

Supplementary Material

Table S1. List of *CaFtsHs* family genes identified in pepper and their sequence characteristics. The proteomic information was obtained from EXPASY (Available online: <http://web.expasy.org/protparam/>).

Number	Name	Gene ID	Chromosome	Number of Intron	Predicted Protein Length	Molecular Weight (KD)	Isoelectric Point	Instability Index
1	CaFstH1	Capana04g000110	4	4	710	76.29	6.00	34.95
2	CaF-stH06	Capana07g001803	7	3	721	77.54	6.29	31.99
3	CaFstH5	Capana05g001818	5	6	721	77.71	9.21	44.65
4	CaFstH4	Capana08g000315	8	4	422	47.31	6.49	42.19
5	CaFstH7	Capana00g003035	un	12	711	76.77	5.97	40.01
6	CaFstH2	Capana00g002383	un	5	692	77.09	7.63	34.24
7	CaFstH8	Capana10g001411	10	5	643	71.82	5.68	33.09
8	CaFstH9	Capana09g001789	9	7	820	90.47	8.39	37.14
9	CaF-stH10	Capana10g001412	10	7	814	89.49	7.98	35.86
10	CaF-stH11	Capana03g002053	3	16	405	44.65	6.29	45.45
11	CaFstH3	Capana03g003013	3	17	452	51.01	4.97	46.07
12	CaF-stH12	Capana06g001351	6	18	480	55.36	5.40	36.37

Table S2. Transcriptome data analysis of *CaFtsHs* family genes in pepper during different tissues development.

GenID	Different tissues										
	L1	L9	F1	F9	FST0	T5	T11	G5	G11	S5	S11
Capana04g000110	286.33	710.58	76.01	63.03	96.75	83.94	160.93	148.43	641.63	31.34	22.46
Capana07g001803	336.21	838.44	53.10	122.26	92.43	124.04	306.94	202.53	755.50	26.44	94.86
Capana05g001818	116.61	178.78	59.29	105.29	77.36	102.68	70.32	84.13	69.05	69.70	76.89
Capana08g000315	31.99	43.70	32.62	51.04	36.30	82.79	137.55	89.20	142.06	46.80	117.04
Capana00g003035	24.66	36.64	20.63	16.29	23.69	27.75	28.15	26.32	33.17	12.28	25.54
Capana00g002383	13.03	17.08	15.18	8.65	11.95	8.73	6.65	9.28	4.76	7.38	7.26
Capana10g001411	5.97	10.20	11.60	10.97	9.88	4.74	4.22	5.30	2.82	1.70	1.24
Capana09g001789	62.70	58.57	71.85	118.29	53.59	56.19	54.93	35.12	50.94	67.42	60.54
Capana10g001412	39.12	42.69	35.14	100.19	39.89	42.91	39.90	42.45	46.92	36.91	21.81
Capana03g002053	59.10	132.34	24.03	18.71	25.03	19.99	18.76	38.73	29.93	8.69	11.22
Capana03g003013	26.19	36.01	18.92	7.61	20.77	12.56	12.80	27.84	24.27	8.78	17.05
Capana06g001351	0.21	0.04	0.37	0.03	0.11	0.13	0.10	0.12	0.21	0.22	0.04

Table S3. Transcriptome data analysis of *CaFtsHs* family genes in pepper during different stress treatments (including heat, salt and osmotic stress).

