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# Supplementary Information

## A Comparative Transcriptomics Method to Infer Gene Coexpression Networks and its applications to Maize and Rice Leaf Transcriptomes

Chang et al.

**Supplementary figures and tables**

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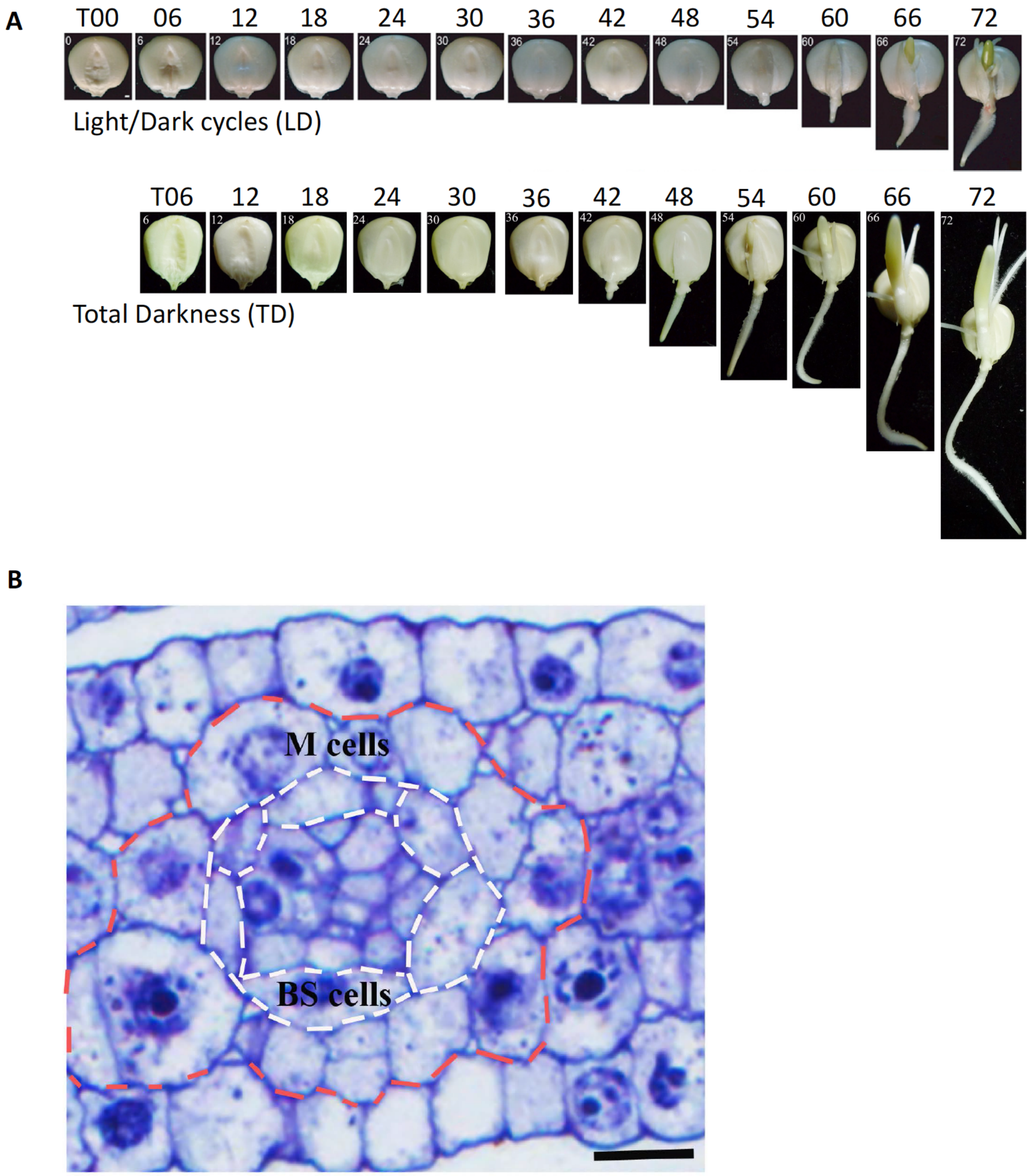
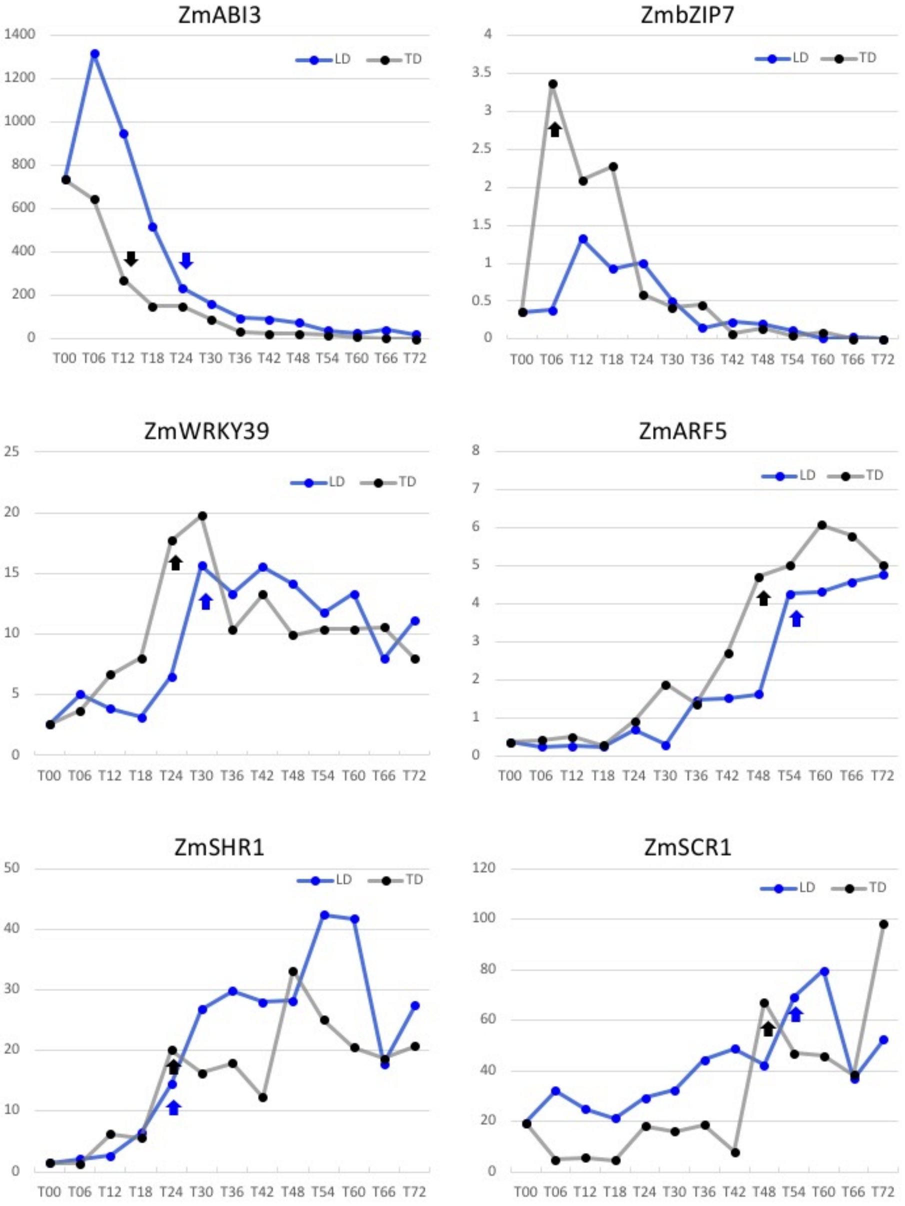
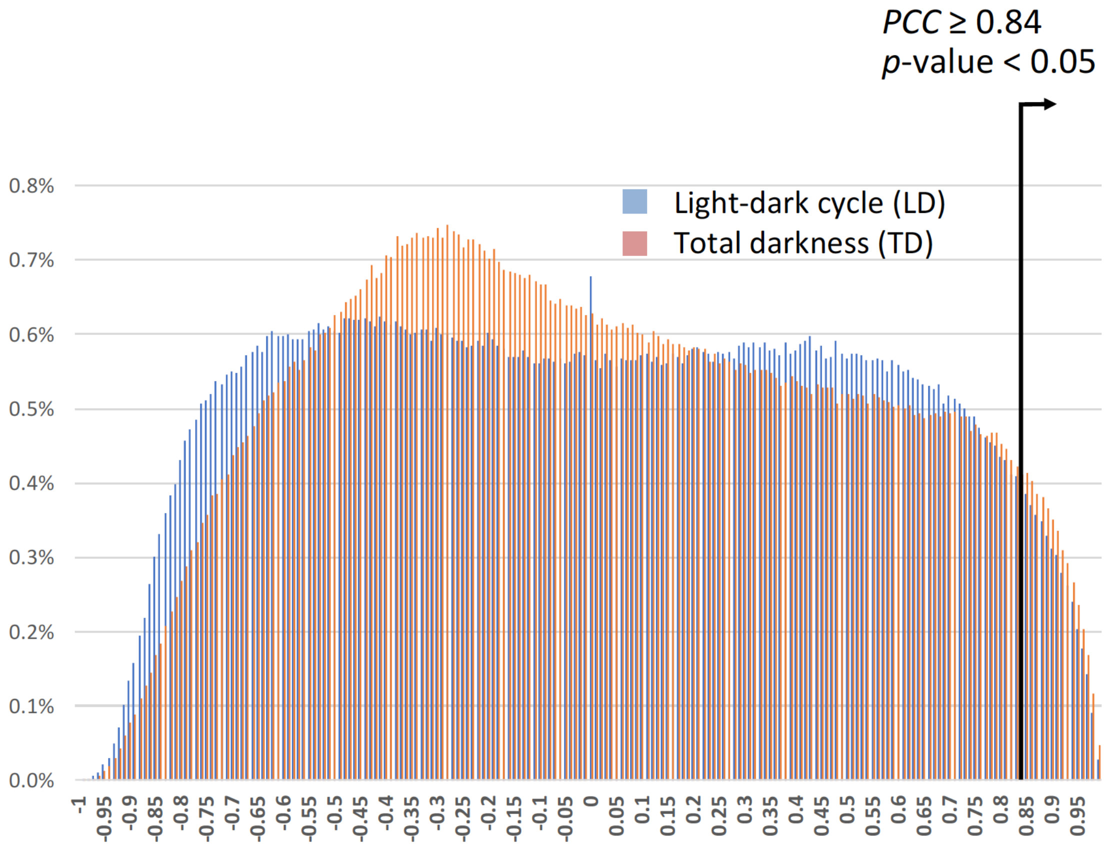
## Supplementary figures



