

HsGSK3 β	-----MSGRPRTTSFA	11
AtBIN2	-----	0
CaSK23	MASIPIGPQHNPENQLYRHPYHLHPNQLMPPPPHQRQPPYYNQVEGGAAGRNAVAGDE	60
HsGSK3 β	ESCKPVQQPSAFGSMKVSRLDKGSKVTTVVATPGQGPDRPQEVSYTDTKVIENGSGFGVVY	71
AtBIN2	-----MADDKEMPAAVVDGHDQVTGHIISTTIGGKNGEKPKTISYMAERVVGTGSFGIIVF	55
CaSK23	GARPETEKEKEMSAAVVEGNGAVTGHIIISTTIGGKNGEKPKTISYMAERVVGTGSFGIIVF	120
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HsGSK3 β	QAKLCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSEKKDEVYLNLV	131
AtBIN2	QAKCLETGETVAIKKVLQDRRYKNRELQLMRVMDHPNVVCLKHCFSTTSK-DELFLNLV	114
CaSK23	QAKCLETGETVAIKKVLQDKRYKNRELQLMRLMDHPNVICLKHCFFSTTSR-DELFLNLV	179
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HsGSK3 β	LDYVPETVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFG-ICHEDIKPNLLLD	190
AtBIN2	MEYVPESLYRVLKHYSSANQRMPLVYVKLYMYQIFRGLAYIHNVAGVCHDLKPNLLVD	174
CaSK23	MDYVPESLSKILRHYSNSNQRMPLIYVKLYIYQIFRGLAYIHNVPRICHDMKPQDLLVD	239
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HsGSK3 β	PDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAEL	250
AtBIN2	PLTHQVKICDFGSAKQLVKGEANISYICSRFYRAPELIFGATEYTTSIDIWSAGCVLAEL	234
CaSK23	PLTHQVKLCDFGSAKQLVNGEANISYICSRHYRAPELIFGATEYSTSIDIWSAGCVLAEL	299
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HsGSK3 β	LLGQPIFGDSCVDQLVEIIKVLGTPTREQIREMNPNYTEFKFPQIKAHPWTKVFRPRT	310
AtBIN2	LLGQPLFPGENAVDQLVEIIKVLGTPTREEIRCMNPHTYDFRFPQIKAHPWHKIFHKRMP	294
CaSK23	LLGQPLFPGENAVDQLVEIIKVLGTPTREEIRCMNPNTYDFRFPQIKAHPWHKVHFHKRMP	359
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HsGSK3 β	PEAIALCSRLLLEYTPARTLPLEACAHSSFFDELDPNVKLPNGRDTPALFNFTTQELSSN	370
AtBIN2	PEAIDFASRLQYSPSLRCTALEACAHFFDELREPNAFLPNGRFPPLFNFKQEVAGSS	354
CaSK23	PEAIDLASRLQYSPSLRCTALEACAHFFDELREPNAFLPNGRFPPLFNFKQELSGAS	419
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HsGSK3 β	PPLATILIPPHARIQAAASTPTNATAASDANTGDRGQTNNAAASASASNST	420
AtBIN2	PELVNKLIPDHIKRLGLSFLNQSGT-----	380
CaSK23	PDLVNKLIPDHVGRQLDLNFPFGATQV-----	447
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(a)

