

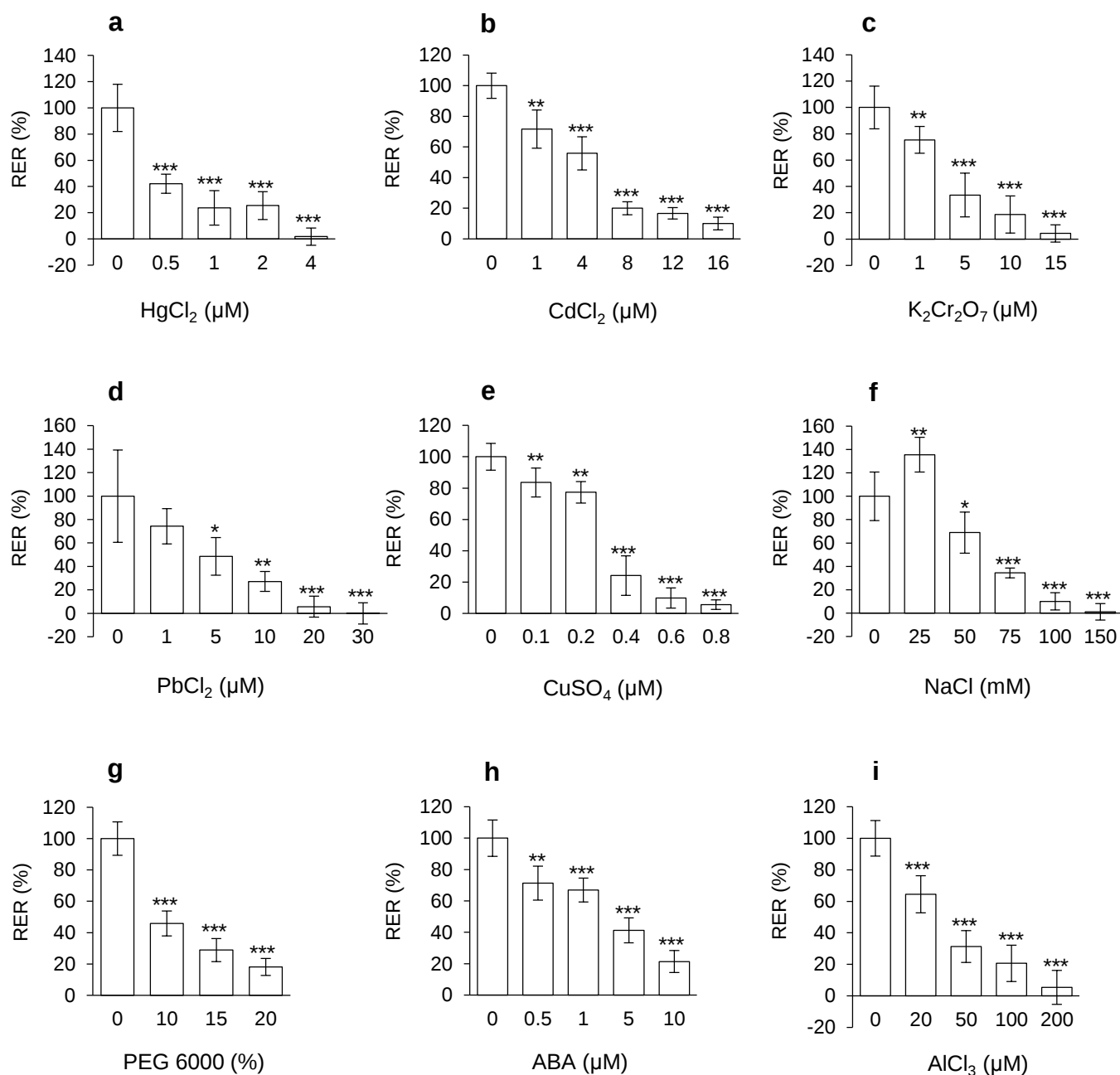


Figure S1. Effects of heavy metal toxicities and other abiotic stresses on root growth in rice.

a-i Four-day-old wild-type rice seedlings were treated for 24 h with different concentrations (as indicated) of heavy metal salts, including HgCl₂ (**a**), CdCl₂ (**b**), K₂Cr₂O₇ (**c**), PbCl₂ (**d**), and CuSO₄ (**e**), and other abiotic stresses, including NaCl (**f**), PEG 6000 (**g**), ABA (**h**), and AlCl₃ (**i**). The effects of these abiotic stresses examined on root elongation were presented as root relative elongation rates (%; RER) compared to the corresponding mock control (100%). Values shown are means $\pm$ SD. Single, double, and triple asterisks indicate $P < 0.01$, 0.001 , and 0.0001 , respectively (t test; compared to the corresponding mock control).

