



Supplementary Information for

Regulators of early maize leaf development inferred from transcriptomes of LCM-isolated embryonic leaf cells

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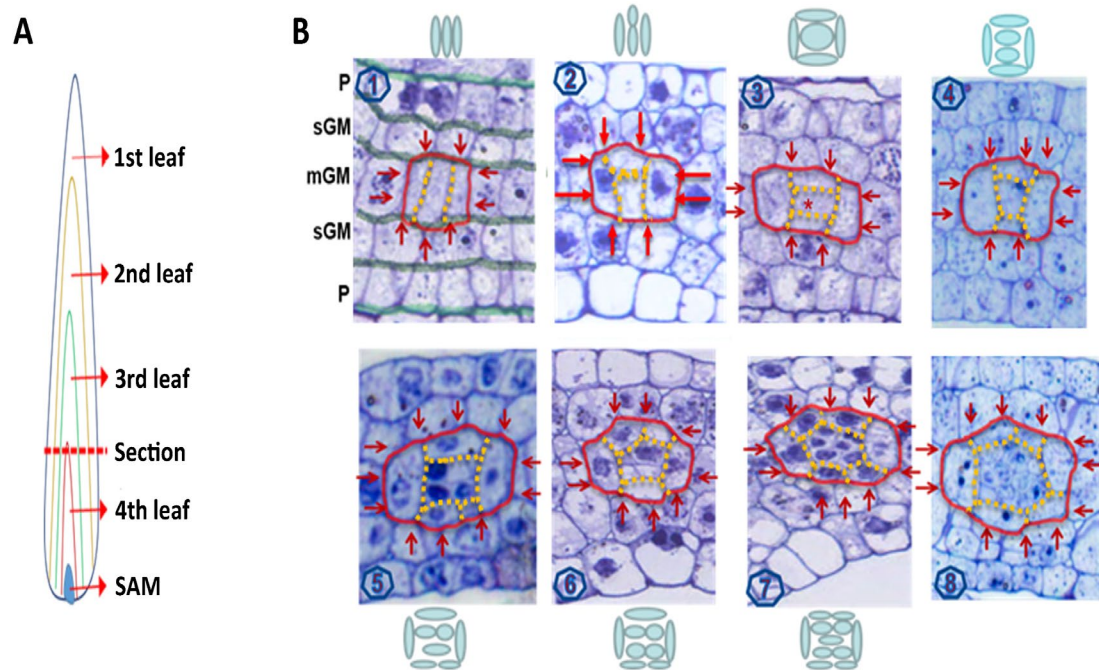


Fig. S1. Early successive stages of minor vein development and contiguous tissue development in transverse sections of the maize embryonic leaves. (A) A sketch of an embryonic leaf used and where each of the stages are located, and isolation of mGM cells and early BS+V cells. **(B)** The figure shows progressive changes in Kranz anatomy development in embryonic leaves. P: primordium; mGM: median ground meristem; and sGM: round-shaped subprotodermal ground meristem. (1) Kranz anatomy development starts from 3 mGM cells. (2) First periclinal division adaxially gives rise to a precursor BS cell. (3) Second periclinal division abaxially gives rise to another BS cell precursor. (4) Division of initial procambial cells. (5) Division of an abaxial BS cell. (6) Division of procambial cells. (7) Division of an adaxial BS cell. (8) Further division of procambial cells and enlargement of BS cells. Arrows indicate developing Kranz anatomy. The star indicates developing or developed BS cells. Scale bars, 10 μm .

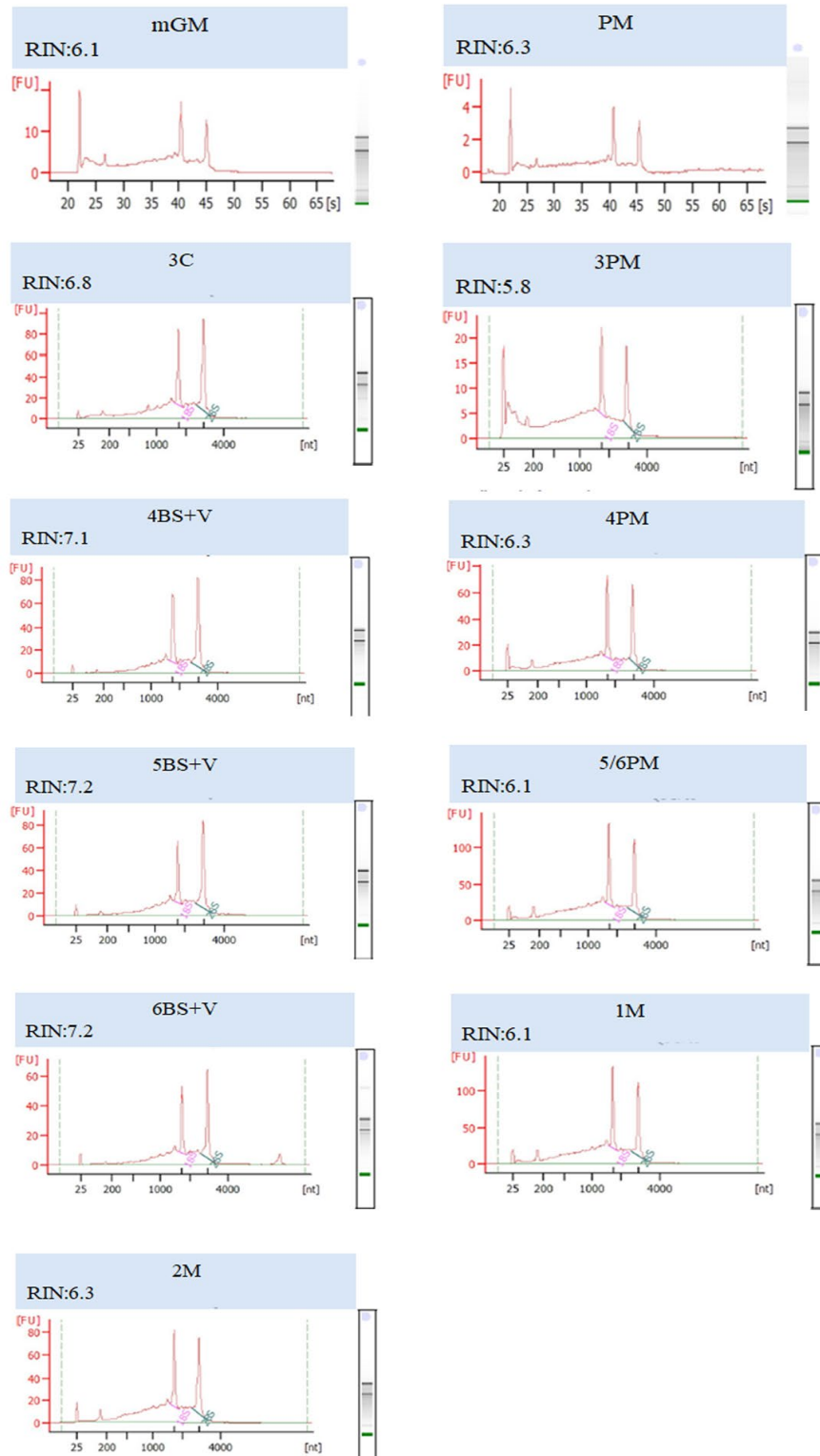


Fig. S2. Representative quality assessments of LCM-derived RNA samples used for RNA sequencing. Electropherograms of RNA samples extracted from the captured pre-Kranz and pre-M cells compartments prior to DNase treatment. RIN, RNA Integrity Number, is a measure of RNA quality.

