

Figure S1

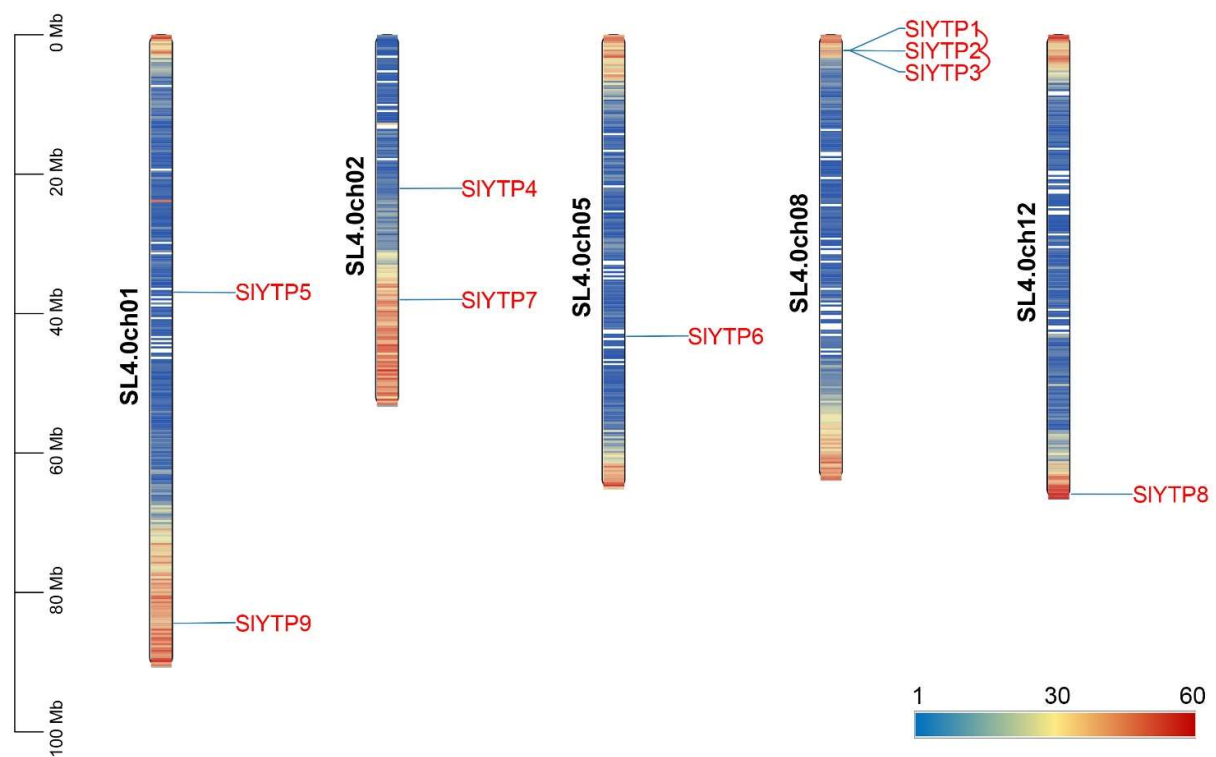


Figure S1. Chromosomal distributions and gene duplications of *SIYTP* genes in tomato genome. The chromosome numbers are shown at the left of each chromosome. Gene pairs from tandem duplication are linked with red lines. Chromosomal length can be calculation via the ruler at the left. Colors in the chromosome frame represented the gene number every 300 kb genome sequence.

