

Figure S1 qPCR assays in teosinte. qPCR quantification of transcripts from immature and mature leaves of teosinte plants grown under inductive short days (SD) and inhibitory night breaks (NB) flowering conditions. These graphs are representative of data obtained for one of the three biological replicates analyzed. Asterisk indicates statistically significant change ($p \leq 0.05$) when it was achieved in the separate analysis of at least two of the three biological replicates.

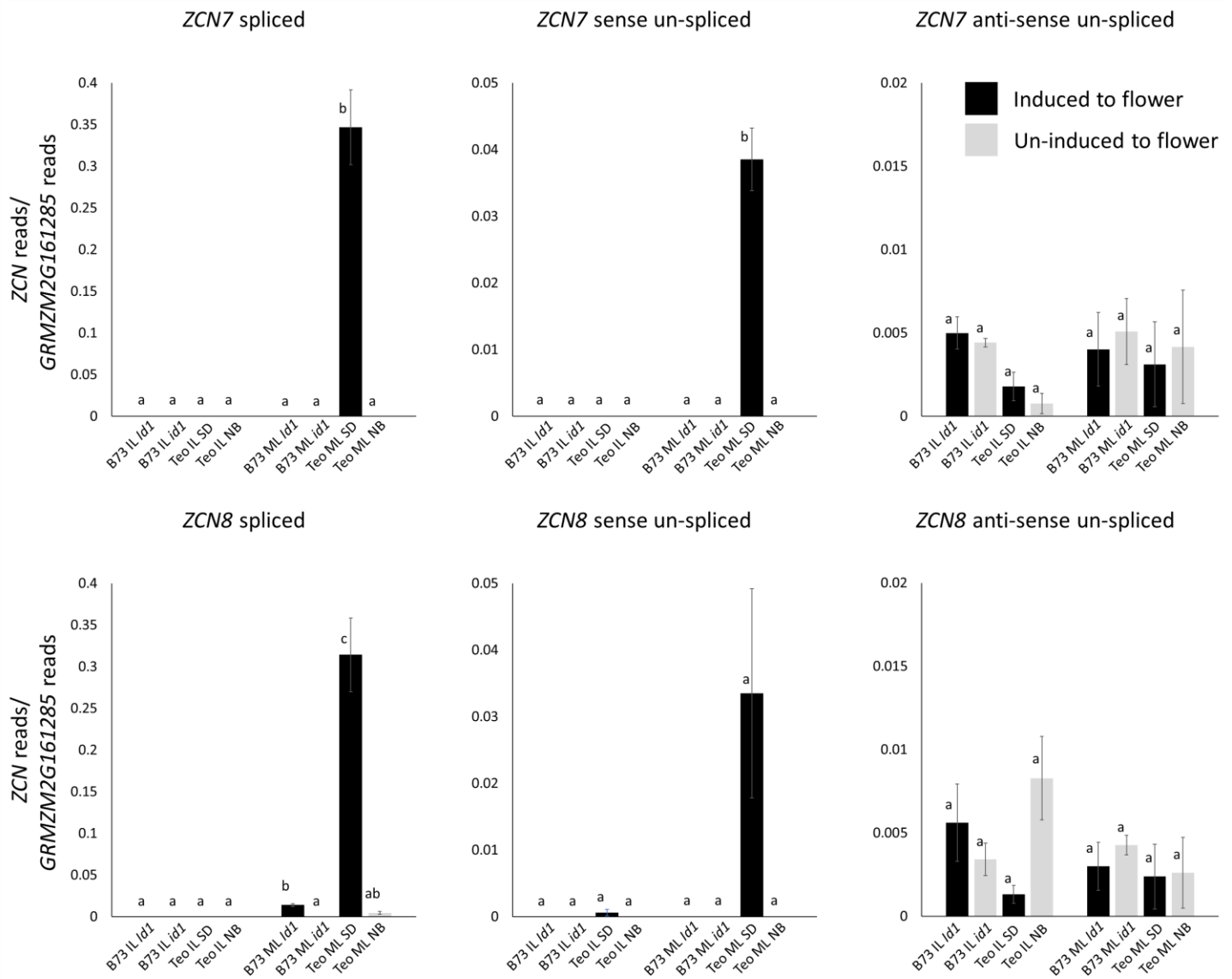


Figure S2 ZCN7 and ZCN8 mapped reads relative to reads mapped to *GRMZM2G161285*. Strand-specific reads from B73 and teosinte (Teo) immature and mature leaf (IL and ML) were mapped to *ZCN7* and *ZCN8* transcripts individually and standardized to the expression of *GRMZM2G161285*. Expression from induced B73 (*Id1*), induced short-day (SD) teosinte, uninduced B73 (*id1*) and uninduced night-break (NB) teosinte was determined for spliced sense, unspliced sense and unspliced anti-sense transcripts. MapQ quality scores were used to resolve reads mapped to both *ZCN7* and *ZCN8*. Reads mapping entirely to exons were removed from *ZCN7* and *ZCN8* unspliced sense transcript quantifications. Letters indicate statistically significant groups ($p \leq 0.05$), as determined through TukeyHSD (both anti-sense transcripts) and Welch t-tests (all other groups) after *fd*r adjustment for multiple comparisons. Error bars denote standard error.