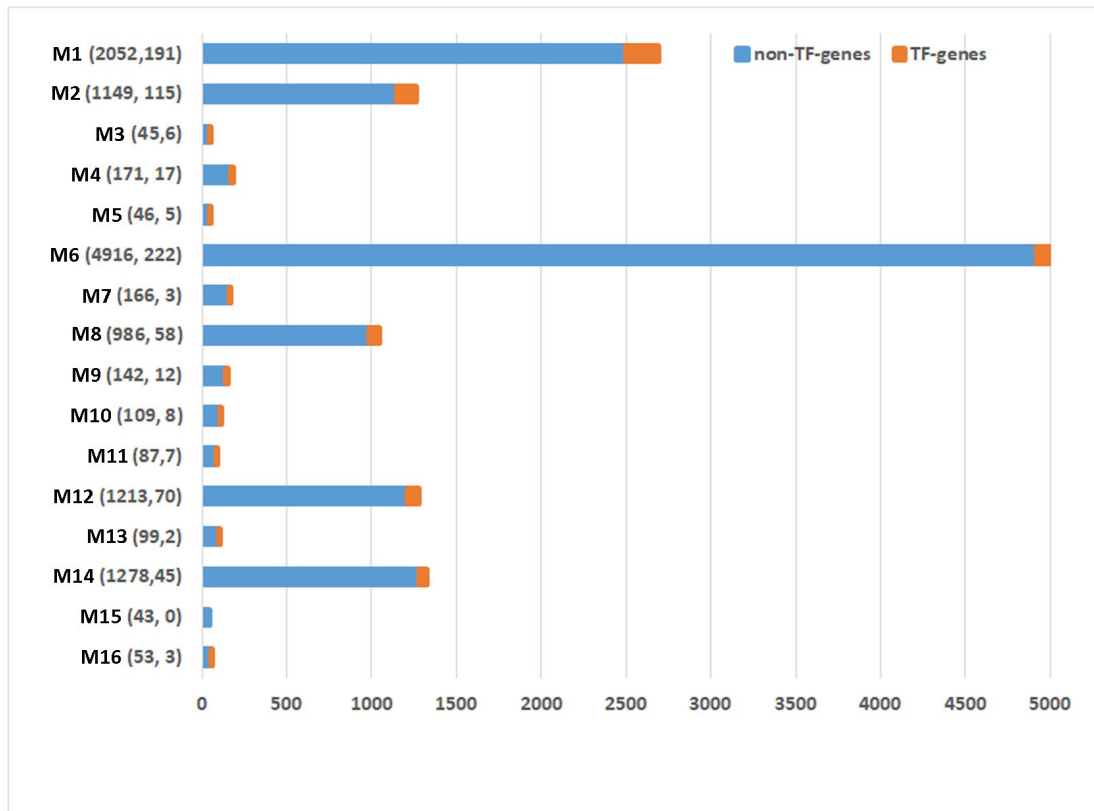
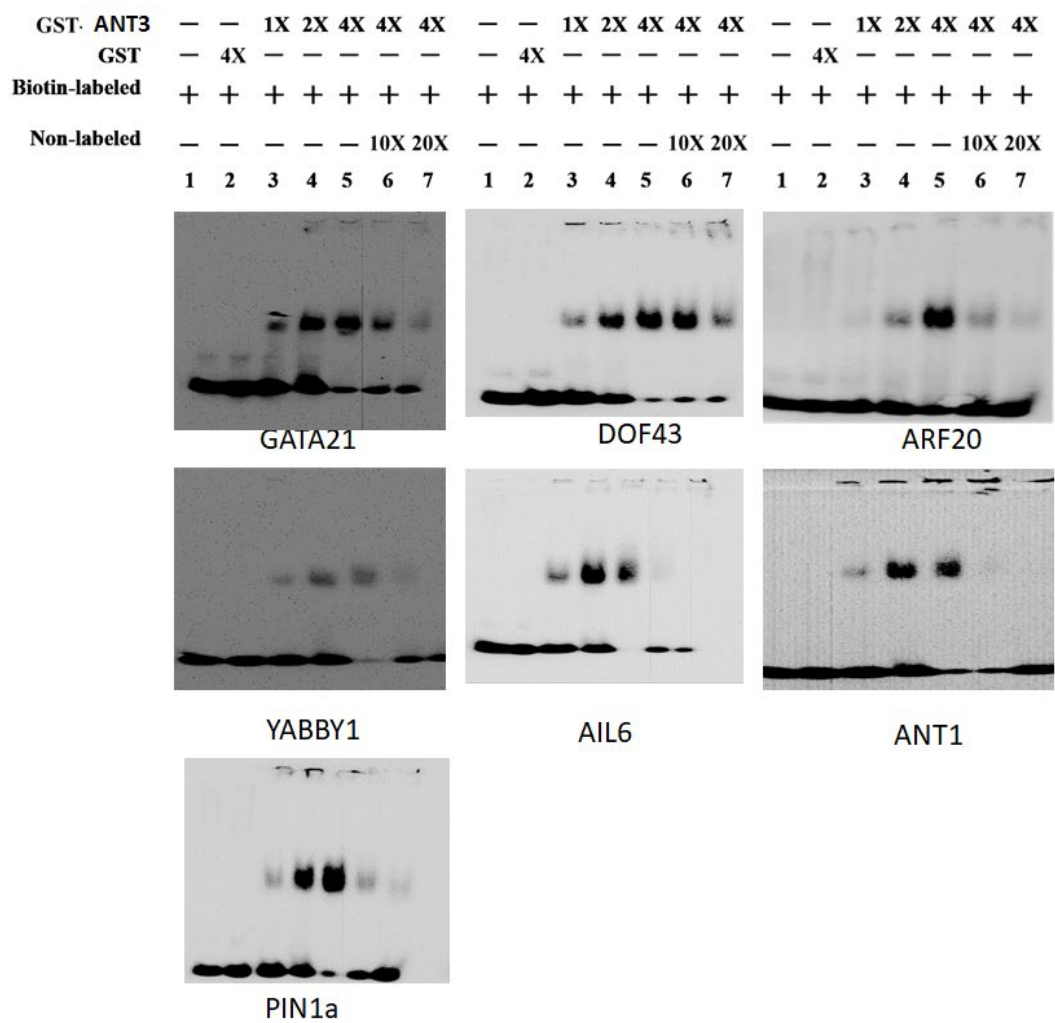
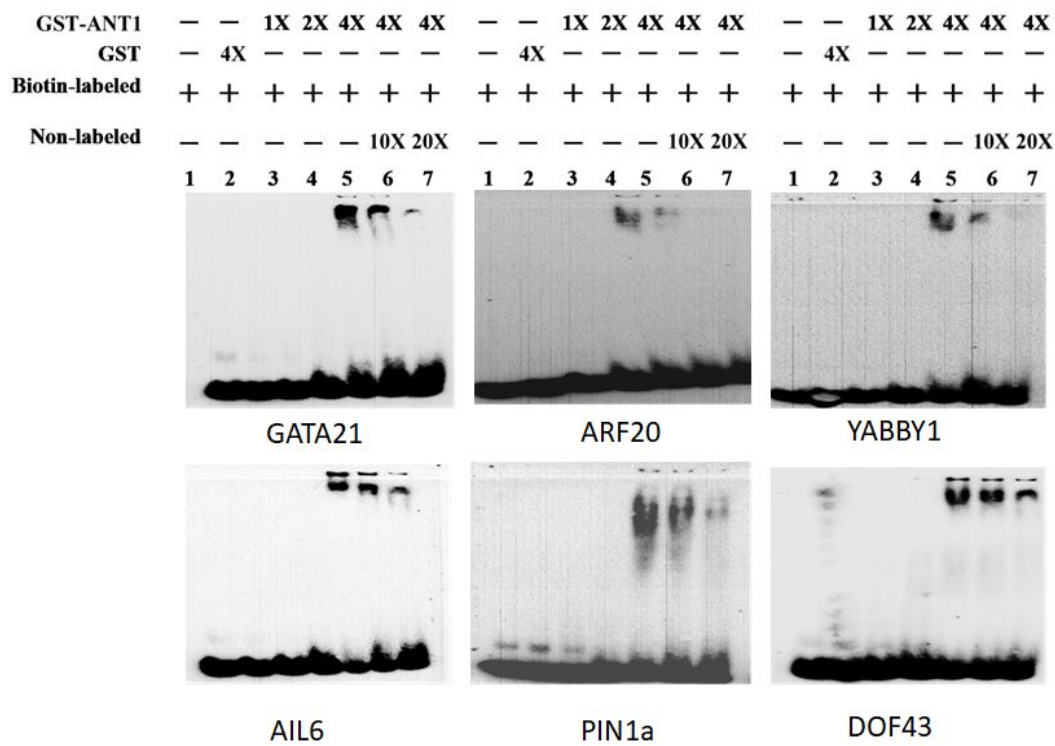
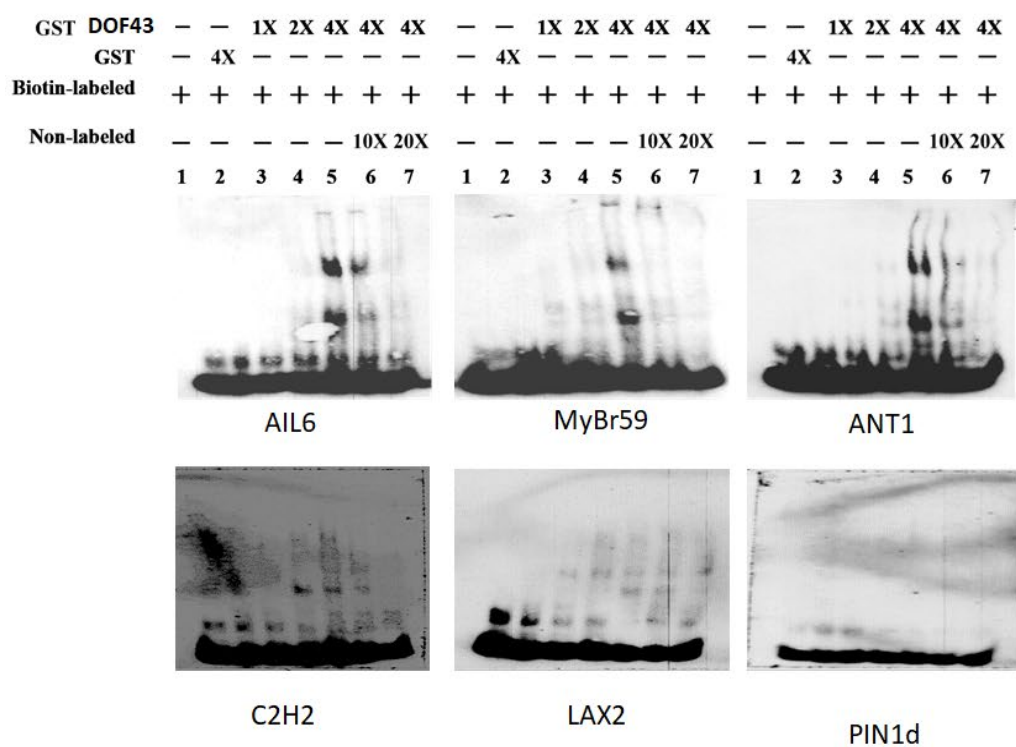
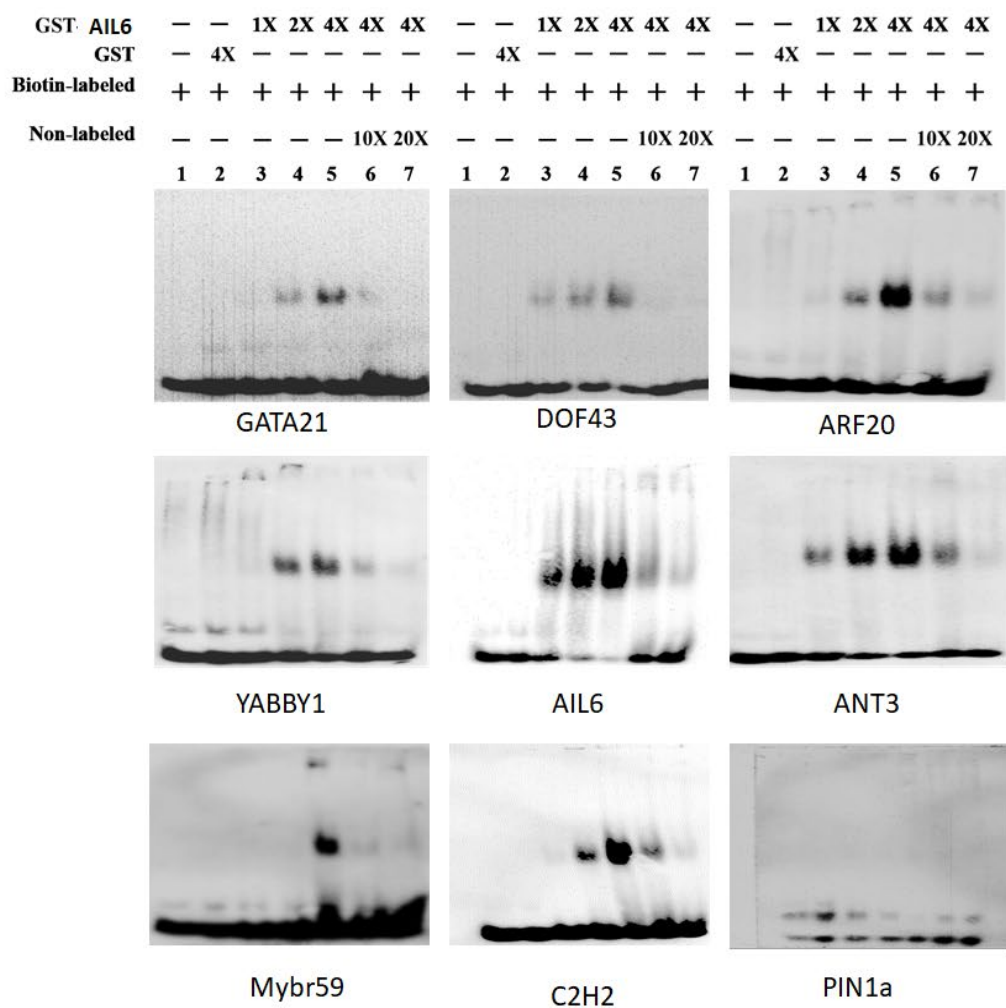
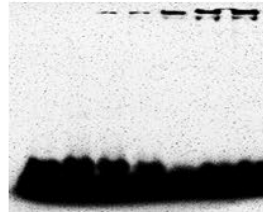


