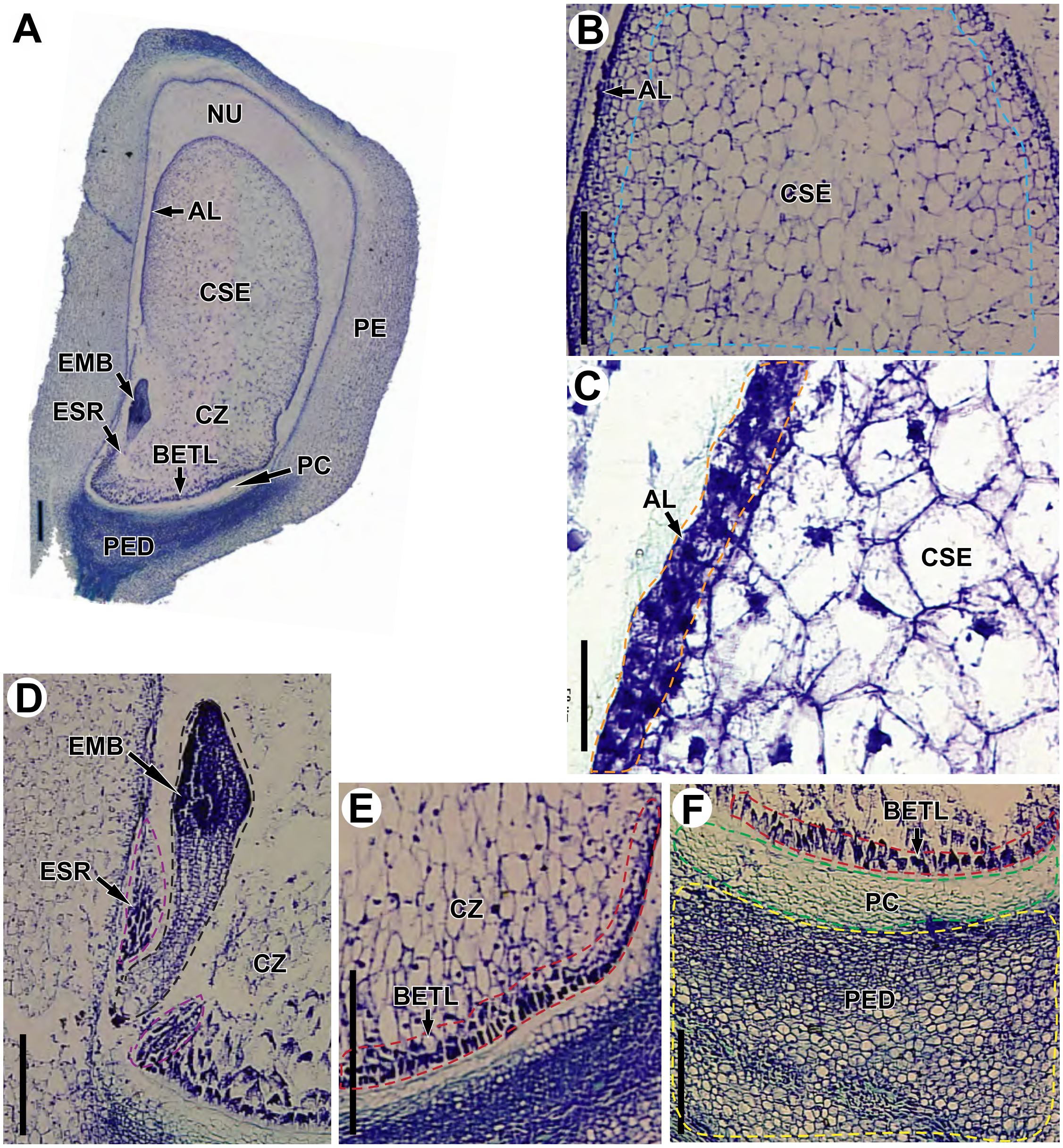
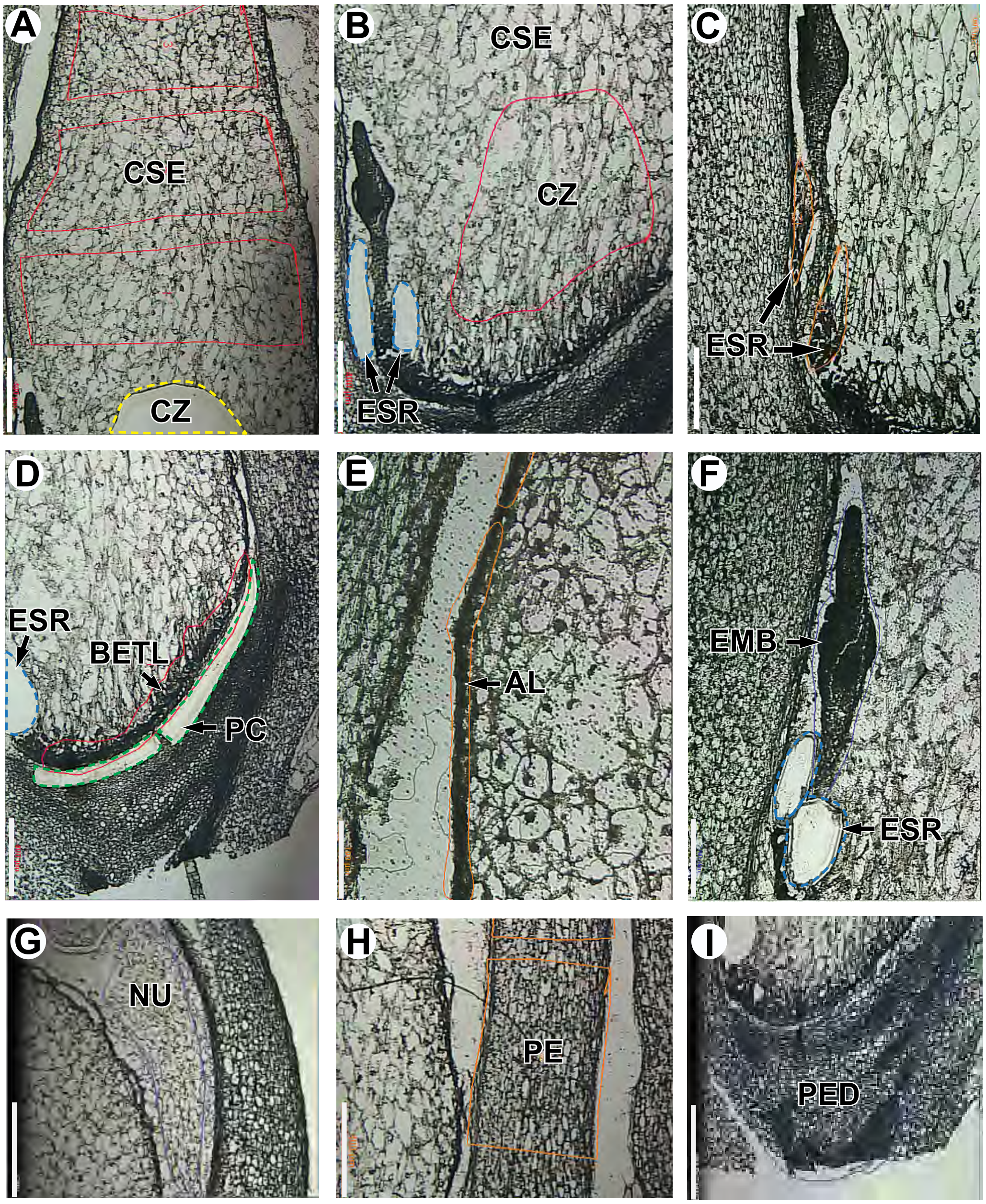


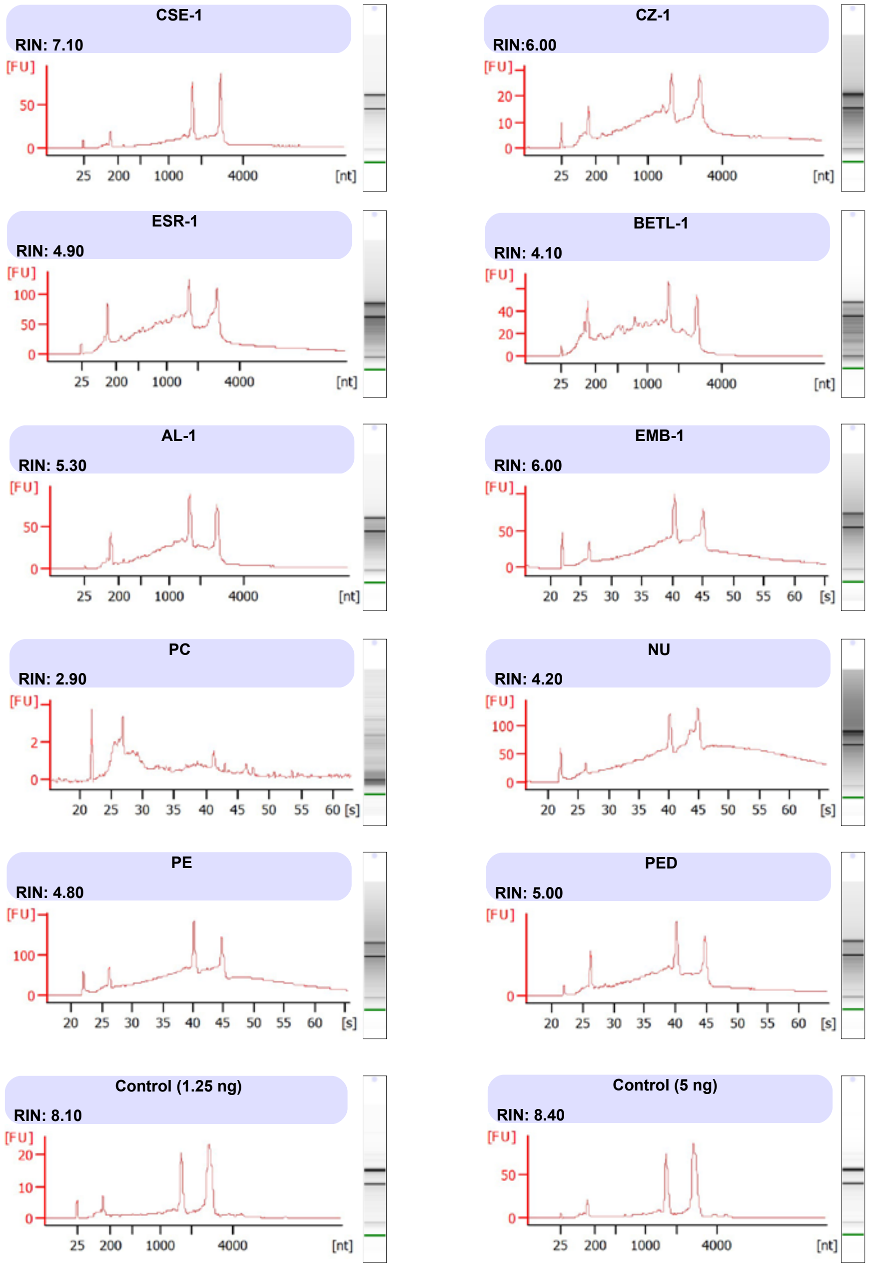
Supplemental Figure 1. Structure of an 8-DAP B73 maize kernel.

(A) Image of a Toluidine Blue-stained section of 8-DAP kernel showing different compartments. Multiple images of a single kernel section obtained using a low-magnification objective lens were merged using Adobe Photoshop CS5, and background was subsequently removed in Adobe Illustrator CS6 to generate the image. **(B)** through **(F)** Details of the captured kernel compartments. Colored dashed lines indicate the margins of excised compartments in a typical laser-capture experiment. Abbreviations: AL, aleurone; BETL, basal endosperm transfer layer; CSE, central starchy endosperm; CZ, conducting zone; EMB, embryo; ESR, embryo-surrounding region; NU, nucellus; PC: placento-chalazal region; PE, pericarp; PED, vascular region of the pedicel. Bars: (A) and (B), 400 μm; (C) and (D), 50 μm; (E), 400 μm; (F), 200 μm.