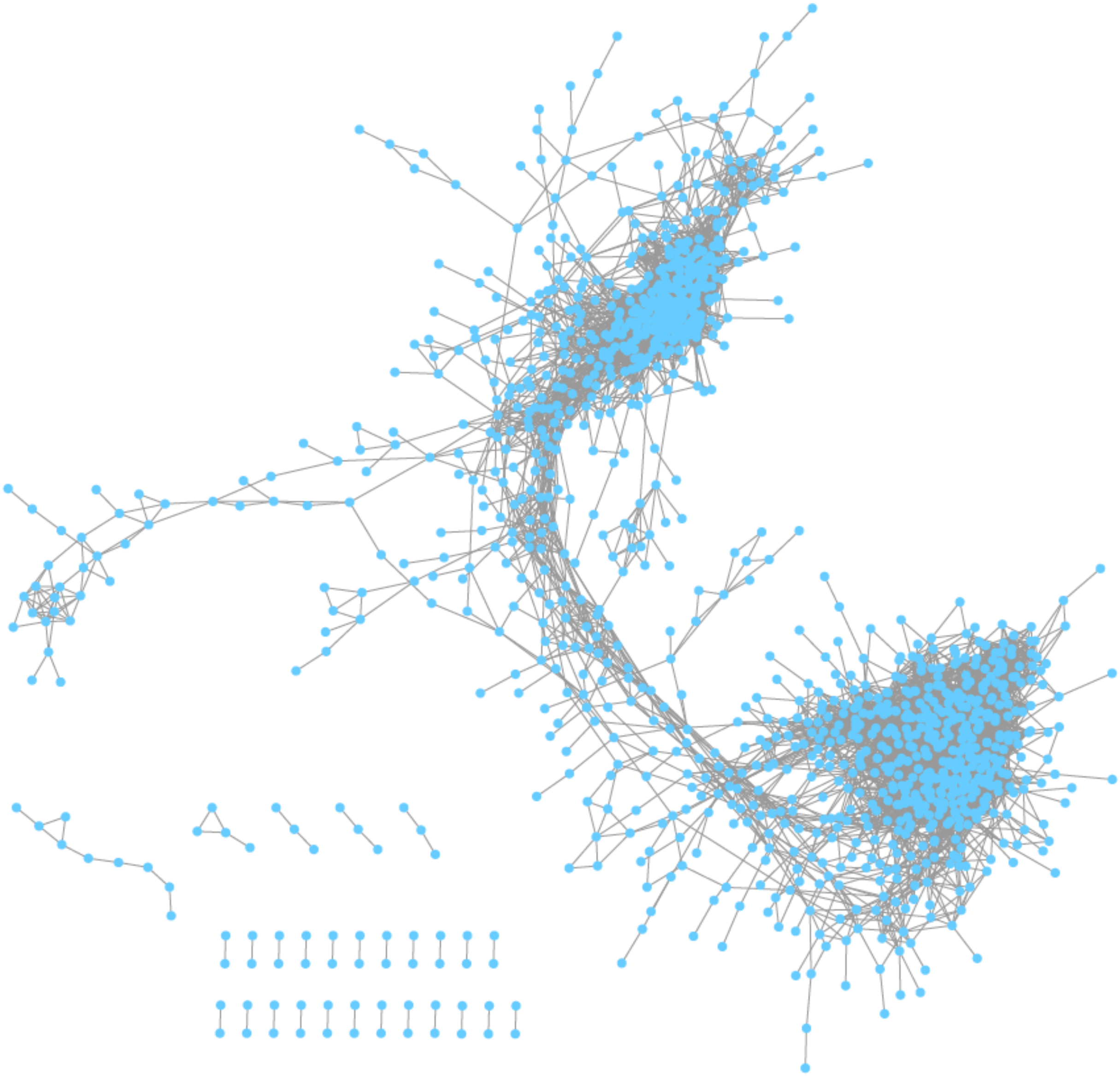
**Supplementary Figure S1.** Time series of maize seed germination and seedling development. (A) Morphologies of seed and germinating seedling from 0 h (T00, dry seed) to 72 h (T72) post imbibition under the natural light/dark (LD) cycle or under total darkness (TD). Scale bars: 1 mm. (B) Cross section of a second order vein under total darkness at 72 h (T72). The Kranz anatomy is shown with one layer of bundle sheath (BS) cells and one layer of mesophyll (M) cells. Scale bar: 10 µm.



