

Transcriptomic variations and network hubs controlling seed size and weight during maize seed development

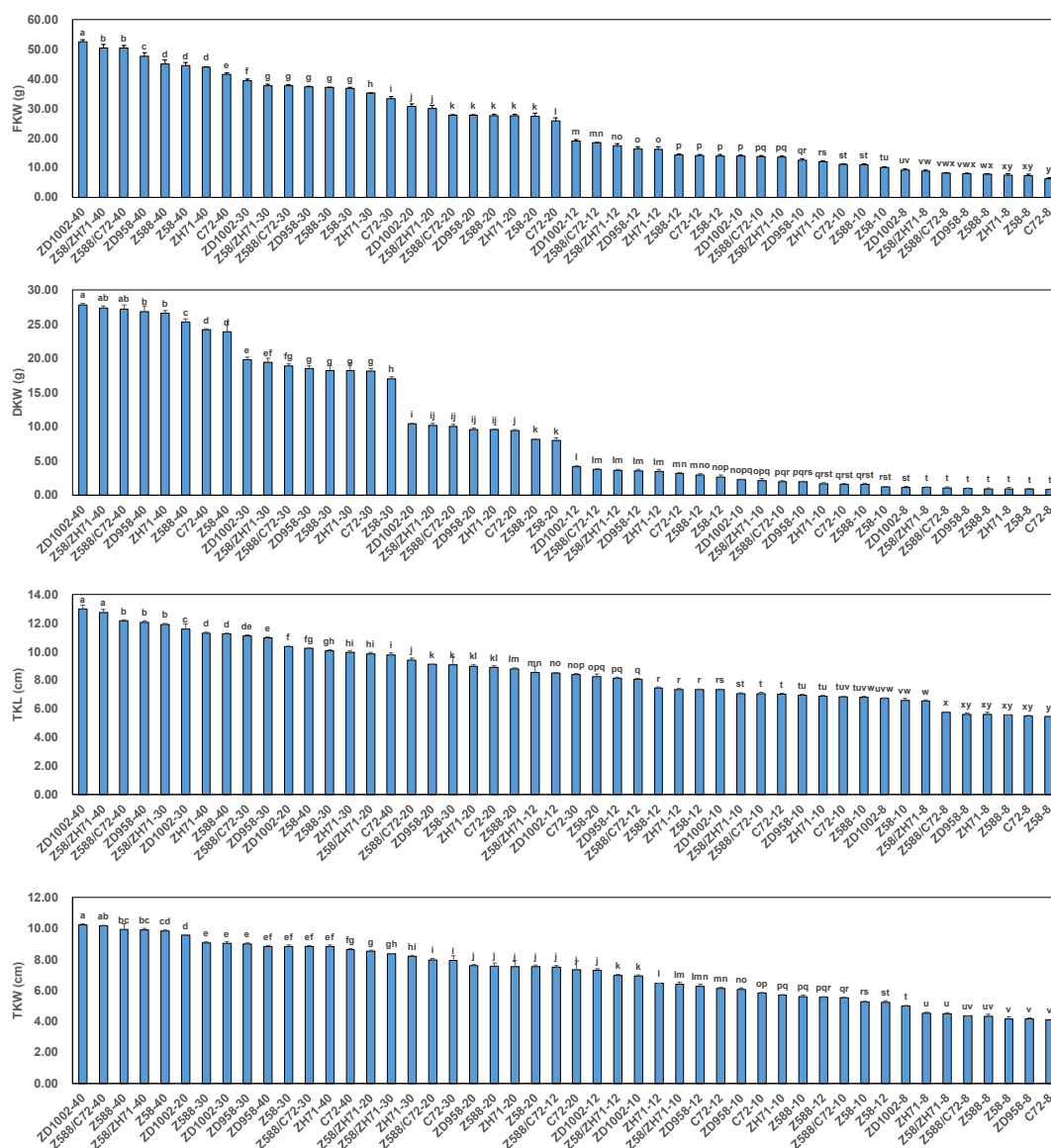
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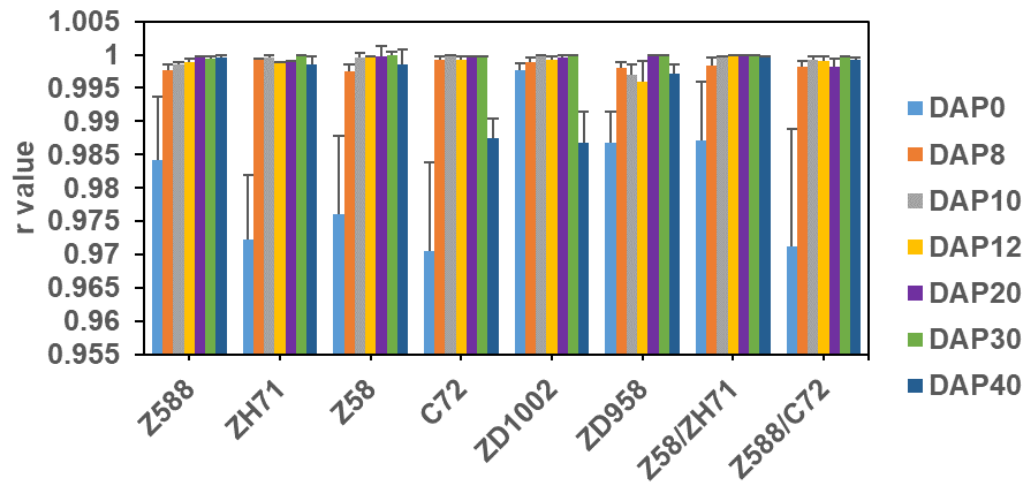
*** Correspondence:**

Yanyong Cao

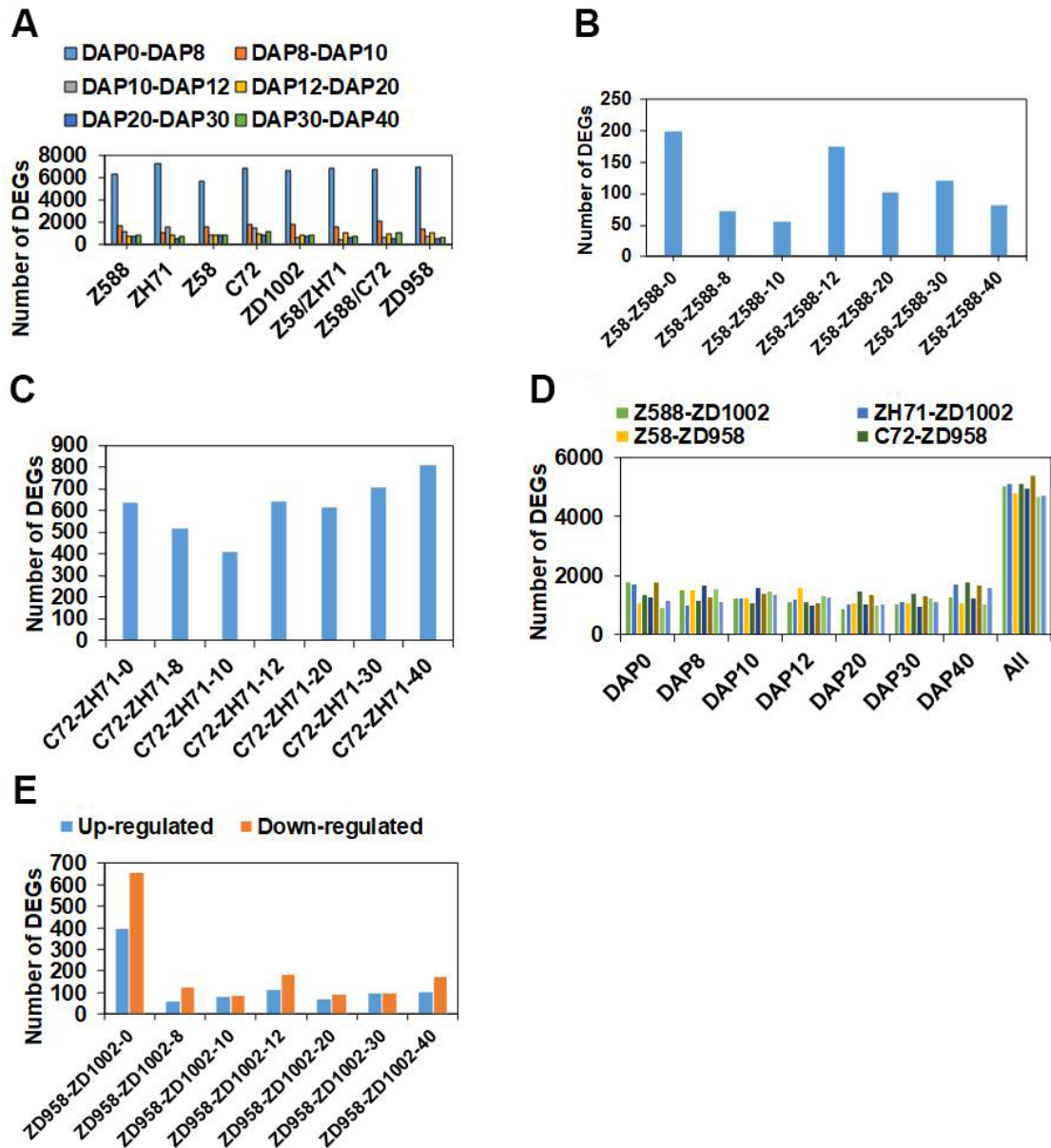
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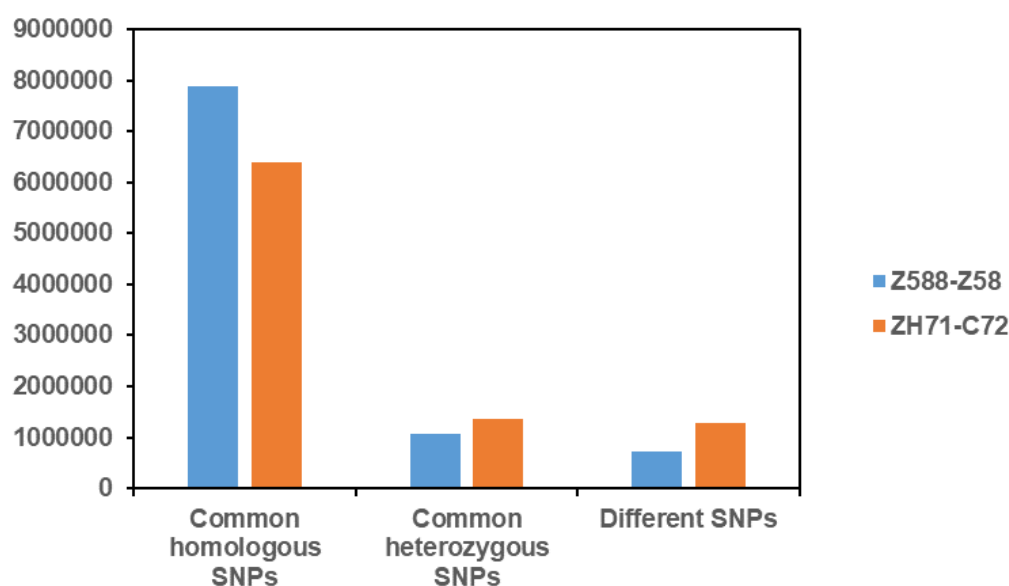
Supplementary Figure 1. Duncan's multiple comparisons of seed size and weight associated traits for eight genotypes during seed development. Data represent the means $\pm$ SD. Lower case letters above error bars represent results of Duncan's multiple comparisons at the 0.05 significant level. Means with different letters are significantly different. DAP8–40 represents 8–40 d after pollination, respectively. FKW, 100-fresh kernel weight; DKW, 100-dry kernel weight; TKL, Ten-kernel length; TKW, Ten-kernel width. Z588, Zheng588; Z58, Zheng58; ZH71, ZhengH71; C72, Chang7-2; ZD958, Zhengdan958; ZD1002, Zhengdan1002.