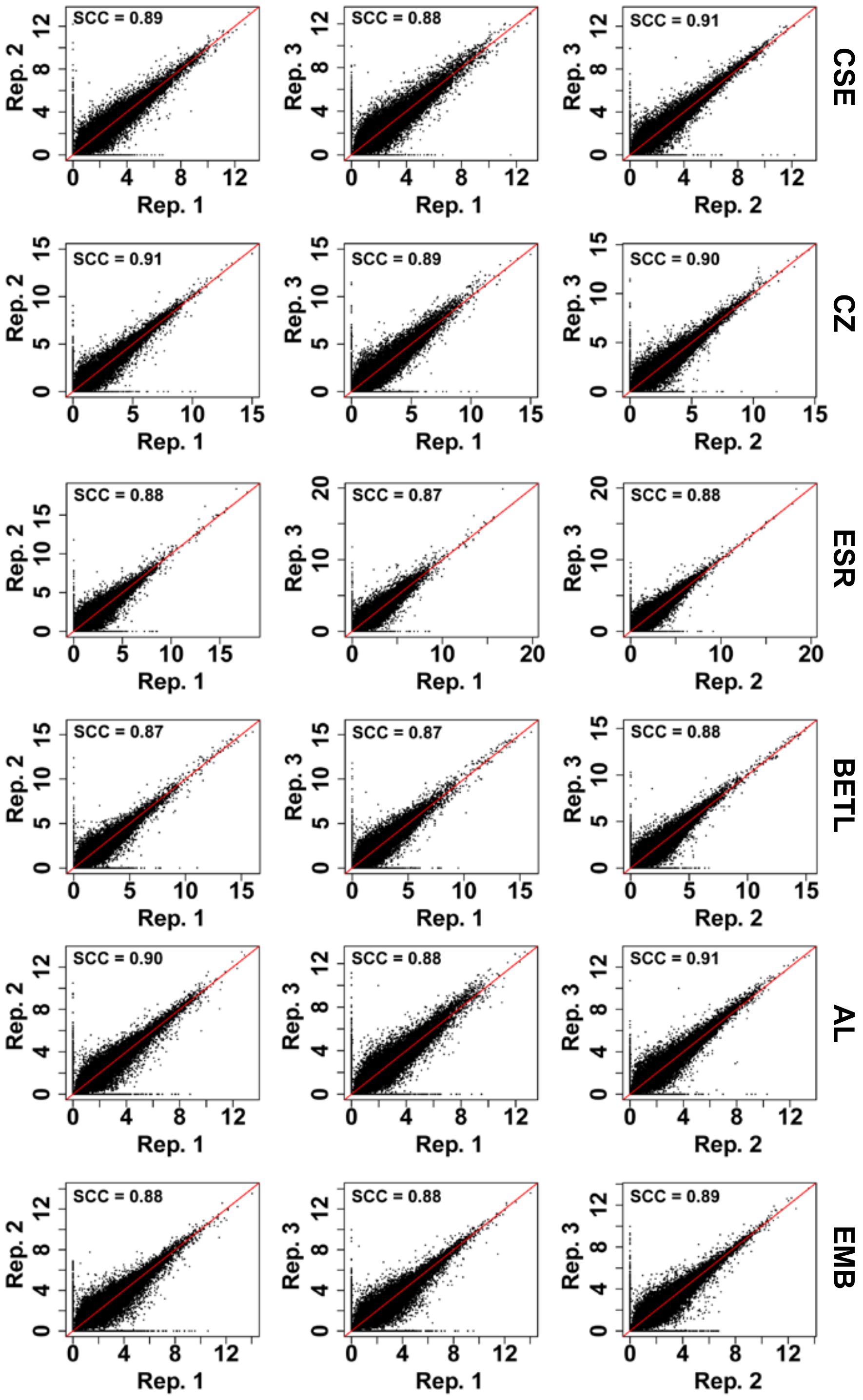


Supplemental Figure 2. Representative images of kernel compartments that were marked and collected for the LCM-RNA-Seq analyses reported in this study.

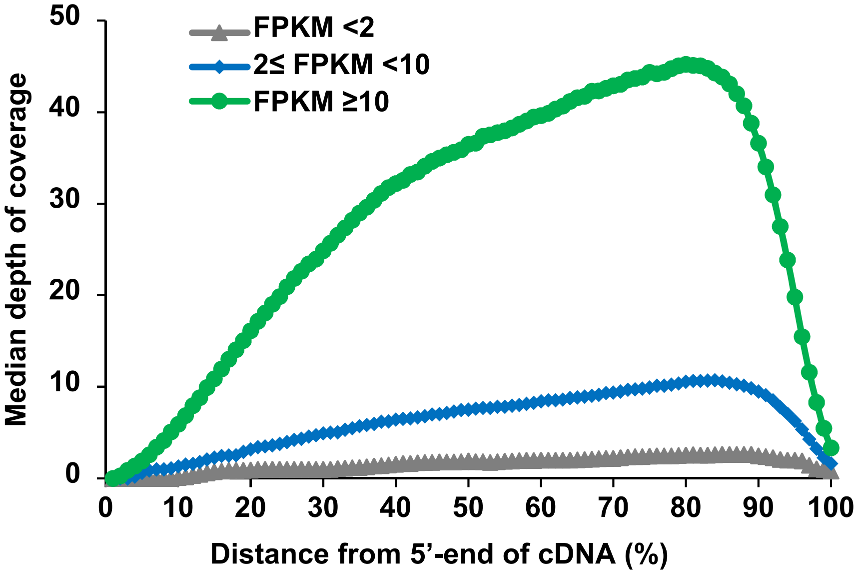
(A) Regions of the CSE and the captured regions of CZ; **(B)** CZ and the captured regions of ESR; **(C)** ESR; **(D)** BETL, and the captured regions of ESR and PC; **(E)** Regions of AL; **(F)** The EMB including suspensor and the captured regions of ESR; **(G)** Regions of NU; **(H)** Region of PE; and **(I)** Regions of PED. Abbreviations same as in Supplemental Figure 1. Bars: (A) and (B), 400 μm; (C), 200 μm; (D), 400 μm; (E), 100 μm; (F), 200 μm; (G), (H) and (I), 400 μm.



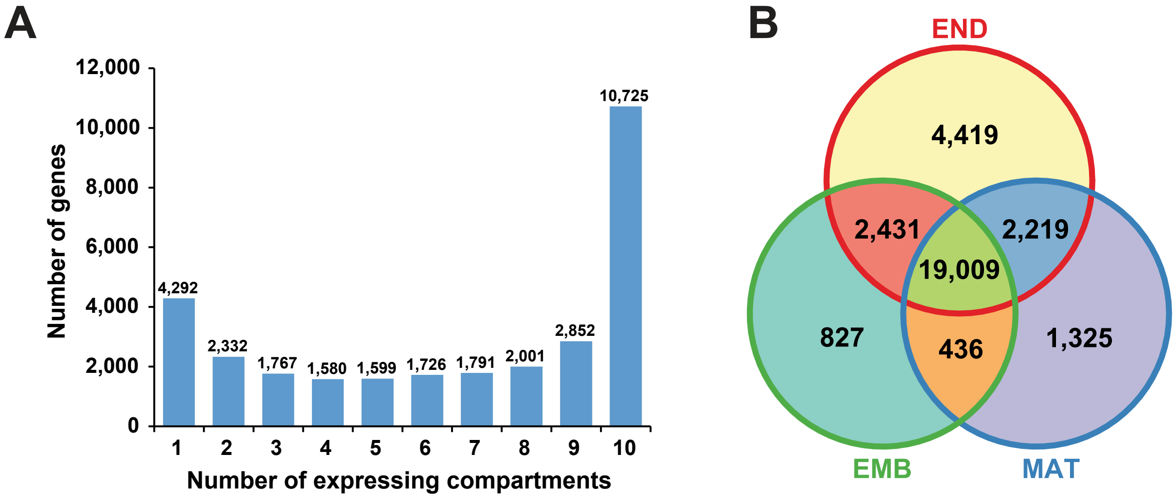
Supplemental Figure 3. Representative quality assessments of LCM-derived RNAs used in sequencing. Electropherograms of sample RNAs extracted from the captured kernel compartments prior to DNase treatment. RIN, RNA Integrity Number, is a measure of RNA quality (Agilent Technologies). Controls refer to known concentrations of total RNA obtained from 2-DAP kernels. Abbreviations: AL, aleurone; BETL, basal endosperm transfer layer; CSE, central starchy endosperm; CZ, conducting zone; EMB, embryo; ESR, embryo-surrounding region; NU, nucellus; PC: placento-chalazal region; PE, pericarp; PED, vascular region of the pedicel.



Supplemental Figure 4. Reproducibility of RNA-Seq reads for each triplicate of the filial compartments. Log_2-transformed FPKM values of the 29,369 genes expressed in at least one of the 22 sequenced samples are shown as scatter plots and were used as input for the Spearman correlation coefficient (SCC) analysis. The red diagonal line in each scatter plot denotes equal FPKMs between two samples. Abbreviations: AL, aleurone; BETL, basal endosperm transfer layer; CSE, central starchy endosperm; CZ, conducting zone; EMB, embryo; ESR, embryo-surrounding region.

