Supplementary Information for:

CACTA-like transposable element in *ZmCCT* attenuated photoperiod sensitivity and accelerated the post-domestication spread of maize

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SI Materials and Methods

Genome-wide association mapping. A GWAS study was performed using the maize panel, CAM508, which includes 256 temperate and 252 tropical/subtropical maize diverse lines (29) (Table S1). The panel was genotyped using the MaizeSNP50 BeadChip, which contains 56,110 SNPs (S1, S2). A subset of 368 lines was genotyped by RNA-seq, resulting in 1.03 million high-quality SNPs (28). We amplified an 800-bp region in the promoter of *ZmCCT*, encoding a CCT domain-containing protein, for each line in the CAM508 panel using the primer pair, MR1 (*SI Appendix,* Table S6). This analysis yielded 52 SNPs and 9 InDels. A total of 557,955 polymorphic sites with MAF ≥0.05 and a missing rate <25% were selected for the GWAS using 368 maize lines. All lines from the CAM508 panel were grown in eight environments at seven locations, which included six long-day (>13 h) and two short-day (<13 h) growing-season environments (Table S2). Flowering time was investigated and measured as days to anthesis (DTA) and days to silking (DTS), which were converted into growing degree days (GDDs). Either anthesis photoperiod response (APR) or silking photoperiod response (SPR) was calculated as the difference between GDDs under long- and short-day conditions. The BLUP (best linear unbiased prediction) values for each trait were used for other data analysis. For APR and SPR, the BLUP values were calculated according to the methods by Hung et al. (18). A mixed linear model (S3), which accounted for population structure and relative kinship (S2), was performed using TASSEL software (S4) to test for associations between flowering-time variation and genotype. The Bonferroni-adjusted significance threshold ($P < 1/557{,}955 = 1.8 \times 10^{-6}$) was used to identify significant associations.

Candidate-gene association mapping. *ZmCCT*-based association mapping was performed using a subset of the maize panel, including 107 temperate and 73 tropical maize lines (Table S1). The *ZmCCT* promoter (~1.8 kb) and coding regions (no introns) were amplified and sequenced using four primer pairs (MR1–MR4). The TE-related PAV was detected using three primer pairs (TED, TELB, and TERB) (*SI Appendix,* Table S6). These sequences were assembled using ContigExpress in Vector NTI Advance 10 (Invitrogen), aligned using MUSCLE (S5), and manually corrected using BioEdit (S6). Polymorphic sites (SNPs and InDels) (MAF≥0.05) were extracted and levels of LD between two sites were calculated in TASSEL 2.1.0 (S4). Associations between extracted SNPs/InDels and flowering time were identified using a mixed model (S3), and incorporated with population structure and kinship (S2) in TASSEL 2.1.0 (S4).

Linkage analysis. Four F_2 populations, including Qi319 × Mo17, Qi319 × Zheng58, Tian77 × Mo17, and Tian77 × Zheng58, were grown at 4 locations: Hainan, Hubei, Beijing, and Jilin (*SI Appendix,* Table S2). Approximately 160–250 F_2 plants from each population were genotyped for the TE-related PAV and scored for 19 agronomic traits, including flowering time, plant height, ear height, and etc (*SI Appendix,* Table S12). The genetic effects of TE in these populations were evaluated via single-factor analysis using one-way ANOVA in Excel 2007 ($\alpha = 0.01$).

Nucleotide diversity and tests for neutrality. *ZmCCT* segments (Fig. 3A) were amplified from 32 teosinte entries (Table S1) using four primer pairs (*SI Appendix,* Table S6). PCR products were cloned into a vector using the pEASY-T5 Zero Cloning kit (Beijing TransGen Biotech Co. Ltd, China), and at least three clones were sequenced for each entry. Nucleotide diversity (π) and Tajima's D-statistic were calculated using DNaSP version 5.0 (S7).

Minimum spanning tree. A sample of 481 maize inbred lines and 93 teosinte entries from all seven subspecies (Table S1) was used to construct a minimum spanning tree for *ZmCCT*. Arlequin version 3.5 (S8) was used to define the haplotypes and calculate the minimum spanning tree among haplotypes. Arlequin's distance matrix output was used in Hapstar-0.6 (S9) to draw the minimum spanning tree.

Functional complementary test. The BAC clone which contained *ZmCCT* was screened from the late-flowering inbred line 1145 (Hap6) BAC library and was subjected to restriction endonuclease digestion using SacI. The resulting 8.1-kb DNA fragment, which contained *ZmCCT* (a 5.4-kb promoter region, 2,547 bp of coding sequences, and a 500-bp 3'-UTR) was inserted into the binary vector pCAMBIA3301. This construct was introduced into the maize hybrid HiII (B73 × A188, Hap1) via *Agrobacterium tumefaciens*-mediated transformation. Transgenic T_0, T_1, and T_2 plants were identified via PCR using two primers pairs, LBCCT and TED (*SI Appendix*, Table S6).

RACE. Total RNA was extracted from young leaf tissues of 1145 plants using a plant RNAprep pure kit (Tiangen Biotech Co. Ltd., China). First-strand cDNA (RACE-ready cDNA) was synthesized using the SMART RACE cDNA amplification kit (Clontech Lab, Palo Alto, CA). *ZmCCT* specific primers (*SI Appendix*, Table S6) were designed to amplify 5'- and 3'-RACE-ready cDNAs. Sequences from 5'- and 3'-RACE products were assembled to obtain full-length *ZmCCT* cDNA.

Sub-cellular localization of *ZmCCT*. Full-length *ZmCCT* cDNA was amplified using the primer pair, NLCCT1 (*SI Appendix*, Table S6), and cloned downstream of the CaMV35S promoter in the pEZS-NL vector. This construct was introduced into onion epidermal cells via particle bombardment using the PDS-1000 system (Bio-Rad) at 1,100 psi helium pressure. Transformed cells were incubated in the dark for 18 h at 28 °C before imaging. The construct was transformed into maize protoplasts as described (S10). The GFP signal was detected using an LSM510 laser scanning confocal system (Zeiss).

Phylogenetic analysis. Protein sequences that contained a CCT-domain were obtained from maize (Maizesequence, http://www.maizesequence.org), rice (Ghd7) (ACA14488.1), sorghum (Sb06g000570) (XP_002446018.1), and *Arabidopsis* (CO and TOC1) (NP_197088.1 and NP_200946.1). These proteins were used to construct a phylogenetic tree using the maximum likelihood method based on the JTT matrix-based model (S11) and MEGA 4.0 (S12).

Expression profiling of *ZmCCT*. Seeds of NIL1 (TE-positive, Hap1) and NIL2 (TE-negative, Hap6) with the Y331 genetic background were planted under either short- (8 h light/16 h dark) or long-day (16 h light/8 h dark) conditions. Temperatures within the chambers were maintained at 26 ˚C during the light period and 22 ˚C during the dark period. At the V4 stage young leaves were harvested every 3 h for 48 h. Three plants were selected at random to serve as biological replicates. T_2 transgenic plants were planted in a greenhouse and maintained at 28˚C during the light period (16 h) and 18˚C during the dark period (8 h). Leaf tissues were collected from these plants at the V6 stage. For each sample total RNA was isolated using a plant RNAprep pure kit (Tiangen Biotech Co. Ltd.), and first-strand cDNA was synthesized using the M-MLV first strand kit (Invitrogen, Carlsbad, CA). *ZmCCT* transcripts were amplified via real-time PCR, using *GADPH* as the internal control (*SI Appendix*, Table S6). Three technical replicates were performed for each reaction under the following conditions: 5 min at 95 ˚C, followed by 40 cycles of 10 s at 95 ˚C, and 20 s at 60 ˚C. The relative quantification method (DDCT) (S13) was used to evaluate gene-expression levels.

For allele-specific expression analysis in transgenic plants the primer pair ASCCT2 (*SI Appendix*, Table S6) was used to amplify *ZmCCT* transcripts, resulting in a 241-bp product from the endogenous gene and a 235-bp product from the exogenous *ZmCCT* transgene. These amplicons could be distinguished through electrophoresis on a 6% non-denaturing polyacrylamide gel.

Transient assays. Three regions of the *ZmCCT* promoter, which contained 641, 2,304, or 4,204 bp, were amplified from the HZS line (Hap1) and cloned into pCAMBIA3301 by replacing the CaMV 35S promoter. Resulting plasmids were 641-bp HZS_{pro}:Gus, 2.3-kp HZS_{pro}:Gus, and 4.2-kb HZS_{pro}:Gus. These three constructs, together with pCAMBIA3301, were transformed into the *Agrobacterium* strain, EHA105. *Nicotiana benthamiana* leaves were infiltrated with the *Agrobacterium* suspension (S14) and placed in a long-day chamber for 3 d. Infiltrated leaves were then subjected to GUS histochemical staining (S15) and examined using a light stereomicroscope.

Bisulfite sequencing. Genomic DNA was isolated from fresh young leaves collected from 1145 (Hap6) and HZS (Hap1) maize lines that were planted under long-day conditions. Unmethylated cytosines were converted to uracils via sodium bisulfite using the EZ DNA Methylation kit (Zymo Research, Orange, CA). After bisulfite conversion, the genomic-DNA samples were subjected to PCR and resulting products were cloned into the pEASY-T1 vector (Transgen Biotech Co. Ltd., China). M12F/R primers were used to sequence 10–15 clones. The CpG island was predicted using MethPrimer (S16), and *cis*-regulatory elements within the promoter were predicted as described (S17).

Construction of an expression network for flowering time. The inbred line HZS (Hap1) and its NIL (Hap6) were used to analyze the *ZmCCT*-related maize flowering pathway. The HZS was crossed to the donor parent, a late-flowering recombination inbred line in a RIL population derived from HZS and CML288 (Hap6), and the F_1 hybrid was backcrossed 7 times to HZS (Fig. S14). One BC_7F_1 plant was self-pollinated to develop the NIL (Hap6), in which the donor size was estimated to be 130kb. Seeds from HZS (Hap1) and its NIL (Hap6) were planted in growing chambers under long-day conditions (16 h light/8 h dark). Young leaves were harvested at stages V3–V7. Total RNA extraction, library construction (≤800-bp insert), and 95-bp paired-end Illumina sequencing were conducted at BGI (Shenzhen). For each sample an average of 27,618,470 raw reads were generated, leading to 2.3 Gb of high-quality raw sequencing data. A total of 29,621 genes were identified, which covered ~72% of all predicted genes in maize. Genes that were differentially expressed ≥1.67-fold between HZS and its NIL at the V3 stage were used for subsequent analyses. These genes were functionally grouped according to GO terms using agriGO (S18) and Interpro database (http://www.ebi.ac.uk /interpro). We then used this data to generate a revise model of the regulatory network that controls flowering time. Previous models from *Arabidopsis* (41) and maize (40) were used as starting points. Real-time PCR was performed to verify RNA-seq data concerning the most critical genes.

Supplementary References

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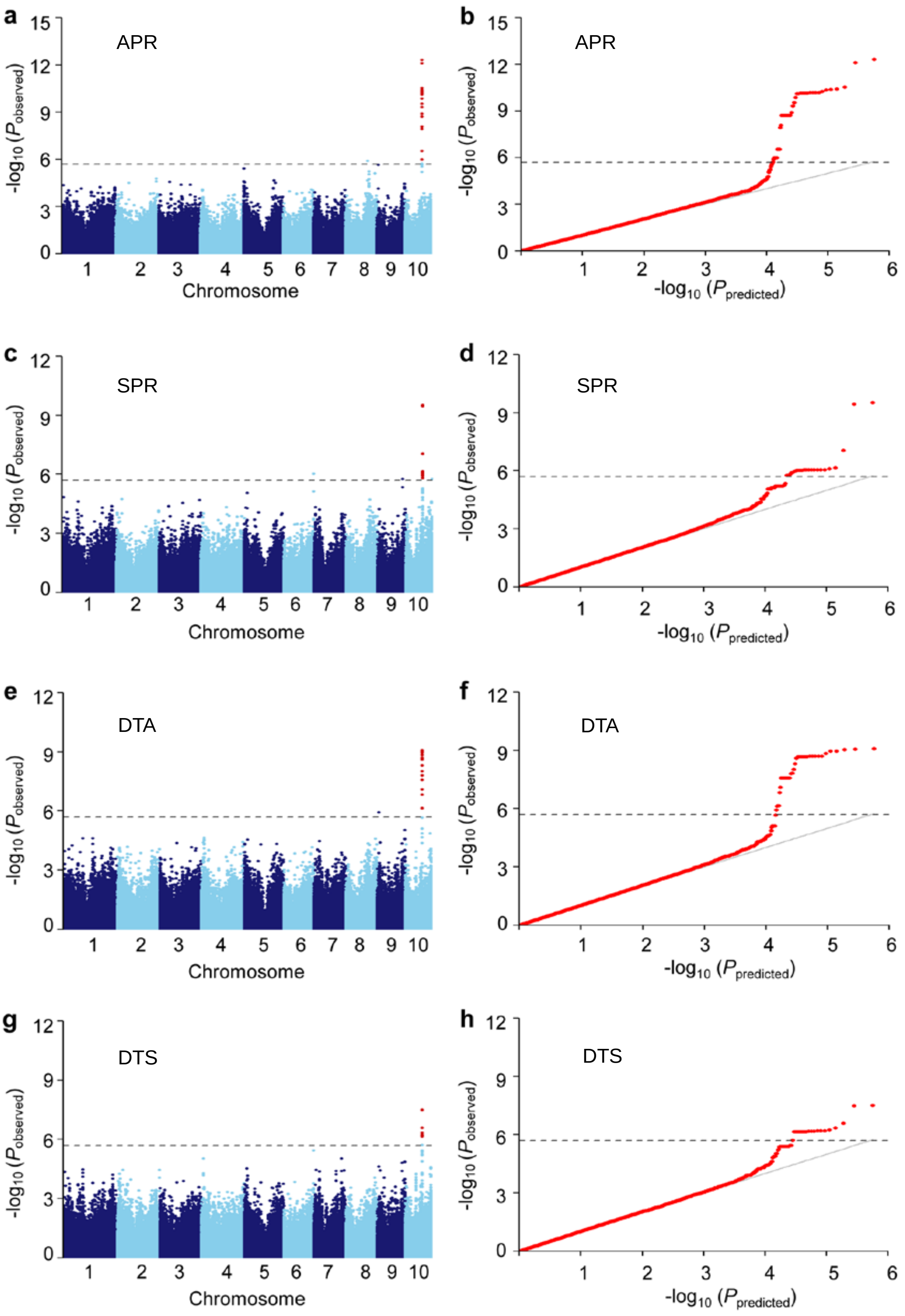

Fig. S1. Manhattan and quantile-quantile plots from the GWAS concerning photoperiod sensitivity (a–d) or flowering time (e–h) under long-day conditions in maize. A panel of 368 lines was analyzed. Dashed horizontal lines indicate the Bonferroni-adjusted significance threshold (1.8×10^{-6}). Significant SNPs in *ZmCCT* are indicated by red dots. APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA, days to anthesis; DTS, days to silking.

