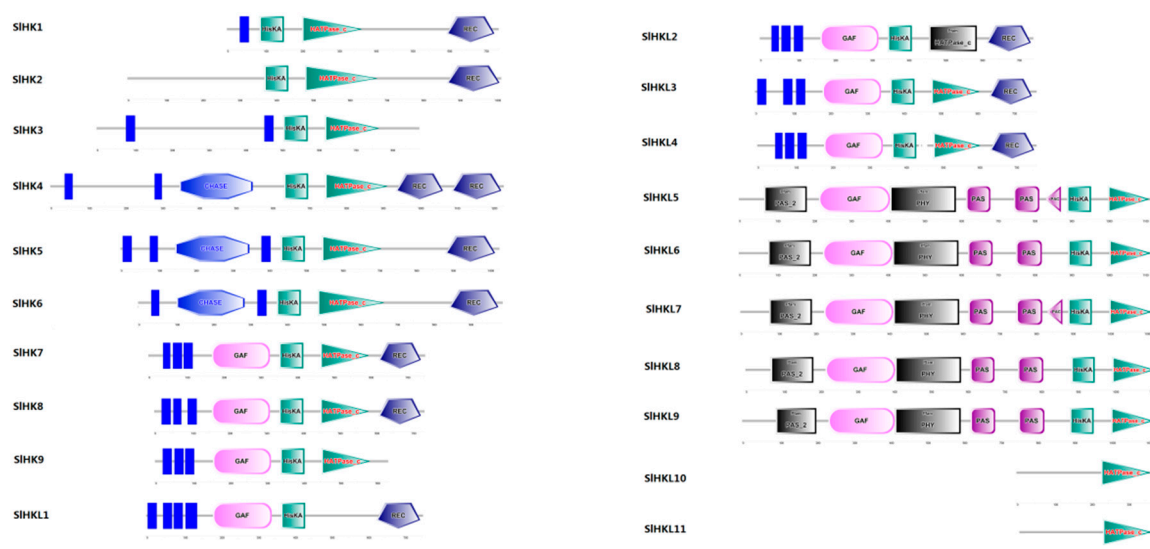
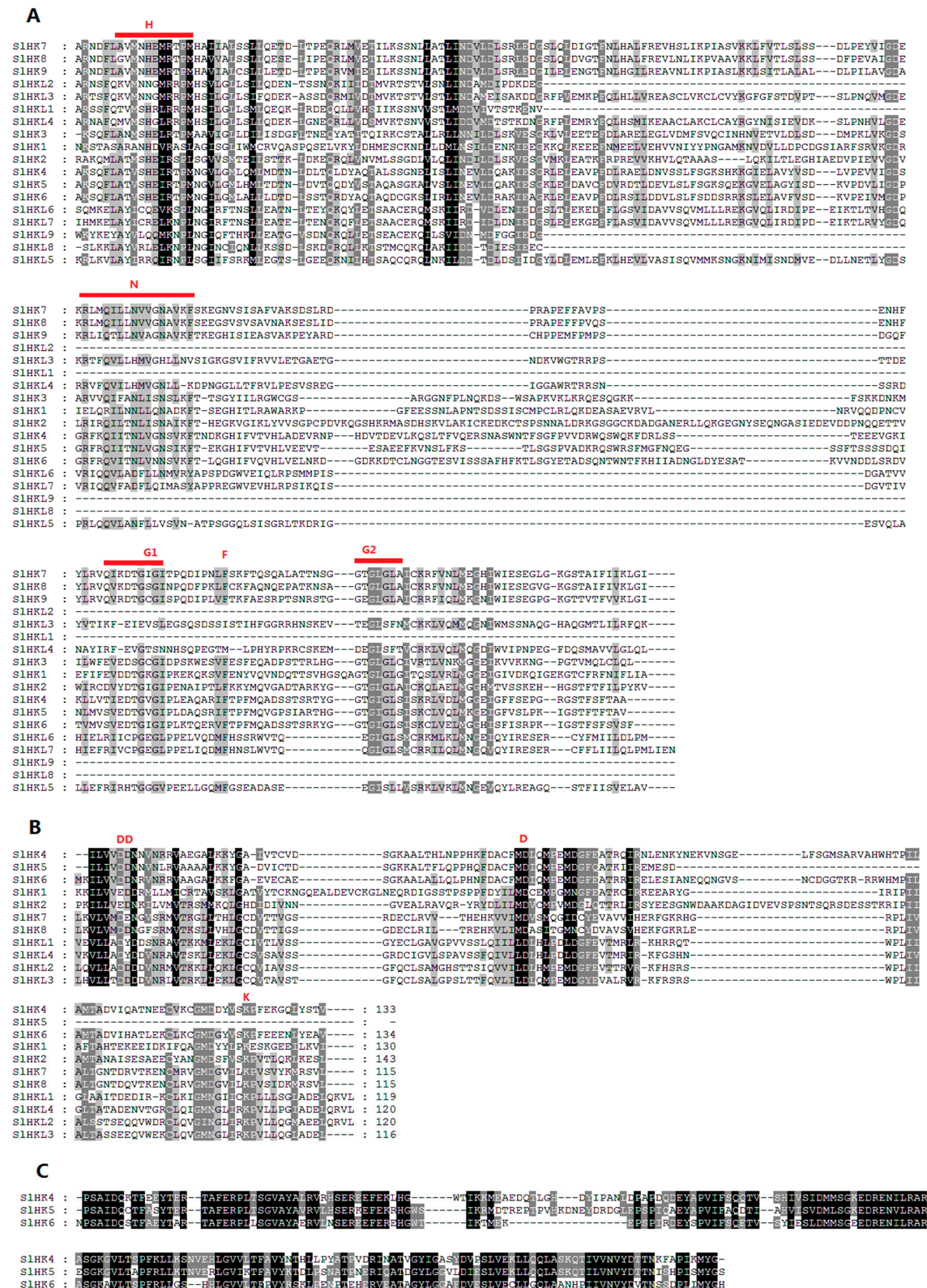


# Supplementary Materials: Genome-Wide Identification and Expression Analysis of Two-Component System Genes in Tomato

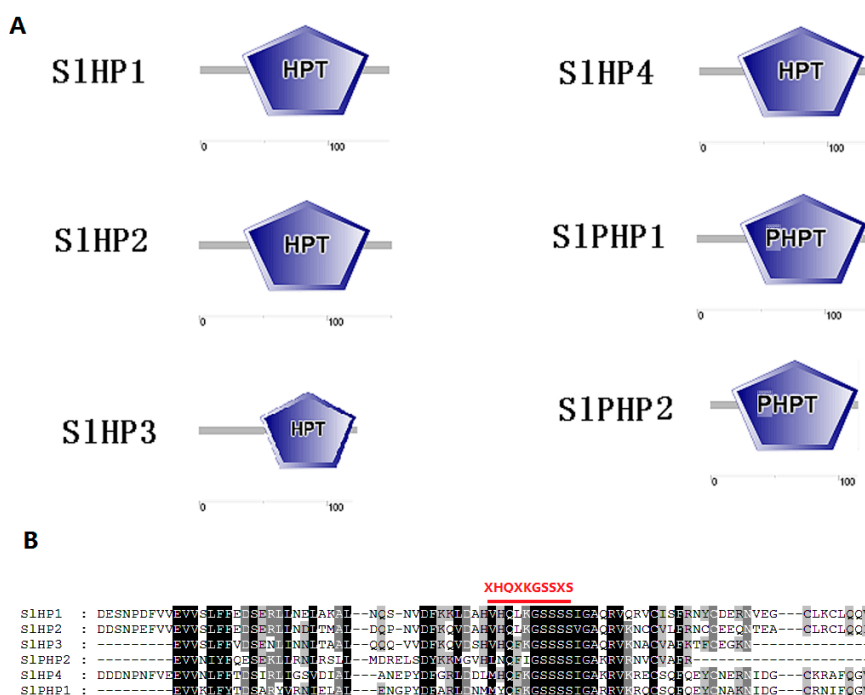
Yanjun He, Xue Liu, Lei Ye, Changtian Pan, Lifei Chen, Tao Zou and Gang Lu



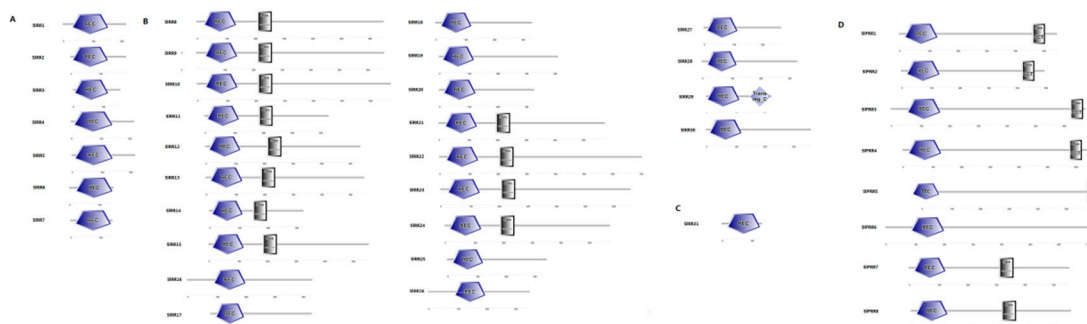
**Figure S1.** Domain structures of SIHK(L)s in tomato. Domain structures were analyzed by SMART online tool and drawn according to their original location and size. TM, transmembrane region; HisKA, Histidine kinase domain; HATPase, Histidine kinase-like HATPases; Rec, receiver domain; CHASE, cyclase/histidine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



