

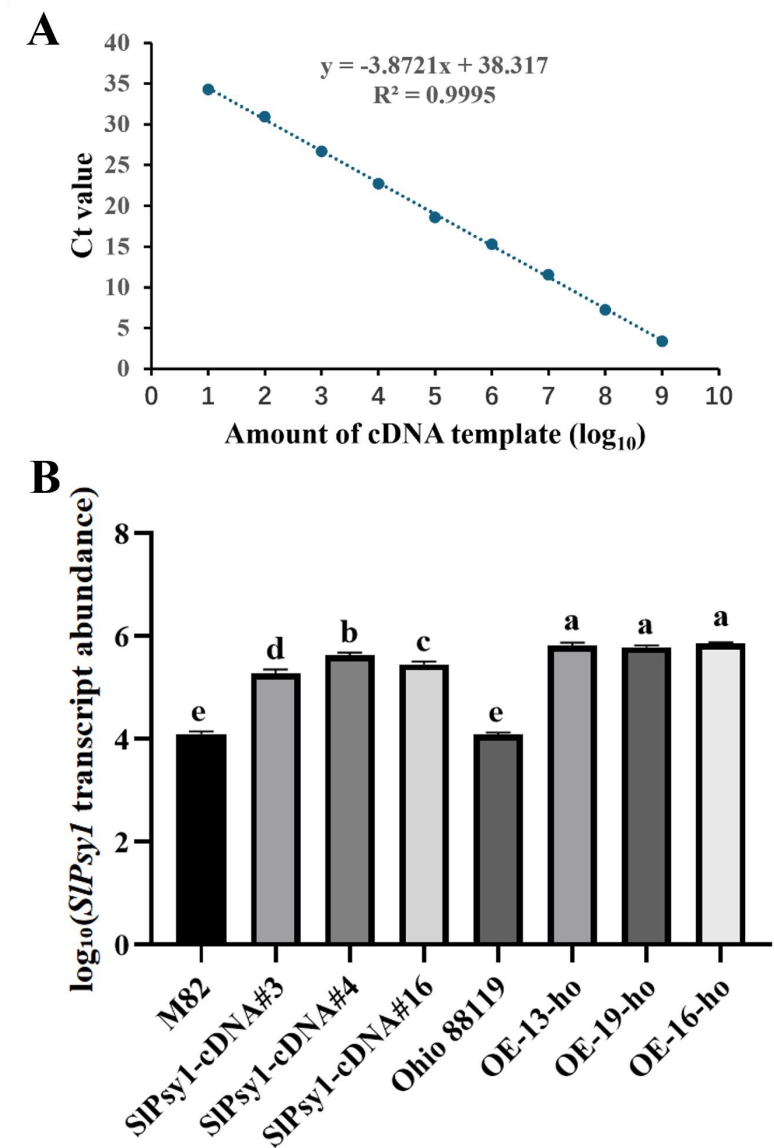


Fig. S4 Abundance of *SIPsy1* transcripts in wild types (M82 and Ohio 88119) and transgenic lines.

A. The standard curve obtained from real-time quantitative PCR amplification of the *SIPsy1* gene. The amount of cDNA template was determined by using NanoDrop2000 Spectrophotometer. B. Transcript abundance of the *SIPsy1* gene in wild types and transgenic lines. SIPsy1-cDNA represents transgenic lines with overexpression of *SIPsy1* cDNA in tomato line M82. OE represents transgenic lines with overexpression of *SIPsy1* gDNA in tomato line Ohio 88119. Means with the same letter indicate no significant difference at 0.05 (Duncan's test).