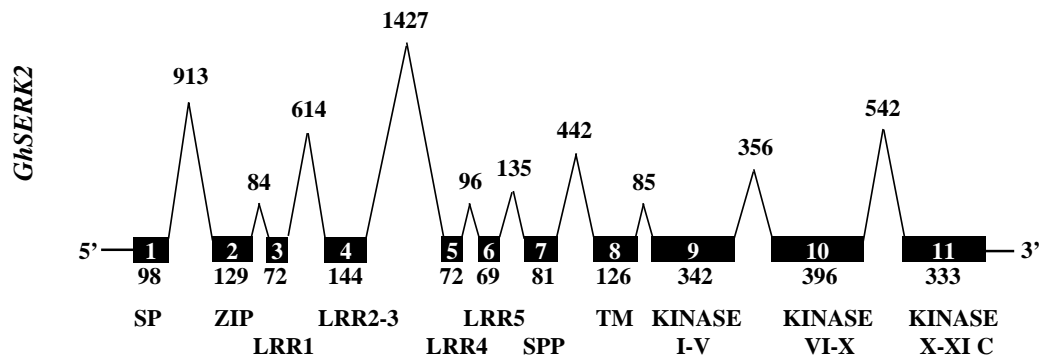
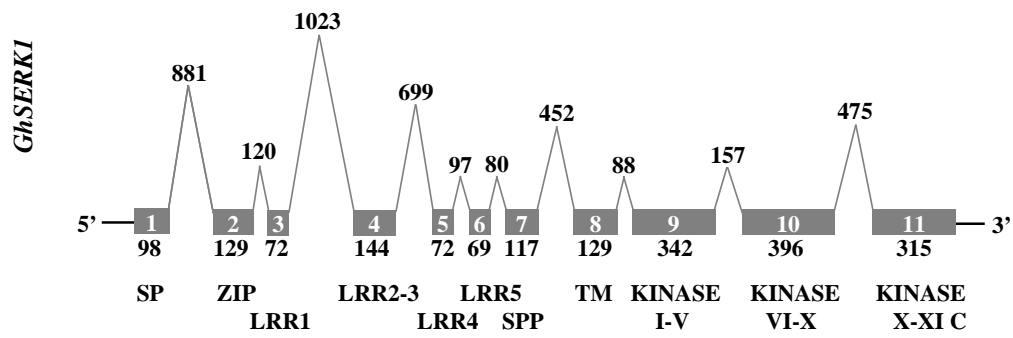
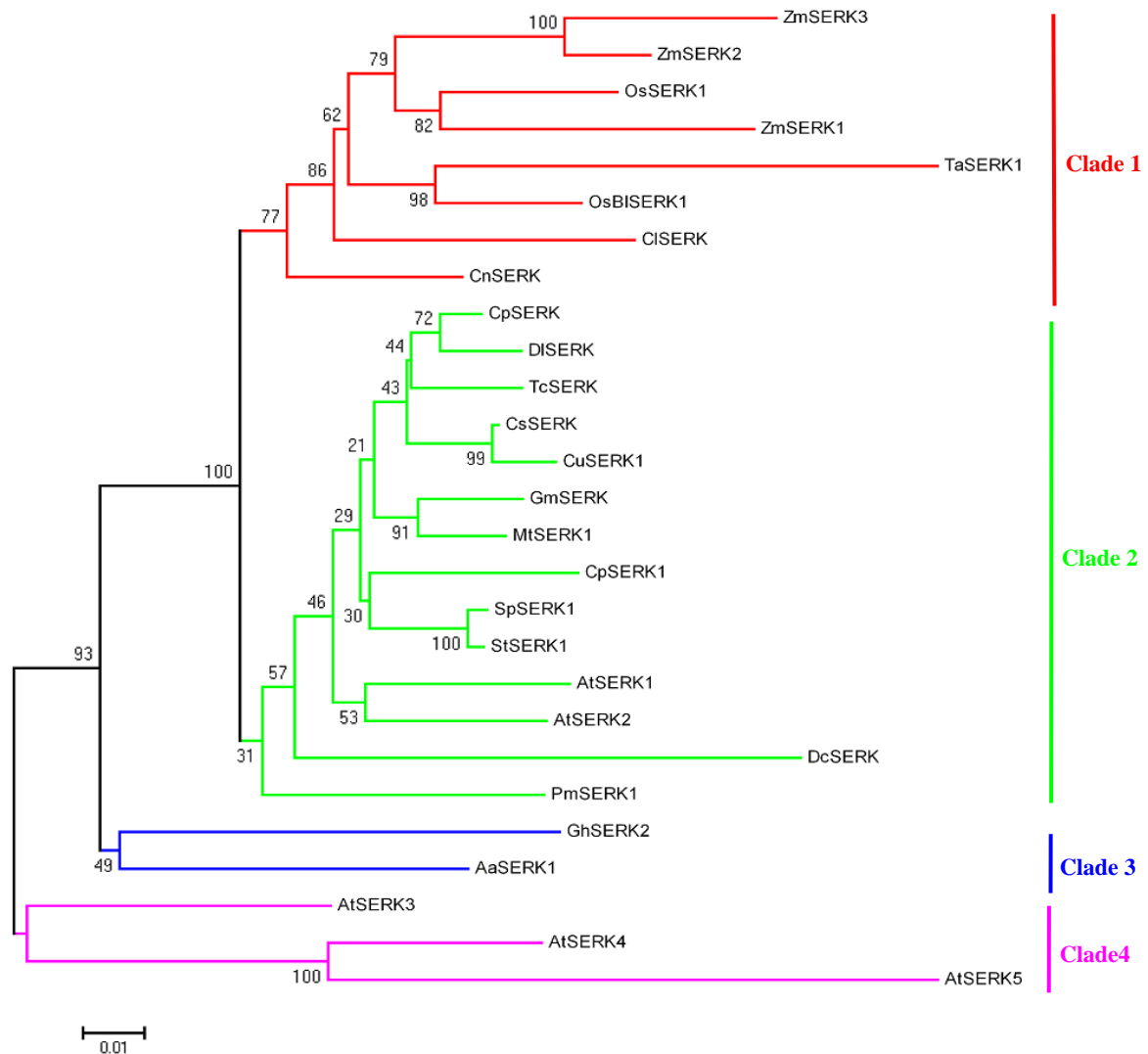


