

Figure S1. The effect of different alleles on the content of p-coumaric acid (SIFM0124).

Boxplot (the middle lines indicate the median, the boxes show the range of the 5-95% of the total data, the whiskers indicate the interquartile range, and the outer dots are outliers) for p-coumaric acid (SIFM0124) content, plotted as a function of genotypes at SNP sf0250353631 (a) and sf0250353789 (b).

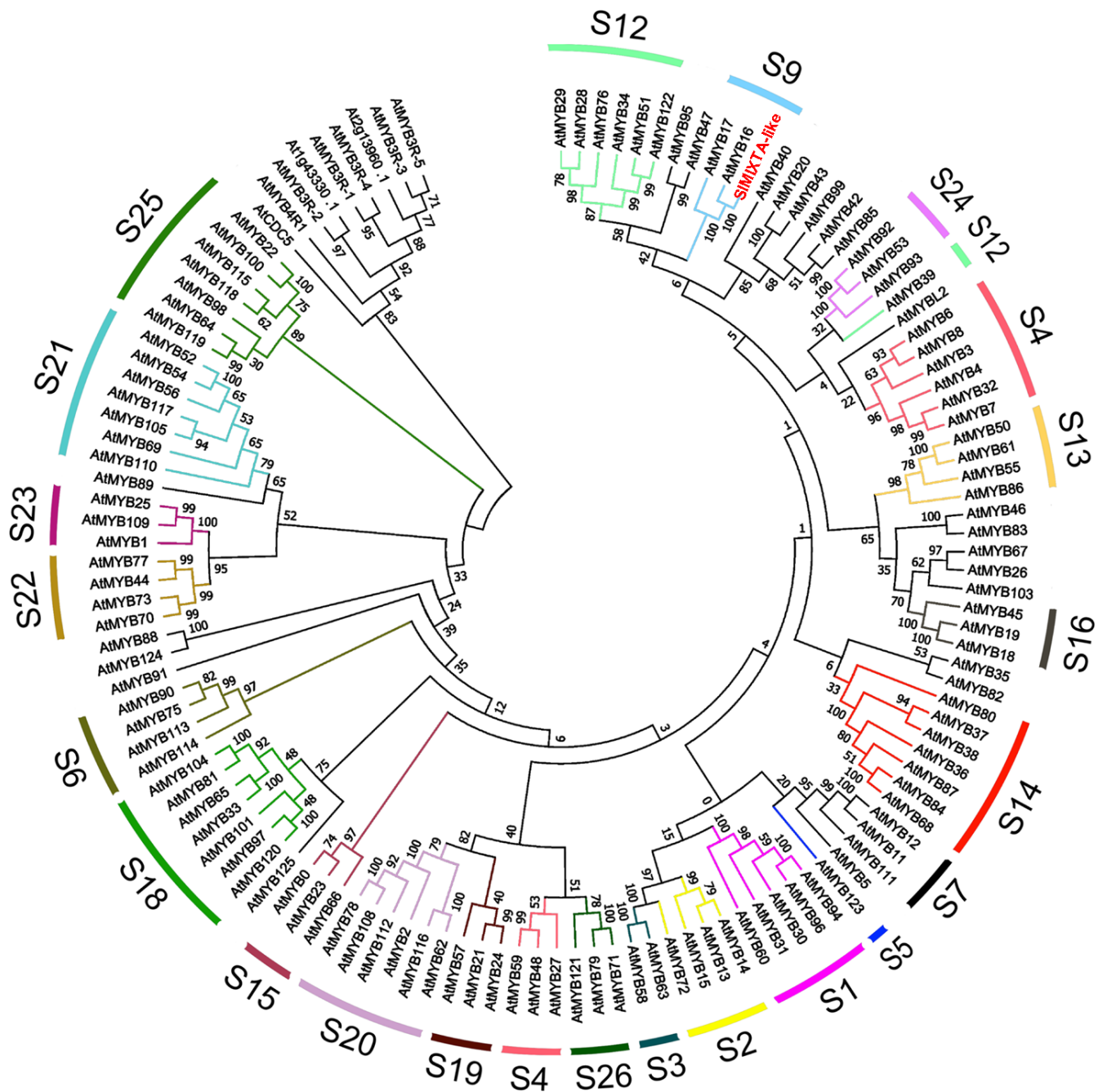


Figure S2. Phylogenetic tree of SIMIXTA-like protein and R2R3-MYB protein family from *Arabidopsis thaliana*. All the R2R3-MYB protein were download from the IT3F database (<http://jicbio.bbsrc.ac.uk/IT3F/>). Protein sequences were aligned using MEGA7.0 and evolutionary relationships were determined using Neighbor-Joining analysis with 1000 bootstrap replicates.