AtCIPK5: MEEERRVLFQKYEMGRLLGKGTFAKVYYGKEITIGGECVAIKVINKDQVMKRPGMMEQIKREISIMKLV : 68
OsCIPK5: MEKKASILMNRYELGRMLGOGTFAKVYHARNLASNQSVAIKVIDKEKVL-RVGMIDQIKREISIMRLV : 67
HsCIPK5: MERKSTILMNRYELGRMLGOGTFAKVYHARSLATNQSVAIKVIDKEKVL-RVGMIDQIKREISIMRLV : 67

AtCIPK5: RHPNIVELKEVMATKTKIFFVMEFVKGGELFCKTISKGLHEDAAARYFQQLISAVDYCHSRGVSHRDL : 136
OsCIPK5: RHPNIVQLHEVMASKSKIYFAMEYVRGGELFSRVARGRLKEDAARKYFQQLICAVDFCHSRGVYHRDL : 135
HsCIPK5: RHPNIVQLHEVMASKSKIYFAMEYVRGGELFARVAKGRLKEDAARKYFQQLICAVDFCHSRDVYHRDL : 135

Activation Loop

AtCIPK5: KPENLLLDENGDLKISDFGLSALPEQILQDGLLHTTCGTPAYVAPEVLKKKGYDGAKADIWSCGVVLY : 204
OsCIPK5: KPENLLVDENGNLKVSDFGLSAFKECQKQDGLLHTTCGTPAYVAPEIINKRGYDGAKADIWSCGVILF : 203
HsCIPK5: KPENLLVDEHGNLKVSDFGLSALKECQKQDGLLHTTCGTPAYVAPEIINKKGYDGEKADIWSCGVILF : 203

AtCIPK5: VLLAGCLPFDENLNMNMYRKIFRADFEFPWFSPPEARRLISKLLVVDPPDRRISTPAIMRTPWLRKNFT : 272
OsCIPK5: VLLAGYLPFHDSNLMMYRKISKGDVKFPQWFTTVRRLLSRLDPNPNIIRITVEKLVEHPWFKKGYK : 271
HsCIPK5: VLLAGYLPFDENLNMNMYRKISKGDVRYPQWFSSDARKLLCRLDPNPNTIRITMDKLIHPWFKKGYK : 271

NAF/FISL Motif

AtCIPK5: PPLAFKIDEPICSSSS-----NNEEEEEEDG-DCENQTEPISPKFFNAFEFTSSMSSGFDLSSSLFES : 333
OsCIPK5: PAV--MLSQPNESNNLKDVHTAFSADHKDNEG-KAKEFASSLKPVSLNAFD-IISLSKGFDSLGLFEN : 335
HsCIPK5: PAV--MLGTPRASKDINDVQAAFSTDHKGDEGSRAEQENSPLKPPASLNAFD-IISLSKGFDSLGLFEK : 336

AtCIPK5: KR--KVQSVFTSRSSATEVMEKIETVTKEMNMKVKRTKDFKVKMEGKTEGRKGRLSMTAEVFEVAPEI : 399
OsCIPK5: DKEQKADSRFMTQKEASAIVSKLEQIAETESFKVKKQDGL-VKLQGSKEGRKGQLAIDAEIFEVTPSF : 402
HsCIPK5: DQEOKSNSRFMTQKEASAIVSKLEQIAETESFKVKKQDGL-VTLQGSKEGRKGQLAIDAEIFEVTPSF : 403

PPI

AtCIPK5: SVVEFCKSAGDTLEYDRLYEEVVRPALNDIVSWHGDNNN--TSSDC----- : 445
OsCIPK5: FVVEVKKSAGDTLEYEKFCKNGLRPSLRDI--CWNGQSEH--PSLAQSSTLTQSSKISRHAT-- : 461
HsCIPK5: YVVEVKKSAGDTLEYERFCKKGLRPSLKDI--CWNGPSEKLEPLVSESVPPTPSSKSTKRNVI-- : 464

Figure S2. Alignment analysis of amino acid sequences among HsCIPK5, OsCIPK5, and AtCIPK5.

a

Gene	Accession number	Gene	Accession number
<i>HsCIPK2</i>	KP638475	<i>HsCIPK23</i>	JN655678
<i>HsCIPK5</i>	KT274758	<i>HsCIPK24</i>	JN655679
<i>HsCIPK9</i>	JN655674	<i>HsCIPK28</i>	KT274759
<i>HsCIPK11</i>	JN655675	<i>HsCIPK29</i>	JN655680
<i>HsCIPK14</i>	JN655676	<i>HsCIPK30</i>	JN655681
<i>HsCIPK17</i>	JN655677	<i>HsCIPK31</i>	JN655682