Figure S2

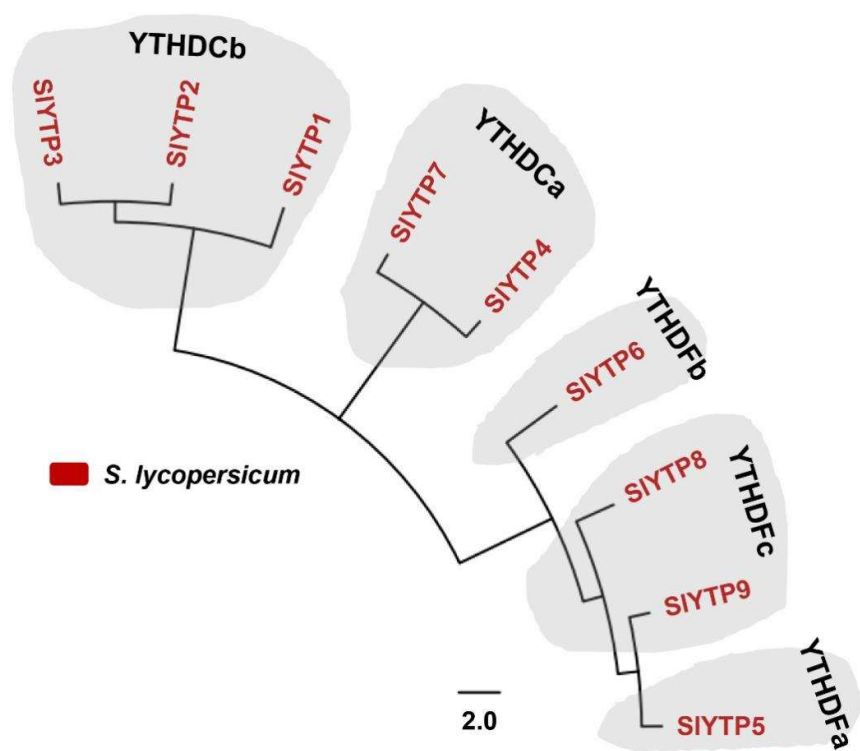


Figure S2. Unrooted phylogenetic tree of YTPs from *S. lycopersicum*. YTPs were divided into five subclasses YTHDCa, YTHDCb, YTHDFa, YTHDFb, and YTHDFc. The phylogenetic tree was constructed by the neighbor-joining method using MEGA7 software with 1000 bootstrap replicates. The scale bar corresponds to a 2.0 genetic distance.

Figure S3

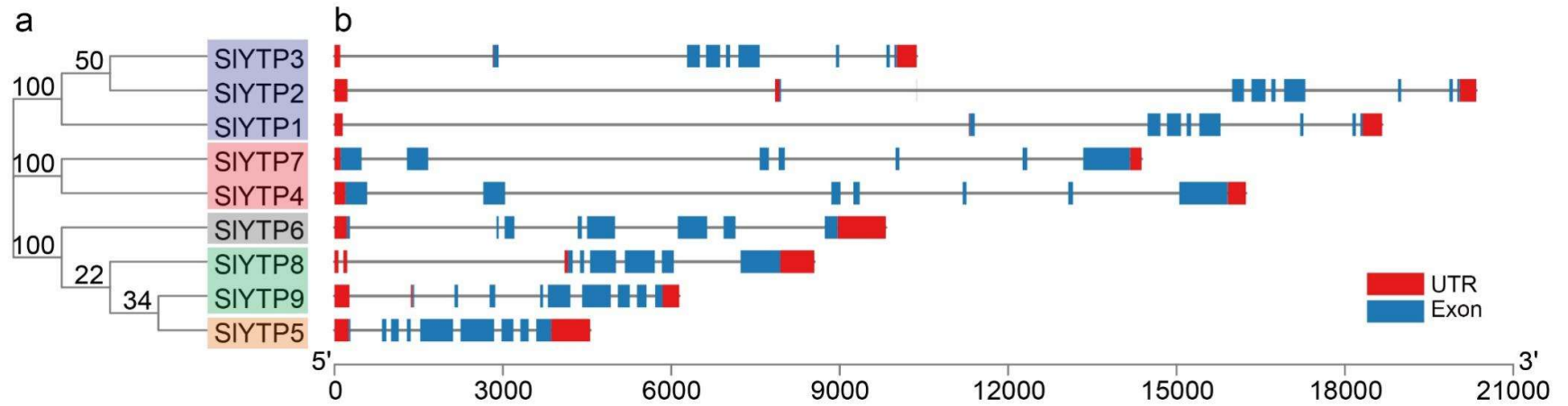


Figure S3. Phylogenetic relationship and gene structure of *SIYTPs*. **a** The phylogenetic tree was constructed based on the full-length sequences of *SIYTPs*. **b** Exon-intron structure of *SIYTPs*. Red boxes indicate untranslated 5'- and 3'-regions; blue boxes indicate exons; and black lines indicate introns.