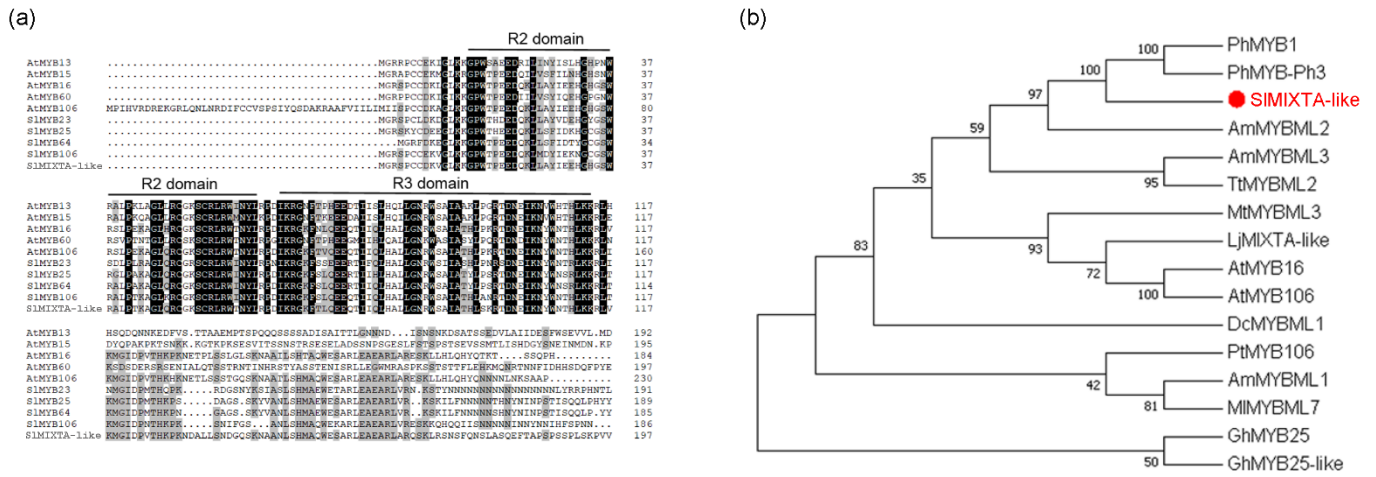


Figure S3. Molecular characterization of SIMIXTA-like. (a) Protein sequence alignment of partial *Arabidopsis thaliana* R2R3 MYB transcription factors and tomatoes. The R2R3 repeats of the DNA binding domain are annotated. (b) Phylogenetic tree of the MIXTA/MIXTA-like protein in different plants. The following protein sequences were used for the analysis: PhMYB1 (CAA78386.1), AtMYB16 (AT5G15310), AtMYB106 (AT3G01140), PhMYB-Ph3(CAA78386.1), AmMYBML2 (AAV70655.1), LjMIXTA-like (AEO27486.1), MtMYBML3 (XM_003621222.2), GhMYB25-like (ADZ55318.1), AmMYBML3 (AAU13905.1), TtMYBML2 (ACN69972.1), MIMYBML7 (AGO03571.1), PtMYB106 (XP_002311313.2), AmMYBML1 (CAB43399.1), GhMYB25 (AAK19616.1), MIMYBML7 (AGO03571.1).

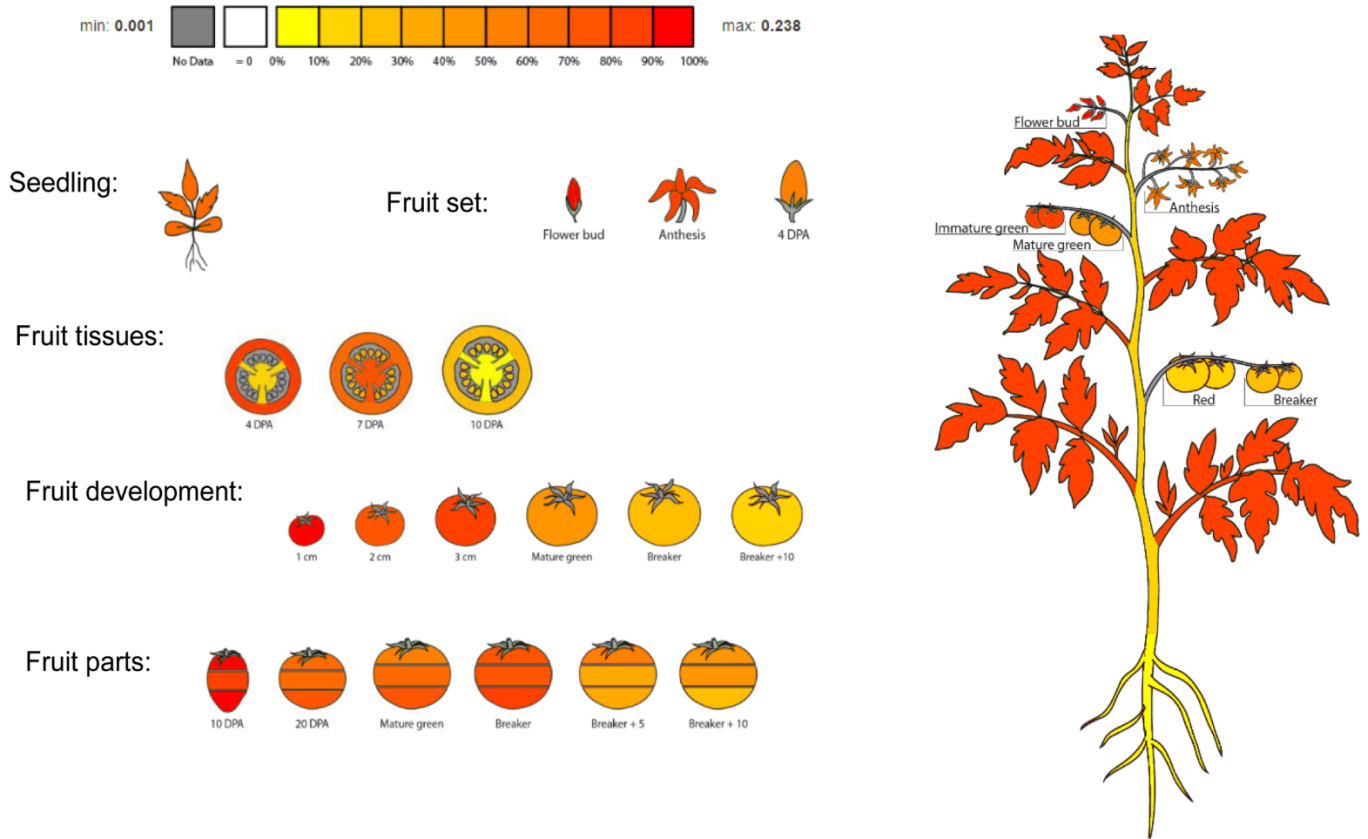


Figure S4. *SIMIXTA-like* expression pattern in tomato. Data was generated in TomExpress website (http://gbf.toulouse.inra.fr/tomexpress/www/welcome_TomExpress.php)