**Supplementary Figure S2.** Examples of gene expression profiles over the time-series transcriptomes under two conditions. Six gene expression profiles are shown over the time course from T00 to T72 (x-axis) under LD (blue line) and under TD (black line); the six TFs are *ZmABI3*, *ZmbZIP7*, *ZmWRKY39*, *ZmARF5*, *ZmSHR1*, and *ZmSCR1*. The up- and down-regulated time points of a gene are indicated by arrows (blue for LD and black for TD).

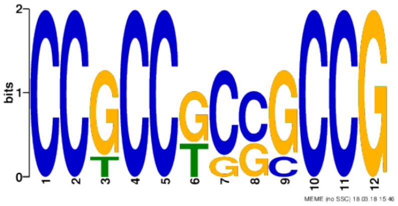


**Supplementary Figure S3.** The distributions of PCC values between TF genes over the time-series RPKM values under LD (blue bars) and under TD (red bars). The cutoff is set to 0.84 with $p < 0.05$.



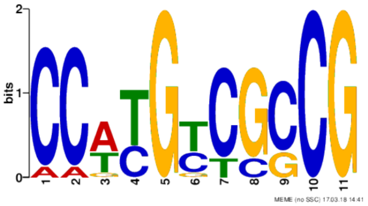
**Supplementary Figure S4.** TF-TF gene coexpression networks with LD+TD+ coexpression relationships (1,275 nodes and 16,281 edges). Each blue node and grey edge in the GCNs represent a TF gene and a coexpression relationship, respectively. The GCNs are visualized using the Cytoscape tool (http://cytoscape.org).

*ZmmTERF-1*



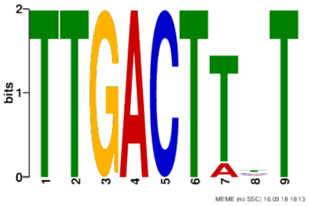
| A | C | G | T |
|---|---|---|---|
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 0.8000 | 0.2000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 0.6000 | 0.4000 |
| 0.0000 | 0.8000 | 0.2000 | 0.0000 |
| 0.0000 | 0.6000 | 0.4000 | 0.0000 |
| 0.0000 | 0.2000 | 0.8000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |

*ZmARF1-2*



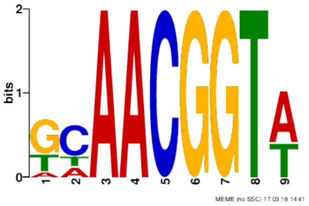
| A | C | G | T |
|---|---|---|---|
| 0.0909 | 0.9091 | 0.0000 | 0.0000 |
| 0.0909 | 0.9091 | 0.0000 | 0.0000 |
| 0.5455 | 0.0000 | 0.0909 | 0.3636 |
| 0.0000 | 0.3636 | 0.0000 | 0.6364 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |
| 0.0000 | 0.3636 | 0.0909 | 0.5455 |
| 0.0000 | 0.8182 | 0.0000 | 0.1818 |
| 0.0000 | 0.1818 | 0.8182 | 0.0000 |
| 0.0000 | 0.7273 | 0.2727 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |

