

Supplementary Table S1. Bioinformatics analysis of CsEIL family.

Gene name	Gene ID	Theoretical pI	Mw(kDa)	Length(aa)	localization	Grp2up	Chromosome	Exon	ORF (bp)
CsEIL 1	orange1.1g007017m	5.27	70.36	622	Nuclear	EIN 3	Chr2 : 954558-957573	4	1866
CsEIL 2	orange1.1g007173m	5.66	69.57	615	Nuclear	EIN	3Chr3 : 266820-271020	4	1825
CsEIL 3	orange1.1g007662m	5.43	67.09	595	Nuclear	EIN 3	chrUn : 874057-876876	4	1785
CsEIL 4	orange1.1g007983m	5.26	66.22	583	Nuclear	EIN 3	Chr2 : 954558-958280	5	1749
CsEIL 5	orange1.1g009140m	6.16	61.85	543	Nuclear	EIN 3	Chr3 : 259802-262917	4	1629
CsEIL 6	orange1.1g012304m	6.11	52.73	467	Nuclear	EIN 3	Chr3 : 267560-271020	3	1401
CsEIL 7	orange1.1g012340m	6.63	52.78	466	Nuclear	EIN 3	Chr2: 954558-957740	4	1398
CsEIL 8	orange1.1g016498m	9.05	44.35	389	Nuclear	EIN 3	Chr3 : 259679-262917	5	1167
CsEIL 9	orange1.1g016840m	5.37	43.96	382	Nuclear	EIN 3	Chr3: 259679-262917	3	1146
CsEIL 10	orange1.1g038853m	5.92	47.35	323	Nuclear	EIN	3Chr1 : 416335-417684	2	1269

Supplementary Table S2. *EIL* genes in sweet orange, *Arabidopsis thaliana*, rice, apple and poplar

Gene id	Gene Name	Gene id	Gene Name
orange1.1g007017m	<i>CsEIL 1</i>	AT5G21120.1	<i>AtEIL5</i>
orange1.1g007173m	<i>CsEIL 2</i>	AT5G65090.1	<i>AtEIL6</i>
orange1.1g007662m	<i>CsEIL 3</i>	AT5G65100.1	<i>AtEIL7</i>
orange1.1g007983m	<i>CsEIL 4</i>	LOC_Os02g36510.1	<i>OsEIL1</i>
orange1.1g009140m	<i>CsEIL 5</i>	LOC_Os03g20780.1	<i>OsEIL2</i>
orange1.1g012304m	<i>CsEIL 6</i>	LOC_Os03g20790.1	<i>OsEIL3</i>
orange1.1g012340m	<i>CsEIL 7</i>	LOC_Os04g38400.1	<i>OsEIL4</i>
orange1.1g016498m	<i>CsEIL 8</i>	LOC_Os07g12210.1	<i>OsEIL5</i>
orange1.1g016840m	<i>CsEIL 9</i>	LOC_Os07g17160.1	<i>OsEIL6</i>
orange1.1g038853m	<i>CsEIL 10</i>	LOC_Os07g48630.1	<i>OsEIL7</i>
AT1G73730.1	<i>AtEIL1</i>	LOC_Os07g48630.2	<i>OsEIL8</i>
AT2G27050.1	<i>AtEIL2</i>	LOC_Os08g39830.1	<i>OsEIL9</i>
AT3G20770.1	<i>AtEIL3</i>	LOC_Os08g39830.2	<i>OsEIL10</i>
AT5G10120.1	<i>AtEIL4</i>	LOC_Os09g31400.1	<i>OsEIL11</i>
NM_001328892.2	<i>MdEIL1</i>	XM_024610055.4	<i>PtEIL4</i>
OU696679.1	<i>MdEIL2</i>	XM_002299212.3	<i>PtEIL5</i>
XM_008347911.3	<i>MdEIL3</i>	XM_002307066.3	<i>PtEIL6</i>
XM_008356616.3	<i>MdEIL4</i>	XM_002307066.3	<i>PtEIL7</i>
XM_017335709.1	<i>MdEIL5</i>	XM_002312805.3	<i>PtEIL8</i>
XM_017335709.2	<i>MdEIL6</i>	XM_002312805.3	<i>PtEIL9</i>
XM_029093268.1	<i>MdEIL7</i>	XM_024598281.1	<i>PtEIL10</i>
OU696691.1	<i>MdEIL8</i>	XM_024598281.1	<i>PtEIL11</i>
OU744993.1	<i>MdEIL9</i>	XM_024598281.1	<i>PtEIL12</i>
OU744998.1	<i>MdEIL10</i>	XM_024600202.1	<i>PtEIL13</i>
OU745005.1	<i>MdEIL11</i>	XM_024605398.1	<i>PtEIL14</i>
XM_008347911.3	<i>MdEIL12</i>	XM_024605398.1	<i>PtEIL15</i>
XM_008347917.3	<i>MdEIL13</i>	XM_024606204.1	<i>PtEIL16</i>
XM_008363268.3	<i>MdEIL14</i>	XM_024606204.1	<i>PtEIL17</i>
XM_008366362.3	<i>MdEIL15</i>	XM_024606204.1	<i>PtEIL18</i>
XM_008367942.3	<i>MdEIL16</i>	XM_024606205.1	<i>PtEIL19</i>
XM_029093454.1	<i>MdEIL17</i>	XM_024606205.1	<i>PtEIL20</i>
XM_029105228.1	<i>MdEIL18</i>	XM_024606205.1	<i>PtEIL21</i>
XM_029105228.1	<i>MdEIL19</i>	XM_024606205.2	<i>PtEIL22</i>
XM_029105229.1	<i>MdEIL20</i>	XM_024606205.3	<i>PtEIL23</i>
XM_029105230.1	<i>MdEIL21</i>	XM_024607301.1	<i>PtEIL24</i>

