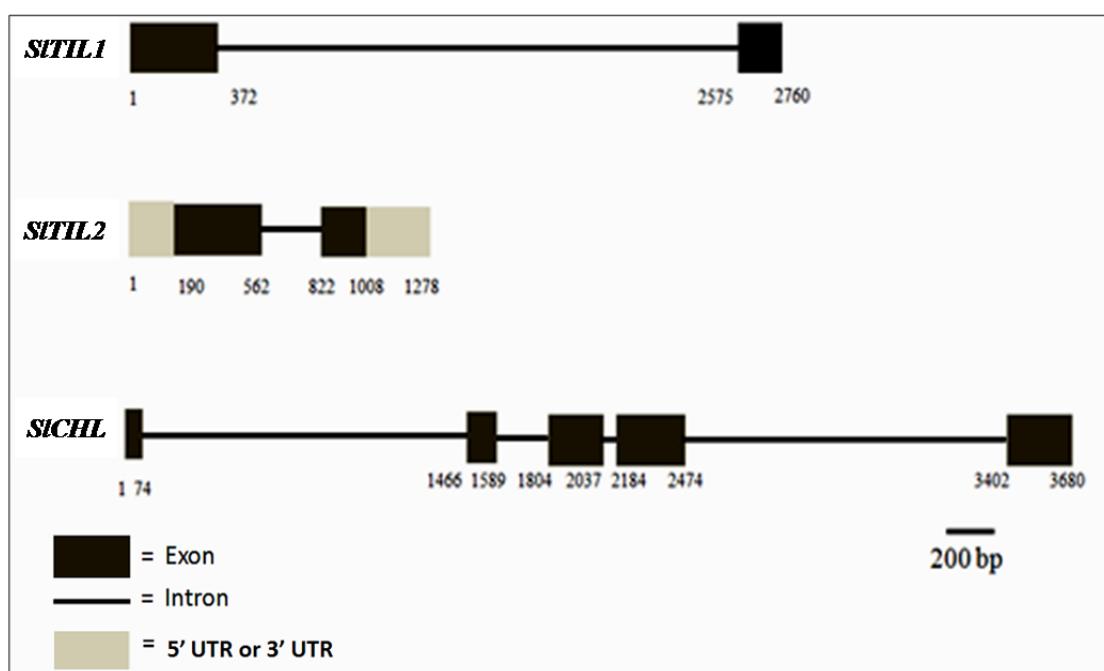
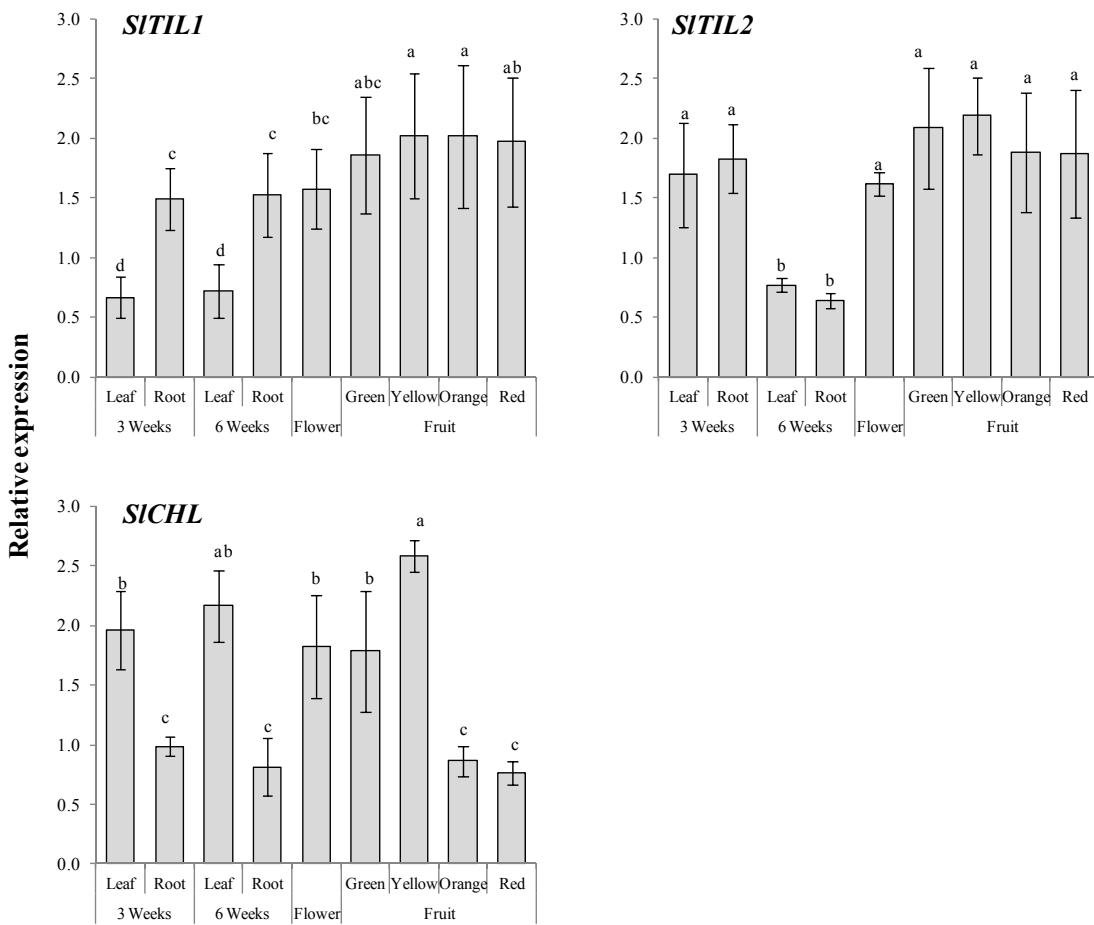


S1TIL1	MATKVMEEVKNLDLKRYMGRWYEIASFPSRFQPKDGVDRATYTLNSDGTVHVLNETWCN	60
S1TIL2	MTTKEMEVVKNLDVEKYMGRWYEIASFPSRNQPKDGVNTRATYTLNQDGTVHVLNETWSG	60
	*:*** *****: : :*****:*****:*****:*****:*****:*****:*****:..	
S1TIL1	GKRGFIEGTAYKADPNSDEAKLKVRFYVPPFLPIIPVTGDYWVLYIDEDYQYALIGQPSR	120
S1TIL2	GKRGSIETAYKADPKSDEAKLKVKFYIPPFLPIIPIVGVDYWVLYIDDDYQYALIGQPSK	120
	**** *****:*****:*****:*****:*****:*****:*****:*****:*****:	
S1TIL1	RYLWILSRQTRLDDEIYNQLVEKAKEEGYDVS KLHKTPQS DSPPDSE DSPKDTKG IWWIK	180
S1TIL2	KYLWILCRQPHLDEE IYNQLVEKAKEVG YDVS KLHKTPQADPPP DGEDAPKDTKG FWWIK	180