Figure S4

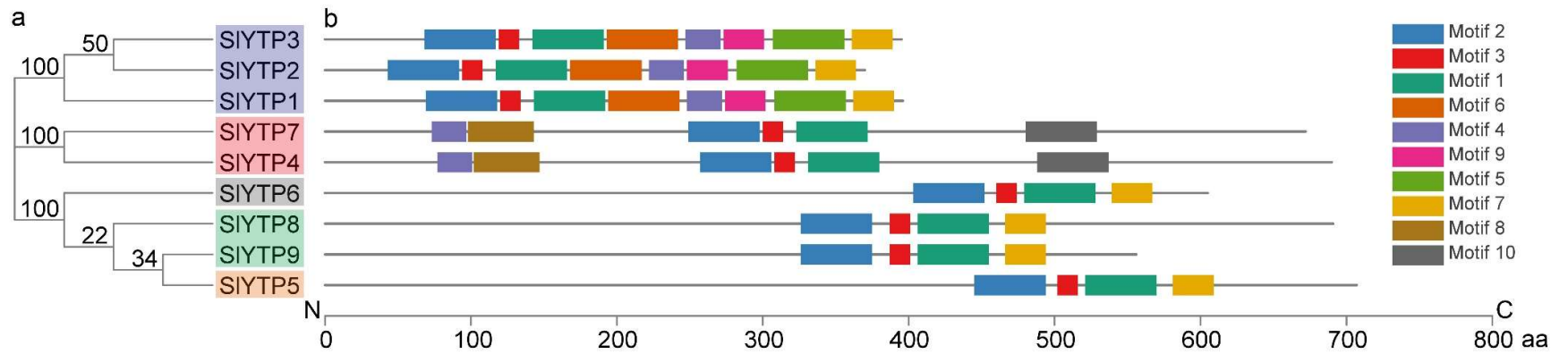


Figure S4. Phylogenetic relationship and architecture of the conserved protein motifs in SIYTPs. **a** The phylogenetic tree was constructed based on the full-length sequences of SIYTPs. **b** The motif composition. The motifs, numbered 1-10, are displayed in different colored boxes. The sequence information for each motif is provided in Fig. S5.

Figure S5



Figure S5. Motif sequence information.

Figure S6

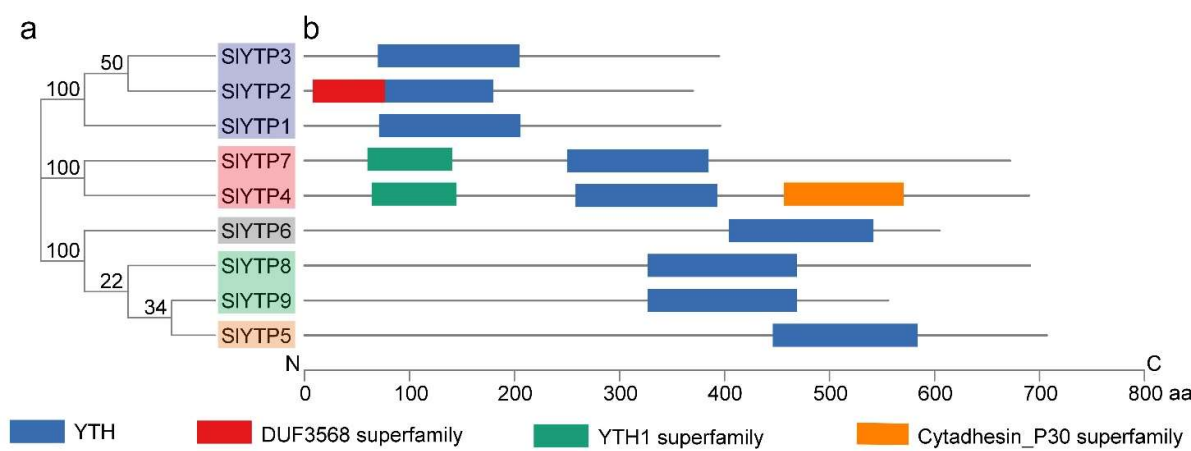


Figure S6. Phylogenetic relationship and conserved protein domains in SIYTPs. **a** The phylogenetic tree was constructed based on the full-length sequences of SIYTP proteins. **b** The YTH domains are shown by blue boxes.

