

Supplementary Data

Fig. 1 Suppl. The ORF sequence and promoter sequence of *CkTPS*. Transcriptional start site is defined as +1; Numbers indicate the positions relative to the transcription start site; ‘ATG’ represents the starting codon.

ABRE

- 792 GAGCACGTATCCAGTGCCAGACAAGTTTGAACCAGTCAAAAAAAAAAGAAAAAGAGGAATGTAAATTTATTTT

- 707 CATTTATGAAGAAGGCCAGATAGGTGTTTGGAGTTGGACTTGGTCTAGAGTGATGCAAGAGGGGTGAGTTGCGAGAGAGATG

TATA-box

- 622 GAGGGAAAAAGAAAAGGCATGTGAGAGAAGAATAAAAACTAAAAACTTTTTATTACTATATTTTGTAGTAAATATTTT

TGACG-motif

- 537 CTTTCTGTTTTCAACAAATCTTGGGTGCCCTGCATGGCATTGACGCTATTGGTTCCTTATAAGCGTACACGAGGATTCTAC

- 452 TGCTTTCTCTCTTTTCTCTATCACTCTGTCAATTCTCTGCCAGAGATTCTGCAGATTTCACCTCTCTACGTACCCGCTTCGTC

TGACG-motif

- 367 TGACTTTAACCCTCTCTGCCTAACCCAGCTGGAGATTGACGCTATTGAACCAGACTTGTCTCTTTGCTTTCACCGTCACTGATTT

- 282 TCGAGGTGTCTCCTGAGCTGGACTTTTAATCTGTTCCCTTAATTTTCACTGCTCTATGACTTGATTATGTTTTGCATCAGATGG

CGTCA-motif

CAAT-box

- 197 GCAATCCGCTTCTGAATATTTCAATATACCTTCTTCCTGCATTGTATTGTTATTTTCATCAATACAATTTTCAGGATTAG

- 112 ACTGCTTCTCTGTTCCAGCACTCTCTTTTGGTATTCCATGAATGTAACAAGCCAGGGATGCGGTGACTCCATTTTCATAT

+1

- 27 ATAGGCTTACGAATGTGAAATTTCCAATCATTTGGTCCACACTGTTGACCCCTTCTGTTGCTTTTGTAAATTCGTGAAACT

P-box

G-box

ABRE

+ 58 GTGCTCTCCTTATTATCTATATTTTCAATTTGATTTTCAAGTGGTCAAAACTTGTCTGGCACTGGATACGTGCTCTCTTTAGATTC

+ 143 TTAATTTTTTTGTTTCTTTTACTATTGTTGTACTCTGTTTGTTCATTAGAAGCTAAATTGAGATGTTTTGTAATTTATTTTTT

CGTCA-motif

+ 228 GTAAACAAAATGCAGGGGAGCAAGTTGGCTGTTTGCACATTGATATTCAACGTCAATGGTTGGATTCCAGAGCGACCATATGCM

+ 313 CTGGAACAAGTACAACGGCGATTGCAATCACATTCCGGGTGCTGTGGAACGGCTTTAAGAGAAAGAGAGTTGAGGGGGTGTGA
P G N K Y N G D S N H I P G R V E R L L R E R E L R G C E

+ 398 GAAGCAAGATGTTGGAAGGGGTTATCGACAGAGGCTTTTGGTGGTGGCTAATAGGTTGCCGGTTTCAGCTATTAGGAAAGGTGAA
K Q D V G R G Y R Q R L L V V A N R L P V S A I R K G E

+ 483 GATTCTTGGTCTCTGGAATAAGTGCCGGTGGACTCGTGAGTGTCTGTTAGGTGTGAAGGAGTTTGAAGCAAGGTGATAGGTT
D S W S L E I S A G G L V S A L L A V K E F E A R W I G

+ 568 GGGCCGGTGTAACGTACCAGATGAGATTGGACAGAAGGCTTTACTAAAGCATTGGCTGAAAAGAGGTGATCCCGTATTCTT
W A G V N V P D E I G Q K A L T K A L A E K R C I P V F L

+ 653 GGATGAAGAGATTGTCCACCAATATTACAATGGCTATTGCAACAACATCTTGTGGCCCTTTTTCATTACCTTGGACTTCCACAA
D E E I V H Q Y Y N G Y C N N I L W P L F H Y L G L P Q

