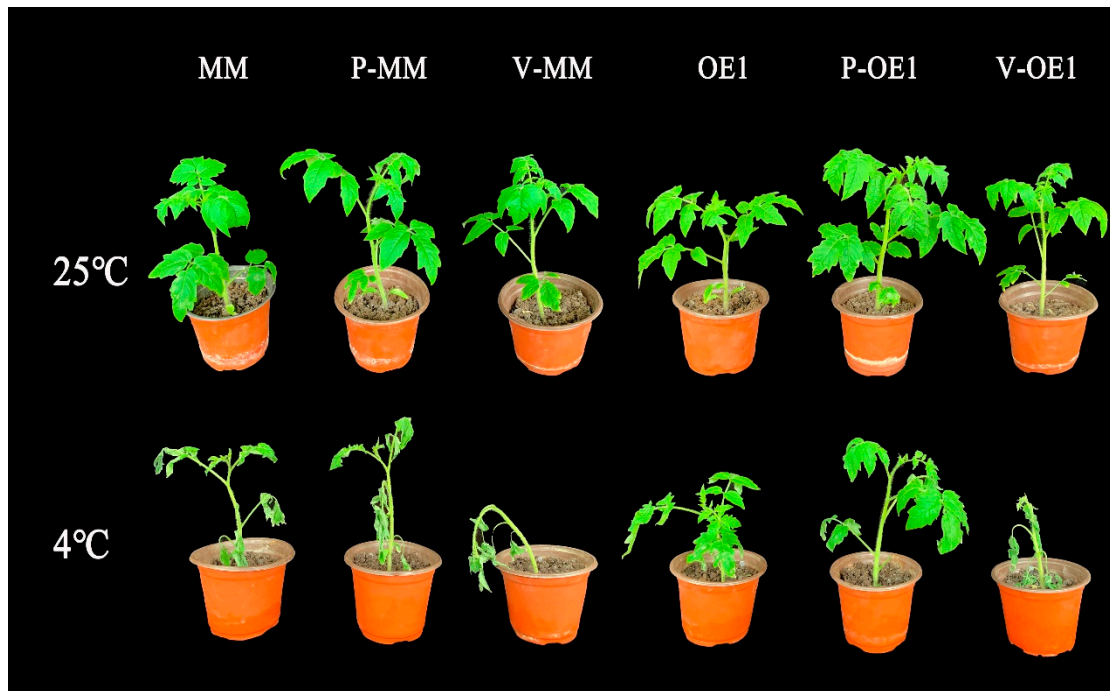
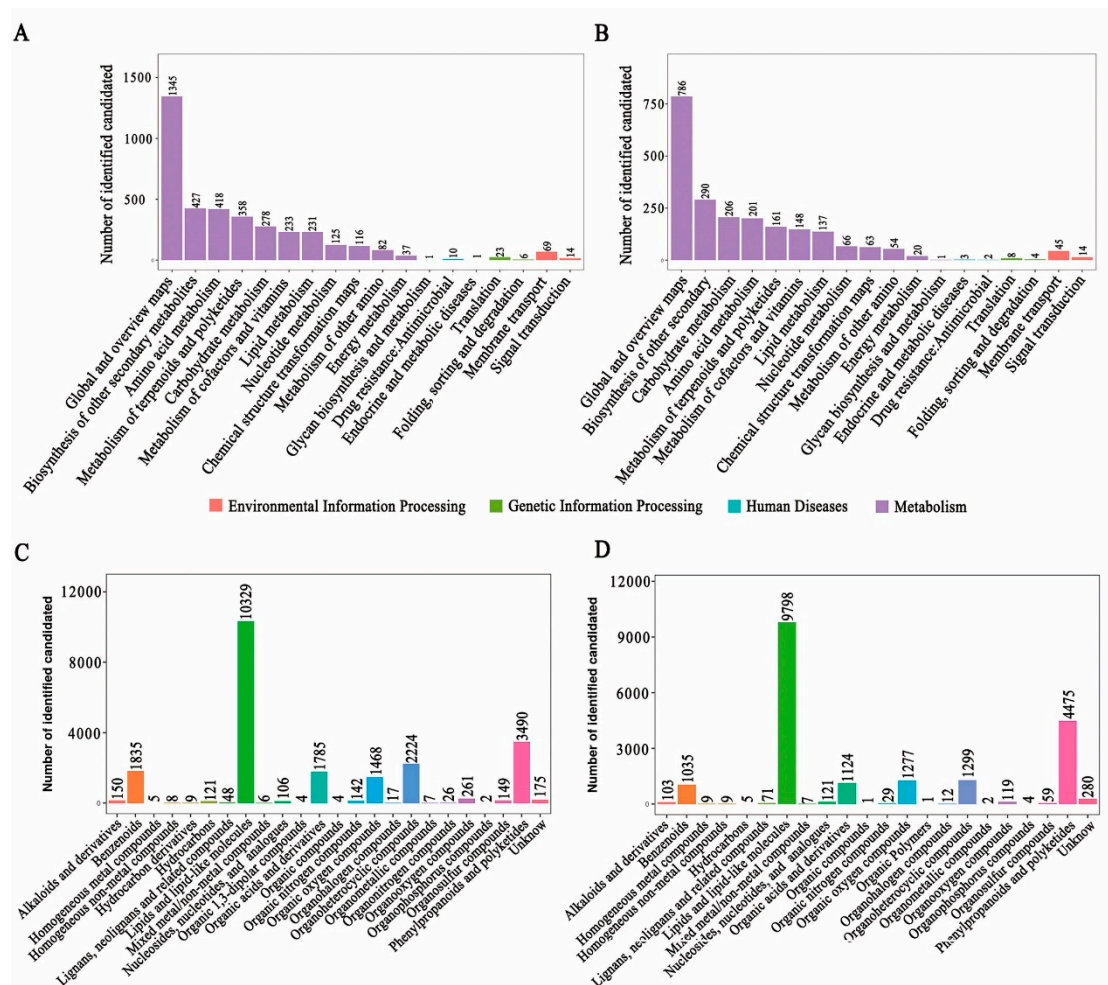