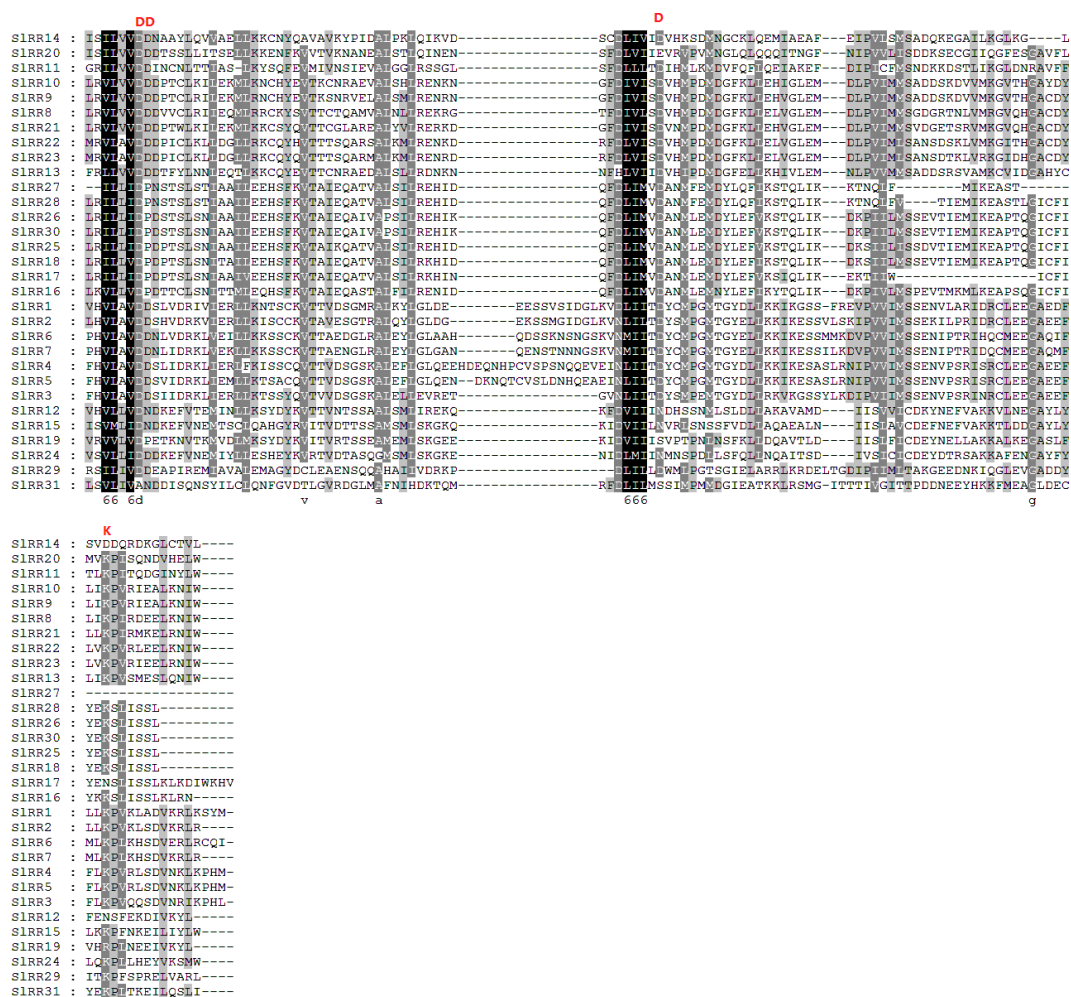
**Figure S2.** Amino acid sequence alignment of SIHK(L)s in tomato. Histidine kinase (like) (A); receiver (B); and cyclase/histidine kinase-associated sensory extracellular (CHASE) (C) domains from SIHK(L) proteins in tomato were aligned by the Clustal X program.