Figure S7

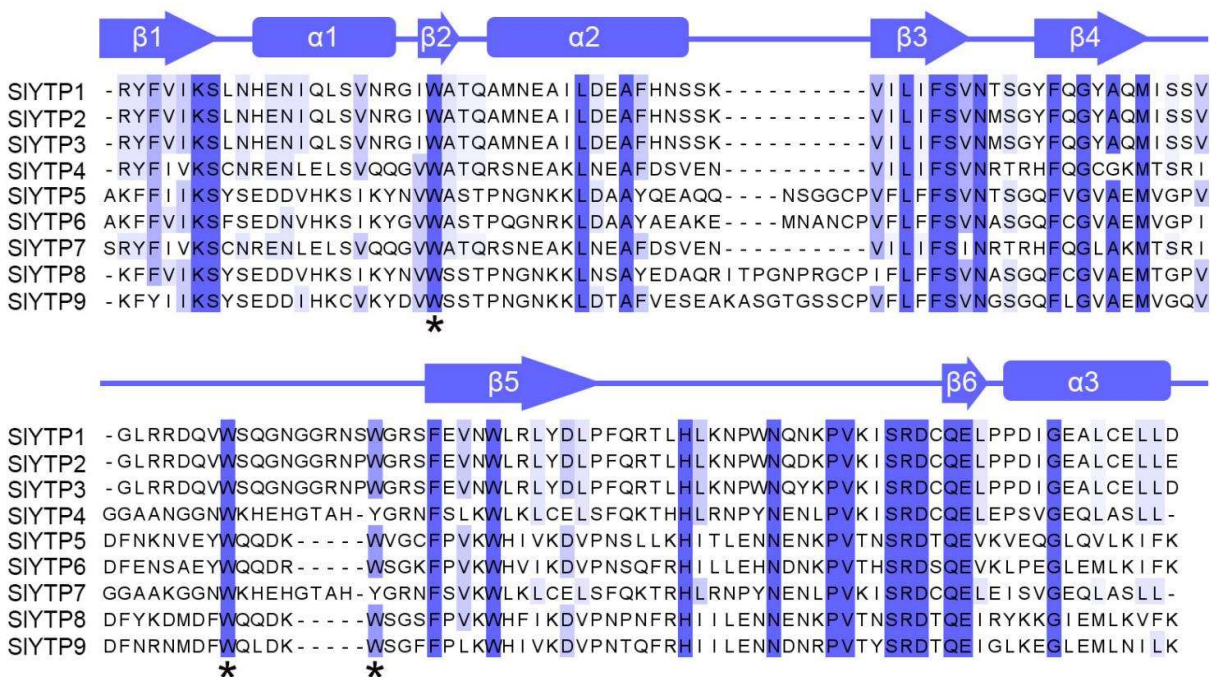


Figure S7. Multiple sequence alignment of the YTH domains of SIYTPs. The alignment was constructed by MUSCLE and visualized by Jalview. Residues in positions conserved more than 50% are shaded. β sheet and α helix are marked. Key residues participating in m^6A binding are marked with *.

Figure S8

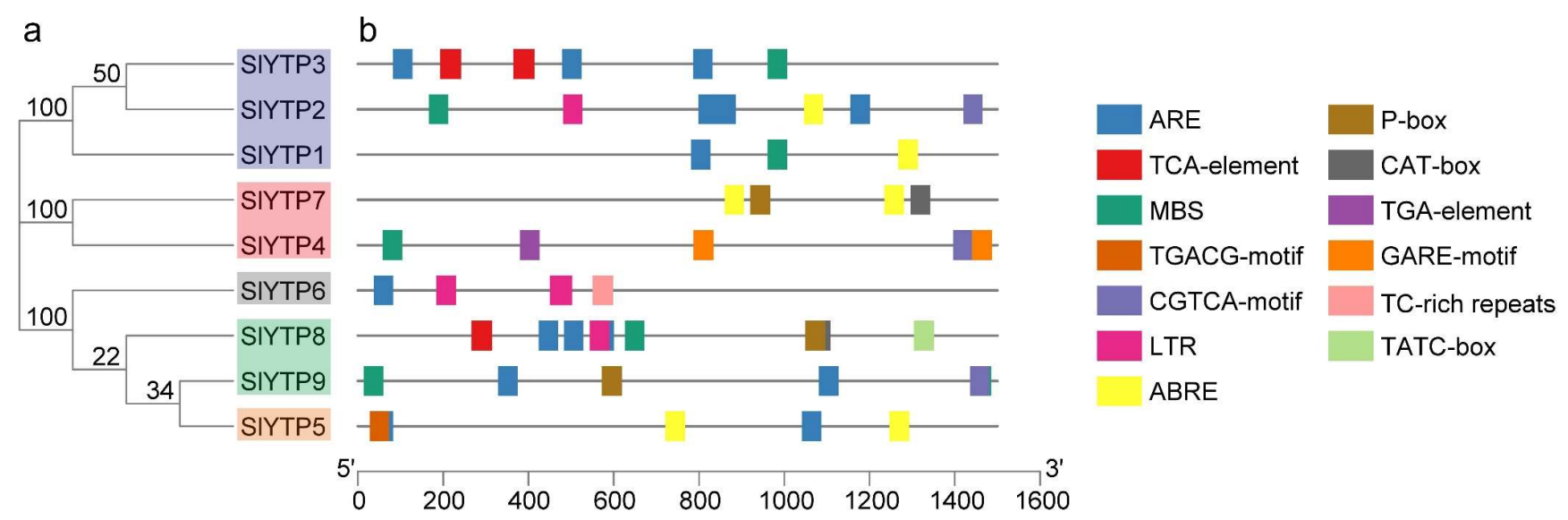


Figure S8. Phylogenetic relationship and prediction of *cis*-acting elements in *SIYTP* promoters. The *cis*-acting elements are displayed in different colored boxes. The number and function information for each *cis*-acting element are provided in Table S4.