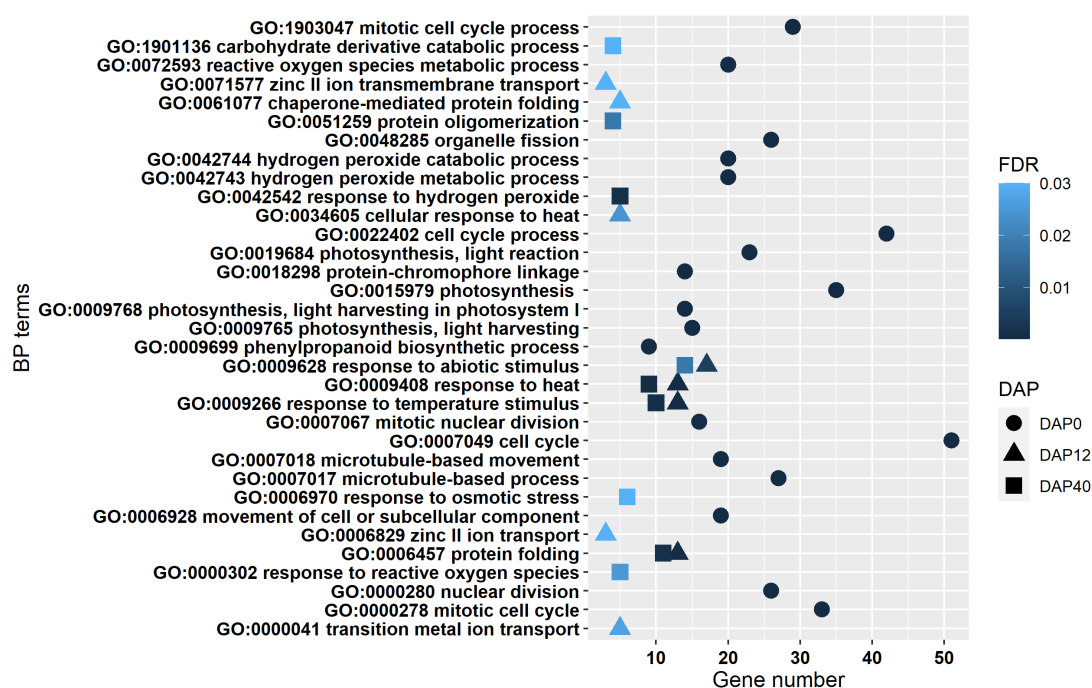
Supplementary Figure 2. The correlations of three biological replicates for eight genotypes at seven developmental stages. DAP0, DAP8, DAP10, DAP12, DAP20, DAP30, and DAP40 represent 0, 8, 10, 12, 20, 30, and 40 d after pollination, respectively. Error bars are represented by SD.



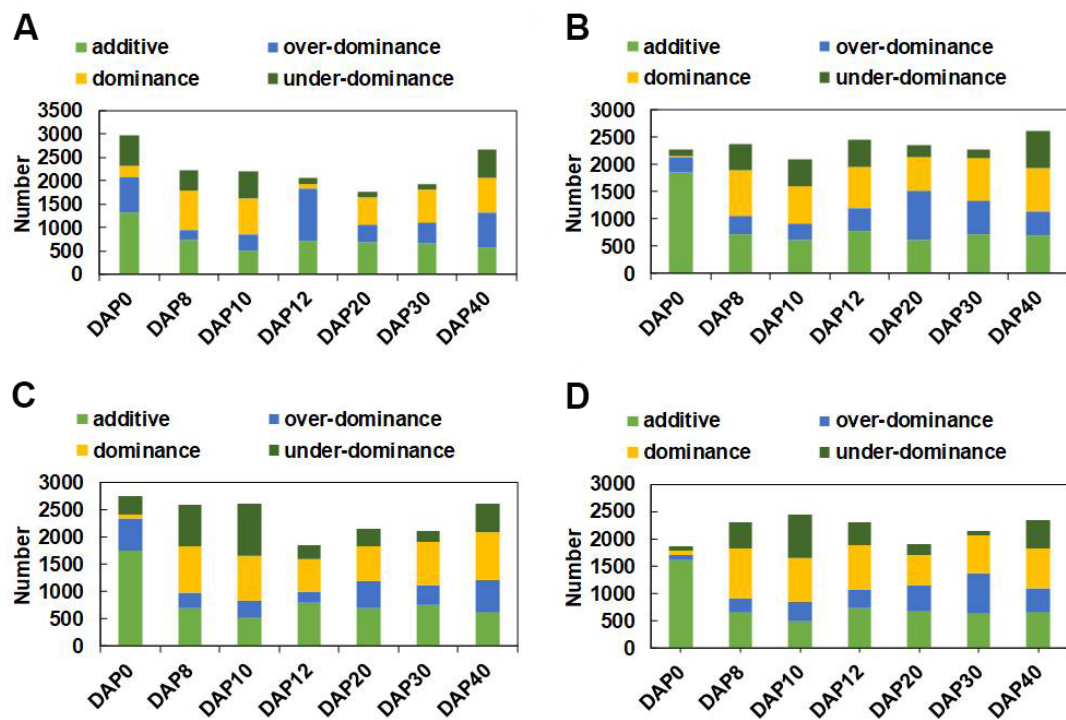
Supplementary Figure 3. Differentially expressed profiles. **(A)** The number of differentially expressed genes (DEGs) between two neighbouring stages. The previous stage is considered as CK. **(B)** The number of DEGs between Z58 and Z588. **(C)** The number of DEGs between C72 and ZH71. **(D)** The number of DEGs between F_1 and their respective parents (CK). **(E)** The number of up-regulated and down-regulated DEGs between ZD958 (CK) and ZD1002. 0, 8, 10, 12, 20, 30, and 40 denote 0–40 d after pollination (DAP). Z588, Zheng588; Z58, Zheng58; ZH71, ZhengH71; C72, Chang7-2; ZD958, Zhengdan958; ZD1002, Zhengdan1002.



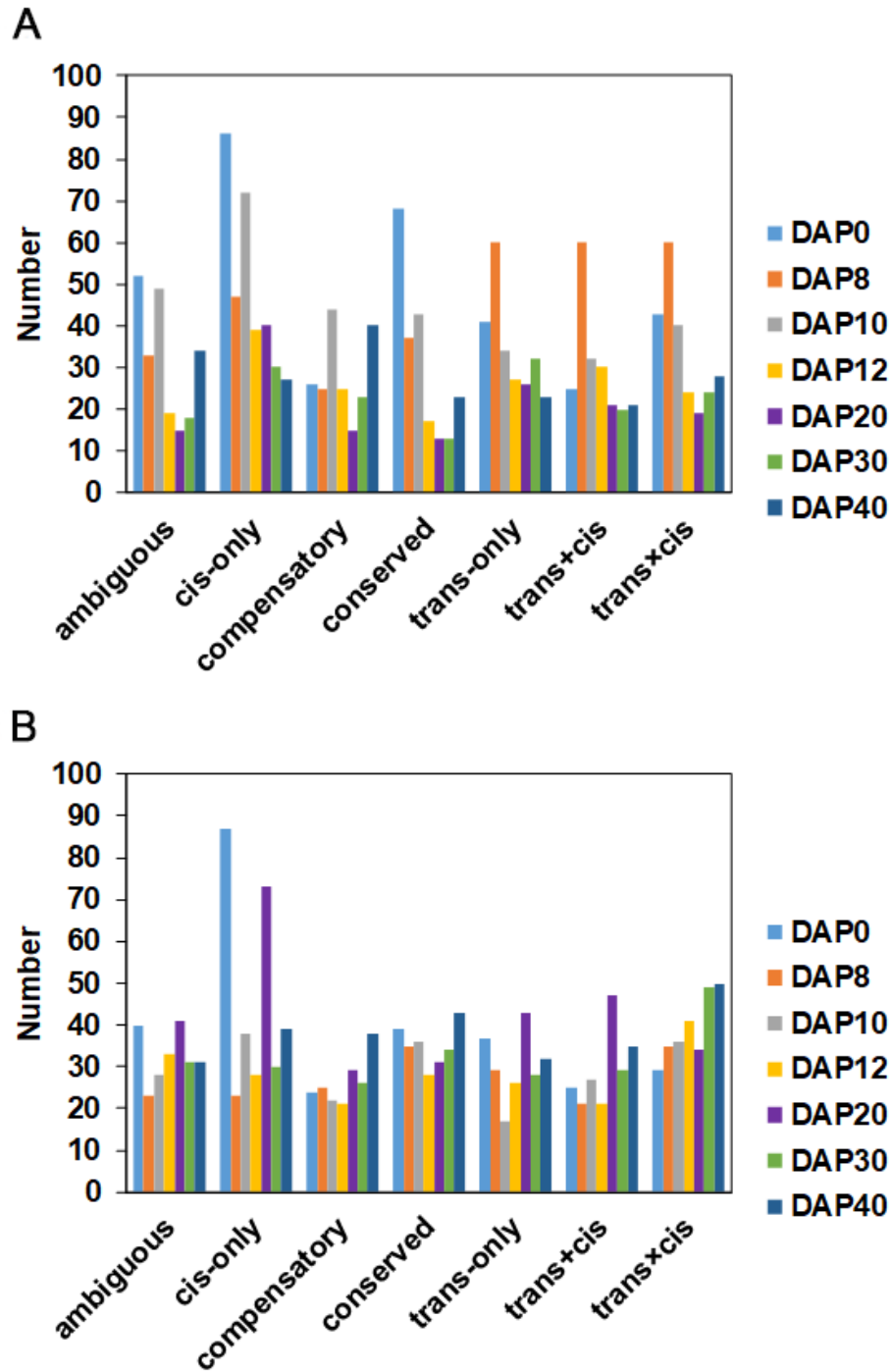
Supplementary Figure 4. The number of common and different SNPs between parents identified from DNA resequencing. Z588, Zheng588; Z58, Zheng58; ZH71, ZhengH71; C72, Chang7-2.