b

	OsCIPK2	OsCIPK5	OsCIPK9	OsCIPK11	OsCIPK14	OsCIPK15	OsCIPK17	OsCIPK23	OsCIPK24	OsCIPK28	OsCIPK29	OsCIPK30	OsCIPK31
HsCIPK2	86.2	62.0	51.5	59.3	59.9	59.4	41.2	55.1	47.1	58.8	40.1	49.8	52.5
HsCIPK5	61.8	85.9	51.3	54.6	58.2	58.2	44.2	56.5	49.2	55.4	40.2	54.3	52.5
HsCIPK9	51.6	51.5	90.3	49.1	46.2	46.3	47.9	67.1	55.0	46.6	37.2	47.2	62.6
HsCIPK11	61.8	54.2	43.8	80.7	58.7	58.2	39.7	50.2	43.7	72.2	40.9	49.7	48.9
HsCIPK14	59.4	56.7	46.3	60.5	82.7	82.8	41.7	49.4	43.5	59.4	39.4	49.1	49.2
HsCIPK15	59.4	57.2	47.1	60.8	83.0	83.0	42.3	50.1	44.2	59.5	39.6	49.1	49.6
HsCIPK17	41.1	42.4	44.7	39.6	40.4	40.4	80.8	47.6	44.0	39.3	34.5	38.3	45.9
HsCIPK23	55.6	54.8	65.5	51.6	50.9	50.8	46.8	94.7	56.6	49.5	39.6	46.9	63.3
HsCIPK24	46.2	47.7	53.8	44.8	44.1	44.6	43.5	56.4	89.1	44.9	39.2	43.8	54.2
HsCIPK28	58.0	53.0	42.6	67.4	59.5	59.2	39.3	49.0	45.5	73.8	42.3	48.2	47.2
HsCIPK29	42.0	40.2	35.7	40.8	42.3	42.1	35.2	38.0	36.7	40.5	70.0	40.6	36.6
HsCIPK30	52.8	54.8	49.3	47.4	50.5	50.1	37.9	48.5	43.0	47.6	38.8	77.3	49.5
HsCIPK31	54.2	52.0	64.7	50.1	49.3	49.2	45.9	63.3	52.5	47.4	35.5	48.4	92.0

c

	AtCIPK2	AtCIPK5	AtCIPK9	AtCIPK11	AtCIPK14	AtCIPK15	AtCIPK17	AtCIPK23	AtCIPK24
HsCIPK2	61.0	55.1	54.5	48.6	48.9	61.6	42.9	55.3	47.2
HsCIPK5	59.3	52.5	51.4	49.3	48.1	58.3	43.3	54.5	48.2
HsCIPK9	46.4	50.8	72.1	44.3	44.1	52.3	47.9	67.8	54.5
HsCIPK11	61.8	54.2	50.1	48.1	45.1	57.2	40.2	48.6	46.2
HsCIPK14	57.3	53.0	49.8	47.4	45.7	56.9	42.4	48.3	44.7
HsCIPK15	57.4	52.9	50.0	47.6	46.2	56.7	42.4	48.9	44.9
HsCIPK17	37.9	41.4	46.5	40.3	37.7	43.9	57.5	44.4	44.1
HsCIPK23	52.2	52.1	67.0	45.3	43.9	53.5	49.9	77.1	57.6
HsCIPK24	44.9	46.1	54.0	42.2	43.7	48.9	46.9	56.2	68.9
HsCIPK28	58.5	50.7	47.5	46.4	45.5	55.9	39.0	46.7	47.1
HsCIPK29	37.3	36.6	34.3	42.9	43.6	40.3	35.0	36.9	37.9
HsCIPK30	50.0	47.3	48.3	42.1	42.7	52.1	40.3	47.2	45.4
HsCIPK31	49.4	49.0	63.0	44.1	41.5	49.6	48.1	64.6	54.0

Figure S3. GenBank accession numbers and homology analysis of HsCIPKs.**a** GenBank accession numbers for 12 *HsCIPK* genes.**b** Homology comparison between HsCIPKs versus OsCIPKs.**c** Homology comparison between HsCIPKs versus AtCIPKs.

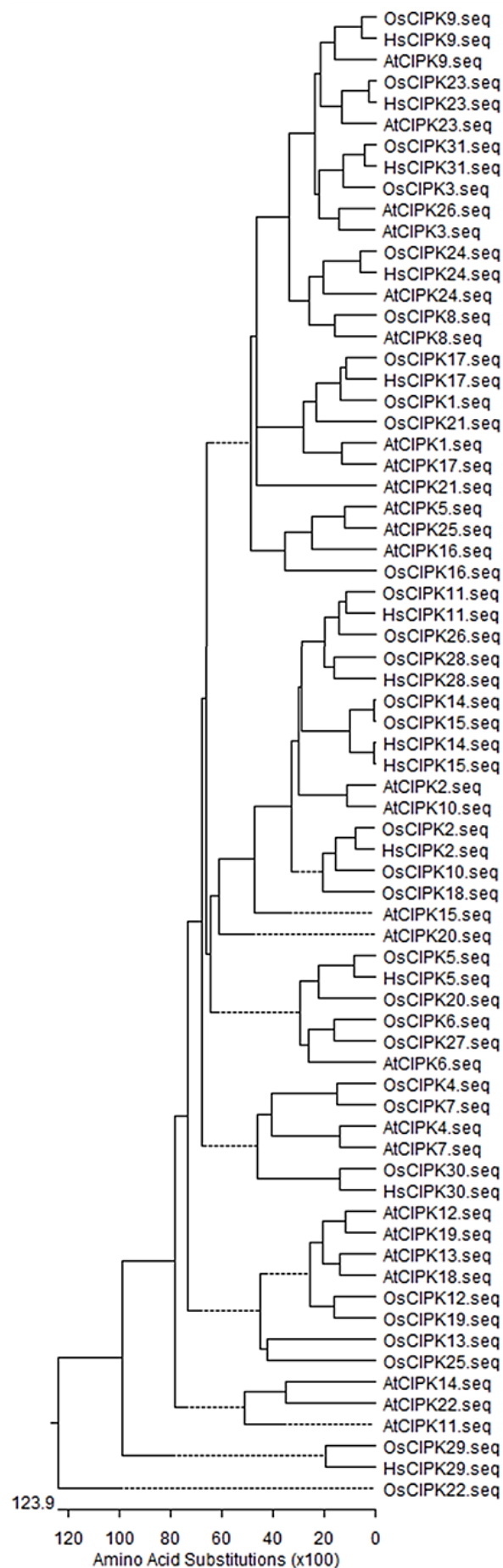


Figure S4. Phylogenetic analysis of HsCIPKs, OsCIPKs, and AtCIPKs.