Fig. S3. Numbers of TF and non-TF genes in each gene coexpression module.

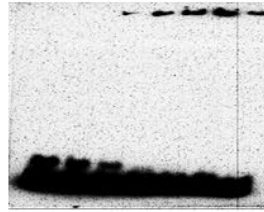




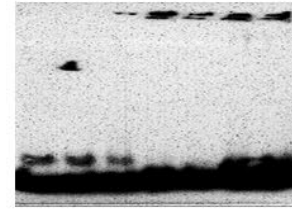
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	GST	—	4X	—	—	—	—	—	—	4X	—	—	—	—	—	—	4X	—	—	—	—	—
Biotin-labeled		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Non-labeled		—	—	—	—	—	10X	20X	—	—	—	—	—	10X	20X	—	—	—	—	—	10X	20X
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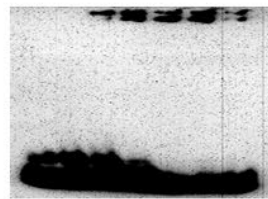
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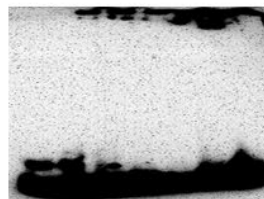
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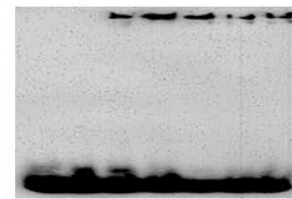
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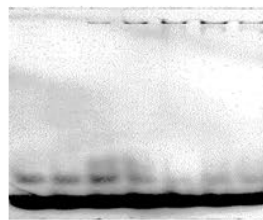
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ARF25



Mybr59

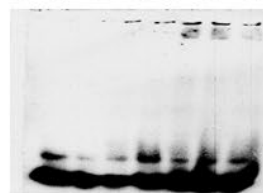


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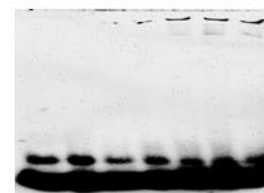


