

Supplementary Materials: Genome-Wide Identification and Expression Analysis of Two-Component System Genes in Tomato

Yanjun He, Xue Liu, Lei Ye, Changtian Pan, Lifei Chen, Tao Zou and Gang Lu

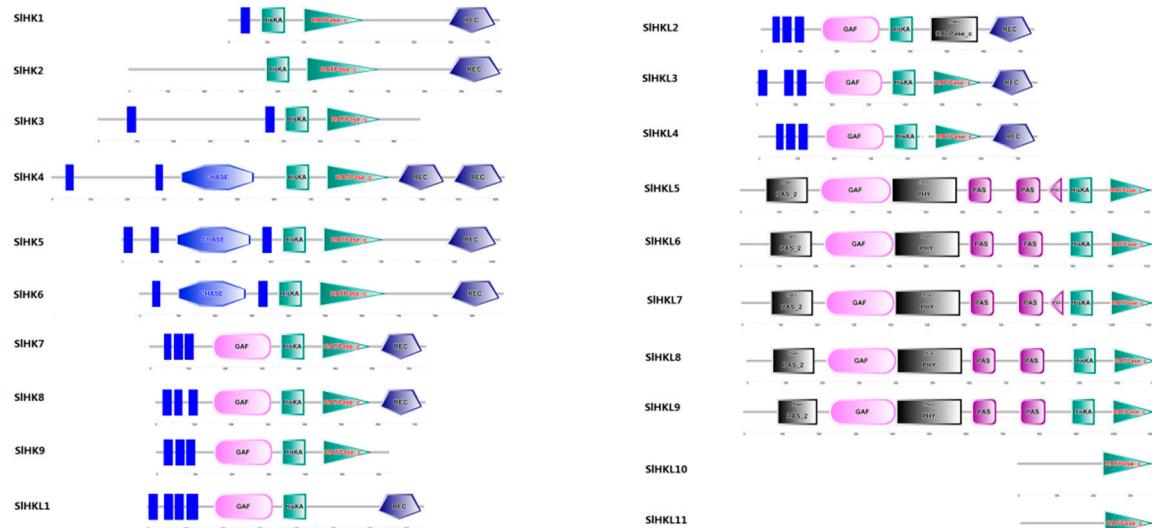


Figure S1. Domain structures of SIHK(L)s in tomato. Domain structures were analyzed by SMART online tool and drawn according to their original location and size. TM, transmembrane region; HisKA, Histidine kinase domain; HATPase, Histidine kinase-like HATPases; Rec, receiver domain; CHASE, cyclase/histidine kinase-associated sensory extracellular domain; GAF, cyclic GMP adenyllyl cyclase FhlA domain; PHY, chromophore-binding domain; PAS, Per/Arndt/Sim folds.

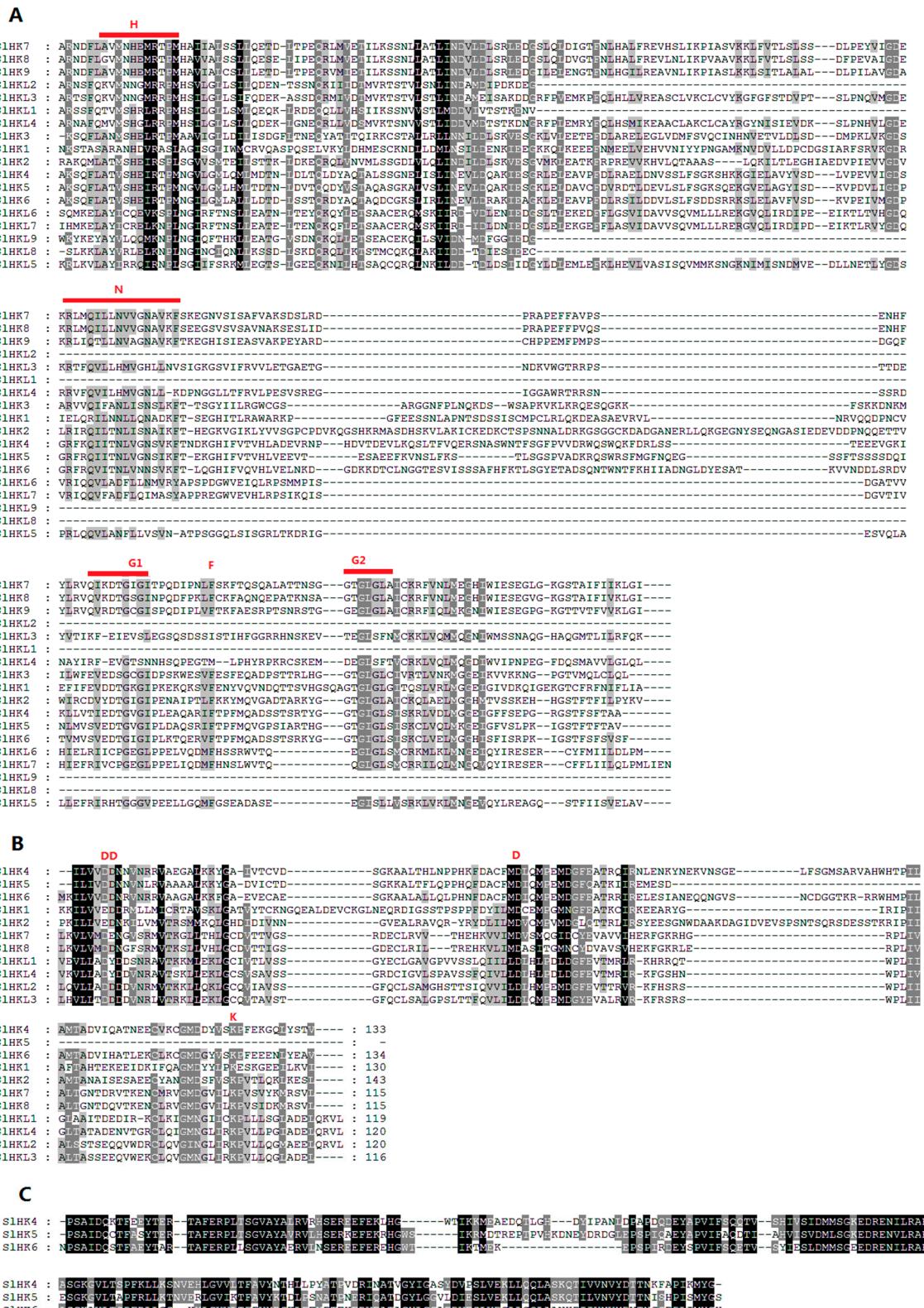


Figure S2. Amino acid sequence alignment of SIHK(L)s in tomato. Histidine kinase (like) (A); receiver (B); and cyclase/histidine kinase-associated sensory extracellular (CHASE) (C) domains from SIHK(L) proteins in tomato were aligned by the Clustal X program.

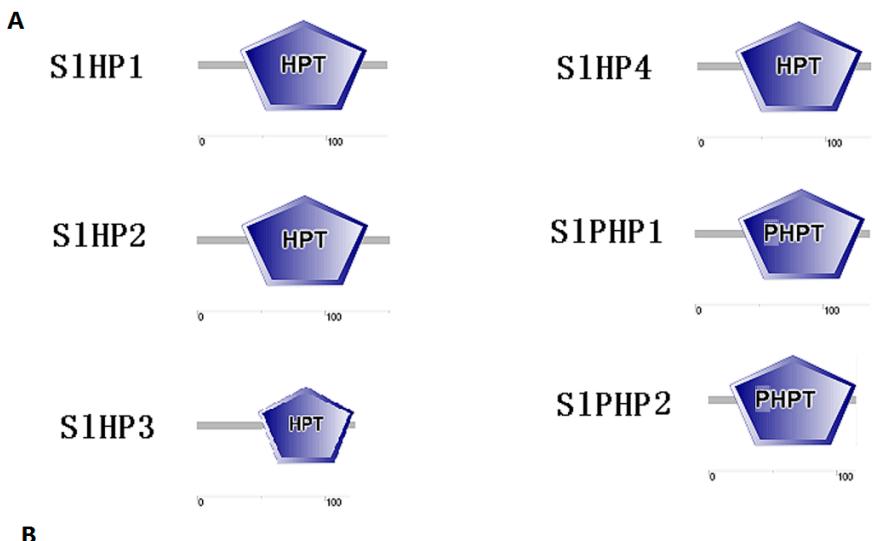


Figure S3. Domain structures and alignment of deduced amino acid sequences of SIHP proteins in tomato. (A) Domain structures were analyzed by SMART online tool and drawn according to their original location and size. Hpt, His-containing phosphotransfer domain; PHPt, pseudo His-containing phosphotransfer domain; (B) Sequences were aligned by the Clustal X program. The Hpt domain has been highlighted by red line. The conserved XHQXKGSSXS motif was also marked above the alignment.