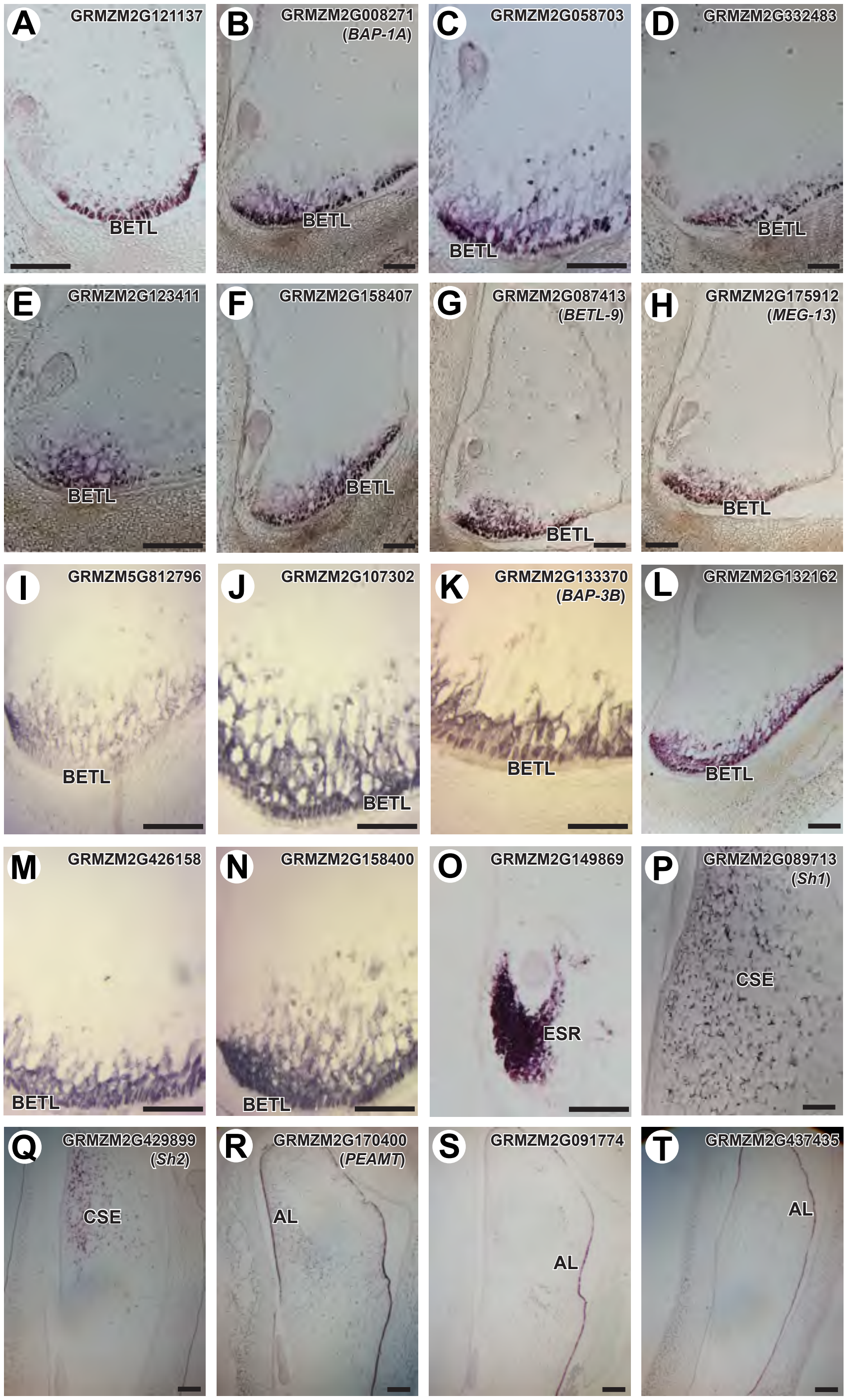


Supplemental Figure 5. Distribution profile of RNA-Seq reads along the length of the gene models. Reads of all 22 sequenced samples were pooled and exonic reads were analyzed for depth of coverage using the available reference gene models to show the combination of Oligo(dT) and random primers provided sufficient coverage of the sequenced cDNAs.



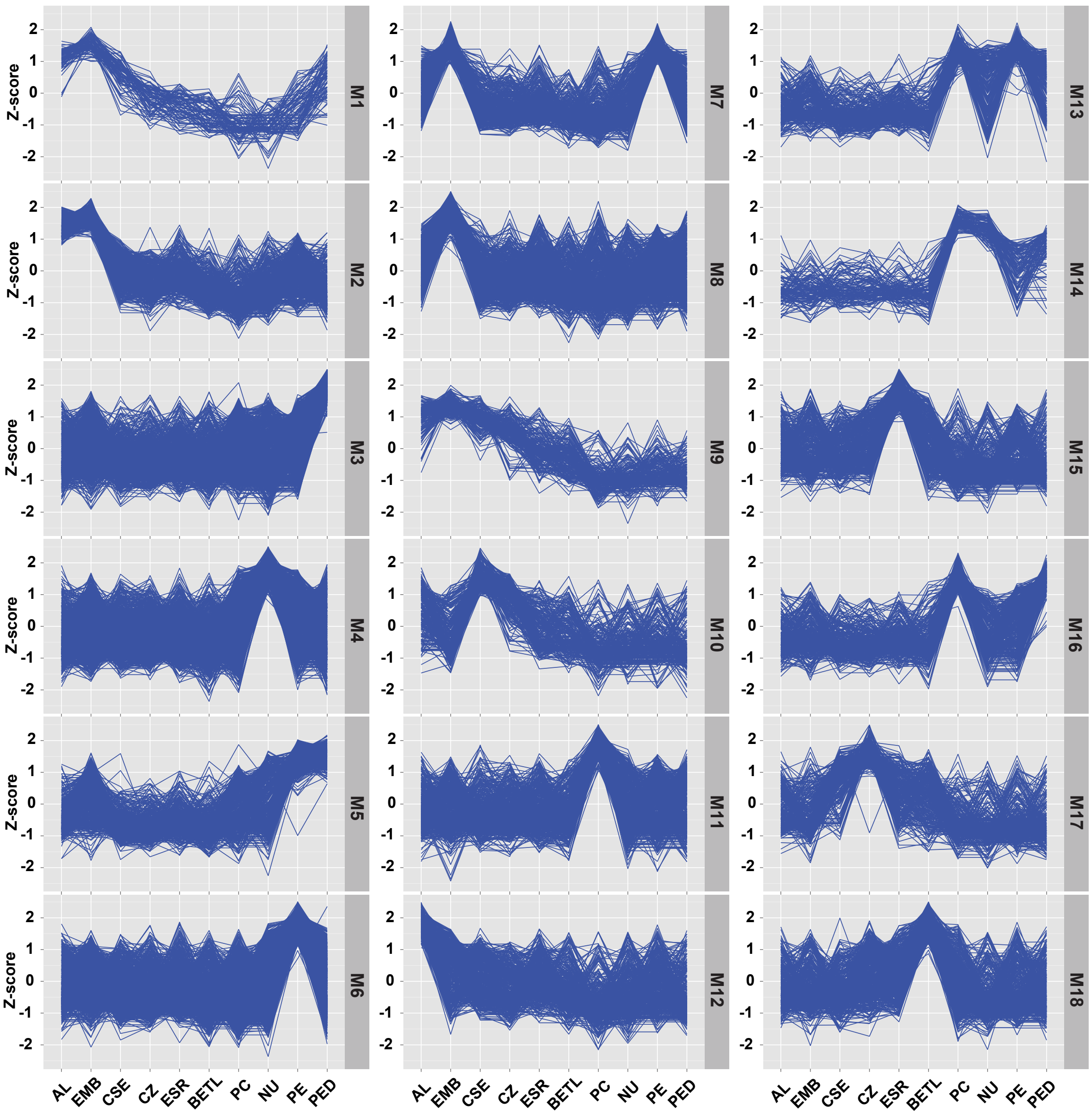
Supplemental Figure 6. Profiles of sequenced RNAs from the captured kernel compartments.

(A) Number of expressed genes detected in one or more kernel compartments. Among the total 30,665 genes that were expressed in at least one compartment, 10,725 were detected in all compartments while expression of 4,292 genes was restricted to single compartments. **(B)** Venn diagram of the numbers of genes expressed in EMB, expressed in at least one captured compartment of endosperm (END), or expressed in at least one maternal compartment (MAT).

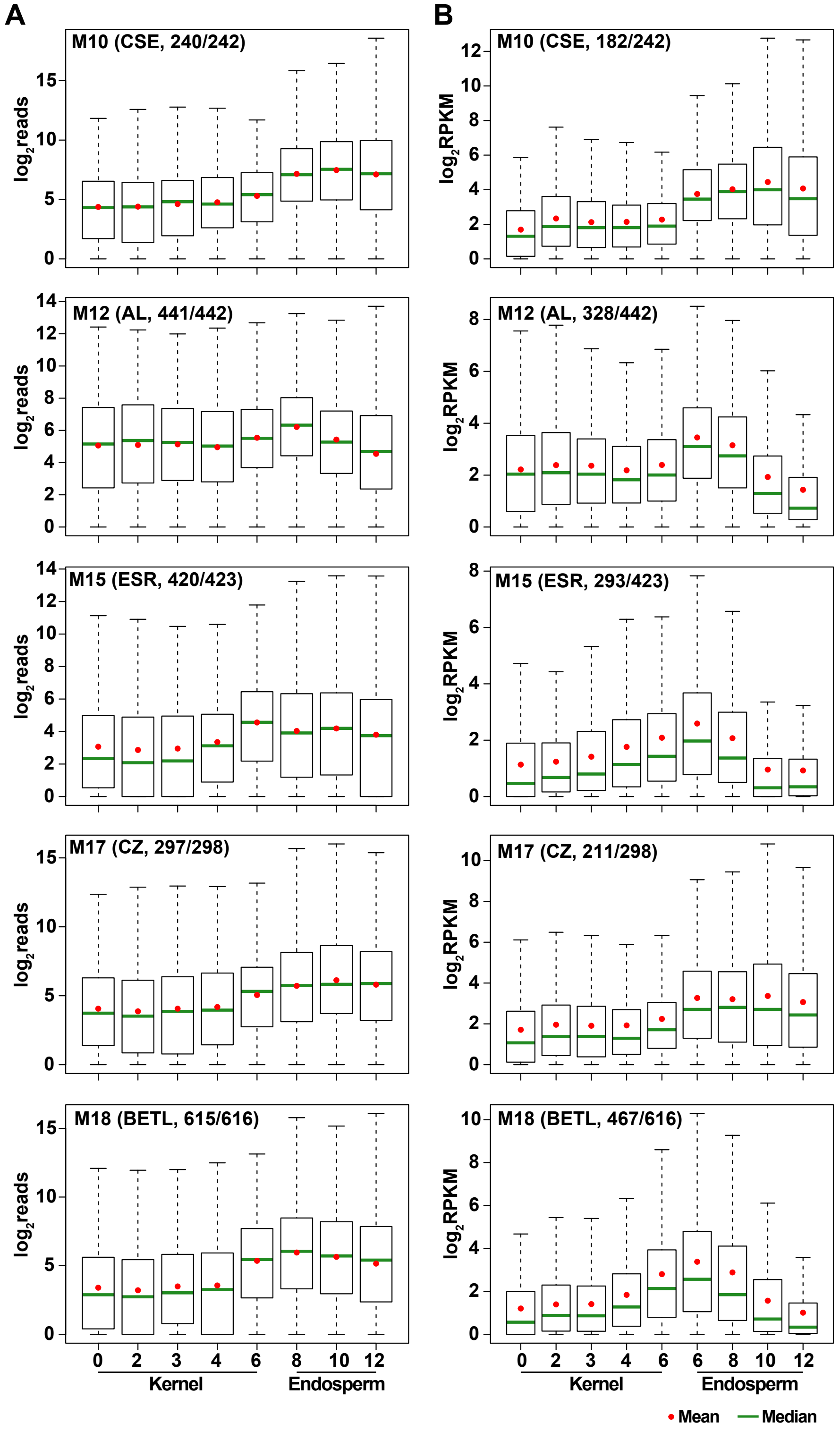


Supplemental Figure 7. Validation of the compartment-specific expression patterns using *in situ* hybridization localization of the mRNAs. For each panel, the gene ID/locus name is indicated.

(A) through **(N)** BETL-specific genes. **(O)** An ESR-specific gene. **(P)** and **(Q)** CSE-specific genes. **(R)** through **(T)** AL-specific genes. Stage of kernels: (A), 6 DAP; (B) through (I), 7 DAP; (J) through (N), 8 DAP; (O) 7 DAP; (P) through (T), 10 DAP. Bars: 2 mm.