+ 738 GAAGACCGCTTGCCACCACGCGTAGTTTCCAGTCTCAGTTTGGCATATGAGAAAGCAAATCAAATGTTTGTGATGTTGTGA
E D R L A T T R S F Q S Q F L A Y E K A N Q M F A D V V

+ 823 ACAAGCATTATGAAGAGGGTGTGTTGTTGGTGCCATGATTACCACCTCATGTTCTTCCAAAATGCTGAAGAAATATAACAG
N K H Y E E G D V V W C H D Y H L M F L P K C L K K Y N S

+ 908 CAAAATGAAAGTTGGATGTTTCTCCACACCCCATTTCCATCTTCTGAAATTCACAGGACACTGCCATCTCGTTCAGAGCTCCTG

K M K V G W F L H T P F P S S E I H R T L P S R S E L L
 + 993 CATTCTGTCTTGCAGCTGATTTAGTTGGTTTTACACCTATGATTATGCAAGACATTTTGTAGTCTGTACTCGCATCCTTG
 H S V L A A D L V G F H T Y D Y A R H F V S A C T R I
 +1078 GACTTGAGGGTACACCTTATGGGGTTGAGTATCAAGGGAAGCTAACTCGAGTTGCCGATTTCGAATTGGGATAGACTCAGAACG
 G L E G T P Y G V E Y Q G K L T R V A A F P I G I D S E R
 +1163 ATTTATACGGGCACTAGACCTTACTCCAGTGCAGAATCACATCAAAGAATTACAAGAAAGATTCAAAGGCAGAAAGGTAATGTTA
 F I R A L D L T P V Q N H I K E L Q E R F K G R K V M L
 +1248 GGTGTGATCGCCTTGATATGATTAAAGGAATCCCTCAGAAAATTCTAGCATTGCAAAAATTTTGAAGAAAAAGAAAATGCTC
 G V D R L D M I K G I P Q K I L A F E K F L E E K E N A
 +1333 ATTGGCGTGGTAAAGTTGTTTGTCTCAAATCGCTGTGCCAACAAGACAGATGTTCTGAATATCAAAGCTTACAAGCCAGGT
 H W R G K V V L L Q I A V P T R T D V P E Y Q K L T S Q V
 +1418 TCATGAAATTGTGGTCGCATCAATGGCAGATTGGAACATTGACTACTGTTCTATACATCACCTGGATCGCTCTCTTGACTTC
 H E I V G R I N G R F G T L T T V P I H H L D R S L D F
 +1503 AATGAACATATGTGCTTGTACGCAGTTACCGATGTAGCGTAGTCACATCTCTGAGGGATGGAATGAATCTTGCAGCTATGAAT
 N E L C A L Y A V T D V A L V T S L R D G M N L V S Y E
 +1588 TTGTGGCCTGCCAGGAGAAAAAGAAAGGGTTCTCATTCTTAGTGAATTTGCTGGTGCAGCGCAGTCTCTAGGTGCCGGGGCAAT
 F V A C Q E K K K G V L I L S E F A G A A Q S L G A G A I
 +1673 TCTGTCAACCCCTGGAACATTACAGAAGTTGCTGATGCAATTGCCCGGGCTCTGAATATGCTACCTGAGGAAAAGAGAAAAGAGA
 L V N P W N I T E V A D A I A R A L N M L P E E R E K R
 +1758 CACAAGCATAATTTTCTTCATGTAATAATCCACACTGCTCAAGAATGGGCAGGAACCTTTTGAAGCGAACTAAATGATACTGTTA
 H K H N F L H V K S H T A Q E W A G T F V S E L N D T V
 +1843 TTGAGGCACAATAAGGACAAGACAAGTTCCGCTGGGCTTCCAACAAAACTGCAATTGACCGTTATCTGCAGTCAACAAATAG
 I E A Q L R T R Q V P P G L P T K T A I D R Y L Q S T N R
 +1928 ATTGCTCATTTTGGGATTCAATGGAACCTTAACTGAACAGTCGAGAAAAACAGGTGATCAGATTAAAGAAATGGAACCTAAGGTG
 L L I L G F N G T L T E P V E K T G D Q I K E M E P K V
 +2013 CATCCAGAATTGAGACAACCTTGACAGCACTTTGCAGTGATCCAAATACCACAGTAGTTGTGCTCAGTGAAGTGGTAGAAAAAG
 H P E L R Q P L T A L C S D P N T T V V V L S G S G R K
 +2098 TCCTAGATGATAACTTCAAAGAATATGACATGTGGTTGGCAGCAGAGAACGGGACGTTTTTACACCCTTCAAAGGGTGAATGGAT
 V L D D N F K E Y D M W L A A E N G T F L H P S K G E W M
 +2183 GACAACAATGCCAGAGCATCTTAGCATGGAATGGGTTGACAGTGTGAAGCATGTTTTCGAGTACTTCACAGAAAGAACCTCGG
 T T M P E H L S M E W V D S V K H V F E Y F T E R T P R
 +2268 TCTCATTTGATTTTCGAGGAGAGGAACTTCACTTGATGGAATTACAAATACGCAGATGTTGAGTTTGGAAAACCTCAAGCAA
 S H F D F E E R E T S L V W N Y K Y A D V E F G K L Q A
 +2353 GGGACATGCTCGGCATCTCTGGACAGGTCCGATTTCGAATCTCTCAGTTGAAGTTGTTCAAGGGAGCCGATCTGTTGAGGTGGC
 R D M L R H L W T G P I S N S S V E V V Q G S R S V E V R
 +2438 AGCTGTTGGTGTACAAAGGGAGCAGCTATTGACCGCATACTGGGAGAGATAGTCCACAGTAAATCCATGACATCACCCATTGAT
 A V G V T K G A A I D R I L G E I V H S K S M T S P I D
 +2523 TATGTTCTTTGTATAGGACATTTTATGGGGAAGGATGAAGATATTTATGCCTTTTTTCGAGCCGGATCTTCTTCTATTGGTGTGG
 Y V L C I G H F M G K D E D I Y A F F E P D L P S I G V
 +2608 GACTTCCGCGAAGTAAGGTAACAACGACAGATCCAGTTAAGTTTCTGCTGAGAGGAAACCGCGTCTTTGAAGATCCCAGCTAG
 G L P R S K V T T T D P V K F P A E R K P P S L K I P A S
 +2693 TAGTAAAAATGGACCAAAGTCATCTCAAAACAAGGCACAGAAGCCAGTGTCAAATCTGATCAGAAGAAAAACAATAATAACCAT
 S K N G P K S S Q N K A Q K P V S N S D Q K K T N N N H
 +2778 ATTTGCAATGAACCACGACGCCCCGCTCCAGAAAAGATATCATGGAACGTCCTTGATCTTAAGAAAGAGAATTACTTCTCATGTG

