

Abbreviations:

ABA, abscisic acid; BP, biological process; BR, brassinosteroid; Ca²⁺, calcium; CC, cellular component; CHI, chalcone isomerase; CHS, chalcone synthase; CI, Chilling damage index; CI, chilling damage index; CTR1, constitutive tripleresponse 1; DEGs, differentially expressed genes; EBF1_2, EIN3-binding F-Box 1_2; EIN2 CEND, carboxyl end of EIN2 protein; EIN2, ethylene-insensitive protein 2; Ein3, ethylene-insensitive protein 3; ERF1, ethylene-responsive factor1; ETH, ethylene; ETR, ethylene receptor; F3H, 3-hydroxylase; Fv/Fm, maximum photochemical efficiency; GA, gibberellin; GA3oX, gibberellin 3 beta-dioxygenase; GO, Gene Ontology; GSH, glutathione; GSTs, glutathione S-transferases; H₂S, hydrogen sulfide; IAA, auxin; JA, jasmonic acid; KEGG, Kyoto Encyclopedia of Genes and Genomes; LHCA, light-harvesting complex I chlorophyll a/b binding protein, LHCB, light-harvesting complex II chlorophyll a/b binding protein; LT, low temperature; MCM, DNA replication licensing factor; MDA, malondialdehyde; MF, molecular function; NO, nitric oxide; NPR1, regulatory protein; PAL, phenylalanine ammonia-lyase; PCA, principal component analysis; PPFD, photosynthetic photon flux density; qRT-PCR, quantitative real-time PCR; RNA-Seq, RNA sequencing; ROS, oxygen species; SA, salicylic acid; SA, salicylic acid; TBARS, thiobarbituric acid reactive substances; t-CA, trans-cinnamic acid; TFs, transcription factors.

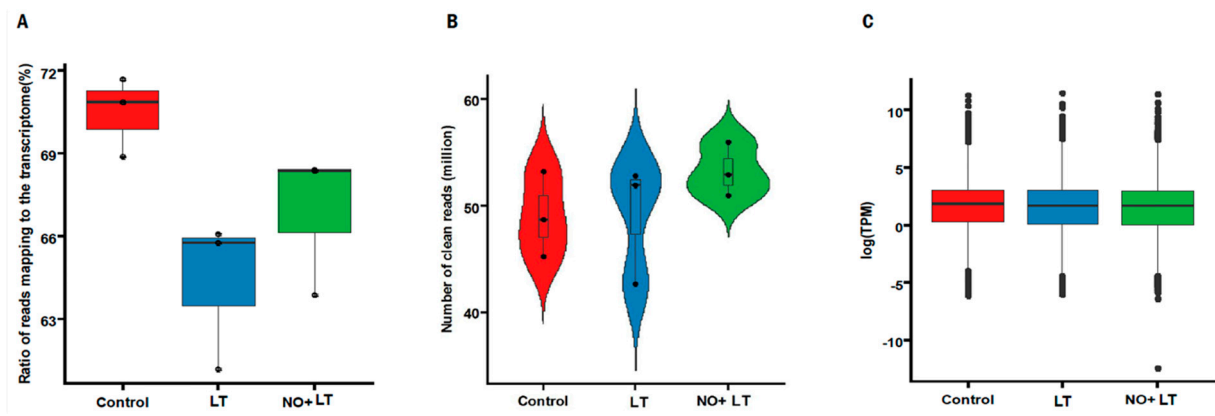


Figure S1. A, the ratio of reads mapping to the transcriptome of each treatment in cucumber plants; B, number of clean reads of each treatment in cucumber plants; and C, Log(TPM) of each treatment in cucumber plants.