Figure S9

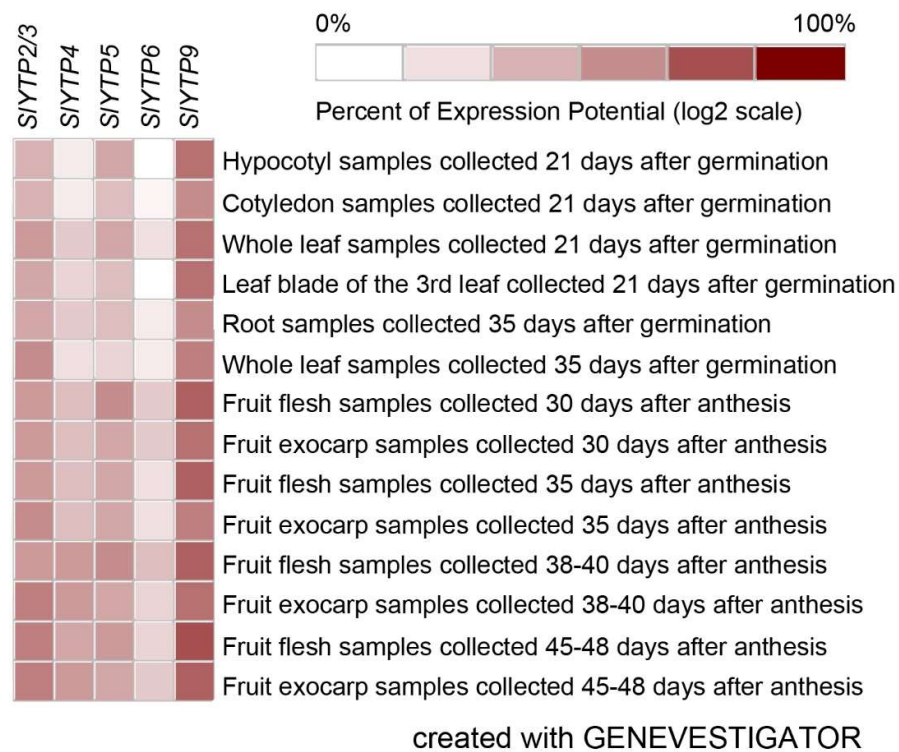


Figure S9. Analyzing expression pattern of *SlYTP2/3/4/5/6/9* in different tissues/organs of Micro-Tom using Genevestigator.

Figure S10

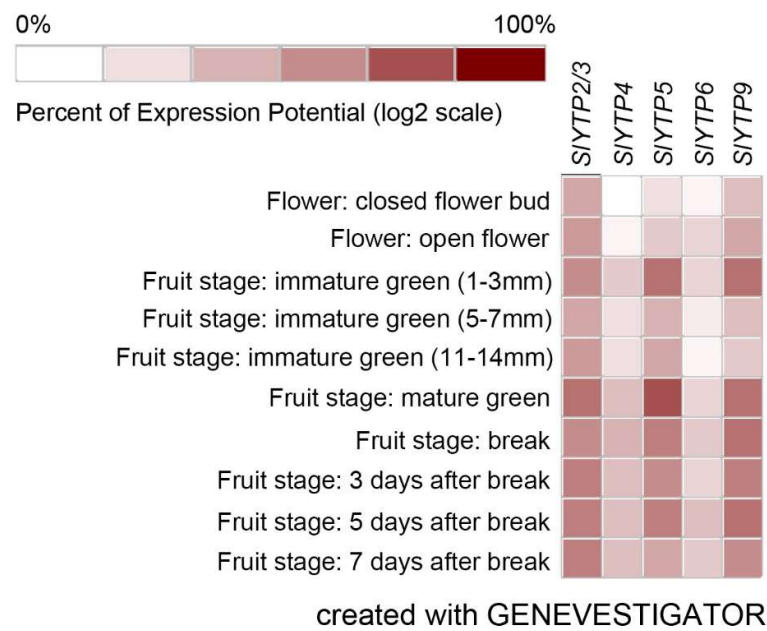


Figure S10. Analyzing expression patterns of *SIYTP2/3/4/5/6/9* in different flower/fruit development stage of Micro-Tom using Genevestigator.