	:*****. ** :**:*****:*****:*****:*****: * ***. **:*****:*****	
S1TIL1	SILGK 185	
S1TIL2	SILGK 185	
	*****	

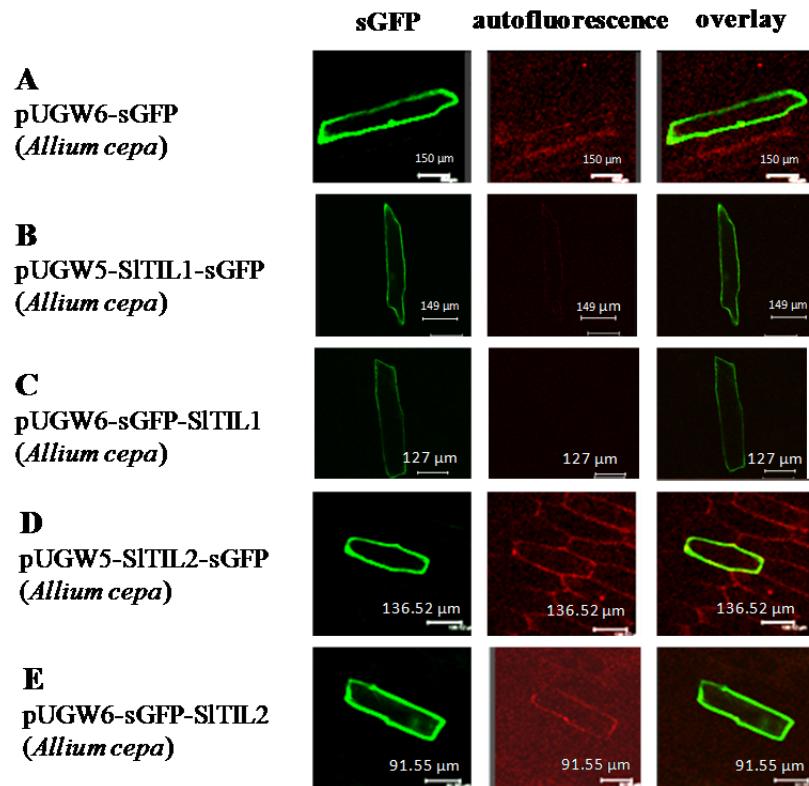
**Figure S1.** The amino acid alignment of S1TIL1 and S1TIL2. Sequences were aligned using CLUSTALW. Asterisk (\*) indicates positions with a single fully conserved residue. Colon (:) indicates conservation between groups with strongly similar properties (scoring > 0.5 in Gonnet PAM 250 matrix). Period (.) indicates conservation between groups with weakly similar properties (scoring = < 0.5 in Gonnet PAM 250 matrix).



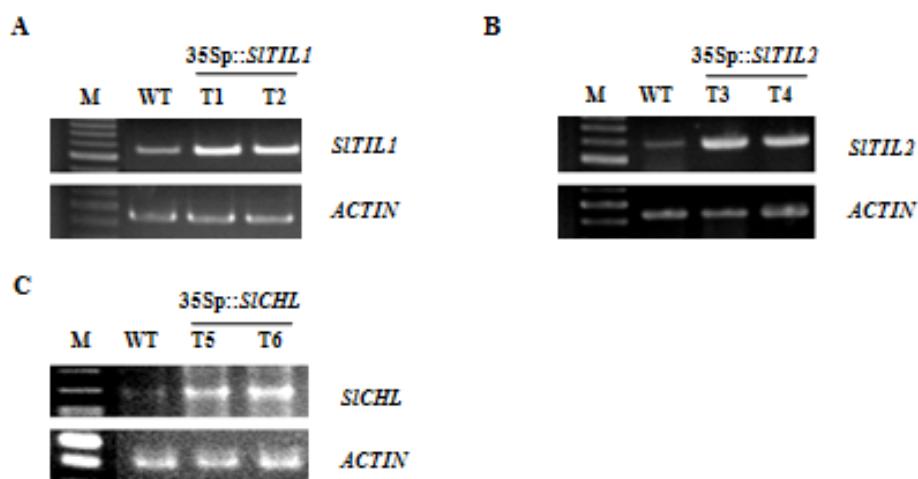
**Figure S2.** Schematic structures of genomic DNA of *SITIL1*, *SITIL2* and *SICHL* genes



**Figure S3.** Gene expression analyses of *SITIL1*, *SITIL2*, and *SICHL* in different tissues of ‘Micro-Tom’ tomatoes. The results of RT-PCR (Figure 2) were quantitated using ImageJ software, and normalized with the value of *ACTIN*. Data are mean values of three separate experiments  $\pm$  SD. Different letters among bars indicate statistical differences by the LSD test ( $P < 0.05$ ). Green: green fruit stage; Yellow: yellow fruit stage; Orange: orange fruit stage; Red: red fruit stage; M: marker.