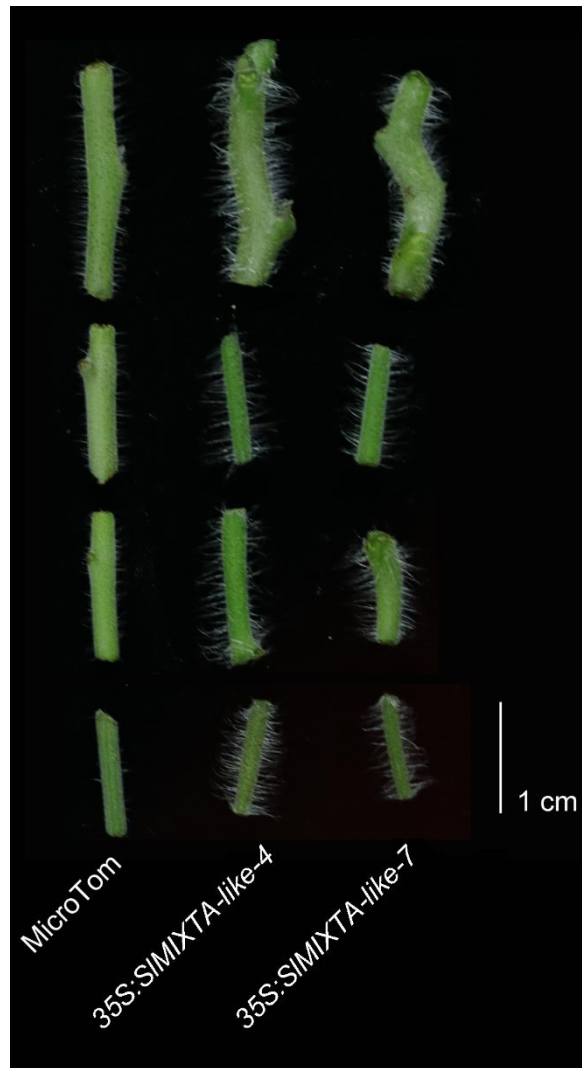


Figure S5. Overexpression of *SIMIXTA-like* in tomato seedlings enhances trichome formation on stems. Both MicroTom and *35S:SIMIXTA-like* stems were visual inspected when first flower opened. Stems on the same row were harvest at comparable part of the seedlings.

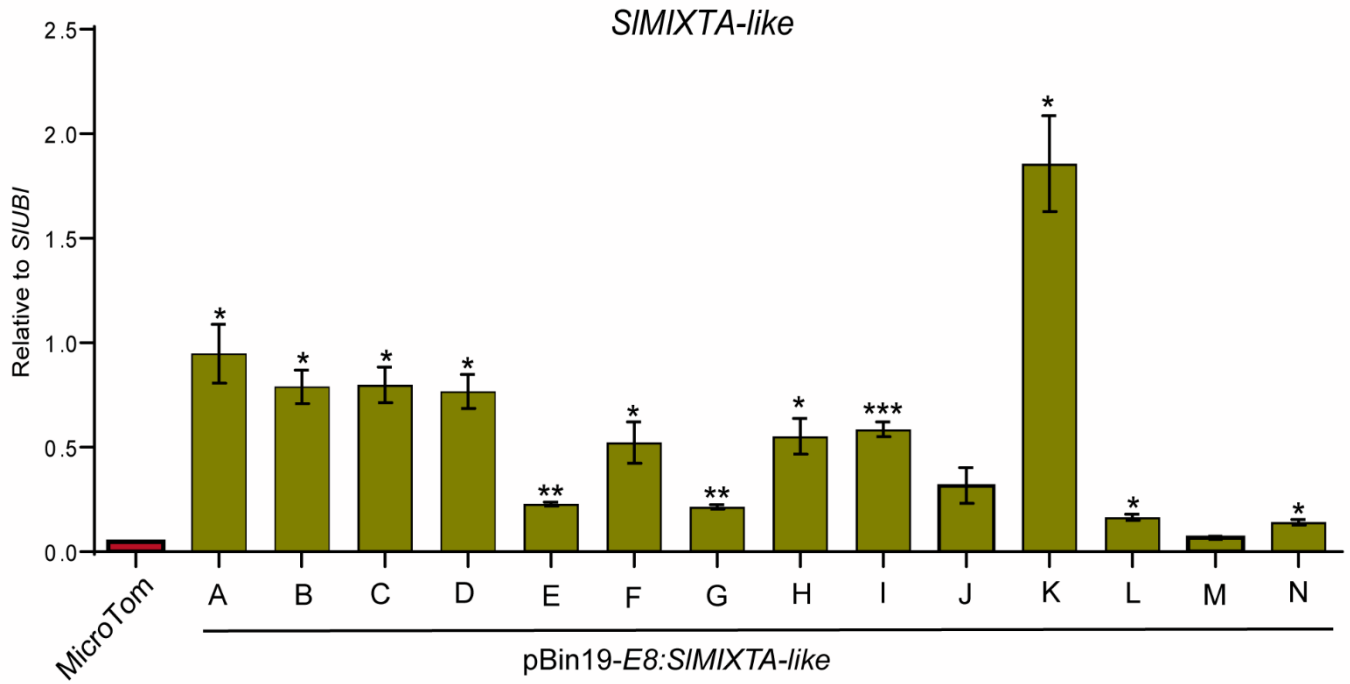


Figure S6. Initial screening of *SIMIXTA-like* expression in T0 pBin19-E8:*SIMIXTA-like* tomato fruits. *SIMIXTA-like* expression in line A to N of T0 transgenic and MicroTom tomato fruits were measured by RT-qPCR. Error bars represent the S.E.M of triplicates (three independent fruit at breaker + 3days). *, $p < 0.05$. **, $p < 0.01$. ***, $p < 0.001$ (Student's t-test). Line K fails to produce any seeds.