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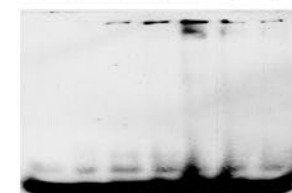
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	GST	—	4X	—	—	—	—	—	—	4X	—	—	—	—	—	—	4X	—	—	—	—	—
Biotin-labeled		+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Non-labeled		—	—	—	—	—	10X	20X	—	—	—	—	—	10X	20X	—	—	—	—	—	10X	20X
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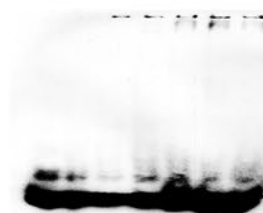
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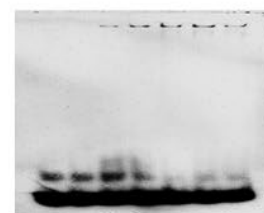
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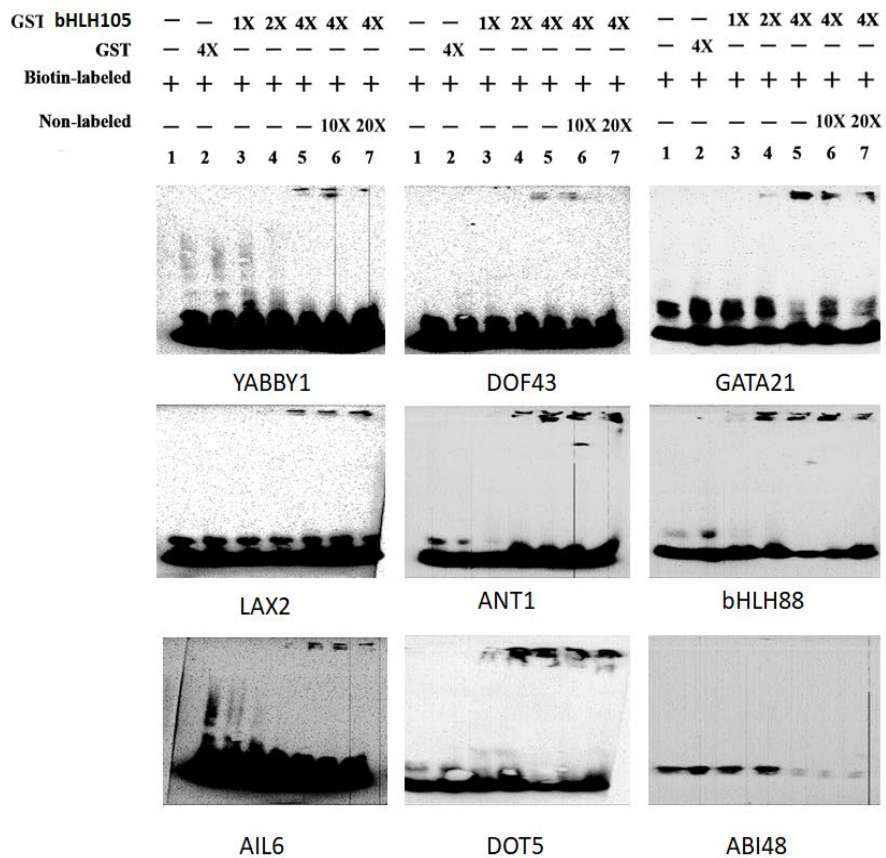
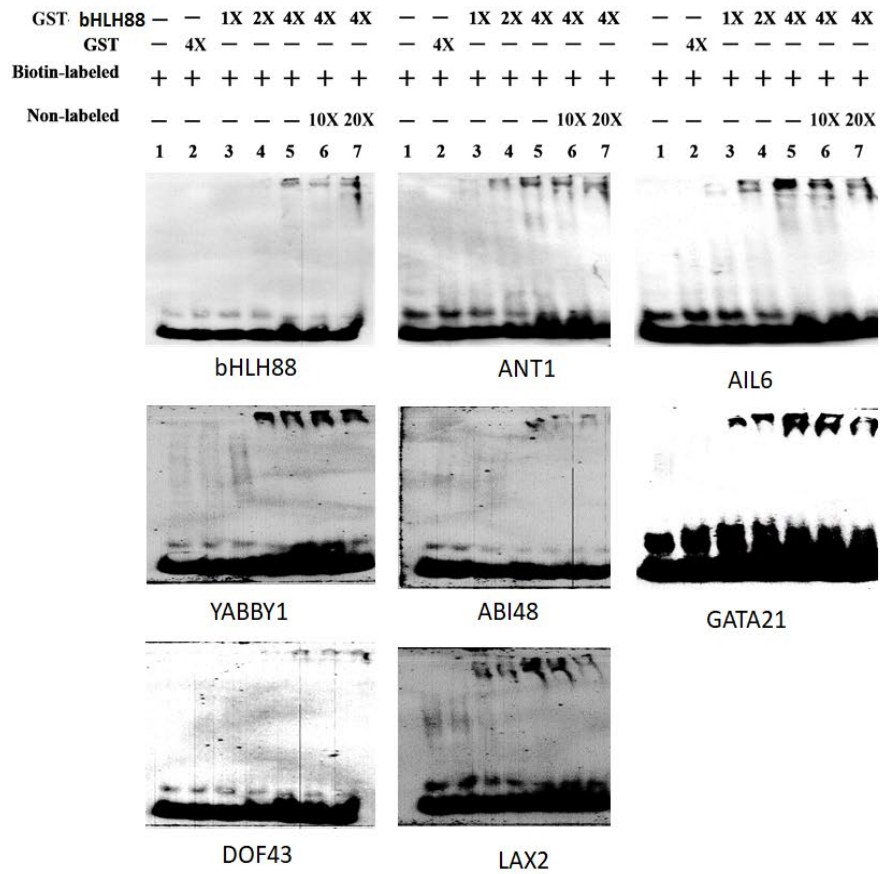
YABBY1



LAX2



PIN1d



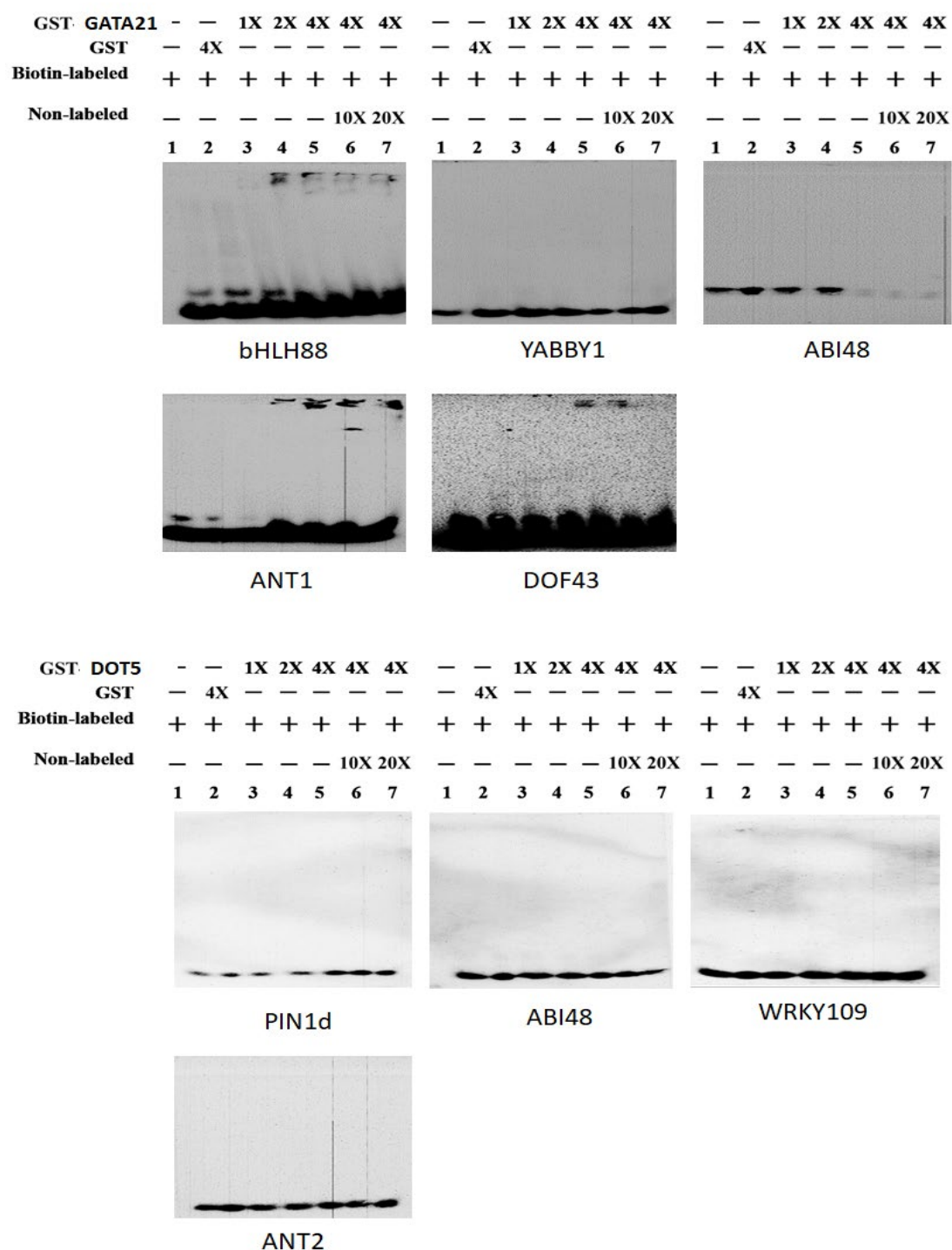


Fig. S4. EMSA assays for ten TFs. EMSA assays for testing the interactions between predicted TFBs in the promoters of putative targets and the purified fusion proteins GST-ZmANT1, GST-ZmAIL6, GST-ZmANT3, GST-ZmDOF43, GST-ZmARF25, GST-ZmARF20, GST-ZmbHLH88, GST-ZmbHLH105, GST-ZmGATA21, and GST-ZmDOT5. In each case, lane 1: biotin-labeled probe alone; lane 2: with increasing amounts of purified GST; lanes 3 to 5: with increasing amounts of GST-TF; and lanes 6 to 7: with increasing amounts of the non-labeled probes.

