

Supplementary materials

A

	Basic Helix Loop Helix Domain	
CabHLH79	A. <u>NKGTEQSSKE</u> .EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	177
AT5G62610.1 NP_001330306	GGSKATEQCKNKE.EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMT	180
StubHLH79-like XP_006344980.1	A. <u>NKGTEQSSKE</u> .EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	191
SlybHLH089 XP_004236164.1	A. <u>NKGTEQSSKE</u> .EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	192
NabHLH79-like XP_019243650.1	V. <u>NKGTEQSSKE</u> .EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	183
CsibHLH79 XP_006476705.1	G. <u>NKPPE</u> .SSKFESEPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	174
ZjbHLH79 XP_015882712.1	D. <u>NKPPE</u> .SSKFESEPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	182
JrbHLH79-like XP_018831619.1	G. <u>NKSTESTKE</u> SEPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	177
CsbHLH79 XP_004138140.1	G. <u>NKLAPEQSPKE</u> .EPPK.DYIHVRARRGQATDSHSLAERARREKISEEMK	174
Consensus	nk tegsskp eppk dyihvrarrgqatdshslaerarreki ser mk	
	H ER RR I R	
CabHLH79	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNHP	227
AT5G62610.1 NP_001330306	ALQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRGASTG	230
StubHLH79-like XP_006344980.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNHP	241
SlybHLH089 XP_004236164.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNHP	242
NabHLH79-like XP_019243650.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNHP	233
CsibHLH79 XP_006476705.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNLT	224
ZjbHLH79 XP_015882712.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNIN	232
JrbHLH79-like XP_018831619.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMGMN	227
CsbHLH79 XP_004138140.1	ILQDLVPGCNKVIKALVLDEIINYIQSLQRCVEFLSMKLEAVNSRMNIT	224
Consensus	ilgdlvpgcnkvigkalvldeiinyiqslrqv efl smkleavnsrmn	
	L LVP K D AS L EA	

B

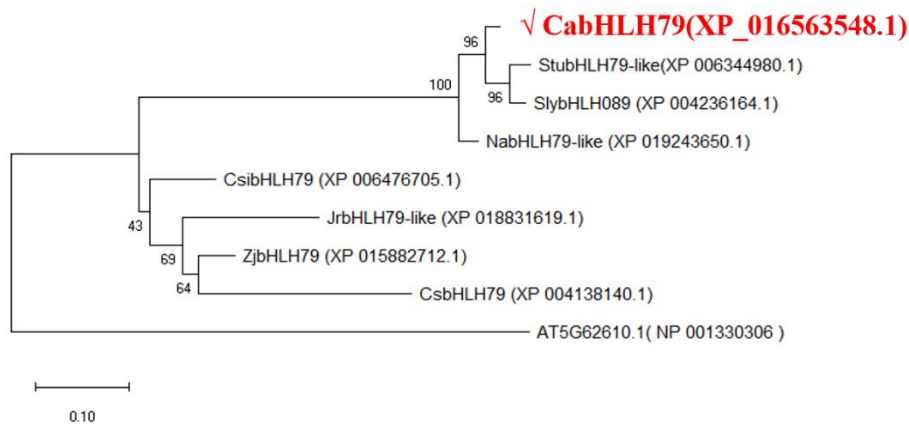


Figure S1. Sequence analysis of the CabHLH79 protein. **(A)** The sequence analysis of *CabHLH79*. The black areas represent homology level 100 %. The pink areas represent a level of homology greater than or equal to 75 %. The blue areas represent a level of homology greater than or equal to 50 %. The consensus subdomains in the bHLH binding domain are shown by thin underlines. **(B)** Phylogenetic relationship of *CabHLH79*(XP_016563548.1) and bHLH from other plant species. The protein sequence of CabHLH79 was used to perform the BLASTP search in the database NCBI Protein Reference Sequences (<https://blast.ncbi.nlm.nih.gov/>). Eight bHLH proteins were selected to construct the NJ phylogenetic tree by MEGA-X (<http://www.megasoftware.net/>) with the following parameters: JTT matrix-based model, bootstrap (1000 replicates), and pairwise deletion gaps.

A



B

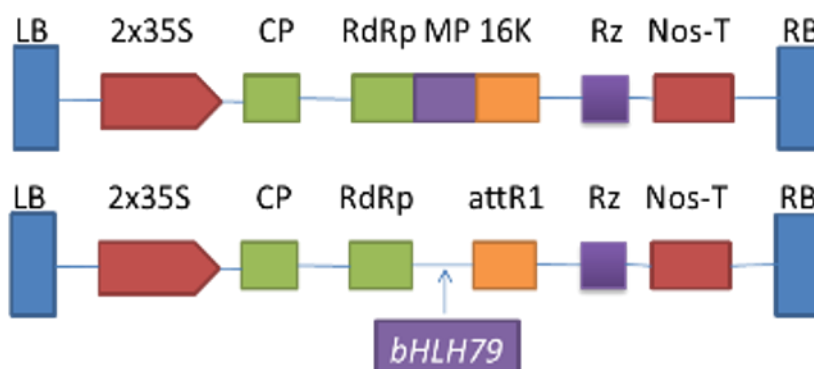


Figure S2. Phenotypes of plants with reduced expression of *CabHLH79*. **(A)** Phenotypes of pepper plants with reduced expression (about 4 weeks after injection). **(B)** Schematic diagram of the construction of VIGS vector. The experiment was conducted with three biological replicates and each replicate contained 3–5 pepper seedlings.