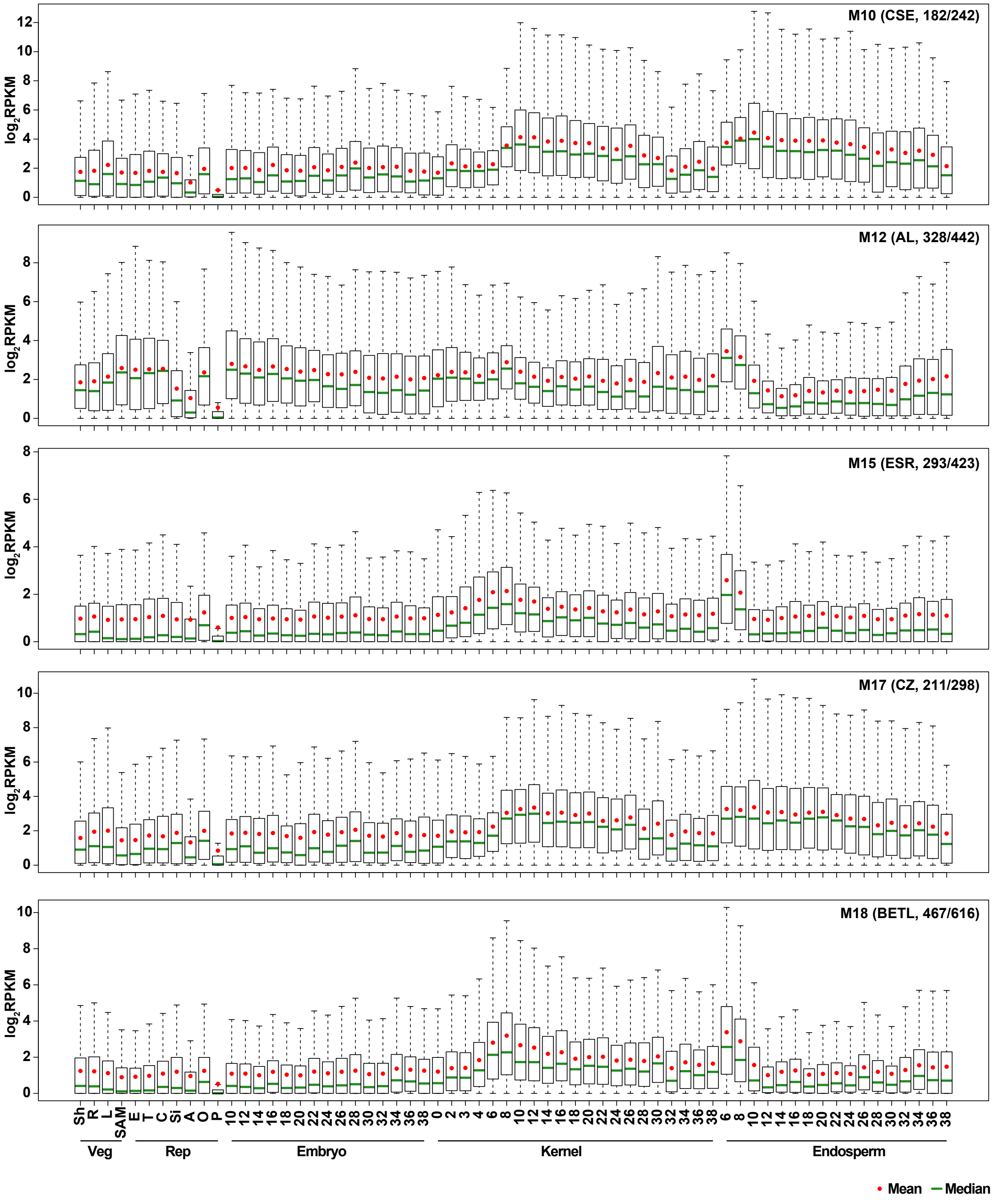


Supplemental Figure 8. Z-score plots showing expression profiles of all genes in the WGCNA-generated co-expression modules M1-M18. Abbreviations same as in Supplemental Figure 1.

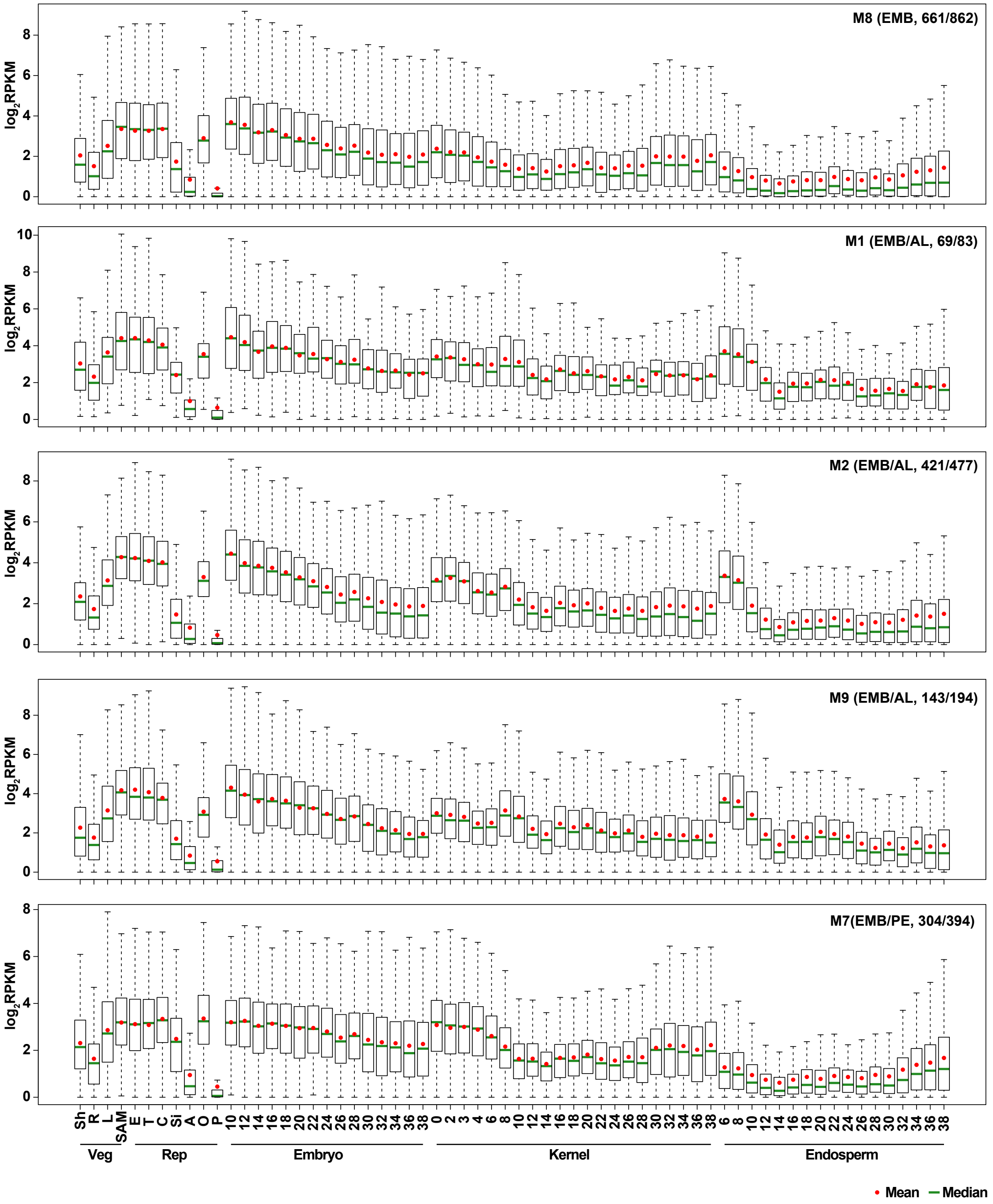


Supplemental Figure 9. Expression pattern of genes in the endosperm-associated modules identified by WGCNA based on previously reported RNA-Seq data.

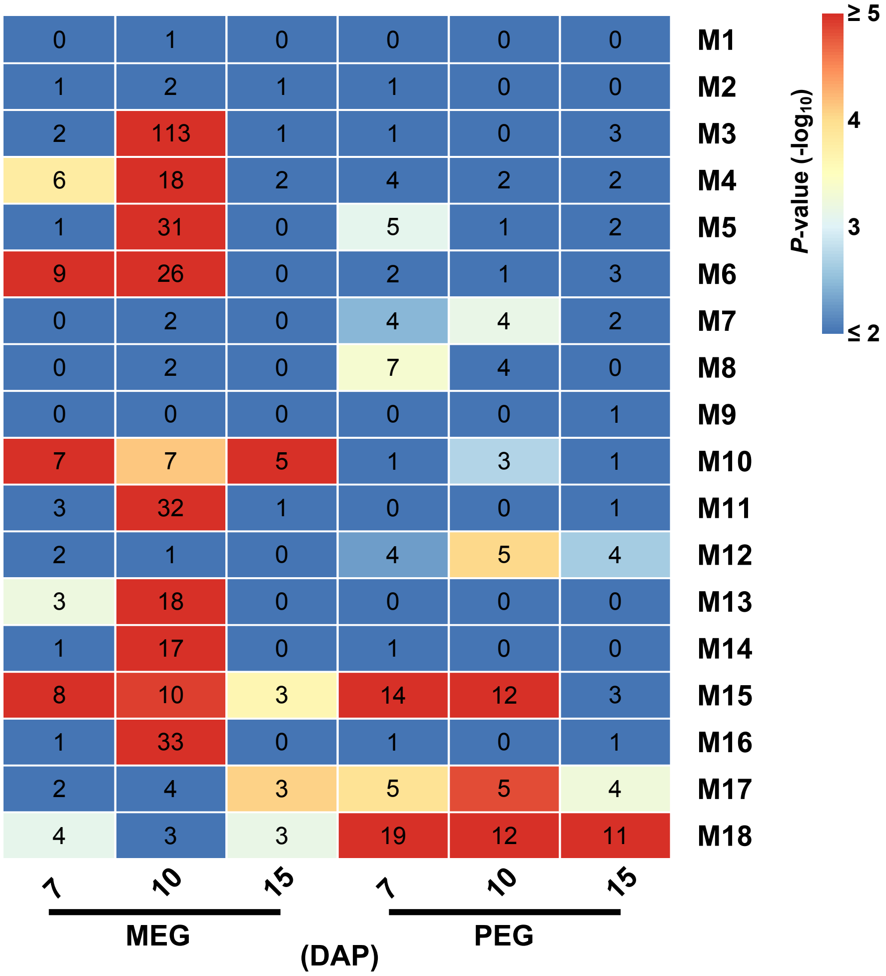
(A) Log$_2$-transformed normalized read counts data from Li et al. (2014). **(B)** Log$_2$-transformed Reads per kilobase of transcript per million mapped reads (RPKM) data from Chen et al. (2014). The selected data included kernels and endosperm of different developmental stages (in days after pollination, DAP). The associated kernel compartment and fractions of genes in each module with available data are indicated in parentheses.



Supplemental Figure 10. Expression pattern of genes in the endosperm-associated modules identified by WGCNA based on RNA-Seq data from Chen et al. (2014). The selected data included vegetative (Veg) tissues shoots (Sh), roots (R), Leaf (L), shoot apical meristem (SAM, Replicate 1); reproductive (Rep) tissues ear (E), tassel (T, Replicate 1), pre-emergence cob (C), silk (Si), Anther (A), ovule (O), pollen (P); and whole kernels, endosperm, and embryos of different developmental stages (in days after pollination, DAP). The associated kernel compartment and fractions of genes in each module that have available data are indicated in parentheses.