**Appendix A** Primers used in this paper.

Primer	Primer sequences (5' →3')	T <sub>m</sub> (°C)	Introductions
P1F	TATTTGCTCGTTGATTCGG	53	To amplify the full-length cDNA /gDNA
P1R	CATCTTCGGTCGTTCCATT	55	
P2F	GGCTGACCCTAATAATGTGTT	56	For amplifying the second intron
P2R	GGAACCAGTTGACCAGTGAGA	59	
P3F	GCAAATCTCACTGGTCAACTG	58	For amplifying the third intron
P3R	CAAGCTCACCAATTCCGTCA	57	
P4F	CGACTACTCTGGGCCAGCTTA	61	For amplifying the fourth intron
P4R	CAATGAGTTGTTGTTGAGACG	56	
P5F	GTCCTTAACTACTATTGACACAC	56	For amplifying the fifth and sixth intron
P5R	GTGGAGCAGGTGGAGGATTA	59	
P6F	CTCCTATCCCACCTACACCT	59	For amplifying the seventh intron
P6R	GTGGAACTAATACCTGATTG	54	
P7F	GAAGGCACCGGATCATTCT	58	For amplifying the eighth intron
P7R	GAAGTGCAGCTCTCCACCT	59	
P8F	GGTTAATGGTAGTGTTCATC	56	For amplifying the ninth intron
P8R	CATCACGGTGGATAATCTTAG	56	
P9F	GTGTTATGCTTCTCGAACTC	56	For amplifying the tenth intron
P9R	CAGAGCCACCTGGATTAGCT	59	
P10F	ATTGTGAGCAACTGGGATGA	58	For semi-quantitative RT-PCR
P10R	GAGTGTGGCAGGGTAGATG	59	
P11F	ATCCACCGTGATGTGAAGGCT	57	For semi-quantitative RT-PCR
P11R	TGTGATGTCGAGTCGGCAATA	56	
P12F	GAAGGCATTCCACCTGACCAAC	61	For qRT-PCR
P12R	CTTGACCTTCTTCTTGTGCTTG	60	
P13F	CGGTTATGGTGTATGCTTCT	56	For qRT-PCR
P13R	GCTCCACTTCTTCGTCTATGT	58	
P14F	CACTGAAGCGGAAGGGACT	60	For identification of transgenic plants by using PCR and southern blotting
P14R	CGATACCGTAAAGCACGAGGAA	60	