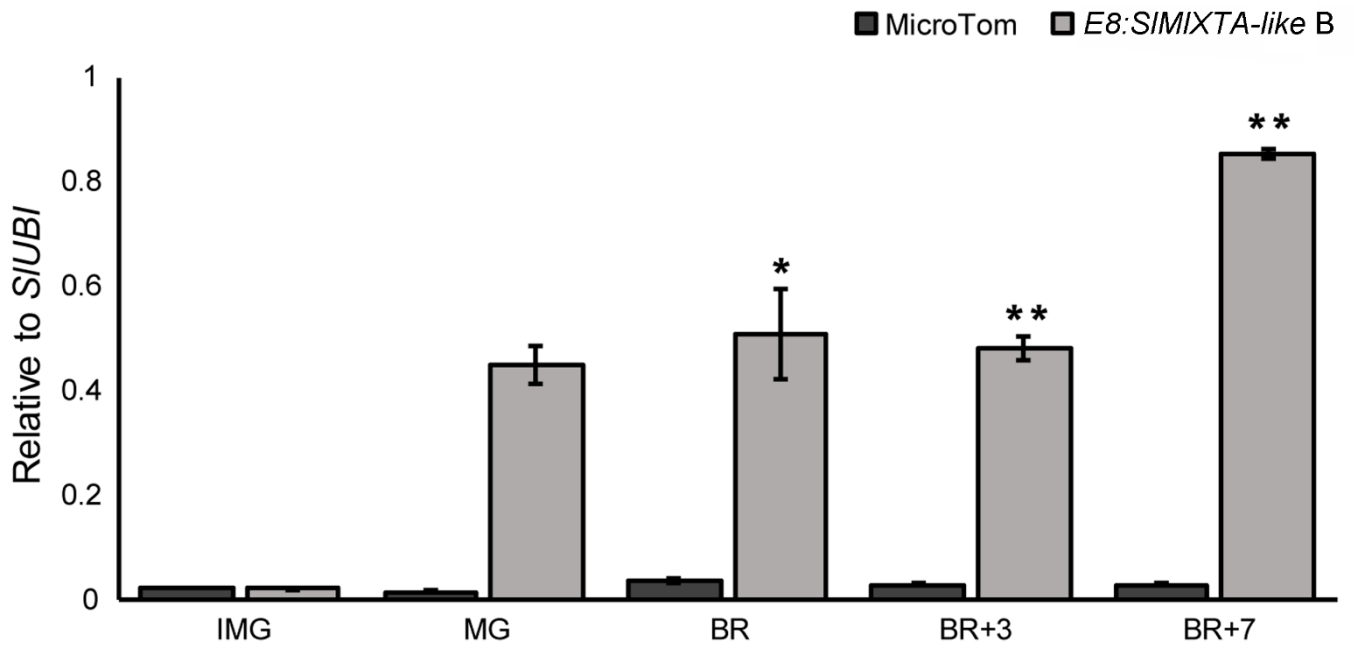


Figure S7. The expression of *SIMIXTA-like* at different fruit development stages for both MicroTom and pBin19-E8:*SIMIXTA-like* B fruit. Data were represented as mean \pm S.E.M (n=3). *, p<0.05 (Student's t-test).

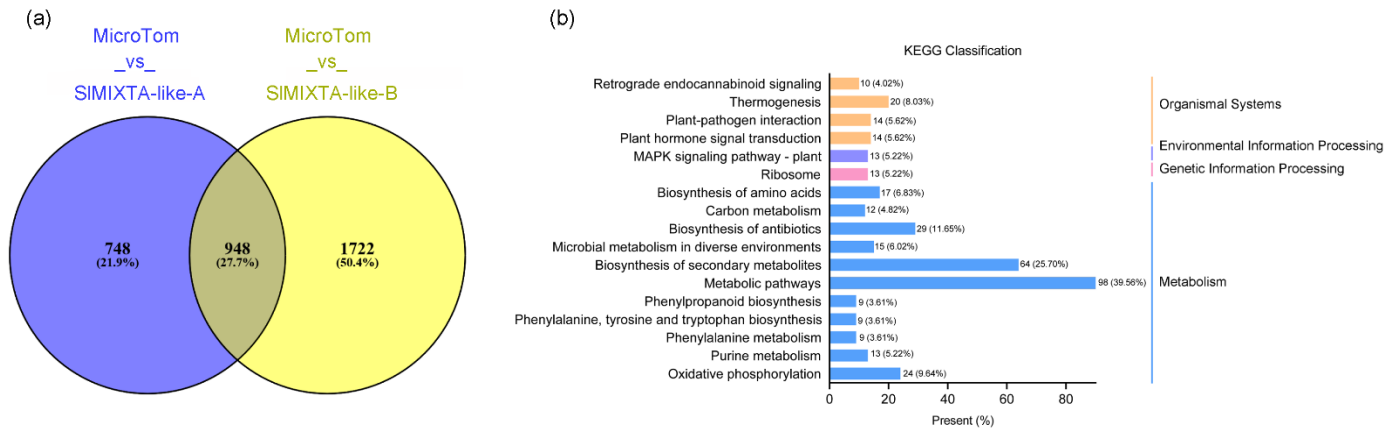


Figure S8. Transcriptome data for *E8:SIMIXTA-like* tomato fruit. (a) The venn map of differently expressed genes in *E8:SIMIXTA-like* line A and B using the Venny 2.1. The number represent the DEGs. (b) The KEGG classification of common DEGs in line A and B.