Supplementary Figure 5. Significant biological process (BP) terms of differentially expressed genes between Zhengdan1002 and Zhengdan958 at 0 d after pollination (DAP0), DAP12, and DAP40. Top20 terms are shown at DAP0 stage, and all significant BP terms are shown at DAP12 and DAP40 stages.



Supplementary Figure 6. Classification of additive and non-additive patterns in Zhengdan1002 (A), Zhengdan958 (B), Zheng588/Chang7-2 (C), and Zheng58/ZhengH71 (D) at seven developmental stages. DAP0, DAP8, DAP10, DAP12, DAP20, DAP30, and DAP40 represent 0, 8, 10, 12, 20, 30, and 40 d after pollination, respectively.



Supplementary Figure 7. Number of seven regulatory patterns at seven developmental stages in Zhengdan1002 (A) and Zhengdan958 (B). DAP0, DAP8, DAP10, DAP12, DAP20, DAP30, and DAP40 represent 0, 8, 10, 12, 20, 30, and 40 d after pollination, respectively.

A				
	FKW	DKW	TKL	TKW
MEblue	0.36	0.38	0.39	0.09
MEmidnightblue	0.17	0.17	0.13	-0.31
MEbrown	0.35	0.36	0.22	0.06
MEdarkorange	0.19	0.15	0.14	0.24
MElightgreen	0.31	0.31	0.37	0.45*
MEpurple	0.02	-0.14	0.27	0.15
MEdarkgrey	0.05	0.06	0.07	0.46*
MEsaddlebrown	-0.34	-0.52**	-0.10	0.08
MEcyan	-0.11	-0.13	-0.23	0.16
MEred	-0.24	-0.26	-0.39	-0.10
MEblack	0.10	0.08	-0.11	-0.04
MEdarkgreen	-0.09	-0.11	-0.27	-0.38
MEgrey	0.07	-0.08	-0.05	0.02

B				
	FKW	DKW	TKL	TKW
MEsalmon	-0.04	-0.10	0.09	-0.07
MEbrown	0.06	0.11	-0.09	-0.05
MEred	0.30	0.35	0.13	0.24
MEdarkorange	0.02	0.08	-0.07	-0.23
MEsteelblue	-0.27	-0.25	-0.25	-0.49*
MEdarkturquoise	0.28	0.27	0.22	0.48*
MElightyellow	0.09	0.09	0.04	0.29
MEroyalblue	0.13	0.04	0.23	0.09
MEdarkmagenta	0.01	-0.06	0.07	-0.01
MEdarkolivegreen	0.32	0.26	0.29	0.27
MEdarkgrey	-0.22	-0.19	-0.27	-0.25
MEblue	-0.39	-0.41	-0.30	-0.39
MEdarkred	-0.17	-0.20	-0.14	-0.02
MEgrey	0.42*	0.44*	0.48*	0.23

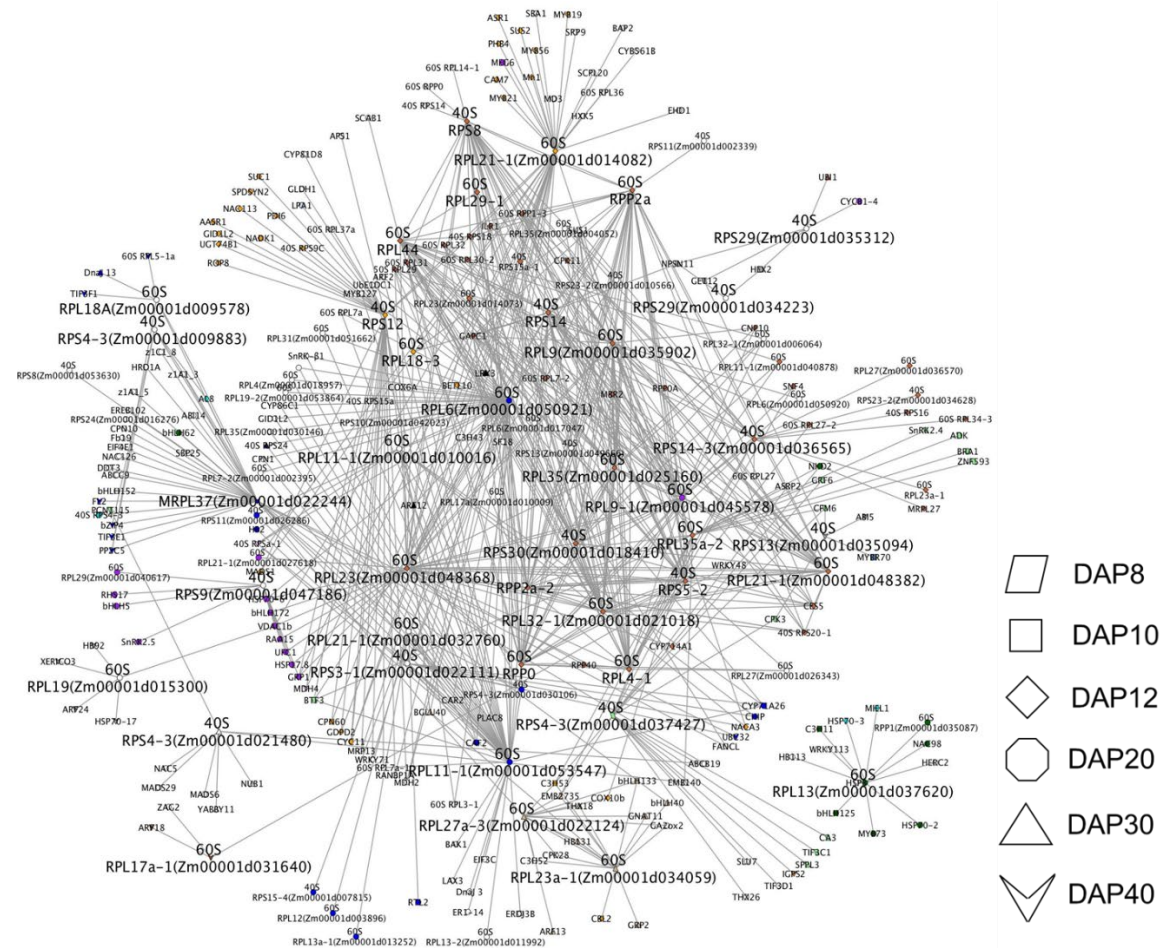
C				
	FKW	DKW	TKL	TKW
MEdarkolivegreen	0.62**	0.56**	0.84**	0.50*
MEfloralwhite	0.48*	0.39	0.60**	0.45*
MEdarkgreen	0.49*	0.44*	0.68**	0.36
MEdarkgrey	-0.04	-0.03	0.36	-0.20
MEcyan	0.26	0.23	0.42*	0.20
MEbrown4	-0.21	-0.25	-0.30	-0.10
MEsaddlebrown	0.28	0.14	0.31	0.32
MEblue	-0.30	-0.31	-0.21	-0.23
MEorange	-0.80**	-0.77**	-0.65**	-0.71**
MEgreen	-0.16	-0.18	0.15	-0.21
MEred	-0.33	-0.36	-0.10	-0.34
MElightsteelblue1	-0.45*	-0.27	-0.73**	-0.24
MEorangered4	-0.54**	-0.37	-0.72**	-0.28
MEsienna3	-0.85**	-0.81**	-0.74**	-0.81**
MEpink	-0.20	-0.23	-0.08	-0.24
MEyellowgreen	-0.29	-0.26	-0.21	-0.33
MEgrey	0.13	0.19	0.01	0.14

D				
	FKW	DKW	TKL	TKW
MElightyellow	-0.18	-0.06	-0.32	-0.28
MElightsteelblue1	0.28	0.45*	0.33	0.30
MEviolet	-0.04	0.23	-0.07	-0.09
MEdarkmagenta	-0.41*	-0.76**	-0.51*	-0.41*
MEsteelblue	0.07	-0.28	0.11	0.16
MEblue	-0.33	-0.72**	-0.32	-0.22
MEdarkgrey	0.07	-0.23	0.15	0.22
MEmidnightblue	0.35	0.29	0.31	0.29
MEdarkgreen	0.37	0.64**	0.35	0.27
MEdarkorange	0.06	0.21	-0.04	-0.08
MEpurple	0.60**	0.89**	0.67**	0.57
MEcyan	0.54**	0.55**	0.67**	0.64**
MEdarkturquoise	0.49*	0.52**	0.59**	0.53**
MEgrey	0.07	0.07	-0.04	-0.13