I C N E P R R P A P E K I S W N V L D L K K E N Y F S C
+2863 CTGTTGGAAGAACTCGAACGAATGCTCGGTATACACTCGGCTCACCAGATGATGTAGTTGCGCTTTTGATGGAAGTAGCAGATGC
A V G R T R T N A R Y T L G S P D D V V A L L M E L A D A
+2948 GTCATTGCAATCTTGAgagtgttcgcaacaaattctctcaaacaccctttccaacactataatttgatgaaattcacgtgagtc
S L Q S *
+3033 ccaccattatggaaatgagaccacaaagttttggcaggattcagatccacgagaatttcacaaatcagtggtgttggaacgag

+3118 tgttagagaatgtgttcataaacactcatcccatcgacaaatatttcccactttgttaaaatattgaatgcctctgtagtttgga
+3203 tgggatgcttcaagttgcagaatttggcattcccttcaagtgaggtttccctctc

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Fig. 2 Suppl. Phylogenetic tree. (A) The phylogenetic tree based on amino acid sequence of *CkTPS* and other homologues sequences. (B) The phylogenetic tree based on amino acid sequence of *CkTPP* and other homologues sequences. The amino acid sequences of the conserved SK domain region were subjected to the Bootstrap test of phylogeny by the MEGA program.