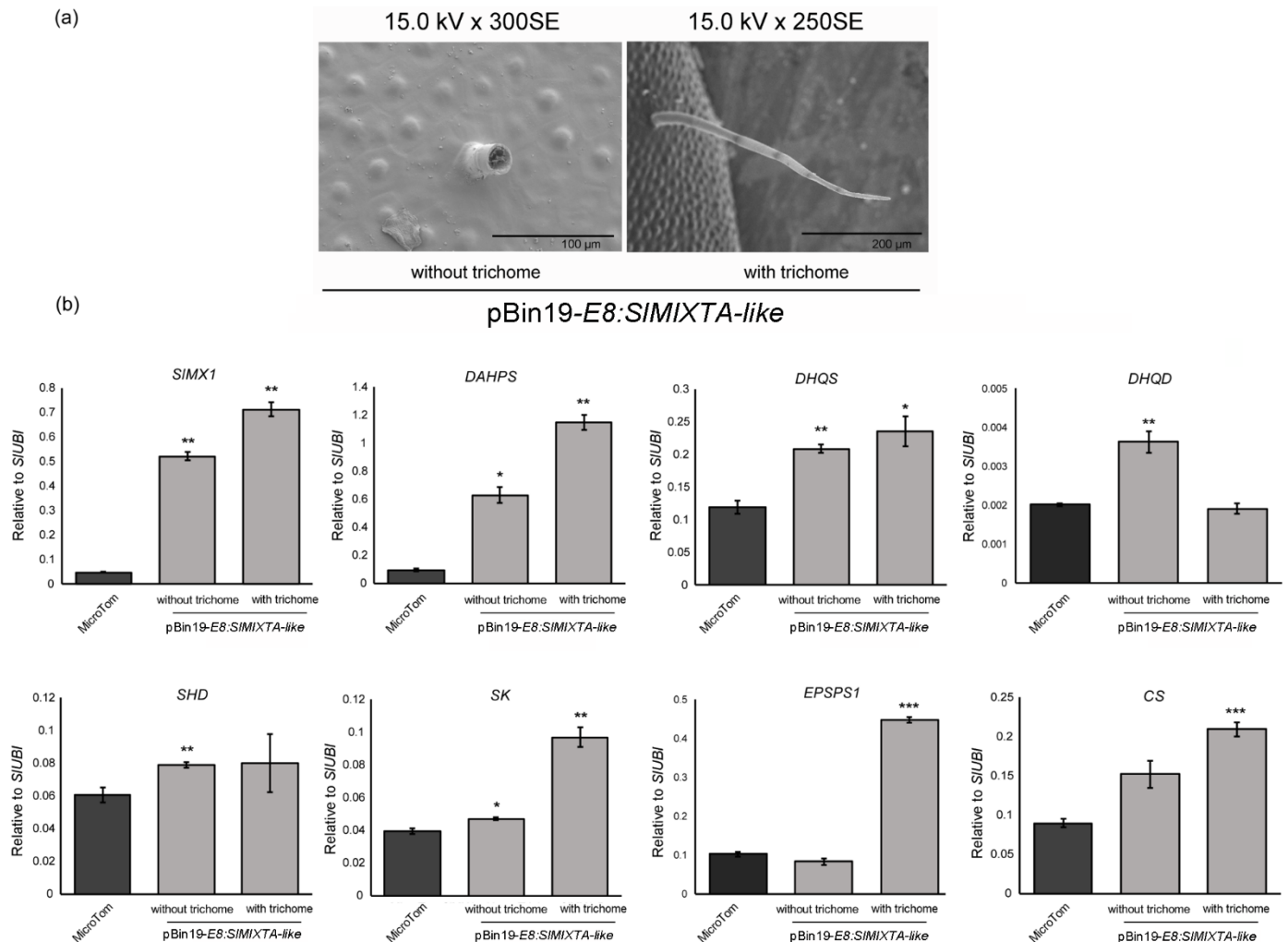


Figure S9. *SIMIXTA-like* changes the expression of primary metabolic genes in the pericarp of *E8:SIMIXTA-like* fruit. (a) SEM of *E8:SIMIXTA-like* B fruit surface after (left) and before (right) removing trichomes. Samples were treated and scanned at 3dpb. (b) Expression of *SIMIXTA-like* and key shikimate pathway genes in the fruit of MicroTom and *E8:SIMIXTA-like* B fruit with(out) trichomes. Samples were harvested at 3dpb. Data were represented as mean \pm S.E.M (n=3). *, p<0.05 (Student's t-test).