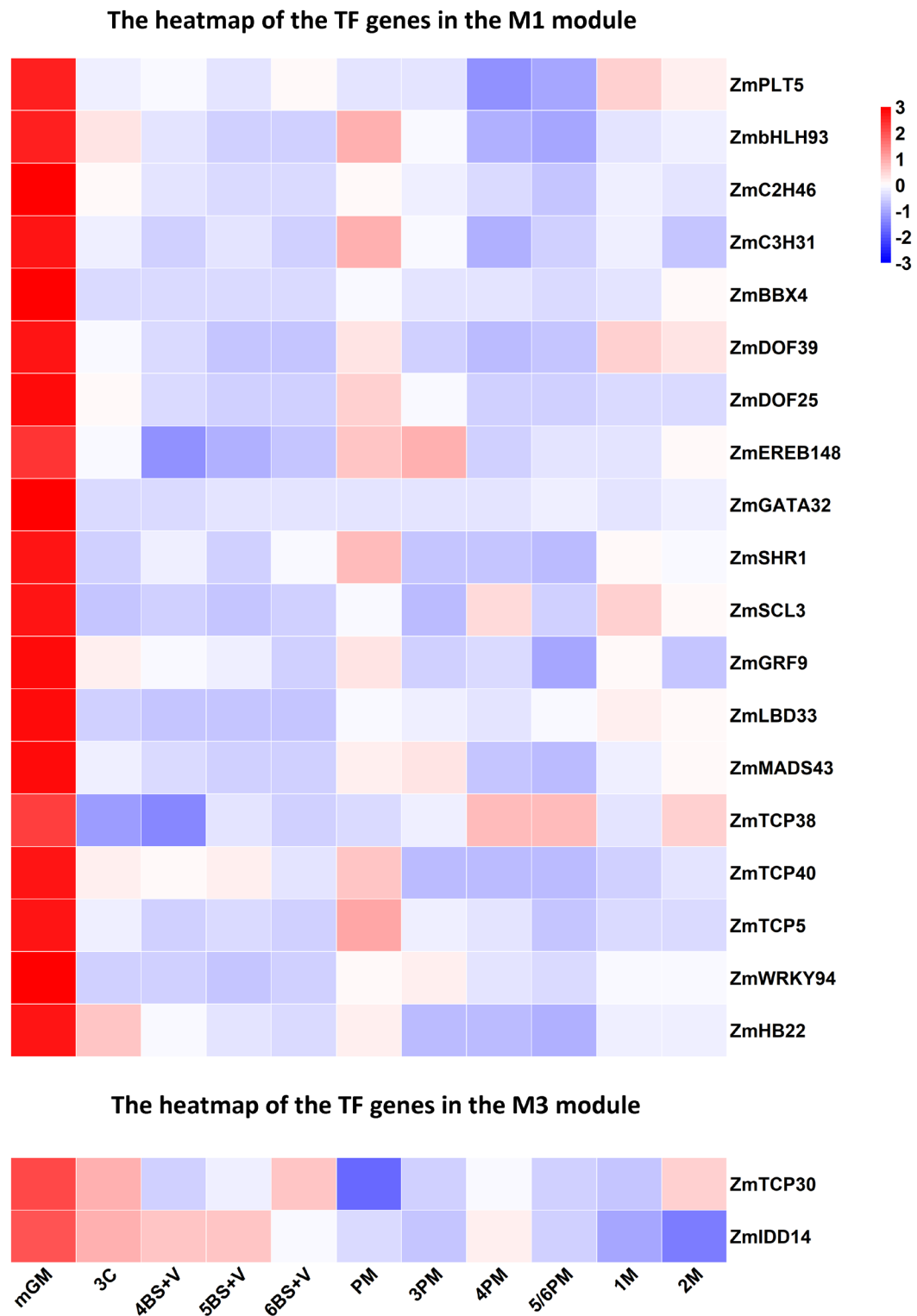


Fig. S5. The heatmap of normalized expression levels (z-scores) of the TF genes in the M1 and M3 module in the 11 cell types. The color bar is shown on the right.

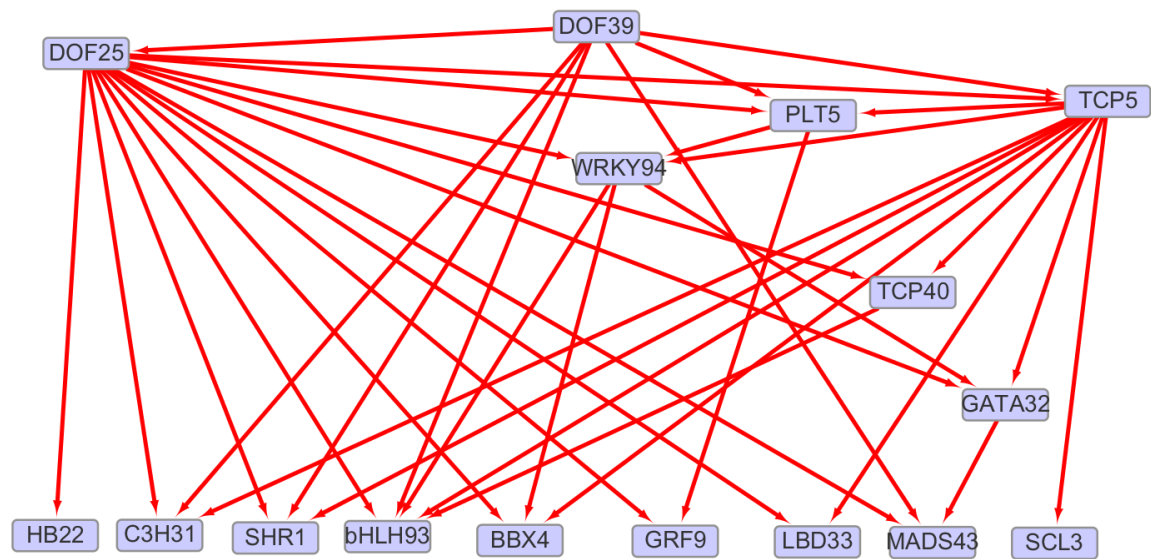


Fig. S6. A regulatory network of predicted connections between the 19 TF genes in the M1 module. The known PWMs of TFs are used to predict the presence of their binding sites in the promoter sequences of their candidate target genes by the CIS-BP method (1) and each successful prediction is indicated by a red line with an arrow in the figure.

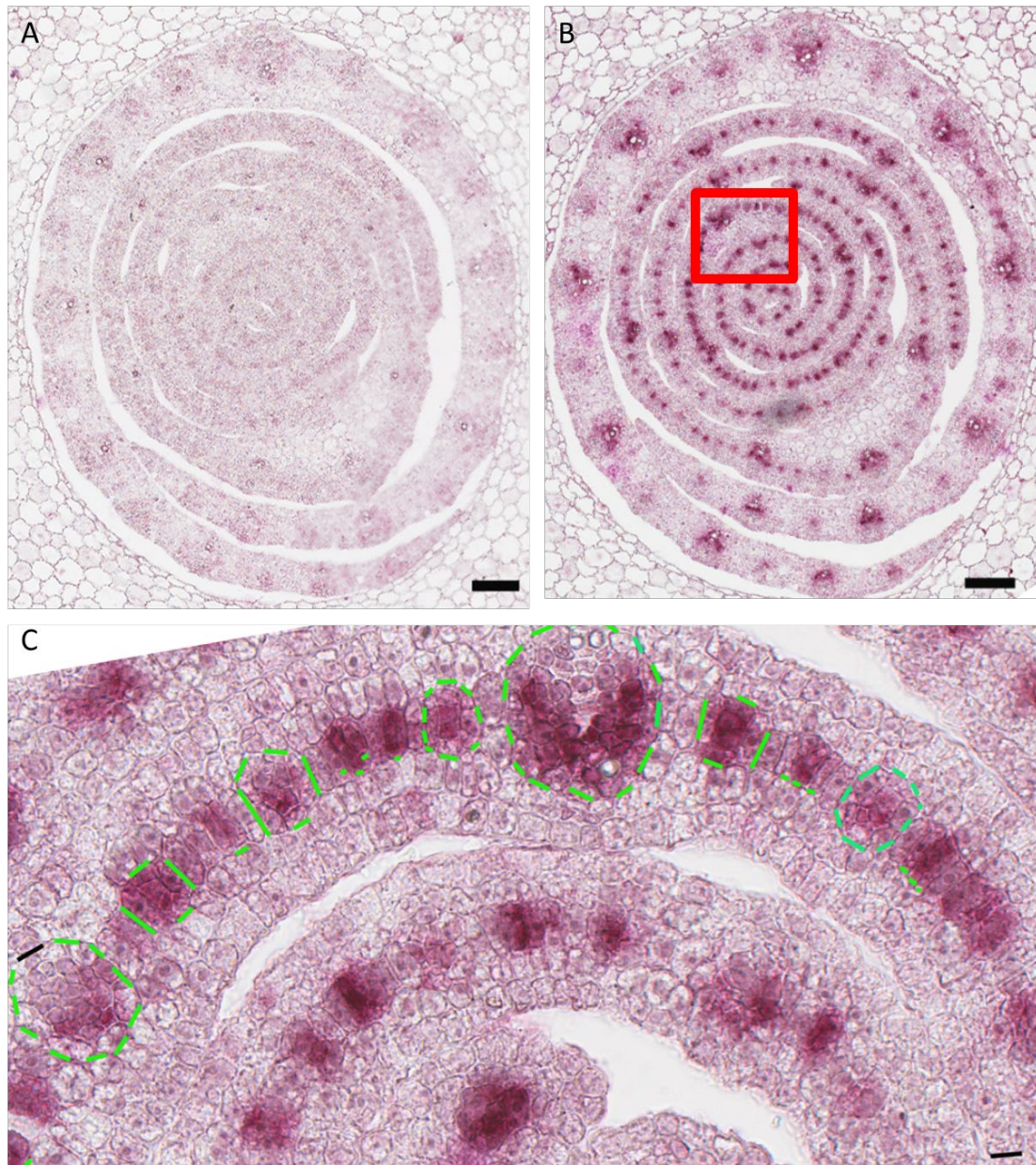


Fig. S8. *In situ* hybridization of *ZmWRKY109* transcript accumulation in the maize seedling shoot. (A and B) Transverse sections of wild-type seedling embryonic leaf. The sections reveal the accumulation pattern of *ZmWRKY109* transcripts (purple) over the vasculature and in the primordia 1 (P1), P2, and P3 prior to the development of vasculature. Gradients of *ZmWRKY109* expression are also noted between vascular bundles in the leaf with (A) the sense probe and (B) the antisense probe. (C) Accumulation of *ZmWRKY109* transcript occurs in vascular tissues of veins in leaf primordia (green circles) in the undifferentiated vascular bundle of the leaf primordia. (Scale bar in A and B, 100 μ m; in C, 20 μ m.)