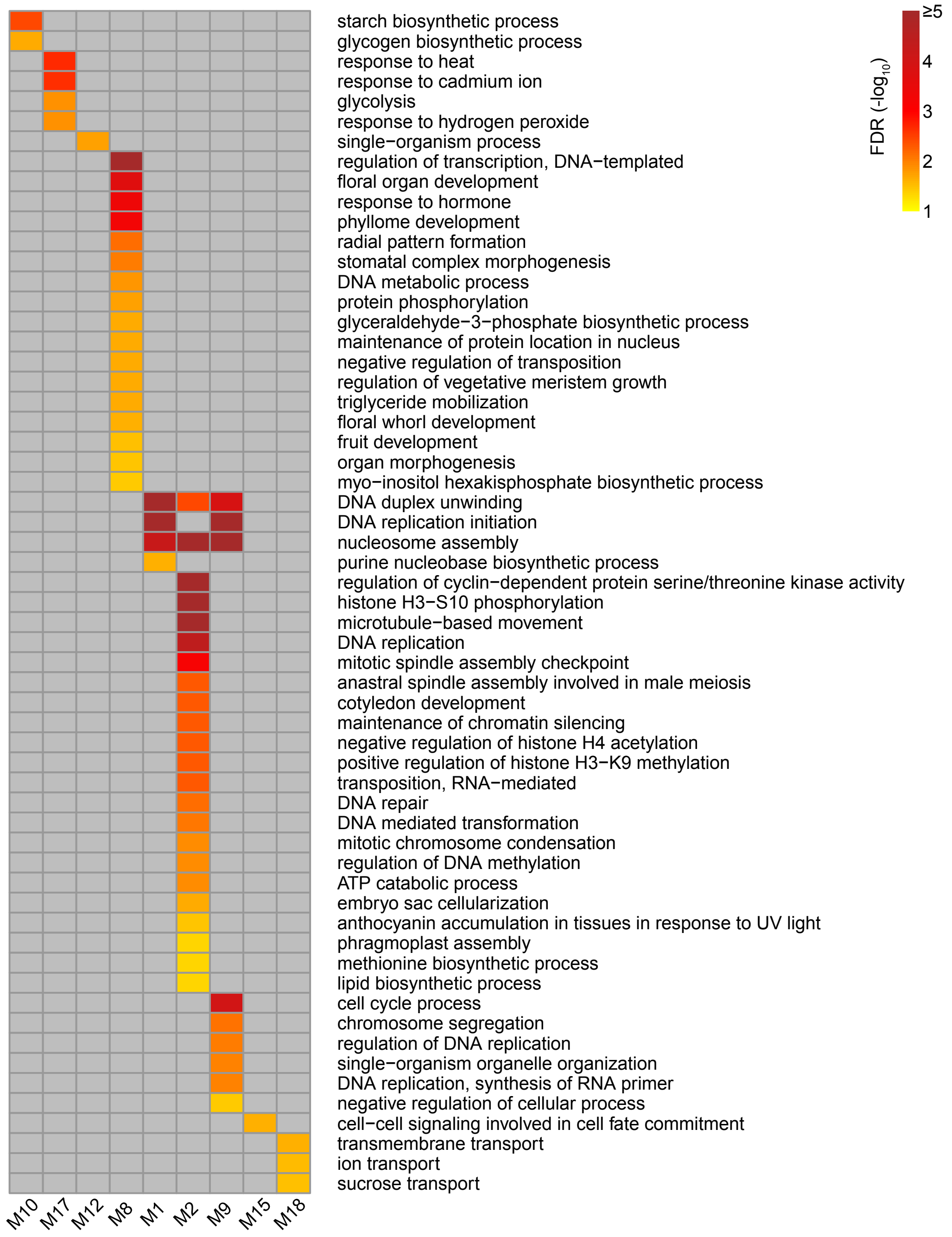


Supplemental Figure 11. Expression pattern of genes in the WGCNA co-expression modules (M1, M2, and M9) associated with both AL and EMB (in comparison to the other two EMB-associated modules M7 and M8) based on RNA-Seq data from Chen et al. (2014). The selected data included the same tissues as Supplemental Figure 10. The associated kernel compartment and fractions of genes in each module with available data are indicated in parentheses.

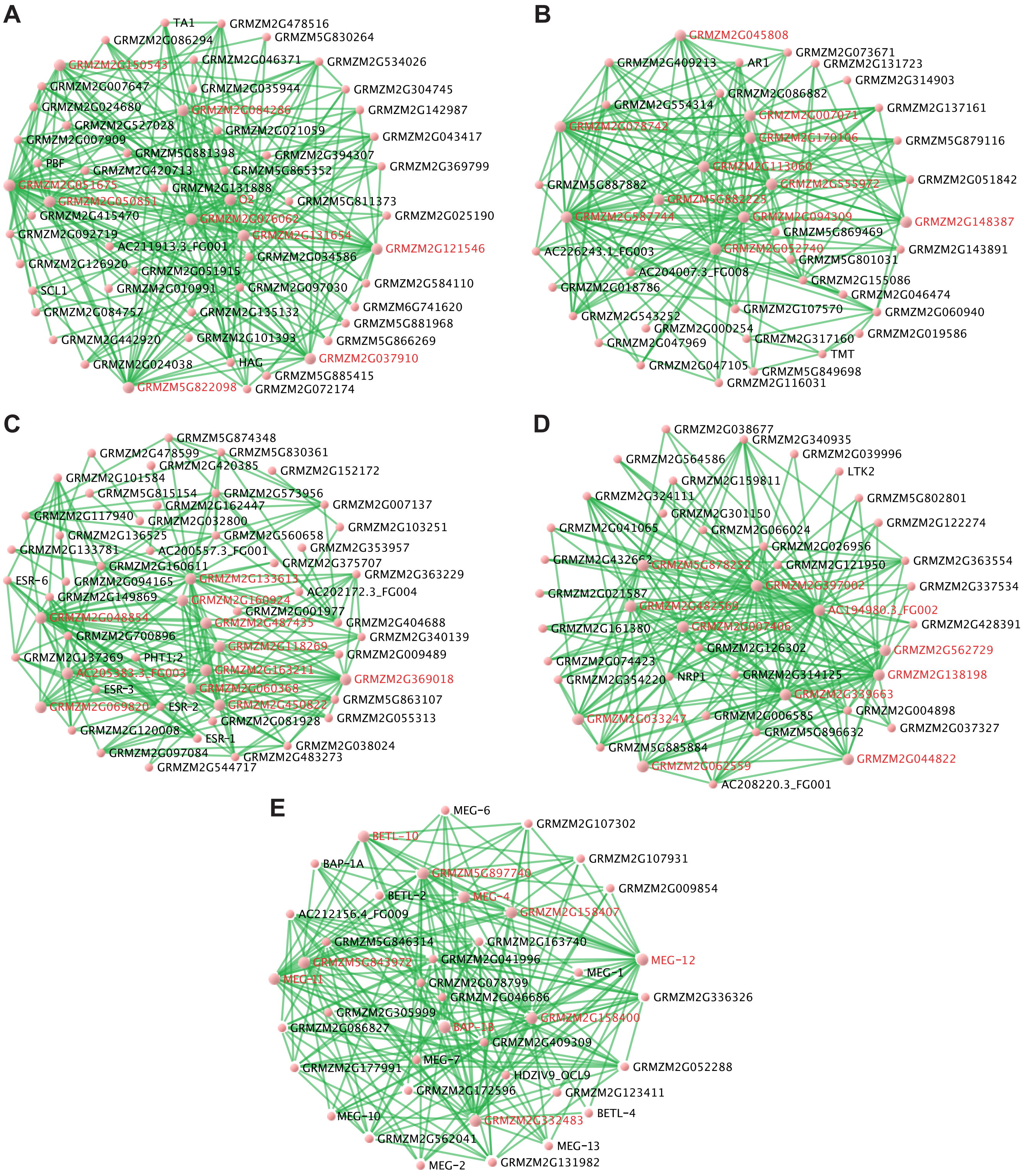


	MEG 7	MEG 10	MEG 15	PEG 7	PEG 10	PEG 15
M1	0	1	0	0	0	0
M2	1	2	1	1	0	0
M3	2	113	1	1	0	3
M4	6	18	2	4	2	2
M5	1	31	0	5	1	2
M6	9	26	0	2	1	3
M7	0	2	0	4	4	2
M8	0	2	0	7	4	0
M9	0	0	0	0	0	1
M10	7	7	5	1	3	1
M11	3	32	1	0	0	1
M12	2	1	0	4	5	4
M13	3	18	0	0	0	0
M14	1	17	0	1	0	0
M15	8	10	3	14	12	3
M16	1	33	0	1	0	1
M17	2	4	3	5	5	4
M18	4	3	3	19	12	11

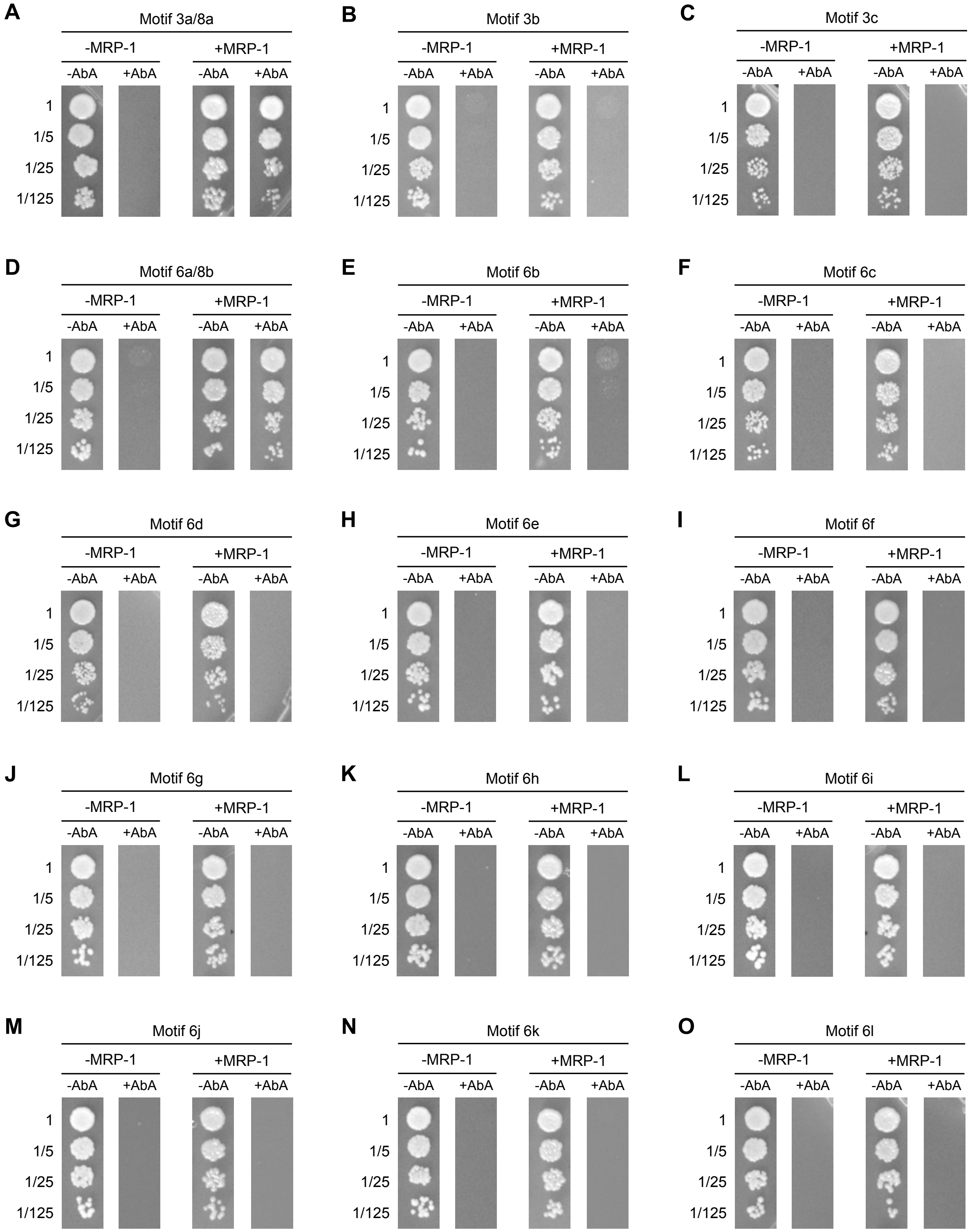
Supplemental Figure 12. Relationships of new sets of allele-biased genes with the co-expression modules obtained using WGCNA. The new allele-biased gene sets were identified using the normalized read data from Xin et al. (2013) by applying less stringent criteria, namely, 75% of the maternal reads and 55% of the paternal reads of the SNP associated reads (with a minimum 20 reads) were defined as maternally and paternally biased genes, respectively. The heat map indicates *P*-values (-$\log_{10}$) of hypergeometric tests of over-representation of genes in a given tested pair of gene sets. Allele-biased gene sets are noted on the x-axis and all WGCNA co-expression modules on the y-axis. Boxes contain the numbers of overlapping genes. Numbers of genes in each allele-biased gene set: 7-DAP MEG, 73; 10-DAP MEG, 451; 15-DAP MEG, 31; 7-DAP PEG, 172; 10-DAP PEG, 111; 15-DAP PEG, 137.