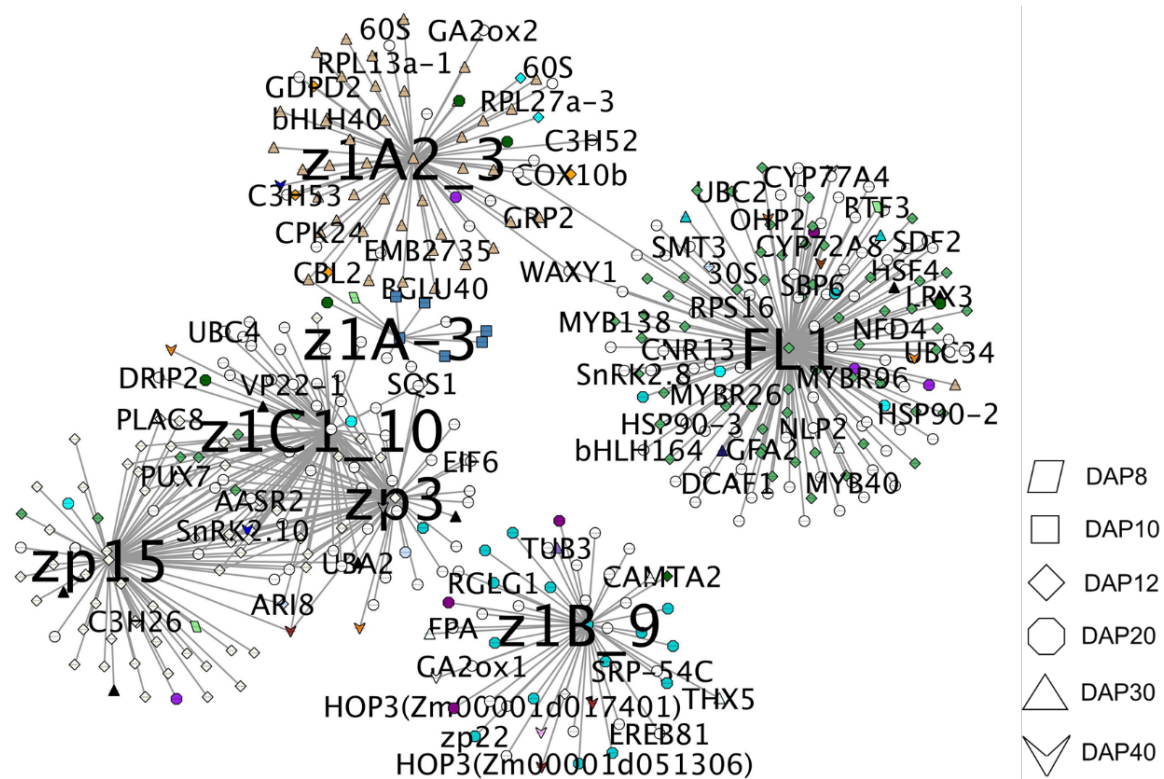
E				
	FKW	DKW	TKL	TKW
MElightsteelblue1	0.29	0.11	0.19	0.39
MEmediumpurple3	-0.58**	-0.30	-0.43*	-0.64**
MEmidnightblue	-0.46*	-0.25	-0.47*	-0.46*
MEorangered4	-0.32	-0.13	-0.19	-0.33
MEdarkorange	-0.04	0.27	0.23	-0.14
MEtan	0.16	0.36	0.46*	0.04
MEdarkturquoise	0.72**	0.70**	0.92**	0.60**
MElightcyan1	0.39	0.61**	0.71**	0.24
MEblack	0.57**	0.61**	0.86**	0.46*
MEdarkgreen	0.18	0.40*	0.63**	0.08
MEsienna3	0.42*	0.25	0.47*	0.37
MEblue	-0.21	-0.25	-0.40	-0.18
MEdarkolivegreen	0.33	0.33	0.35	0.25
MEivory	0.41*	0.39	0.33	0.38
MEgrey	0.11	0.15	0.07	0.14

F				
	FKW	DKW	TKL	TKW
MEdarkmagenta	-0.38	-0.23	-0.24	0.03
MEdarkolivegreen	-0.35	0.01	-0.09	-0.18
MEsaddlebrown	-0.47*	-0.59**	-0.53**	0.10
MEbrown	-0.81**	-0.62**	-0.73**	-0.39
MEgrey60	-0.75**	-0.84**	-0.90**	-0.38
MEplum1	-0.74**	-0.87**	-0.88**	-0.18
MEblue	-0.25	-0.55**	-0.52**	-0.14
MEdarkgreen	0.38	0.01	0.15	0.39
MEdarkgrey	-0.16	-0.44*	-0.35	0.14
MElightsteelblue1	0.23	0.02	0.12	0.37
MEdarkorange	0.72**	0.58**	0.70**	0.56**
MEdarkturquoise	0.19	0.20	0.26	0.35
MEgrey	-0.11	-0.08	-0.21	-0.18

Supplementary Figure 8. Module-trait relationship of the module eigengene correlation with seed size and weight at different development stages using WGCNA. **(A):** 8 d after pollination (DAP8). **(B):** DAP10. **(C):** DAP12. **(D):** DAP20. **(E):** DAP30. **(F):** DAP40. Modules are represented by colors. Shown are correlation values, and * and ** represent 0.05 and 0.01 significant level, respectively. FKW, 100-fresh kernel weight; DKW, 100-dry kernel weight; TKL, ten-kernel length; TKW, ten-kernel width.



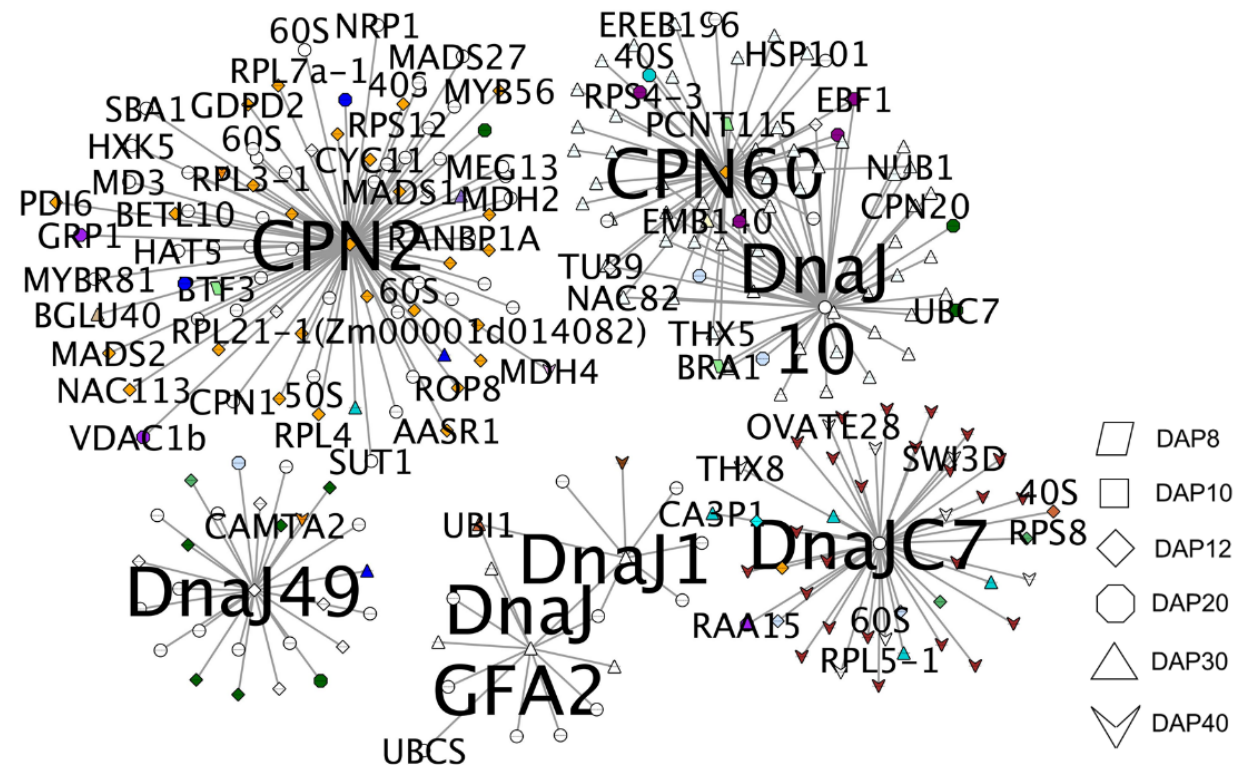
Supplementary Figure 10. Gene networks of hub genes associated with ribosomal proteins at DAP8–40 stages. Top 10% genes with annotations are shown according to their weight value with these hub genes. Different colors represent different module. Circle and geometric figures with no colors denote genes that appeared more than two stages or modules. DAP8–40 represents 8–40 d after pollination, respectively.



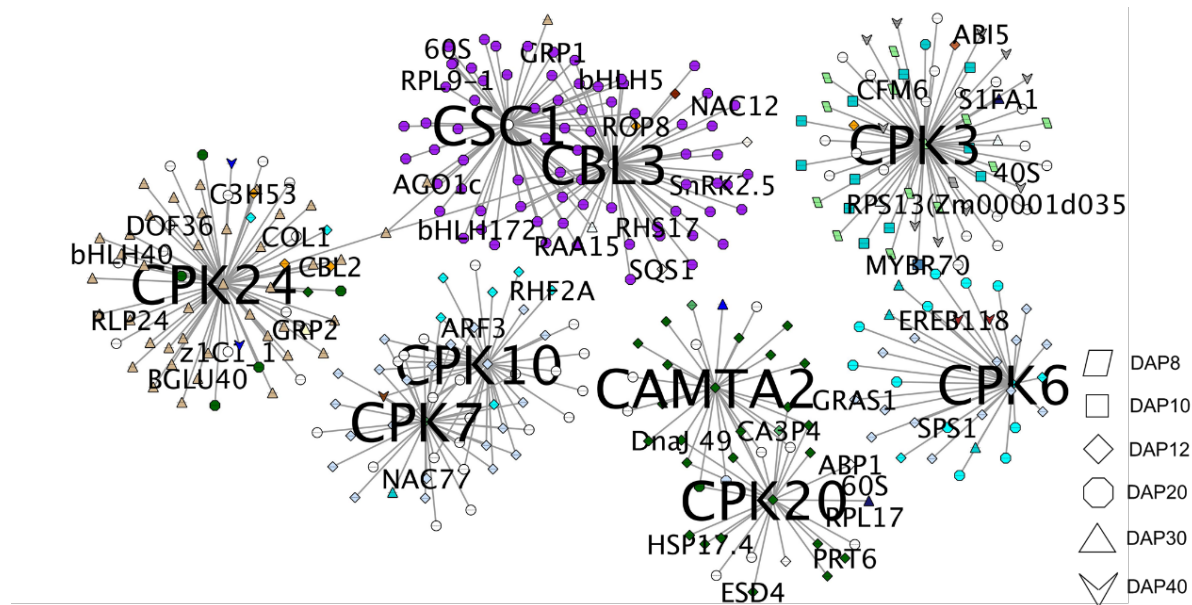
Supplementary Figure 11. Gene networks of hub zein genes at DAP8–40 stages. Top 10% of genes with weight value ≥ 0.1 are shown according to their weight value with these hub genes. Different colors represent different modules. Circle and geometric figures with no colors denote genes that appear in more than two stages or modules. DAP8–40 represents 8–40 d after pollination.