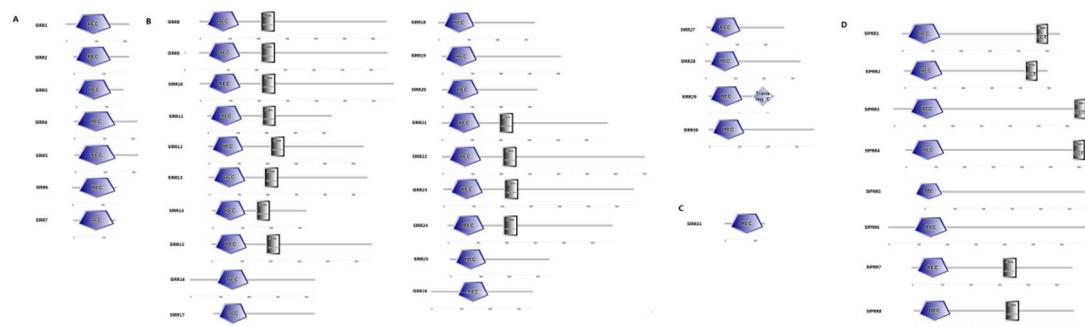


Figure S4. Domain structures of SIRR genes in tomato. Domain structures were analyzed by SMART online tool and drawn according to their original location and size. Rec, receiver domain; PRec, pseudo receiver domain; Myb, Myb DNA-binding domain; CCT, plant-specific CCT motif. (A–D) represent the domain structures of type-A RR, type-B RR, type-C RR, and PRR, respectively.

D

S1RR14 : ISITWVSDNAAYLCWAEIIRKCNVQAVAKYPIDATPDKOIKVD-----	SCDILVIVVHKSDLNGCKBQEMIAEAF--EIPVTSVSADOKEGAIILKGKRG---L
S1RR20 : ISITWVSDTSSLLITSEIIRKENFKVTVVKNANEALSTCQINEN-----	SEDLVITIEVPLPVNLQIQQCITNGF--NIPVWLMISSDRSECGLIGCFESAEVL
S1RR11 : GEIIVVVEIDINCNIETTAS-LKYSQFEIMVNSIEVLAGG-RSSGL-----	SEDLVITVHHLKDVFGQETQEIAKEF--DIPVPCMISNDKDKTSTINGLDRNRAVF
S1RR10 : DSVVIVVEIDPCTCLRIIEKMLRNCHYDITCKNRAEVLSHRENKN-----	GEIIVVVEISVH-PDIDGFKEIIEHIGLEM--DLPVNMISADDSDKDVUMMGVTHACDY
S1RR9 : DSVVIVVEIDPCTCLRIIEKMLRNCHYDITCKNRAEVLSHRENKN-----	GFIIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISADDSDKDVUMMGVTHACDY
S1RR8 : DSVVIVVEIDVVCERLIEQMLRKCSYQTTTCGCLAREILYVREKRG-----	TDFIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISGGDGRNTLVMRGVRCACDY
S1RR21 : DSVVIVVEIDPTEWLIEKMLRKCSYQTTTCGCLAREILYVREKRG-----	GFIIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISVGDGETSRVMRGVRCACDY
S1RR22 : MSVIAVADEPDICLKDQGILRKCYHQTTTQSARSLKRNRENRD-----	REFIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISANSDSKLVMRGITHACDY
S1RR14 : MSVIAVADEPDICLKDQGILRKCYHQTTTQSARSLKRNRENRD-----	REFIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISANSDTKLVRGIDHACDY
S1RR13 : FELIVVVEIDPTEFLYNNIEQMLRKCYHQTTTQSARSLKRNRENRD-----	NEHIVVVEISVH-PDIDGFKEIIEHVGLEM--DLPVNMISADDSSRVAMWCVIDAHCY
S1RR17 : --IHLVILPNSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----MIKEAST-----
S1RR26 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR2 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR30 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR21 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR10 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR17 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR16 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR1 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR2 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR6 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR7 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR4 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR4 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR3 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR12 : DEIILVILPDSTSLSNAAIEEHFSKTAIECATVLSHREHID-----	QEDIVVVEISVH-PDIDGFKEIIEHVGLEM--KTNQIF-----TIEMIKEAESTICFI
S1RR15 : ISVMLILNDKRFVNEITSCQAHGYYRITVDTTSSMSNRGRQ-----	KIEVITDHSNNLSLDLARAVAMD---IISVYVCDKYNEFVKVVKINECAYLY
S1RR15 : ISVMLILNDKRFVNEITSCQAHGYYRITVDTTSSMSNRGRQ-----	KIEVITDHSNNLSLDLARAVAMD---IISVYVCDKYNEFVKVVKINECAYLY
S1RR24 : VSVLLILNDKRFVNEITSCQAHGYYRITVDTTSSMSNRGRQ-----	KIEVITDHSNNLSLDLARAVAMD---IISVYVCDKYNEFVKVVKINECAYLY
S1RR29 : RSIILVILDEAPIREMIAVLEMAGYDCLAEANSQQLHAIIVDRKP-----	ISVPTPNNSFKLIDQAVTLDD---IISIPICDNEYNELLAKRAKRECASLF
S1RR31 : LSVZVANDISQNSYILOCQNFGVDTLGRDGMFNLHKDTGM-----	ISVPTPNNSFKLIDQAVTLDD---IISIPICDNEYDTRSAKRAFEN-AAYF
S1RR31 : LSVZVANDISQNSYILOCQNFGVDTLGRDGMFNLHKDTGM-----	ISVPTPNNSFKLIDQAVTLDD---IISIPICDNEYDTRSAKRAFEN-AAYF

66 6d v a 666 g

K

S1RR14 : SVDDQRDKGLCTVU-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR20 : MVEPISQNDWHELN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR11 : TIKP-TODGINLYN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR10 : LIPKPRRIEALKNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR9 : LIPKPRRIEALKNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR8 : LIPKPRDEELKNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR21 : LIPKPRMKELRNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR22 : LIPKPRLEELKNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR23 : LIPKPRLEELKNN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR13 : LIPKPSMELQNIW-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR27 : -----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR22 : YERGSIISSL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR20 : YERGSIISSL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR30 : YERGSIISSL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR25 : YERGSIISSL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR18 : YERGSIISSL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR17 : YERGSIISSLKLRDIWKHV	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR16 : YERGSIISSLKLRDIWKHV	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR1 : LIPKPKLADVKRKLKSYN-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR2 : LIPKPKLSDVKRKL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR6 : MIKEPKHKSINVERLRCQI-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR7 : MIKEPKHKSINVKRKR-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR4 : FIRPKVRLSUVNKKLPHM-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR5 : FIRPKVRLSUVNKKLPHM-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR3 : FIRPKVQSDUVNKKRPHL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR12 : FENFSFERDIDVYK-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR15 : LKQPFNKEILLYIW-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR19 : VEPDPINEELIVKYL-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR24 : LQKPLILHEYVKSNW-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR29 : ITRGFSFRELVALR-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI
S1RR31 : YERGSIISSLQSLI-----	QEDIVVVEAN-LEYDYLEEVRSIQLIK--EKTIHW-----ICFI

Figure S5. Alignment of deduced amino acids sequences of REC domain from RR proteins in tomato. Sequences were aligned by the Clustal X program and the highly conserved amino acids are highlighted.