Table S1. The primer sequences for qRT-PCR

| Gene ID | Forward primer | Reverse primer |
|--------------------------------------|-----------------------------|-----------------------------|
| <i>Actin</i> (CsaV3_6G041900.1) | 5'-ATGTGCCTGCTATGTATGTTG-3' | 5'-GCTCCGATGGTGATGACTT-3' |
| <i>WRKY</i> (CsaV3_2G013650.1) | 5'-TTGAGTATGGATGGCAGCGT-3' | 5'-GCTCCCTTCTTCTCCTCTAGC-3' |
| <i>MYB</i> (CsaV3_7G004040.1) | 5'-ACAAAATTACCCGGACGAACC-3' | 5'-CTCCTCCTCATGCTTCTTTGC-3' |
| <i>HD-ZIP</i> (CsaV3_6G045240.1) | 5'-TCAGTCGATGTTGGATGGCT-3' | 5'-TTTCTCTCCGGTTCGAGCTT-3' |
| <i>b-ZIP</i> (CsaV3_3G037220.1) | 5'-GGATGAGGTTTGGTCCGAGA-3' | 5'-GTGTGGCAGATTCCGGATTC-3' |
| <i>Peroxidase</i> (CsaV3_5G005000.1) | 5'-TTCTCCAAAGCACTGCCCTA-3' | 5'-ACAATGGAGGGTAGGTTGGG-3' |
| <i>MCM5</i> (CsaV3_2G003500.1) | 5'-GTCAAGGACCAAGGCAAAGG-3' | 5'-TGGTTCTTCTCCAGGCTGAG-3' |
| <i>MCM6</i> (CsaV3_6G053180.1) | 5'-ACATCAGGGATCAGGTTGCA-3' | 5'-TAGTGTGGCCTGTATTCCGG-3' |
| <i>PAL</i> (CsaV3_6G039690.1) | 5'-GGCAGCAATTATGGAGCACA-3' | 5'-AGGCTTTTGGAGGGGATCAA-3' |
| <i>NPR1</i> (CsaV3_3G040450.1) | 5'-ATCTTGGCGGCTAGGAGTTT-3' | 5'-TACTACTCCCTGTCGACGGA-3' |
| <i>LHCA1</i> (CsaV3_5G025740.1) | 5'-GGAGAAGTGCCAGAGAACCT-3' | 5'-GCTTTAACCCAGTTGCCCAA-3' |
| <i>LHCB1</i> (CsaV3_6G051520.1) | 5'-GTTTGGTGAAGCTGTGTGGT-3' | 5'-CCCATCAACACAACCTGGCA-3' |
| <i>GA3ox</i> (CsaV3_7G032870.1) | 5'-CATAAACTCAAGGCCGCTCG-3' | 5'-ATGAGGCCAGAGTTTTCGGA-3' |
| <i>PR1</i> (CsaV3_7G007620.1) | 5'-GGACCTGTCAGTTGGGATGA-3' | 5'-CCCATATGGCCCGTTAGAGT-3' |
| <i>ERF1</i> (CsaV3_3G012170.1) | 5'-CCTAATCTCCGAGGGCACAT-3' | 5'-GGCGGCGAACTCCTCTATAA-3' |

Table S2. Data description of RNA-Seq reads for the three cucumber samples with three replicates

| samples | Total reads (M) | Total bases (G) | Mapping ratio | Clean total reads (M) | Clean total bases (G) | Q30 bases |
|-----------|-----------------|-----------------|---------------|-----------------------|-----------------------|-----------|
| Control 1 | 48.72 | 7.31 | 71.67 | 48.56 | 7.25 | 0.93 |
| Control 2 | 45.28 | 6.79 | 70.85 | 45.14 | 6.75 | 0.93 |
| Control 3 | 53.18 | 7.89 | 68.88 | 53 | 7.92 | 0.93 |
| LT1 | 42.68 | 6.4 | 61.18 | 42.51 | 6.36 | 0.93 |
| LT2 | 52.75 | 7.91 | 65.75 | 52.59 | 7.86 | 0.93 |
| LT3 | 51.94 | 7.79 | 66.06 | 51.74 | 7.73 | 0.93 |
| NO + LT 1 | 51.02 | 7.65 | 63.85 | 50.84 | 7.6 | 0.93 |
| NO + LT 2 | 55.94 | 8.39 | 68.41 | 55.74 | 8.34 | 0.93 |
| NO + LT 3 | 52.85 | 7.93 | 68.35 | 52.72 | 7.88 | 0.94 |