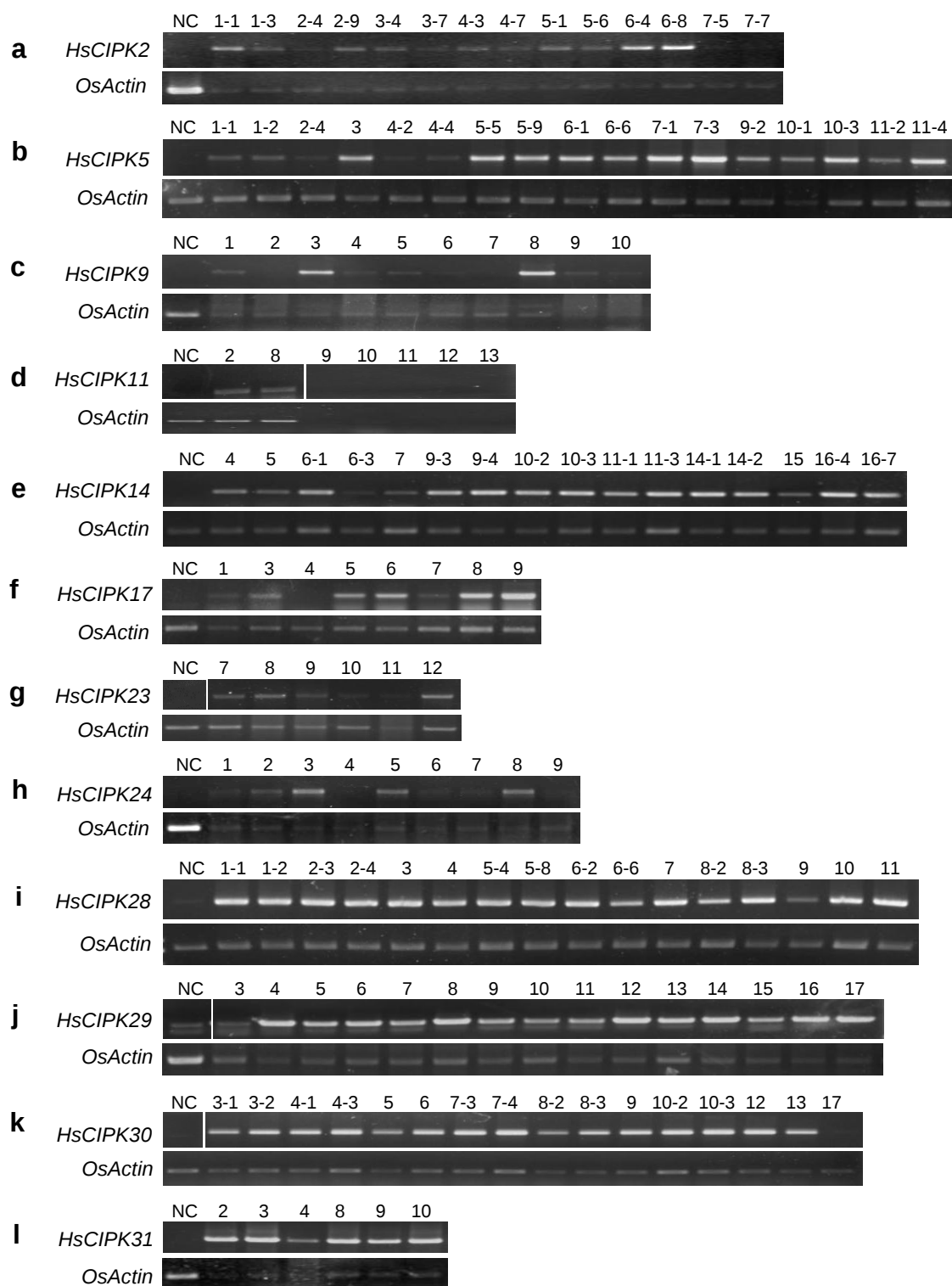


Figure S5. Molecular identification of *HsCIPK* overexpression in rice. RT-PCR assays were performed in T1 G418-resistant individual transgenic lines (**a-l**) under the control of 35S promoter. NC, the negative control (wild-type Nipponbare). Numbers show different transgenic lines whereas number-dash-numbers indicate the transgenic plants regenerated from the same callus.

Table S1. Accession numbers of rice and *Arabidopsis* CIPK cDNA in NCBI database.