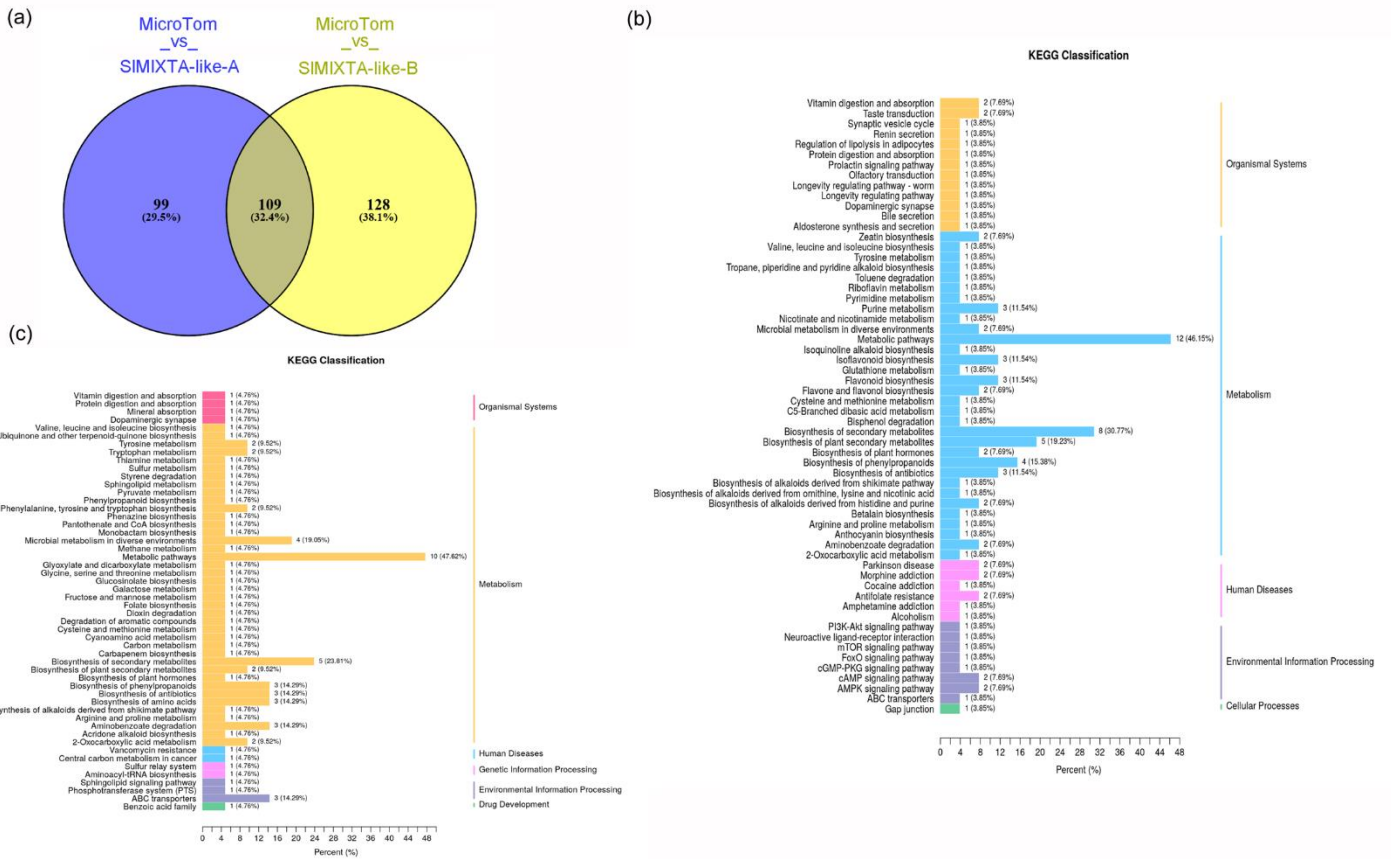


Figure S10. Metabolic profiling for *E8:SIMIXTA-like* tomato fruit (a) The venn map of differently accumulated metabolites *E8:SIMIXTA-like* line A and B using the Venny 2.1. The number represent the difference compounds. (b) The KEGG classification bar graph for metabolites up-regulated in both line A and B. (c) The KEGG classification for metabolites down-regulated in both line A and B.