**Figure S1** Verification of RNA-seq results by qRT-PCR (MM-12h vs OE-12h).

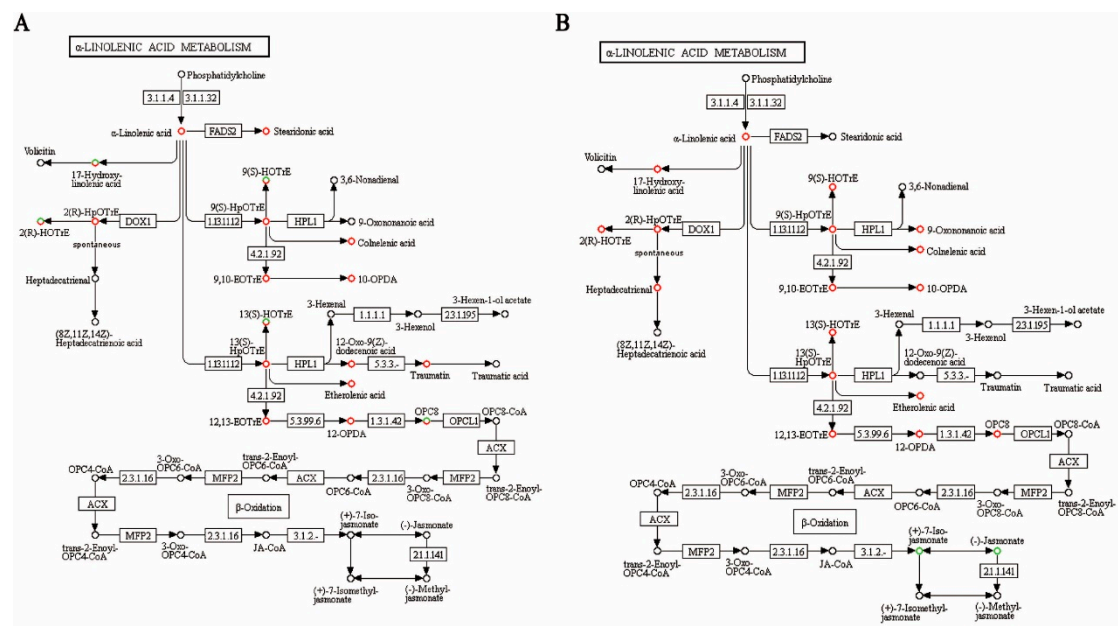


**Figure S2** Phenotypic changes of MM, *SICCX1-like*-silenced MM, OE1, *SICCX1-like*-silenced OE1 seedlings under chilling stress. MM, control plants; P-MM, empty vector control plants; V-MM, *SICCX1-like*-silenced MM plants; OE1, overexpression of *SlHSP17.7* plants; P-OE1, empty vector OE1 plants; V-OE1, *SICCX1-like*-silenced OE1 plants.



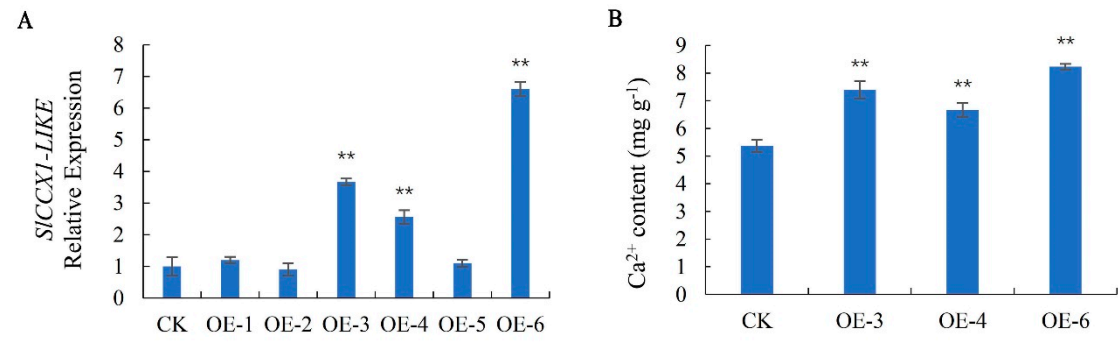
**Figure S3** Metabolite identification. A. MS1-KEGG/pos; B. MS1-KEGG/neg; C. MS1-HMDB/pos; D. MS1-HMDB/neg.





**Figure S5** The differential metabolites in alpha-linolenic acid metabolism before (A) and after chilling stress for 12 h (B). The red circle indicates the up-regulated expression of this metabolite in OE1 plants.





**Figure S7** Overexpression of *SlCCX1-like* in Micro-Tom (CK) increased calcium concentration of the leaves. (A) The expression of *SlCCX1-like* in *SlCCX1-like* OE lines. (B) The content of Ca<sup>2+</sup> in *SlCCX1-like* OE plants.