*ZmWRKY39*



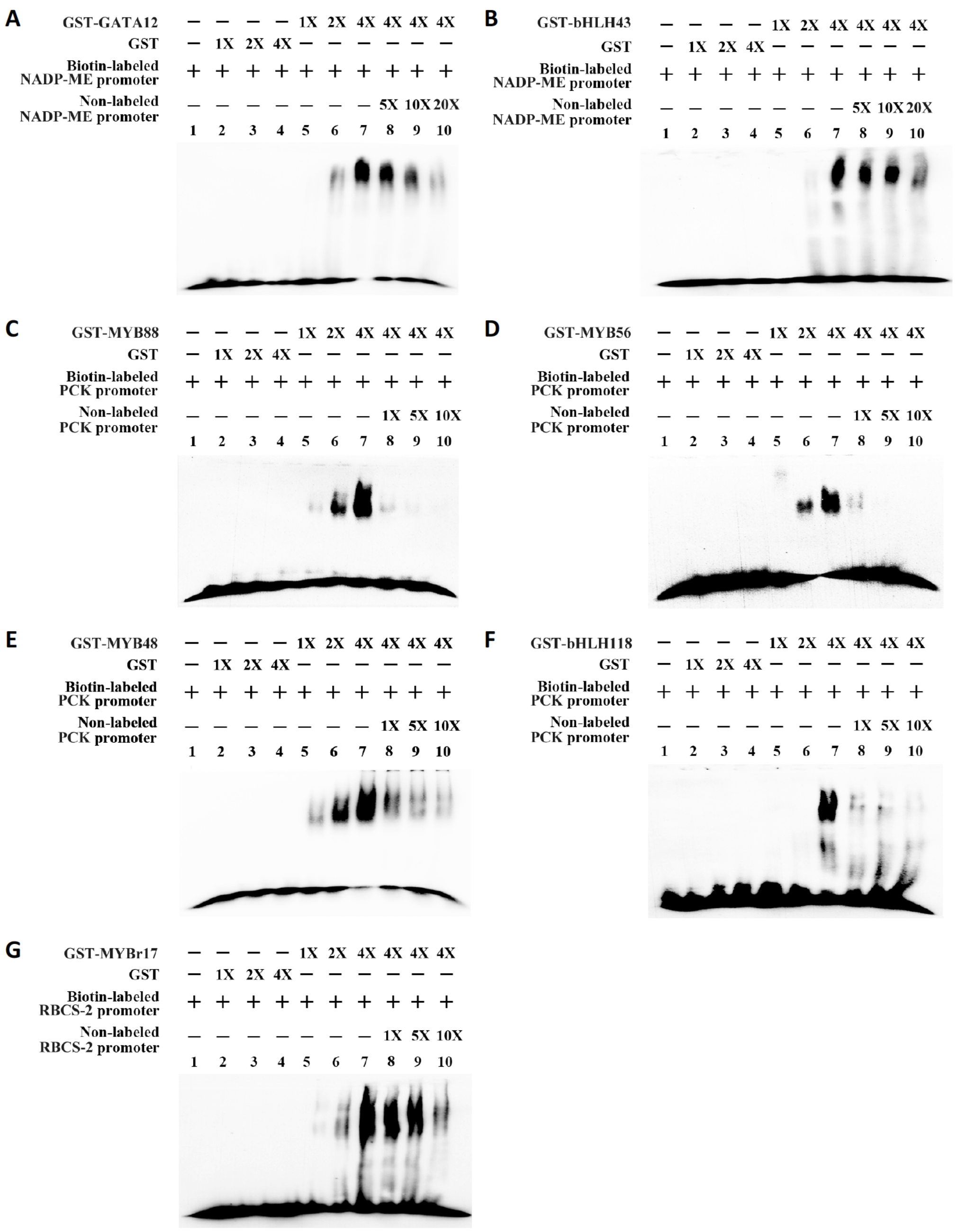
| A | C | G | T |
|---|---|---|---|
| 0.0000 | 0.0000 | 0.0000 | 1.0000 |
| 0.0000 | 0.0000 | 0.0000 | 1.0000 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |
| 1.0000 | 0.0000 | 0.0000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 0.0000 | 1.0000 |
| 0.1250 | 0.0000 | 0.0000 | 0.8750 |
| 0.2500 | 0.2500 | 0.1250 | 0.3750 |
| 0.0000 | 0.0000 | 0.0000 | 1.0000 |