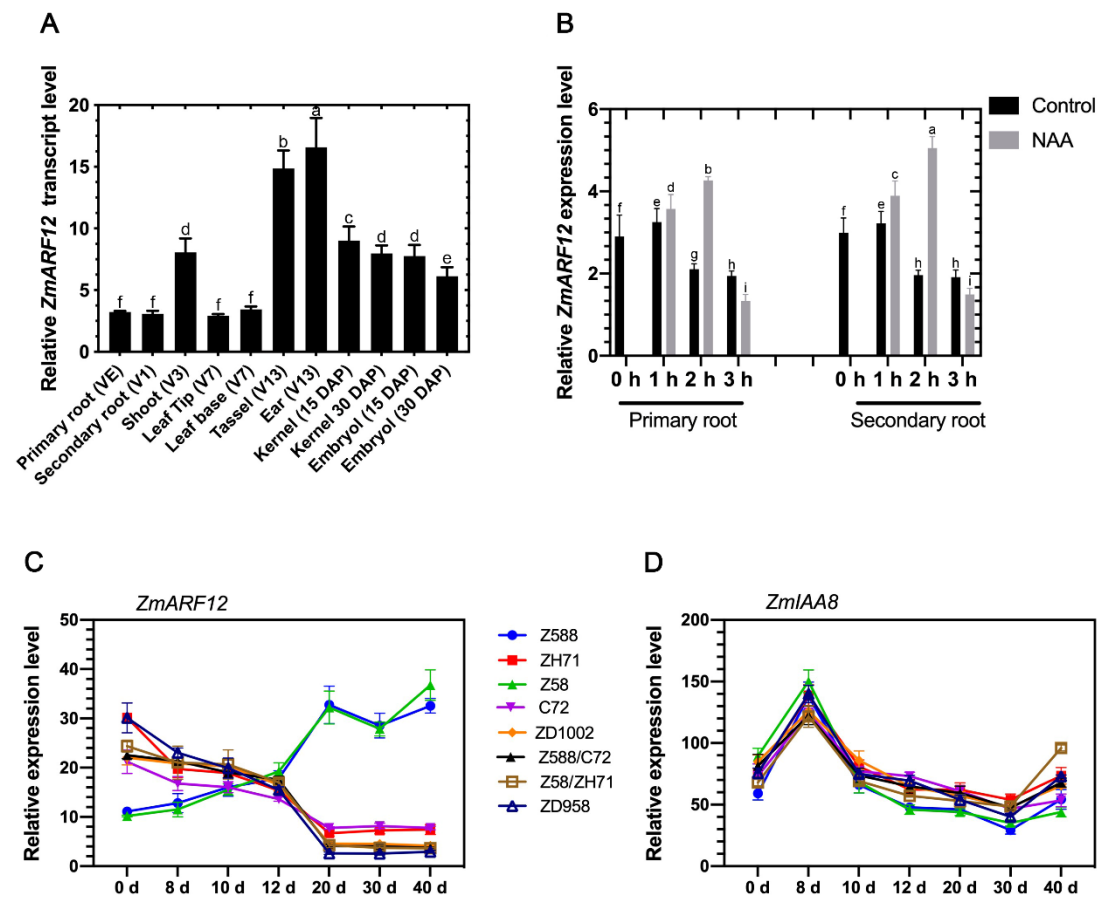
Supplementary Figure 12. Gene networks of hub genes associated with ubiquitin proteins at DAP8–40 stages. Top 10% of genes with weight value ≥ 0.1 are shown according their weight value with these hub genes. Different colors represent different module. Circle and geometric figures with no colors denote genes are appeared more than two stages or modules. DAP8–40 represents 8–40 d after pollination.



Supplementary Figure 13. Gene networks of hub genes associated with chaperone proteins at DAP8–40 stages. Top 10% of genes with weight value ≥ 0.1 are shown according their weight value with these hub genes. Different colors represent different module. Circle and geometric figures with no colors denote genes are appeared more than two stages or modules. DAP8–40 represents 8–40 d after pollination.

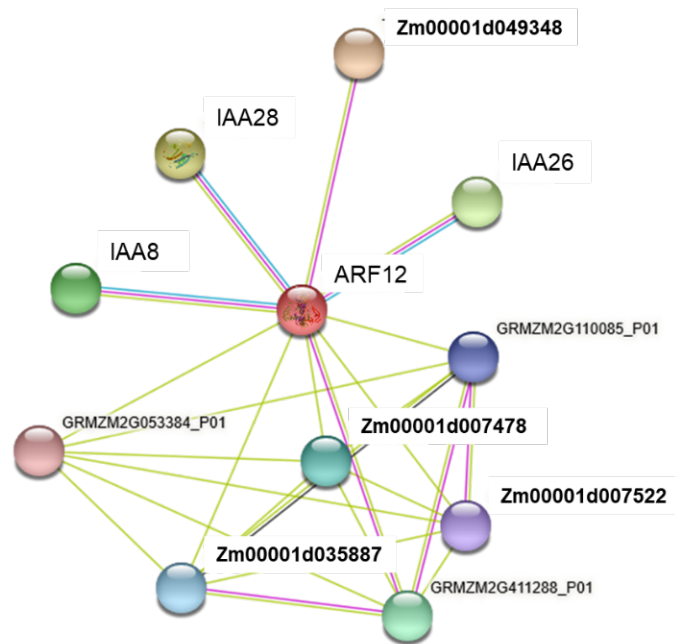


Supplementary Figure 14. Gene networks of hub genes associated with calcium-dependent protein kinases at DAP8–40 stages. Top 10% of genes with weight value ≥ 0.1 are shown according their weight value with these hub genes. Different colors represent different module. Circle and geometric figures with no colors denote genes are appeared more than two stages or modules. DAP8-40 represents 8–40 d after pollination.



Supplementary Figure 15. The expression levels of *ZmARF12* and its potential interactor in different tissues, under auxin stimuli, and different time points post fertilization. **(A)** Real-time RT-PCR analysis of *ZmARF12* in different tissues. For each sample, the primary root and secondary root was cut from seedlings that had germinated for 8 d (vegetative emergency, VE) and V1 stage, respectively; the shoots were collected from plants at the V3 collar stage; the

leaf tip and leaf base were cut from plants at the V7 growth stage; and the tassel and ear were cut from plants at the V13 stage. Kernels were peeled off the ears at 15 d after pollination (DAP15) and DAP30, and the embryos were excised from the ears at 15 DAP and 30 DAP. **(B)** Fold change of *ZmARF12* conditioning exogenous auxin treatment. The primary and lateral roots of 8-day-old maize seedlings were isolated after 0 h, 1 h, 2 h and 3 h of incubation in 5 μ M α NAA and Hoagland's solution control and subjected to real-time PCR analysis. **(C)** and **(D)** The expression profiles of *ZmARF12* and its potential interacting factor *ZmIAA8* during ear fertilization. The kernels of four hybrids (ZD1002, Zhengdan1002; Z588/C72, Zheng588/Chang7-2; Z58/ZH71, Zheng58/ZhengH71; ZD958, Zhengdan958) and their parental inbred lines (Z588, Zheng588; ZH71, ZhengH71; Z58, Zheng58; C72, Chang7-2) were harvested 0 d, 8 d, 10 d, 12 d, 20 d, 30 d, and 40 d after pollination and used for real-time RT-PCR. Relative mRNA abundance of each tested gene was averaged for triplicate reactions and the values were normalized according to the *Ct* of the internal control of ubiquitin gene by using the $2^{-\Delta\Delta C_t}$ method. All bars represent means $\pm$ SD ($n = 6$ repeats). Different letters indicate significant difference ($P < 0.05$) as determined by Tukey-Kramer test.



Supplementary Figure 16. Protein-protein interaction networks of ARF12 revealed by String database. The protein-protein interaction enrichment *P*-value was 5.21E-05.

ZmARF11 1 AGCAGCAGCTCACGAAACAGGAGCGTCATAAAGACATGGTCGTCGCAGGATAGCCTCAGACCCAGCGACGCAGCGGCAGCGACCCAGGAAGCAACAGCGA
 ZmARF12 1 -----
 ZmARF23 1 -----
 ZmARF24 1 -----
 ZmARF26 1 -- CGTAGTCCATAGTACTCCATTTGCA AATTGCATTGCCACACC -- TCGGCTCATCCCCACCT CACCTCGGCCTCACTTCACAAGTTCACATCAC

 ZmARF11 101 CCGGCATCGATCGCGGCAGCCGAGGCGGGGGACGGGAGGAGGGAGGGAGCGCTCGCCGAGGAGCAGAGCGGCA CGGCATGGGGTCCTGAGTGACTGA
 ZmARF12 1 ----- CTTCCCAACACTTCCCTCCCTTC -- CCGCTACAGCAAGCCGCCCAGCCATTATGGCCATCACCC
 ZmARF23 1 ----- CGCAGGGGCGTGGGGGACGGGACTGGCATTTGCACCTGCCAGCCGCGGGAGCGGCCCTTCGGGGGGA -----
 ZmARF24 1 --- TATAGGCCTCGGCCCCCATTCATGGCCATTACCAAGATGTGTACCCACACACCGCCCTCTCCGATGCTGCCTCCCTCATG ATAACCCCTCTCC
 ZmARF26 91 --- GAAACAGGAGCGTCATAAAGACATGGGCGTCGCAGGGTAGCCTCAGACGGTCAGACCAGTGACGCAGCGGCAGCGGCAGCGGGCATGGGGTC-----