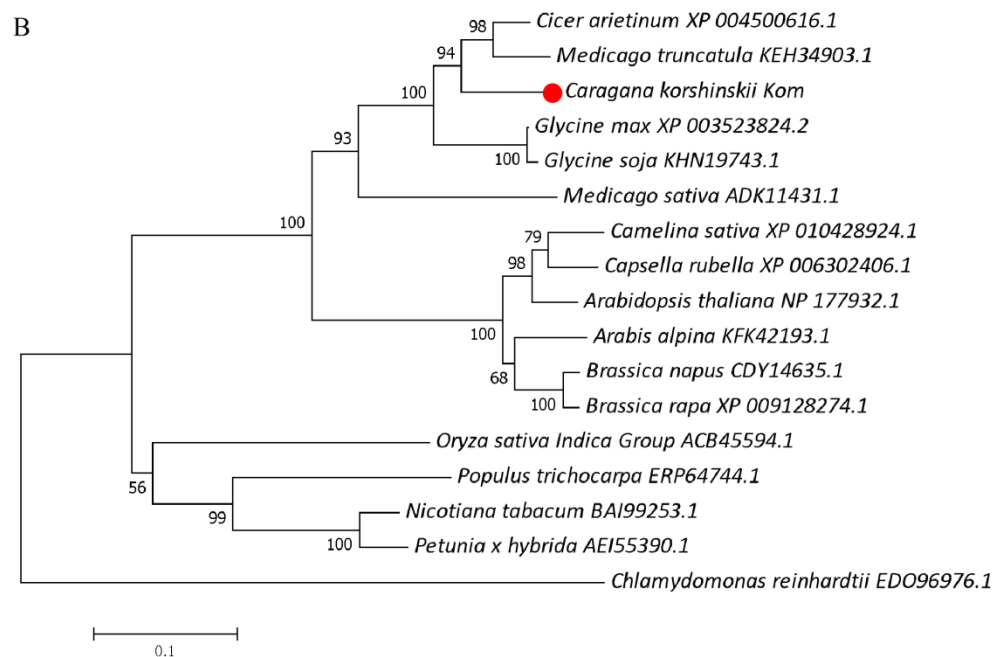
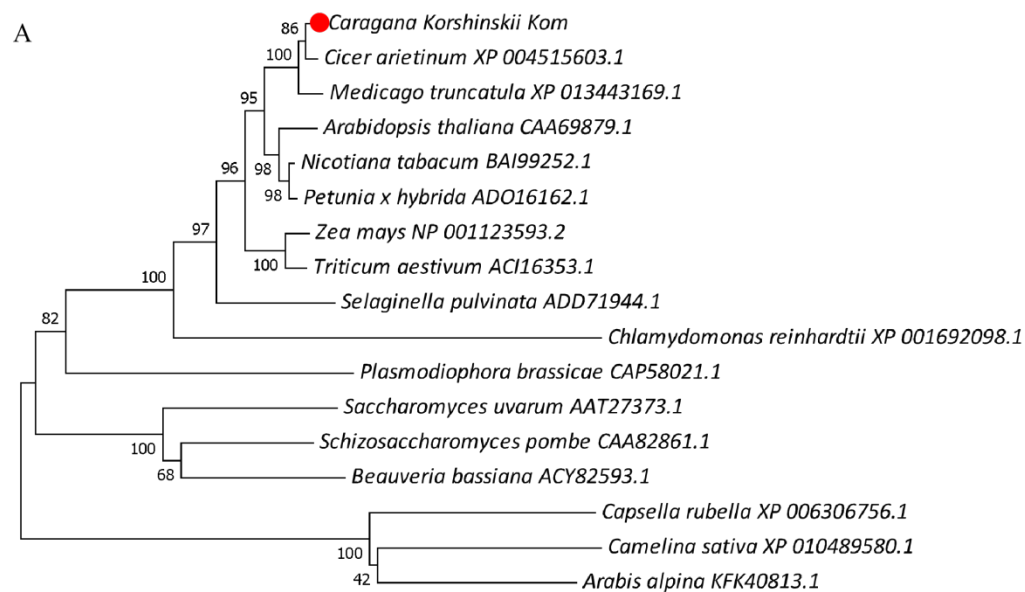


Fig. 3 Suppl. The ORF sequence and promoter sequence of *CkTPP*. Transcriptional start site is defined as +1; Numbers indicate the positions relative to the transcription start site; ‘ATG’ represents the starting codon.