*ZmMYB117*

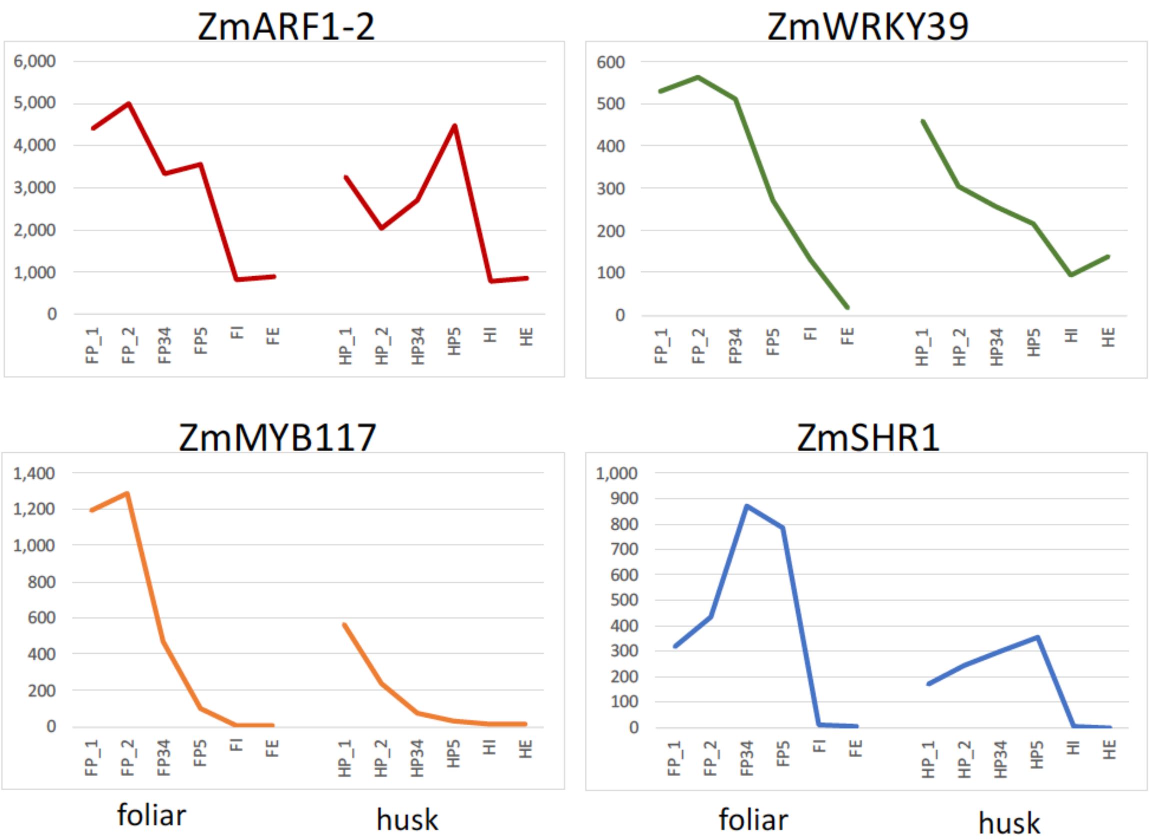


| A | C | G | T |
|---|---|---|---|
| 0.1000 | 0.0000 | 0.6000 | 0.3000 |
| 0.2000 | 0.6000 | 0.0000 | 0.2000 |
| 1.0000 | 0.0000 | 0.0000 | 0.0000 |
| 1.0000 | 0.0000 | 0.0000 | 0.0000 |
| 0.0000 | 1.0000 | 0.0000 | 0.0000 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |
| 0.0000 | 0.0000 | 1.0000 | 0.0000 |
| 0.0000 | 0.0000 | 0.0000 | 1.0000 |
| 0.6000 | 0.0000 | 0.0000 | 0.4000 |

**Supplementary Figure S5.** The predicted TFBSs of four upstream regulators of *ZmSHR1*. The four regulators are *ZmmTERF-1*, *ZmARF1-2*, *ZmWRKY39*, and *ZmMYB117* and in each case the motif logo and position weight matrix are shown in the left and right hand panel, respectively.



**Supplementary Figure S6.** EMSA validation of predicted upstream regulators of the C$_4$ enzyme genes. The regulators tested were ZmGATA12, ZmbHLH43, ZmMYB88, ZmMYB56, ZmMYB48, ZmbHLH118, and ZmMYBr17. GST- ZmGATA12 (A), GST- ZmbHLH43 (B), GST- ZmMYB88 (C), GST- ZmMYB56 (D) and GST- ZmMYB48 (E), GST- ZmbHLH118 (F), GST- ZmMYBr17 (G), were isolated from *E. coli* and were separately incubated with probes corresponding to the predicted TF binding site in the *ZmNADP-ME* (A and B), *ZmPCK* (C-F), and *ZmRbcS2* (G) promoters, respectively. In each case EMSA was conducted with the biotin-labeled probe alone (lane 1), with increasing amounts of purified GST (lanes 2-4) or with GST-TF (lanes 5-7) and the biotin-labeled probe. The DNA-binding specificity of a TF was tested by adding excess of the unlabeled probe (lanes 8-10).



**Supplementary Figure S7.** Expression profiles of four TF genes in maize foliar ($C_4$) and husk ($C_3$-type) embryonic leaves. The analysis used the data from Wang et al. (1).

## Supplementary tables

**Supplementary Table S1**. Read count statistics of the RNA sequencing data for the 12 time points under total darkness (TD). The data were obtained using Illumina HiSeq2000 with the paired-end 2*101nt format.

| | Quality filtering | | Mappable reads | |
|---|---|---|---|---|
| Sample (TD) | Total reads | Rate (%) | Total reads | Rate (%) |
| T06 | 622,278,182 | 92.8 | 502,136,866 | 80.7 |
| T12 | 631,190,482 | 92.9 | 529,141,296 | 83.8 |
| T18 | 654,440,380 | 92.6 | 550,918,931 | 84.2 |
| T24 | 507,710,021 | 94.3 | 422,194,745 | 83.2 |
| T30 | 564,950,902 | 91.6 | 477,864,256 | 84.6 |
| T36 | 520,170,828 | 94.0 | 441,941,333 | 85.0 |
| T42 | 589,910,974 | 92.7 | 499,591,439 | 84.7 |
| T48 | 441,648,581 | 95.1 | 370,185,791 | 83.8 |
| T54 | 478,353,359 | 95.0 | 403,373,361 | 84.3 |
| T60 | 619,109,440 | 93.0 | 524,564,651 | 84.7 |
| T66 | 594,676,837 | 93.7 | 500,542,333 | 84.2 |
| T72 | 732,667,006 | 91.9 | 621,034,074 | 84.8 |

**Supplementary Table S2.** Numbers of genes and TF-gene pairs in eight expression correlation types under LD and TD growth conditions.

| | **Coexpression type** | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | LD+TD+ | LD+TD0 | LD0TD+ | LD0TD− | LD−TD0 | LD−TD− | LD+TD− | LD−TD+ |
| **# genes** | 17,457 | 22,227 | 22,645 | 23,096 | 22,460 | 15,874 | 294 | 1,384 |
| **(# TF genes)** | (1,538) | (1,698) | (1,702) | (1,703) | (1,654) | (1,398) | (102) | (329) |
| **# TF-gene pairs** | 431,974 | 547,762 | 671,020 | 546,822 | 704,620 | 539,624 | 239 | 3,710 |
| **(#TF-TF pairs)** | (16,281) | (18,984) | (25,907) | (14,394) | (29,727) | (15,951) | (9) | (160) |

Note that the coexpression type of LD0TD0 means no coexpression under both conditions, so we exclude it in this study.