**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.



**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.

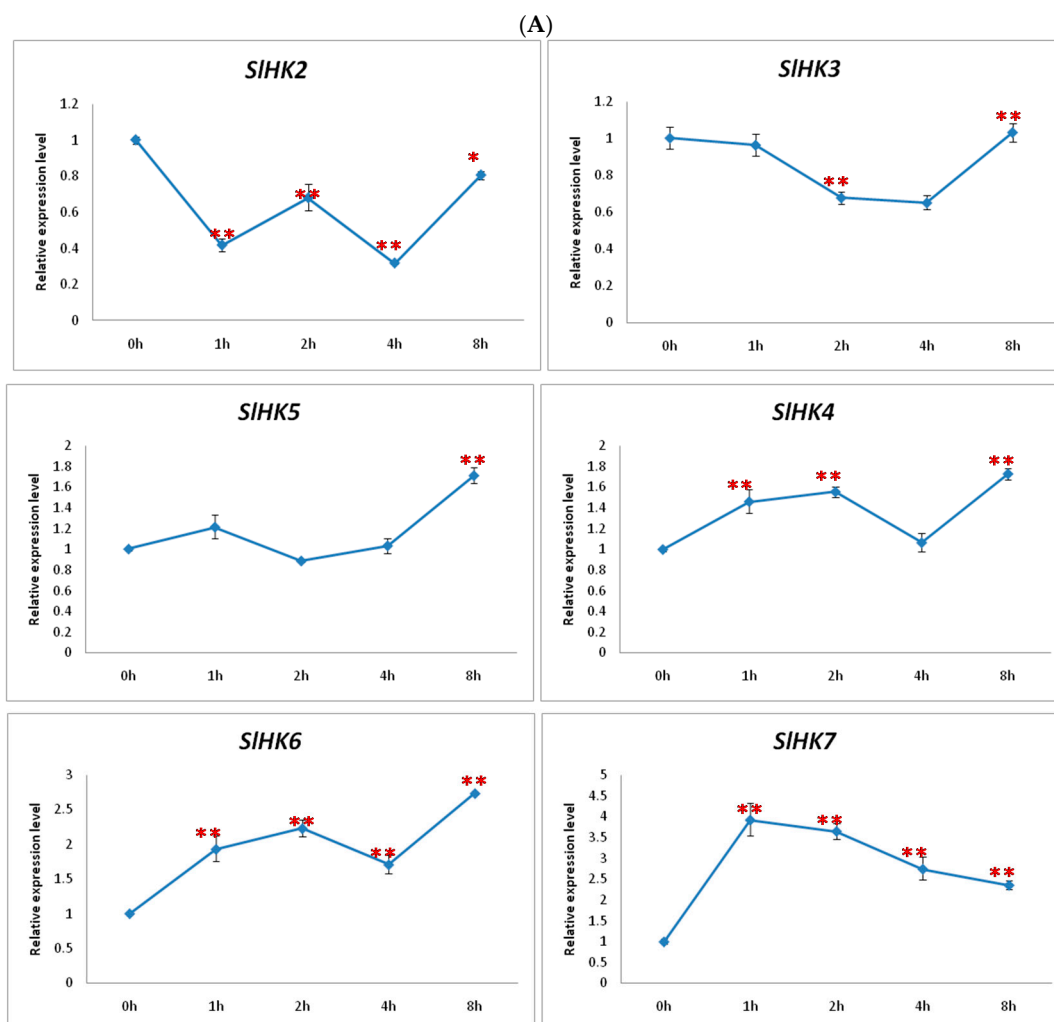


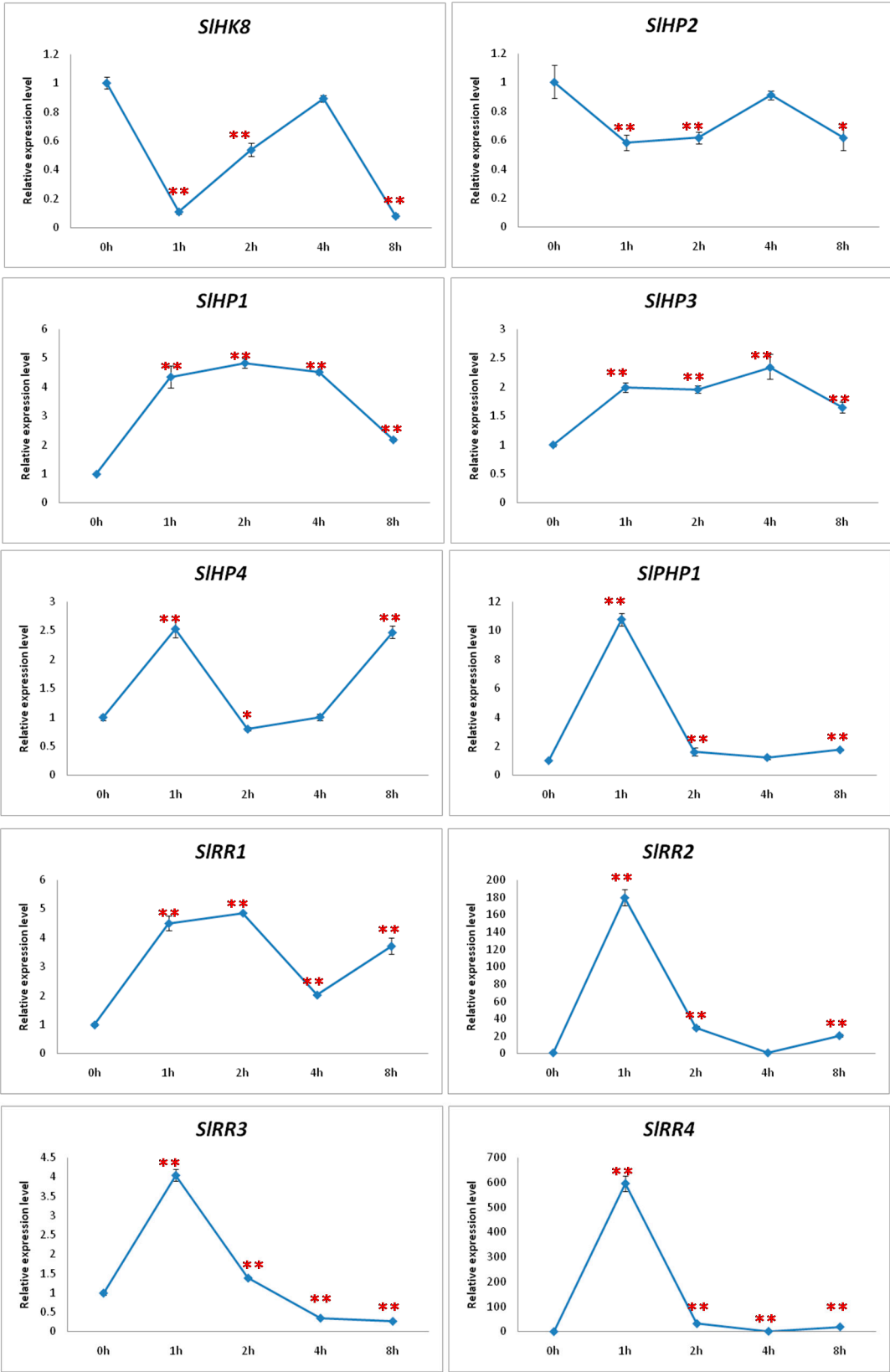
**Figure S6.** The conserved motif LOGO of HK(L) (A); HP (B); and RR (C) genes in tomato.

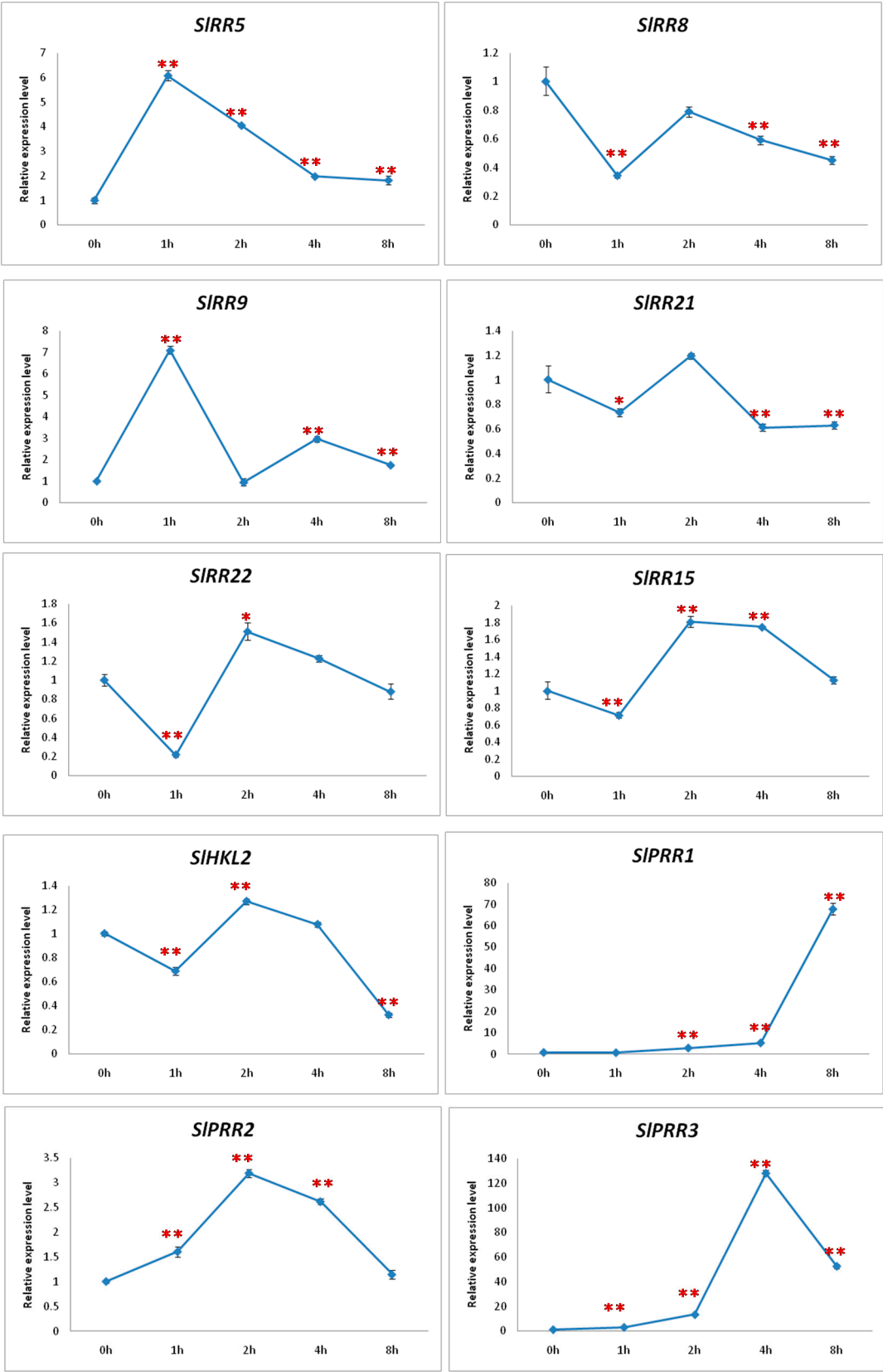


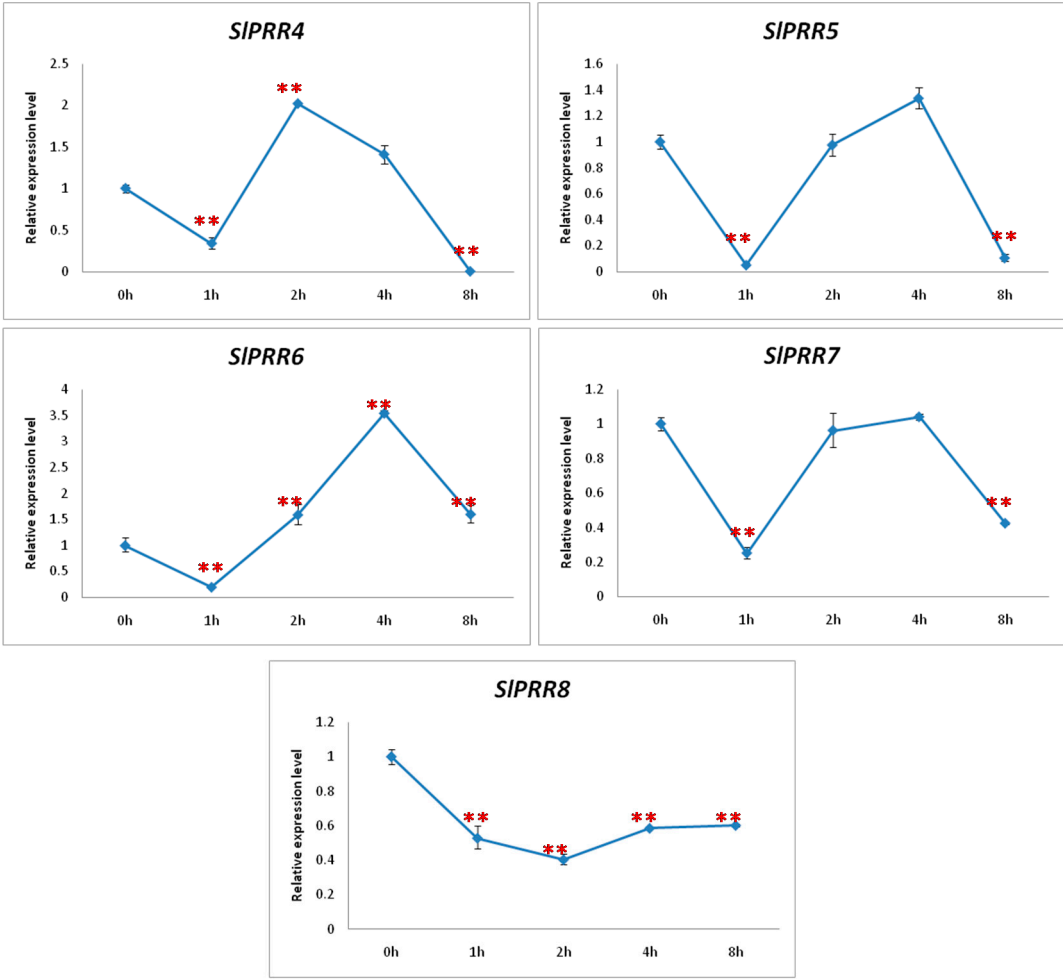
**Table S4.** The KEGG pathway enrichment analysis for tomato TCS genes.