GenID	Leaf							Root						
	CL0	HL1	HL2	HL3	HL4	HL5	HL6	CR0	HR1	HR2	HR3	HR4	HR5	HR6
Capana04g000110	318.17	275.51	216.52	241.03	179.11	137.19	338.77	214.31	28.35	174.37	13.33	13.62	7.56	13.56
Capana07g001803	424.00	330.98	277.39	295.8	515.21	546.42	633.80	372.34	34.21	226.23	37.04	49.2	41.57	63.05
Capana05g001818	34.36	22.78	19.36	40.33	85.56	70.33	62.84	38.04	48.50	49.21	41.92	48.80	44.01	34.23
Capana08g000315	47.43	26.86	27.94	43.93	76.47	98.42	98.53	40.4	45.64	39.58	48.98	71.64	80.41	110.85
Capana00g003035	17.77	14.91	10.65	8.61	18.00	16.93	24.13	13.68	16.09	13.38	14.02	15.34	10.41	29.94
Capana00g002383	5.87	3.38	3.48	4.08	10.04	12.49	15.00	7.47	9.85	7.64	9.89	10.75	13.42	15.18
Capana10g001411	5.14	0.95	0.47	0.60	2.34	5.30	6.94	3.68	4.37	3.61	1.51	2.75	1.09	1.54
Capana09g001789	69.67	23.64	18.05	19.55	33.14	40.48	50.1	54.31	53.91	54.42	31.22	37.52	30.09	37.02
Capana10g001412	25.91	15.11	11.76	12.42	24.46	28.19	31.36	24.58	29.64	30.59	21.27	21.86	16.74	17.88
Capana03g002053	65.87	49.26	46.94	39.26	40.09	107.39	64.72	62.98	10.16	33.31	5.08	9.02	11.19	18.86
Capana03g003013	21.41	11.36	7.88	8.27	7.66	14.22	16.39	14.2	8.97	7.95	5.88	5.39	6.05	23.12
Capana06g001351	0.39	0.16	0.16	0.00	0.09	0.13	0.12	0.38	0.16	0.04	0.07	0.04	0.00	0.11

Table S4. Primer sequences were used for qRT-PCR.

Gene name	Accession Number	Forward primer (5'→3')	Reverse primer (5'→3')
<i>CaUbi3</i>	AY486137	ATGGGTTCTGCTTCAATGG	TCATACTTTTTTACTGTTTGATGTTAG
<i>CaFtsH06</i>	Capana07g001803	ATGGCTACTTCATCAGTATGC	ATTAGGTGGATGAGTGTATGAAT
<i>AtHSP101</i>	At1G74310	TGCATTAGCTGGTGCTTTGAT	CCACCGGCACTAGAGATTGC
<i>AtAPX2</i>	At3G09640	AATATGCTGCAGATGAGGATGC	CAAGAATCAAGGAGGTAGGAGATG
<i>AtSOD1</i>	At1G08830	TCAACTGGAAATATGCAAGCGAGGT	ACCACACAGCTGAGTTGAGCAAA
<i>AtCAT1</i>	At1G20630	AGCGCTTTCGGAGCCTCGTG	GGCCTCACGTTAAGACGAGTTGC
<i>AtGPX3</i>	AT2G43350	GGGTCAATCAGCGAGCTAC	CGATGGCGAAGAAGGGTATC
<i>AtMYB44</i>	AT5G67300	GGAAGTGGTAACATCAGGAGGC	TTCTTTGCTCTCTTCTGTATCCATC
<i>AtRD29a</i>	AT5G52310	TGTGCCGACGGGATTTG	CTGATGCCTCACCGTATCCA
<i>AtDREB2A</i>	AT5G05410	AAGGATTTGGGGTAAATGGGTTG	CAGCCTCATCATAAGCAGAAGCA
<i>AtActin2</i>	At3G18780	CTGTACGGTAACATTGTGCTCAG	CCGATCCAGACACTGTACTTCC

Table S5. Primers for subcellular localization of *CaFtsH06*.

Primer Name	Primer sequence (5'→3')	Enzymes
<i>CaFtsH6</i>	F: CGGGATCCATGGCTACTTCATCAGTATGC	<i>BamH I</i>
	R: GGGGTACCATTAGGTGGATGAGTGTATGAAT	<i>Kpn I</i>

Note: Highlighted text indicated the enzymes.

Table S6. The CDS sequence of *CaFtsH06* (Accession no. Capana07g001803).