**Supplementary Table S3.** First to fourth order upstream TF candidates of *ZmSHR1.*

| Gene ID AGPv4 | TF family | TO-GCN level | Order of candidate | Gene name | TFBS ID |
|---|---|---|---|---|---|
| Zm00001d043969 | GATA | 11 | 1st | *GATA20* | C2C2gata_tnt.GATA19_colamp_a_m1 |
| Zm00001d020037 | C2H2 | 11 | 1st | *DOT5* | C2H2_tnt.WIP5_colamp_a_m1 |
| Zm00001d012731 | ARF | 11 | 1st | *ARF3-2* | ETT_TGTCGGAA |
| Zm00001d037117 | GRF | 11 | 1st | *GRF5* | GRF_tnt.AtGRF6_col_a_m1 |
| Zm00001d022295 | HSF | 11 | 1st | *HSFB4* | HSF_tnt.HSFB4_col_a_m1 |
| Zm00001d049443 | HD-ZIP | 11 | 1st | *ML1* | M0852_1.02 |
| Zm00001d034204 | AP2 | 11 | 1st | *ANT1* | M2364_1.02 |
| Zm00001d052256 | TCP | 11 | 1st | *TCP14* | MA1063.1 |
| Zm00001d025669 | WRKY | 11 | 1st | *WRKY2* | MA1078.1 |
| Zm00001d048493 | NAC | 11 | 1st | *NAC086* | NAC_tnt.ANAC028_col_a_m1 |
| Zm00001d031463 | NAC | 11 | 1st | *CUC3* | NAC_tnt.CUC3_col_a_m1 |
| Zm00001d022613 | bZIP | 11 | 1st | *FD* | pTH7315_AREB2_AT3G19290 |
| Zm00001d002075 | AP2 | 11 | 1st | *AP2* | TOE1_CCTCGTAC |
| Zm00001d002829 | YABBY | 11 | 1st | *YAB3* | **unknown** |
| Zm00001d004889 | WOX | 11 | 1st | *WOX3* | **unknown** |
| Zm00001d017784 | ZF-HD | 11 | 1st | *ZFHD5* | **unknown** |
| Zm00001d025944 | YABBY | 11 | 1st | *YAB1* | **unknown** |
| Zm00001d027991 | HD-ZIP | 11 | 1st | *HB6* | **unknown** |
| Zm00001d028371 | C2H2 | 11 | 1st | *ZFP4* | **unknown** |
| Zm00001d036356 | MYB-related | 11 | 1st | *SANT1* | **unknown** |
| Zm00001d040186 | bHLH | 11 | 1st | *bHLH110* | **unknown** |
| Zm00001d042588 | ERF | 11 | 1st | *CRF3* | **unknown** |
| Zm00001d048309 | bHLH | 11 | 1st | *bHLH* | **unknown** |
| Zm00001d051471 | B3 | 11 | 1st | *NGA2-3* | **unknown** |
| Zm00001d002794 | WRKY | 11 | 1st | *WRKY12* | WRKY12_CGTTGACC |
| Zm00001d002562 | B3 | 10 | 1st | *NGA2-1* | ABI3VP1_tnt.NGA4_col_a_m1 |
| Zm00001d017618 | B3 | 10 | 1st | *NGA2-2* | ABI3VP1_tnt.NGA4_col_a_m1 |
| Zm00001d013699 | HD-ZIP | 10 | 1st | *HB14* | HB_tnt.ATHB15_col_a_m1 |
| Zm00001d041489 | HD-ZIP | 10 | 1st | *PHB* | M2366_1.02 |
| Zm00001d032194 | MYB/MYB-related | 10 | 1st | *MYB117* | MYB_tnt.MYB105_col_a_m1 |
| Zm00001d014814 | bHLH | 10 | 1st | *bHLH93* | **unknown** |
| Zm00001d020774 | ZF-HD | 10 | 1st | *ZHD1-2* | ZFHD_tnt.ATHB25_col_a_m1 |
| Zm00001d015243 | ARF | 10 | 2nd | *ARF20* | ARF_ecoli.MP_col_m1 |
| Zm00001d034163 | Dof | 10 | 2nd | *OBP2* | Dof5.7_ACGTTAAC |
| Zm00001d039006 | ARF/B3 | 10 | 2nd | *ARF3-1* | ETT_TGTCGGAA |