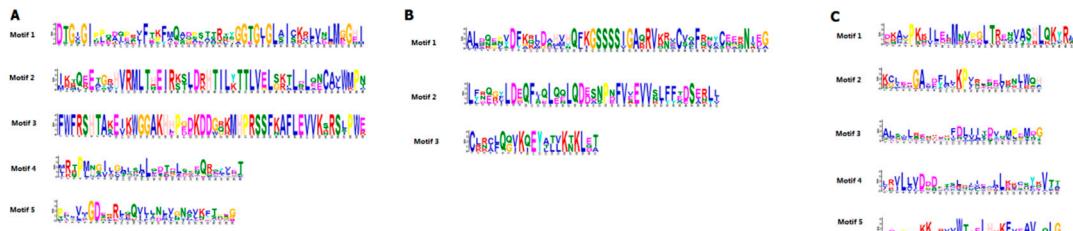
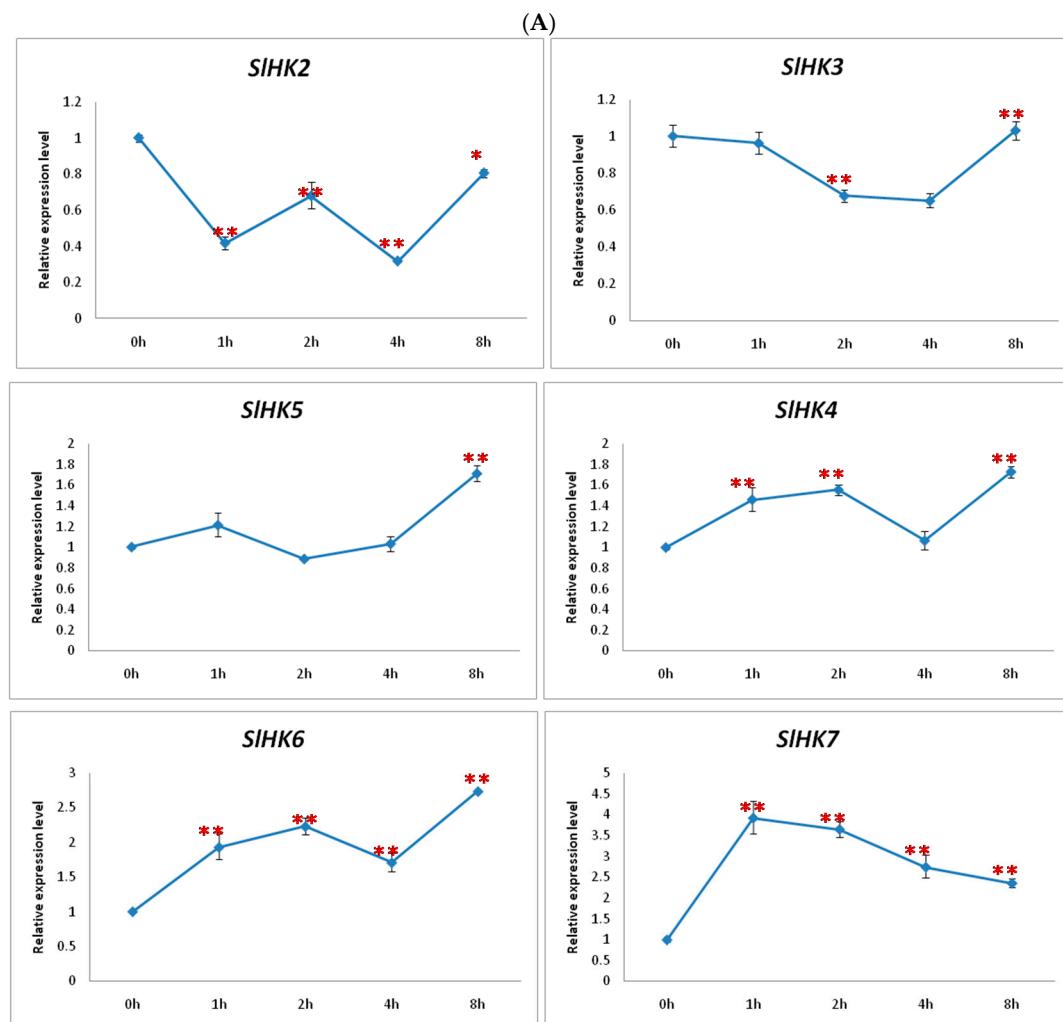
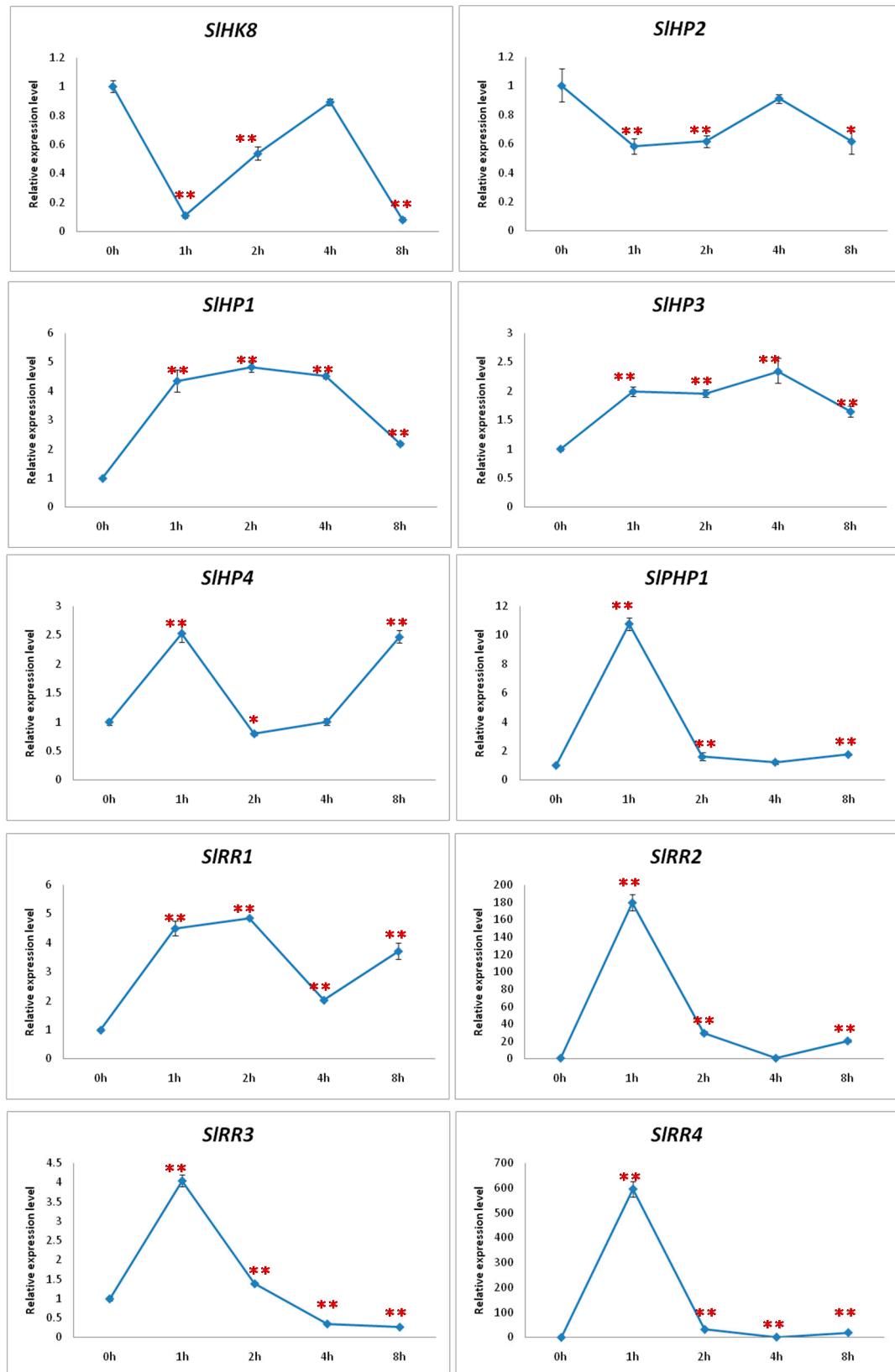


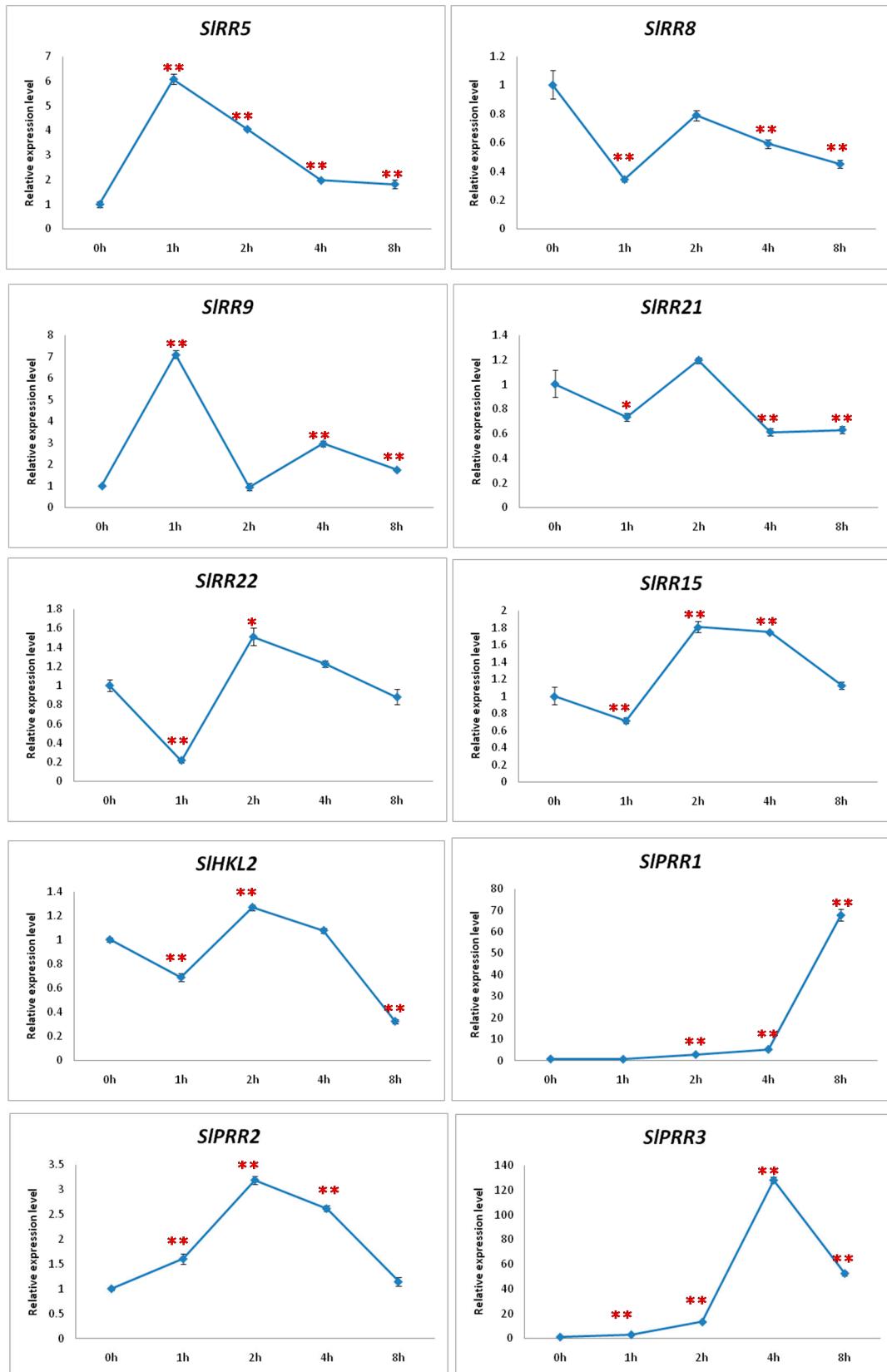
Figure S6. The conserved motif LOGO of HK(L) (A); HP (B); and RR (C) genes in tomato.