Pathway ID	Pathway	KO List	Gene l1st
ko02020	Two-component system	ko:K07657	<i>SIRR29</i>
ko04075	Plant hormone signal transduction	ko:K14489	<i>SIHK4, SIHK5, SIHK6</i>
		ko:K14490	<i>SIHP1, SIHP2, SIHP3, SIHP4, SIHP1, SIHP2</i>
		ko:K14491	<i>SIRR8, SIRR9, SIRR10</i>
		ko:K14492	<i>SIRR1, SIRR2, SIRR3, SIRR4, SIRR5, SIRR6, SIRR7</i>
		ko:K14509	<i>SIHK7, SIHK8, SIHK9, SIHKL1, SIHKL2, SIHKL3, SIHKL4</i>
ko04712	Circadian rhythm-plant	ko:K12120	<i>SIHKL5, SIHKL8</i>
		ko:K12121	<i>SIHKL6, SIHKL7</i>
		ko:K12127	<i>SIPRR1, SIPRR2</i>
		ko:K12129	<i>SIPRR5, SIPRR6</i>
		ko:K12130	<i>SIPRR3, SIPRR4</i>

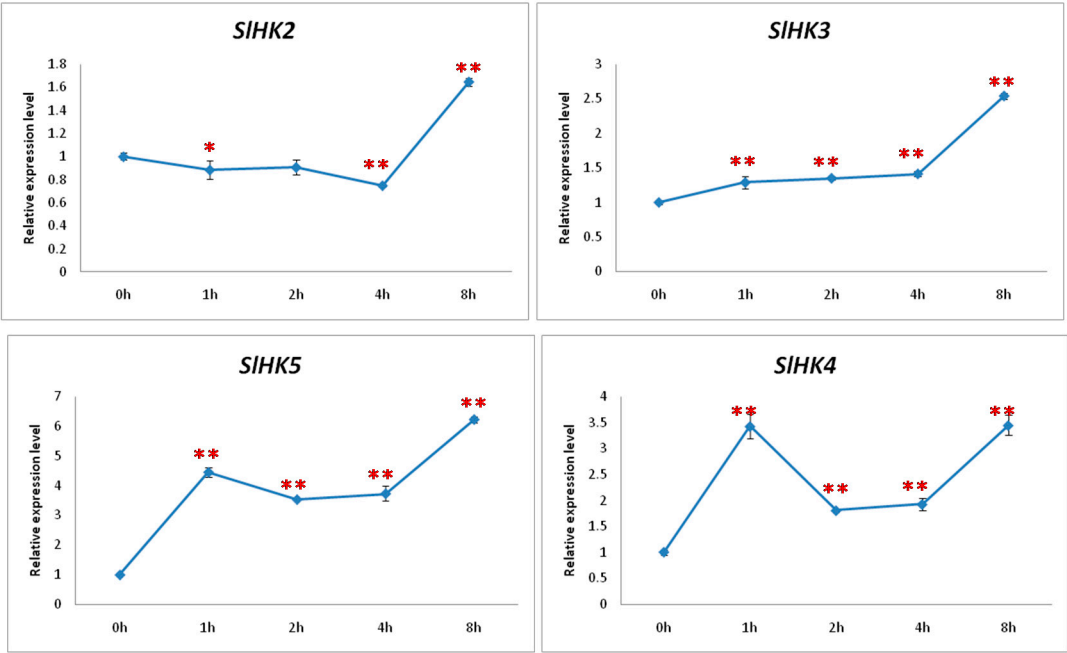
**Table S5.** The expression patterns of tomato TCS genes in response to various hormone (ZT (A) and ABA (B)) and stresses (drought (C) and salt (D)). The second true leaves were collected at 0, 1, 2, 4, and 8 h after the onset of treatments. Asterisks on the top of bars (SE values) indicate statistically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