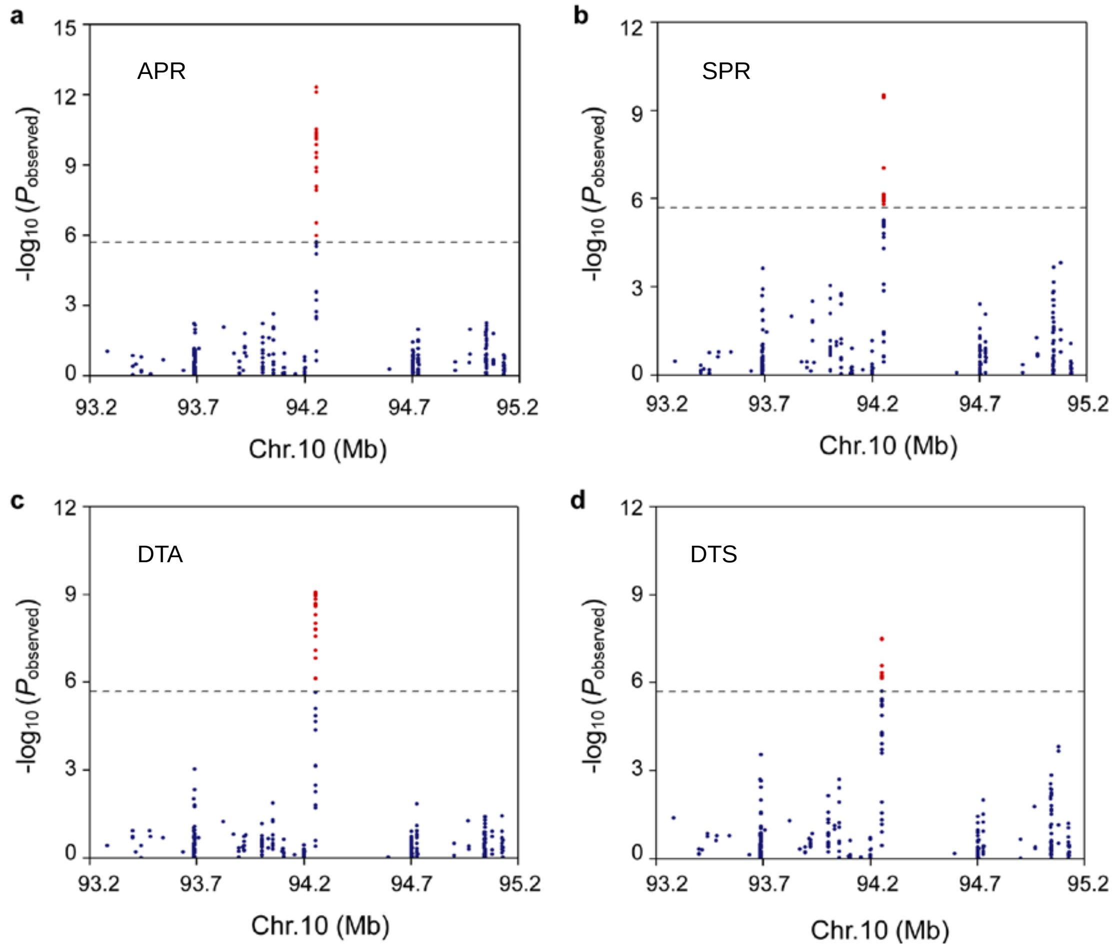

Fig. S2. Manhattan plots of associations between SNPs on chromosome 10 near *ZmCCT* and photoperiod sensitivity (a, b) or flowering time (c, d) under long-day conditions in maize. A panel of 368 lines was analyzed. Dashed horizontal lines indicate the Bonferroni-adjusted significance threshold (1.8×10^{-6}). Significant SNPs within the promoter of *ZmCCT* are indicated by red dots. APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA, days to anthesis; DTS, days to silking.

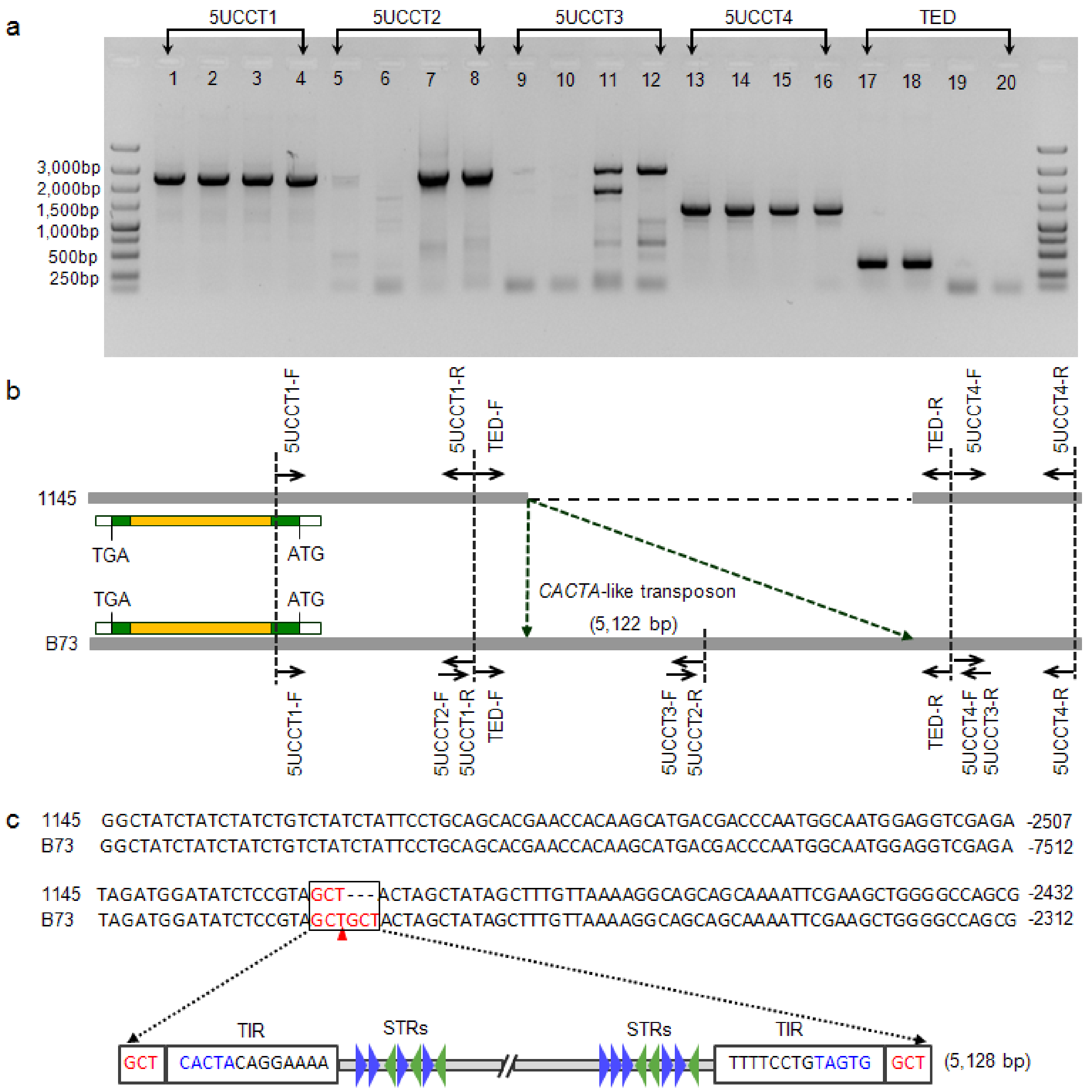

Fig. S3. Identification of a CACTA-like transposon in the *ZmCCT* regulatory region using an overlapping PCR strategy. (a) PCR amplification of the *ZmCCT* regulatory region from photoperiod sensitive (1145 and Qi319) and insensitive (B73 and Mo17) lines of maize. Five pairs of overlapping primers were used (5UCCT1, 5UCCT2, 5UCCT3, 5UCCT4, and TED). Lanes 1, 5, 9, 13, and 17 represent line 1145. Lanes 2, 6, 10, 14, and 18 represent line Qi319. Lanes 3, 7, 11, 15, and 19 represent line B73. Lanes 4, 8, 12, 16, and 20 represent line Mo17. (b) Schematized alignment of *ZmCCT* loci from 1145 and B73. A CACTA-like transposon was detected 2,543 bp upstream of the *ZmCCT* ORF in B73. Primers used to analyze the *ZmCCT* regulatory region are represented by arrows. Within the *ZmCCT* gene, green boxes represent exons, yellow boxes represent introns, and open boxes represent UTRs. (c) Structure of the CACTA-like transposon. The CACTA ends (blue text) and the GCT target size duplication (red text) are shown. The 13-bp terminal inverted repeat (TIR) sequences are also shown. Blue and green arrows indicate forward and reverse duplications of sub-terminal repeats (STRs), respectively. The STR sequence is 5'-TTTCCGACGG-3'.

Fig. S4. *ZmCCT* gene structures based on maize inbred line B73 genomic sequence.

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   1 TAATATACGG ATTCTCAATC CAAGGTGCAG GCGTACCCGA ATCAAATCAA ATATGAGGCT

  61 ATCTATCTAT CTGTCTATCT ATTCCTGCAG CACGAACCAC AAGCATGACG ACCCAATGGC

                                        TE 5,122bp
 121 AATGGAGGTC GAGATAGATG GATATCTCCG TAGCT.. ....GCTACTAGC TATAGCTTTG

 181 TTAAAAGGCA GCAGCAAAAT TCGAAGCTGG GGCCAGCGGC CATTGATTCC TGATGGATGC

 241 ACATACGTGC ATCCATATCG ATGCTGTCGC TGCCTCCGTC GTCTCGTCTC GCCACAACCG

 301 CGCTACACGC AAAAGCTATG CGGATTCTGT TTCTGTGTAA ACAACCAACA CTCTCTTTAT

 361 TCCAATGGAC AATGCTCCAT CTCTCTTGTG CCCCCCGCAG GACAGAATTG GCTAGGCGGC

 421 GATTCCACGT GCCATCACAT TTCCAATTCT GAAGTTAGCC TATCCCACCG TTGCTTCCTA

 481 CACGTGTCGA CCATCCGGAC CATATATAGA CAGCTATACC ACACCCGCGT GGATGCATGC

 541 ATGGCTCATC CCTTACTTGT GATGTATAGA CAATTCACAC TATATATATA TATATATATA

 601 TATATATATA TATATATATA TATTGCTTTG ATTTTTGATC TCTGATATAT ATATATCGCC


                                                         Resequence start
 661 AGCATATTAT CACTGGCACC ACTTATCCTC GCTCGATCTC TCAGAAACAA TAATAACATA

 721 GAGAGTTTAT ATAGTTCGAA CATTAGTATC G---TTTTTT ATTTGCAATA GATTCTAATG

 781 TAACTCT--- -TTAGTACTG GTTGTAAC-A AAAAAAAACC AGTACTACAT ACTAAGTTTT

 841 CAACAACAAC TGATACTAAA ATTATTTTAT TAGTTTTCTA CAAACAATAT GATATTAACA

 901 GAGAGTACAT TAATAATTAT GTGCATATAC AAATATACAA GTTCTTTCCA ATGGATATGT

 961 GCACATACAA AAATACAAGT ACTTTCCAAT AGATATGAGC AGATACAAAC ATACAAAC--

1021 --ATCCAA-- --ATATACAT ATAGCTTCTT TATTGAATAT ATAAATTTTA GGAGAGTACA

1081 TATTATATA- TTTTTA--GT ACAAGGAAAG TGTGAAAACA CGTCT-GATT CC---C----

1141 ---------- ---------T TCTCTA-TTT TTTCGTCTCA GTTCCTGCTT C-TTCCCAAA

1201 CCTAT----T ACTGCAACCC TAC-TTCCTC TTGTGCGGAG -G--TTAGGT CAAGGGATTC

1261 CAAACCAACT ACGGGTTTAA TGTGAGGGAC GAAGATGCTC TTACAACCAA CTAGCCCTTG

1321 AAGTAGGAAA TAGAATGTAT TTTCTTATTT CCTGCCATAG GACTAGTTCA TTTTTCAAGA

1381 TCTTCTCCAT TTCACTATGA CCAATGCGAG GATGGTTTCT ATG-AAAAAA ATATACAAAA

1441 CAG--AAAAA ATAGAGTTCA AAACAAATGG TGTAATAGTT ATATATGGAC AGTAAACAAA

1501 AAATAAAAAA CATGGATGAA TATCATTTTG CGAATGTGTA AAAAATACTC GAGGCACGTG
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1561 ACATTTGTGT TGTATTGATA ATTAACACAC TATGTGACAT TTACTCAAAA CTTTCATTGG