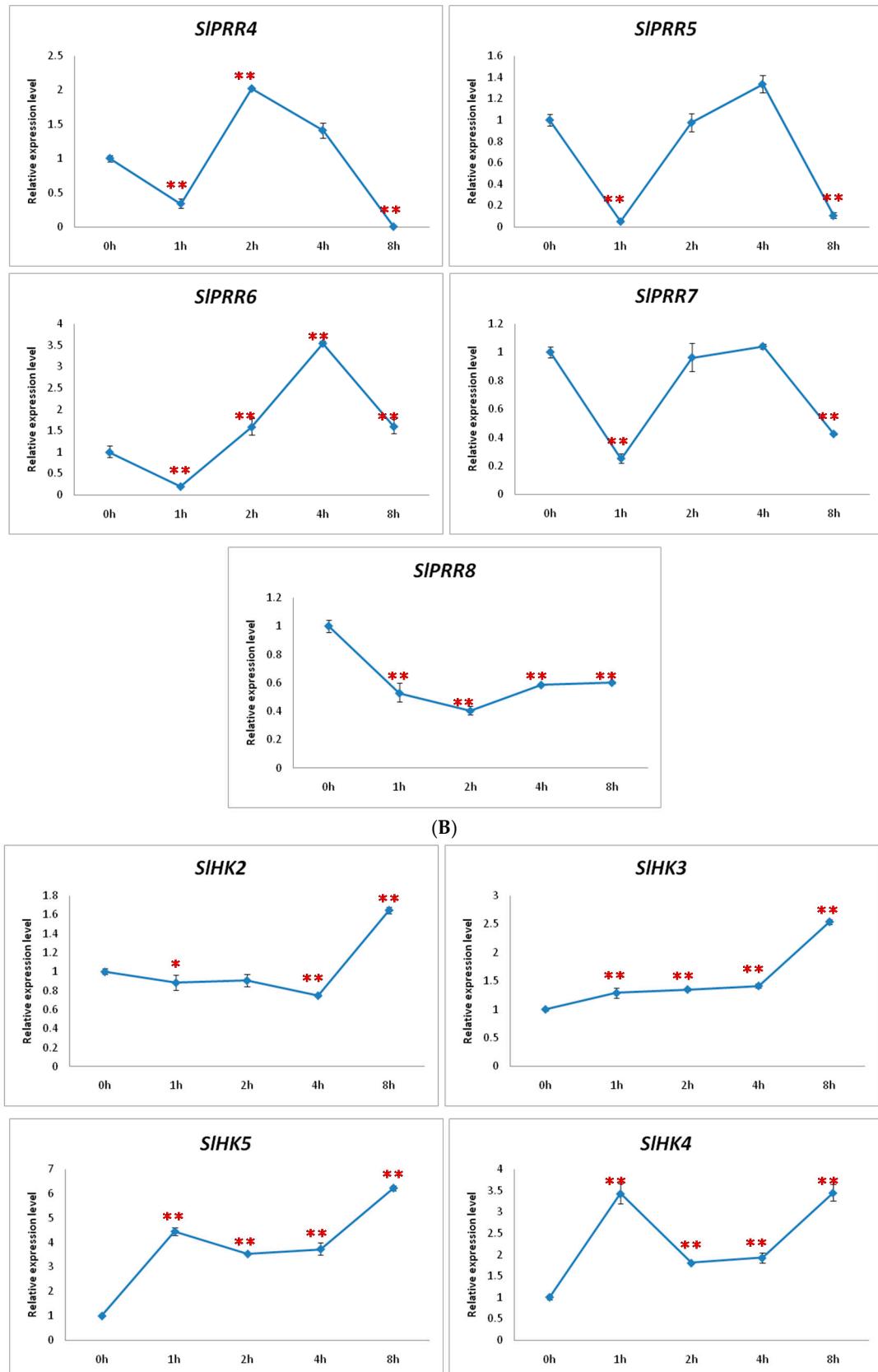
Table S4. The KEGG pathway enrichment analysis for tomato TCS genes.

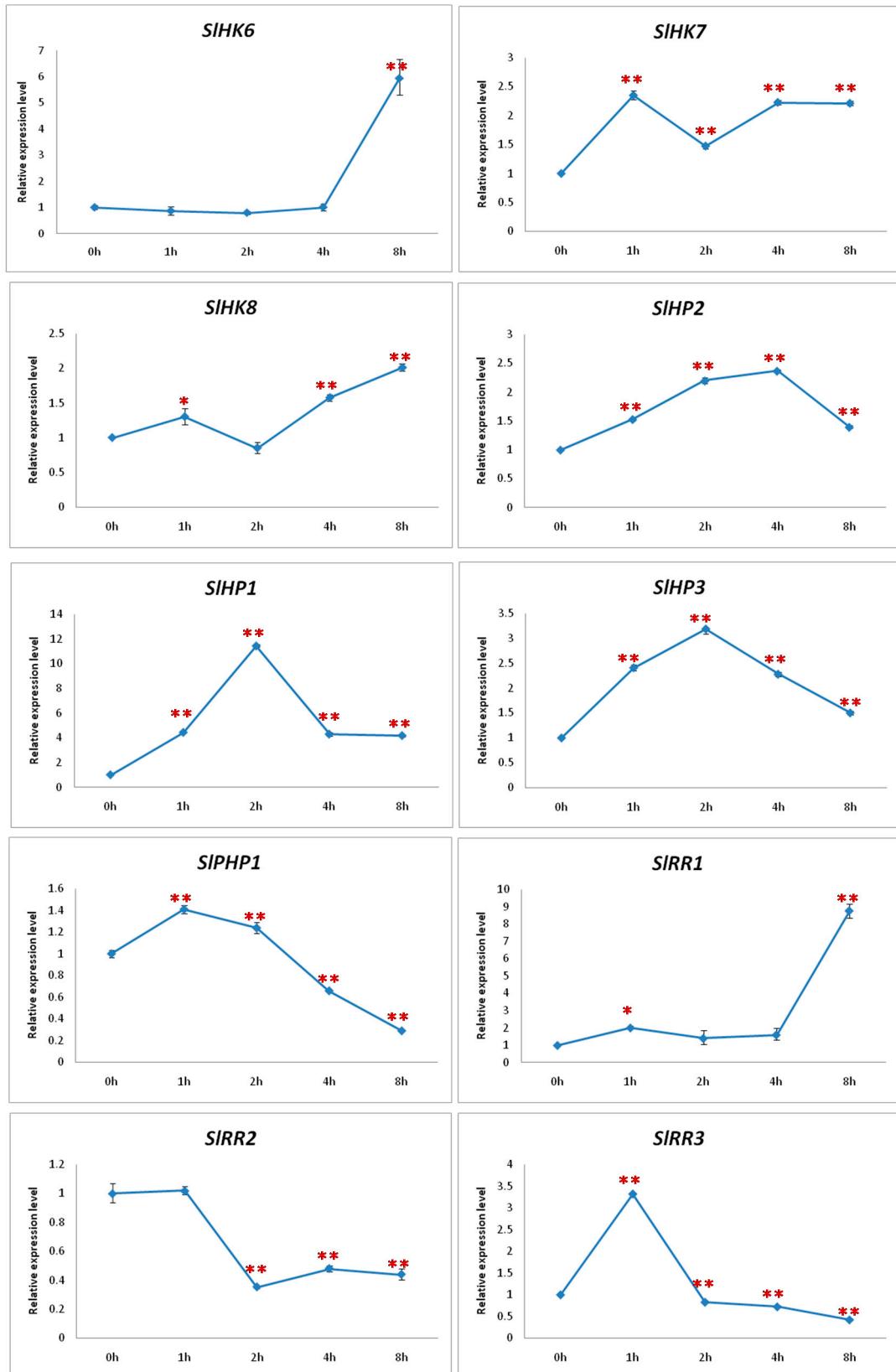
Pathway ID	Pathway	KO List	Gene List
ko02020	Two-component system	ko:K07657	<i>SIIRR29</i>
ko04075	Plant hormone signal transduction	ko:K14489 ko:K14490 ko:K14491 ko:K14492 ko:K14509	<i>SIHK4</i> , <i>SIHK5</i> , <i>SIHK6</i> <i>SIHP1</i> , <i>SIHP2</i> , <i>SIHP3</i> , <i>SIHP4</i> , <i>SIPHP1</i> , <i>SIPHP2</i> <i>SIIRR8</i> , <i>SIIRR9</i> , <i>SIIRR10</i> <i>SIIRR1</i> , <i>SIIRR2</i> , <i>SIIRR3</i> , <i>SIIRR4</i> , <i>SIIRR5</i> , <i>SIIRR6</i> , <i>SIIRR7</i> <i>SIHK7</i> , <i>SIHK8</i> , <i>SIHK9</i> , <i>SIHKL1</i> , <i>SIHKL2</i> , <i>SIHKL3</i> , <i>SIHKL4</i>
ko04712	Circadian rhythm–plant	ko:K12120 ko:K12121 ko:K12127 ko:K12129 ko:K12130	<i>SIHKL5</i> , <i>SIHKL8</i> <i>SIHKL6</i> , <i>SIHKL7</i> <i>SIPRR1</i> , <i>SIPRR2</i> <i>SIPRR5</i> , <i>SIPRR6</i> <i>SIPRR3</i> , <i>SIPRR4</i>