**Figure S4.** Subcellular localization of SITIL1, SITIL2, SlCHL in onion epidermal cells. (A) Fluorescent microscopic images of pUGW6-sGFP in onion epidermal cells. (B) Fluorescent microscopic images of pUGW5-SITIL1-sGFP fusion protein in onion epidermal cells. (C) Fluorescent microscopic images of pUGW6-sGFP-SITIL1 fusion protein in onion epidermal cells. (D) Fluorescent microscopic images of pUGW5-SITIL2-sGFP fusion protein in onion epidermal cells. (E) Fluorescent microscopic images of pUGW6-sGFP-SITIL2 fusion protein in onion epidermal cells.



**Figure S5.** The expression of *SITIL1* (A), *SITIL2* (B), and *SICHL* (C) in leaves of wild-type plants and over-expressed plants. The numbers of T1, T2 in the figure illustrate representative results from independent transgenic lines shown in Figure 4.

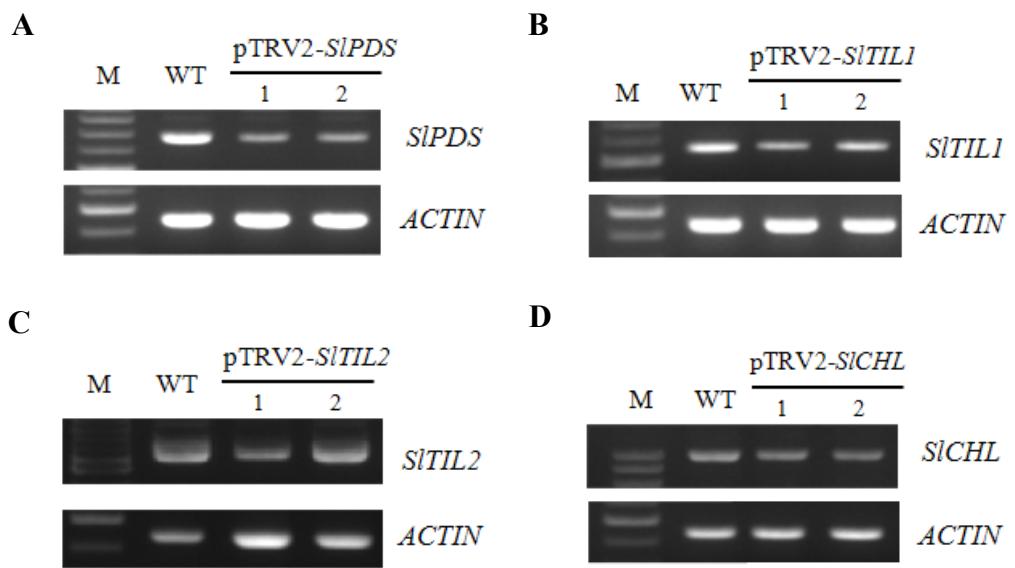
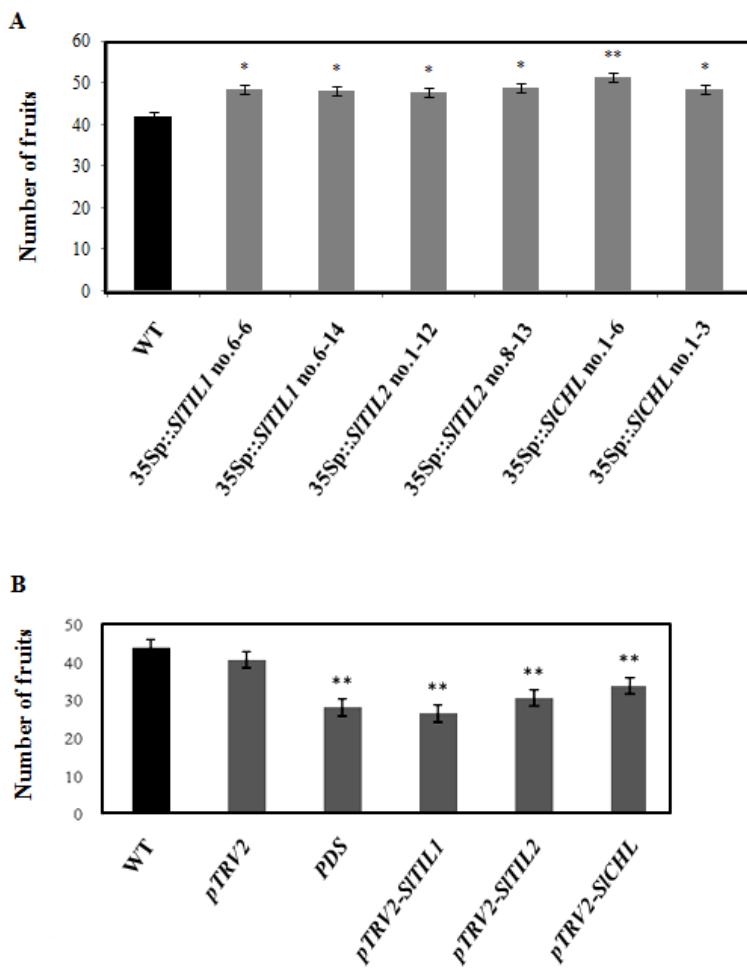
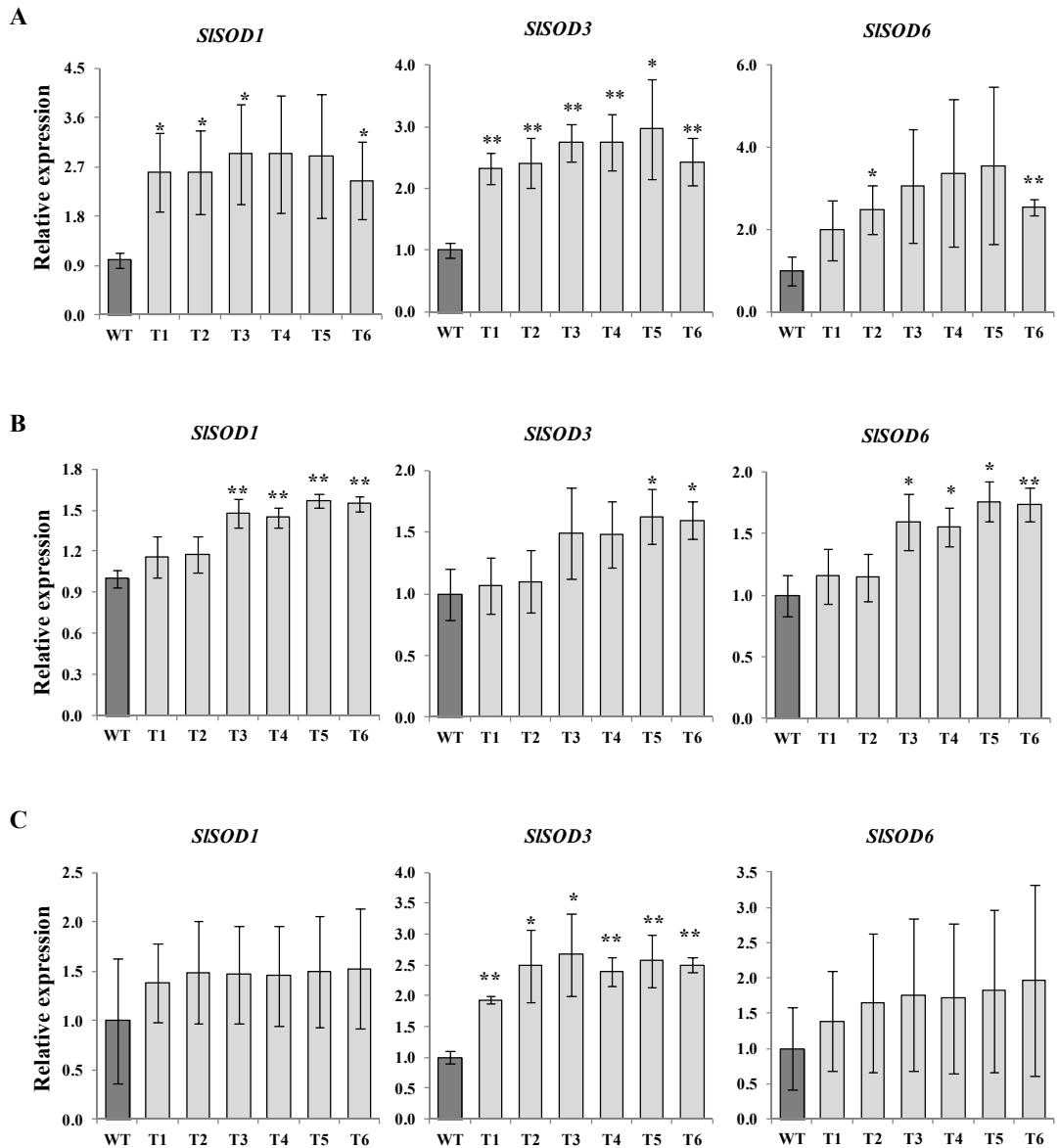


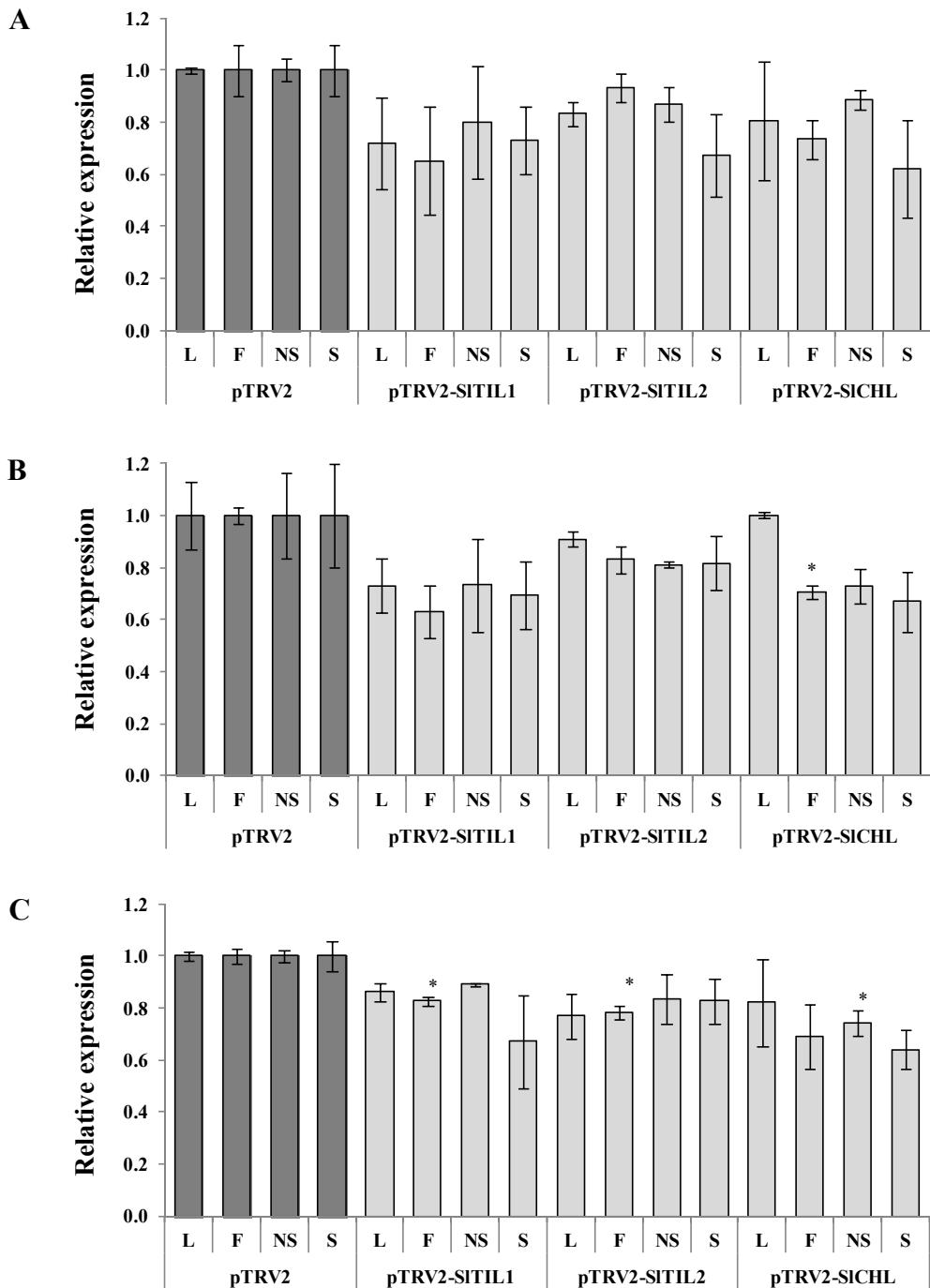
Figure S6. The expression of *SlPDS* (A), *SlTIL1* (B), *SlTIL2* (C), and *SlCHL* (D) in leaves of wild-type plants and silenced plants by VIGS. The numbers of 1, 2 in the figure illustrate representative results from independent experiments.



**Figure S7.** The numbers of fruits in over-expressed *SITIL1*, *SITIL2* and *SICHL* transgenic tomato plants (A) and their gene silenced plants (B). Data are mean values of three separate experiments  $\pm$  SD. \* and \*\* indicate a significant difference from that of WT at  $P < 0.05$  and  $P < 0.01$ , respectively, by Student's *t*-test.