TATA-box

-1495 TGAGGCTATATGTGGCTTTGATTGGAGTCAGGACCTTCAATTAAGACATACTGCATTTTGAAATTATTTGAAGTTGTTGCTGAA

MRE

-1410 TGCTGATCAAGCTTGGTTTGTATGCTCACAAGGTGTTGTCTAAAGTCCTCGTTGAAGACATGCTAGTTTTTGGTTTACTACATC

-1325 TGTGATGCAAAATTGGAGATTTTATTCTTACTGTTGTGCTGGATCTGAGATTGCAGAAGATTGATTTGGACTCTGGATCATCTG

-1240 TATTTGAGATGGTTTCATTCAGTCTGAGAGGGAAGAATTACTTCATCTATTTGCACTTAGAGGTTACAAAACCAGAATAATGTG

ABRE

-1155 GTTCAATTATGGTCTCGTGACTTCATTTGCTCTTAGTGTGTGGAAGTGTGACTTGCTGCAGTGTACACCACTGGTGGTATTT

GARE-motif **ARE**

-1070 GAACTCTGTGATTGTTTTGCTTTTCAGTTCATTGGTTTGGCTTGAATTGGCTTGTGATATTTGCTTCTGCCTTATGGTG

- 985 GTTAAGCATTGTAGCTTCTGTTAAGTGGTTAAGCCTTGAGTTATGGCTTCTGCTTAATGGTTAAGCTTTGGATTGTTGCTTCTGC

- 900 CAAGTGGTTAAGCCTTGAGTTGTGGCTTCTGCTTGGTGGTTAAGCTTTTGTCTTATGGCTTTGATTCAACCGATGTATTTCCG

- 815 GCATTTCTCTTTGATTGTTGCTTTGATTGATATGCGTCTGTATTGCTCATCCCAAGCTGGAAGTGTGTGAACACCTTCCAGCT

- 730 TGCGGGGGGCTGTTAGAGATATAGGAAATTAGAGTATTAGAGTTAGTTGGTTACTAGTTTGGTAGCCTATATAAAGACATGATG

Skn-1-motif **TC-rich repeats**

- 645 TAATCACTTTGTCATTACACTTACTCATTAGTCAATACCAAATTTACATTTATGTGAAGTCTCTCTCAATTTATTTTCTCTCTC

- 560 CATAGATGTATGTTTCTCAACATGGTCAACCCATTAACCCACCTGGTGTCCGTAAGGTTGAATAAAGCAGTTTGGCGTTTC

CGTCA-motif

- 475 TTTAAAAACAGACCACTGCTGTTTCGTGATTTTCAGGAAGAACAATTTTCGAGATGTATAGCATTGCTCTTTCAAAAATAAATTT

- 390 AGAAGAATCAATTTTATTTAAATTATAACCAATTAATTATGCCTCCATTAACCTAAGAATATGTTCTGATAAAACAACCTGGAAG

- 305 CACCGGTGTTCTCTTTTGAATGAGACCGAGGTGCCCTTTTAACATGGTAAATTAATGTCACGAAGTTACATGATCCACTTGCA

- 220 GTGTAGCTAGGTTCCAAATTATTAGTAGTACTATTTTACAGTAGAAAAGGTAATGAAAAAGGAGGTTAGTAGTGGTCCCTC

- 135 CATTCGCATATTTAGTATAGTTGCGGAGAAGTACAATATTATGGCCAGGAAAGATAAGTGGTTGTTTGTTCGTCGGTTTGTGCC

Box-W1 **+1**

- 50 GTGAAAGTGAAACCATGTTTATAAATTGACCAAAACACCCCTCCCTGCTTTGTGACTCGACCAGAGCTAGCCAGCCAGCCAGCCA

+ 35 ACCCGTGAAGTAACCTGATTCAGATTTTCTTCCCCGCAACTTTTCTTCTTATAAAGCCCTCATTTACGCGGACGAAGAAGCC

G-box

+ 120 ACGTACTATAATATCGAGTCTCTTCTCCTTCCCTTCTCCCTTGTGTTGATTCCCATTTACCACTCTTTGTTGGTAACTTA