<i>Arabidopsis thaliana</i>		<i>Oryza sativa</i>	
Gene	Accession No.	Gene	Accession No.
<i>AtCIPK1</i>	AF302112	<i>OsCIPK1</i>	EU703792
<i>AtCIPK2</i>	AF286050	<i>OsCIPK2</i>	EU703793
<i>AtCIPK3</i>	AF286051	<i>OsCIPK3</i>	Os07g48760
<i>AtCIPK4</i>	AY007221	<i>OsCIPK4</i>	NM_001073746
<i>AtCIPK5</i>	AF285105	<i>OsCIPK5</i>	EU703795
<i>AtCIPK6</i>	AF285106	<i>OsCIPK6</i>	AP004703
<i>AtCIPK7</i>	AF290192	<i>OsCIPK7</i>	AK111510
<i>AtCIPK8</i>	AF290193	<i>OsCIPK8</i>	NM_001049794
<i>AtCIPK9</i>	AF295664	<i>OsCIPK9</i>	AC104427
<i>AtCIPK10</i>	AF295665	<i>OsCIPK10</i>	EU703796
<i>AtCIPK11</i>	AF295666	<i>OsCIPK11</i>	EU703797
<i>AtCIPK12</i>	AF295667	<i>OsCIPK12</i>	EU703798
<i>AtCIPK13</i>	AF295668	<i>OsCIPK13</i>	AP003052
<i>AtCIPK14</i>	AF295669	<i>OsCIPK14</i>	AB264036
<i>AtCIPK15</i>	AF302111	<i>OsCIPK15</i>	AK121773
<i>AtCIPK16</i>	AY030304	<i>OsCIPK16</i>	AK061220
<i>AtCIPK17</i>	AY036958	<i>OsCIPK17</i>	EU703799
<i>AtCIPK18</i>	AY034099	<i>OsCIPK18</i>	EU703800
<i>AtCIPK19</i>	AY030303	<i>OsCIPK19</i>	AK069486
<i>AtCIPK20</i>	AY035225	<i>OsCIPK20</i>	AK107068
<i>AtCIPK21</i>	AY034100	<i>OsCIPK21</i>	NM_001066932
<i>AtCIPK22</i>	AF450478	<i>OsCIPK22</i>	AC117264
<i>AtCIPK23</i>	AY035226	<i>OsCIPK23</i>	EU703802
<i>AtCIPK24</i>	AF395081	<i>OsCIPK24</i>	AK102270
<i>AtCIPK25</i>	AF448226	<i>OsCIPK25</i>	AK065374
<i>AtCIPK26</i>	NM_180530	<i>OsCIPK26</i>	EU703805
		<i>OsCIPK27</i>	NM_001069722
		<i>OsCIPK28</i>	AC144743
		<i>OsCIPK29</i>	AK111746
		<i>OsCIPK30</i>	AK069231
		<i>OsCIPK31</i>	NM_001056484

Table S2. Primer sequences for *HsCIPKs* cloning.

Primer Name	Primer Sequences
<i>HsCIPK2</i> -Sacl-F	TCC <u>GAGCTC</u> ATGGGGGAGCAGAAGGGGAATATTCTGAT
<i>HsCIPK2</i> -Xbal-R	ACT <u>TCTAGAT</u> CAACAAGATTGCTGCTGCGGCTGCGGC
<i>HsCIPK5</i> -KpnI-F	CGGGG <u>TACCAT</u> GAGAGGAAGTCCACCATCCTCATG
<i>HsCIPK5</i> -Xbal-R	TGCT <u>TCTAGAT</u> TAAATGACATTCCTTTTGGTCGACTT
<i>HsCIPK9</i> -SmaI-F	CCT <u>CCCGGG</u> ATGGCTAGCAAATCGAAGATATACATGG
<i>HsCIPK9</i> -Xbal-R	TGCT <u>TCTAGACT</u> AAAGCACATTCAGGATGCCTGTTAG
<i>HsCIPK11</i> -KpnI-F	CGGGG <u>TACCAT</u> GATGAGAGGAGGACTATATTGATGG
<i>HsCIPK11</i> -Xbal-R	TGCT <u>TCTAGAT</u> CATCCGATATTGCTAGCATGTGAATCTT
<i>HsCIPK14</i> -KpnI-F	CGGGG <u>TACCAT</u> GAGAACAGTGGGAAGATTGTAATG
<i>HsCIPK14</i> -Xbal-R	TGCT <u>TCTAGACT</u> AACCATCAGCCCCATGCCAGGCCCAT
<i>HsCIPK17</i> -KpnI-F	ACCGGT <u>ACCAGC</u> AGCGGGCAGCAGAAAGATG
<i>HsCIPK17</i> -Xbal-R	CCAT <u>TCTAGAT</u> CACAAGGCAACCAAGTGGTGTC
<i>HsCIPK23</i> -SmaI-F	CCT <u>CCCGGG</u> ATGGTTGATTTCGAGCGCGGGTGGGAAGA
<i>HsCIPK23</i> -Xbal-R	TGCT <u>TCTAGAT</u> CATGGAGACCTCCGGTGCCGGGTCT
<i>HsCIPK24</i> -Sacl-F	ACC <u>GAGCTC</u> ATGGCAGGCGCGCCGAGGAAGAAGCTGG
<i>HsCIPK24</i> -Xbal-R	TGCT <u>TCTAGACT</u> AGCAAGTGGTTGTCCTCAGCAATGC
<i>HsCIPK28</i> -KpnI-F	CGGGG <u>TACCAT</u> GGAAGACAGGAGTGTTTTGACCAAAC
<i>HsCIPK28</i> -Xbal-R	TGCT <u>TCTAGAT</u> TATTGTGGCAGTGGGGAGAAAGCATTTG
<i>HsCIPK29</i> -BamHI-F	AATG <u>GATCC</u> ATGCCGTCCGCCTCCAGCGC
<i>HsCIPK29</i> -Xbal-R	ATT <u>TCTAGAT</u> CACACTGCCTGAGGCTTCACGGCC
<i>HsCIPK30</i> -KpnI-F	CGGGG <u>TACCAT</u> GGCCATGGAGAAGAACCAAGATTCC
<i>HsCIPK30</i> -Xbal-R	TGCT <u>TCTAGAT</u> CAGGAATTCGTGTTTGGCCTAGGCAC
<i>HsCIPK31</i> -SmaI-F	CCT <u>CCCGGG</u> ATGTATCGGGCCAAGAGAGCCGCATTGT
<i>HsCIPK31</i> -Xbal-R	TGCT <u>TCTAGAT</u> CATGCCGCGGTGCTGTTATCTTCTAC