**Appendix B** Structure comparison between *GhSERK1* and *GhSERK2*. A schematic drawing of *GhSERK1* and *GhSERK2* genomic sequences shows the conserved exon/intron structure made up of 11 exons and 10 introns. Boxes represent exons and lines represent introns. Numbers represent sequence length (bp). SP, signal peptide; ZIP, leucine zipper; LRR, leucine rich repeats; SPP, serine-proline proline domain; TM, transmembrane region; Kinase, kinase catalytic domains; C, C-terminal domain.



**Appendix C** Phylogenetic analysis of GhSERK2 and other plant SERK proteins based on the full length amino acid sequences. Accession numbers of SERKS: CnSERK (*Cocos nucifera*), AAV58833.2; OsBISERK (*Oryza sativa*), AAU88198.1; OsSERK1 (*Oryza sativa Japonica Group*), AAU88198.1; ZmSERK3 (*Zea mays*), CAC37642.1; CpSERK (*Carica papaya*), ABY60783.1; DISERK (*Dimocarpus longan*), ACH87659.3; TcSERK (*Theobroma cacao*), AAU03482.1; CsSERK (*Citrus sinensis*), ACP20180.1; SpSERK (*Solanum peruvianum*), ABR18800.1; StSERK (*Solanum tuberosum*), ABO14172.1; CpSERK1 (*Cyclamen persicum*), ABS11235.1; DcSERK (*Daucus carota*), AAB61708.1; PmSERK1 (*Pinus massoniana*), ACZ56417.1; The other sequences of GenBank accession numbers are in accordance with the sequences in Fig. 1.

**Appendix D** The results of blast between *GhSERK2* sequence and *G. raimondii* chromosome database.

Query (Q.)	Subject (S.)	Identity (%)	Alignment length (bp)	Mismatches	Gap opens	Q. start	Q. end	S. start	S. end	E-value	Bit score
GhSERK2	Chr5	99.25	400	3	0	1134	1533	37441680	37441281	0	723
GhSERK2	Chr5	99.71	343	1	0	793	1135	37442373	37442031	6.00E-178	628
GhSERK2	Chr5	99.4	334	2	0	1530	1863	37440915	37440582	3.00E-171	606
GhSERK2	Chr12	93.02	401	28	0	1134	1534	2451846	2451446	4.00E-165	586
GhSERK2	Chr12	90.77	401	37	0	1134	1534	2435229	2434829	4.00E-150	536
GhSERK2	Chr12	92.42	343	26	0	793	1135	2452570	2452228	3.00E-136	490
GhSERK2	Chr12	81.44	334	47	5	1530	1863	2450843	2450525	1.00E-66	259
GhSERK2	Chr12	84.81	237	36	0	1530	1766	2434256	2434020	1.00E-60	239
GhSERK2	Chr11	91.77	401	33	0	1134	1534	24818103	24817703	9.00E-157	558
GhSERK2	Chr13	91.25	400	35	0	1134	1533	26744903	26744504	7.00E-153	545
GhSERK2	Chr13	88.03	401	46	2	1134	1533	26699081	26698682	3.00E-131	473
GhSERK2	Chr13	88	400	45	2	1134	1533	26716838	26716442	4.00E-130	470
GhSERK2	Chr13	85.66	244	35	0	1530	1773	26744129	26743886	4.00E-66	257
GhSERK2	Chr10	84.9	384	58	0	1150	1533	22748044	22748427	1.00E-105	388