+ 205 CTAAAGGCTTTGAAGTTGAAGGGAAGTTAATAAGATGACGAAACAGAATGTGGTGACTACTCTGAAGTCAAGTTATGTATTAA

ERE

+ 290 CACGCTTATTGCCATGGCAGCGTCCAATTATTTCAAACTCACCCGTGTTACCAAGCGCAGCTGTGCTTGGTGAGTTAATTTTATG

+ 375 AAGAGGTTGGAAGGAGCTAAAGTTAGCGCATGGATTGATTCAATGAGAGCAGCTTCTCCAACCTCGTGTCAAATCTTCTGAAAACC

M R A A S P T R V K S S E N Q

+ 460 AAGAAAAAATCTTGGACTCTTAAACATCCTTCAGCGCTGAAGTGTGTTGATCGGATAGTACATAACTCCAATGGAAAGCAGAT

E K N S W T L K H P S A L N L F D R I V H N S N G K Q I

+ 545 TGTCATTTTCTTGACTACGATGGAAGTCTCTCCCGATTGTTTCAGATCCTGATAAGGCTTTCATGACTAGAAAGATGAGAGCG

V I F L D Y D G T L S P I V S D P D K A F M T R K M R A

+ 630 ACGCTGCAGGACATAGCAAGACATTTCCACAGCCATAGTGACCGGAAGATGCAGAGACAAGGTATTTAACTTTGTAATAATGG

T L Q D I A R H F P T A I V T G R C R D K V F N F V K L A

+ 715 CGGAAGTGTACTACGCAGCAAGCCATGGAATGGACATCATGGGGCCAACAAAAAGTCGAAGTGCTGAGAAAAAGTAATAATAATA
E L Y Y A A S H G M D I M G P T K S R S A E K S N N N N
+ 800 TGCAGTGTGTTCCAACCTGCTAGTCAATTCCTGCCAATGATCGATGAGGTGTACATAATATTGTTAGAAAAACAAAGTCTGTG
A V L F Q P A S Q F L P M I D E V Y I I L L E K T K S V
+ 885 CCAGGTGCTAAGGTAGAGAACAACAAATTTTGCTTGCCGTGCACTTCCGTTGTGTTGACGAAAAGAGTTGGGCAGTGTAGCGG
P G A K V E N N K F C L S V H F R C V D E K S W A V L A
+ 970 AGAAAGTTAGATTGGTGCTCAATGAATACCCAAAACCTTAGGCTAACCCAAGGAAGGAAAGTGCTGGAGATCCGTCCAACCATCAA
E K V R L V L N E Y P K L R L T Q G R K V L E I R P T I K
+1055 ATGGAACAAGGGCAGGGCCCTTGAATTCTTGTTAGAATCTTTAGGATACGAGAATTCAGTGATGTATTTCCAATATATATTGGT
W N K G R A L E F L L E S L G Y E N S S D V F P I Y I G
+1140 GATAATCGAACTGATGAGGATGCTTTTAAGGTTTTGCGCAGAAGGGGTCAAGGGATTGGGATTCTTGTTTCTATATTTCCAAAAG
D N R T D E D A F K V L R R R G Q G I G I L V S I F P K
+1225 AAACAGATGCTTCCTACACCTACAAGATCCATCAGAGGTTGAGTAAtttttgcggcgattggaggaggaaagatcgagtac
E T D A S Y T L Q D P S E V E *
+1310 tgtgacccccacaagtgtagagagttgcagattgtagatgatcagccaaggaattgacaccacttcgagctcga

Table 1 Suppl. Primers used in this study.