1621 TACTCAACAC GTCCGGTGCT CACGAATGAG AAAGGCAGGT TGCGCTTATA GGAGACACCC

1681 CTA-GCCAAT AACTTGTACC AAATCCTTCA CTTTTAGTGT TGGTTATTTA AAAGAATCGG

1741 TGCTAAACTA ATTTTGGCGG GAATT----- TCAATTGCTC TGGCAGGATT GGAAAATATC

1801 TTTCTATATC GGTTCTTTAT AAAAAAC--- ---------- ---------- ----------

1861 ---------- ------GGTT CTAAATAAAC ACAATATTTC CAACCAGTAC TAAAGACTTA

1921 AAATTTAGTA TCGATTCTAT AAAAGAACCG ATACTAAAGA TATTGGAGAT GTTCTCTTCG

1981 AA-------- ---------- ---------- ---TAATCCA T--AGAGA-A AAAACACTGT

2041 GGAAGC---- ----TTAGTG CAGATTAAAG TCAAGCCTAA TTAGTGCTGG TTCTTAGGTT

2101 GAACTAGCAG TGCTAGATAA C--TTAATAT TAAGTAT--- -TAGTTGCAT ACAACAACCC

2161 ATACTGATAT CATATCCTCT GCACGGAC-- --TATATTTT AAAACGGTGC TAAAGCTAGT

2221 ACTAATATTG GAACAAATAA AATTGGACGG AAACCCCATT CTCCGGTAGG GAATAATGAT

2281 TTGTTTTTCT TCTTGCACTT TAATTTGTTT AGTTTATATT CTCGCTAGCT TGACGACATA

2341 AATACATGTG TGTAGATAGA ACATTGCCTA TATACCCAGA GATGGAGTCT CGTCCATGCA

5’-UTR

2401 TATCTATTCG GCAGCGGGCA TTGGCTACCA GATTCTGCGA TATGGAACAT CTGCTTTTCT

2461 TTCTGCTGCT TCGTCTCTGG CCTTTGCTTT TCCTTCACTA CGACTTAAAT AAAAGTAACT

2521 AGCCCTAGCA GCTAGCTATC AAGCTTTATT TATCTGCTCC TTCCTCCATC TCCCTGCTGG

2581 CCTGCCTGAT CAGTATATAT AACTCTCAAT TCCATCAACA AATCTCCCTC CCAAGCTAGT

2641 CGATCCAT-- -CTTGTG--C ACAC---ACA GCGGATATAC CTCTCTATCG ATCAACAGCG

Translation Start

-1 +1

2701 GCCATGTCGT CGGGGCCAGC AGCATGCGGT GTGTGCGGCG CGGCCGCCTG CTGCCCGCAC

1st exon

2761 CTCTTGCACA CCGGTGACGG CAACGACGAC GACCTC---A TCAGCCGGGC CTTCTTCTCC

2821 GTCTTCCCTG TCGTCGGTCA TCACCGTCGT CATGAGTCCA CCAGCAGCCC CGCCATGCAG

2881 CAGCCATCGG GGTGCCTGCA CGAGTTCCAG TTCTTTGGCC ATCAGGACG- --ACCACCAC

2941 CACCAAGAAA CCATCGCCTG GCTCTTGGAC CACCCACCGC CACCTGCGCC CGAGCTTGGC

3001 GGCGACGACG GCCCGTCCCC AGCTGGTGAT GAGAACGACG ACCAGCCTGC GTTTCACCCG

3061 TTTGGGACAC CACAGTACCA CCACCCCGGA AAA------G GGAACGGGAA CGGGCTCACC

3121 TTTGAGCTGG ACGCCACGCT GGGCCTCGGC ACCGCGCGGC AAACCACTGA GACAGCAGAA

3181 GCAAGCGCCA CCATCGTAAG TATTGCTCCC GAATTATCTT AAGTAAGTTC AGATAATTCA

3241 CATGCATGGT TTCTAATTGG AATTTGGTCC CAAGCTGGAC -ACCCTTTTT TTATCTTCCG

3301 TT----TTCT CAACTCTCTT ATCGATCACC TGCATAAAGG ACCTTTGTAT CAAGTACCAA

3361 GAGNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

3421 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

3481 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

3541 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

3601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

3661 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

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4261 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4321 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4381 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4441 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4561 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

4621 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNA TACATATGAC CAAAGTACTA ATTAATTAGT

4681 TG-CTGCAGT TATTAGCTGT CCAAAATTTG CTTTGATCAT CATGCAATAA TATACACATG

4741 CAGAAACTAA AATG-AATAA CATATATAAA TCCATGCATG CACATGCA-G CATAC-----

2st exon

4801 TAATTATTGC TATTAATTAA TTGCAGATGT CATTCTCTGG GAGCACATTC ACGGACGCTG

4861 CAAGCAAGGA GCCAGCACTG ATCGACGACG GCAATGAGCT GCAAATGCCG GTAGATCAGT

4921 CGTCGACGGA GAGGGAGGTT AAGTTGATGA GGTACAAGGA GAAGAGGATG AGGAGGTGCT

4981 TTGAGAAGCA GATAAGATAT GCATCCAGGA AAGCCTATGC GCAGGTGAGA CCCAGGGTGA

Stop codon

5041 AAGGCCGCTT TGCCAAGGTA ACCGAATGAC GAAGCCTGCT AGCTAGCTCC ACCACAGCAG

3′-UTR

5101 ACGACGACGC CTGAATCT-- ----TATGTA --TATATGTA TGTATAGTTA GTAAATGTAG

5161 TAC------C CCTCTATTCT TTTTTATTTG TCGCCGATTA GTTTAAAAAT AAACTAGCG-

5221 -GACGACAAA TATTCGAGAA CAGAGGTAGT ATATGTTATG TCTCAATTGC CAACTGCAAT

5281 A

//

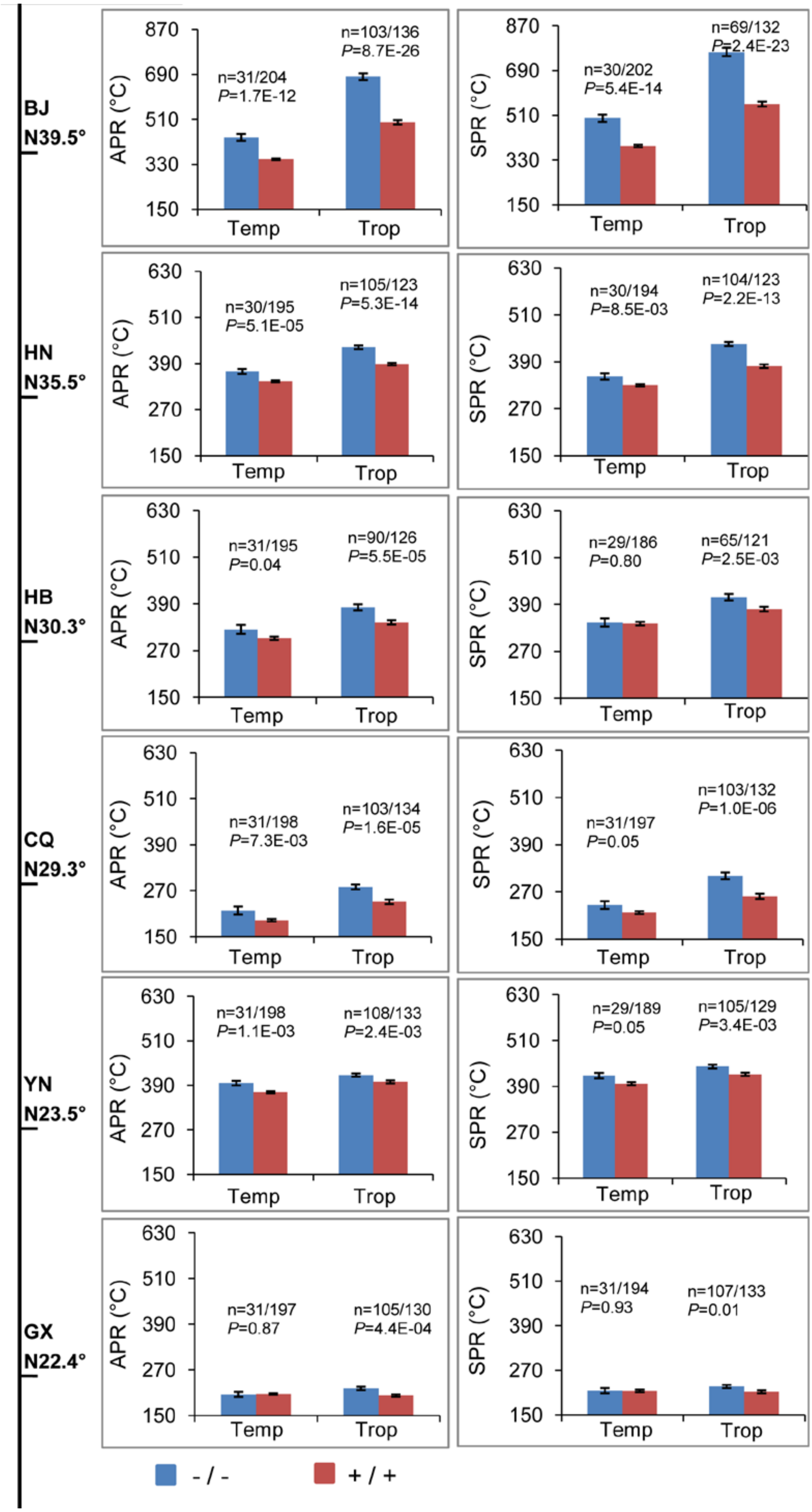
BJ
N39.5°
APR (°C)
870
690
510
330
150
n=31/204
P=1.7E-12
n=103/136
P=8.7E-26
Temp
Trop
SPR (°C)
870
690
510
330
150
n=30/202
P=5.4E-14
n=69/132
P=2.4E-23
Temp
Trop
HN
N35.5°
APR (°C)
630
510
390
270
150
n=30/195
P=5.1E-05
n=105/123
P=5.3E-14
Temp
Trop
SPR (°C)
630
510
390
270
150
n=30/194
P=8.5E-03
n=104/123
P=2.2E-13
Temp
Trop
HB
N30.3°
APR (°C)
630
510
390
270
150
n=31/195
P=0.04
n=90/126
P=5.5E-05
Temp
Trop
SPR (°C)
630
510
390
270
150
n=29/186
P=0.80
n=65/121
P=2.5E-03
Temp
Trop
CQ
N29.3°
APR (°C)
630
510
390
270
150
n=31/198
P=7.3E-03
n=103/134
P=1.6E-05
Temp
Trop
SPR (°C)
630
510
390
270
150
n=31/197
P=0.05
n=103/132
P=1.0E-06
Temp
Trop
YN
N23.5°
APR (°C)
630
510
390
270
150
n=31/198
P=1.1E-03
n=108/133
P=2.4E-03
Temp
Trop
SPR (°C)
630
510
390
270
150
n=29/189
P=0.05
n=105/129
P=3.4E-03
Temp
Trop
GX
N22.4°
APR (°C)
630
510
390
270
150
n=31/197
P=0.87
n=105/130
P=4.4E-04
Temp
Trop
SPR (°C)
630
510
390
270
150
n=31/194
P=0.93
n=107/133
P=0.01
Temp
Trop
- / -
+ / +

Fig. S5. Genetic effect of the TE-related PAV on photoperiod sensitivity in temperate and tropical maize germplasms grown in multiple environments. Maize adaptation, temperate and tropical, was categorized mainly by the population structure estimated by 926 SNPs (Yang et al, 2011, Mol Breed, 28:511-526) and 36,618 SNPs (Li et al, 2012, PLoS ONE, 7: e36807), which consisted TST (Tropical or Subtropical), SS (Stiff Stalk) and NSS (NonStiff Stalk). When the membership probability of TST group was the highest for a maize inbred line, we defined the line as a tropical line, otherwise as a temperate line. Furthermore, the adaptation categorizations of some confused inbred lines were also corrected by the pedigree information and flowering time in different environments. Environments and corresponding latitudes are indicated to the left. BJ, Beijing; HN, Henan; HB, Hubei; CQ, Chongqing; YN, Yunnan; GX, Guangxi. Temp, temperate maize lines; Trop, tropical or subtropical maize lines; -/-, TE-negative genotypes; +/+, TE-positive genotypes; APR, anthesis photoperiod response; SPR, silking photoperiod response.

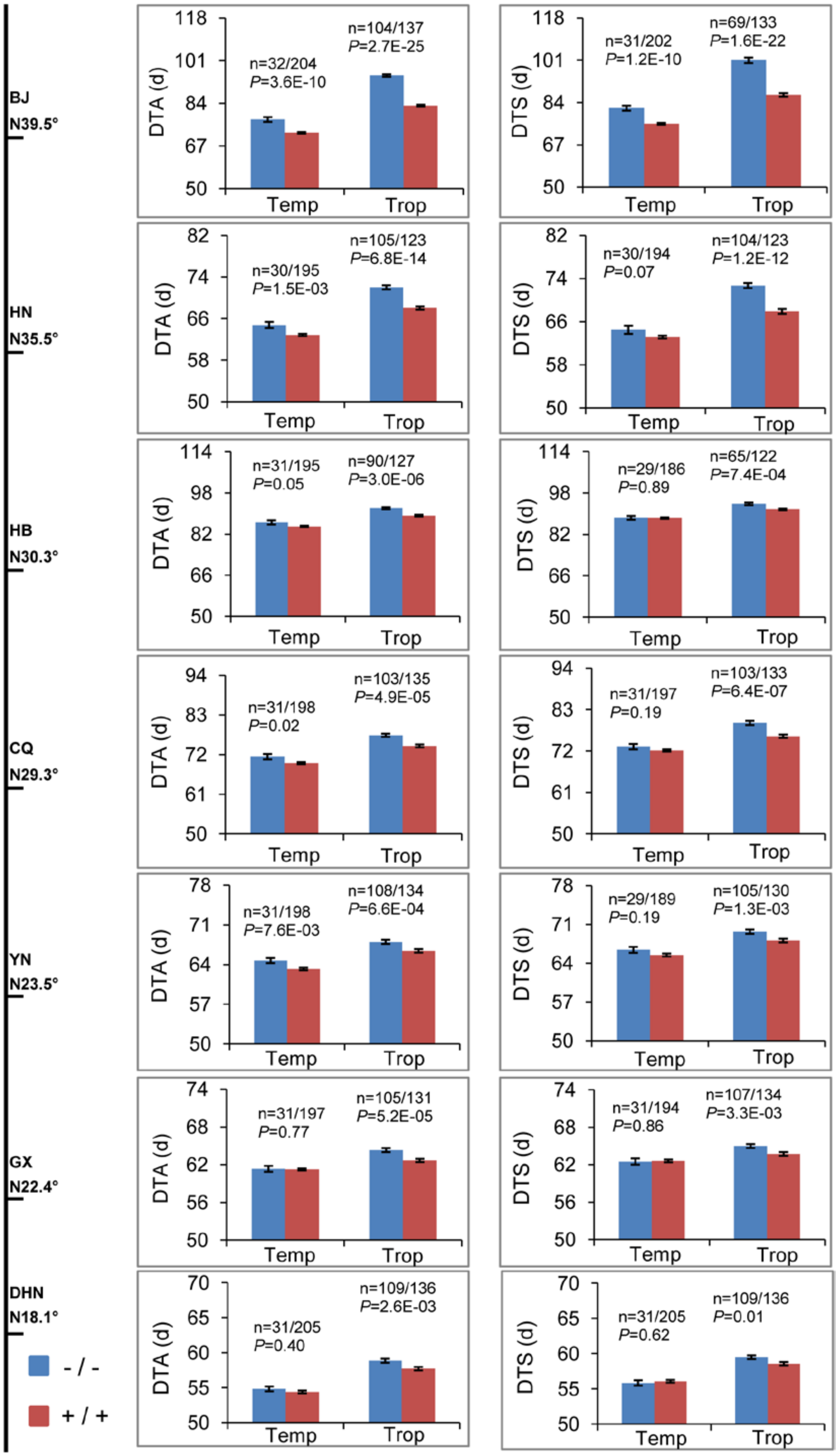
BJ
N39.5°
HN
N35.5°
HB
N30.3°
CQ
N29.3°
YN
N23.5°
GX
N22.4°
DHN
N18.1°
🟦 - / -
🟥 + / +
DTA (d)
DTS (d)
Temp
Trop
n=32/204
P=3.6E-10
n=104/137
P=2.7E-25
n=31/202
P=1.2E-10
n=69/133
P=1.6E-22
n=30/195
P=1.5E-03
n=105/123
P=6.8E-14
n=30/194
P=0.07
n=104/123
P=1.2E-12
n=31/195
P=0.05
n=90/127
P=3.0E-06
n=29/186
P=0.89
n=65/122
P=7.4E-04
n=31/198
P=0.02
n=103/135
P=4.9E-05
n=31/197
P=0.19
n=103/133
P=6.4E-07
n=31/198
P=7.6E-03
n=108/134
P=6.6E-04
n=29/189
P=0.19
n=105/130
P=1.3E-03
n=31/197
P=0.77
n=105/131
P=5.2E-05
n=31/194
P=0.86
n=107/134
P=3.3E-03
n=31/205
P=0.40
n=109/136
P=2.6E-03
n=31/205
P=0.62
n=109/136
P=0.01
118
101
84
67
50
82
74
66
58
114
98
94
83
72
61
78
71
64
57
68
62
56
70
65
60
55