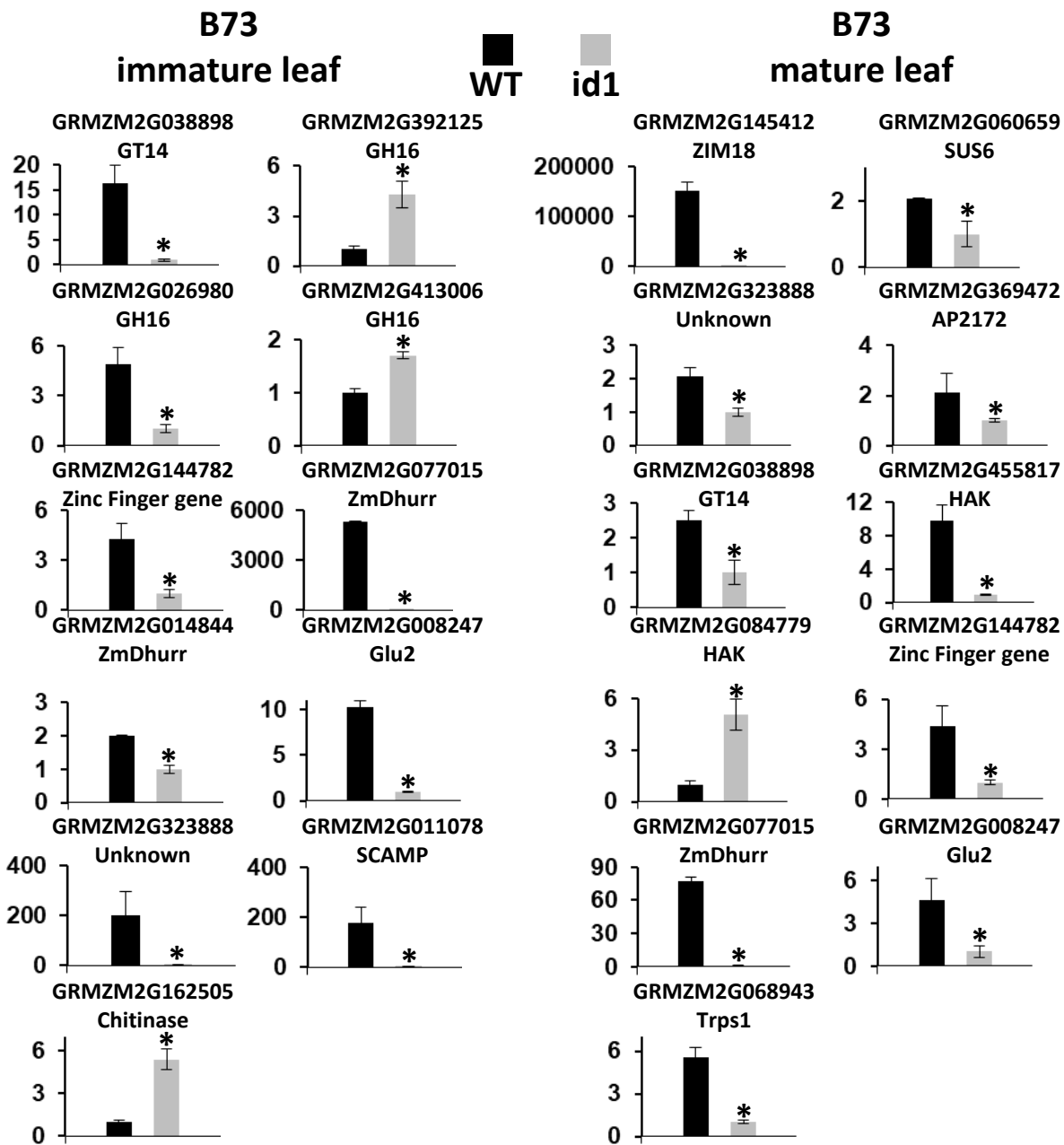


Figure S3 qRT-PCR assays in maize B73 inbred. qPCR quantification of transcripts from immature and mature leaves of maize B73 WT and *id1* mutant (*id1*) plants. These graphs are representative of data obtained for one of the three biological replicates analyzed. Asterisk indicates statistically significant change ($p \leq 0.05$) when it was achieved in the separate analysis of at least two of the three biological replicates.

Supplemental Table S9. List of primers used in qRT-PCR. a: Name of amplified sequence. b: sub-species. c: Forward (F) and reverse (R) primers reported in 5'-3' orientation.

Sequence ^a	Sub-species	Primer combination ^b
GRMZM2G323888	teosinte and maize	F CCTCCACGACGCCATGT R TACACAAAAGCGGGCGGA
GRMZM2G144782	teosinte and maize	F GTCACAAAATGCCAGGGAGATG R TGAATAGCCCCACTAATCCTGC
GRMZM2G038898	teosinte and maize	F TCAAACAAACAGGCCGTTGAC R AACAAAATTGGCTTTGGCCG