Table S3. Primer sequences for qRT-PCR assay in Tibetan Plateau annual wild barley.

Primer Name	Primer Sequences
<i>qHsCIPK2-F</i>	CACCGTGATTTGAAGCCCGAGAAC
<i>qHsCIPK2-R</i>	GATACCCAGCCATAAGCACAAAGAGGA
<i>qHsCIPK5-F</i>	GAAGGCAGCAGGGCAGAACCAACCA
<i>qHsCIPK5-R</i>	TGGATCCCTGCAGCGTCACAAGTC
<i>qHsCIPK9-F</i>	TTATTTCAAGGTCGGCGGGATTCAA
<i>qHsCIPK9-R</i>	ACCTTTTCTTCCTGTCTTGTCACCTTTCA
<i>qHsCIPK11-F</i>	ACCGAGCCTGAAGCAACGCACAC
<i>qHsCIPK11-R</i>	AAACCGTTCTTCCCTGCGACCAT
<i>qHsCIPK14-F</i>	GCCCGAGAACCTATTGCTTGATGA
<i>qHsCIPK14-R</i>	AACAGGATGACACCGCAAGACCAGA
<i>qHsCIPK17-F</i>	GTGAGCTATTGCCATGGAAAGGGTGTCTAC
<i>qHsCIPK17-R</i>	TACTCCACAAGACCAGATATCCGACAATGA
<i>qHsCIPK23-F</i>	ATTTTGGACTCAGCGCCCTATCG
<i>qHsCIPK23-R</i>	ATCGGCCTTGGCTCCATCATAACC
<i>qHsCIPK24-F</i>	GCAGCAGATATTTGGTCATGTGGTGTT
<i>qHsCIPK24-R</i>	GATCATTGACTTGGCCCCTGGAGAG
<i>qHsCIPK28-F</i>	GCGGCGCCGAGGGAAGGAAAGA
<i>qHsCIPK28-R</i>	CTGCTGAACATCGCCGTGCCATCC
<i>qHsCIPK29-R</i>	AACCCGGCCACGCGCATTGACA
<i>qHsCIPK29-F</i>	GTCCCGCGCCATGTCCTCCTTGAA
<i>qHsCIPK30-F</i>	GCCCGTCGCTCGCCGCTACTTTC
<i>qHsCIPK30-R</i>	CGTGCGCGTCGAGGAGGAGGTTCT
<i>qHsCIPK31-F</i>	CACCTCGCAATGCCCTCCAAAAG
<i>qHsCIPK31-R</i>	CTTCGCCTTTTTTCAGCTCAACCACA
<i>qHvActin-F</i>	CCAAAAGCCAACAGAGAGAA
<i>qHvActin-R</i>	GCTGACACCATCACCAGAG

Table S4. Primer sequences for RT-PCR assay in rice transgenic lines.