Fig. S6. Genetic effect of the TE-related PAV on flowering time in temperate and tropical maize germplasms grown in multiple environments. Environments and corresponding latitudes are indicated to the left. BJ, Beijing; HN, Henan; HB, Hubei; CQ, Chongqing; YN, Yunnan; GX, Guangxi; DHN, Hainan; Temp, temperate maize lines; Trop, tropical or subtropical maize lines; -/-, TE-negative genotypes; +/+, TE-positive genotypes; DTA, days to anthesis; DTS, days to silking.

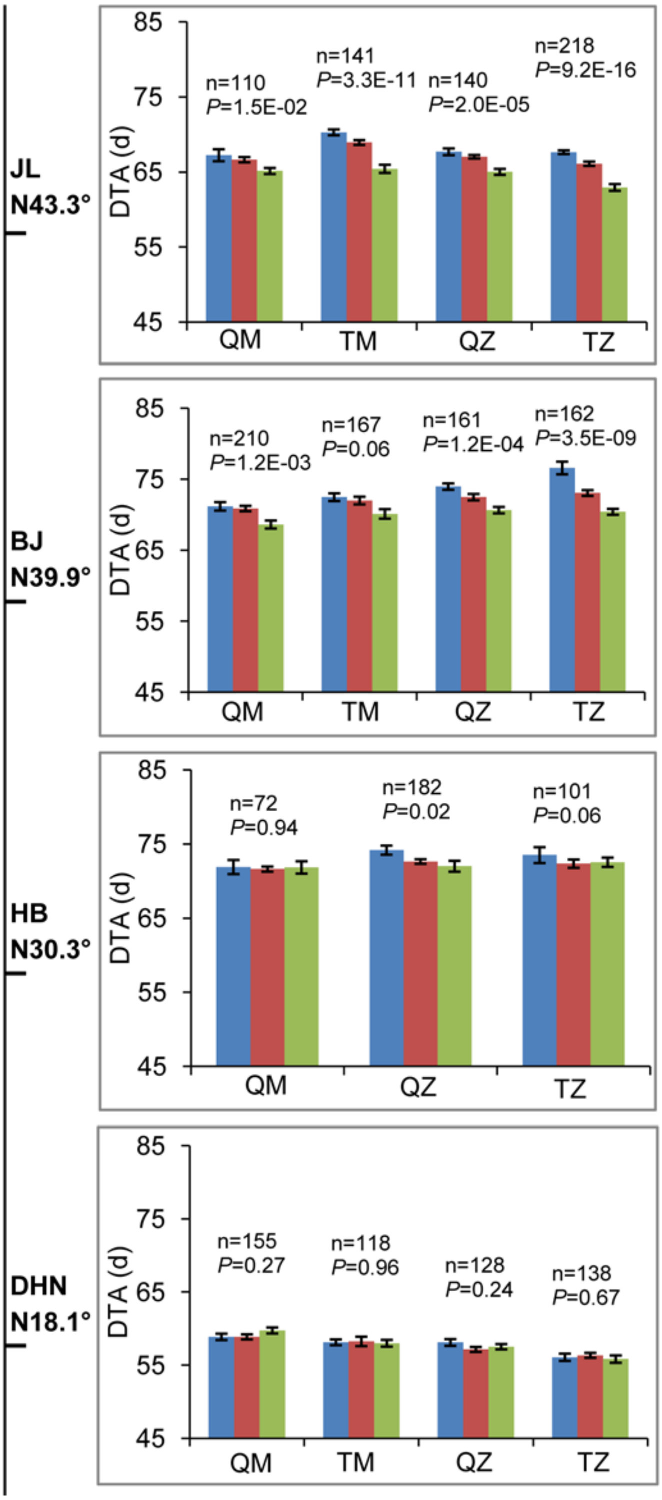

Fig. S7. Genetic effect of the TE-related PAV on DTA in F_2 populations grown in multiple environments. Environments and corresponding latitudes are indicated to the left. Colored bars represent homozygous TE-negative genotypes (blue), heterozygous genotypes (red), and homozygous TE-positive genotypes (green). JL, Jilin; BJ, Beijing; HB, Hubei; DHN, Hainan; DTA, days to anthesis.

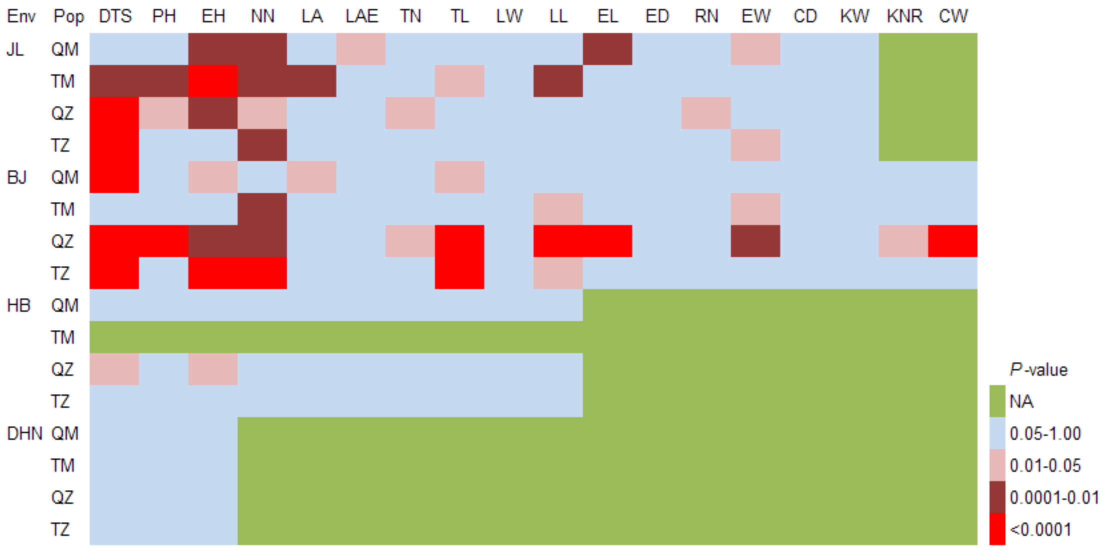

Fig. S8. Heat map indicating effects of the CACTA-like TE on 18 measured traits. Four F_2 populations were analyzed in four environments. Colors indicate significance levels associated with differences among three genotypes. Unabbreviated traits are listed in Table S12. QM, Q319 × MO17; TM, Tian77 × MO17; QZ, Q319 × Zheng58; TZ, Tian77 × Zheng58; JL, Jilin; BJ, Beijing; HB, Hubei; DHN, Hainan.

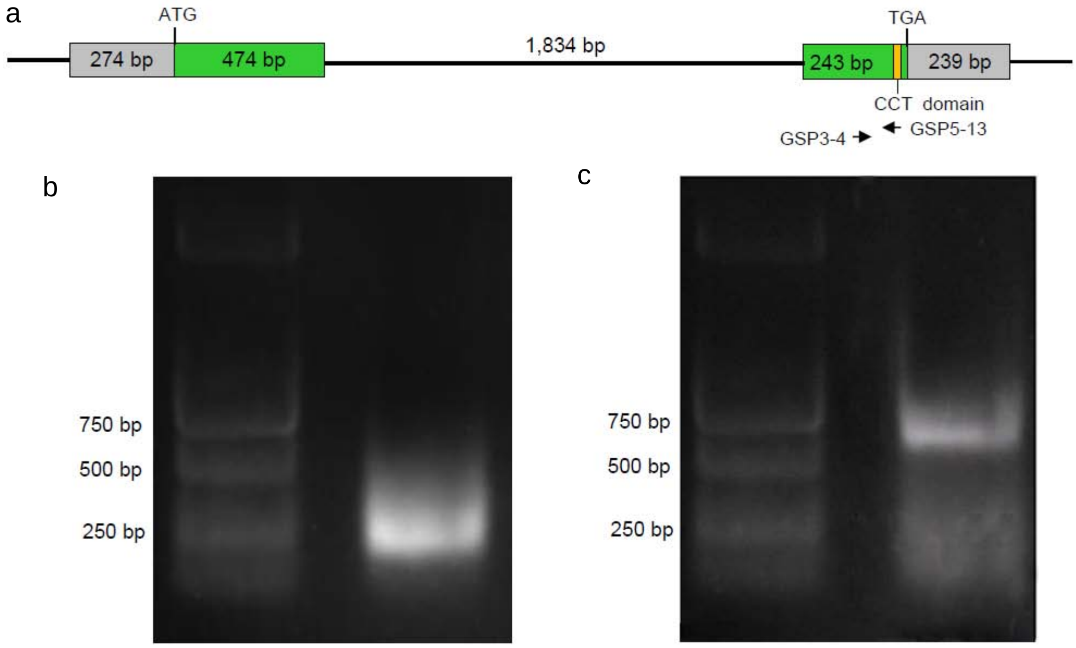

Fig. S9. Structure of the *ZmCCT* gene and isolation of a full-length *ZmCCT* cDNA. (a) Diagram of the *ZmCCT* gene. Green boxes represent exons, grey boxes represent UTRs, orange box represents the CCT domain, and the thin line between exons represents an intron. Primers used to amplify the full-length cDNA are indicated. Leaf tissue from 1145 was subjected to (b) 3’ RACE of *ZmCCT* using the GSP3-4 primer, and (c) 5’ RACE of *ZmCCT* using the GSP5-13 primer.

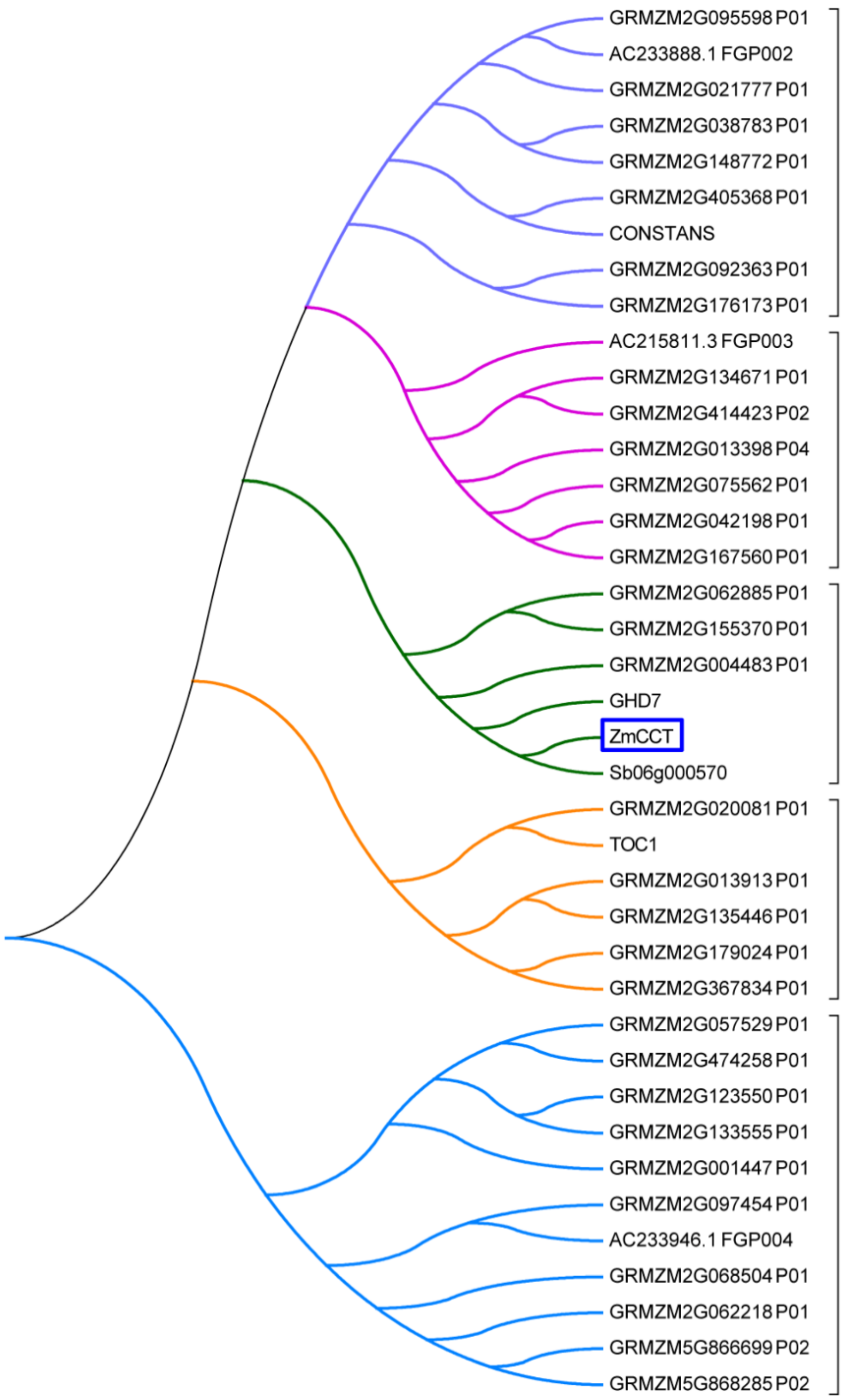

Fig. S10. Phylogenetic analysis of the CCT gene family in maize using the maximum likelihood method.