ATGGCTACTTCATCAGTATGCATAGCAGGAAATGGTTTGTGTC-
 TACACATAAAACACAGAAAGTCTTTAAGAAGGATGTTTATGGAAGGAAAATTTTATATTCCCTCAAATCTTCCATCGTCTGGTAA
 AACGTCAAGAGTAGTTGTAAAAGCATCTCTTCAGCAAAGGCCGGATGAAGGAAGAA-
 GAGGCTTTCTTAAATTATTGCTTGGAATGTTGGGCTTGGAGCGCTGCTTTGTTAGGTAATGGAAAAGCCTATGCTGATGAGC
 AAGGTGTTTCTAACTCAAGGATGTCTTATTCTAGATTTTTGGAATATCTGGACAAGGA-
 TAGGGTGCAAAAAGTAGATTTGTTTGAAAACGGAACCATAGCTATTGTTGAGGCTGTATCTCCAGAATTAGGAAACCGGGTGCA
 AAGAGTTAGGGTACAACCTACCCGGGCTCAGCCAGGAACCTTCTTCAAAAGTTCCGG-
 GAAAAAACATCGATTTTGCTGCTCACAATGCTCAAGAGGACTCAGGTTCTCTCATATTCAACTTGATTGGAAATCTGGCATTCTC
 CCGCTTATTTTGATTGGTGGTCTTTTCTGCTATCAAGGCGGTCTAACGGAGGAATGG-
 GAGGTCTGGTGGGCTGGTAACCCACTAGCATTTGGTCAATCAAAAGCTAAGTTCCAAATGGAACCAACACTGGTGTGACAT
 TTGATGATGTTGCTGGTGTAGATGAAGCAAAACAAGATTTTATGGAGGTTGTAGAATTTTT-
 GAAGAAACCTGAGAGGTTCACTGCAGTGGGGCTCGTATTCCAAAAGGTGTTCTTCTTGTGGTCTCCTGGTACGGGGAAGAC
 CCTGCTAGCAAAGCAATTGCTGGTGAA-
 GCGGGTGTTCCATTTTTCTCAATTTTCAGGTTTCAGAATTCGTCGAGATGTTTGTGGTGTGGAGCCTCTCGAGTCCGTGATCTT
 TTCAAGAAGGCCAAGGAAAATGCTCCCTGCATTTGATTTGTTGATGAAATTGATGCTGTT-
 GGGCGACAAAGAGGGACTGGAATCGGAGGAGGGAATGATGAAAGAGAACAGACCTGAACCAACTATTGACGGAAATGGATGGT
 TTTGAAGGAAATACTGGTATAATAGTTGTTGCAGCAACCAATCGTGCAGATATTTCTCGAT-
 TCGGCTTTGCTGTGACAACCTGGTGCTGCTGGTGATTTGTCAGCAGATCACCAGTTTGGCAAAACAGATGGTTGTCACTTTTGGGA
 TGTCTGAACTTGGCCAGACCAGGACGCTTTGATAGACAAGTATCTGTGGATGTTCCAGA-
 CATCAAGGGAAGAACAGAGATCTTAAAGGTTTCATGCCGGCAACAAGAAGTTCGATTTCAGATGTGTCTCTTGAAGTTATTGCCAT
 GAGGACACCTGGCTTCAGTGGAGCAGATCTTGCTAACCTCTTGAATGAAGCAGCCATTCTT-
 GCAGGTGCGGCTGGTAAAACAGCAATCGCATCCAAAGAGATTGATGATTCAATTGACAGGATAGTGGCTGGAATGGAAGGAACA
 GTAATGACTGATGGCAAGAGCAAGAGTCTTGTGGCATATCACGAAGTT-
 GGACATGCCATCTGTGGAACCTCTCACTCCAGGGCATGATCCTGTTCAAAAGGTCCTCTAATCCCACGTGGTCAGGCAAAAGGT
 TTGACCTGGTTCATTCTGTCAGATGATCCAACCTTAATATCCAAGCAGCAACTCTTCGCTA-
 GAATTGTCGGTGGACTTGGTGGAAGAGCTGCAGAGGAAGTGATCTTTGGTGCACCTGAAGCCTGGTCACTCATGGATGCTTCAG
 CCCAAAGTGGTGATGTAATCATGAGAATGATGGCCAGGAACCTCAATGTCAGAAAA-
 GCTAGCTGAAGACATCGATGCTGCTGTGAAGAGGCTTTTCAGACAGTGCATATGAGATTGCGTTGAGCCAAATCCGCAGCAACCG
 TGAAGCCATTGATAAGATTGTGGAAGTCCCTCCTTGAAAAGGAGACGATGACAGGA-
 GATGAATTCCGTGCTATTCTCTCAGAATTTGTGGAAATTCCTGCTAAACCCGTGTCCCTGCTGCTGTACCTACCCCAGCAGCCG

Table S7. Primers for gene silencing of *CaFtsH06*.

Primer Name	Primer sequence (5'→3')	Enzymes
<i>CaFtsH6</i>	F: CGGGATCCATTCCCTCAAATCTTCCATCG	<i>BamH I</i>
	R: GGGGTACCTGCACCCGGTTTCCTAA	<i>Kpn I</i>

Note: Highlighted text indicated the enzymes.

Table S8. Primer pairs for transformation of *CaFtsH06*.