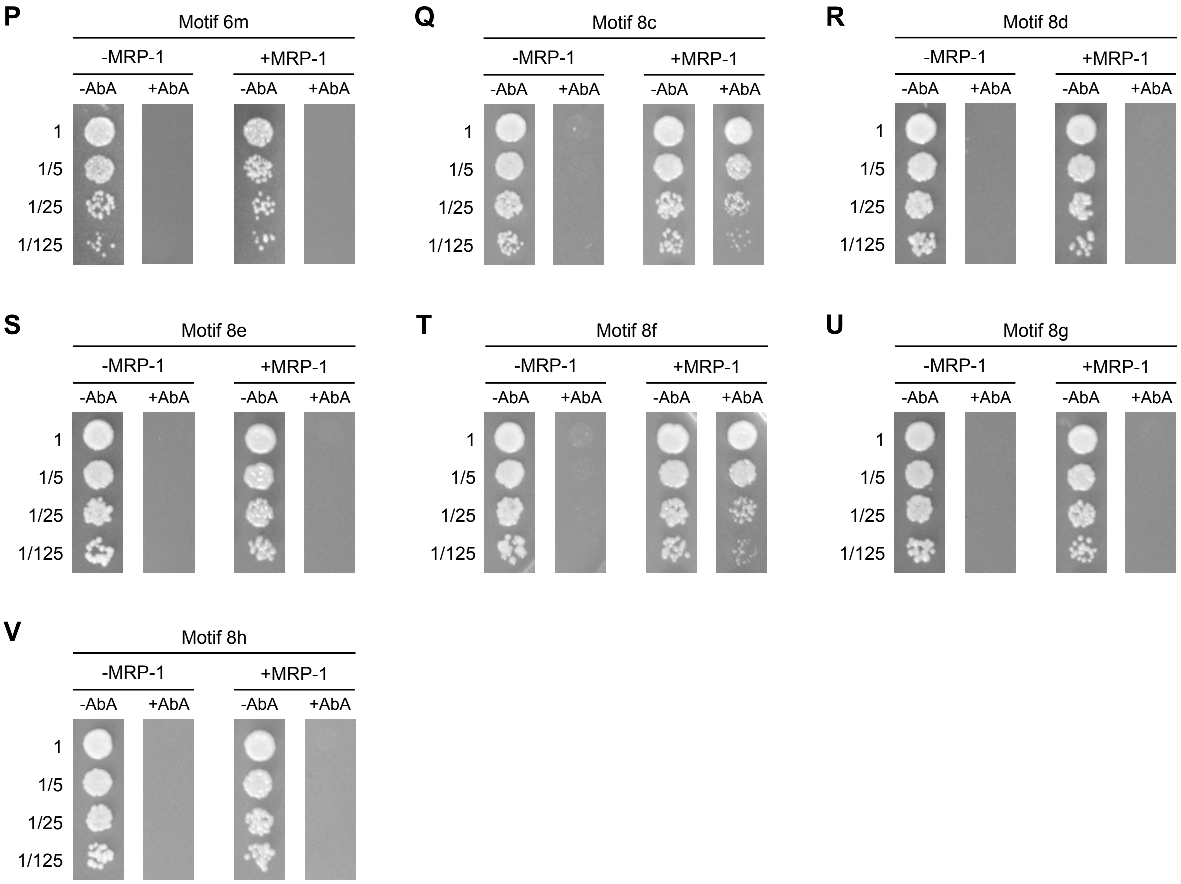


Supplemental Figure 13. Enrichment of biological processes in the filial compartment-correlated modules. The heat map indicates enriched GO terms detected for modules M1, M2, M8, M9, M10, M12, M15, M17, and M18 based on FDR (-log$_{10}$). The grey boxes represent GO terms that are not significantly enriched.

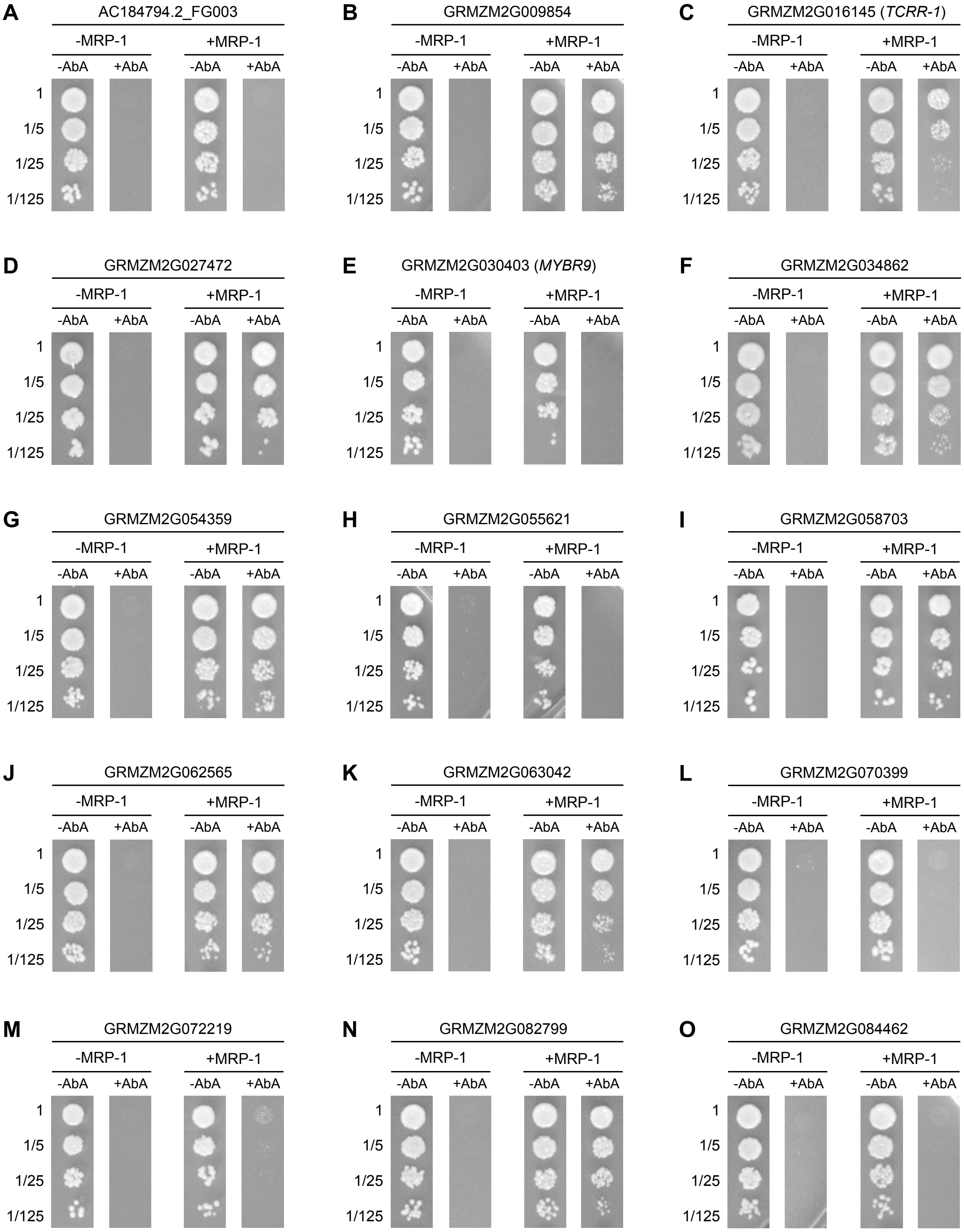


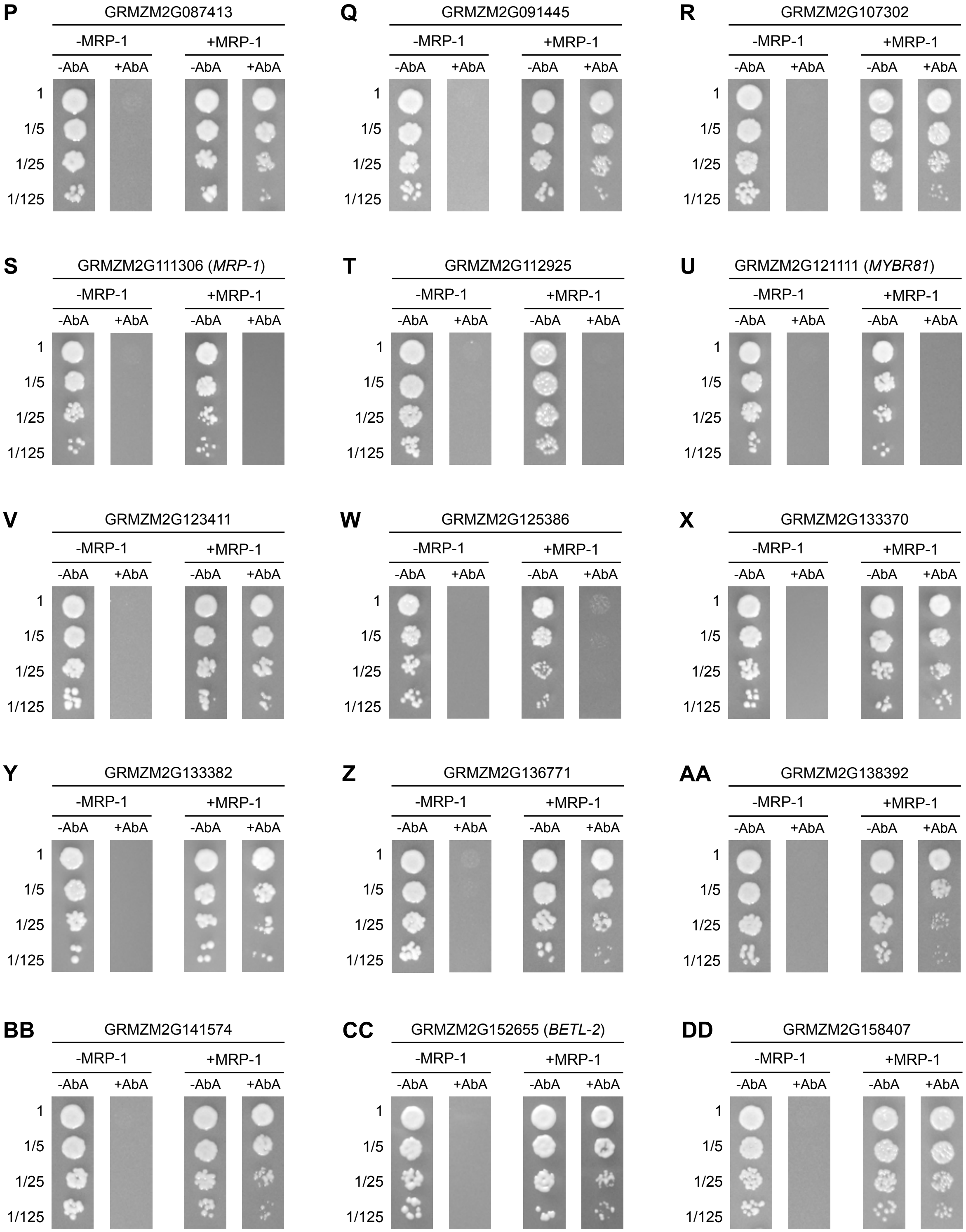
Supplemental Figure 14. Visualization of the five endosperm compartment-correlated co-expression modules using the VisANT program. The top 200 connections among top 100 intramodular hub genes (based on kME) are shown for modules M10 **(A)**, M12 **(B)**, M15 **(C)**, M17 **(D)**, and M18 **(E)** corresponding to CSE, AL, ESR, CZ, and BETL, respectively. Either a locus name (if available) or a gene ID is used to identify each gene. The 10 to 11 genes with the highest number of connections are shown in a bigger node size with red names/gene IDs.