**Figure S8.** The expression of *SISOD1*, *SISOD3*, and *SISOD6* in leaves (A), flowers (B) and fruits (C) of wild-type plants and *SlTIL1*, *SlTIL2* and *SlCHL* over-expressed plants. WT: wild-type plants. T1, T2: 35Sp::*SlTIL1* over-expressed plants; T3, T4: 35Sp::*SlTIL2* over-expressed plants; T5, T6: 35Sp::*SlCHL* over-expressed plants. The results of RT-PCR (Figure 8 A, B and C) were quantitated using ImageJ software, and were normalized with the value of *ACTIN*. The gene expression of different tissues in wild-type plants was used as calibrators (value = 1). Data are mean values of three separate experiments  $\pm$  SD. \* and \*\* indicate a significant difference from that of WT at  $P < 0.05$  and  $P < 0.01$ , respectively, by Student's *t*-test.



**Figure S9.** The expression of *SISOD1* (A), *SISOD3* (B), and *SISOD6* (C) in leaves, flowers, and fruits of *SITIL1*, *SITIL2* and *SICHL* silenced plants. L: leaves; F: flowers; NS: non-silenced fruits; S: silenced fruits. The results of RT-PCR (Figure 8 D) were quantitated using ImageJ software, and were normalized with the value of *ACTIN*. The gene expression of different tissues in wild-type plants was used as calibrators (value = 1). Data are mean values of three separate experiments  $\pm$  SD. \* indicates a significant difference from that of WT at  $P < 0.05$  by Student's *t*-test.