Gene id	Gene Name	Gene id	Gene Name
XM_029106284.1	<i>MdEIL22</i>	XM_024607301.2	<i>PtEIL25</i>
XM_024610055.1	<i>PtEIL1</i>	XM_024608163.1	<i>PtEIL26</i>
XM_024610055.2	<i>PtEIL2</i>	XM_024608164.1	<i>PtEIL27</i>
XM_024610055.3	<i>PtEIL3</i>	XM_024610055.1	<i>PtEIL28</i>

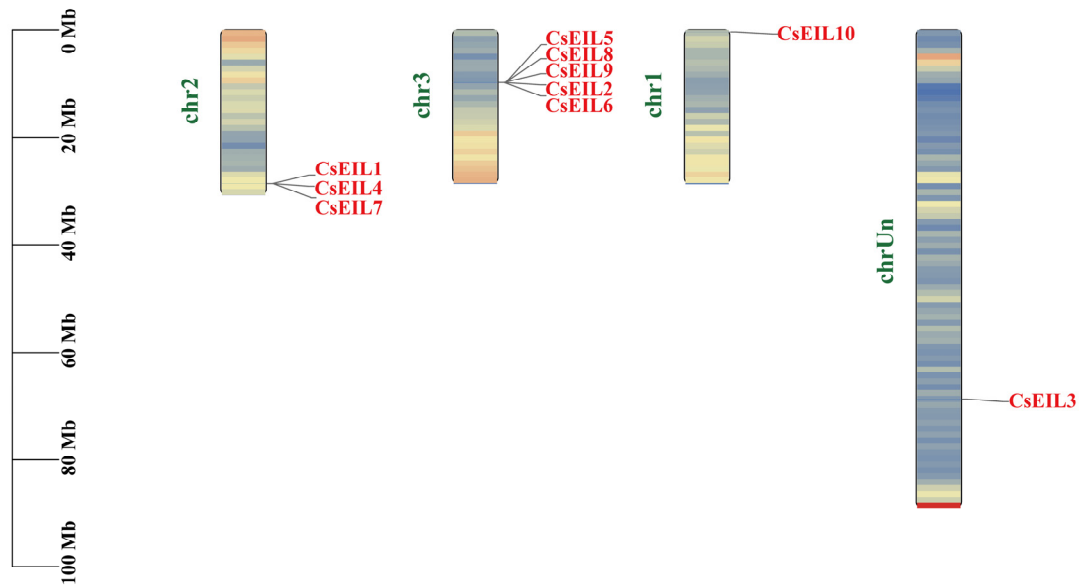
Supplementary Table S3. Collinearity analysis of sweet orange, *Arabidopsis thaliana*, rice, apple and poplar