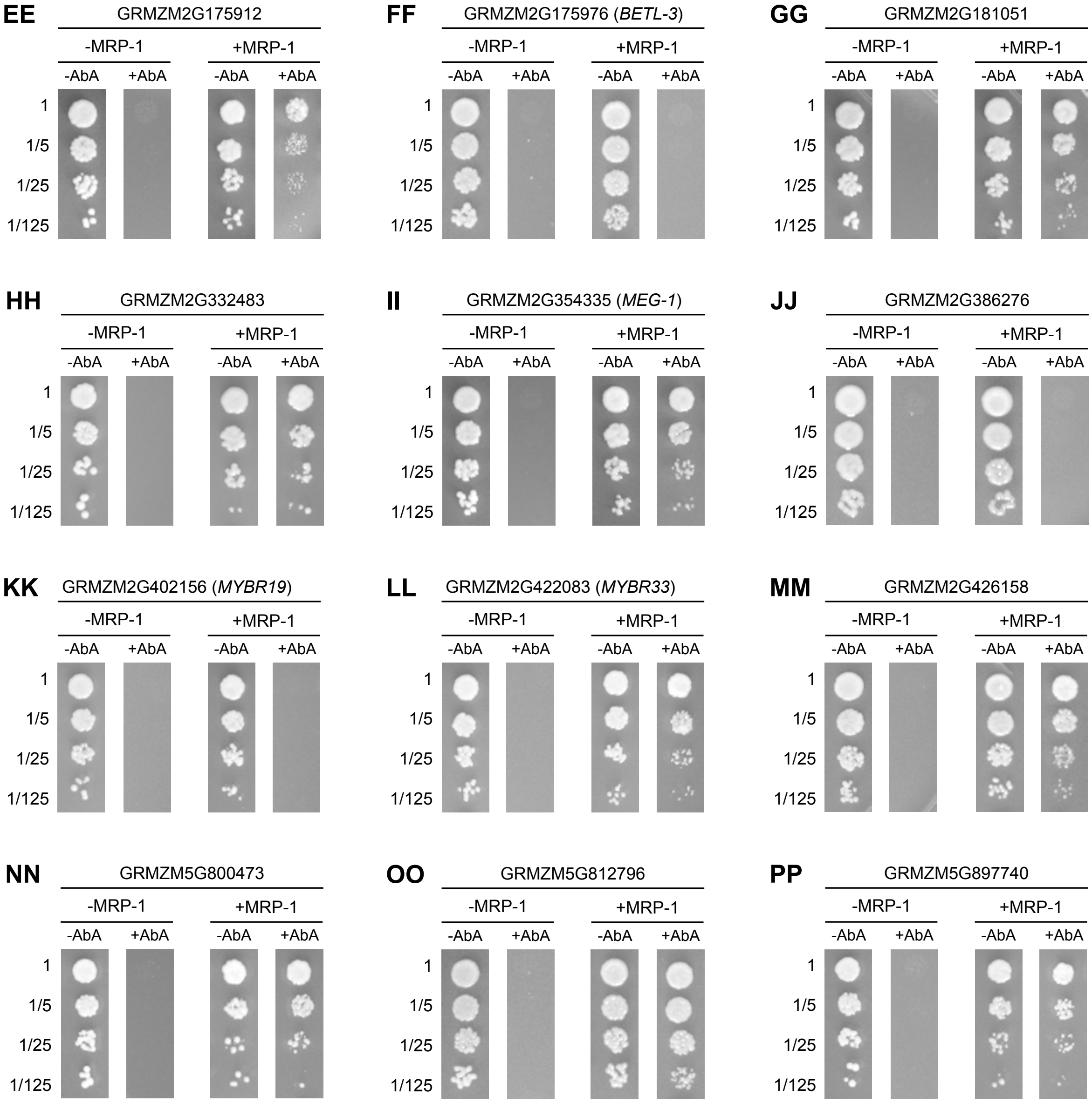

A
Motif 3a/8a
B
Motif 3b
C
Motif 3c
D
Motif 6a/8b
E
Motif 6b
F
Motif 6c
G
Motif 6d
H
Motif 6e
I
Motif 6f
J
Motif 6g
K
Motif 6h
L
Motif 6i
M
Motif 6j
N
Motif 6k
O
Motif 6l
-MRP-1
+MRP-1
-AbA
+AbA
1
1/5
1/25
1/125



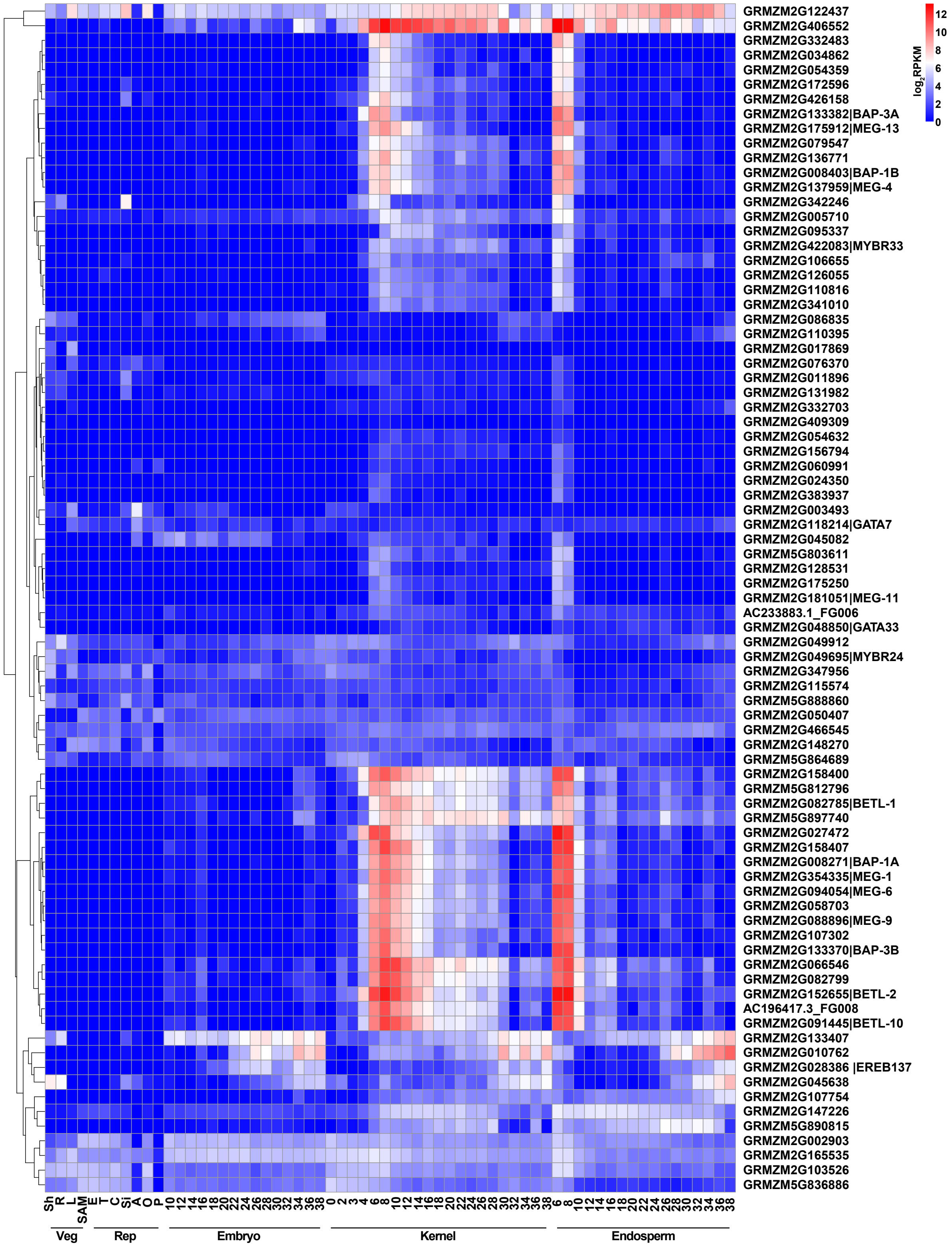
Supplemental Figure 15. Yeast one-hybrid assays for binding of MRP-1 to the sequence motifs listed in Table 1. For each motif, two yeast strains were tested, one lacking MRP-1 (-MRP-1) and one expressing MRP-1 (+MRP-1). Each strain was spotted onto plates containing (+AbA) and lacking (-AbA) Aureobasidin A. Each strain was spotted in a 1:5 dilutions series.


A
AC184794.2_FG003
B
GRMZM2G009854
C
GRMZM2G016145 (*TCRR-1*)
D
GRMZM2G027472
E
GRMZM2G030403 (*MYBR9*)
F
GRMZM2G034862
G
GRMZM2G054359
H
GRMZM2G055621
I
GRMZM2G058703
J
GRMZM2G062565
K
GRMZM2G063042
L
GRMZM2G070399
M
GRMZM2G072219
N
GRMZM2G082799
O
GRMZM2G084462
-MRP-1
+MRP-1
-AbA
+AbA
1
1/5
1/25
1/125


P
GRMZM2G087413
Q
GRMZM2G091445
R
GRMZM2G107302
S
GRMZM2G111306 (*MRP-1*)
T
GRMZM2G112925
U
GRMZM2G121111 (*MYBR81*)
V
GRMZM2G123411
W
GRMZM2G125386
X
GRMZM2G133370
Y
GRMZM2G133382
Z
GRMZM2G136771
AA
GRMZM2G138392
BB
GRMZM2G141574
CC
GRMZM2G152655 (*BETL-2*)
DD
GRMZM2G158407
-MRP-1
+MRP-1
-AbA
+AbA
1
1/5
1/25
1/125



Supplemental Figure 16. Yeast one-hybrid assays for binding of MRP-1 to the promoters of the genes listed in Supplemental Table 12. For each promoter, two yeast strains were tested, one lacking MRP-1 (-MRP-1) and one expressing MRP-1 (+MRP-1). Each strain was spotted onto plates containing (+AbA) and lacking (-AbA) Aureobasidin A. Each strain was spotted in a 1:5 dilutions series.



Supplemental Figure 17. Expression pattern of the 93 genes containing MRP-1-binding sub-motifs based on RNA-Seq data from Chen et al. (2014). Genes were hierarchically clustered based on Euclidean distance. The selected data included the same tissues as Supplemental Figure 10.

Supplemental Table 1. The origins, quality and quantities of RNAs isolated using laser-capture microdissection.

	# kernels			**# sections used**			**Total area (mm^2)**			**RNA quality as RNA Integrity Numbers (RINs)**			**Total amount of RNA (ng)**		
	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3
CSE	9	8	7	26	23	23	36.64	34.69	33.67	7.10	6.80	6.10	236.98	183.70	203.13
CZ	9	7	7	95	137	95	22.04	33.53	35.58	6.00	6.20	5.10	143.65	156.20	195.80
ESR	20	9	9	150	246	208	6.86	10.69	7.25	4.90	6.50	4.20	343.18	191.40	314.60
BETL	6	6	7	150	149	150	15.75	14.77	19.34	4.10	4.90	3.50	556.92	200.20	422.40
AL	8	6	6	57	68	63	10.77	6.43	8.73	5.30	6.30	5.00	242.01	244.20	334.40
EMB	11	3	3	89	61	87	8.86	11.15	9.52	6.00	5.50	4.00	101.20	235.40	458.04
PC	-	-	7	-	-	118	-	-	6.09	-	-	2.90	-	-	25.62
NU	-	14	-	-	110	-	-	27.15	-	-	4.20	-	-	171.60	-
PE	-	11	-	-	10	-	-	19.70	-	-	4.80	-	-	193.60	-
PED	-	12	-	-	41	-	-	19.39	-	-	5.00	-	-	411.40	-
Control (10 ng)	-	-	-	-	-	-	-	-	-	8.40	9.00	9.00	-	-	-
Control (5 ng)	-	-	-	-	-	-	-	-	-	8.40	9.30	9.10	-	-	-
Control (2.50 ng)	-	-	-	-	-	-	-	-	-	8.80	9.40	9.20	-	-	-
Control (1.25 ng)	-	-	-	-	-	-	-	-	-	8.10	8.10	9.30	-	-	-

Supplemental Table 2. Summary statistics of RNA-Seq reads and mapping.