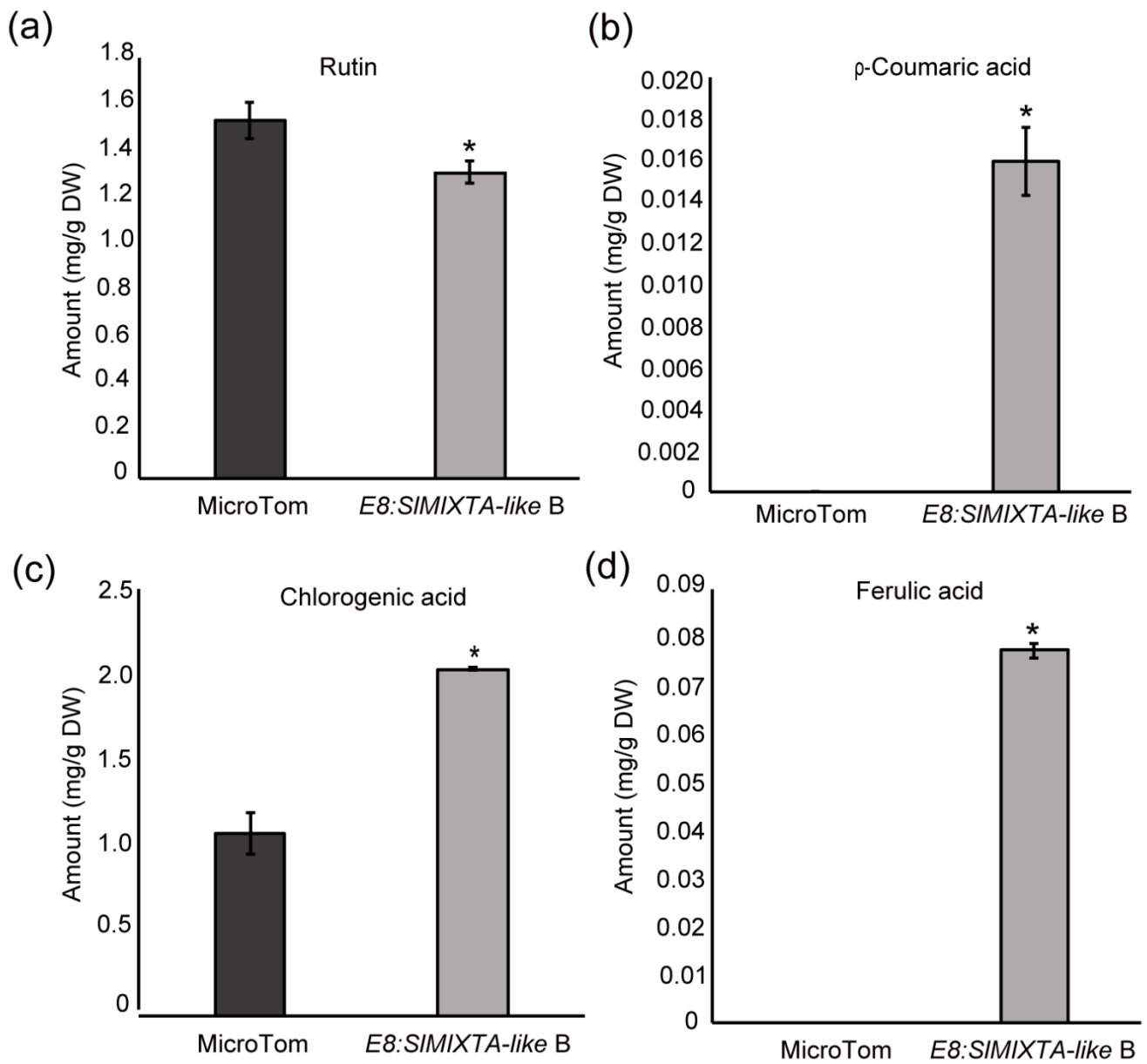


Figure S11. The contents of rutin (a), ρ -coumaric acid (b), chlorogenic acid (c) and ferulic acid (d) in *E8:SIMIXTA-like B* and MicroTom. Data were represented as mean \pm S.E.M (n=3). *, p<0.05 (Student's t-test).

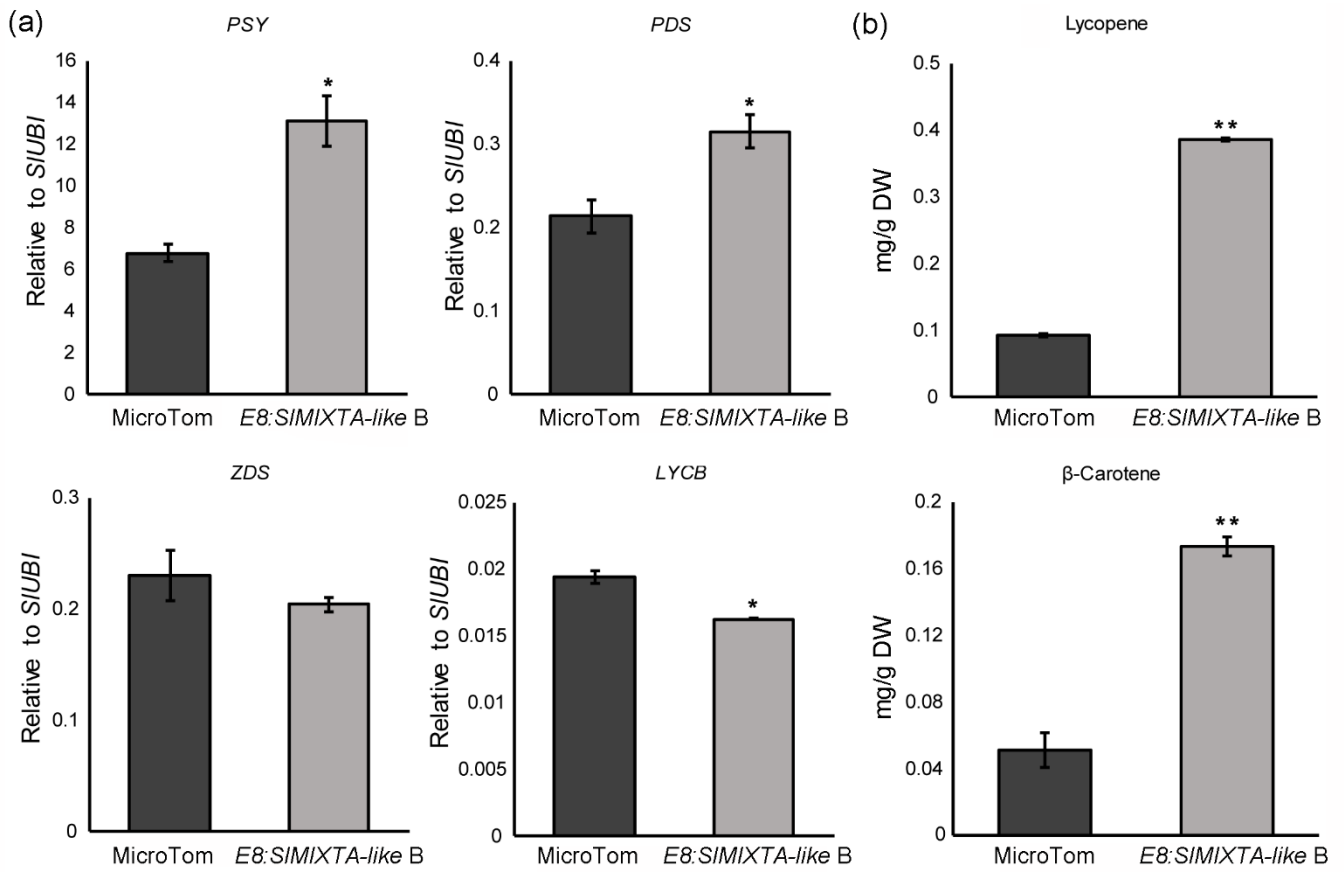


Figure S12. Expression of carotenoid pathway genes (a) and carotenoid contents (b) in *E8:SIMIXTA-like B* and *MicroTom* fruit. Samples were harvested at 7dpb. Data were represented as mean \pm S.E.M (n=3). *, $p < 0.05$ (Student's t-test).