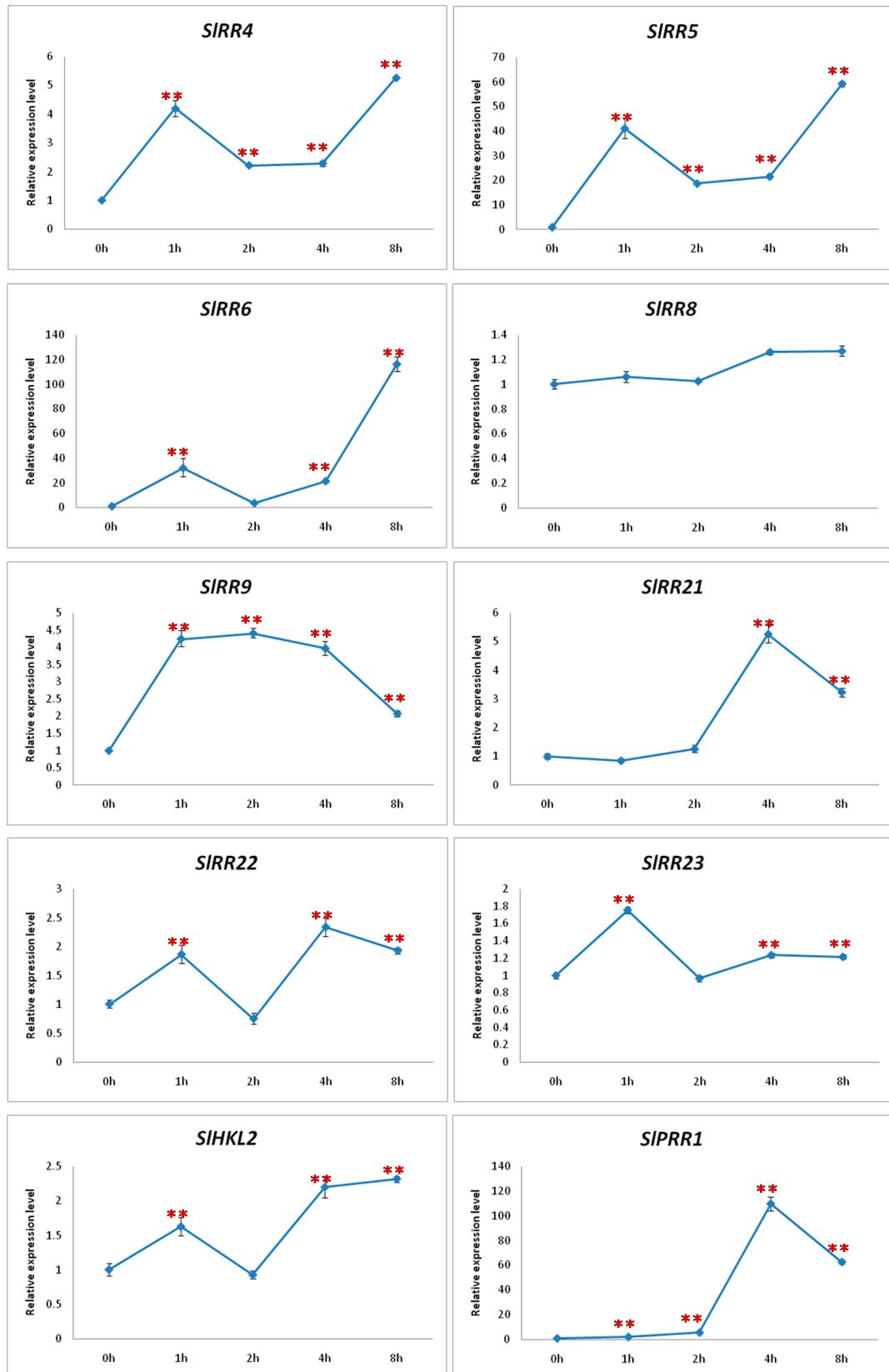
Table S5. The expression patterns of tomato TCS genes in response to various hormone (ZT (A) and ABA (B)) and stresses (drought (C) and salt (D)). The second true leaves were collected at 0, 1, 2, 4, and 8 h after the onset of treatments. Asterisks on the top of bars (SE values) indicate statistically significant difference between the compared pairs (* $p < 0.05$; ** $p < 0.01$).