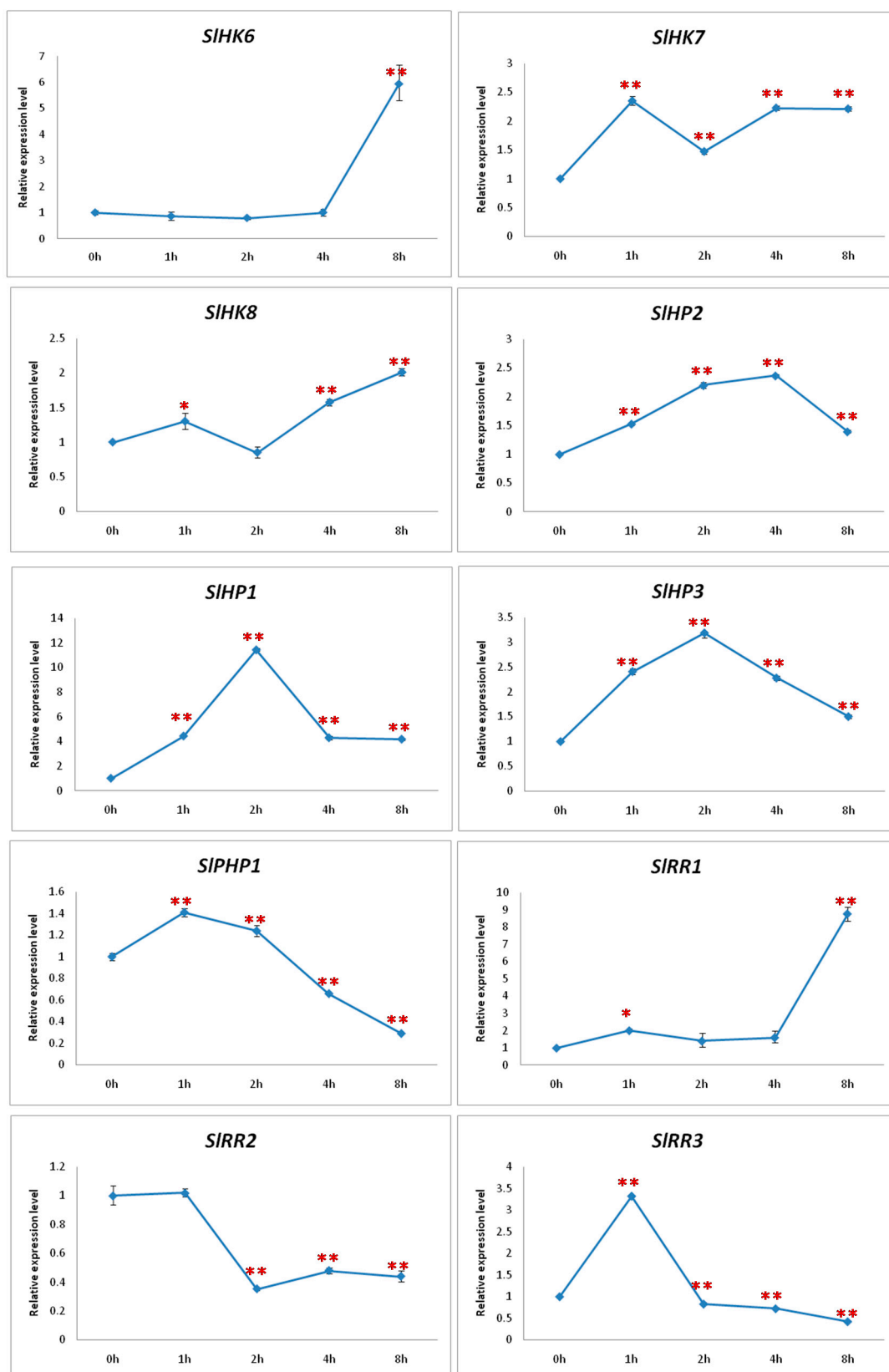


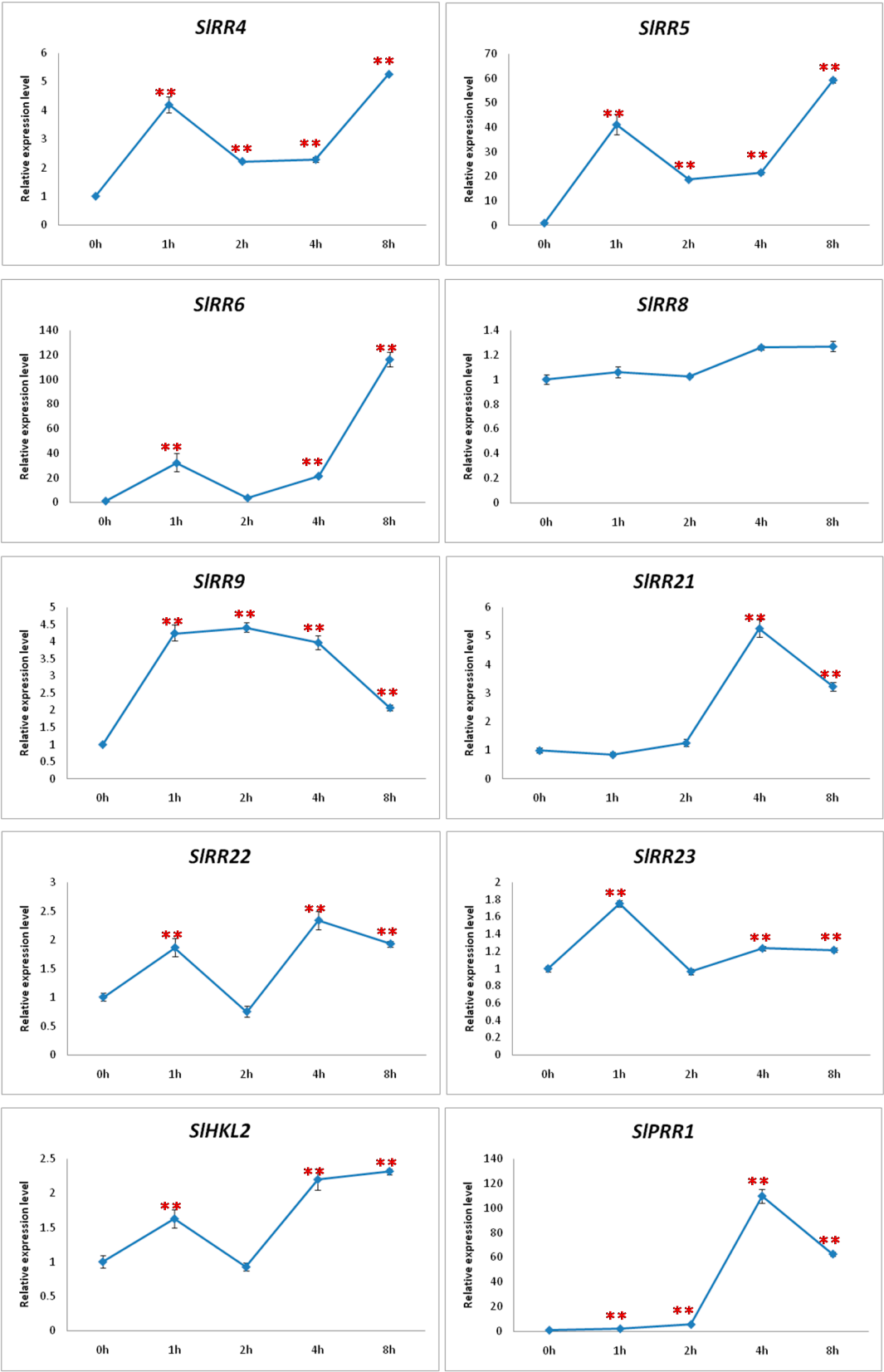


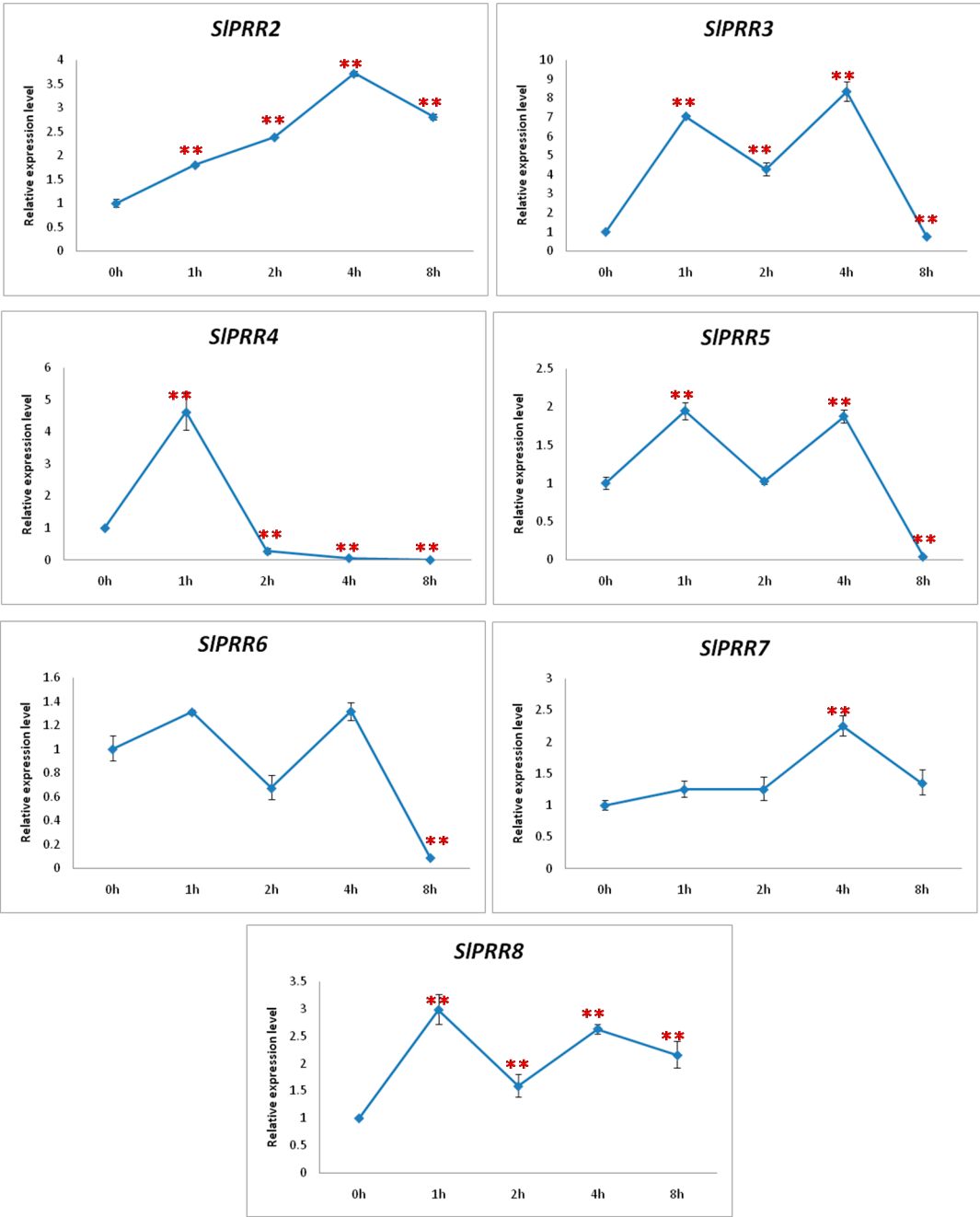
(B)