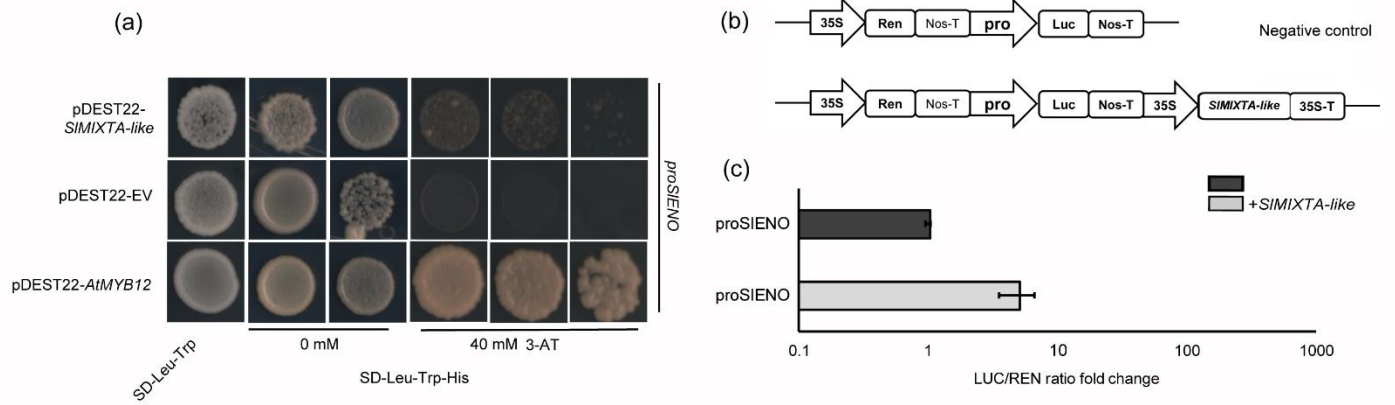


Figure S13. SIMIXTA-like can't directly bind to the promoter of *SIENO*. (a) Yeast one-hybrid indicates SIMIXTA-like cannot directly interact with *SIENO* promoter. AtMYB12 was used a positive control. (b) Schematic representation of fused vector and negative control vector in Dual-LUC assay. (c) Dual-luciferase assay indicates SIMIXTA-like can't bind to the promoter region of *SIENO* to induce its expression. Error bars show S.E.M (n=3). No significant difference ($P < 0.05$) was observed.

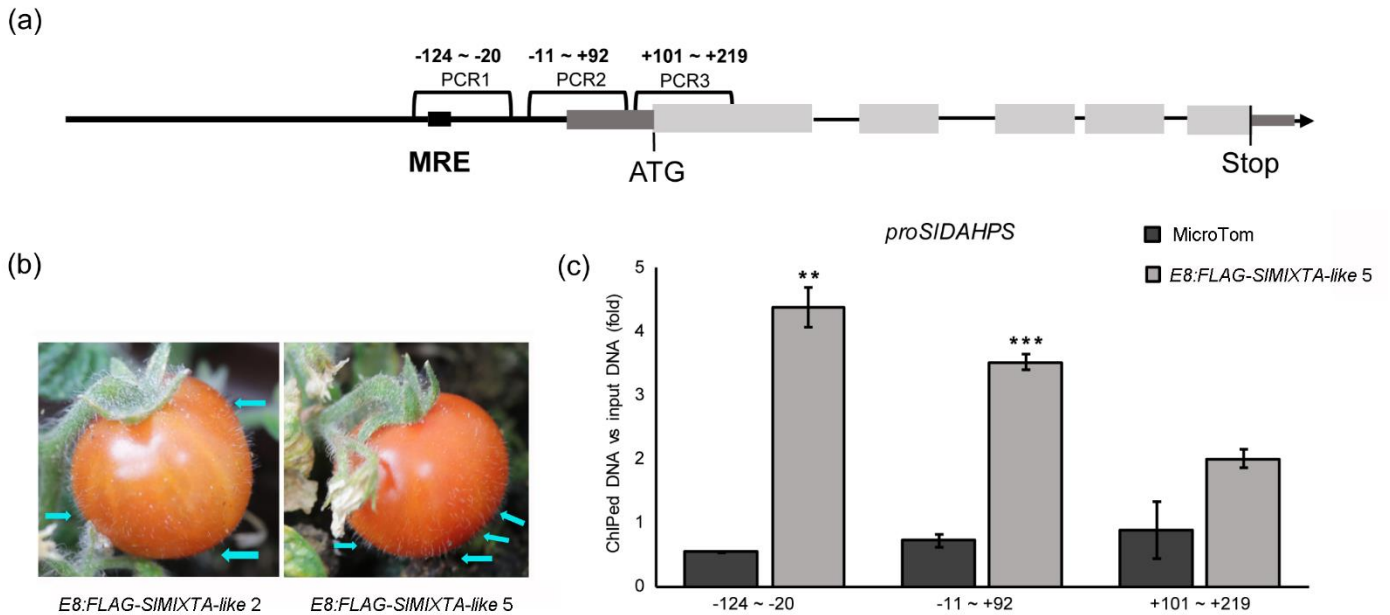


Figure S14. ChIP-qPCR indicates SIMIXTA-like directly binds to the promoter of *SIDAHPS* *in vivo*. (a) schematic representation of *SIDAHPS* gene structure and PCR primers design. Black box indicates MYB recognition site (MRE). (b) *E8:FLAG-SIMIATA-like* fruit show enhanced trichome density on ripe fruit. (c) Binding of SIMIATA-like to the *proSIDAHPS* was confirmed by ChIP-qPCR. Fruit were analyzed at 5dpb. The numbers on the horizontal axis below the bars correspond to the left and right borders of the amplified regions relative to the initial transcription start site. Data were represented as mean \pm S.E.M (n=3). *, p<0.05 (Student's t-test).