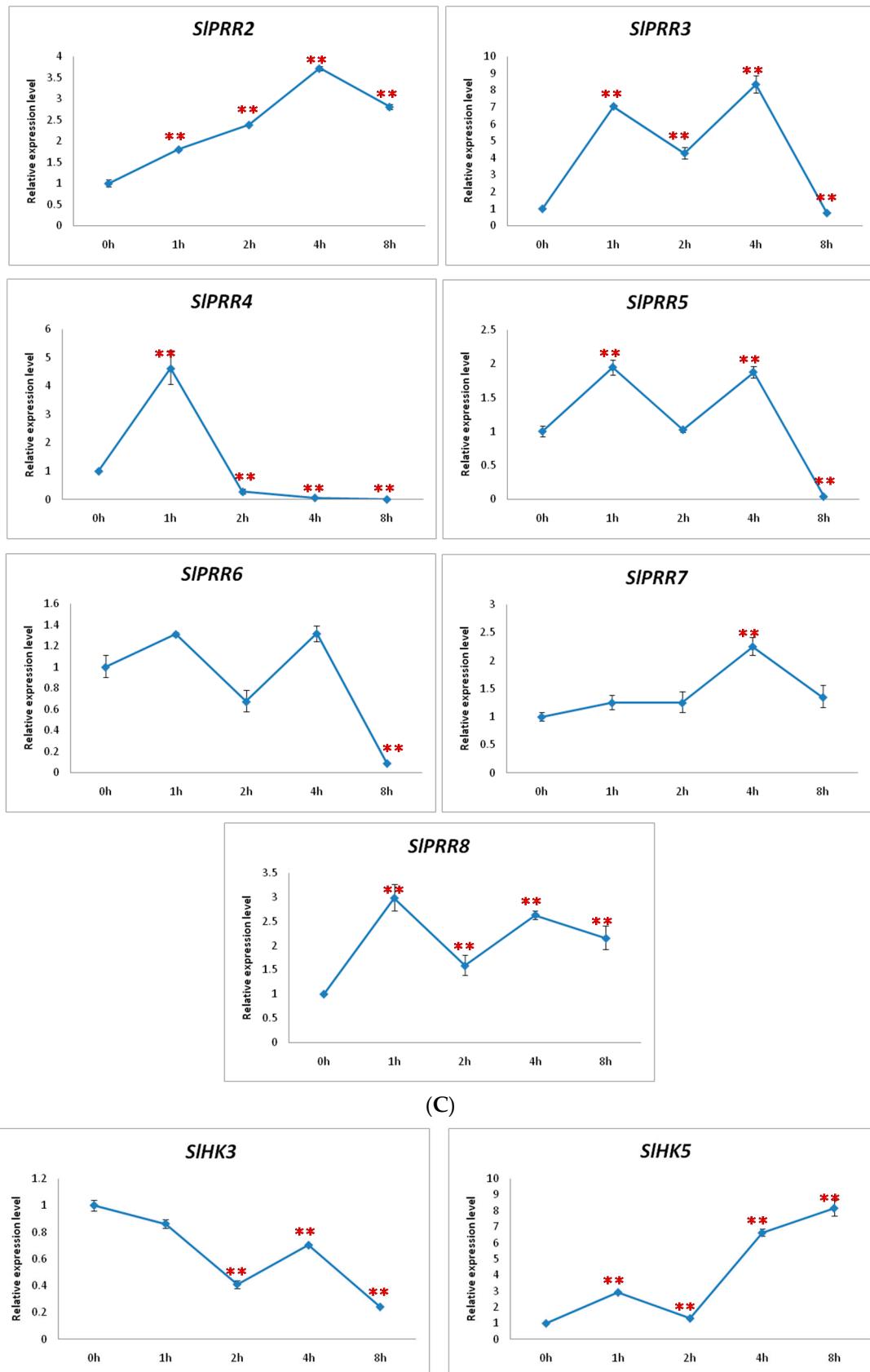


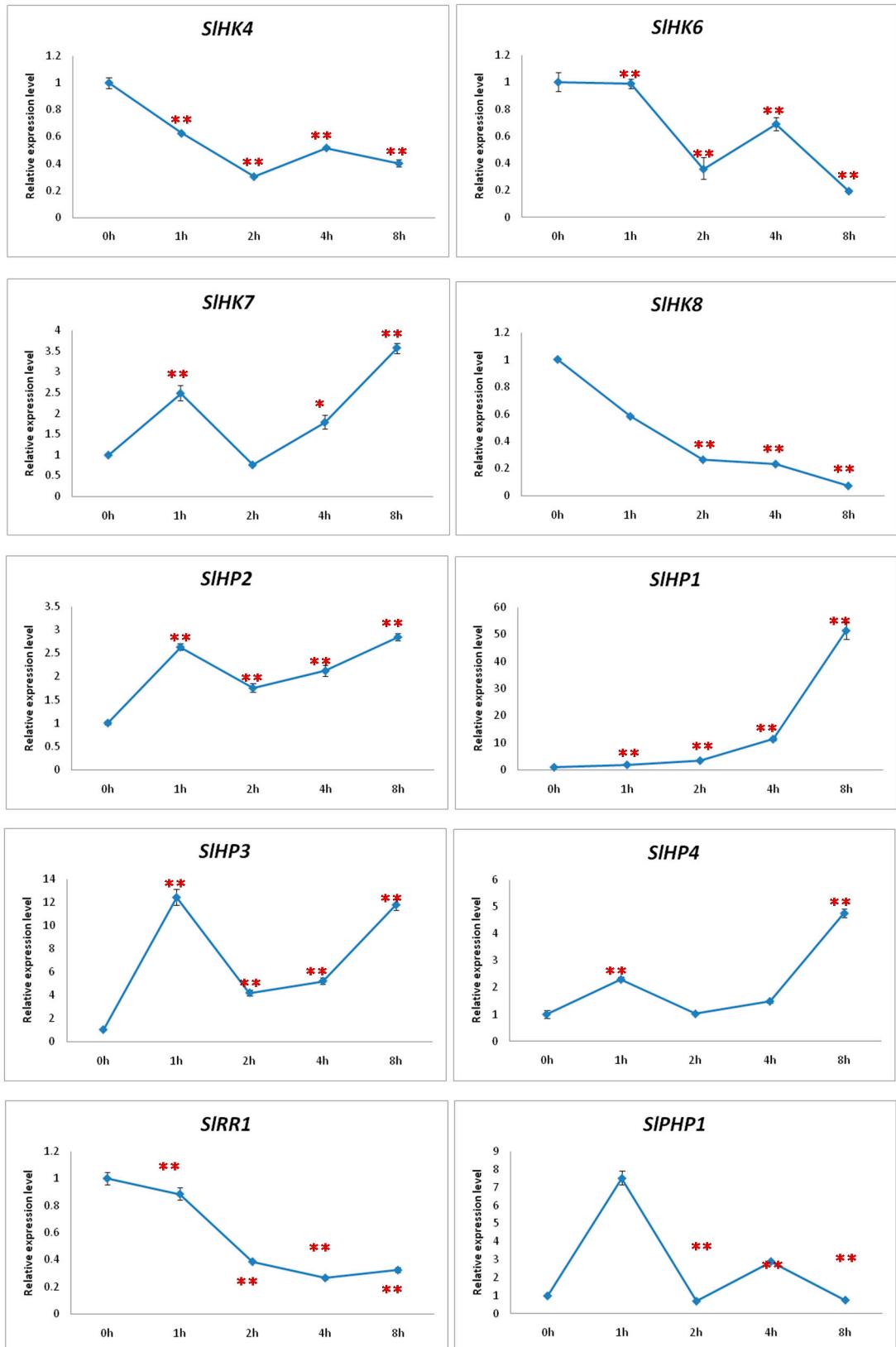


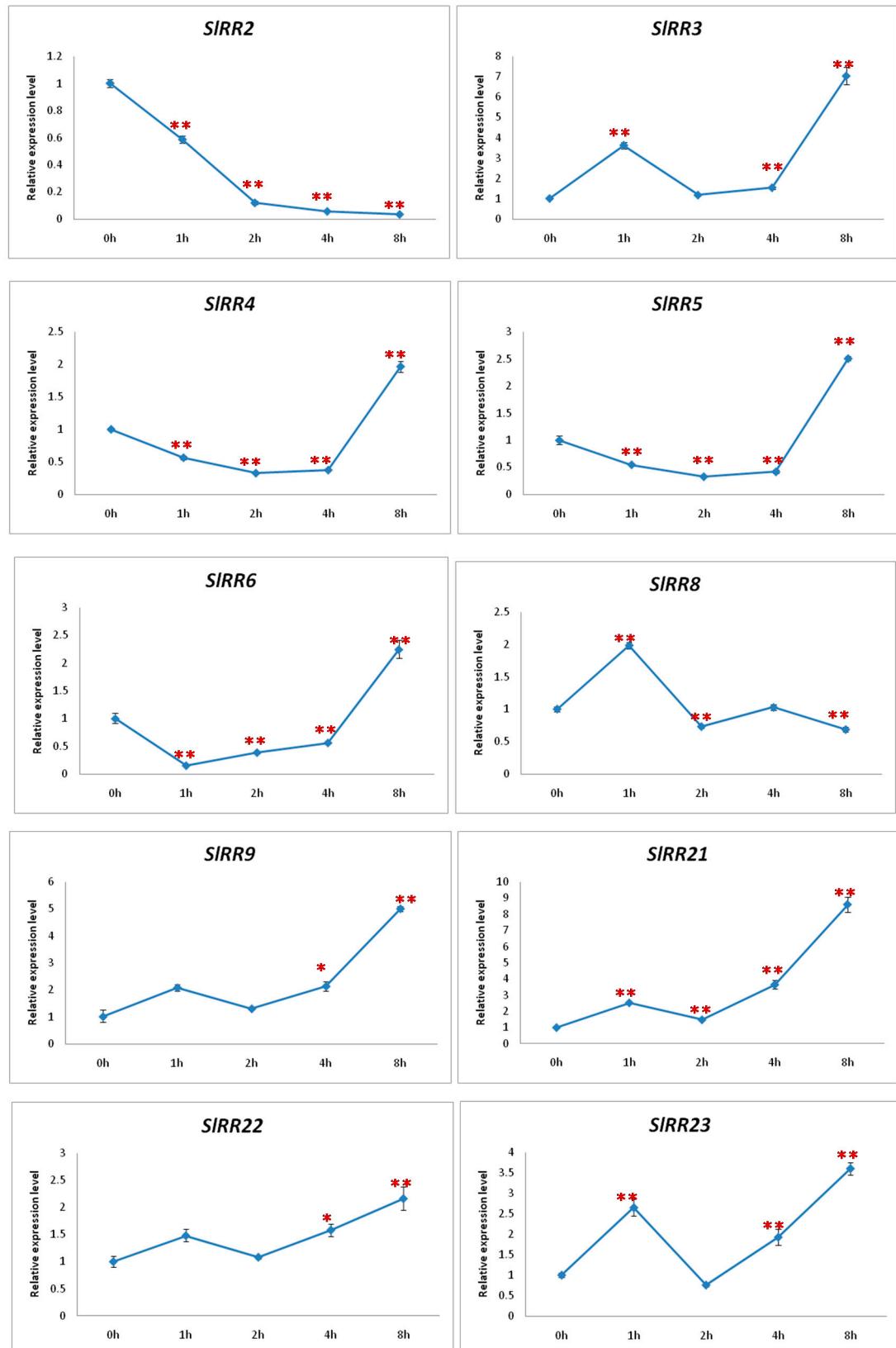


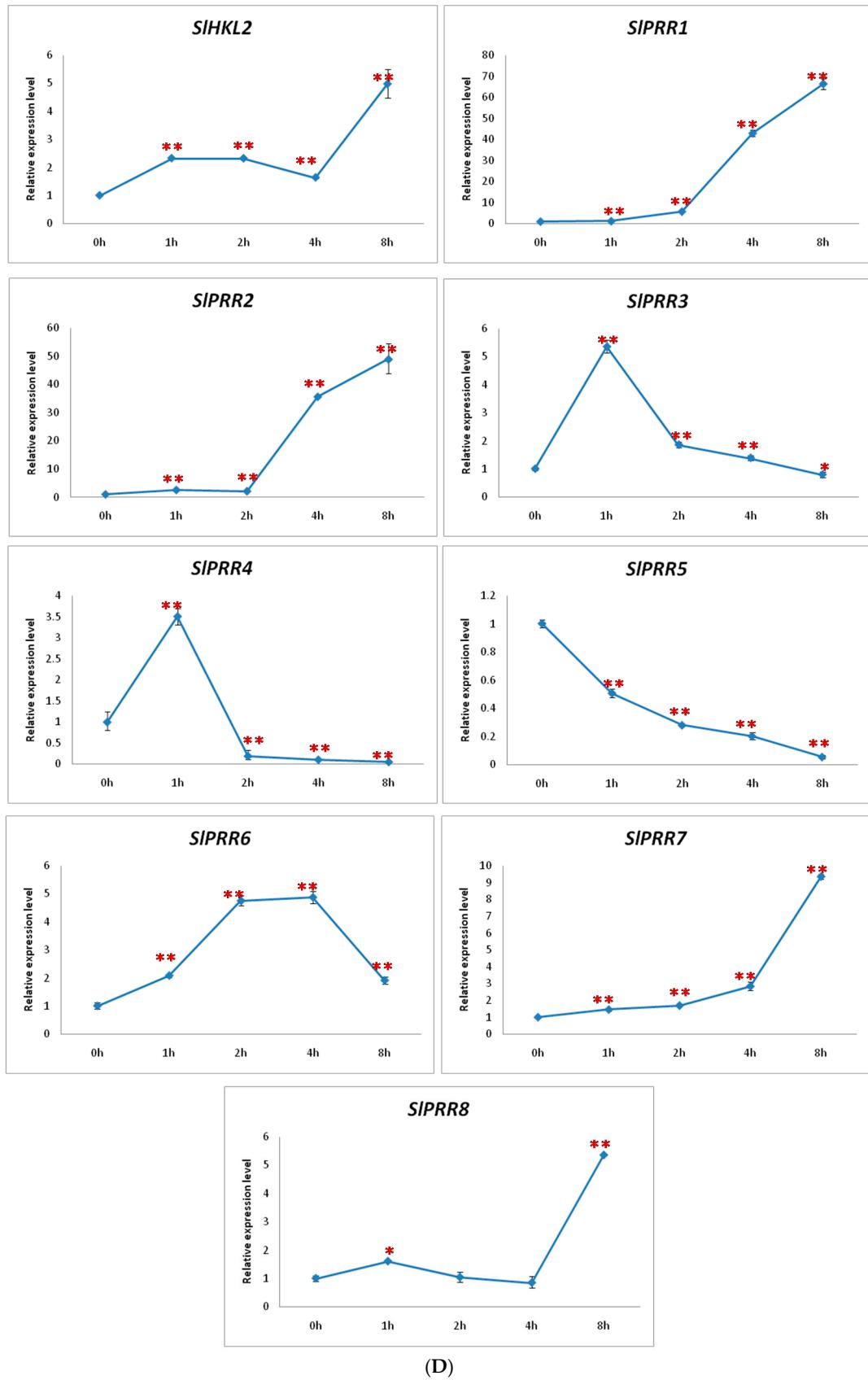




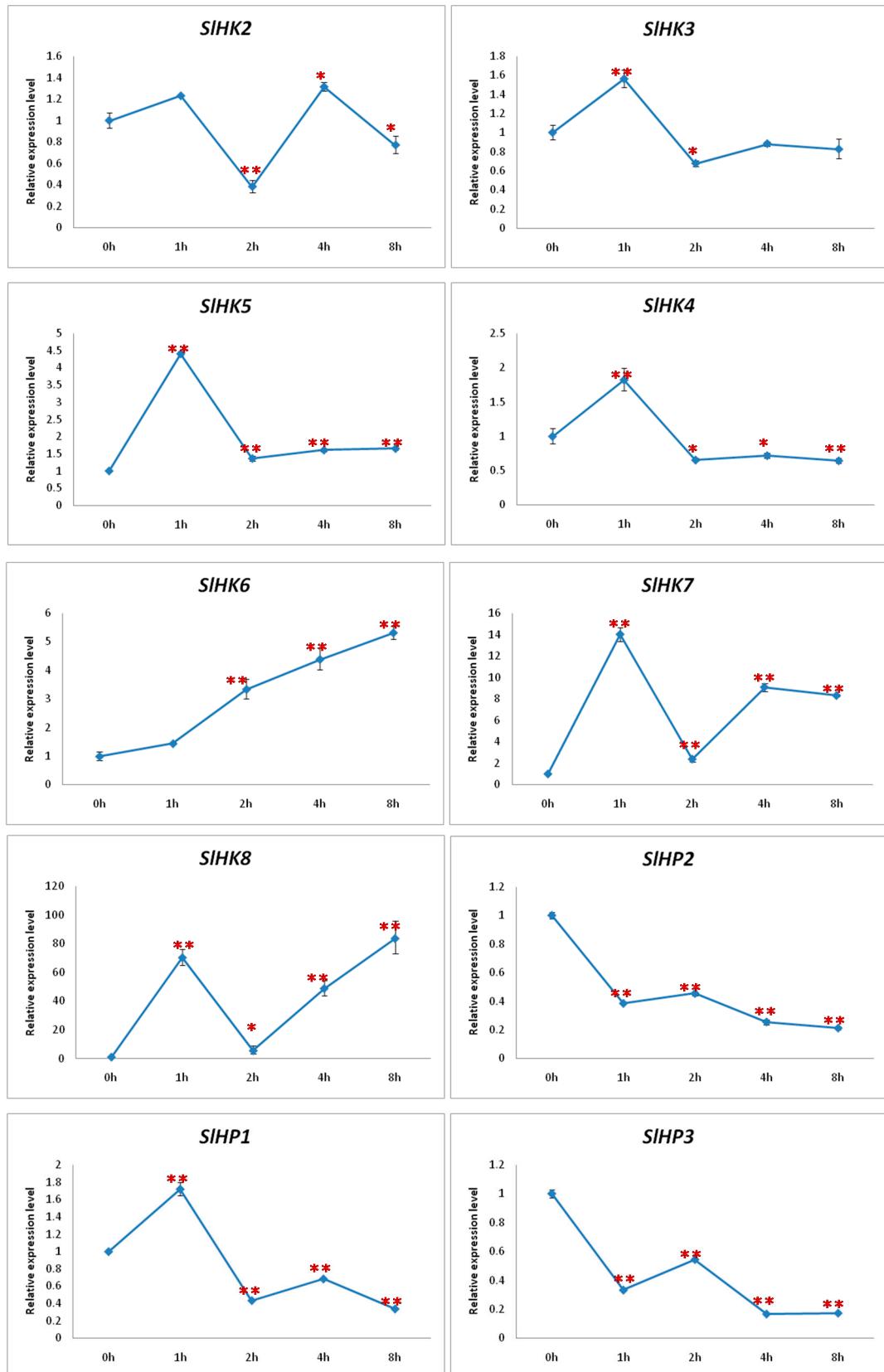


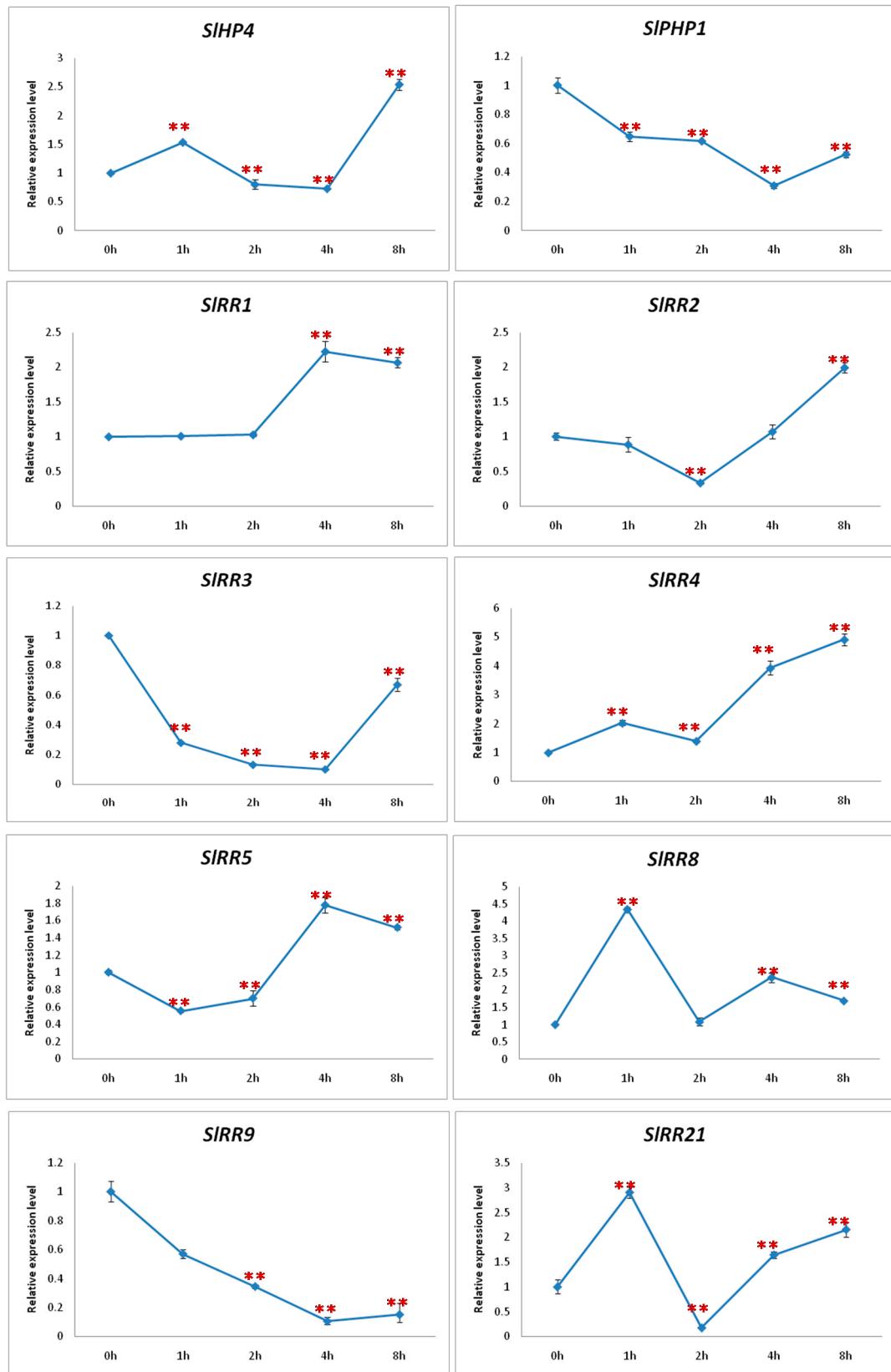


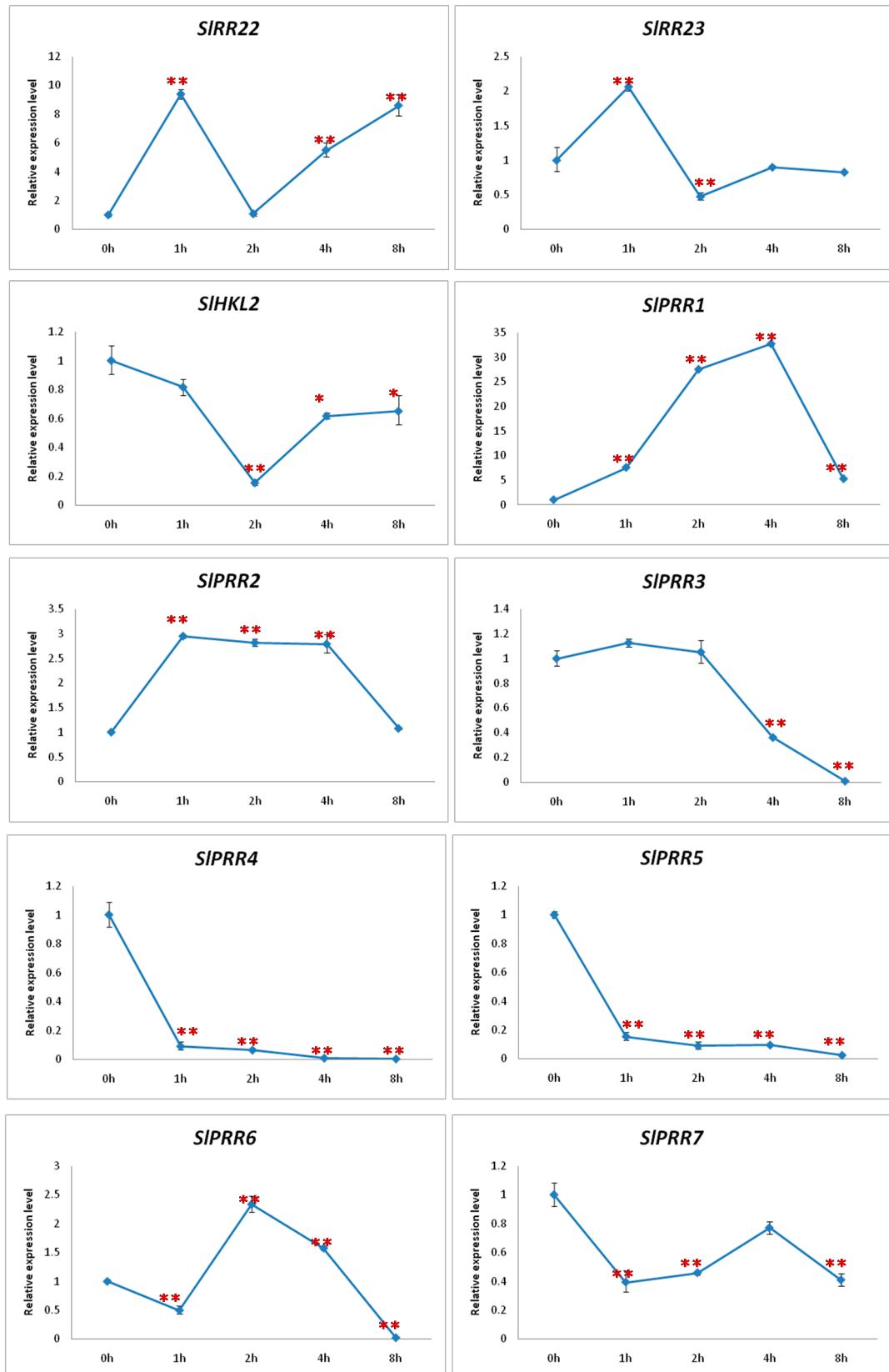


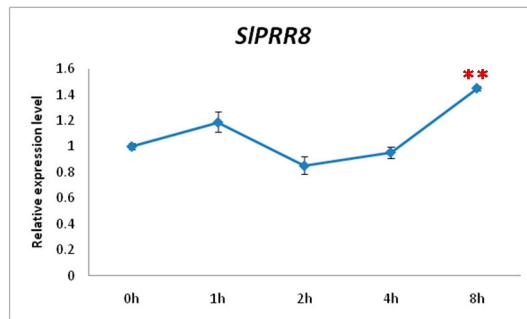


(D)







**Table S6.** Gene-specific primers of selected TCS genes used for subcellular localization and qRT-PCR analysis.**Primers used for subcellular localization**

Primer-S	Primer-A	Gene Name
CGGGATCCTGGTGTGATAAGATAAGAG	GCTCTAGACACACTGTATTCTGATTTC	SIHK8
CGGGATCCAAGGAAATGGAAGTGGG	GCTCTAGAATCCCGTAAGCATTGAG	SIHP2
CGGGATCCCTTCTCCCCACATCAAA	GCTCTAGACATGTTCACCTGCTGC	SIHP3
CGGGATCCAGTGGAGATGCCAAGAAATG	GCTCTAGAAATGGGAGAGGAGGGC	SIRR1