Figure S11

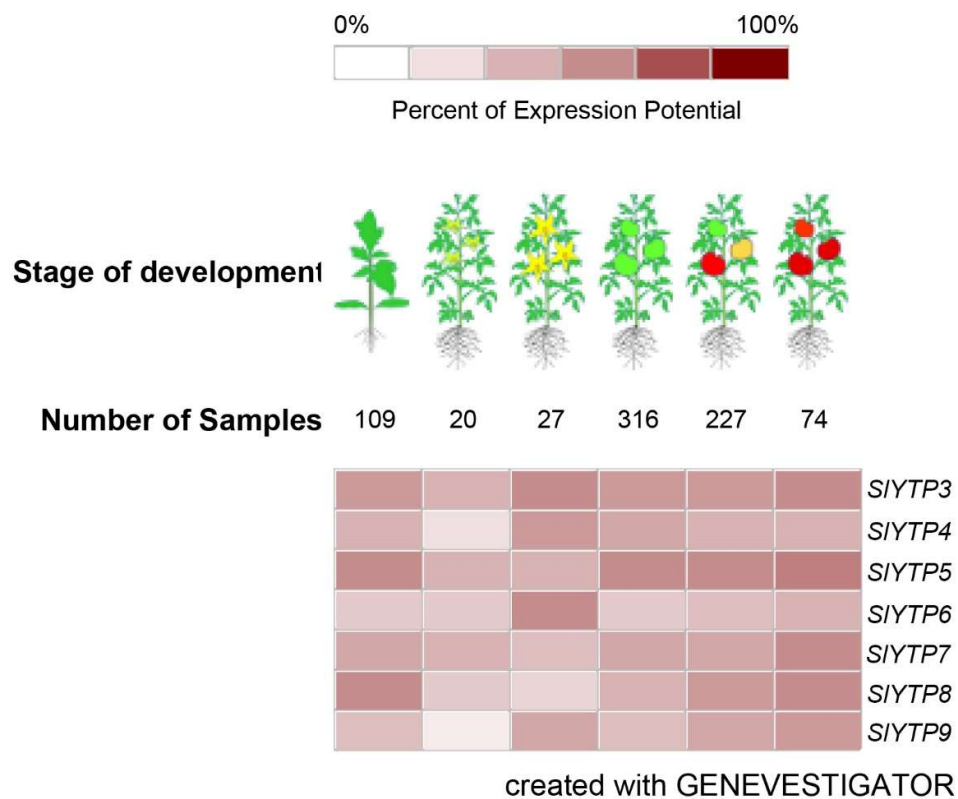


Figure S11. Analyzing expression pattern of *SIYTP2/3/4/5/6/9* in different development stage of tomato using Genevestigator.

Figure S12

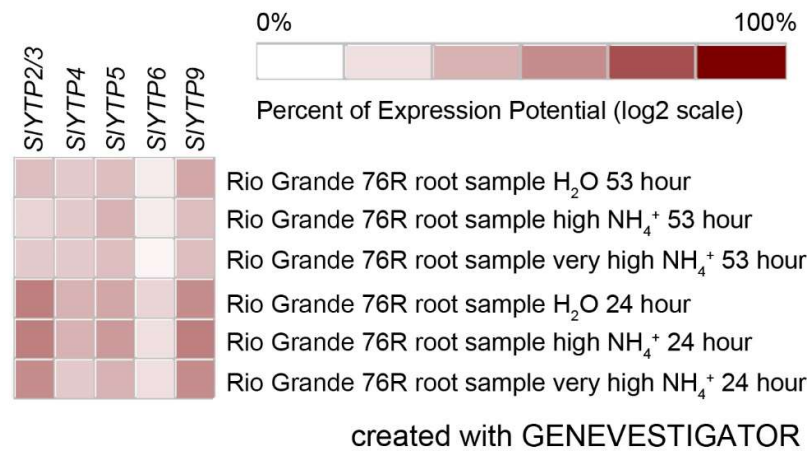


Figure S12. Analyzing expression pattern of *SiYTP2/3/4/5/6/9* under high NH₄⁺ condition in tomato root using Genevestigator.

Figure S13

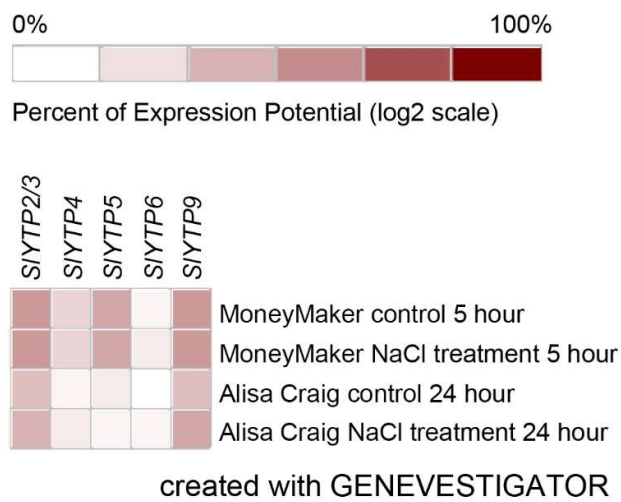


Figure S13. Analyzing expression pattern of *SlYTP2/3/4/5/6/9* under high NaCl condition in tomato using Genevestigator.