 ZmARF11 200 CTGACTGACGACTGAGTGTCTGACTGAGAGGAGATGGCTGGAGCGCGACGGCCCCG AGCCAT TAATGGGGCGTCATCTCTCTCGT CCTCCCACT
 ZmARF12 67 ACCA----- CCAATGTGTGCGCGCCA CTCCACCTCCACCTCCACCCCACTCCTCTCACCAGCAACCTAAACCC GCCTCCCTCGCTCCTCACCCG
 ZmARF23 68 ----- CAAGCGCATTAATGCCACTTGCCGCTCCGCGGATTTAACTCCCCGC CTCTAT C ----- GCCCTCACCT --- TCAC CTGTACGCC
 ZmARF24 96 CTGGTGGTTG TTCTTTGCTTGTGTCG TGCAAGCTCCACC CCACCTCCTCATTAATCAC TTGCTAGCTCCCTGCTCCCTCCCGGCTCCCGCT
 ZmARF26 183 ----- CTGAGTGACCACTTGCGAAGGAGATGGCTGGAGCGCGACGGCCCCG AGCCAT TAATGGGGTCCTCATCTCTCTCC CCTCCT CG

 ZmARF11 297 CCTCGCTCCCCCCCGCA GGTCGCGGTCTGGCTCTTTTAAACGGGCTTGTCTTGAGCGGGGCGAAGCGCGAACCTCACGGGCGCCGAACACGAA
 ZmARF12 155 CTCCCTGTCCGTCCATCCATCGCTCTGCGCGCTCTGTGTCGGCTTTG CTCCAGCTGCGG CGACGGGGGCCATG ----- GCGGG
 ZmARF23 145 GTCCCGCTTCGCTTCGAGAGGTGCTGCTGCTGCTGCCATCAAC GTTCCCTCGCTGTTGAGGTAGACCC
 ZmARF24 192 CCCCCCTCTCTGTC TTGCGGCCCCCGCAGCAGCCATGCGGGGATCGACCTCAAGACACCGTGGAGGAGGACGAG ----- GAGGA
 ZmARF26 269 CCTCCTCCTCCGCCGGCTCGCGGACGCGGTCTGGCTCCGCTTTTAAACGGGCTTCTCCGGAGCGGGCG

 ZmARF11 396 CCGGAACCTTAGTGGTGGTGGTGGT --- GGCGCGCCCATGGGCATCGACCTCAACATGGCGGACGGCGAGAGCCAGAGCGCGCCCGCGCGCGG
 ZmARF12 235 CATCGACCTCAACACCGT --- GAGGAGGAGGACGAGGAG GAGCGGAGGCGCTGCCCTTTGCC CGG ACCCG GTGGCGG TGGCGCG
 ZmARF23 217 ACCGACCCCCAGTACTAGTCTGGGAC --- AGAG --- ATGGGCATTGATCTCAACGCCGTGGG --- GGAGGACGACCCCGCGGGCGCGG
 ZmARF24 273 GCGGAGCCCGGCAACGCCCTGCTCCAGCAGAGCGGACAGCTCCGCGGCCAGCTTCCGCGCGCGCGCGCA ACCAGCGAGGCGGAGCGCGCGG
 ZmARF26 337 CCGGAACCTTAGTGTGCTGGTGGCAAGCGGCGCGCCCATGGGCATCGATCTCAACATGGTGGACGGCGAGGGCCAGAGCGCGCCCGCGCGCGGTGA

 ZmARF11 492 TGTGCCGGGAGCTGTGGCAGCGTGCAGGGGCCCCGTGCTTCCGCTACCGCGCGGGGAGCCTGCTCGTGTACCTGCCGCAAGGCCACCTAGCCCGGC
 ZmARF12 318 TGTGCCGGGAGCTGTGGCAGCGTGCAGGGGCCCCGTCCCGCGCGTGGCGCGGAAGGGCAGCGCGCTCGTGTACCTGCCGAGGGGCCACCTCGAGCACAT
 ZmARF23 295 TGTGCCGGGAGCTGTGGCAGCGTGCAGGGGCCCCGTGAGTGGCGCTGCCGCGCGGGGAGCGCGTGTGTACCTGCCAGCCACCTCGCGCGGG
 ZmARF24 371 TGTGCCCGAGCTGTGGCAGCGTGCAGCGGGCCCCGTCCCGCGCTGCCGAGGAAAGGAGCGCTGCTGTGTACCTCCCGCAGGGACACATCGAGCACCT
 ZmARF26 437 CGTGCCGGGAGCTGTGGCAGCGTGCAGGGGCCCCGTGCTTCCGCTACCGCGCGGGGAGCCTGCTCGTGTACCTGCCGAGGGGCCACCTGGCGCGGC

ZmARF11 592 CGGCGGCG ----- GCAACGTCGCTGTGGAAC ----- TGCCGCCGCACGTGGCTGCGCGCTCGCGATGTCGAGTTATGCGCGGAT
 ZmARF12 418 CGGCGGCGACGCGGC GC GAGGAGCAGCAGTTTGGCGGT ----- GCCGCCGCACGTGCTTGCCGCTCGTCGACGTACCCCTCCACGCGGAC
 ZmARF23 395 CGGCTGCGACCGGTGG ----- TGGGGTGTGGCGCGCGGCCCGCGCGCGGTGCCGCCGCACGTGGTGTGTGCGGTGCTCGACGTGAGCTACGCGCGGAT
 ZmARF24 471 CGGCGACGCGCGCGCGCGCGGAGGCCGCGCGCGCGCGCTCGCCC ----- TGCCGCCCCACGTCTTTTGCCGCTCGTCGACGTCACTCTCATGCGGAC
 ZmARF26 537 GGGCGGCG ----- GGAACGTCGCTGCGGAAC ----- TGCCGCCGCACGTGGTGTGCCGCTCGCGATGTCGAGCTATGCGCGGAT

 ZmARF11 668 GCGGCGACGACGAGGTGTACGCGCGGCTGGCGCTGGTCCGGAGGCGAGG --- CATTTGGGAGAAATCTGCGTGGTGGTGGAGTCGATGGG --- GACG
 ZmARF12 506 GCGGCGACAGACGAGGTGTACGCGCGGCTGTGCTGCTGCTGCCGAGGACGAGGACGCGGAGAACGGGCGCAGGCGCAGGCGCGGCTCCGGAGGACGAGG
 ZmARF23 489 GCGGCGACGACGAGGTGTACGCGCGGCTTGCGCTGGTGGCGATGGATACGA --- TGTTTGGCCGAAACATCAATGATGGTGAAACCTGAAGAG --- AAGA
 ZmARF24 568 GCGTCCACGACGAGGTGTACGCGCAGCTGCGCTCTGCTGCCGAGAACGAGGATGTCGCGAGGCGGCTGCGCGGACGGTCCGAGGACGCGCAGCGCGGAGG
 ZmARF26 613 GCGGCGACGACGAGGTGTGCGCGCGGCTGGCGCTGGTTGCCGAGGCGAGG --- CATTCGGGAGCAATCTGGCGGCTGGTGGAGTTGAAGGG --- GACG

 ZmARF11 762 AT ----- GACATGGAGGATTTTTCATGTTGAAAGGAAGTCC --- CGGATGTTGCACATGTTCTGCAAACGCTTACAGCCTCTGACACAAGCACACATGG
 ZmARF12 606 ACCGCCGCGACGGCGAGGACGGCGCGCCATGAGGCGCTCGCACGGAAGCCGCACATGTTCTGCAAGACGCTCACGGCATCCGATACCAGCACGCAACGG
 ZmARF23 583 AT ----- GGCGAGGAAGAGGATGGCGACGGAGAAAGAAAG --- CACGCATCACACATGTTCTGCAAGACACTCACAGCTTCTGATACCAGCACACATGG
 ZmARF24 668 AC ----- GGCGACGAAGGGGAAACCGTGAAAGCAGCGGTTCTCGCGGATGCCGCACATGTTCTGCAAGACGCTCACGGCCTCCGACACCAGCACGCAACGG
 ZmARF26 707 AT ----- GGCATGGAAGATTTTCGATGCTGAAAGGAAGTCC --- CGGATGCTGCACATGTTCTGCAAACGCTTACGGCCTCTGACACAAGCACGCATGG

 ZmARF11 853 AGGCCTTCTCTGTTCCTCGTCGTGCTGCTGAGGACTGTTCCTCCGCGCTCTGGATTATAATCAGCTCAGGCCCTTCTCAAGAGCTGCTTGCCAAGGATTTGCAAT
 ZmARF12 706 CGGTCTTCTCAGTCCGCGCGCGCGCGCGGAGGACTGTTCCTCCGCGCGCTGGACTACAGCCAGCAGAGGCCGCTCTCAGGAGCTCTGTGGCCAAGGATCTACAC
 ZmARF23 674 GGGATTTCTCTGTTCCACGCGGAGCTGCAGAGGACTGCTTCCACCATTTGGACTATGACAGCTTAGGCCCTTCCCAAGAGCTTATTTGCCAAGGATTTGCAAT
 ZmARF24 762 CGGCTTCTCCGTGCCACGCGCGCGCGCGGAGGACTGTTCCTCCGCGCTCTGGACTACAGCCAGCAGCGACCGTCCGAGGAGCTTGTGGCCAAGGATTTGCAC
 ZmARF26 798 AGGCCTTCTCTGTTCCTCGCCGTGCTGCTGAGGACTGTTCCTCCGCGCTCTGGATTATAATCAGCTCAGGCCCTTCTCAAGAGCTGCTTGCCAAGGATTTGCAAT

 ZmARF11 953 GGAGCCAAAGTGGAAATTTTCGTCATATATATAGGGGTCAGCCTCGTAGGCATCTCTTGACTACTGGATGGAGTTCAATTTGTCAATAAAAGAAACTGCTTTT
 ZmARF12 806 GGCACGGAGTGGAAAGTTCCGSCATATCTATCGAGGTGAGCCAGGAGCATCTCTTAACCACTGGATGGAGTGCATTTTGTAAATAGGAAGAACTCATTTT
 ZmARF23 774 GGCATGAAATGGAGGTTCCGTCATATCTATAGAGGTCAACCTCGAAGGCATCTCTGACAACTGGATGGAGTTCAATTTATCAATAAGAAGAAACTAGTCT
 ZmARF24 862 GGAACCFAGTGGAGGTTCCGCCACATTTATCGAGGCGAGCCCGCAGACACCTTTTAACCACTGGATGGAGTGCCTTTTGTCAAAGAAGAACTGTGCT
 ZmARF26 898 GGAGCCAAAGTGGAAAGTTTCGTCATATATATAGGGGTCAGCCTCGTAGGCATCTCTTGACTACTGGATGGAGTTCAATTTGTCAATAAAAGAAACTGCTTTT