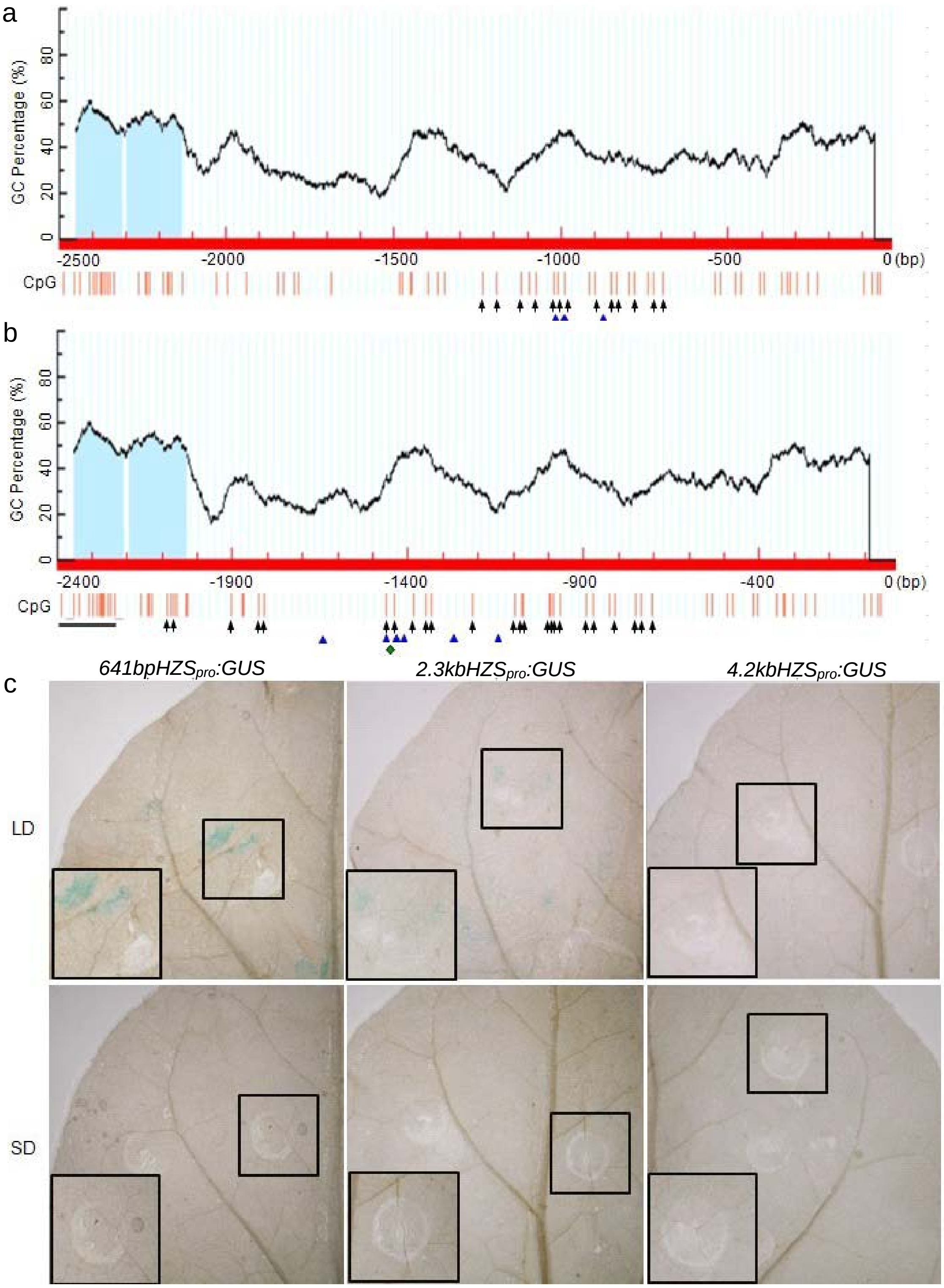

Fig. S11. DNA methylation within the *ZmCCT* promoter and transient expression of transgenic constructs. DNA methylation within the *ZmCCT* promoter was reduced in 1145 (a) compared to HZS (b), which is consistent with the photoperiod responses of these maize lines. For both 1145 and HZS, no DNA methylation was observed within ~700bp of the start codon (0 bp). Light-blue regions represent CpG islands. The grey bar indicates a region that was not sequenced from HZS. Black arrows indicate methylated CpG sites, blue triangles indicate methylated CHG sites, the green square indicates a methylated light responsive motif (INRNTPSADB). (c) Different *ZmCCT* promoter fragments from HZS were use to drive transient expression of GUS in epidermal cells of the tobacco leaf under long-day (LD) or short-day (SD) conditions. Insets show higher magnifications of injection areas (boxed).

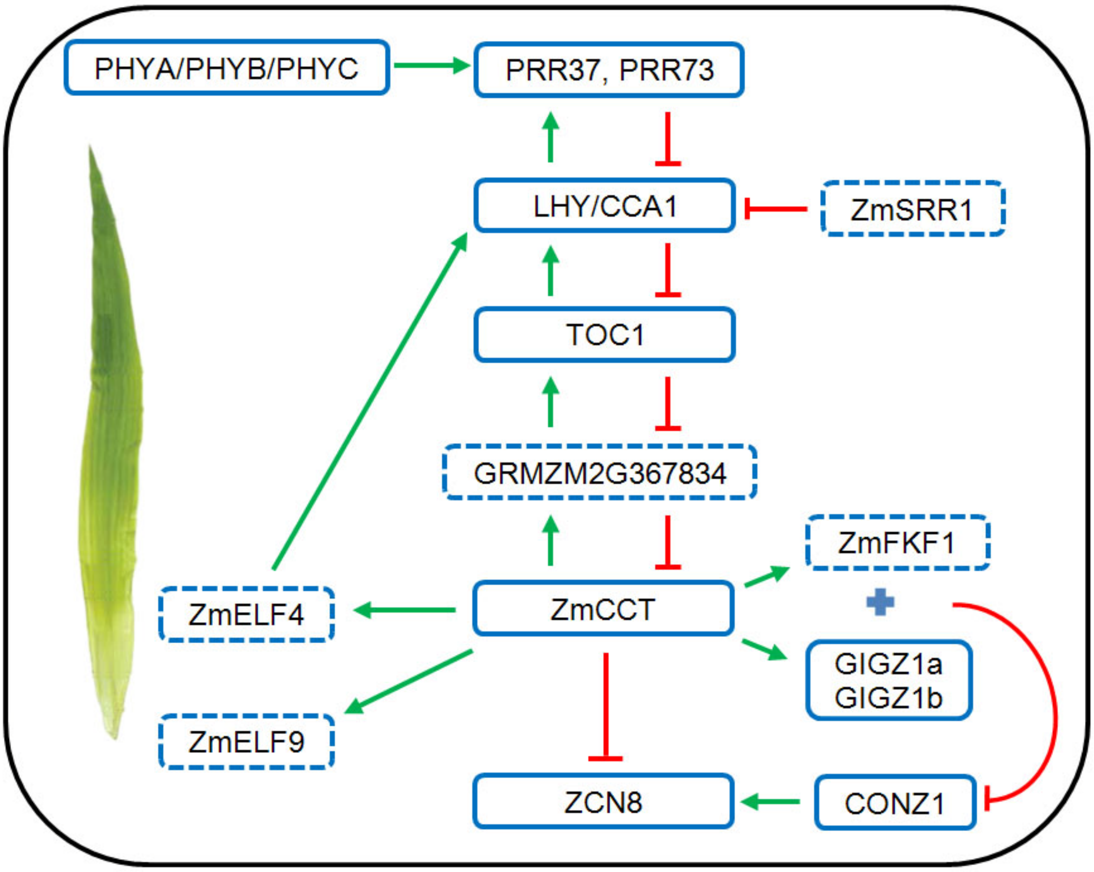

Fig. S12. Model of the photoperiod pathway in maize. Green arrows indicate positive regulation. Red t-bars indicate suppression. Dashed boxes indicate genes we have added to the previous model of the photoperiod pathyway (8, 40). conz1, a maize CONSTANS-like gene; ZmELF4&ZmELF9, early flowering; ZmFKF1, flavin binding, kelch repeat, F-box; GIGZ1a&b, gigantea-like1 a&b; LHY, late elongated hypocotyl; PRR37&73, pseudo-response regular protein 37 & 73; ZmSRR1, sensitivity to red light reduced 1; TOC1, timing of cab expression 1; ZCN8, *Zea mays* centroradialis 8.

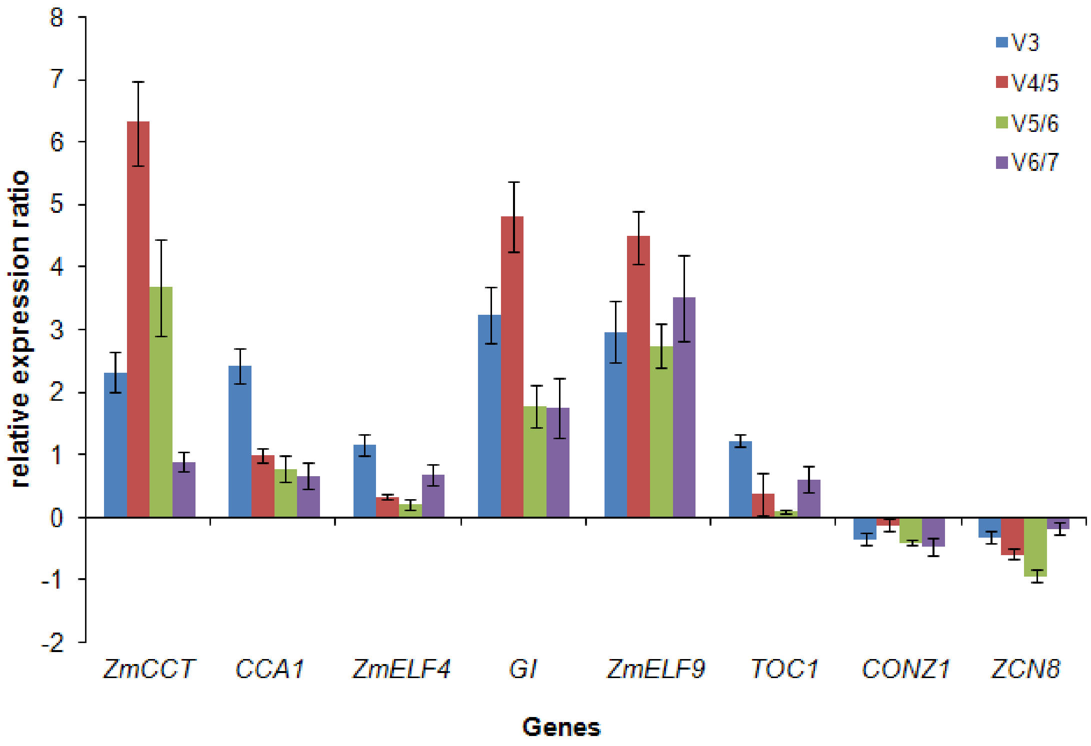

Fig. S13. Relative expression ratio between HZS and its NIL of genes involved in the photoperiod pathway at different developmental stages (V3–V7) under long-day conditions. Expression levels were normalized to 18S RNA. Error bars represent SE (n = 3). The relative expression ratio = (relative expression of NIL – relative expression of HZS) / relative expression of HZS. For HZS, V3, V4, V5, and V6 represent the vegetative-growth stage, the early floral-transition stage, the floral-transition stage, and the reproductive stage, respectively. For the NIL, V3, V5, V6, and V7 represent the vegetative-growth stage, the early floral-transition stage, the floral-transition stage, and the reproductive stage, respectively.

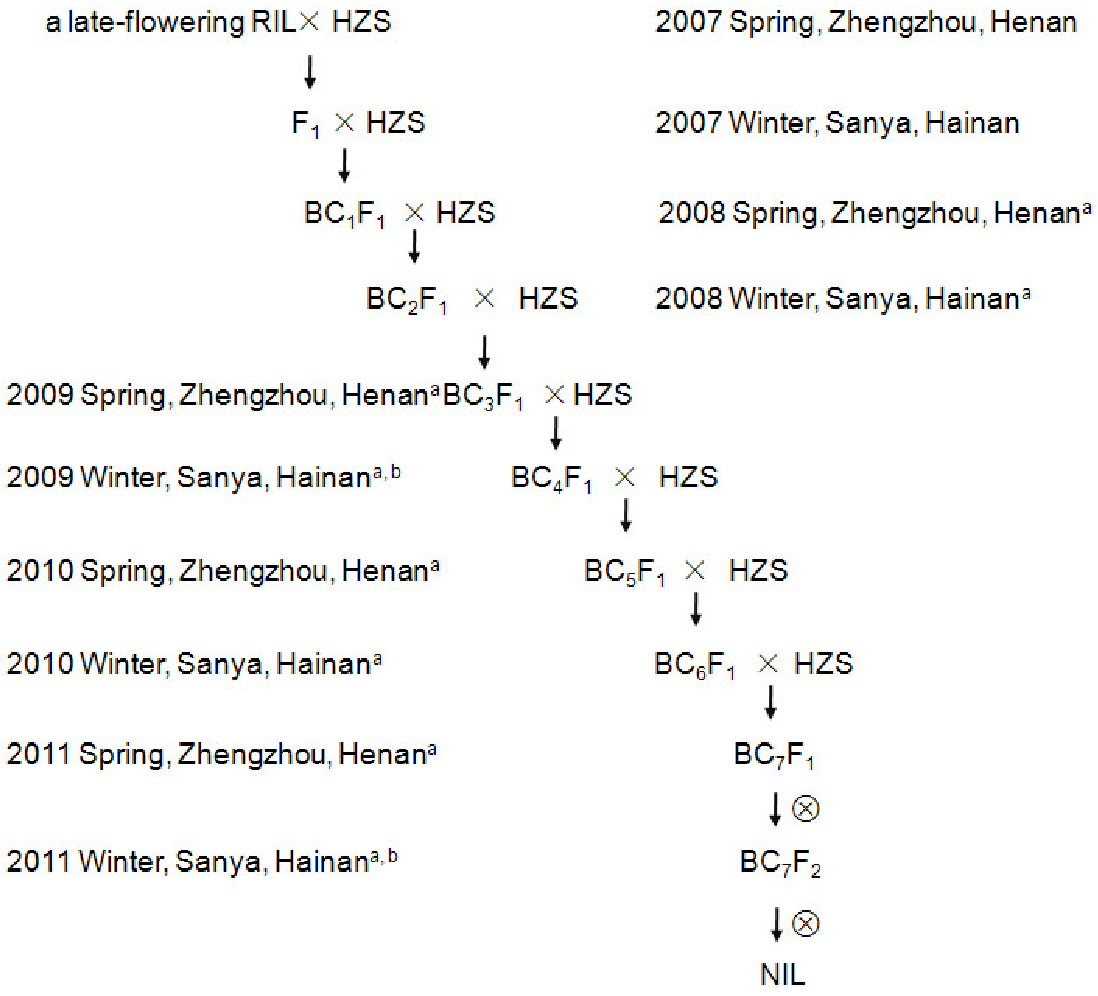

Fig. S14. Schematic diagram of NIL development. The late-flowering RIL was one line in a RIL population derived of a single cross between a tropical line CML288 (Hap6) and a temperate line HZS (Hap1). [a]Foreground selection using the flanking markers; [b]Foreground selection using the flanking markers and background selection using 230 polymorphic SSR markers.