SI Appendix tables

Table S1. The quality and quantities of RNAs isolated using laser-capture microdissection.						
Sample	RNA quality in terms of RNA Integrity Numbers (RINs)			Total amount of RNA (ng)		
	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3
mGM	6.1	6.3		11	16.9	
3C	6.1	6.8	6.8	72.8	55.4	45.6
4BS+V	7.1	7.0		38.3	54.9	
5BS+V	7.2	6.8		42.8	48.4	
6BS+V	7.2	6.6		30.3	31.7	
PM	6.3	5.7		19.6	34.3	
3PM	5.7	5.8	5.8	62.9	23.5	30.06
4PM	6.3	6.1	5.9	33.5	40.7	40.1
5/6PM	6.1	5.9		66,2	66.9	
1M	6.4	6.0	6.4	57.6	10.1	12
2M	6.3	6.4	6.2	42.2	18.6	13.5

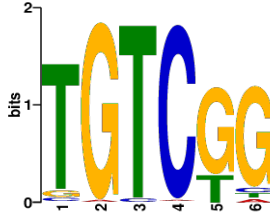

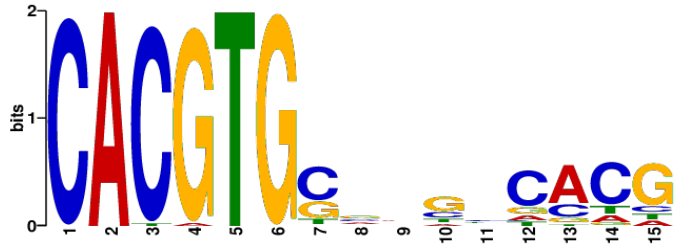
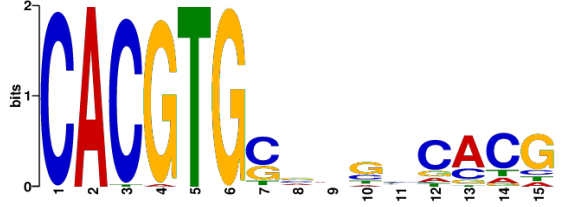
Table S2. Summary statistics of RNA-seq reads for different maize cell types and read mapping to the genome					
Sample	Total of reads	Reads processed	Reads processed (%)	mappable reads	Read mappable rate (%)
mGM	84,568,114	75,532,038	89.32	47,099,502	62.36
mGM	84,099,008	66,847,230	79.49	45,881,690	68.64
3C	140,867,096	131,288,298	93.20	86,999,584	66.27
3C	100,866,768	87,869,226	87.11	64,106,808	72.96
3C	94,328,266	81,349,868	86.24	54,746,719	67.30
4BS+V	103,977,188	90,985,098	87.50	64,446,843	70.83
4BS+V	111,035,694	93,894,470	84.56	63,369,283	67.49
5BS+V	86,416,264	78,721,692	91.10	52,532,706	66.73
5BS+V	101,552,318	84,956,446	83.66	55,528,683	65.36
6BS+V	99,302,934	87,293,198	87.91	62,753,096	71.89
6BS+V	111,826,974	94,428,722	84.44	64,235,756	68.03
PM	82,822,744	66,641,460	80.46	42,898,259	64.37
PM	80,162,768	63,615,724	79.36	39,043,770	61.37
3 PM	87,144,740	80,608,314	92.50	46,049,444	57.13
3 PM	89,725,470	82,154,384	91.56	46,206,002	56.24
3 PM	105,091,420	51,837,604	49.33	33,901,708	65.40
4 PM	95,365,742	88,239,084	92.53	57,922,760	65.64
4 PM	87,844,574	79,709,836	90.74	49,577,841	62.20
4 PM	87,943,214	56,202,360	63.91	37,877,147	67.39
5/6 PM	89,808,354	83,081,640	92.51	45,433,708	54.69
5/6 PM	187,347,952	174,882,490	93.35	125,083,549	71.52
1 M	92,933,774	81,539,552	87.74	50,196,988	61.56
1 M	86,595,430	79,340,284	91.62	45,404,456	57.23
1 M	90,506,336	78,281,728	86.49	50,153,676	64.07
2 M	90,002,406	82,512,660	91.68	47,750,930	57.87
2 M	92,066,900	81,503,244	88.53	45,725,448	56.10
2 M	88,219,038	66,257,336	75.11	41,752,521	63.02

Table S3. Expression levels (FPKMs) of selected differentially expressed genes of the M2 gene coexpression module

Gene Id	Gene name	mGM	3C	4BS+V	5BS+V	6BS+V	PM	3PM	4PM	5/6PM	1M	2M
Zm00001d034204	ANT1	88.39	43.31	18.49	13.90	15.82	40.38	42.64	4.49	4.24	11.60	8.76
Zm00001d048004	ANT2	20.25	16.22	5.97	6.15	6.56	5.36	9.96	2.27	2.97	5.58	4.88
Zm00001d018731	ANT3	97.91	58.84	31.19	25.18	24.55	27.97	36.96	8.91	10.00	20.28	12.90
Zm00001d007840	ANT3-1	49.80	19.41	10.18	6.02	3.77	16.50	15.90	4.05	4.13	12.46	9.69
Zm00001d027878	AIL6	118.7	62.22	9.14	4.31	4.59	43.62	54.38	2.12	1.51	2.95	1.92
Zm00001d015243	ARF20	12.37	15.15	4.44	2.22	2.42	3.34	4.45	0.62	0.81	2.32	1.61
Zm00001d011953	ARF25	77.60	63.17	52.42	48.24	54.85	65.00	47.78	31.00	30.73	37.83	34.92
Zm00001d044355	ABI48	22.37	15.13	8.88	9.60	8.20	14.18	13.38	9.41	8.09	9.39	8.82
Zm00001d026046	bHLH134	17.69	6.66	6.42	4.80	4.31	8.44	5.66	1.81	2.16	2.10	2.78
Zm00001d020790	bHLH105	17.02	9.55	4.49	4.75	4.22	8.49	12.93	2.27	2.96	6.73	8.50
Zm00001d000291	bHLH88	28.14	19.00	14.81	14.97	13.72	15.23	16.97	6.19	4.16	11.44	9.22
Zm00001d053006	C2H2	20.23	7.01	4.98	4.10	3.94	5.31	10.48	2.82	1.98	6.20	3.88
Zm00001d020037	DOT5	36.79	21.83	8.71	5.28	5.81	9.08	6.73	1.57	1.37	5.74	4.86
Zm00001d051577	DOF43	9.61	10.64	3.69	3.03	3.07	3.07	2.46	0.54	0.59	1.76	1.95
Zm00001d009604	GATA21	8.09	3.09	0.17	0.80	0.12	2.56	3.40	0.00	0.08	1.58	0.20
Zm00001d028380	Mybr59	18.03	15.09	8.34	9.88	11.93	9.75	10.41	9.06	10.52	9.42	7.10
Zm00001d013709	WRKY109	8.05	4.41	3.99	4.49	3.71	3.65	3.18	2.18	2.38	2.84	2.06
Zm00001d017391	YABBY1	188.4	89.57	60.81	59.13	61.95	114.8	56.10	28.41	33.50	49.87	48.68
Zm00001d028401	LAX2	221.0	90.83	24.10	19.01	17.00	64.12	70.10	9.22	14.14	26.90	24.80
Zm00001d044812	ZmPin1a	32.82	20.33	11.09	9.48	7.47	13.36	16.47	5.93	5.77	14.40	11.35
Zm00001d052442	ZmPin1d	31.08	14.68	5.88	5.91	6.15	19.17	13.56	5.65	4.30	7.99	10.29

Table S4. PWMs of the TFs in Figure 8.