 ZmARF11 1053 CTGGGGATGCGGTCTTATTTCTCCGAGGTGATGATGGTGAACTAAGGCTGGGCGTACGGAGGGCCATTTCAGCTTAAAAATGAGGCCCTTTTTTGACGATTT
 ZmARF12 906 CTGGAGATGCAGTTCTCTTCCCTCGAGGCGAAGATGGAGTGCTTCGACTGGGAGTGCGCCGAGCAGCCAGCTAAAAATGTTAACTCCTATTTCTTGCAACC
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 ZmARF26 998 CAGGGGATGCTGTCTTATTTCTCCGAGGTGATGACGGTGAACTAAGGCTGGGTGTGCGGAGGCTATTTCAGCTTAAAAATGAGGCCCTTTTTTGAAGATTT

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ZmARF24	1062	TTATAACCAGTGCTTAAATCTTGGTTCACTACCTAATGTTTGCACATGCTGTGGCCACAAAAGTGTTTCCACATCTACTACAACCCAGATTAAGCCAA
ZmARF26	1098	CAATAGTGCACGACAAAACGGCATTTCTTTGACGGCTGTAGCTGATTCTTGAAGAACAGAAGTGTTTTTCACATTTCTTACAATCCAAGAGCTACTGCT
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ZmARF24	1502	-----AAATG-----GAAGCGGTCTGCTCTGATTTTCCGGAATCTGCCCAATTCCACAAGGTCTTGCAAGGT
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 ZmARF23 1770 GTTCGACCATTGTGATTATGTGCAGAG-----ATCAGATGCAACTCAAGGATACGCTCTCCAGCAGTTTAAATCTGCCAGC-----
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 ZmARF24 1954 CCAATCTCAATCCCTCATCCCCACCATCTGTCCGTGATGTTTCAACGAGGTGATCCAAAGATGTCCCATTTGAAATTTGGGCATTTCCACGTGAATAAGAAAG
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 ZmARF23 2128 GTTTCTCCCTGACTGAGAAGATCCTTGGAAAGGATGGTGGTGGTGTAAGGAAGGGAACTACGAAGTGGACCGTCAAACTCCCAGGGTGCTA-GACTTGT
 ZmARF24 2240 GCATATCTTTGACCGAGAAGGTTCCAGCAATGAAGAAAAAGGGCTGTGGTGACATCAACACCAACTATCCATCCCCCTTCCTGTCTTTGAAGCAACAAGT
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 ZmARF11 2430 TCGGGTACAACCTGCTCAGCCCCAAGTGCTGCTCTTCAGCTCTGTGTGCTGCC---CCCTTTTGAATGTGATGCTACTTCAATAACGCTGCTGAGTAT-T
 ZmARF12 2263 GCCAAAATCGCTAGGCAGCTGTTGGGCCACTGTTCACGAGCAAGGCCCTGTTGT-TGGCAGGGTGGTTGACGCTCTCGGCGACAGATATG-TGATCTG--
 ZmARF23 2227 TTGGGCACG---GTTCTACGCC---TGGAGCTCTGCATGCTCTCTGTGCTGCT---CCCTTGGGAATATGATGCTGTT-----CTGCCTAGTTTT--
 ZmARF24 2340 GCCGAAATCGCTGGGCAACAGCTGTGCCACCGTTCATGAGCAGAGGCCTGTGTTGT-TGCTAGGGTGATTGACGTTTCAACAGTTGGATATGATGATCTG--
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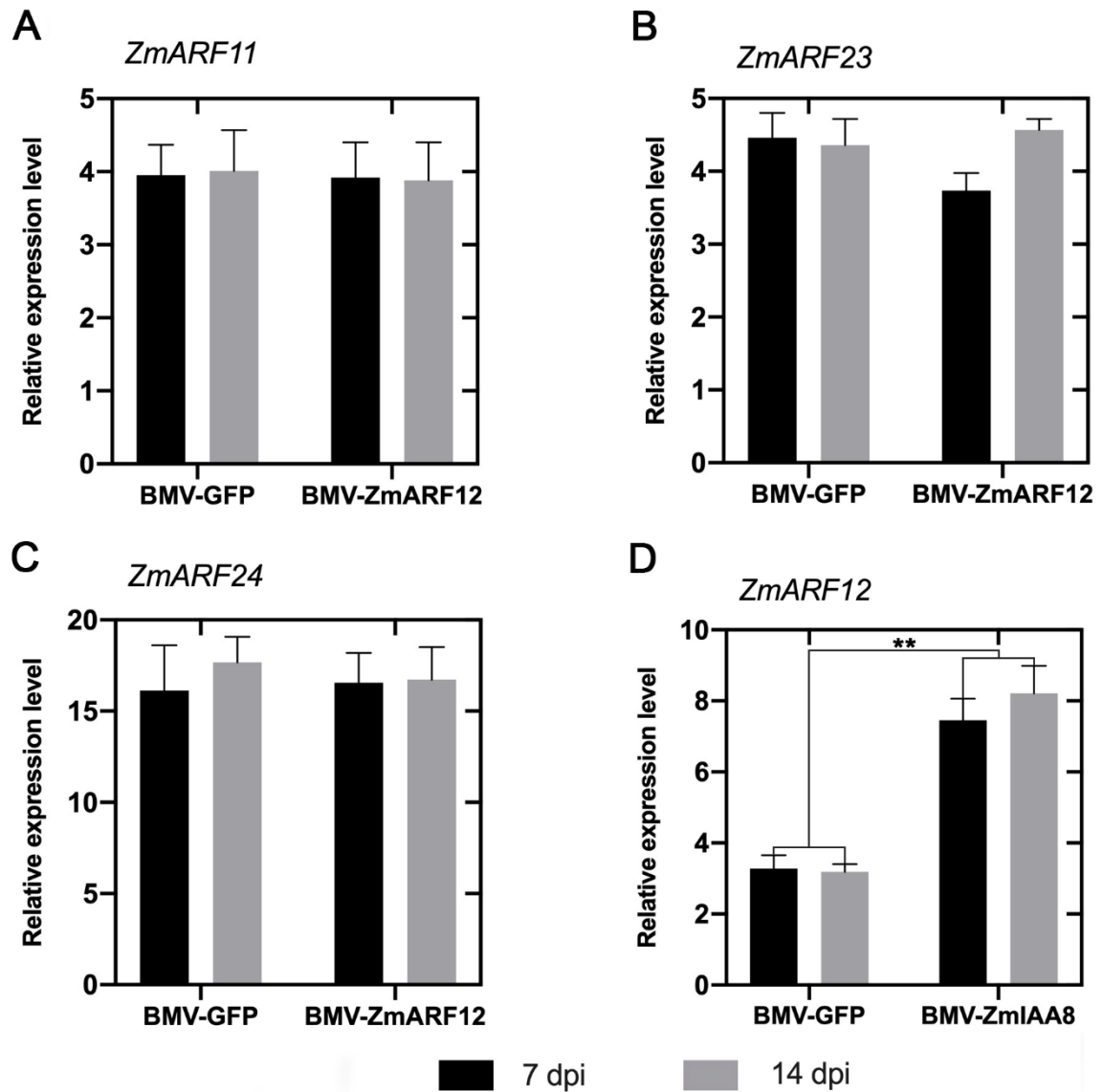
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 ZmARF23 2306 ---TAC---AACAGTTAGATTTTATGTAATCCTTCAGCCATTTTCATCGCGTTGTACTTTGACCAATATGT---CCA---CGGTATGATTTCCAGTT
 ZmARF24 2435 ---ATGTATT---GGAAACCTGTCTGGAGGCTGTGTTGCGTAGTGTGGACA-GTGTGCGTTTGATGGTTCCG---TATCGTGAAGACGGGAATTTGATT
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 ZmARF11 2621 AAGCAGTCAATTTGCACAAGTAAACAAAGGATCGTTGATGATCCACTTCTCGCCATGCCCTCACCTATCGCTAAGA-TATTGTAAATTAGTCTTAGGATACG
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 ZmARF23 2390 T-TAAATTGTATGCTGATGCTA-CATATCCCTCTTTGAGATCCA-TGCATGAGAATTCTGGCAGAAATGAACAGAGGTA---AATTGATGTCCAG-----
 ZmARF24 2525 GAGGATCTGGCCAGATTTGTATCCTAGTTGTAGCTGTGTAGAGCACTTTGTATGACAACCGTGAGTGCTCCGTGT-TATCAGCAGTAGTTGCTGCTCACA
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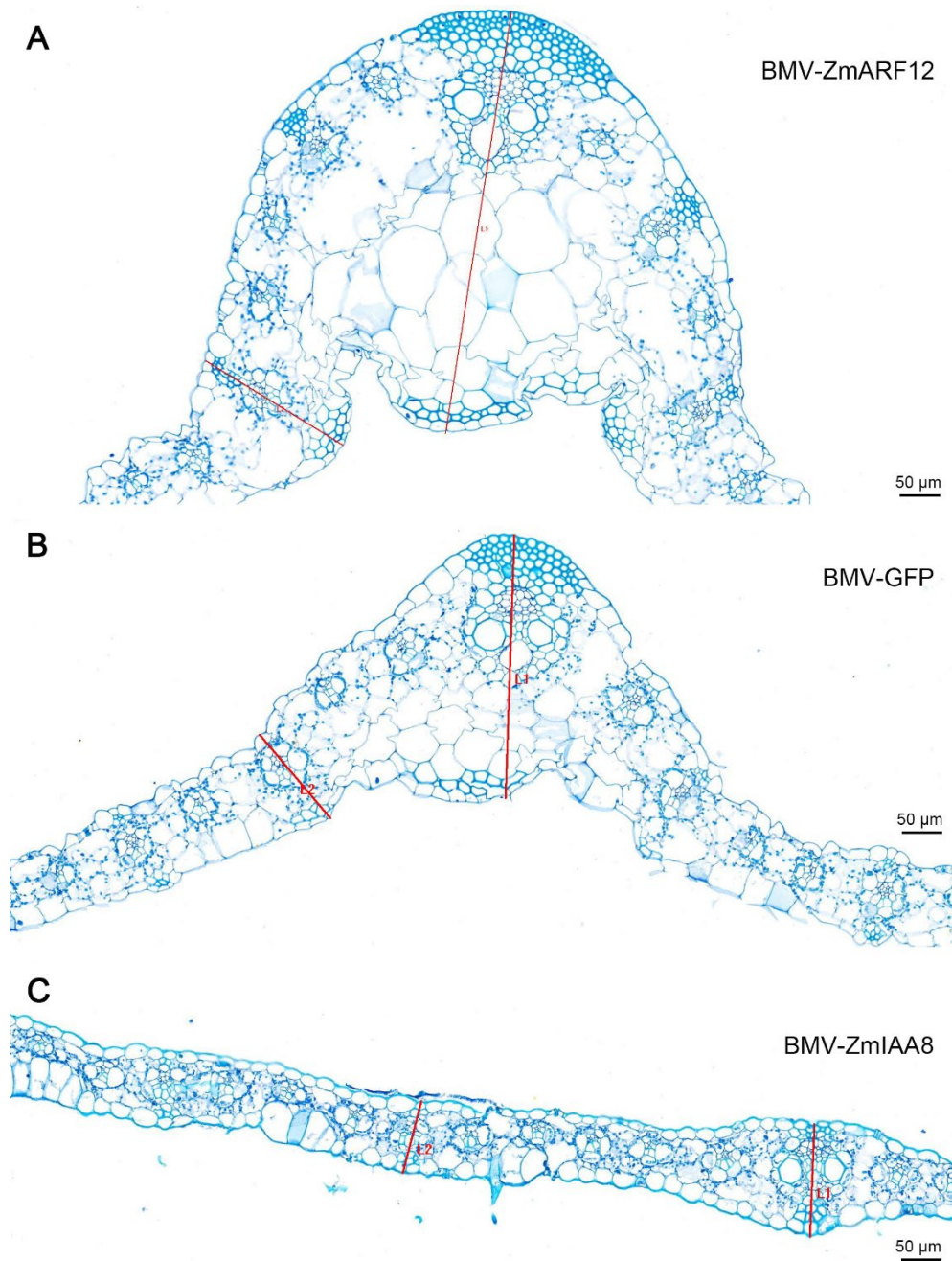
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 ZmARF23 2476 -----
 ZmARF24 2623 ACTTGCCCTCTATGTTTATAATCTGTATGCCATGTGAGACCATTATAGAGGGTTTGTGTTGCTTGGCATAGTTCTAGACTTAAAGCATTATTTATGAGAAC
 ZmARF26 2734 CAGAGACACCACATTG-TAA-----CTTATGTGATGATCCTTCAGAACTGTTGTGCGATGAAGCTAACAATTTGCTCTAAAAGTACTTTGCTTGC-