Table S1 List of maize inbred lines and teosinte entries used in the current study (see a separate file)

Table S2 Environments used to evaluate association and linkage populations

Population	Environment	Longitude and latitude	Mean day lengths (h)
Association panel	Sanya, Hainan, 2011	E109.3 , N18.1	10.3
	Sanya, Hainan, 2012	E109.3 , N18.1	10.3
	Chongqing, 2011	E106.3 , N29.3	13.5
	Honghe, Yunnan, 2011	E102.4 , N23.5	13.4
	Nanning, Guangxi, 2011	E108.2 , N22.4	13.2
	Hebi, Hennan, 2011	E114.1 , N35.5	14.2
	Wuhan, Hubei, 2011	E114.2 , N30.3	13.4
	Beijing,2012	E116.2 , N39.5	13.7
Linkage populations	Sanya, Hainan, 2011	E109.3 , N18.1	10.9
	Wuhan,Hubei, 2012	E114.2 , N30.3	13.4
	Beijing, 2012	E116.2 , N39.5	14.7
	Gongzhuling, Jilin, 2012	E124.5 , N43.3	14.8

Table S3 Statistic summary of photoperiod responses and flowering times in 508 maize inbred lines

Trait[a]	Mean ± SE			Range			Repeatability[b] ± SE (%)
	All lines	Temperate	Tropical	All lines	Temperate	Tropical	
APR (°C)	334.9±2.2	304.9±1.7	365.6±3.0	186.9-481.7	186.9-393.9	244.7-481.7	75.1±0.02
SPR (°C)	355.4±2.2	326.2±1.9	385.5±3.0	254.4-520.5	254.4-420.1	275.6-520.5	72.8±0.02
DTA_LD (d)	72.6±0.2	69.8±0.2	75.5±0.2	62.0-84.5	62.0-79.0	66.9-84.5	88.9±0.01
GDD_DTA_LD (°C)	1021.6±3.2	975.0±2.7	1069.2±4.0	846.4-1212.5	846.4-1130.6	926.6-1212.5	89.1±0.01
DTS_LD (d)	74.5±0.2	71.9±0.2	77.1±0.2	63.8-88.2	63.8-80.4	69.0-88.2	86.5±0.01
GDD_DTS_LD (°C)	1053.1±3.0	1011.4±2.8	1096.1±3.9	876.3-1268.2	876.3-1152.4	962.0-1268.2	86.8±0.01
DTA_SD (d)	56.4±0.2	54.6±0.2	58.2±0.2	45.6-67.0	45.6-67.0	51.2-64.8	95.4±0.01
GDD_DTA_SD (°C)	686.4±1.4	670.2±1.6	702.9±1.7	599.1-789.4	599.1-789.4	636.0-767.8	95.0±0.01
DTS_SD (d)	57.5±0.2	56.2±0.2	58.9±0.2	45.7-66.9	45.7-66.9	52.6-65.7	93.2±0.01
GDD_DTS_SD (°C)	697.6±1.3	685.3±1.6	710.2±1.7	602.8-787.6	602.8-787.6	650.3-778.9	92.6±0.01

[a] APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA_LD, days to anthesis under long-day condition in days; GDD_DTA_LD, days to anthesis under long-day conditions in GDDs; DTS_LD, days to silking under long-day conditions in days; GDD_DTS_LD, days to anthesis under long-day conditions in GDDs; DTA_SD, days to anthesis under short-day conditions in days; GDD_DTA_SD, days to anthesis under short-day conditions in GDDs; DTS_SD, days to silking under short-day conditions in days; GDD_DTS_SD, days to anthesis under short-day conditions in GDDs.

[b] The repeatability for each trait was estimated using the methods by Knapp et al (Crop Science, 1985, 25:192–194).

Table S4 Pearson coefficients among flowering time traits in 508 maize inbred lines.

Trait[a]	APR (°C)	SPR (°C)	DTA_LD (d)	DTS_LD (d)	DTA_SD (d)	DTS_SD (d)
APR (°C)	1.00					
SPR (°C)	0.89	1.00				
DTA_LD (d)	0.93	0.87	1.00			
DTS_LD (d)	0.85	0.93	0.94	1.00		
DTA_SD (d)	0.56	0.60	0.82	0.80	1.00	
DTS_SD (d)	0.50	0.51	0.74	0.78	0.90	1.00

[a] APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA_LD, days to anthesis under long-day condition in days; DTS_LD, days to silking under long-day condition in days; DTA_SD, days to anthesis under short-day condition in days; DTS_SD, days to silking under short-day condition in days.

Table S5 Polymorphic sites significantly associated with photoperiod sensitivity and flowering time in a maize panel of 368 lines

SNP	Chromosome	Position[a]	Allele[b]	MAF[c]	P-value[d]	Lead trait[e]	Other trait[f]	Candidate gene[g]	Annotation[h]
M2c7358967	1	7358967	C/G	0.15	1.5×10^{-5}	SPR		GRMZM2G095968	RlpA-like double-psi beta-barrel domain (IPR009009)
M2c223285513	2	223285513	C/G	0.11	1.6×10^{-5}	APR		GRMZM2G172297	Myc-type, basic helix-loop-helix (bHLH) domain (IPR011598)
M2c10697661	4	10697661	T/G	0.31	9.2×10^{-6}	DTS		GRMZM2G426294	Protein of unknown function DUF538 (IPR007493)
M2c1046572	5	1046572	T/G	0.06	3.7×10^{-6}	APR		GRMZM2G313481	NAC domain (IPR003441)
M2c13396311	5	13396311	A/T	0.05	8.7×10^{-6}	SPR		GRMZM2G170338	Unknown
M2c164140644	6	164140644	T/G	0.21	7.5×10^{-6}	SPR		GRMZM2G079832	Ribosomal protein S2, conserved site (IPR018130)
M2c164140645	6	164140645	T/G	0.21	7.5×10^{-6}	SPR			
M2c164552177	6	164552177	T/G	0.07	9.5×10^{-7}	SPR	DTS	GRMZM2G318183	Unknown
M2c153729937	7	153729937	A/G	0.35	9.4×10^{-6}	DTS		GRMZM2G027344	Small GTPase superfamily, Rab type (IPR003579)
M2c124842646	8	124842646	T/G	0.11	1.2×10^{-6}	APR		GRMZM2G093404	Zinc finger
M2c131255321	8	131255321	A/G	0.48	5.7×10^{-6}	APR		GRMZM2G054588	Unknown
M2c132201362	8	132201362	T/C	0.15	8.6×10^{-6}	APR		GRMZM2G474726	Integral membrane protein TerC (IPR005496)
M2c132047401	8	132047401	T/G	0.38	1.7×10^{-5}	APR		GRMZM2G700665	DNA-binding domain with a 2-layer beta(3)-alpha fold (IPR016177)
PZE-108118075	8	166913953	A/G	0.06	7.8×10^{-6}	APR		GRMZM2G095709	Unknown
M2c7614751	9	7614751	T/C	0.07	1.2×10^{-6}	DTA	APR	GRMZM2G079949	Alpha/beta-Hydrolases superfamily
M2c138799623	9	138799623	T/C	0.16	1.7×10^{-6}	SPR	DTS	GRMZM2G020982	Ankyrin_rpt-contain_dom
M2c138799811	9	138799811	A/G	0.17	4.3×10^{-6}	SPR			
M2c154088454	9	154088454	A/T	0.35	1.4×10^{-5}	DTA		GRMZM2G143244	Per1-like (IPR007217)
M2c154093370	9	154093370	T/C	0.22	9.1×10^{-6}	DTA		GRMZM2G143213	Protein kinase like-domain (IPR011009)
M2c94053899	10	94053899	C/G	0.21	1.4×10^{-5}	SPR		GRMZM2G006871	Unknown
M10c94252249	10	94252249	G/A	0.21	1.9×10^{-9}	APR	SPR, DTA, DTS	GRMZM2G381691	*ZmCCT*, a gene encoding a CCT-domain protein
M10c94252257	10	94252257	A/G	0.20	1.9×10^{-9}	APR	SPR, DTA, DTS		

SNP	Chromosome	Position[a]	Allele[b]	MAF[c]	P-value[d]	Lead trait[e]	Other trait[f]	Candidate gene[g]	Annotation[h]
M10c94252266	10	94252266	A/C	0.20	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252284	10	94252284	A/G	0.20	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252303	10	94252303	0/9/1	0.09	1.2×10^{-8}	APR	SPR, DTA, DTS		
M10c94252308	10	94252308	G/A	0.21	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252320	10	94252320	0/4	0.20	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252322	10	94252322	G/A	0.21	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252325	10	94252325	A/C	0.20	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252330	10	94252330	G/A	0.21	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252347	10	94252347	A/C	0.20	1.2×10^{-9}	APR	SPR, DTA, DTS		
M10c94252362	10	94252362	C/T	0.21	1.9×10^{-9}	APR	SPR, DTA, DTS		
M10c94252435	10	94252435	A/C/G	0.07	4.6×10^{-10}	APR	SPR, DTA, DTS		
M10c94252441	10	94252441	C/T	0.19	4.1×10^{-11}	APR	SPR, DTA, DTS		
M10c94252473	10	94252473	T/C	0.19	6.7×10^{-11}	APR	SPR, DTA, DTS		
M10c94252480	10	94252480	C/T	0.20	6.7×10^{-11}	APR	SPR, DTA, DTS		
M10c94252529	10	94252529	0/3	0.20	6.7×10^{-11}	APR	SPR, DTA, DTS		
M10c94252541	10	94252541	G/A	0.10	2.9×10^{-7}	APR	SPR, DTA		
M10c94252554	10	94252554	2/0	0.20	6.8×10^{-11}	APR	SPR, DTA, DTS		
M10c94252590	10	94252590	T/C	0.27	4.7×10^{-13}	APR	SPR, DTA, DTS		
M10c94252594	10	94252594	C/T	0.10	2.9×10^{-7}	APR	SPR, DTA		
M10c94252597	10	94252597	A/T	0.19	3.7×10^{-11}	APR	SPR, DTA, DTS		
M10c94252609	10	94252609	0/3	0.23	5.5×10^{-11}	APR	SPR, DTA, DTS		
M10c94252614	10	94252614	A/G	0.09	2.9×10^{-7}	APR	SPR, DTA		
M10c94252665	10	94252665	A/G	0.19	6.9×10^{-11}	APR	SPR, DTA, DTS		
M10c94252679	10	94252679	T/C	0.19	6.9×10^{-11}	APR	SPR, DTA, DTS		

SNP	Chromosome	Position[a]	Allele[b]	MAF[c]	P-value[d]	Lead trait[e]	Other trait[f]	Candidate gene[g]	Annotation[h]
M10c94252687	10	94252687	G/A	0.20	6.9×10^{-11}	APR	SPR, DTA, DTS		
M10c94252712	10	94252712	0/4	0.19	7.0×10^{-11}	APR	SPR, DTA, DTS		
M10c94252713	10	94252713	G/C	0.08	9.8×10^{-7}	APR	SPR, DTA		
M10c94252722	10	94252722	T/C	0.27	7.4×10^{-13}	APR	SPR, DTA, DTS		
M10c94252734	10	94252734	G/A	0.20	7.0×10^{-11}	APR	SPR, DTA, DTS		
M10c94252767	10	94252767	C/T/-	0.10	8.1×10^{-9}	APR	SPR, DTA, DTS		
M10c94252774	10	94252774	4/0/12	0.11	2.9×10^{-10}	APR	SPR, DTA, DTS		
M10c94252788	10	94252788	G/T	0.09	9.8×10^{-7}	APR	SPR, DTA		
M10c94252804	10	94252804	A/T	0.24	2.2×10^{-6}	APR	SPR, DTA		
M10c94252827	10	94252827	T/A	0.20	7.5×10^{-11}	APR	SPR, DTA, DTS		
M10c94252832	10	94252832	G/T	0.09	9.8×10^{-7}	APR	SPR, DTA		
M10c94252888	10	94252888	A/G	0.19	7.6×10^{-11}	APR	SPR, DTA, DTS		
M10c94252889	10	94252889	T/C	0.20	2.8×10^{-11}	APR	SPR, DTA, DTS		
M10c94252957	10	94252957	C/A	0.19	4.2×10^{-11}	APR	SPR, DTA, DTS		
M10c94252990	10	94252990	T/C	0.08	9.8×10^{-7}	APR	SPR, DTA		
M10c94253000	10	94253000	4/0	0.09	6.4×10^{-6}	APR			
M10c94253003	10	94253003	T/G	0.08	1.9×10^{-6}	APR			
M10c94253071	10	94253071	G/A	0.09	2.8×10^{-6}	APR	SPR, DTA		
M10c94253073	10	94253073	A/G	0.08	9.8×10^{-7}	APR	SPR, DTA		
M10c94253076	10	94253076	C/T	0.20	1.4×10^{-10}	APR	SPR, DTA, DTS		
M2c139854704	10	139854704	T/C	0.08	1.4×10^{-5}	DTA		GRMZM2G303768	Protein kinase-like domain (IPR011009)
M2c145196768	10	145196768	T/G	0.09	1.7×10^{-6}	SPR		GRMZM2G086030	Tetratricopeptide TPR-1 (IPR001440)
M2c145196818	10	145196818	T/C	0.09	1.7×10^{-6}	SPR			

[a] Position in base pairs for the polymorphic sites according to version 5b.60 of the B73 reference sequence (MaizeSequence, http://www.maizesequence.org). [b] Major allele (first), minor allele. Favorable alleles are underlined. [c] Minor allele frequency (MAF). [d] *P*-value of associations between the polymorphic site and the lead trait. [e] The associated trait whose significance level is the highest among the measured traits. [f] All of the associated traits except for the lead trait. APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA, days to anthesis under long-day conditions in days; DTS, days to silking under long-day conditions in days. [g] The plausible candidate gene (based on function) or the annotated gene that is closest to the significant polymorphic site. [h] Each candidate gene is annotated according to InterProScan (http://www.ebi.ac.uk/interpro).