Primer Name	Primer sequence (5'→3')	Enzymes
<i>CaFtsH6</i>	F: CGGGATCCATGGCTACTTCATCAGTATGC	<i>BamH I</i>
	R: GGGGTACCTATTAGGTGGATGAGTGTATGAAT	<i>Kpn I</i>

Note: Highlighted text indicated the enzymes.

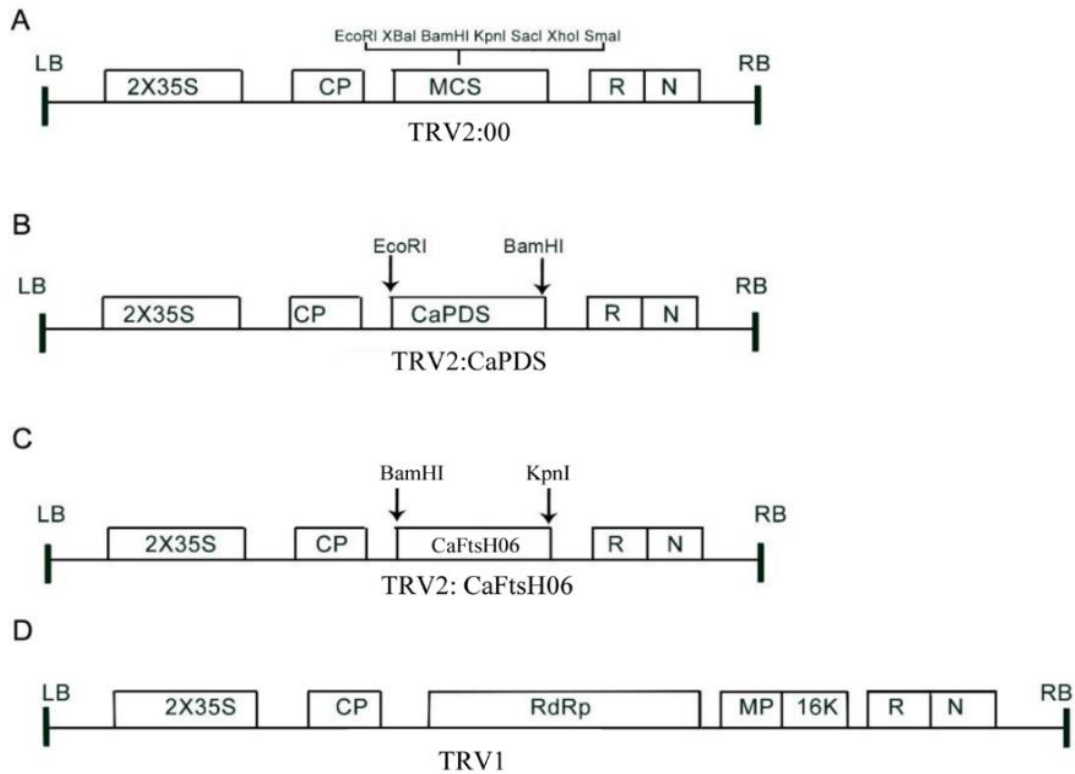


Figure S1. Structure of TRV2 vector for VIGS system. (A) the empty TRV2 vector; (B) TRV2:CaPDS vector; (C) TRV2:CaFtsH06 vector; (D) TRV1 vector. LB and RB: the left and right borders of TRV2 vector DNA; CP: coat protein; MP: movement proteins; 2 × 35S: two copies of the TRV2 with 35 promoter; RdRp: RNA-dependent RNA polymerase; 16 K: 16 KDa protein; MCS: multiple cloning sites; R and N: ribozyme and no-terminator.