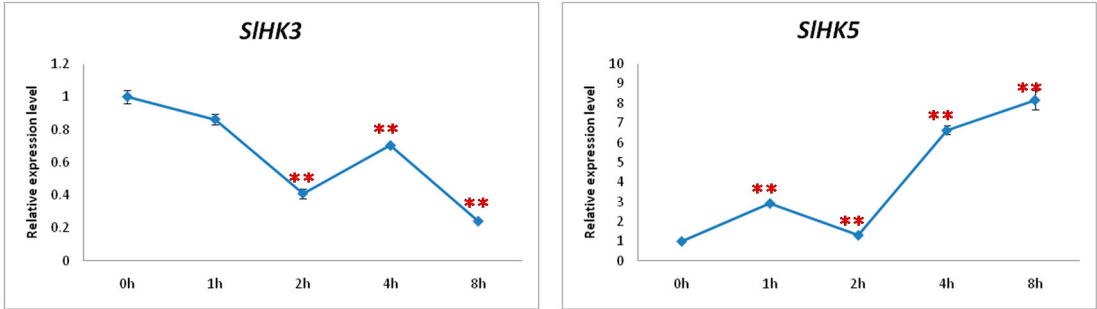


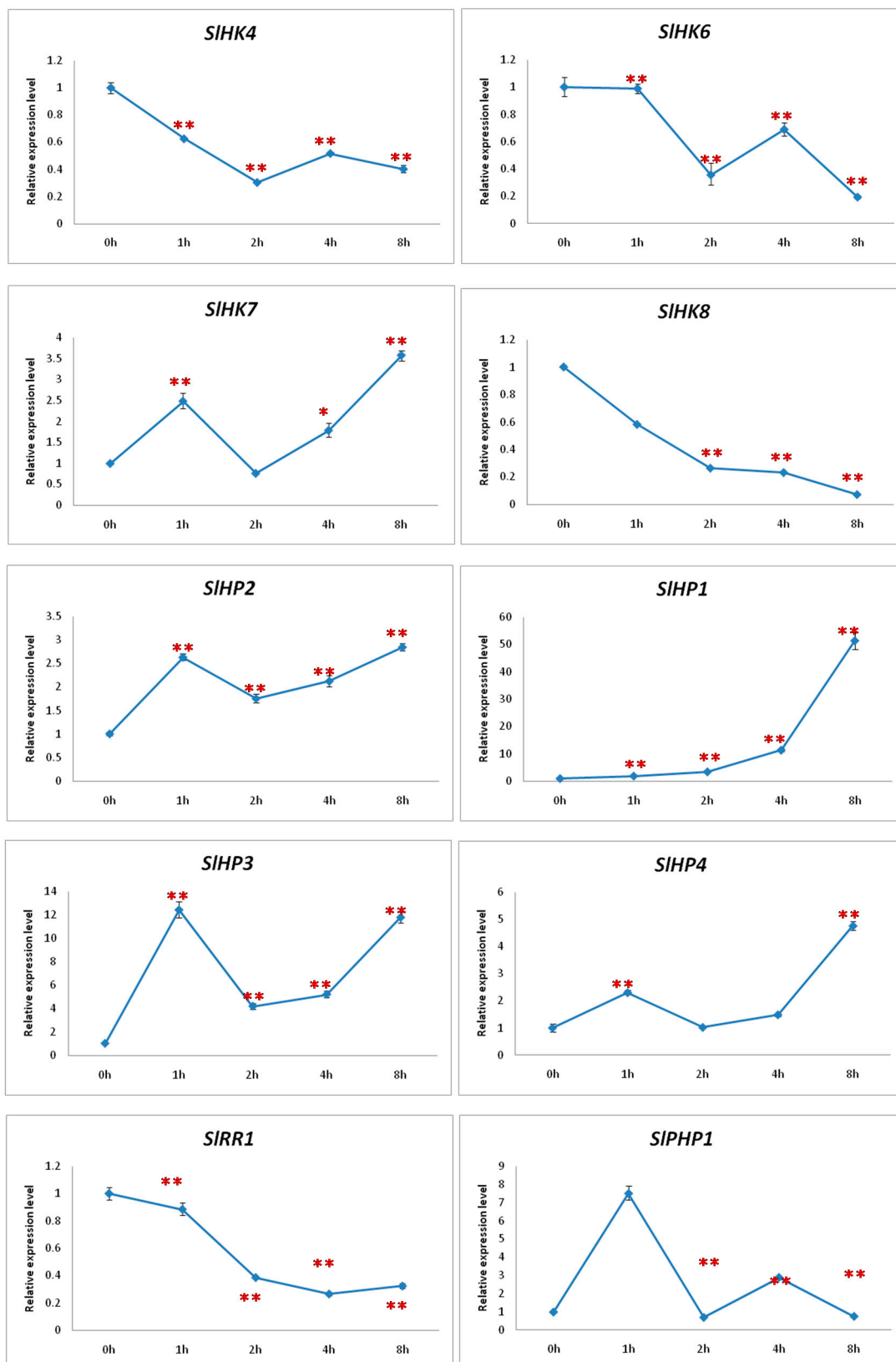




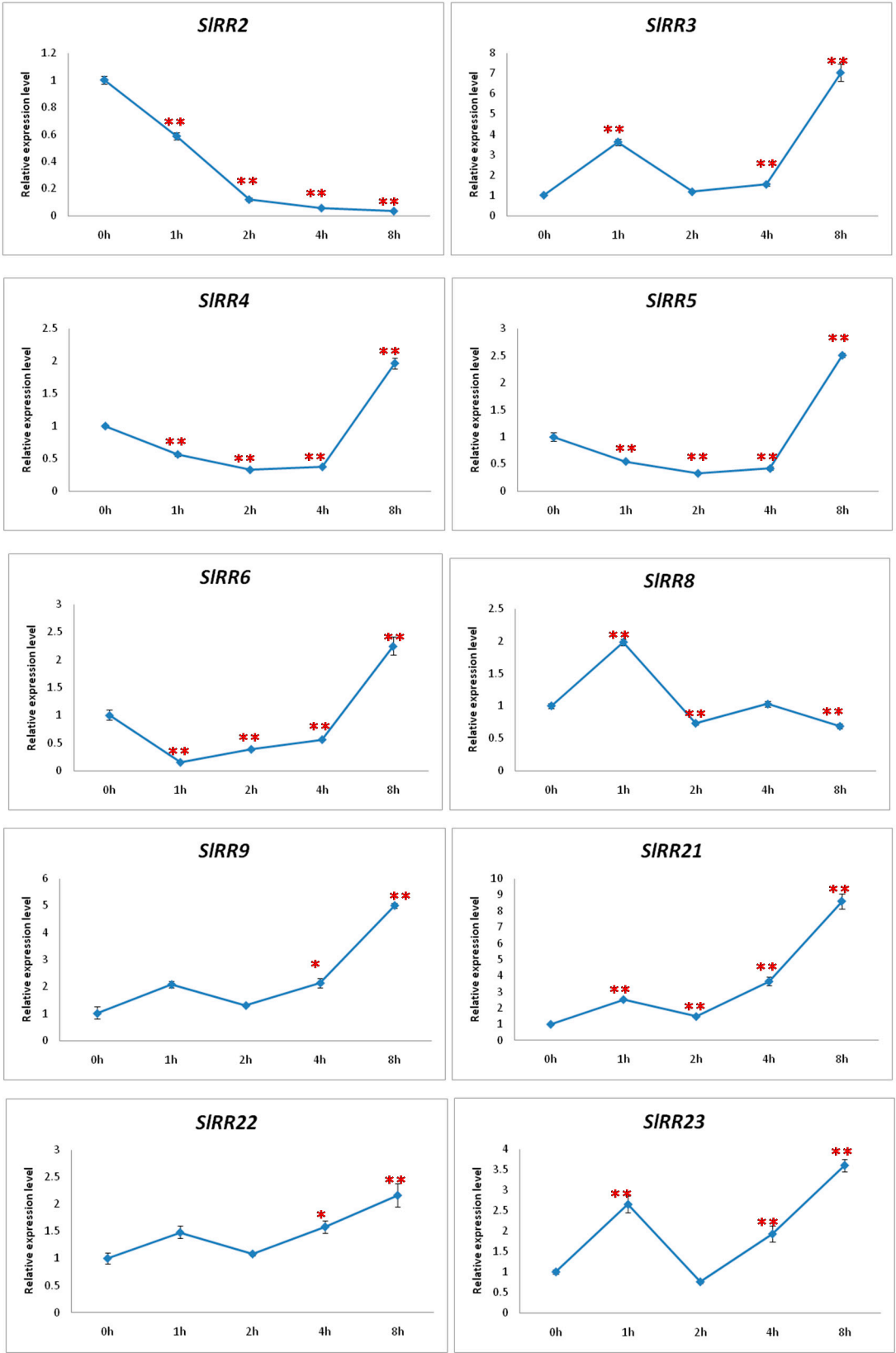


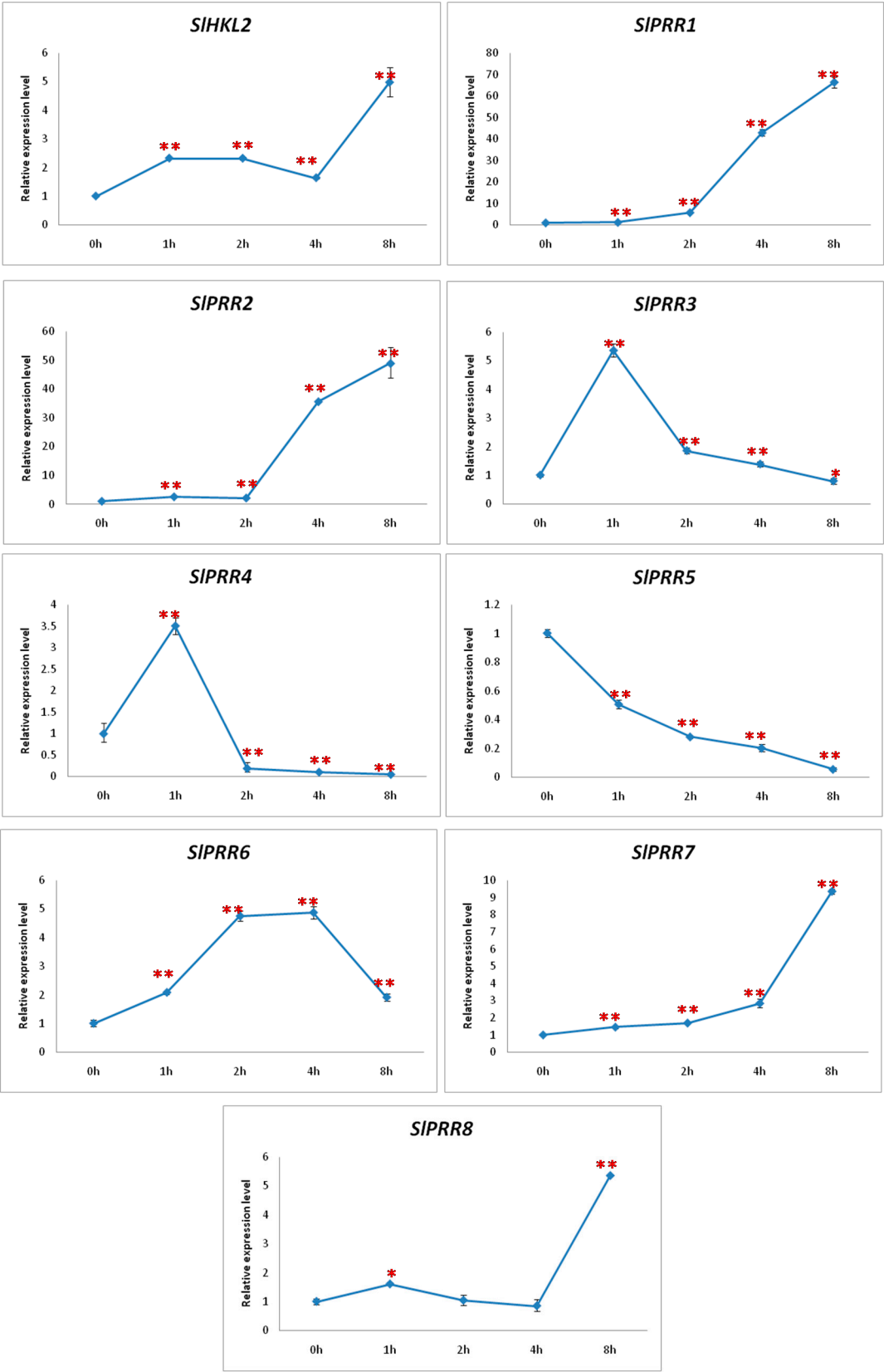
(C)