Figure S14

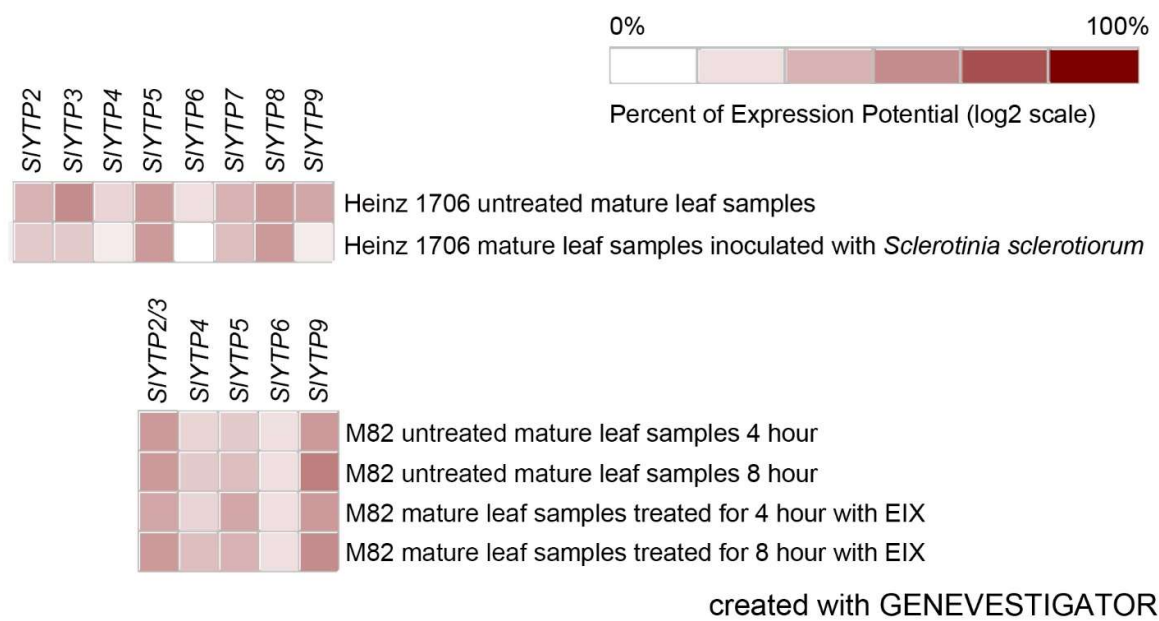


Figure S14. Analyzing expression pattern of *SIYTP2/3/4/5/6/9* after pathogen infection in tomato leaf using Genevestigator.

Figure S15

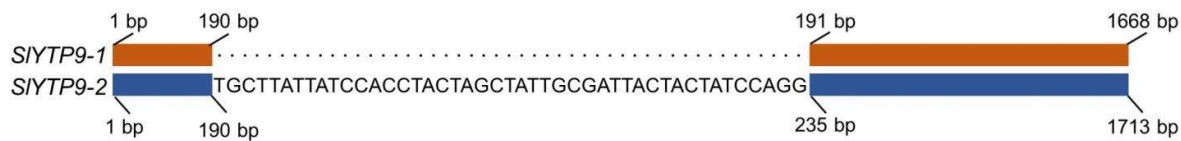


Figure S15 Sequence alignment schematic of *SIYTP9* two transcripts, *SIYTP9-1* and *SIYTP9-2*, which we cloned from Micro-tom tomato leaves. The *SIYTP9-2* transcript has a 45-bp length sequence insertion in the 190-bp location, comparing to the *SIYTP9-1* transcript. The whole coding region of the two transcripts are listed in Table S3.

Figure S16

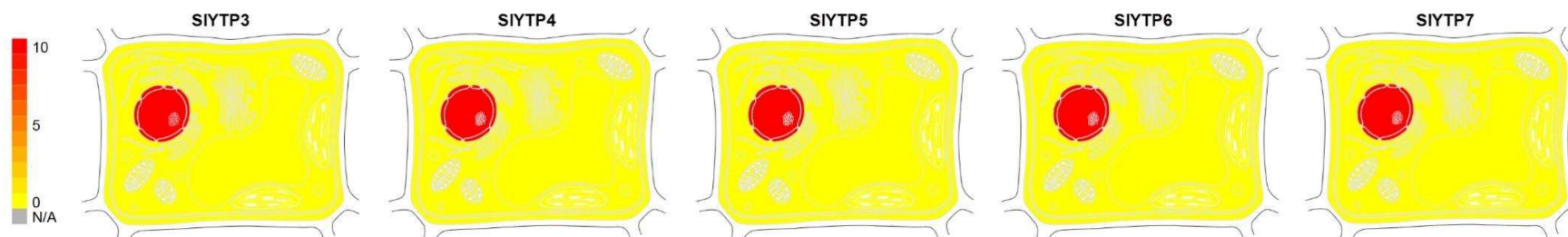


Figure S16. Prediction subcellular localizations of SIYTP3/4/5/6/7.