Table S1. Primers were used for the RT- qPCR.

Gene name	Primer Abbreviation	Primer Sequence (5'–3')
1	<i>CaUbi3-F</i>	TGTCCATCTGCTCTCTGTTG
2	<i>CaUbi3-R</i>	CACCCCAAGCACAATAAGAC
3	<i>CabHLH79-F</i>	CCAGCAGCTGTGTTCCACTA
4	<i>CabHLH79-R</i>	ACGAGACGACCATGAACATACA
5	<i>CaSOD-F</i>	TATGGAGCCTTAGAACCTGC
6	<i>CaSOD-R</i>	CCATTGAACTTGATAGCACCT
7	<i>CaPOD-F</i>	TCCTCCTCCTACTTCTAACC
8	<i>CaPOD-R</i>	ACAGACCTCTTTTGCTCACT
9	<i>CaCAT2-F</i>	GAAGCCAAATCCTAAGTCCC
10	<i>CaCAT2-R</i>	CCAACCTCGGATTGCCTCTT
11	<i>CaAPX1-F</i>	AGAGGACAAGCCAGAACCAC
12	<i>CaAPX1-R</i>	CCTTGTCTGATGGCAACTGT

13	<i>ERD15-F</i>	CCAGCGAAATGGGGAAAC
14	<i>ERD15-R</i>	ACAAAGGTACAGTGGTGGC
15	<i>CaCBF1A-F</i>	TGAGGCTGTCTGAGTCTTTC
16	<i>CaCBF1A-R</i>	AGGTGGAGGTAGCGTTAGT
17	<i>AtActin-F</i>	TGTTATGGTAGGGATGGGTC
18	<i>AtActin-R</i>	TTCTCTCTATTTGCCTTGGG
19	<i>AtCAT2-F</i>	GCAACTACCCCGAGTGGAAA
20	<i>AtCAT2-R</i>	TGTTTCAGAACCAAGCGACCA
21	<i>AtPOD-F</i>	TCCGGGAGCCACACCATTGG
22	<i>AtPOD-R</i>	TGGTCGGAATTCAACAG
23	<i>AtSOD-F</i>	ATGAGAAGTTCTATGAAGAG
24	<i>AtSOD-R</i>	GTCTTTATGTAATCTGGT
25	<i>AtRD29A-F</i>	AACCACCACTCAACACACAC
26	<i>AtRD29A-R</i>	AGTCGCACCATTCTCATGATG
27	<i>AtKIN1-F</i>	GCGAAAGATCAAACCTCCCA
28	<i>AtKIN1-R</i>	TCCTTCTGTGTGTTTGGAAGA
29	<i>AtCBF1-F</i>	GTTTGGGATGCCGACTTTGTTGG
30	<i>AtCBF1-R</i>	GTCACCATCTCCTTCGCCGTCAT

Table S2. List of the 10 proteins selected following the Y1H screening.

Numbering	Gene ID	GenBank Accession
1	Capsicum annuum transcription factor MYC2-like (LOC107870881), mRNA	XM_016717573.1
2	Capsicum annuum ferredoxin-dependent glutamate synthase, chloroplastic (LOC107852264), mRNA	NM_001324694.1
3	Capsicum annuum transcription factor BIM1 (LOC107862352), transcript variant X2, mRNA	XM_016707907.1
4	Capsicum annuum transcription factor bHLH79 (LOC107862470), mRNA	XM_016708062.1
5	Capsicum annuum FGGY carbohydrate kinase domain-containing protein (LOC107877499), mRNA	XM_016724156.1
6	Capsicum annuum abscisic acid 8'-hydroxylase 1-like (LOC107850059), mRNA	XM_016694530.1
7	Capsicum annuum uncharacterized LOC107867496(LOC107867496), mRNA	XM_016713756.1
8	Capsicum annuum protein BRASSINAZOLE-RESISTANT 1-like (LOC107867043), mRNA	XM_016713134.1
9	Capsicum annuum phosphatidylinositol:ceramide inositolphosphotransferase 2-like (LOC107842870), mRNA	XM_016686913.1
10	Capsicum annuum transcription factor MYC2-like (LOC107850747), mRNA	XM_016695492.1