Table S6 Primers used in this study

Type	Name	Primer sequence (5’-3’)	
Transgenic plant test	LBCCT	Forward	TGTGGAATTGTGAGCGGATA
		Reverse	TAGCTAGCTCCACCACAGCA
qRT-PCR primers	CTT8	Forward	AACGACGACGACCTCATCAG
		Reverse	ACTGGAACTCGTGCAGGCAC
	ASCCT2	Forward	GACCACCACCACCAAGAAAC
		Reverse	CTGCTGTCTCAGTGGTTTGC
	GADPH1	Forward	ATCAACGGCTTCGGAAGGAT
		Reverse	CCGTGGACGGTGTCGTACTT
RACE primers	GSP5-13	Reverse	TCCGTGAATGTGCTCCCAGAGAAT
	GSP3-4	Forward	ATTCACGGACGCTGCAAGCAAGGAG
Primers for full-length cDNA	NLCCT1	Forward	CCGCTCGAGTATCGATCAACAGCGGCCAT
		Reverse	CGGAATTCCTTCGGTTACCTTGGCAAAGC
Primers for genotyping upstream region of *ZmCCT*	5UCCT1	Forward	CATCCGGACCATATATAGAC
		Reverse	CTGGTCGTCGTTCTCATCAC
	5UCCT2	Forward	TCTCTGGCCTGGTGTAGTGA
		Reverse	AAGTAAGGGATGAGCCATGC
	5UCCT3	Forward	GGGTGTTTGAAGCTCCATTG
		Reverse	AGCACCTTGGGCATTCCTAT
	5UCCT4	Forward	TTCAATGGAGCTTCAAACAC
		Reverse	GGTTGTGCGTTCTTGACATC
	TED	Forward	GCACAAGAGAGATGGAGCATT
		Reverse	ATTCTCAATCCAAGGTGCAG
	TERB	Forward	CCTAAGAACCGTCGGAAACA
		Reverse	CGAGCGTTTTCGACATAACA
	TELB	Forward	AAACGCTGACACTTCCGACT
		Reverse	GTCGACACGTGTAGGAAGCA
Primers for genotyping the whole gene and upstream of *ZmCCT* in teosinte	MR1	Forward	CACTTATCCTCGCTCGATCTCT
		Reverse	GGACGTGTTGAGTACCAATGAA
	MR2	Forward	GTCTCAGTTCCTGCTTCTTCC
		Reverse	ACATGGCCGCTGTTGATC
	MR3	Forward	TGGCTACCAGATTCTGCGATAT
		Reverse	TGTGCGTAAAGTGCAACTCATG
	MR4	Forward	GCATGTAGGCCCATTCAGC
		Reverse	GAGCTTGTTATCGAGATGAGGA
	TR1	Forward	CGGATTCTGTTTCTGTGTAAAC
		Reverse	GATCTTGAAAAATGAACTAG
	TR2	Forward	CTAGTTCATTTTTCAAGATC
		Reverse	ATATCGCAGAATCTGGTAGCCA
	TR3	Forward	ATGTAGGCCCATTCAGCATATC
		Reverse	TATTGCAGTTGGCAATTGAGAC
Primers for bisulfite-sequencing	1M-1	Forward	TTTTGATGGTTAAAGAATTGGAATT
		Reverse	TTCCTCCATCTCCCTACTAACCTA

Type	Name	Primer sequence (5’-3’)	
PCR of 1145 promoter	1M-2	Forward	TAGGTTAGTAGGGAGATGGAGGAA
		Reverse	ACCTATATACCCAAAAATAAAATCTC
	1M-3	Forward	TTATTTTTGGGTATATAGGTAATGTTTTAT
		Reverse	TCAAACCTAATTAATACTAATTCTTAAATT
	1M-4	Forward	AATTTGTATTAAGTTTTTATAGTGTTTTT
		Reverse	CTTATACTAAATCCTTCACTTTTAATATTA
	1M-5	Forward	TTATAATATTAAATTTATTTGTATTTTTAG
		Reverse	ACATATAATCATATCCTCCCTAAATC
	1M-6	Forward	TGGTTTTTGAATTATTGTTTTTGAG
		Reverse	AAATACATACATAACTCATCCCTTACTTAT
	1M-7	Forward	AAGGGATGAGTTATGTATGTATTTA
		Reverse	AACAATACTCCATCTCTCTTATACCC
	1M-8	Forward	TAAGAGAGATGGAGTATTGTTTATTGGA
		Reverse	ATAACTTTATTAAAAAACAACAACAAAATT
	1M-9	Forward	TGTGTATTTATTAGGAATTAATGGT
		Reverse	TCAAATATAAAACTATCTATCTATCTATCT
Primers for bisulfite-sequencing PCR of HZS promoter	HM-1	Forward	TTTTGATGGTTAAAGAATTGGAATT
		Reverse	TTCCTCCATCTCCCTACTAACCTA
	HM-2	Forward	TAGGTTAGTAGGGAGATGGAGGAA
		Reverse	ACCTATATACCCAAAAATAAAATCTC
	HM-3	Forward	TTATTTTTGGGTATATAGGTAATGTTTTAT
		Reverse	TCAAACCTAATTAATACTAATTCTTAAATT
	HM-4	Forward	AGTATTGTTAGTTTAATTTAAGAATTAGTA
		Reverse	ACTAAAAATATTAAAAATATTCTCTTC
	HM-5	Forward	GAAGAGAATATTTTTAATATTTTTAGTAT
		Reverse	AAAAAACACCCCTAACCAATAACTTATA
	HM-6	Forward	ATTGGTTAGGGGTGTTTTTTATAAG
		Reverse	AAAAACATAAATAAATATCATTTTAC
	HM-7	Forward	TTGAAAAATGAATTAGTTTTATGGTAGG
		Reverse	AATCAAAAAATTCCAAACCAACTAC
	HM-8	Forward	GTTTGGAATTTTTTGATTTAATTTT
		Reverse	AATTCTTTCCAATAAATATATACACATACA
	HM-9	Forward	TGTATATATTTATTGGAAAGAATTTGTATA
		Reverse	ACAATAAATTCTAATATAACTCTTTAATAC
	HM-10	Forward	AGTGGTGTTAGTGATAATATGTTGG
		Reverse	AATACATACATAACTCATCCCTTACTTATA
	HM-11	Forward	AAGGGATGAGTTATGTATGTATTTA
		Reverse	AACAATACTCCATCTCTCTTATACCC
	HM-12	Forward	TAAGAGAGATGGAGTATTGTTTATTGGA
		Reverse	ATAACTTTATTAAAAAACAACAACAAAATT
Primers used for promoter constructs	HP-1	Forward	CACTGTGGAAGCTTAGTGCAG
		Reverse	GGCCGCTGTTGATCGATAG
	HP-2	Forward	TGATTCCTGATGGATGCACAT

Type	Name	Primer sequence (5’-3’)	
		Reverse	GGCCGCTGTTGATCGATAG
	HP-3	Forward	GGCATCAAATGAGGCTGGTT
		Reverse	GGCCGCTGTTGATCGATAG
Real-time PCR primers for critical genes in the *ZmCCT* pathway	ZmCCT	Forward	TCCGTCTTCCCTGTCGT
		Reverse	CCAGGCGATGGTTTCTT
	ZmCCA1	Forward	GTAAAAATGGTAGGCGAT
		Reverse	CTCTTGGGTGTTGGGGTT
	ZmCONZ1	Forward	CTTGCACTGGATGGTGACAGATA
		Reverse	AGTTGACGAACAGCACAAATAC
	ZmZCN8	Forward	GCAGATCGGAGCACGGCAACA
		Reverse	GATGACGGCGACCTCGGCATC
	ZmTOC1	Forward	CGTTTGGAGTTTGGGTATGG
		Reverse	GCCGCCCTCGTAGTTGA
	ZmELF4	Forward	CGGCAGCGATAGCATGGAGTT
		Reverse	CGGGCGATATTAGTGTTGAGC
	ZmELF9	Forward	CCATCTCTGAGCTACACTCCGC
		Reverse	CTGGTCCACATCATTGCCTTTC
	GI	Forward	GATCACTGACATATTGCTAGCC
		Reverse	CCAGATCCTCGGCTGC
	18S	Forward	CCTGCGGCTTAATTGACTC
		Reverse	GTTAGCAGGCTGAGGTCTCG

Table S7 Associations between *ZmCCT* polymorphisms and four flowering time traits in 180 maize inbred lines

Location	Site[a]	Allele[b]	Frequency	*P* value			
				APR	SPR	DTA	DTS
Promoter	-2543	+/-	142/37	1.1×10^{-6}	7.5×10^{-6}	4.1×10^{-6}	1.8×10^{-5}
	-1875	C/A	153/27	2.1×10^{-4}	0.02	2.1×10^{-4}	4.0×10^{-3}
	-1807	C/T	26/154	6.1×10^{-5}	0.01	6.0×10^{-5}	1.5×10^{-3}
	-1806	G/A	26/154	6.1×10^{-5}	0.01	6.0×10^{-5}	1.5×10^{-3}
	-1745	A/T	27/153	2.1×10^{-4}	0.02	2.1×10^{-4}	3.8×10^{-3}
	-1648	A/G	18/162	6.1×10^{-5}	0.01	6.1×10^{-5}	1.5×10^{-3}
	-1636	C/T	38/142	3.7×10^{-6}	2.8×10^{-5}	2.2×10^{-5}	8.7×10^{-5}
	-1626	4/0	27/153	2.1×10^{-4}	0.02	2.1×10^{-4}	3.8×10^{-3}
	-1598	A/G	27/153	2.1×10^{-4}	0.02	2.1×10^{-4}	3.7×10^{-3}
	-1590	C/T	27/153	2.1×10^{-4}	0.02	2.1×10^{-4}	3.7×10^{-3}
	-1575	G/A	27/153	2.1×10^{-4}	0.02	2.0×10^{-4}	3.7×10^{-3}
	-1505	T/A	27/153	2.1×10^{-4}	0.02	2.0×10^{-4}	3.6×10^{-3}
	-1498	C/T	38/142	3.7×10^{-6}	2.7×10^{-5}	2.0×10^{-5}	7.9×10^{-5}
	-1460	0/2	27/153	2.1×10^{-4}	0.02	2.0×10^{-4}	3.6×10^{-3}
	-1435	3/0	27/153	2.1×10^{-4}	0.02	2.0×10^{-4}	3.5×10^{-3}
	-1386	T/C	26/154	6.1×10^{-5}	0.01	5.7×10^{-5}	1.3×10^{-3}
	-1379	C/T	27/153	2.1×10^{-4}	0.02	2.0×10^{-4}	3.5×10^{-3}
	-1347	T/C	26/154	6.1×10^{-5}	0.01	5.7×10^{-5}	1.3×10^{-3}
	-1228	C/A	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.8×10^{-3}
	-1225	A/G	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.8×10^{-3}
	-1211	A/G	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.8×10^{-3}
	-1187	G/A	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.7×10^{-3}
	-1160	G/A	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.7×10^{-3}
	-1152	A/G	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.7×10^{-3}
	-1127	C/T	28/152	2.8×10^{-4}	0.02	2.3×10^{-4}	2.8×10^{-3}
	-1003	T/C	21/149	2.1×10^{-4}	0.02	1.9×10^{-4}	3.4×10^{-3}
5'UTR	-19	4/0	31/147	7.0×10^{-6}	1.5×10^{-4}	9.7×10^{-5}	5.9×10^{-4}
Intron	601	0/4	13/165	5.7×10^{-5}	3.4×10^{-3}	3.8×10^{-3}	0.03
3'UTR	2491	A/G	10/134	9.5×10^{-5}	1.6×10^{-6}	1.4×10^{-3}	3.1×10^{-5}

[a] Relative position of polymorphic sites in *ZmCCT* (Fig. S4). The start codon is denoted as +1 bp.

[b] The favorable allele for the corresponding trait is underlined.