Figure S17

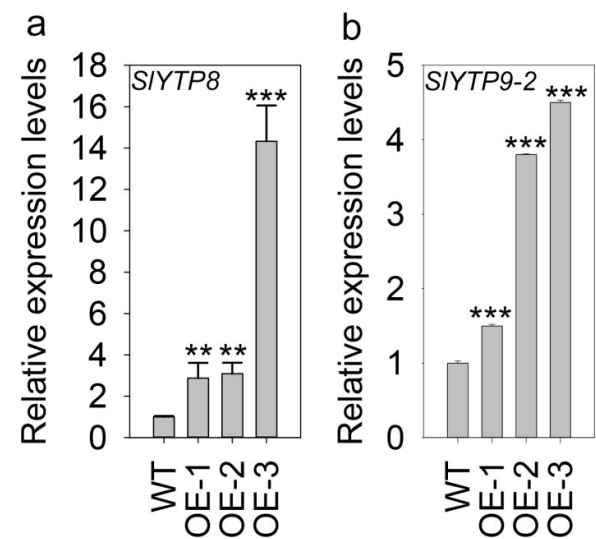


Figure S17. Expression levels of *SIYTP8* and *SIYTP9-2* in WT and OE transgenic tomato plants.

Figure S18

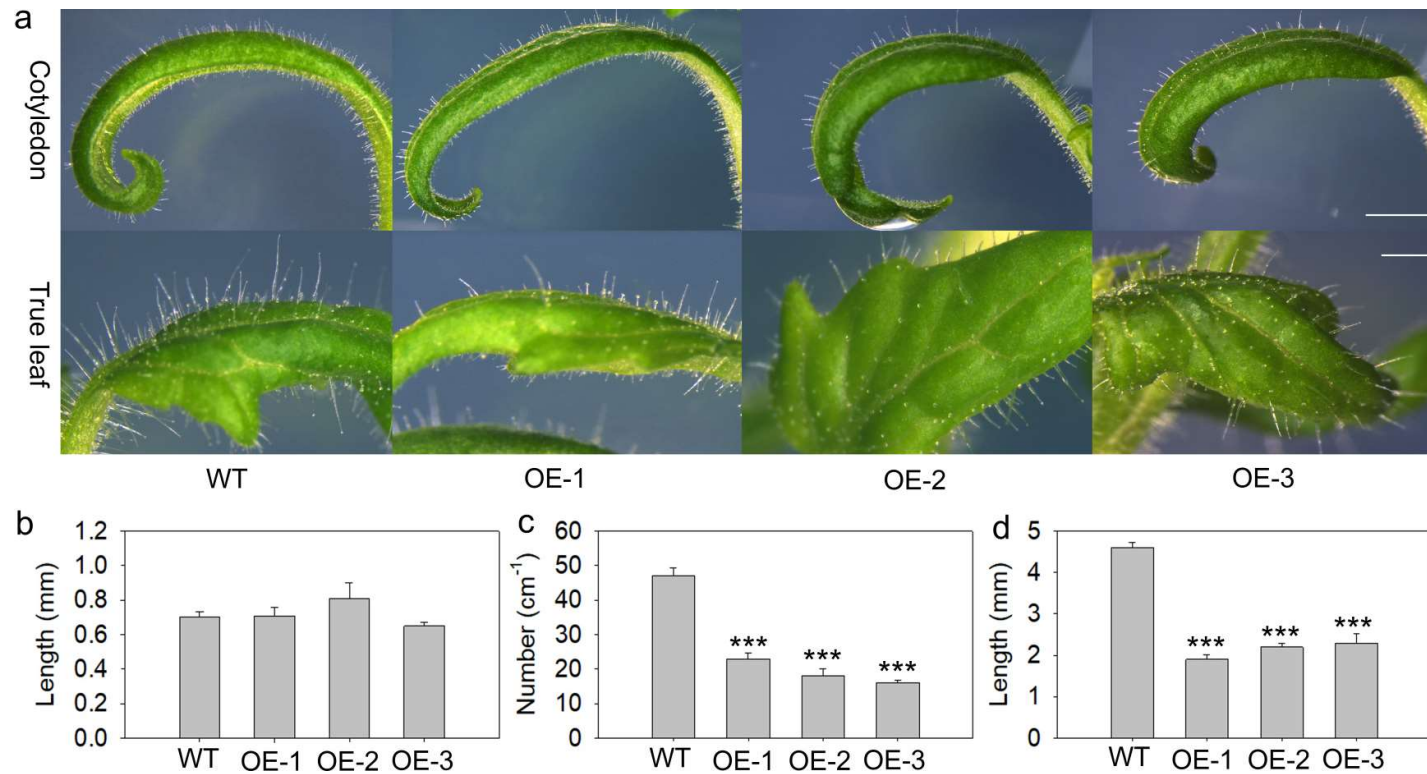


Figure S18. Observation of trichomes in the epidermis of WT and SIYTP8 transgenic tomatoes leaves. **a.** Morphology of trichomes on tomato cotyledons and true leaves, scale length = 5 mm; **b.** Statistical analysis of trichome length in the midsection of cotyledons, showing no significant difference between WT and *SIYTP8* OE plants; **c.** Statistical analysis of the quantity of trichomes in the midsection of cotyledons, indicating a significant reduction in transgenic tomatoes compared to WT; **d.** Statistical analysis of trichome length in the midsection of true leaves in transgenic and WT tomatoes.