Gene ID	TF Name	Source	PWM (Forward)
Zm00001d034204	ANT1	DAP-seq	
Zm00001d048004	ANT2	Prediction	Same as that of ANT1 (DBD sim=89.1%)
Zm00001d018731	ANT3	DAP-seq	
Zm00001d007840	ANT3-1	Prediction	Same as that of ANT3 (DBD sim=95.6%)
Zm00001d027878	AIL6	DAP-seq	

Zm00001d015243	ARF20	Prediction	
Zm00001d011953	ARF25	DAP-seq	
Zm00001d000291	bHLH88	DAP-seq	
Zm00001d020790	bHLH105	Prediction	 Inferred from bHLH88 (DBD seq id =45%) by our DAP-seq

Zm00001d017391	YABBY1	DAP-seq	<p>Sequence logo for YABBY1 DAP-seq binding site. The y-axis is 'bits' from 0 to 2. The x-axis shows positions 1 to 13. The sequence is approximately AATCCATTCATTAG.</p>
Zm00001d044355	ABI48	Prediction	<p>Sequence logo for ABI48 Prediction binding site. The y-axis is 'bits' from 0 to 2. The x-axis shows positions 1 to 15. The sequence is approximately CAGGTG.</p> <p>Inferred from NGA2 (DBD seq id = 39%) by our DAP-seq</p>

Table S5. Predicted binding elements in the promoters of 15 TFs. Each prediction successfully validated by EMSA is indicated by a “V”, and otherwise by an “X” (failed) or “--” (not determined).

Target promoter	TF	Binding element (sequence)	EMSA
bHLH88	bHLH88	ACTGTGAACCACATG	V
bHLH88	GATA21	GATCCACCCGT	V
bHLH88	bHLH105	ACTGTGAACCACATG	V
GATA21	bHLH88	CCCGTTTCACGTGGCCGCCCT	V
GATA21	bHLH105	CCCGTTTCACGTGGCCGCCCT	V
GATA21	ANT1	GCCCGCGTCCCCAGG	V
GATA21	ANT3	TGCGCCTCGTGATCGGCGA	V
GATA21	AIL6	AGCGCGAACGCCTGGGAGACTGCT	V
GATA21	ARF25	ACCGACA	V
GATA21	ARF20	CAGACAT	V
ARF25	ARF20	CAGACAGAC	V
WRKY109	DOT5	TTATTATATACCAAGAGAAA	X
ARF20	ANT1	CCCTTGGTCTTCGTGAG	V
ARF20	AIL6	CCCTTGGTCTTCGTGAG	V
ARF20	ANT3	CCCTTGGTCTTCGTGAG	V
YAABY1	GATA21	CCGGTCAGATCGGCCGTG	X
YAABY1	ANT1	GGCAACAGTCTCGAGATGCCGACC	V
YAABY1	ANT3	GGCAACAGTCTCGAGATGCCGACC	V
YAABY1	AIL6	GGCAACAGTCTCGAGATGCCGACC	V
YAABY1	ARF25	GGCAACAGTCTCGAGATGCCGACC	V
YAABY1	bHLH88	GGCAAGATCCACATGCAGTAGTAG	V
YAABY1	bHLH105	GGCAAGATCCACATGCAGTAGTAG	V
DOT5	bHLH88	ATGTCGTTGCACGTGCAAGCACCC	--
DOT5	bHLH105	ATGTCGTTGCACGTGCAAGCACCC	V
DOT5	ANT3	TGCACAGCTACAGAG	--
AIL6	ANT1	GGCACGGCCCCAAGACAA	V
AIL6	ANT3	GGCACGGCCCCAAGACAA	V
AIL6	AIL6	GGCACGGCCCCAAGACAA	--
AIL6	bHLH88	TTGGGCCGGCACGTG	V
AIL6	bHLH105	TTGGGCCGGCACGTG	V
AIL6	DOF43	ATAAACGTCAAAAAGGAGACT	V
AIL6	ABI48	CACGAAATCACCTGA	--
MYBr59	DOF43	ATTCTACTTTTGTACGCATT	V
MYBr59	ARF20	CAGACA	V

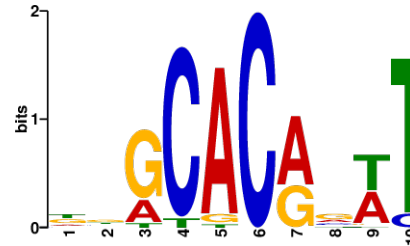
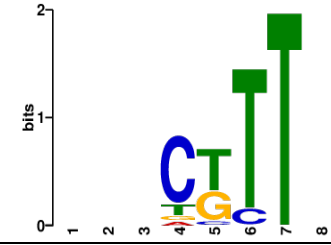
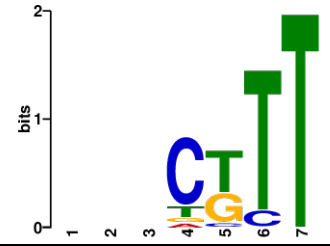
MYBr59	AIL6	GTTCGTTGAGTTCTGTATC	V
LAX2	DOF43	AAAGAAAACGAAAAGCACAGG	V
LAX2	bHLH88	CGCCTGTCGGACGTG	V
LAX2	bHLH105	CGCCTGTCGGACGTG	V
LAX2	ARF20	CGCCTGTCGGACGTG	V
LAX2	ARF25	GGAAGACA	V
LAX2	ABI48	CAAAAGAACTCCTGG	--
ABI48	DOT5	TTTGTGCTGGATGCT	X
ABI48	bHLH88	CACGAGCAGGATCTG	V
ABI48	bHLH105	CACGAGCAGGATCTG	X
ABI48	GATA21	TGGATGGGGTC	X
ANT1	GATA21	AACCCAATCCT	V
ANT1	ARF20	CCGACC	V
ANT1	DOF43	TCATTCCTTTTGCACGCCTTT	V
ANT1	bHLH88	CACATGCGACCAGAG	V
ANT1	bHLH105	CACATGCGACCAGAG	V
ANT1	ANT3	CACACACAAACCGAAGCCC	V
ANT1	AIL6	CACACACAAACCGAAGCCC	V
Pin1a	ARF20	<u>TGTCGG</u>	V
Pin1a	ANT1	TGCACGGACGTCGAGGA	V
Pin1a	ANT3	TGCACGGACGTCGAGGA	V
Pin1a	AIL6	TCGTGTCGGGGAGTGTGCA	X
ANT2	DOT5	GAGCTCGAGAGTAAC	X
DOF43	ANT1	CGCGCGGGCCTCAAGGA	V
DOF43	ANT3	CGCGCGGGCCTCAAGGA	V
DOF43	AIL6	ACGCCTCGGGATGCGAACT	V
DOF43	ARF25	<u>TGTCTCCA</u>	V
DOF43	ARF20	CCGACA	V
DOF43	GATA21	ATTCACATCTC	V
DOF43	bHLH88	GACGTGTCTCCACTG	V
DOF43	bHLH105	GACGTGTCTCCACTG	V
Pin1d	DOF43	GACAACATCATAAAGCACACT	X
Pin1d	DOT5	CAGATTCTCCGGGGT	X
Pin1d	ARF20	TGTCTGCC	V
Pin1d	ARF25	TGTCTGCC	V
C2H2	AIL6	AATTATCGAGATTTGTAAA	V
C2H2	DOF43	AAAAAAAAAAAAAGGAGCAG	V

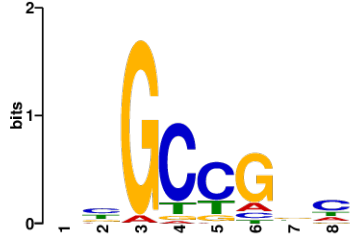
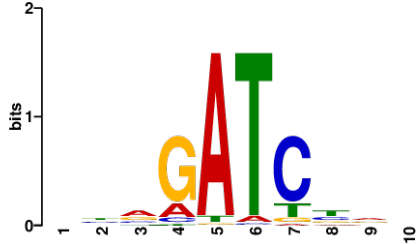
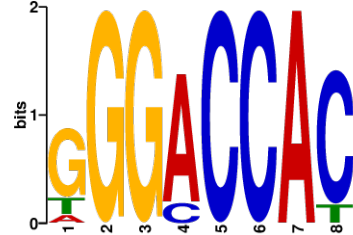
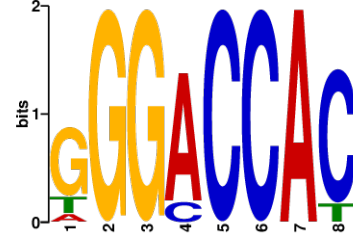
Table S6. Functions of the candidate TF genes of the M1 gene coexpression module.