GRMZM2G026980	teosinte and maize	F ACAACTACTGCACCGATAAGTACC R TTCTACTCATCTACTACTGGCCG
GRMZM2G011078	teosinte	F CAGTAGGGTTGGCGTCTTGT R ACCTGGAGGGCTCAAAACAC
GRMZM2G011078	maize	F GCGACAGCGTCATTGTTGG R CGCCTCATCTCCGCTTCT
GRMZM2G413006	teosinte and maize	F TGATCTACAACACTGCACCGAC R ATCTCTGGTCTGAAGTGAACGAC
GRMZM2G392125	teosinte and maize	F TACTGCGCCGACACCAAG R AATTGACCCGTGCGTCGT
GRMZM2G154628	teosinte	F CGCGGTCATCTACAACAAGG R GGAAACAGAACAGGGCGTCA
GRMZM2G111324	teosinte	F CACGGATCTTGTGTTTATGCTGG R ATTCTGCAAAGACTGCATGGTTC
GRMZM2G026050	teosinte	F CCTGGGTGGGTGAATAGGC R AGCAGTTGACGATGGCAGAA
GRMZM2G369472	teosinte and maize	F CTGATGAGGCTGGACGAAGG R TAGTTGAACGGCTGGGATCTG
GRMZM2G177340	teosinte	F GAGATGGCCAGGCTCTACTTC R TGGAGCTCGAGGCCGTAG
GRMZM2G145412	teosinte and maize	F ATTCCTGTTCGGTGTCCCTAC R ACGTGCAACTGTGTTTTTCAG
GRMZM2G103666	teosinte	F CATGGTGTTCGTGCTGTTCC R TTGCAGTTGAAGTTGTGCCG
GRMZM2G051338	teosinte	F TCAACTGCCAGCGTGAGG R CACGAGTACATCCTCCTGCC