| | | | | | |
|---|---|---|---|---|---|
| Zm00001d002005 | SBP | 10 | 2nd | *SPL8* | M2371_1.02 |
| Zm00001d001879 | ARF | 10 | 2nd | *ARF8* | MA0944.1 |
| Zm00001d012067 | bHLH | 10 | 2nd | *bHLH62* | pTH7309_AT1G68920_AT1G68920 |
| Zm00001d017350 | TCP | 10 | 2nd | *TCP21* | TCP_tnt.At5g08330_colamp_a_m1 |
| Zm00001d021236 | HD-ZIP | 9 | 2nd | *ANL2* | HB_tnt.ANL2_colamp_a_m1 |
| Zm00001d051527 | G2-like | 9 | 2nd | *KAN2-2* | KAN1_CGAATAT.T |
| Zm00001d030727 | Dof | 9 | 2nd | *DOF5.1-1* | M2712_1.02 |
| Zm00001d026590 | ARF | 9 | 2nd | *ARF6* | MA0944.1 |
| Zm00001d041866 | TCP | 9 | 2nd | *TCP8-2* | MA1063.1 |
| Zm00001d011953 | ARF | 9 | 2nd | *ARF2-2* | ARF_tnt.ARF2_col_v31_m1 |
| Zm00001d039439 | BES1 | 9 | 2nd | *BEH4* | BZR_tnt.At4g18890_colamp_a_m1 |
| Zm00001d017702 | G2-like | 9 | 2nd | *KAN2-1* | KAN1_CGAATAT.T |
| Zm00001d039907 | RAV | 9 | 2nd | *RAV1* | M0013_1.02 |
| Zm00001d006110 | bHLH | 9 | 2nd | *bHLH137* | M0166_1.02 |
| Zm00001d041549 | Dof | 9 | 2nd | *DOF5.1-2* | M2712_1.02 |
| Zm00001d033965 | WRKY | 9 | 2nd | *WRKY39-2* | WRKY_tnt.WRKY7_colamp_a_m1 |
| Zm00001d023565 | TCP | 8 | 3rd | *TCP8-1* | MA1063.1 |
| Zm00001d049824 | SBP | 8 | 3rd | *SPL13B-2* | SBP_tnt.SPL13_col_a_m1 |
| Zm00001d021285 | SRS | 8 | 3rd | *SRS3* | **unknown** |
| Zm00001d013307 | WRKY | 8 | 3rd | *WRKY39* | WRKY_tnt.WRKY7_colamp_a_m1 |
| Zm00001d003601 | ARF | 8 | 4th | *ARF1-2* | ARF_tnt.ARF2_col_v31_m1 |
| Zm00001d038698 | ARF/B3 | 8 | 4th | *ETT-1* | ETT_TGTCGGAA |
| Zm00001d015585 | mTERF | 8 | 4th | *mTERF-2* | **unknown** |
| Zm00001d024468 | AP2/ERF | 8 | 4th | *AIL1* | **unknown** |
| Zm00001d038158 | mTERF | 8 | 4th | *mTERF-3* | **unknown** |
| Zm00001d050781 | ARF | 7 | 4th | *ARF1-1* | MA0942.1 |
| Zm00001d012015 | SBP | 7 | 4th | *SPL13B-1* | SBP_tnt.SPL13_col_a_m1 |
| Zm00001d031533 | mTERF | 7 | 4th | *mTERF-1* | **unknown** |
| Zm00001d005931 | ZF-HD | 7 | 4th | *ZHD1-1* | ZFHD_tnt.ATHB25_col_a_m1 |

**Supplementary Table S4.** Sequences of gene cloning primers for protoplast transient assay (PTA).

| Gene ID | Level in the TO-GCN: gene name | Forward primer | Reverse primer |
|---|---|---|---|
| Zm00001d003601 | L8: ZmARF1-2 | GAATTCATGGACGCGCCCAACCCT | GAGCTCTCATTCAGACAGTGAGTTCGCAGC |
| Zm00001d013307 | L8: ZmWRKY39 | GAATTCATGGAGGCGATGGAGGAGG | AAGCTTCAGGCTGGCTGGGCTAGAA |
| Zm00001d032194 | L10: ZmMYB117 | GAATTCATGCCGTGCTCGTCGCC | AAGCTTTCATGTGGCTCCGACCCC |
| Control | GFP | ATGGTGAGCAAGGGCGAGGAG | TACTTGTACAGCTCGTCCATGC |

**Supplementary Table S5.** Statistics of level order changes with different initial seeds

| TF gene ID of initial seed | TF family | Gene name | Proportion of TFs with level change | Mean of level change [a] | STDEV of level change |
|---|---|---|---|---|---|
| Zm00001d013074 | bZIP | ZmbZIP25 | 16% | -0.06 | 0.39 |
| Zm00001d018941 | HSF | ZmHSFA6B | 10% | -0.05 | 0.32 |
| Zm00001d040775 | GATA | ZmGATA16 | 11% | -0.11 | 0.32 |
| Zm00001d046974 | MYB_related | ZmRVE6 | 13% | -0.12 | 0.34 |
| Zm00001d050242 | NF-YB | ZmNF-YB12 | 8% | -0.07 | 0.28 |
| Zm00001d013202 | G2-like | ZmHHO5 | 17% | -0.12 | 0.39 |
| Zm00001d030907 | B3 | ZmABI46 | 9% | -0.09 | 0.29 |
| Zm00001d043992 | bZIP | ZmGBF3 | 14% | -0.06 | 0.38 |
| Zm00001d001837 | MYB | ZmMYB133 | 13% | -0.08 | 0.34 |
| Zm00001d031723 | bZIP | ZmbZIP127 | 15% | -0.12 | 0.37 |
| Zm00001d007339 | C2H2 |  | 10% | 0.04 | 0.32 |

[a] For each node, the positive and negative number represent its level changes to lower or higher level, respectively, in the new TO-GCN against the original one. Zero represents no change between two TO-GCN. For example, a node belongs to level 5 in the original TO-GCN and changes to level 4 in the new one then the level change number is -1.