gene id	gene name	gene id	gene name	chr id	Cs start/end	At start/end
orange1.1g007017m	CsEIL1	AT2G27050.1	AtEIL2	Cs chr2/At chr2	954558-957573	11545656-11548293
orange1.1g007983m	CsEIL4	AT2G27050.1	AtEIL2	Cs chr2/At chr2	954558-958280	11545656-11548293
orange1.1g012340m	CsEIL7	AT2G27050.1	AtEIL2	Cs chr2/At chr2	954558-957740	11545656-11548293
orange1.1g038853m	CsEIL10	AT5G65090.1	AtEIL6	Cs chr1/At chr5	416335-417684	7182589-7184342
orange1.1g007017m	CsEIL1	AT5G21120.1	AtEIL4	Cs chr2/At chr5	954558-957573	26003882-26006851
orange1.1g007983m	CsEIL4	AT5G21120.1	AtEIL4	Cs chr2/At chr5	954558-958280	26003882-26006851
orange1.1g012340m	CsEIL7	AT5G21120.1	AtEIL4	Cs chr2/At chr5	954558-957740	26003882-26006851
orange1.1g007173m	CsEIL2	XM_008347917.3	MdEIL12	Cs chr3/Md chr2	266820-271020	32069916-32073820
orange1.1g009140m	CsEIL5	XM_008347917.3	MdEIL12	Cs chr3/Md chr2	259802-262917	32069916-32073820
orange1.1g012304m	CsEIL6	XM_008347917.3	MdEIL12	Cs chr3/Md chr2	267560-271020	32069916-32073820
orange1.1g016498m	CsEIL8	XM_008347917.3	MdEIL12	Cs chr3/Md chr2	259679-262917	32069916-32073820
orange1.1g016840m	CsEIL9	XM_008347917.3	MdEIL12	Cs chr3/Md chr2	259679-262917	32069916-32073820
orange1.1g007173m	CsEIL2	XM_029105228.1	MdEIL19	Cs chr3/Md chr7	266820-271020	4954483-4958869
orange1.1g009140m	CsEIL5	XM_029105228.1	MdEIL19	Cs chr3/Md chr7	259802-262917	4954483-4958869
orange1.1g012304m	CsEIL6	XM_029105228.1	MdEIL19	Cs chr3/Md chr7	267560-271020	4954483-4958869
orange1.1g016498m	CsEIL8	XM_029105228.1	MdEIL19	Cs chr3/Md chr7	259679-262917	4954483-4958869
orange1.1g016840m	CsEIL9	XM_029105228.1	MdEIL19	Cs chr3/Md chr7	259679-262917	4954483-4958869
orange1.1g038853m	CsEIL10	XM_008366362.3	MdEIL15	Cs chr1/Md chr15	416335-417684	35505799-35513442
orange1.1g007017m	CsEIL1	XM_024605398.1	PtEIL7	Cs chr2/Pt chr9	954558-957573	11613079-11617694
orange1.1g007983m	CsEIL4	XM_024605398.1	PtEIL7	Cs chr2/Pt chr9	954558-958280	11613079-11617694