Primer name	Primer sequences
<i>HsCIPK2-F</i>	TGACGGCGCCAAGGCTGACATCT
<i>HsCIPK2-R</i>	TTAACATGGTTGCTGCTGCGGCTG
<i>HsCIPK5-F</i>	ATGGAGAGGAAGTCCACCATCCTCATG
<i>HsCIPK5-R</i>	TTAAATGACATTCCTTTTGGTCGACTT
<i>HsCIPK9-F</i>	ATGGCTAGCAAATCGAAGATATACATGG
<i>HsCIPK9-R</i>	CTAAAGCACATTCAGGATGCCTGTTAG
<i>HsCIPK11-F</i>	ATGGATGAGAGGAGGACTATATTGATGG
<i>HsCIPK11-R</i>	TGGTGGTTGTTCTGCTGCTCCTG
<i>HsCIPK14-F</i>	ATGGAGAACAGTGGGAAGATTGTAATG
<i>HsCIPK14-R</i>	CGGTACATCTCTATCAAGTTCTGACCTT
<i>HsCIPK17-F</i>	ATGGTGCGGACGGGCGACGC
<i>HsCIPK17-R</i>	TACTCCACAAGACCAGATATCCGACAATGA
<i>HsCIPK23-F</i>	ATGGTTGATTCGAGCGCGGGTGGGAAGA
<i>HsCIPK23-R</i>	TCATGGAGACCTCCGGTGCCGGGTCT
<i>HsCIPK24-F</i>	ATGGCAGGCGCGCCGAGGAAGAAGCTGG
<i>HsCIPK24-R</i>	CTAGCAAGTGGTTGTCCTCAGCAATGC
<i>HsCIPK28-F</i>	AAGTGGCGAGATGGTCTGCTCCACACCG
<i>HsCIPK28-R</i>	ACCGGGCCTCCCTTTGACTATATCTTTC
<i>HsCIPK29-F</i>	ATGCCGTCCGCCTCCAGCGC
<i>HsCIPK29-R</i>	TCCACTGCCTGAGGCTTCACGGCC
<i>HsCIPK30-F</i>	ATGGCCATGGAGAAGAACCAAGATTCCAAAG
<i>HsCIPK30-R</i>	ATGGTGATCCGGGTGTTGGGGTTTCG
<i>HsCIPK31-F</i>	GCACCATCGGGGAAGGGACATT
<i>HsCIPK31-R</i>	CTTCGCCTTTTTTCAGCTCAACCACA
<i>OsActin2-F</i>	GGAAGTGGTATGGTCAAGGC
<i>OsActin2-R</i>	AGTCTCATGGATACCCGCAG

Table S5. Summary of endogenous *HsCIPK* responses to heavy metal toxicities.

Gene	20 μ M HgCl ₂ (roots)	20 μ M CdCl ₂ (roots)	0.5 mM K ₂ Cr ₂ O ₇ (roots)	20 μ M PbCl ₂ (roots)	1 mM CuSO ₄ (roots)
<i>HsCIPK2</i>	↑ (6.6±0.19) ***	↑ (7.6±0.25) ***	↑ (3.9±0.10) ***	↑ (1.8±0.03) ***	↑ (3.0±0.20) ***
<i>HsCIPK5</i>	↑ (2.2±0.36)	↑ (2.3±0.03) ***	↑ (7.9±0.54) ***	↑ (1.8±0.32)	↑ (14.1±1.22) ***
<i>HsCIPK9</i>	—	↑ (11.5±0.57) ***	↑ (4.5±0.54) **	↑ (6.1±0.71) **	↑ (2.91±0.14) ***
<i>HsCIPK11</i>	↑ (3.6±0.33) **	↑ (4.0±0.05) ***	↑ (4.8±0.19) ***	↑ (1.48±0.53) **	↑ (4.3±0.59) **
<i>HsCIPK14</i>	↑ (4.7±0.48) **	↑ (13.3±1.24) ***	↑ (4.2±0.10) ***	↑ (4.8±0.53) **	↓ (0.59±0.03) ***
<i>HsCIPK17</i>	↑ (30.6±2.40) ***	↑ (70.9±1.76) ***	↑ (15.7±0.62) ***	↑ (6.7±0.68) **	↑ (12.7±0.77) ***
<i>HsCIPK23</i>	↑ (10.7±0.49) ***	↑ (5.2±0.16) ***	↑ (4.8±0.25) ***	↑ (2.6±0.18) ***	↑ (3.1±0.09) ***
<i>HsCIPK24</i>	↑ (6.4±0.59) ***	↑ (7.1±0.39) ***	↑ (8.1±0.32) ***	↑ (3.3±0.36) **	↑ (1.8±0.12) **
<i>HsCIPK28</i>	↑ (4.0±1.24) *	—	↓ (0.55±0.07) **	↑ (2.3±0.16) **	↑ (2.6±0.61) *
<i>HsCIPK29</i>	↑ (9.5±0.78) ***	↑ (66.6±2.6) ***	↑ (6.1±0.46) ***	↑ (4.2±0.03) ***	↑ (6.9±0.24) ***
<i>HsCIPK30</i>	↑ (12.9±1.41) **	↑ (3.9±0.46) **	↑ (12.1±1.25) **	↑ (1.9±0.15) **	↑ (14.3±3.11) **
<i>HsCIPK31</i>	↑ (5.5±0.06) ***	↑ (69.5±8.32) **	↓ (0.4±0.03) ***	↓ (0.46±0.01) ***	↑ (7.1±0.50) ***

↑, ↓, and — indicate elevation, reduction, and no changes at *HsCIPK* mRNA levels relative to the 0-h time point, respectively. The expression levels of *HsCIPKs* being three times higher than the mock control are shown in Fig. 2 and Fig. 3. The numbers in brackets show the maximum levels of elevation or reduction at the *HsCIPK* mRNA levels relative to the corresponding mock control (0-h time point) during treatments. Single, double, and triple asterisks indicate $P < 0.01$, 0.001 , and 0.0001 , respectively (t test; compared to the 0-h time point mock control).

Table S6. Summary of endogenous *HsCIPK* responses to other abiotic stresses.