Gene ID_V4	At_gene ID	TF family	Gene Symbol	Gene Function	Reference
Zm00001d002025	AT5G57390	AP2	PLT5	AtPLT5 is required to maintain high levels of PIN1 expression at the periphery of the meristem and to modulate local auxin production in the central region of the SAM, which underlies phyllotactic transitions.	(2, 3)
Zm00001d036382	AT5G65640	bHLH	bHLH93	AtbHLH093 is involved in several developmental characteristics, including a downward curling of rosette leaves and impaired bolting, stem growth, and differentiation of stomatal guard cells.	(4, 5)
Zm00001d024534	AT1G32360	C3H	ZmC3H31	ZmC3H31 is related to root hair traits	(6)
Zm00001d033325	AT5G39660	Dof	ZmDOF39	AtDOF5.2 appears to act as a positive regulator of somatic embryo, and the timing of the transition from the vegetative to the reproductive phase	(7, 8)
Zm00001d034163	AT1G07640	Dof	ZmDOF25	OBP2 regulates auxin concentration and cell size in leaves	(9)
Zm00001d009103	AT2G47520	ERF	ZmEREB148	AtERF071 plays a role in promoting cell growth."	(10)
Zm00001d010785	AT5G25830	GATA	ZmGATA32	AtGATA12 is involved in xylem vessel formation	(11)
Zm00001d042127	AT1G50420	GRAS	ZmSCL3	AtSCL3 could have a similar function to SCR	(12)
Zm00001d021973	AT4G37650	GRAS	ZmSHR1	A well-known regulator of Kranz anatomy development	(13)
Zm00001d051456	AT2G36400	GRF	ZmGRF9	AtGRF3 regulates genes in leaf development.	(14)
Zm00001d011748	AT4G09960	MIKC_MADS	ZmMADS43	AtSTK is involved in flower development and periodic lateral root formation	(15)

Zm00001d034353	AT1G30210	TCP	ZmTCP5	AtTCP24 is involved in heterochronic regulation of leaf differentiation	(16)
Zm00001d022256	AT1G30210	TCP	ZmTCP38	AtTCP24 is involved in heterochronic regulation of leaf differentiation	(16)
Zm00001d025033	AT1G72010	TCP	ZmTCP40	AtTCP22 regulates cell proliferation and leaf development	(17)
Zm00001d050195	AT4G31550	WRKY	ZmWRKY94	AtWRKY15 plays an important role in regulating protoxylem vessel formation in the development of the root vascular cylinder	(18)
Zm00001d038717	AT3G02550	LBD	ZmLBD33	LOB DOMAIN-CONTAINING PROTEIN 41	
Zm00001d026684	AT1G75710	C2H2	ZmC2H46	Function unknown	
Zm00001d051047	#N/A	CO-like	BBX4	uncharacterized protein	
Zm00001d020774	#N/A	ZF-HD	ZmHB22	uncharacterized protein	
Functions of the candidate TF genes of the M3 gene coexpression module.					
Zm00001d020683	AT1G68130	C2H2	ZmIDD14	The SHR/SCR/IDD network might wire auxin and BR signaling to coordinate leaf vein density.	(19, 20)
Zm00001d034353	AT1G30210	TCP	ZmTCP30	AtTCP24 is involved in heterochronic regulation of leaf differentiation	(16)

Table S7. The DNA binding motifs (PWMs) of 9 TFs in the M1 gene coexpression module from the CIS-BP database

Gene ID	TF Name	Source (CIS-BP)	PWM (Forward)
Zm00001d002025	PLT5	M02647_2.00	
Zm00001d033325	ZmDOF39	M00862_2.00	
Zm00001d034163	ZmDOF25	M00862_2.00	

Zm00001d009103	ZmEREB148	M00717_2.00	 <p>Sequence logo for ZmEREB148. The y-axis represents information content in bits (0 to 2). The x-axis shows positions 1 to 8. The sequence is approximately G C C G.</p>
Zm00001d010785	ZmGATA32	M00727_2.00	 <p>Sequence logo for ZmGATA32. The y-axis represents information content in bits (0 to 2). The x-axis shows positions 1 to 10. The sequence is approximately G A T C.</p>
Zm00001d022256	ZmTCP38	M01313_2.00	 <p>Sequence logo for ZmTCP38. The y-axis represents information content in bits (0 to 2). The x-axis shows positions 1 to 8. The sequence is approximately G G G A C C A C.</p>
Zm00001d034353	ZmTCP5	M01313_2.00	 <p>Sequence logo for ZmTCP5. The y-axis represents information content in bits (0 to 2). The x-axis shows positions 1 to 8. The sequence is approximately G G G A C C A C.</p>

Zm00001d025033	ZmTCP40	M00891_2.00	
Zm00001d050195	ZmWRKY94	M00731_2.00	
The DNA binding motifs (PWMs) of 2 TFs in the M3 gene coexpression module from the CIS-BP database			
Zm00001d020683	IDD14	M06805_2.00	
Zm00001d034353	TCP30	M01313_2.00	

Table S8. Sequences of the primers used to generate the clones for the *in situ* hybridization probes.

Gene ID	Symbol name	Forward Primer	Reverse Primer
Zm00001d027878	Ereb130 (AIL6)	TAC GGC CAC CCC ATG AAA CTG	GGC AAA ATT GTC GCC ATC TTG C
Zm00001d034204	ANT1	GGC AAC TGC ATG ACG GAC ACC T	CGT ACC CTG GTA ATG ACA CGG ATG
Zm00001d018731	ANT3	TCG TAC CAC TCG ATC CAC CGA TT	GGC CTC CAT TTT ACA AAA CCC C
Zm00001d044355	Abi48	ACG ATC ACC TTG GTG GAT GAG G	TGA ACC GTG CAA TTG GTA AGC C
Zm00001d020790	bHLH105	CGG CCA CAT GGT GCT CTA CTC GTT	GAA CAG CGT CTG CAC CTG TCC A
Zm00001d000291	bHLH88	CAG CCT TGC ATT TGC GAA TCG	CAG CCT TGC ATT TGC GAA TCG
Zm00001d020037	DOT5	AGA TCC TGG TCG GCT CCA CGC AG	GCC GTT GTC GTC AAA AGT CTG CA
Zm00001d051577	DOF43	GAG CAG GAA TCG ATG GAG GTG AAG	ATT CGT CCC AAG CTC TCT AAG TTC T
Zm00001d009604	GATA21	GGG ATC CGG TAC AAG AAG GAG G	TTG ACA TGC GAA CTT CAG CGT C
Zm00001d013709	WRKY109	AGG GGC TAC TAC AAA TGC AGC A	AGG GGC TAC TAC AAA TGC AGC A
Zm00001d017391	YABBY 1	GGG CCC ATT TCC CAC ACA TCC AT	GCC GCA CAT CGT CAT ACA CAT AAC AAC
Zm00001d028401	LAX2	CAT GAC AAA CTT CGT CCG CCA GAT C	CTC TAT GCG GCT GTA GAA ATG GAT TC
Zm00001d044812	ZmPin1a	GGC AGT CAT CTT CGG CAT GC	CAC TCG CCC GCT TTG ATG TC

Table S9. Sequences of the primers used to generate the constructs to test the promoters by EMSA assays.

Gene ID	TF name	Forward Primer	Reverse Primer
Zm00001d027878	Ereb130 (AIL6)	AAA GGT ACC ATG GAC ATG AAC AAC GGG TGG C	AAA GGT ACC GGA GGA GGC TTG CAG TAG C
Zm00001d034204	ANT1	AAAGGA TCC ATG ACC AGC AAC AGC AGC CA	AAA GGA TCC TGC GTC GGT CCA CGC CGG CGA ACA
Zm00001d018731	ANT3	AAA GGT ACC GGC GTC GGT CCA GGC GGC GAA	AAA GGA TCC ATG CCA ACG AAA ACA ATG GCA ACG
Zm00001d015243	ARF20	AAA GAA TTC ATG AAG CAG TCC CCG GCC AGC T	AAA CTC GAG TCA CTC AAA TTG GTC GTA GAA CCC G
Zm00001d011953	ARF25	AAA CCC GGG AAT GCC GCC CGC AGC CAT GGC GCT	AAA CTC GAG CTA CTC GTT TGC GGC GGC GGC GGC GCA GCC TT
Zm00001d000291	bHLH88	AAA CAT ATG CAG CCC ACT ACG CGG GAA	AAA GAG CTC ACG GCT TCG ACA CGG ACG
Zm00001d020790	bHLH105	AAA GGA TCC ATG GCA CTG GAG GCC GTG	AAA GGT ACC CTC TAA GCT GCC GCC GCC TTG T
Zm00001d020037	DOT5	AAA CAT ATG CAC AGC TAC AGA GCC ATG C	AAA GAG CTC TAG ATG ACG ACC ATG TCG CT
Zm00001d051577	DOF43	AAA CAT ATG ATG GCC GGG GCA CCG	AAA GGA TCC TTA GAT GGC CGC CGA GGA GC
Zm00001d009604	GATA21	AAA CAT ATG CTG CAG AAG GAG CTT CCG	AAA GAG CTC TAG TAG TAC GGG GAC AGA GTG C

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