CGGGATCCTGGTCTCAATGGTAAGTATG	GCTCTAGATCATGGGAACTTGAGACC	SIRR8

Primers used for qRT-PCR

Primer-S	Primer-A	Gene Name
ATAACCAACTCCTCTTCGTCC	AAGTCCTTCGTAACTCAGCC	SIHK1
TCAACGGGAGCAAATACTAAC	GATGTCCTCTTCACCGCAAAC	SIHK2
GGTTAGAGAGAAATGGGGTGC	TATGACAAAAGGTGATGAGGC	SIHK3
CTTGTCCTTGGTGGGTG	TGCTTACGTTGAACGGTCC	SIHK4
CACCTCTTTATTCCCTCTCATC	CACATCAAACACCTAACCCC	SIHK5
TGTCAGGAGAGGAGGATCG	GAATGTAAAACAACACCAAGG	SIHK6
AACGGGAAACACAGACAGAG	CACCAAGAAATCCAAAGACG	SIHK7
TATTGGAGATGAAAAACGGC	CAACTGGGAAATCCTGAG	SIHK8
CTCTGCTACCTATGCCCTCC	ATCCCACCATCATCTCCAC	SIHK9
GACTTCAAGAAACTGGATGCTC	TTACGGAAGGAAATGCACAC	SIHP1
GGTAATCCAAGCAACAAAGC	CCAAGAATCCCTCACGAAAC	SIHP2
CGATGAGCATTGATTGGTA	GAATTGATGTGGGGAGA	SIHP3
AGATGATGATAACCTAACCTCG	GAGCACTCTTTCACTTTTG	SIHP4
CTATGATTGCTAGGCTGGA	CATTGTCCTTTACTCTCTGGC	SIPHP1