**Supplementary Table S6.** Sequences of qRT-PCR primers.

| Gene ID | Level in the TO-GCN: gene name | Forward primer | Reverse primer |
|---|---|---|---|
| Zm00001d021973 | L11: ZmSHR1 | CCAACGCATCCTACAACTAC | TGTTGCCGCATTCTTCTT |
| Zm00001d032194 | L10: ZmMYB117 | CCTTTGAAGGGACGACAAGA | AAGCTTTCATGTGGCTCCGACCCC |
| Zm00001d013307 | L8: ZmWRKY39 | GAGATGGTTAAGAGGAGCAATC | ATGTCTGAGAGCCACTAACT |
| Control | GFP | AAGCAGCACGACTTCTTC | CACCTTGATGCCGTTCTT |
| Control | ZmACT | CTGAGGTTCTATTCCAGCCATCC | CCACCACTGAGGACAACATTACC |

**Supplementary Table S7.** EMSA primer sequences for regulator-target pairs in the upstream regulatory pathway of *ZmSHR1*.

| TF | Target gene | Probe | |
|---|---|---|---|
| Level: Gene name | Level in the TO-GCN: Gene name | Forward primer | Reverse primer |
| L8: ZmARF1-2 | L8: ZmWRKY39 | ACGCTCGCTCGTCGTCACCACCA | ATGGTGGTGACGACGAGCGAGCG |
| L8: ZmWRKY39 | L10: ZmMYB117 | ATGGCCAGTCAAGCGTTGCAGAG | ACTCTGCAACGCTTGACTGGCCA |
| L10: ZmMYB117 | L11: ZmSHR1 | AATCCGAACCATTCCTTAG | AACTAAGGAATGGTTCGGA |

**Supplementary Table S8.** Predicted TFBSs with cross-species conservation.

| Target C4 enzyme | Regulator gene name | Arabidopsis (DBD identity %)[a] | Motif ID | Conservation [b] |
|---|---|---|---|---|
| BS: ZmNADP-ME | ZmGATA12 | AT5G49300 (70%) | C2C2gata_tnt.GATA16_col_a_m1 | 1 |
| BS: ZmNADP-ME | ZmbHLH43 | AT1G09530 (79%) | M2863_1.02 | 3 |
| BS: ZmNADP-ME | ZmERF | AT1G36060 (86%) | AP2EREBP_tnt.At1g36060_col_a_m1 | 4 |
| BS: ZmNADP-ME | ZmNAC | AT5G18270 (73%) | NAC_tnt.ANAC087_col_v3a_m1 | 2 |
| BS: ZmPCK | ZmMYB48 | AT5G59780 (86%) | MYB59_GTTAGGTA | 1 |
| BS: ZmPCK | ZmMYB88 | AT5G59780 (83%) | MYB59_GTTAGGTA | 1 |
| BS: ZmPCK | ZmMYB56 | AT5G59780 (86%) | MYB59_GTTAGGTA | 1 |
| BS: ZmPCK | ZmbHLH118 | AT5G54680 (71%) | M0167_1.02 | 2 |
| BS: ZmRbcS2 | ZmMYBr17 | AT5G47390 (82%) | MYBrelated_tnt.At5g47390_colamp_a_m1 | 3 |
| M: ZmCA | ZmABI33 | AT1G13260 (73%) | RAV_tnt.RAV1_colamp_a_m1 | 1 |
| M: ZmCA | ZmRAV | AT1G13260 (77%) | RAV_tnt.RAV1_colamp_a_m1 | 1 |
| M: ZmPEPC | ZmRAV | AT1G13260 (77%) | RAV_tnt.RAV1_colamp_a_m1 | 1 |

[a] DNA-binding domain (DBD) sequence identity between a maize TF and its best homologous Arabidopsis TF

[b] Four reference species were used, including *Brachypodium distachyon, Oryza sativa, Sorghum bicolor, and Setaria italica.* The number refers to the number of species in which the TFBS was observed.

**Supplementary Table S9.** Sequences of the cloning primers for predicted regulator genes of $C_4$ enzyme genes.

| Regulator Gene ID | Clone ID | Regulator gene name | Forward cloning primer | Reverse cloning primer |
|---|---|---|---|---|
| Zm00001d037605 | PUT6147 | ZmGATA12 | GAATTCATGATGATGGATTCCGCGGA | AAGCTTCTAGCCATGTAGCAGCGTGGATCT |
| Zm00001d033267 | PUT4131 | ZmbHLH43 | GAATTCATGAACCAGTTCGTGCCGGA | AAGCTTTCATCTAAGAGCGCCCATCTGCAG |
| Zm00001d048623 | PUT5992 | ZmMYB88 | GAATTCATGGTGACTGTGAGAGAGGAGATGC | AAGCTTCCCACCCTTTCACATCATGATTTC |
| Zm00001d030678 | PUT5678 | ZmMYB56 | GAATTCCCCTTCACCATGGTGACAGTGAG | AAGCTTTCAGAAGCAGGGCCCAACTCCTTC |
| Zm00001d038357 | PUT3433 | ZmbHLH118 | GAATTCTTCACCATGAGCTGCGCGGG | CTCGAGACCCTTCTAGGCGACCGGCGG |
| Zm00001d044409 | PUT3161 | ZmMYBR17 | GAATTCATGGCTAGGAAGTGCTCACACTGTG | AAGCTTTCATGTTCCGATGGATGGGGCA |

**Supplementary Table S10.** EMSA primer sequences for TF genes and their target $C_4$ enzyme genes.

| TF gene name | Target gene name | Target gene ID | Forward EMSA primer | Reverse EMSA primer |
|---|---|---|---|---|
| ZmGATA12 | ZmNADP-ME | Zm00001d000316 | ACATCATCACCAGCAACATATAAAG | TATCTTTATATGTTGCTGGTGATGA |
| ZmbHLH43 | ZmNADP-ME | Zm00001d000316 | AACGTCACACGTGAAAAGC | AAGCTTTTCACGTGTGACG |
| ZmMYB88 | ZmPCK | Zm00001d028471 | AAATGACCGAACATCAG | AACTGATGTTCGGTCAT |
| ZmMYB56 | ZmPCK | Zm00001d028471 | AAATGACCGAACATCAG | AACTGATGTTCGGTCAT |
| ZmbHLH118 | ZmPCK | Zm00001d028471 | AATAACACGTGAGTAGGG | AACCCTACTCACGTGTTA |
| ZmMYBR17 | ZmRbcS2 | Zm00001d004894 | AATCAGGATAGGCCAGGC | AAGCCTGGCCTATCCTGA |

1. Wang P, Kelly S, Fouracre JP, & Langdale JA (2013) Genome-wide transcript analysis of early maize leaf development reveals gene cohorts associated with the differentiation of C4 Kranz anatomy. *Plant J* 75(4):656-670.