Gene	400 mM NaCl (roots)	20% PEG 6000 (seedlings)	20 μ M AlCl ₃ (roots)	4°C Cold (seedlings)	35°C Heat (seedlings)	20 μ M ABA (roots)
<i>HsCIPK2</i>	↑ (4.0±0.25) ***	↑ (1.3±0.05)	↑ (2.0±0.01) ***	↓ (0.83±0.18)	↓ (0.38±0.05) *	↑ (3.8±0.46) **
<i>HsCIPK5</i>	↑ (2.9±1.10) *	↑ (1.29±0.22)	—	—	↑ (2.9±0.94) *	↑ (1.8±0.46)
<i>HsCIPK9</i>	—	↑ (3.0±0.02) ***	↓ (0.27±0.01) ***	↑ (10.6±1.0) ***	↑ (2.1±0.06) ***	↑ (1.7±0.67) *
<i>HsCIPK11</i>	↑ (1.5±0.12) *	↑ (1.5±0.01) **	↑ (1.7±0.03) ***	—	↓ (0.7±0.05) **	↑ (1.5±0.01) **
<i>HsCIPK14</i>	↓ (0.39±0.01) ***	↓ (0.2±0.01) ***	—	—	↓ (0.4±0.01) ***	↓ (0.78±0.08) *
<i>HsCIPK17</i>	↑ (3.2±0.11) ***	↓ (0.8±0.02) **	↑ (1.6±0.14) *	—	↑ (1.5±0.15) *	↑ (7.4±0.42) ***
<i>HsCIPK23</i>	—	↓ (0.8±0.06) *	↓ (0.6±0.03) ***	—	↓ (0.87±0.07)	—
<i>HsCIPK24</i>	↑ (3.1±0.38) **	↑ (1.2±0.03) **	↑ (2.3±0.21) **	↓ (0.89±0.11)	↑ (1.3±0.10) *	↓ (0.77±0.06) *
<i>HsCIPK28</i>	↓ (0.76±0.16) *	↑ (1.9±0.3) *	↑ (2.9±0.09) *	—	↑ (1.4±0.45)	↓ (0.90±0.11)
<i>HsCIPK29</i>	↑ (3.2±0.06) **	↑ (2.5±0.31) *	↑ (2.7±0.45) *	—	↑ (1.4±0.34)	—
<i>HsCIPK30</i>	↑ (10.1±0.40) ***	—	↑ (4.3±0.23) ***	↑ (2.8±0.19) ***	—	—
<i>HsCIPK31</i>	↑ (2.6±0.05) ***	↑ (3.7±0.02) ***	↑ (4.8±0.06) ***	↑ (5.8±0.30) ***	↓ (0.8±0.07) *	↑ (5.4±0.72) **

↑, ↓, and — indicate elevation, reduction, and no changes at *HsCIPK* mRNA levels relative to the 0-h time point, respectively. The expression levels of *HsCIPKs* being two times higher than the mock control are shown in Fig. 4. The numbers in brackets show the maximum levels of elevation or reduction at the *HsCIPK* mRNA levels relative to the corresponding mock control (0-h time point) during treatments. Single, double, and triple asterisks indicate $P < 0.01$, 0.001 , and 0.0001 , respectively (t test; compared to the 0-h time point mock control).

Table S7. Summary of root growth tolerance to abiotic stresses in rice transgenic lines overexpressing *HsCIPKs*.

Gene	0.5 μ M HgCl ₂	5 μ M CdCl ₂	5 μ M K ₂ Cr ₂ O ₇	5 μ M PbCl ₂	0.25 μ M CuSO ₄	50 mM NaCl	10% PEG 6000	1 μ M ABA	50 μ M AlCl ₃
<i>HsCIPK2</i>	↑*	—	↑*	—	—	↑*	—	↑*	—
<i>HsCIPK5</i>	—	—	↑*	—	↑**	↑**	—	—	—
<i>HsCIPK9</i>	—	↑*	↑*	—	—	—	—	—	↓**
<i>HsCIPK11</i>	—	↑**	—	—	—	—	—	—	—
<i>HsCIPK14</i>	↑*	↑**	—	—	—	—	—	—	↓*
<i>HsCIPK17</i>	↑*	↑**	↑*	↓*	—	↑*	↑*	↑**	↓*
<i>HsCIPK23</i>	—	↑*	—	—	—	—	↑*	—	—
<i>HsCIPK24</i>	—	↑***	—	—	↑*	—	—	↓*	—
<i>HsCIPK28</i>	—	—	—	↓*	—	↑*	—	—	—
<i>HsCIPK29</i>	—	↑*	—	↓*	↑*	↑**	↑**	↓*	—
<i>HsCIPK30</i>	—	—	↑*	↓*	—	↑**	—	—	↓*
<i>HsCIPK31</i>	—	—	↓*	—	↑*	—	↑**	—	—

↑, ↓, and — indicate elevation, reduction, and no changes in root growth tolerance to stress treatments relative to the wild-type control NT seedlings, respectively. The detailed data are shown in Fig. 5 and Fig. 6. The numbers in brackets show the maximum levels of elevation or reduction at the *HsCIPK* mRNA levels relative to the corresponding mock control (0-h time point) during treatments. Single, double, and triple asterisks indicate $P < 0.05$, 0.01 , and 0.001 , respectively (t test; compared to the wild-type control NT seedlings).