CCTCCCCTAATTCTCGTCTC	GCAATGCTGAACCTGC	SIPHP2
TGAACAAGAGAAAGTGCAG	AGAGGTCAACTGATGAGGGTG	SIRR1
TAGATGTTGGAGGAAGGTGC	GGGATGGTATTGATTGTGTCG	SIRR2
AGCAGCAACAAACAACACAG	TGCGAGCGAGAGATTACAC	SIRR3
GATTACTGTATGCCCTGGATG	GCCCCTCTCTAACGATCTAC	SIRR5
GCTTAGAAGAAGGGCAG	TGGGGCTTTACATTGG	SIRR4
AGATGGTCTGAGGGCTTCTAG	GATGACATGATCACAACGGTAC	SIRR6
GAAAATCAAGGAATCGTCG	GTAATTAGCACCCAAACACAAC	SIRR7
ACCTCTGCCCTGTATTGC	CTGGTTGAGTCCCTGTC	SIRR8
GCATGGTATGCCAAAGGC	GCATCCCACAAACAGCAC	SIRR9
GGAGTCACTACAGAACATTGG	CAACCTCACTCATTAGTTACACAC	SIRR13
GAAGGATCATTCTTGCTTCTCG	GGTATTCTTAGACGGTAGGTG	SIRR16
TGTAGCTCTATCCATTCTCG	TCATTTCAATCGTCACCTCTG	SIRR18
GTGTTGTTCACTGCCAGC	CCAATCCAAGGAATCGT	SIRR21
AGGAGAAGGCAGAACAGAGG	AGCCCAAACACAGCAGG	SIRR22
GCTCAGGAAATGCCAGTATC	CAAGACCAACAAGTTCAAGAAG	SIRR23