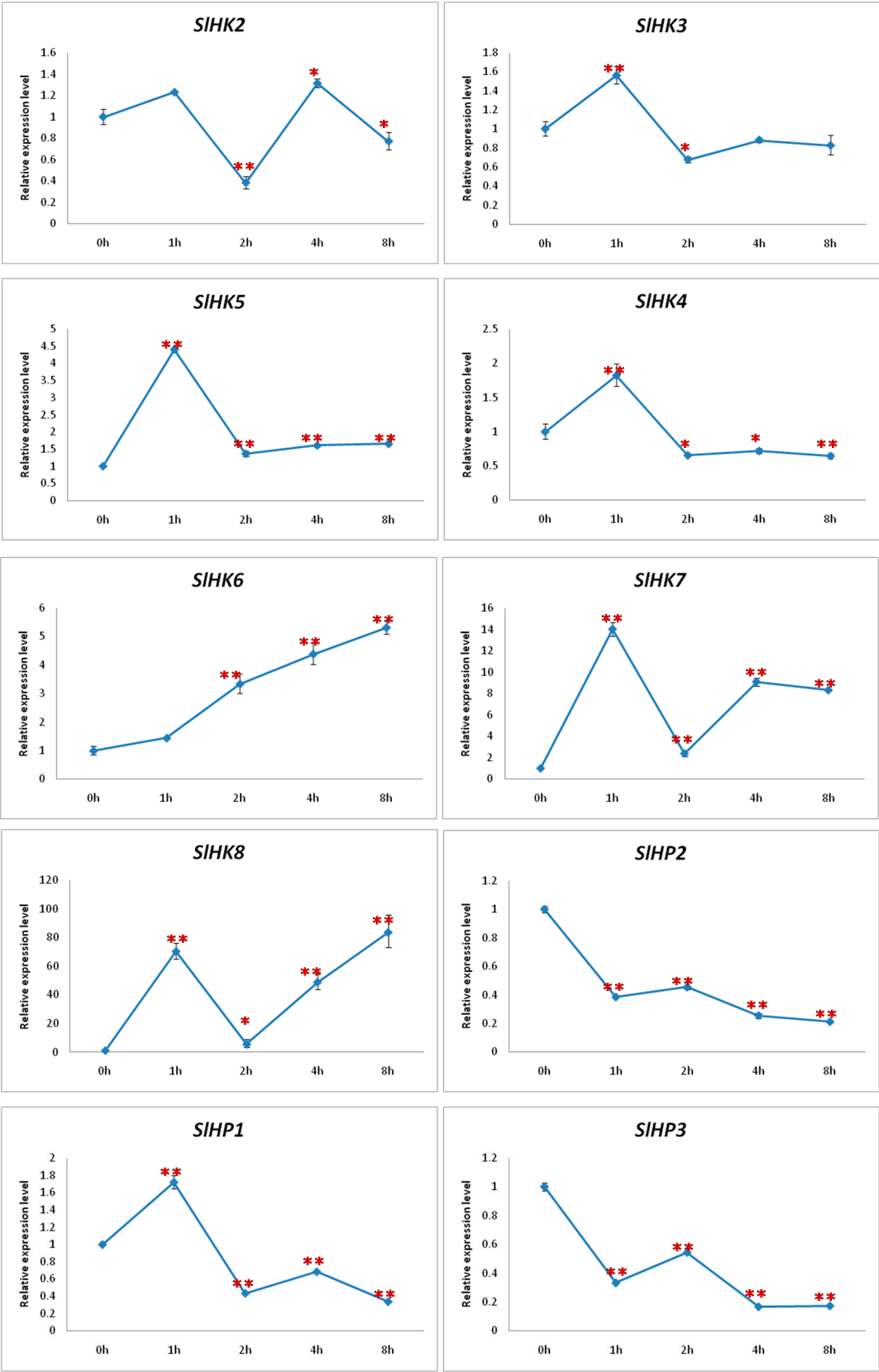


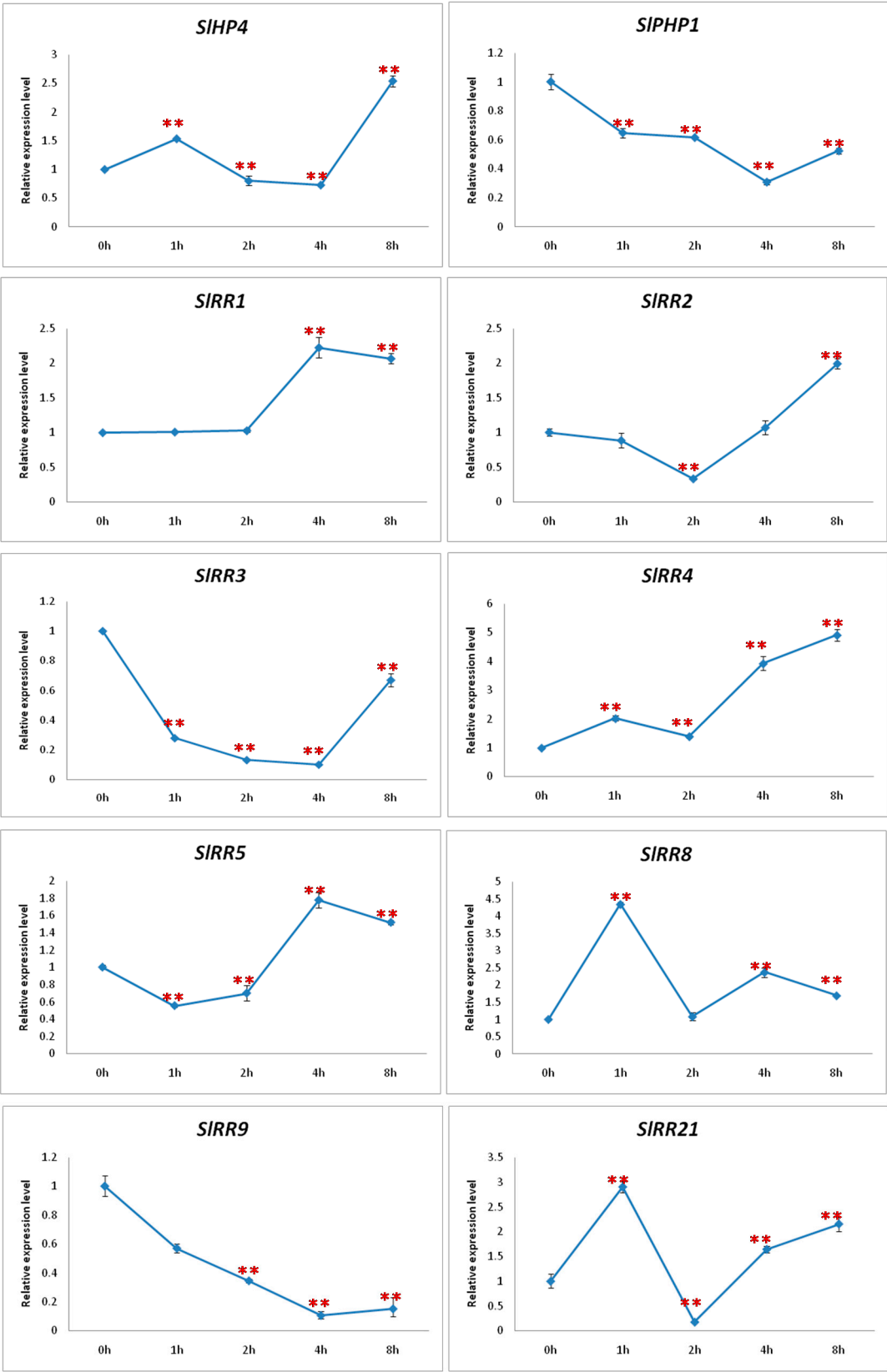




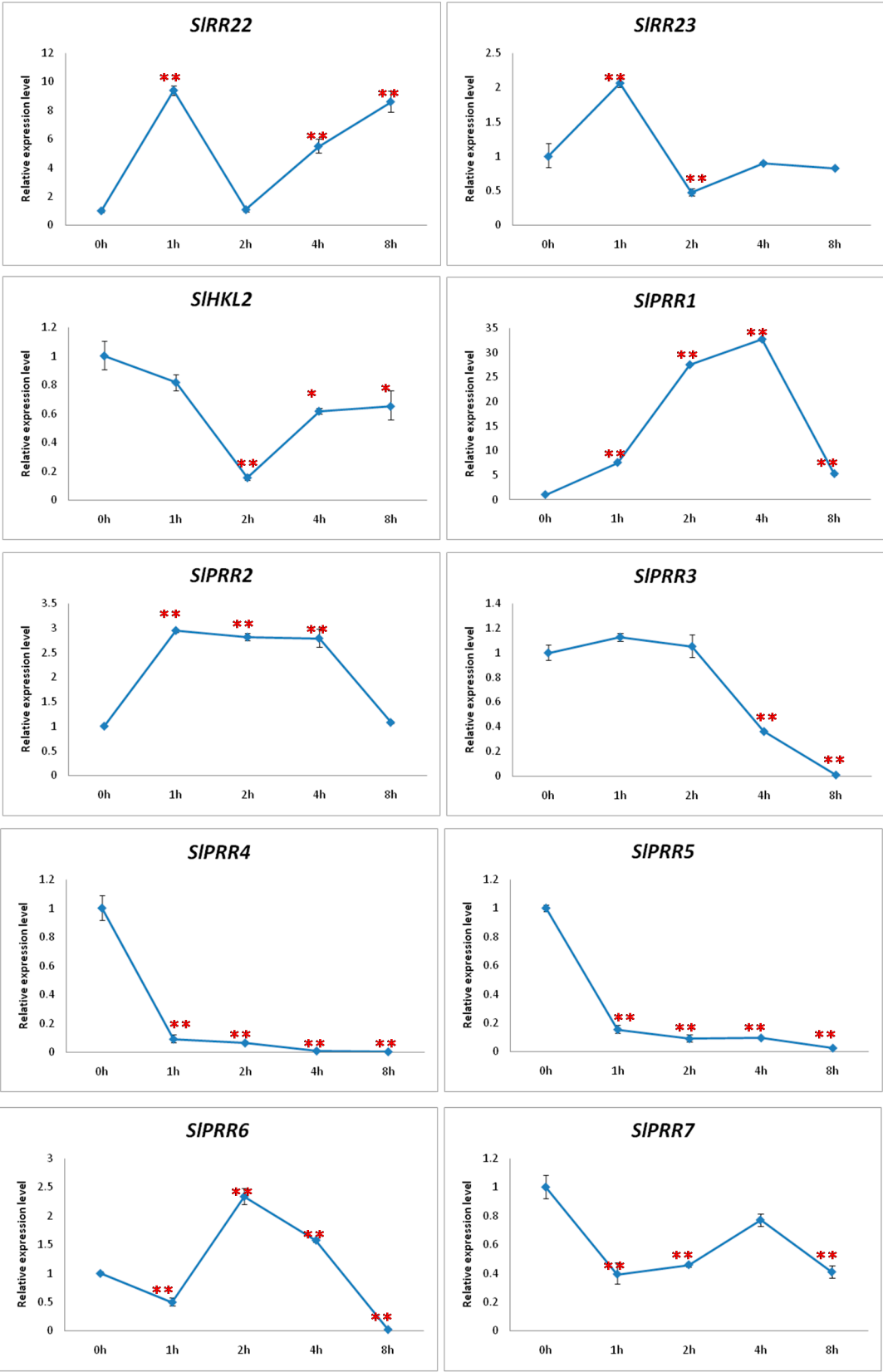


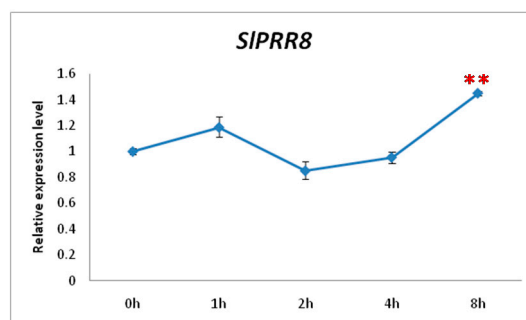
(D)









**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	<i>SIHK8</i>
CGGGATCCAAGGAAATGGAAGTGGG	GCTCTAGAATCCCGTAAGCATTGAG	<i>SIHP2</i>
CGGGATCCCTTCTCCCCACATCAA	GCTCTAGACATGTTTCACCTGCTGC	<i>SIHP3</i>
CGGGATCCAGTGAGATGGCAAGAAATG	GCTCTAGAATGGGAGAGGAGGGC	<i>SIRR1</i>
CGGGATCCTGGTCTTCAATGGTAAGTATG	GCTCTAGATCATGGGGAACCTGAGACC	<i>SIRR8</i>

**Primers used for qRT-PCR**

Primer-S	Primer-A	Gene Name
ATAACCAACTCCTCTTCGTCC	AAGTCCTTTCGTAACCTCAGCC	<i>SIHK1</i>
TCAACGGGAGCAAATACTAAC	GATGTCCTCTTCACGCAAAC	<i>SIHK2</i>
GGTTAGAGAGAAATGGGGTGC	TATGACAAAAGGTGATGAGGC	<i>SIHK3</i>
CTTTGTCTTTGGTGGGGTG	TGCTTACGTTGAACTGGTCC	<i>SIHK4</i>
CACCTTCTTTATTCCTCTCATC	CACATCAAACACCTAACCCC	<i>SIHK5</i>
TGTCAGGAGAGGAGGATCG	GAATGTCAAACAACACCAAGG	<i>SIHK6</i>
AACGGGGAACACAGACAGAG	CACCAAGAAATCCAAAGACG	<i>SIHK7</i>
TATTGGAGATGAAAAACGGC	CAACTTGGGGAAATCCTGAG	<i>SIHK8</i>
CTCTGCTACCTATGCCTCC	ATCCCACCATCATCTCCAC	<i>SIHK9</i>
GACTTCAAGAACTGGATGCTC	TTACGGAAGGAAATGCACAC	<i>SIHP1</i>