gene id	gene name	gene id	gene name	chr id	Cs start/end	At start/end
orange1.1g01 2340m	CsEIL7	XM_0246053 98.1	PtEIL7	Cs chr2/Pt chr9	954558-957740	11613079- 11617694
orange1.1g00 7173m	CsEIL2	XM_0246062 04.1	PtEIL12	Cs chr3/Pt chr8	266820-271020	626979- 631297
orange1.1g00 9140m	CsEIL5	XM_0246062 04.1	PtEIL12	Cs chr3/Pt chr8	259802-262917	626979- 631297
orange1.1g01 2304m	CsEIL6	XM_0246062 04.1	PtEIL12	Cs chr3/Pt chr8	267560-271020	626979- 631297
orange1.1g01 6498m	CsEIL8	XM_0246062 04.1	PtEIL12	Cs chr3/Pt chr8	259679-262917	626979- 631297
orange1.1g01 6840m	CsEIL9	XM_0246062 04.1	PtEIL12	Cs chr3/Pt chr8	259679-262917	626979- 631297
orange1.1g00 7173m	CsEIL2	XM_0246100 55.1	PtEIL24	Cs chr3/Pt chr10	266820-271020	4954483- 4958869
orange1.1g00 9140m	CsEIL5	XM_0246100 55.1	PtEIL24	Cs chr3/Pt chr10	259802-262917	4954483- 4958869
orange1.1g01 2304m	CsEIL6	XM_0246100 55.1	PtEIL24	Cs chr3/Pt chr10	267560-271020	35505799- 35513442
orange1.1g01 6498m	CsEIL8	XM_0246100 55.1	PtEIL24	Cs chr3/Pt chr10	259679-262917	22117946- 22122347
orange1.1g01 6840m	CsEIL9	XM_0246100 55.1	PtEIL24	Cs chr3/Pt chr10	259679-262917	22117946- 22122347
orange1.1g03 8853m	CsEIL10	XM_0023070 66.3	PtEIL6	Cs chr1/Pt chr5	416335-417684	5747051- 5751372
orange1.1g03 8853m	CsEIL10	XM_0246053 98.1	PtEIL11	Cs chr1/Pt chr7	416335-417684	11613079- 11617694
orange1.1g00 7662m	CsEIL3	XM_0245982 81.1	PtEIL8	Cs chrUn/Pt chr3	874057-876876	20939771- 20942987

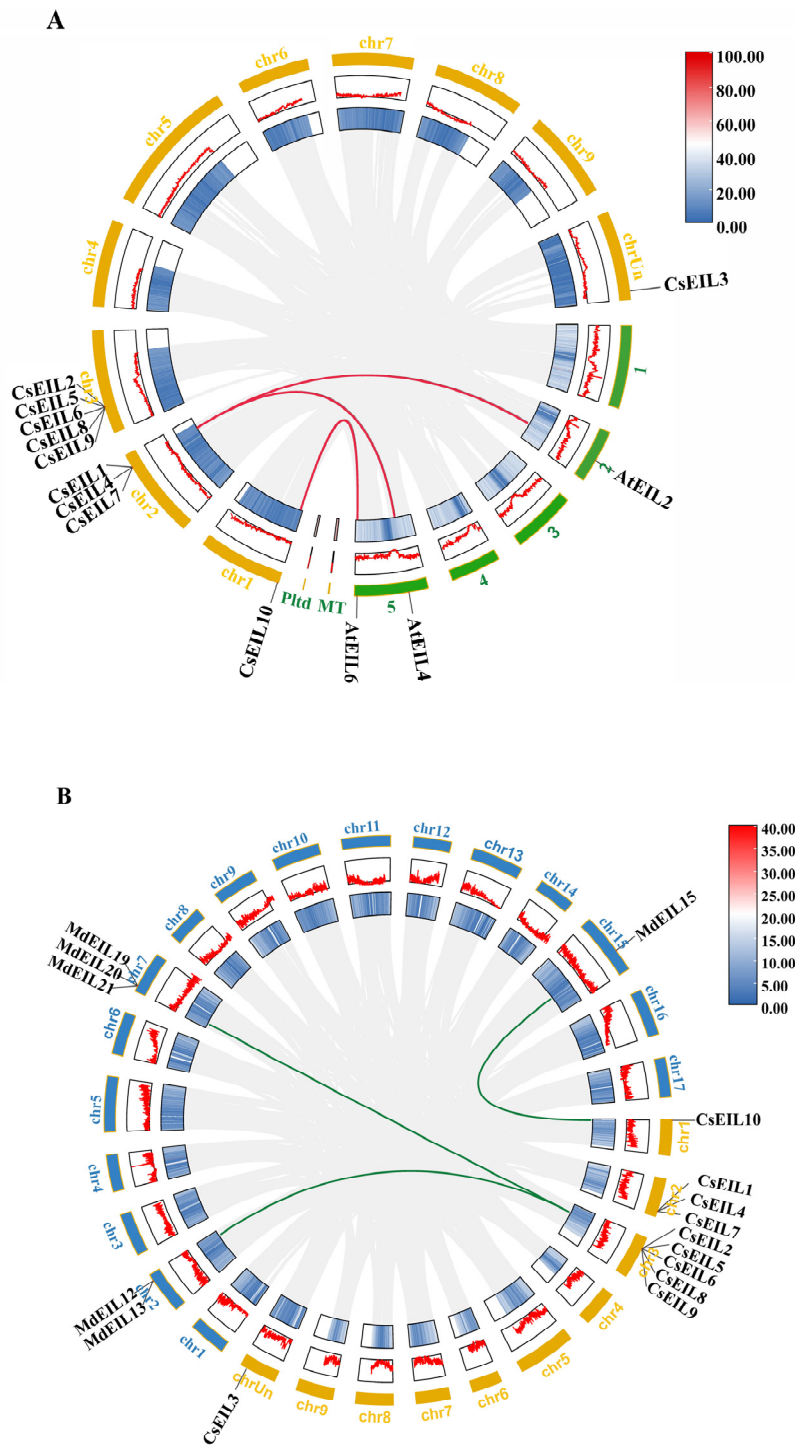
Supplementary Table S4. List of qRT-PCR primers

Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')
<i>CsEIL1</i>	ACTCTTGTCGGCTCTCATGC	TGATCACTGCCGTCAACACA
<i>CsEIL2</i>	ATTCGACCGTAATGGCCCTG	GCTTGGAAAGTGGGGGTTCT
<i>CsEIL3</i>	CCAGCAGCCATAGCGAAGTA	TTGGAGAAAGGAGTTCCGCC
<i>CsEIL4</i>	GTCCACCCCGTACAAGAAG	CGGGAGTGGCTCATTATCA
<i>CsEIL5</i>	GCTTGGAAAGTGGGGGTTCT	CCGAAAGCTTGTTGCGCAAT
<i>CsEIL6</i>	ACAATCTCCGTGAGTGGTGG	AGAGTTGCAAGACACCACCC
<i>CsEIL7</i>	CCGCTGGAAAAAGGTGTTGC	TGGCGGTAATTAACCA
<i>CsEIL8</i>	TGCTAAGCAGCGTCAATCCC	CCTGTGAGTTTCCCCAGTGT
<i>CsEIL9</i>	GAAGGAGAGGCGTTTCTGGA	ATGTCTCGGGCACAAGATGG
<i>CsEIL10</i>	ACTCTTGTCGGCTCTCATGC	CAATCAGGAGGAGGCCTTGG
<i>CsCOX</i>	GTATGCCACGTCGCATTCCAGA	GCCAAACTGCTAAGGGCATTCT



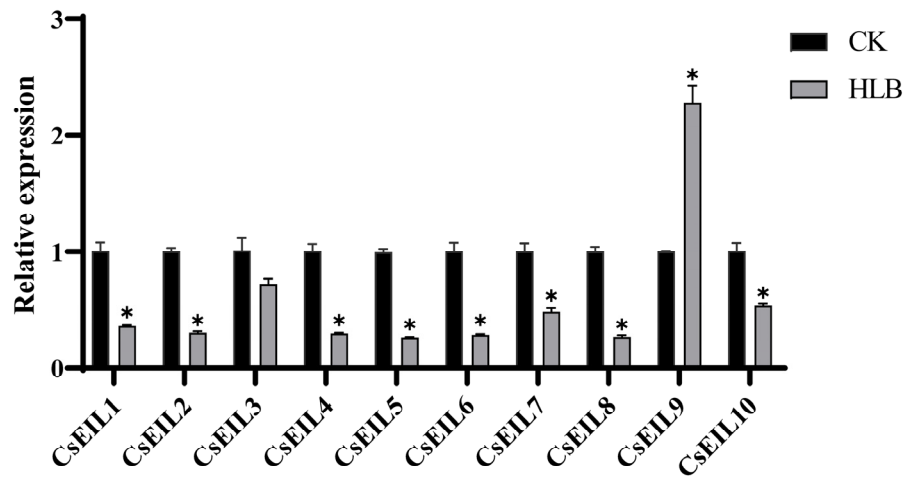
Supplementary Figure S1. Chromosome localization of the *CsEIL* genes.

The size of chromosomes is estimated based on their relative lengths, and chromosome numbers are shown on the left of each chromosome. Gene density is represented by a color bar (a blue to red scale indicates low to high gene density).