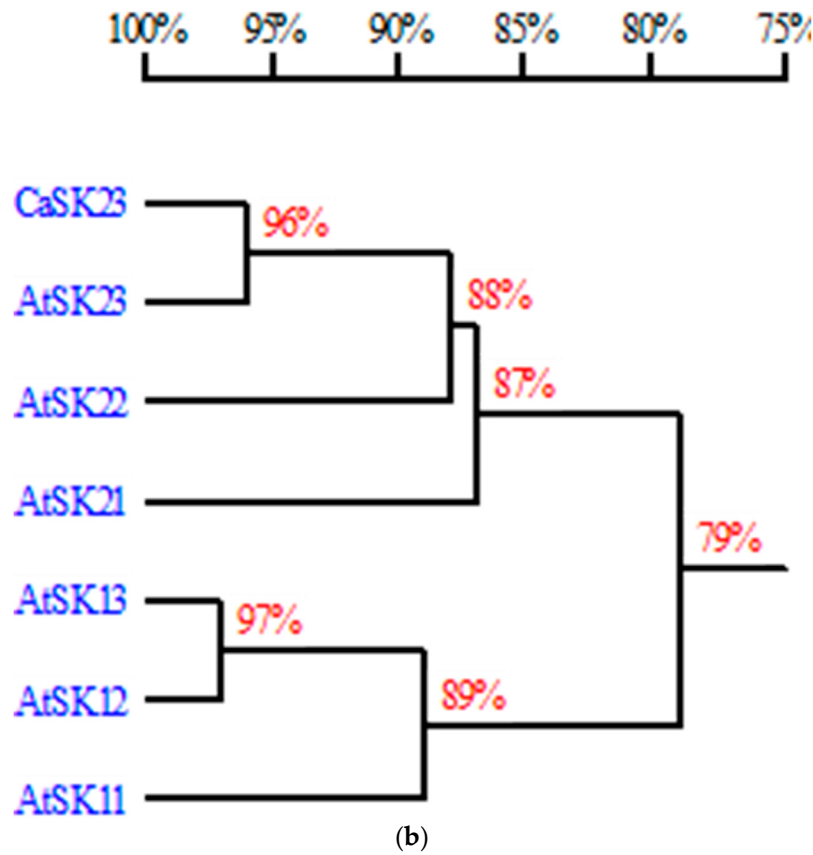


Figure S1. (a) Comparison of amino acid sequences of CaSK23 with *Homo sapiens* GSK3 β (HsGSK3 β , NP_001139628) and *Arabidopsis thaliana* BIN2 (AtBIN2, At4G18710) with DNAMAN5.0. The kinase domain is highlighted in yellow, and the conserved tyrosine (Y265 in CaGSK23) whose phosphorylation is required for kinase activity is highlighted in green. The conserved phosphate-binding residues (R144, R229, and K254 in CaSK23) that interact with prime-phosphorylated substrates are highlighted in red. The conserved TREE domain is in cyan. The figure was made based on the figure of Saidi et al [54]. (b) Phylogenetic tree analysis was made by DNAMAN5.0 with amino acid sequences of CaSK23 and its homologues in Arabidopsis including At5G26751 (AtSK11), At3G05840 (AtSK12), At5G14640 (AtSK13), At4G18710 (AtSK21/AtBIN2), At1G06390 (AtSK22), and At2G30980 (AtSK23).

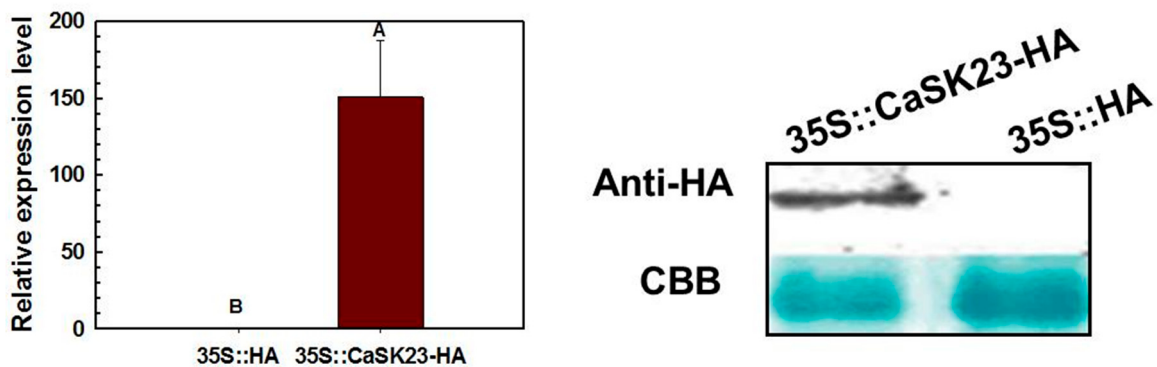


Figure S2. Expression of CaSK23-HA in pepper leaves via agroinfiltration. a. The transcript levels of CaSK23 in agro-infiltrated pepper leaves with GV3101 cells containing 35S::CaSK23-HA or 35S::HA by qRT-PCR with a specific primer pair of CaSK23 at 24hpi. Data represent the means $\pm$ SD obtained from five independent experiments. Different

letters above the bars indicate significant differences among means ($p < 0.01$), determined by Fisher's protected LSD test. b. The expression of CaSK23 in agro-infiltrated pepper leaves with GV3101 cells containing 35S:: *CaSK23-HA* by western blotting, and the total proteins of *CaSK23-HA* transiently overexpressing pepper leaves were isolated at 24 hpi and were immunoblotted with antibodies of HA.

Table S1. Primers for PCR and qRT-PCR used in this study.

Gene	Accession No.	Forward primers (5'→3')	Reverse primers(5'→3')
*Primers used for construction of over-expression & subcellular localization vectors			
<i>CaSK23</i>		AAAAAGCAGGCTACATGGCTTCTA TACCCATTGGT	AGAAAGCTGGGTCCTACACTTGTG TTGCACCGG
*Primers used for construction of VIGS vector			
<i>CaSK23</i>		AAAAAGCAGGCTACCAGAAAAT ATAGGGAGTCCCTTG	AGAAAGCTGGGTCCATAAGTAGA CAGGATTACAC
*Primers used for qRT-PCR analyses in pepper plants			
<i>CaSK23</i>		TGGCAGAGCGAGTTGTCGGTAC	TGAGCGGCATCCTTTGATTGTA
<i>CaPR1</i>	AF053343	GCCGTGAAGATGTGGGTCAATGA	TGAGTTACGCCAGACTACCTGAGT A
<i>CaSAR82A</i>	AF313766	CCATAGAGGT TCATATGGAA GTCC	GGAAAGTGAA TAGGACCTTT
<i>CaPIN2</i>	AAB94771	GCAACTATTACAGCGTCATCGG	GGGTCAGACTCTCCTTCACAAA
<i>CaACC Oxidase</i>	AB434925	CCATTGTGGTCAACCTTGGC	GCATCGCTTCCTGGATTGTAA
<i>CaActin</i>	AY572427	AGGGATGGGTCAAAAGGATGC	GAGACAACACCGCCTGAATAGC
*Primers used for qRT-PCR analyses in tobacco plants			
<i>NtNPR1</i>	U76707	GGCGAGGAGTCCGTTCTTTAA	TCAACCAGGAATGCCACAGC
<i>NtPR2</i>	M60460	TGATGCCCTTTTGATTCTATG	AGTTCCTGCCCCGCTTT
<i>NtPR1b</i>	X66942	AACCCATCCATACTATTCTTG	GCCGCTAACCTATTGTCCC
<i>NtEFE26</i>	Z29529	CGGACGCTGGTGGCATAAT	CAACAAGAGCTGGTGCTGGATA
<i>NtEF1a</i>	D63396	TGCTGCTGTAACAAGATGGATGC	GAGATGGGGACAAAGGGGATT

* The utilizations of the primes were listed in the lines with gray background.