Table S8 All haplotypes composed of 13 polymorphic sites in 461 maize inbred lines

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
150	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
238	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
268	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
501	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
647	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
812	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
1462	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
3411	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
5213	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
5237	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
5311	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
7327	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
8902	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
9782	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
81162	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
526018	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
04K5686	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
04K5702	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
05W002	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
07KS4	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
303WX	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
3H-2	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
4F1	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
835B	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
975-12	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
A619	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B110	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B111	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B113	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B114	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B73	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
B77	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BEM	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BS16	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY4839	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY4944	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY4960	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY804	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY807	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY809	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY813	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY815	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY843	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
BY855	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site												Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
BZN	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
C8605	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CA47	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CF3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CHANG3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CHANG7-2	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CHENG698	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CHUAN48-2	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CI7	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL1	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL103	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL111	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL112	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL113	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL114	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL116	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL119	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL120	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL121	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL122	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL123	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL125	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL133	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL134	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL137	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL138	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL139	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL140	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL141	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL143	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL144	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL145	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL146	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL147	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL148	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL153	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL154	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL155	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL16	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL17	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL30	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL38	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL42	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL47	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL5	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
CIMBL51	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL52	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL55	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL57	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL58	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL59	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL6	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL61	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL66	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL71	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL72	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL73	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL77	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL8	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL83	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL85	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL86	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL87	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL88	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL9	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL90	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL97	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML113	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML114	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML115	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML116	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML121	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML134	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML162	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML163	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML166	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML191	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML223	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML290	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML304	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML307	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML32	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML323	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML324	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML325	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML326	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML360	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML361	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML415	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML422	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML430	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
CML431	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML480	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML493	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML497	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML50	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CML51	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DAN3130	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DAN340	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DAN360	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DE.EX	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DH29	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
DONG237	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
EN25	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ES40	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
FCD0602	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS1	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS10	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS18	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS2	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS20	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS25	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS27	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS28	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS29	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS30	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS31	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS37	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS41	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS44	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS45	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS46	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS48	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS50	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS51	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS52	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS53	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS54	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS56	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS57	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS58	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS59	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS60	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS61	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS62	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS63	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
GEMS64	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS65	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GEMS66	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY1007	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY1032	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY220	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY237	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY246	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY386	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY462	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY798	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
GY923	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HB	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HSBN	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HTH-17	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HU803	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HUANGC	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HYS	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
HZS	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
IRF291	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
IRF314	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
J4112	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JH59	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JI53	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JI63	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JI842	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JI846	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
JI853	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
K10	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
K12	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
K14	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
K22	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
L3180	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LIAO138	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LIAO159	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LIAO5114	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LIAO5263	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LK11	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LV28	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LXN	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
LY042	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
M153	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
M165	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
M97	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
MN	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
MO113	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
MO17	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
NAN21-3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
P178	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
Q1261	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
R08	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
R15	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
R15X1141	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY684	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY697	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY713	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY729	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY732	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
RY737	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
S22	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
S37	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SC55	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SHEN5003	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SI273	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SI444	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SI446	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1032	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1035	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1039	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1052	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1077	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY1128	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY3073	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY998	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
SY999	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TIE7922	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TT16	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TX5	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY1	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY10	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY11	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY2	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY4	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY5	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY6	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY7	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY8	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
TY9	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
U8112	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
W138	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
WMR	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1

Line	Site												Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
WU109	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
XI502	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
XUN971	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
XZ698	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YAN414	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YE107	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YE478	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YE515	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YE52106	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YE8001	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YU374	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
YU87-1	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZAC546	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZB648	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZH68	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG22	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG29	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG32	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG35	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG58	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHENG653	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZHI41	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZI330	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZONG3	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZONG31	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
ZZ01	+/+	A	C	C	A	4	T	C	0	A	C	0	G	Hap1
CIMBL10	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL15	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL19	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL29	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL4	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL46	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL62	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL63	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL76	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL78	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL89	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL96	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CML170	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CML171	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CML172	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CML225	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CML411	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
SW92E114	+/+	A	C	C	T	4	T	C	0	A	C	0	G	Hap2
CIMBL69	+/+	A	C	C	A	4	T	C	0	A	C	0	C	Hap8
CIMBL80	+/+	A	C	C	A	4	T	C	0	A	C	0	C	Hap8

Line	Site												Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
CIMBL95	+/+	A	C	C	A	4	T	C	0	A	C	0	C	Hap8
CML122	+/+	A	C	C	A	4	T	C	0	A	T	1	G	Hap9
CML139	+/+	A	C	C	A	4	T	C	0	A	T	1	G	Hap9
CIMBL60	+/+	A	C	C	A	4	T	C	0	A	T	1	G	Hap9
CML118	+/+	A	C	C	T	4	T	C	0	A	C	0	C	Hap10
CIMBL99	+/+	A	C	C	T	4	T	C	0	A	C	0	C	Hap10
7884-4HT	+/+	A	A	A	T	12	C	T	3	G	T	9	A	Hap11
DONG46	+/+	A	A	A	T	12	C	T	3	G	T	9	A	Hap11
CIMBL40	-/-	A	C	C	A	4	C	C	0	A	C	0	C	Hap12
CIMBL74	-/-	A	C	C	A	4	C	C	0	A	C	0	C	Hap12
CIMBL115	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL127	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL136	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL149	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL157	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL33	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL34	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL39	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL75	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CIMBL82	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML226	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML27	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML287	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML300	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML305	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML31	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML364	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML426	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML470	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
GEMS32	-/-	A	C	C	A	4	C	C	0	A	C	0	G	Hap3
CML228	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL45	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL49	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL79	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL93	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL94	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL156	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
GEMS4	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
GEMS5	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
GEMS11	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
GEMS19	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
GEMS23	-/-	A	C	C	A	4	C	C	3	A	C	0	G	Hap4
CIMBL106	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL107	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL108	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL109	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
CIMBL11	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL110	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL118	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL12	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL128	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL129	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL13	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL150	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL18	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL24	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL25	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL26	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL27	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL28	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL44	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL48	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL50	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL67	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL68	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL70	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL81	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL91	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CIMBL92	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML189	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML192	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML20	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML286	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML408	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML423	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML451	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML473	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
CML479	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
GEMS12	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
GEMS13	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
GEMS14	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
GEMS15	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
GEMS47	-/-	A	A	A	T	12	C	T	3	G	T	9	A	Hap5
177	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
1323	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
7381	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
05WN230	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
18-599	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
B151	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CIMBL105	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CIMBL117	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CIMBL20	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6

Line	Site												Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
CIMBL7	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML298	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML327	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML412	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML428	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML465	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML474	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
CML486	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
D047	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
D863F	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
DAN598	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
DAN599	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
DH3732	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
JIAO51	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
JY01	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
LG001	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
LIAO5262	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
QI319	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
SHEN135	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
SHEN137	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
TIAN77	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
ZHENG30	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
ZZ03	-/-	G	C	A	T	0	C	C	3	C	T	1	G	Hap6
9642	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
384-2	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL101	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL124	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL126	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL23	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL56	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CIMBL65	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML28	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML338	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML432	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML433	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML471	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
LY	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
YUN46	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
ZHONG69	-/-	G	C	A	T	0	C	C	3	G	T	1	G	Hap7
CML169	-/-	A	A	A	T	12	C	T	3	G	T	1	G	Hap13
CIMBL43	-/-	A	A	A	T	12	C	T	3	G	T	1	G	Hap13
CIMBL151	-/-	A	A	A	T	12	C	T	3	G	T	1	G	Hap13
CIMBL14	-/-	A	A	A	T	12	C	T	3	G	T	9	C	Hap14
CIMBL31	-/-	A	A	A	T	12	C	T	3	G	T	9	C	Hap14
CIMBL53	-/-	A	A	A	T	12	C	T	3	G	T	9	C	Hap14
CIMBL84	-/-	A	A	A	T	12	C	T	3	G	T	9	C	Hap14

Line	Site													Haplotype
	TE	-1983	-1884	-1875	-1722	-1692	-1636	-1565	-1518	-1341	-1267	-1206	-1145	
B11	-/-	A	A	A	T	12	C	C	3	C	T	1	G	Hap15
CIMBL22	-/-	A	A	A	T	12	C	C	3	C	T	1	G	Hap15
CML454	-/-	A	A	A	T	12	C	C	3	C	T	1	G	Hap15

Table S9 Effect of *ZmCCT* promoter haplotypes (MAF ≥ 0.01) on photoperiod sensitivity and flowering time in a maize panel of 508 lines. Only one site is shown when the sites are in complete LD

Haplotype	TE	-1983	-1884	-1875	-1722	-1518	-1341	-1206	N[a]	Temp[b]	Trop[c]	Trait (Means±SE)[d]					
												APR (°C)	SPR (°C)	DTA (d)	DTS (d)	GDD_DTA_LD (°C)	GDD_DTS_LD (°C)
Hap1	+/+	A	C	C	A	0	A	0	300	193	107	325.7±0.2	345.8±0.2	71.7±0.01	73.6±0.01	1008.0±0.3	1039.7±0.4
Hap2	+/+	A	C	C	T	0	A	0	18	0	18	311.4±2.0	328.9±2.3	71.5±0.2	72.9±0.2	1003.7±3.0	1027.6±3.2
Hap3	-/-	A	C	C	A	0	A	0	20	0	20	361.4±1.8	387.0±2.0	74.5±0.2	76.3±0.2	1050.9±2.7	1082.9±2.8
Hap4	-/-	A	C	C	A	3	A	0	12	4	8	330.6±3.0	362.3±3.4	72.4±0.3	74.8±0.3	1016.8±4.6	1057.8±4.8
Hap5	-/-	A	A	A	T	3	G	9	41	5	36	356.9±1.0[fghi]	370.3±1.1	74.2±0.1[fh]	75.8±0.1	1048.0±1.5[h]	1074.5±1.6
Hap6	-/-	G	C	A	T	3	C	1	32	18	14	360.1±1.3[fghi]	381.7±1.5[fghi]	74.5±0.1[fghi]	76.3±0.1[fghi]	1053.5±1.9[fghi]	1080.9±2.1[fghi]
Hap7	-/-	G	C	A	T	3	G	1	16	2	14	372.9±2.2[fghi]	388.8±2.5[fghij]	75.0±0.2[fghi]	76.6±0.2[fghi]	1059.2±3.4[fghi]	1086.3±3.5[fghi]

[a] The number of maize lines. [b] The number of temperate germplasms. [c] The number of tropical germplasm. [d] Means and SE, least square means of photoperiod responses in GDDs and flowering time in days and GDDs under long-day conditions for each haplotype after correcting for the population structure and kinship. [f, g, h, i, j] Refer to the corresponding haplotype was significantly different from Hap1, Hap2, Hap3, Hap4 and Hap5, respectively ($P < 0.05$), $P < 1.6 \times 10^{-9}$ for all the six traits between haplotypes with TE and without TE. APR, anthesis photoperiod response; SPR, silking photoperiod response; DTA, days to anthesis; DTS, days to silking; GDD_DTA_LD, GDD of days to anthesis under long-day conditions; GDD_DTS_LD, GDD of days to silking under long-day conditions.

Table S10 Light-responsive elements identified in the *ZmCCT* promoter

Cis-element name	Sequence motif	Number of copies in the *ZmCCT* promoter (1145)	Number of copies in the *ZmCCT* promoter (HZS)
EVENINGAT	AAAATATCT	1	1
GT1CONSENSUS	GRWAAW	16	17
IBOX	GATAAG	2	1
IBOXCORE	GATAA	5	5
INRNTPSADB	YTCANTYY	4	4
SORLIP1AT	GCCAC	2	1
SORLIP2AT	GGGCC	1	1

Table S11 All haplotypes composed of 8 polymorphic sites in 26 NAM founders

Lines	TE	-1983	-1884	-1875	-1722	-1518	-1341	-1206	Haplotypes
CML52	+/+	A	C	C	A	0	A	0	Hap1
CML247	+/+	A	C	C	A	0	A	0	Hap1
Tzi8	+/+	A	C	C	A	0	A	0	Hap1
Ki3	+/+	?	C	C	A	0	A	0	Hap1
Mo18W	+/+	A	C	C	A	0	A	0	Hap1
CML69	+/+	A	C	C	A	0	A	0	Hap1
CML103	+/+	A	C	C	A	0	A	0	Hap1
CML322	+/+	A	C	C	A	0	A	0	Hap1
M162W	+/+	A	C	C	A	0	A	0	Hap1
NC350	+/+	?	C	C	A	0	A	0	Hap1
Tx303	+/+	A	C	C	A	0	A	0	Hap1
MS71	+/+	A	C	C	A	0	A	0	Hap1
HP301	+/+	A	C	C	A	0	A	0	Hap1
NC358	+/+	A	C	C	A	0	A	0	Hap1
M37W	+/+	A	C	C	A	0	A	0	Hap1
Oh7B	+/+	A	C	C	A	0	A	0	Hap1
B97	+/+	A	C	C	A	0	A	0	Hap1
Mo17	+/+	A	C	C	A	0	A	0	Hap1
Oh43	+/+	A	C	C	A	0	A	0	Hap1
Il14H	+/+	A	C	C	A	0	A	0	Hap1
B73	+/+	A	C	C	A	0	A	0	Hap1
P39	+/+	A	C	C	A	0	A	0	Hap1
CML333	+/+	A	C	C	T	0	A	0	Hap2
Ki11	-/-	A	C	C	A	3	A	0	Hap4
CML228	-/-	A	C	C	A	3	A	0	Hap4
CML277	-/-	A	A	A	T	3	G	9	Hap5
Ky21	-/-	A	A	A	T	3	G	9	Hap5

Table S12 Traits analyzed in this study

Trait	Description	Units
Days to anthesis (DTA)	Number of days after planting for anthers exsertion on the tassel	d
Days to silking (DTS)	Number of days after planting that silks are visible on ears	d
Growing degree days to anthesis (GDD_DTA)	Accumulation of thermal time from sowing to anthesis after a (10°C and 30°C) adjustment	°C
Growing degree days to silk (GDD_DTS)	Accumulation of thermal time from sowing to silking after a (10°C and 30°C) adjustment	°C
Anthesis photoperiod response[a] (APR)	The difference in growing degree days to anthesis between long- and short-day environments	°C
Silking photoperiod response[a] (SPR)	The difference in growing degree days to silking between long- and short-day environments	°C
Plant height (PH)	Height from the ground to the tip of the main tassel branch	cm
Ear height (EH)	Height from the ground to the ear	cm
Node number (NN)	Node number above the ground	
Leaf angle (LA)	Angle between the first leaf above the top ear and the stem	°
Leaf numbers above the ear (LAE)	Number of leaves above the top ear	
Tassel blanch number (TBN)	Number of tassel branches	
Tassel length (TL)	Length of the main stem of the tassel	cm
Leaf width (LW)	Leaf width of the top ear	cm
Leaf length (LL)	Leaf length of the top ear	cm
Ear length (EL)	Length of the ear	cm
Ear diameter (ED)	Diameter of the ear	mm
Kernel row number (KRN)	Number of rows of kernels around an ear	
Ear weight (EW)	Weight of the ear	g
Cob diameter (CD)	Diameter of the cob	mm
Kernel weight (KW)	One hundred kernel weight	g
Row kernel number (KNR)	Number of kernels per row	
Cob weight (CW)	Weight of the cob	g

[a] The average of daily min and max was used as daily average temperature, and the following adjustments were implemented: 1) temperatures below 10 degrees C are set at 10 degrees C, and 2) temperatures above 30 degrees C are set at 30 degrees C. GDDs $=\sum[(T_{max} + T_{min})/2 - 10]$ (Veldboom et al. 1994, Theor Appl Genet, 88:7-16).