ZmARF11	2819	GATTTTATGATTCATGTGGGAGGTTTGTCTAGCTCAGCTTTTAAATGTACTGGTTATGTATCTTTAAATCAGCTGCTGTACGACTTTTTTTTTTAGCTC-CAAG
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ZmARF23	2476	-----
ZmARF24	2723	AAATTTTG-----CTCTGCACCGTATCTTTCTTACTTTCAAGTTGGCAACGGATTACGGTGGAGGAGATGATCTGAGAGGTTAGTTG
ZmARF26	2823	-----TCTAAAAGTACCGGCTATGTATATTTAAATCAGCACCTGTATCAGTTTTTTTTTAGCCCTCACAAG
ZmARF11	2918	CCCTGGTTGCAGTCGCCTAGGCCGTGTGATTGTATCAGTATGTAAGACATGCTATATTTTAATATTCTTATCGATATTTATTCTGATGC-----
ZmARF12	2701	-----
ZmARF23	2476	-----
ZmARF24	2805	TGCGACGTATTAATGGTGTTACATATATTATGCTTAGGAGCATTTCTGCCAGCTCATTTATCATATACATGTCAGCACTTGATTTGTTAAGTGTAGTTAGT
ZmARF26	2888	CCCTGGTTGCAGTCGACCTAGGCCGTGTGATTGTATTAGTATGCTAT-CTTTTAAACTGT---CGCTTATGAGTCTTTATTCTAGTGCATTGTGTGAAT
ZmARF11	3006	-----
ZmARF12	2701	-----
ZmARF23	2476	-----
ZmARF24	2905	AGC-----
ZmARF26	2983	ACTCTGTTTCATCGCATGCAAGTCTTGTCTTCTGTTTCTGTTGGCTTGGTAGGAGATACTCTGATTTTATAACATGTCAGATTTTTTATTGGTCAATTCAAC
ZmARF11	3006	-----
ZmARF12	2701	-----
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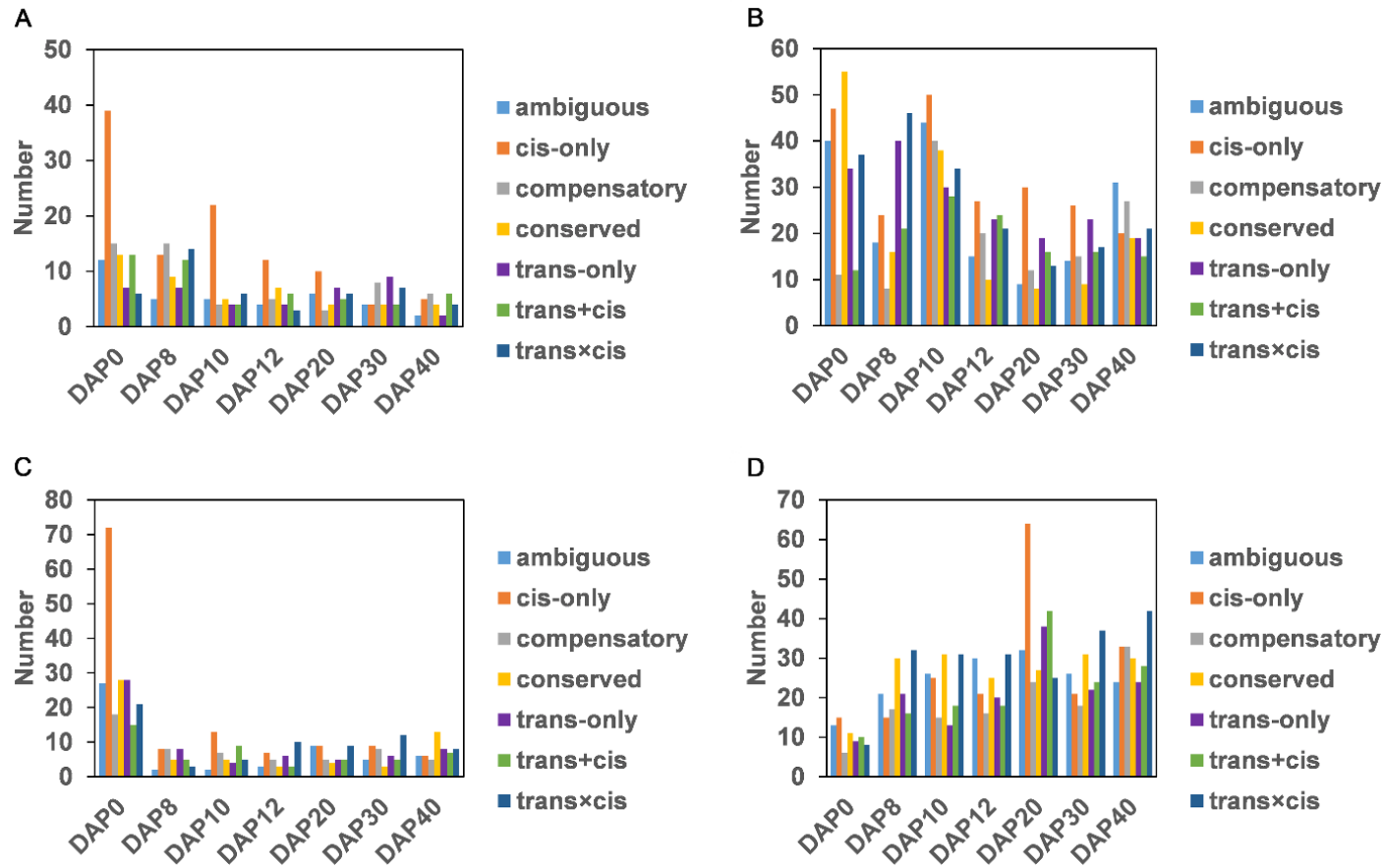
Supplementary Figure 17. The alignment of different *ZmARF* orthologues. The alignment was performed using BioEdit (v7.2.5, <http://www.mbio.ncsu.edu/bioedit/bioedit.html>). Sequences of *ZmARF* genes analyzed in the alignment were obtained from MaizeGDB. Accessions were as follows: *ZmARF11*, GRMZM2G056120; *ZmARF12*, GRMZM2G437460; *ZmARF23*, GRMZM2G441325; *ZmARF24*, GRMZM2G030710; and *ZmARF26*, GRMZM5G874163.



Supplementary Figure 18. The expression level of *ZmARF11*, *ZmARF12*, *ZmARF23*, and *ZmARF24* in *ZmARF12*- and *ZmIAA8*-silenced maize seedlings. (A) to (C) The silencing specificity of *ZmARF12* was evaluated by detecting the expression levels of *ZmARF11*, *ZmARF23* and *ZmARF24*, which share high identities with *ZmARF12*, in the relevant systemic leaves using qRT-PCR at 7 days and 14 days post inoculation (dpi), respectively. (D) The relative transcript level of *ZmARF12* in the *ZmIAA8* transient knocked-down plants was evaluated by using real-time RT-PCR at 7 dpi and 14 dpi, respectively. Values are means $\pm$ SD, * $P < 0.05$, ** $P < 0.01$ (paired Student's *t*-test); ns, not significant.



Supplementary Figure 19. Microscopic analysis of the leaf disk of the *ZmARF12*- and *ZmIAA8*-silenced plants. The leaf disks were dissected from the second systemic leaves above the inoculated leaves of the *ZmARF12* transient silencing, *ZmIAA8*-silenced and control plants, respectively. The cells along the two red lines (L1 and L2) were calculated, respectively. The scale bar = 50 μ m.



Supplementary Figure 20. Regulatory category assignments of additive (A), (C) and nonadditive (B), (D) differentially expressed genes in Zhengdan1002 (A), (B) and Zhengdan958 (C), (D). DAP0, DAP8, DAP10, DAP12, DAP20, DAP30, and DAP40 represent 0, 8, 10, 12, 20, 30, and 40 d after pollination, respectively.