Primer name	Primer sequence
CkActin-F	5'-GTTGGAAGGTGCTGAGGGA-3'
CkActin-R	5'-TGACAGGATGAGCAAGGAGA-3'
qCkTPP-F	5'-TTCCGTTGTGTTGACGAAAAGAG-3'
qCkTPP-R	5'-ACTTTCCTTCCTTGGGTTAGCCT-3'
qCkTPS-F	5'-TTGACCGCATACTGGGAGAGATA-3'
qCkTPS-R	5'-GACGGCGGTTTCCTCTCAGC-3'
TPPZJ-F1	5'-TTYYTNGAYTAYGAYGGNAC-3'
TPPZJ-F2	5'-TTYYTNCNATGATHG-3'
TPPZJ-R	5'-CYTTRAANGCRTCYTC-3'
TPP-J-F1	5'-AGTTGGGCAGTGTTAGCGGAGAA-3'
TPP-J-F2	5'-AGGAAGGAAAGTGCTGGAGAT-3'
TPP-J-R1	5'-CCGCTAACACTGCCCAACTCT-3'
TPP-J-R2	5'-CTCTACCTTAGCACCTGGGAC-3'
CkTPP-full-F	5'-TCCGTGCACTTCCGTTGTGT-3'
CkTPP-full-R	5'-CGAGCTCGAAGTGGTGTCAATTCC-3'
TPS-J-F1	5'-GAGGAGAGGGAACTTCACTTG-3'
TPS-J-F2	5'-TTGGCAGCAGAGAACGGGATGT-3'
TPS-J-R1	5'-GTTCCAAATCTGCCATTGATGCGACC-3'
TPS-J-R2	5'-TGTTCTTGTTGGCACAGAGATT-3'
TPS-ZJ-F1	5'-GCNGCNTGYGGNACNGCNTG-3'
TPS-ZJ-F2	5'-CNACNACNTGYGCNAC-3'
TPSZJ-R	5'-ANGCNCCNCCNGTNCC-3'
CkTPS-full-F	5'-ATGCCTGGGAACAAGTACA-3'
CkTPS-full-R	5'-TCAAGATTGCAATGACGCA-3'
TPP-SP1-1	5'-GTTGTTCTCTACCTTAGCACCTGGGA-3'
TPP-SP1-2	5'-GGTCACTATGGCTGTGGGAAAATGTC-3'
TPP-SP1-3	5'-CAGAAGATTTGACACGAGTTGGAGAAG-3'
TPP-SP2-1	5'-CAGAAGATTTGACACGAGTTGGAGAAG-3'
TPP-SP2-2	5'-CGCTGAAATGAGGGGCTTTATAGGAA-3'
TPP-SP2-3	5'-ACAATGGTTTCACTTTCACGGCACA-3'
TPP-SP3-1	5'-ACAATGGTTTCACTTTCACGGCACA-3'
TPP-SP3-2	5'-CGGTGCTTCCAAGTTGTTTTATCAGA-3'
TPP-SP3-3	5'-TCTTCCTGAAAATCACGAACTGACG-3'
TPS-SP1-1	5'-ACATGAGGTGGTAATCATGGCACCAAACAA-3'
TPS-SP1-2	5'-AGAGCCTTCTGTCCAATCTCATCTGGTACG-3'
TPS-SP1-3	5'-TCTCTTAAAAGCCGTTCCACACGACCCG-3'
TPS-SP2-1	5'-TGAATATCAATGTCGAAACAGCCAACCTT-3'
TPS-SP2-2	5'-TCCAGTGCCAGACAAGTTTTGAACCA-3'
TPS-SP2-3	5'-AGTCACCGCATCCCTGGGCTTGTTAC-3'

pCkTPS-F	5'-TCCAGTGCCAGACAAGTTTTGAA-3'
pCkTPS-R	5'-ATGGTCGCTCTGGAATCCAACCAT-3'
pCkTPP-F	5'-TGAGGCTATATGTGGCTTTGATTGGAG-3'
pCkTPP-R	5'-GCTAAAGTTAGCGCATGGATTGATTCA-3'
pCkTPS-F2	5'-CGGATCCTCCAGTGCCAGACAAGTTTTGAA-3'
pCkTPS-R2	5'-GCGAGCTCATGGTCGCTCTGGAATCCAACCAT-3'
pCkTPP-F2	5'-GCGTCGACTGAGGCTATATGTGGCTTTGATTGGAG-3'
pCkTPP-R2	5'-GCGAGCTCGCTAAAGTTAGCGCATGGATTGATTCA-3'
pORE-F	5'-ACTGAAGGCGGGAAACGACAAT-3'
pORE-R	5'-TTTCACGGGTTGGGGTTTCTAC-3'
GUS-F	5'-TCAACGGGGAAACTCAGCAAGC-3'
GUS-R	5'-CCTCATTGTTTGCCTCCCTGCT-3'
Actin2-F	5'-GCACCACCTGAAAGGAAGTACA-3'
Actin2-R	5'-CGATTCTGACCTGCCTCATC-3'
CkTPP-BamHI-F	5'-AGAACACGGGGGACTCTAGAACATGGCAGTGTTAGC GGATGGATTG-3'
CkTPP-BamHI-R	5'-CGTTGCAAACGTAAGTGTTGAAGTGGTGTCAATTCC TTGGAC-3'
CkTPS-XbaI-F	5'-CGCTCTAGAATGCCTGGGAACAAGTACA-3'
CkTPP-BamHI-R	5'-CGTGGATCCTCAAGATTGCAATGACGCA-3'
PBI101-35S-F	5'-AGGAAGGTGGCTCCTACAAATG-3'

Fig. 4 Suppl. Genome PCR and RT-PCR identification of transgenic *Arabidopsis* lines. (A) Three transgenic lines of *Pro.CkTPS*. (B) Three transgenic lines of *Pro.CkTPP*.