GRMZM2G122277	maize	F ACATCAACATACCCACATCCAC R TCACCATATCATCATCAGGGCAG
GRMZM5G840560	maize	F CTCGTGGGCATAATCTTTGTCAATT R AATAGCTGACCTCATAGTTTGTGCTA
GRMZM2G077015	maize	F AAAGACGCAATAGACCTGGGAG R ATGCCCGTCTGTCTTTCTTCT
GRMZM2G014844	maize	F GTGTATGGCCGTGGGATGAA R TGAACCCTTGGTGTTGCCT
GRMZM2G008247	maize	F AGTGGTTAAAAGAGTTCAACTGCG R AGAATATGACTCCACTACCTCTCA
GRMZM2G162505	maize	F CGACCGCCCTGTGTCTT R TGGTCAGGGAGGAGACGG
GRMZM2G060659	maize	F GGACCAGATCAGTGTATTATGTGA R TCTCTTTACATCATCCAGCTCTCC
GRMZM2G455817	maize	F AGGCAGTCTACGCTGAGGA R GTGAGGAGTGGGGTCTTGC
GRMZM2G084779	maize	F ACTGCTCCGGTTGGAATG R ACCACCTGCCTGCTTTGA
GRMZM2G415359	maize	F GCCTGTGATTTGCACGACATT R TAGGCACCAGGAAAGCAACAA
GRMZM2G141584	maize	F ACAGCCCGGTTTCAGTCA R CAGCCATCGTCCTCTTCTTC
GRMZM2G381709	maize	F ACGCATGATTGCTGGTGTT R TCCCCTGCCTTCGTATTT
MEP	teosinte and maize	F TGTACTCGGCAATGCTCTTG R TTTGATGCTCCAGGCTTACC
UBPC	teosinte and maize	F CAGGTGGGGTATTCTTGGTG R ATGTTCCGGTGGAAAACCTT

Supplemental Table S10. List of primers used in stem-loop qRT-PCR. See Materials and Methods and Varkonyi-Gasic et al. (2007) for details of the technology and meaning and use of primer type. Primers are written in 5'-3' orientation. UPL probe 21 reverse complement sequence is highlighted in bold.

miR166	miRNA sequence UCGGACCAGGCUUCAUUCCC RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACGGGAAT forward primer GCAGCTTCGGACCAGGCTTC
miR399e/i/j	miRNA sequence (miR399e) UGCCAAAGGAGAGUUGCCCUG RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACCAGGGCAA forward primer CGAACGGGTGCCAAAGGAGAG
miR399c/a/h	miRNA sequence (miR399c) UGCCAAAGGAGAAUUGCCCUG RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACCAGGGCAA forward primer GCGACGGGTGCCAAAGGAGAA
miR399b/d	miRNA sequence (miR399b) UGCCAAAGGAGAGCUGUCCUG RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACCTGGTC forward primer CCATGTCTGTGCCAAAGGAGAGCT
miR156	miRNA sequence UGACAGAAGAGAGUGAGCAC RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACGTGCTC forward primer GCGGCGGTGACAGAAGAGAGT
miR166	miRNA sequence UCGGACCAGGCUUCAUUCCC RT primer GTTGGCTCTGGTGCAGGGTCCGAGGTAT TCGCACCAGAGCCAACGGGAAT forward primer GCAGCTTCGGACCAGGCTTC
Universal	Reverse primer GTGCAGGGTCCGAGGT