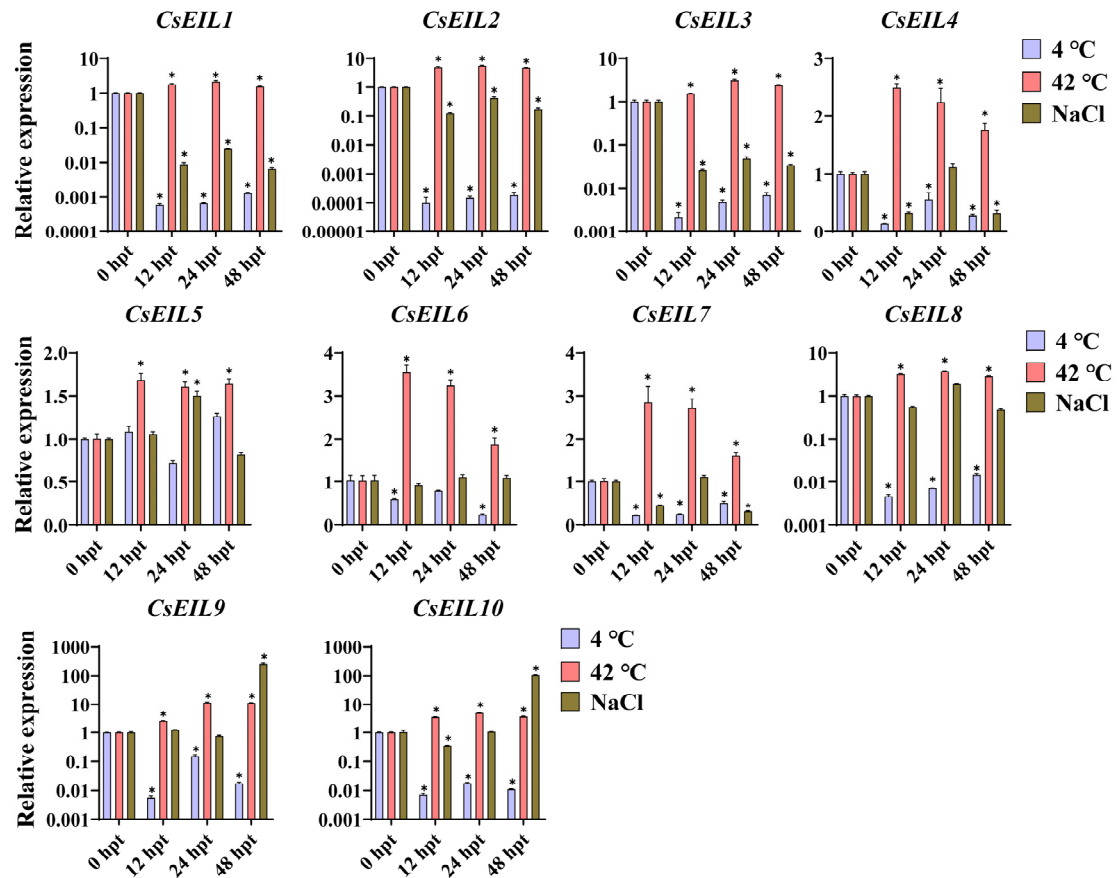
Supplementary Figure S2. Replication and collinearity analysis of *EIL* genes in sweet orange, Arabidopsis, and apple.

Supplementary Figure S2A shows the collinear relationship between sweet orange and Arabidopsis, while Supplementary Figure S2B shows the collinear relationship between sweet orange and apple. The gray lines represent all collinear regions, and the other colored lines represent homologous gene pairs (the blue to red scale indicates the gene density from low to high)



Supplementary Figure S3. Expression level of *CsEIL* genes after *Candidatus Liberibacter asiaticus* inoculation.

CK is a healthy plant and HLB is a CLas-infected plant. The experiment was conducted with three biological replicates in all panels, and similar outcomes were observed. The asterisk (*) indicates a significant difference ($P < 0.05$).



Supplementary Figure S4. Expression levels of *CsEIL* genes under different abiotic stresses.

The X-axis represents the different time points after exposure to various abiotic stress treatments, while the Y-axis shows the relative gene expression levels of *CsEIL*. The purple bar represents treatment at 4°C, the pink bar represents treatment at 42°C, and the brown bar represents NaCl treatment. The experiment was performed with three biological replicates, and the asterisk (*) indicates significant difference ($P < 0.05$).