GGTAATCCAAGCAACAAAGC	CCAAGAATCCCTCACGAAAC	<i>SIHP2</i>
CGATGAGCATTGATTGGTA	GAATTTGATGTGGGGGAGA	<i>SIHP3</i>
AGATGATGATAACCCTAACTTCG	GAGCACTCTCTTTTCACTCTTTTG	<i>SIHP4</i>
CTATGATTTTGCTAGGCTGGA	CATTGTCTTTTACTCTTCTGGC	<i>SIPHP1</i>
CCTCCCCTAATTCGTCTC	GCCAATGCTTGAACCTGC	<i>SIPHP2</i>
TGAACAAGAGAAAGTTGCCAG	AGAGGTCAAGTGATGAGGGTG	<i>SIRR1</i>
TAGATGTTTGGAGGAAGGTGC	GGGATGGTATTGATTGTGTCG	<i>SIRR2</i>
AGCAGCAACAACAACAACAG	TGCGAGCGAGAGATTACAC	<i>SIRR3</i>
GATTACTGTATGCCTGGGATG	GCCCCTTCTTCTAAGCATCTAC	<i>SIRR5</i>
GCTTAGAAGAAGGGGCAG	TGGGGCTTTTACATTGG	<i>SIRR4</i>
AGATGGTCTGAGGGCTTTAG	GATGACATGATCACAACCTGGTAC	<i>SIRR6</i>
GAAAATCAAGGAATCGTCG	GTAATTAGCACCCAACACAAC	<i>SIRR7</i>
ACCTTCTTGCCTTGTATTGC	CTGGTTTGAGTTCCTGTC	<i>SIRR8</i>
GCATGGTATCGCAAAGGC	GCATCCCACAAACAGCAC	<i>SIRR9</i>
GGAGTCACTACAGAACATTGG	CAACCTCACTTCATTAGTTACACAC	<i>SIRR13</i>
GAAGGATCATTCTTTGCTTTTCG	GGTATTTCTTTAGACGGTAGGTG	<i>SIRR16</i>
TGTAGCTCTATCCATTCTCCG	TCATTTCAATCGTCACCTCTG	<i>SIRR18</i>
GTGTTGTTTCAGTGCCAGC	CCAATCCAAAGGAATCGT	<i>SIRR21</i>
AGGAGAAGGCGAAAGAGG	AGCCCAAACCTACACGAGG	<i>SIRR22</i>
GCTCAGGAAATGCCAGTATC	CAAGACCAACAAGTTCAAGAAG	<i>SIRR23</i>