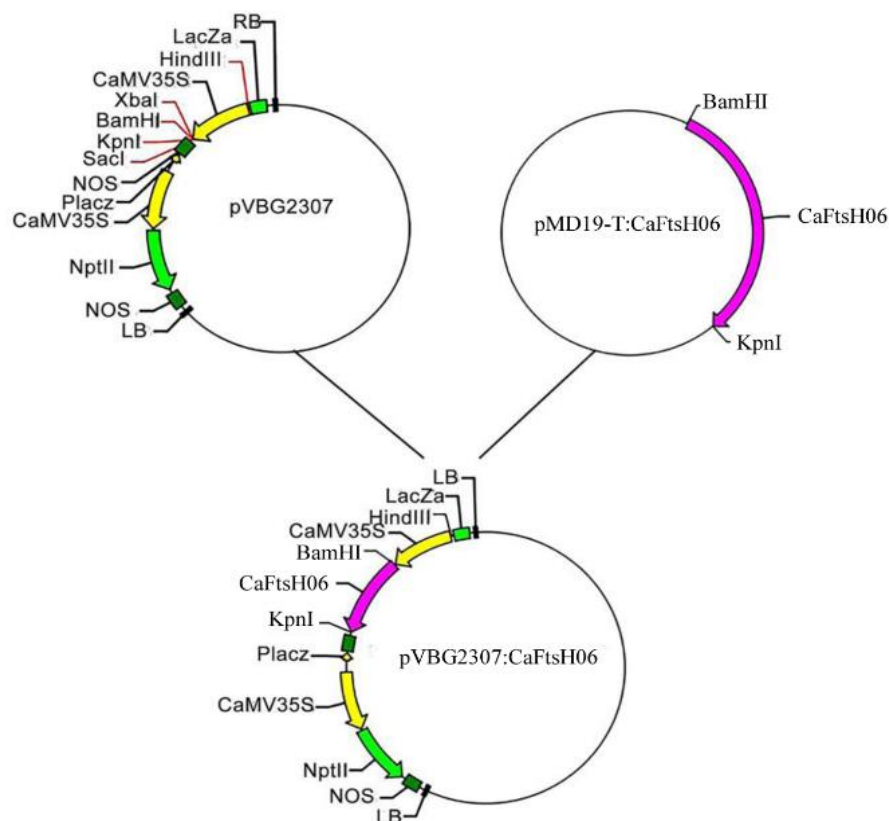


Figure S2. Structure of pVBG2307 vector for transgenic *Arabidopsis*.

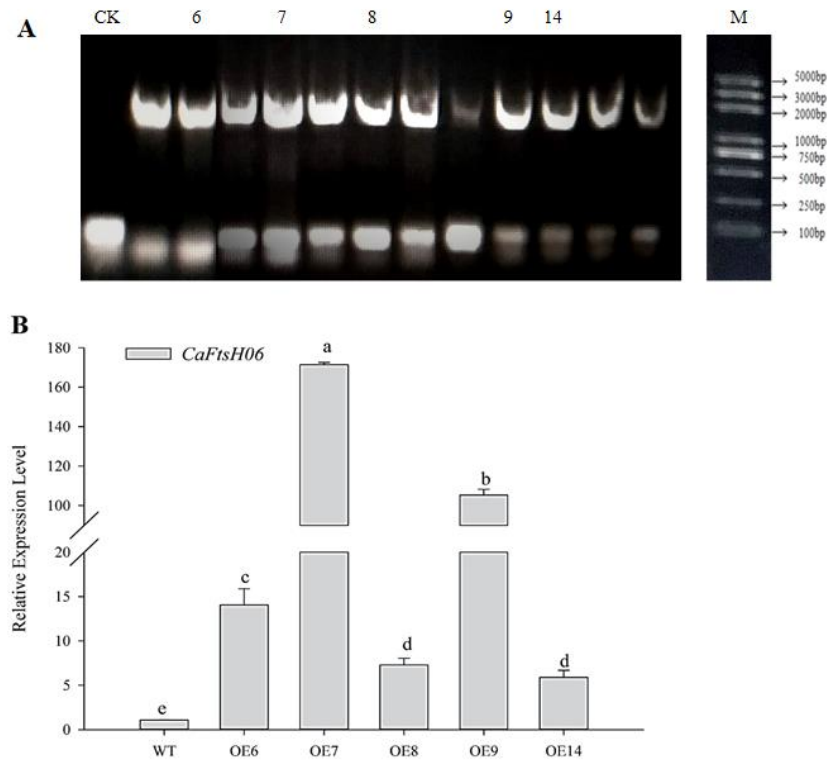


Figure S3. Detection and selection of the transgenic *Arabidopsis* lines. **(A)** PCR analysis of the *CaFtsH06* gene in wild type (WT) and *CaFtsH06*-OE *Arabidopsis*; **(B)** Relative expression level of WT and *CaFtsH06*-OE *Arabidopsis* lines (OE6, OE7, OE8, OE9, OE14) under normal conditions; The error bars represent SD for three biological replicates, and the lowercase showed the significant level at $\alpha = 0.05$.