Samples[a]	Total # reads	All mapped reads		Mapped to exons	
		#	%	#	% (of mapped)
CSE-1	10,222,204	8,861,426	86.7	3,299,695	37.2
CSE-2	31,450,130	25,808,488	82.1	8,616,333	33.4
CSE-3	33,686,796	27,230,237	80.8	8,924,753	32.8
CZ-1	29,475,616	24,887,580	84.4	9,755,319	39.2
CZ-2	36,099,924	28,111,041	77.9	10,407,325	37.0
CZ-3	31,555,056	24,171,723	76.6	7,456,103	30.8
ESR-1	40,439,606	34,729,514	85.9	11,344,960	32.7
ESR-2	33,883,182	26,160,199	77.2	8,323,640	31.8
ESR-3	32,478,306	29,137,023	89.7	8,238,762	28.3
BETL-1	17,109,048	14,341,367	83.8	4,599,768	32.1
BETL-2	27,823,360	21,678,667	77.9	6,237,856	28.8
BETL-3	29,420,758	20,380,515	69.3	6,319,413	31.0
AL-1	11,496,690	9,247,655	80.4	3,581,977	38.7
AL-2	30,289,840	23,899,741	78.9	7,937,483	33.2
AL-3	21,498,076	16,487,384	76.7	5,114,948	31.0
EMB-1	23,091,244	12,142,139	52.6	4,792,036	39.5
EMB-2	21,651,262	13,972,219	64.5	4,075,913	29.2
EMB-3	22,895,586	11,973,058	52.3	3,284,420	27.4
PC	28,140,418	21,025,363	74.7	5,095,299	24.2
NU	24,447,238	15,850,406	64.8	4,363,845	27.5
PE	23,581,668	16,044,397	68.0	3,549,164	22.1
PED	21,838,282	13,136,224	60.2	3,363,514	25.6

[a] Biological replicates are indicated as -1, -2 and -3.

Supplemental Table 3. Number of genes expressed in each of the ten compartments.

Compartment	Protein-coding genes	Transposable elements	Pseudogenes	miRNAs	TFs		Total #
					#	%	
CSE	19,928	664	544	0	1,137	5.4	21,136
CZ	20,775	819	646	0	1,172	5.3	22,240
ESR	22,228	925	699	1	1,305	5.5	23,853
BETL	19,281	704	550	0	1,105	5.4	20,535
AL	20,646	680	578	0	1,173	5.4	21,904
EMB	21,392	685	623	3	1,343	5.9	22,703
PC	15,605	354	305	0	964	5.9	16,264
NU	15,173	397	340	0	899	5.7	15,910
PE	17,615	417	369	1	1,057	5.7	18,402
PED	16,740	366	338	0	1,040	6.0	17,444

Supplemental Table 4. Number of genes expressed at different FPKM levels in the ten compartments.

Compartment	FPKM < 2		2 ≤ FPKM < 10		10 ≤ FPKM < 200		FPKM ≥ 200	
	#	%	#	%	#	%	#	%
CSE	14,501	47.29	7185	23.43	8,509	27.75	470	1.53
CZ	14,438	47.08	7570	24.69	8,237	26.86	420	1.37
ESR	13,859	45.19	7244	23.62	9,315	30.38	247	0.81
BETL	15,585	50.82	6104	19.91	8,685	28.32	291	0.95
AL	12,839	41.87	8204	26.75	9,182	29.94	440	1.43
EMB	11,112	36.24	9395	30.64	9,765	31.84	393	1.28
PC	15,613	50.91	7098	23.15	7,647	24.94	307	1.00
NU	14,905	48.61	7699	25.11	7,748	25.27	313	1.02
PE	11,176	36.45	10197	33.25	9,001	29.35	291	0.95
PED	12,354	40.29	9273	30.24	8,712	28.41	326	1.06

Supplemental Table 5. Summary of principle component analysis (PCA) of the ten compartments. Ten principle components (PCs) of each of the ten kernel compartments, the standard deviation of each PC, and the percentage of variance explained by each PC are shown.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
AL	-91.9	66.0	-1.3	57.3	0.6	17.4	34.3	93.6	-20.3	1.7E-12
BETL	-72.2	-125.1	26.8	-64.2	-18.2	-70.6	-58.0	42.6	12.9	-2.1E-13
CSE	-99.2	-6.0	-12.1	32.0	41.2	81.2	-15.1	-15.5	55.4	6.8E-13
CZ	-102.3	-51.3	-0.9	-14.6	34.3	51.8	-29.3	-46.6	-54.7	-3.8E-13
EMB	-55.3	152.4	3.7	58.4	-31.7	-82.5	-33.9	-44.8	2.3	9.1E-13
ESR	-71.3	-44.3	8.3	-47.5	-32.0	-31.7	105.5	-35.6	7.2	4.3E-13
NU	112.3	-30.5	-180.6	5.5	27.0	-22.9	1.5	3.3	-1.6	-8.6E-13
PC	146.2	-106.4	58.8	99.4	-73.0	22.4	-1.4	-8.7	-2.6	-1.2E-12
PE	97.0	111.6	7.6	-107.5	-71.9	62.0	-16.1	9.1	0.9	-8.3E-13
PED	136.7	33.8	89.8	-18.8	123.7	-27.0	12.5	2.7	0.5	-2.2E-13
Standard deviation	107.6	90.5	70.8	63.4	59.4	55.8	45.1	42.7	27.3	2.5E-13
% of variance	28.9	20.5	12.5	10.0	8.8	7.8	5.1	4.6	1.9	0.0
Cumulative % of variance	28.9	49.4	61.9	71.9	80.7	88.5	93.6	98.1	100.0	100.0

Supplemental Table 6. Summary of the available *in situ* hybridization and promoter analysis data for endosperm cell-specific genes.

Gene ID	Locus Name	Cell Type	CS Score	Assays	References
GRMZM2G170400	PEAMT	AL	0.94	*In situ* hybridization	This study
GRMZM2G437435	-	AL	0.90	*In situ* hybridization	This study
GRMZM2G091774	-	AL	0.87	*In situ* hybridization	This study
GRMZM2G069095	VPP1	AL	0.70	*In situ* hybridization	Wisniewski et al. (2004)
GRMZM2G091054	AL-9	AL	0.51	*In situ* hybridization; promoter fusion	Li et al. (2014); Gómez et al. (2009)
AC199820.4_FG006	-	BETL	0.99	*In situ* hybridization	Li et al. (2014)
GRMZM2G016145	TCRR-1	BETL	0.99	*In situ* hybridization	Muñiz et al. (2006)
GRMZM2G426158	-	BETL	0.99	*In situ* hybridization	This study
GRMZM2G111306	MRP1	BETL	0.99	*In situ* hybridization	Gómez et al. (2002)
GRMZM2G133382	BAP-3A	BETL	0.99	*In situ* hybridization	Serna et al. (2001)
GRMZM2G132162	-	BETL	0.99	*In situ* hybridization	This study
GRMZM2G072219	-	BETL	0.99	*In situ* hybridization	Li et al. (2014)
GRMZM2G073290	BETL-4	BETL	0.97	*In situ* hybridization	Hueros et al. (1999)
GRMZM2G158400	-	BETL	0.97	*In situ* hybridization	This study
GRMZM2G332483	-	BETL	0.97	*In situ* hybridization	This study
GRMZM2G121137	-	BETL	0.96	*In situ* hybridization	This study
GRMZM2G354335	MEG-1	BETL	0.96	*In situ* hybridization; promoter fusion	Gutiérrez-Marcos et al. (2004)
GRMZM2G008271	BAP-1A	BETL	0.95	*In situ* hybridization	This study; Serna et al. (2001)
GRMZM2G107302	-	BETL	0.94	*In situ* hybridization	This study
GRMZM2G123411	-	BETL	0.93	*In situ* hybridization	This study
GRMZM2G175912	MEG-13	BETL	0.93	*In situ* hybridization	This study
GRMZM2G058703	-	BETL	0.92	*In situ* hybridization	This study
GRMZM2G158407	-	BETL	0.92	*In situ* hybridization	This study
GRMZM2G152655	BAP-2	BETL	0.89	*In situ* hybridization	Hueros et al. (1999)
GRMZM5G812796	-	BETL	0.89	*In situ* hybridization	This study
GRMZM2G167733	EBE-2	BETL	0.86	*In situ* hybridization; promoter fusion	Magnard et al. (2003)
GRMZM2G082785	BETL-1	BETL	0.79	*In situ* hybridization	Hueros et al. (1995)
GRMZM2G401374	CC8	BETL	0.76	*In situ* hybridization	Massonneau et al. (2005)
GRMZM2G087413	BETL-9	BETL	0.74	*In situ* hybridization; promoter fusion	This study; Royo et al. (2014)
GRMZM2G090264	TCRR-2	BETL	0.57	*In situ* hybridization	Muñiz et al. (2010)
GRMZM2G138727	27-kD γ-zein	CSE	0.96	*In situ* hybridization	Woo et al. (2001)
GRMZM2G060429	16-kD γ-zein	CSE	0.95	*In situ* hybridization	Woo et al. (2001)
GRMZM2G089713	Sh1	CSE	0.89	*In situ* hybridization	This study
GRMZM2G369799	-	CSE	0.77	*In situ* hybridization	Li et al. (2014)
GRMZM2G429899	Sh2	CSE	0.68	*In situ* hybridization	This study
GRMZM2G023872	SCL1	CSE	0.60	*In situ* hybridization	Li et al. (2014)
GRMZM2G154182	ASN1	CSE	0.47	*In situ* hybridization	Li et al. (2014)
GRMZM2G006585	-	CZ	0.70	*In situ* hybridization	Li et al. (2014)
GRMZM2G315601	ESR-2	ESR	0.99	*In situ* hybridization	Li et al. (2014)
GRMZM2G048353	ESR-6	ESR	0.99	*In situ* hybridization	Balandín et al. (2005)
GRMZM2G149869	-	ESR	0.99	*In situ* hybridization	This study
GRMZM2G120008	-	ESR	0.99	*In situ* hybridization	Li et al. (2014)
GRMZM2G046086	ESR-1	ESR	0.99	*In situ* hybridization	Li et al. (2014)
GRMZM2G372553	AE3	ESR	0.54	*In situ* hybridization	Magnard et al. (2000)

Supplemental Table 7. Robustness of WGCNA-generated co-expression modules based on a permutation test of average topological overlap (TO).

Module	Mean TO observed[a]	Mean TO random[b]	Maximal TO random[c]	*P*-value[d]
1	0.20032682	0.04206503	0.05808373	$< 10^{-5}$
2	0.13829484	0.03242548	0.03794889	$< 10^{-5}$
3	0.05589406	0.03135009	0.03492353	$< 10^{-5}$
4	0.05180793	0.03119400	0.03506029	$< 10^{-5}$
5	0.11182849	0.03251804	0.03856629	$< 10^{-5}$
6	0.05307235	0.03117166	0.03413336	$< 10^{-5}$
7	0.10177977	0.03284855	0.03858159	$< 10^{-5}$
8	0.05829481	0.03152054	0.03555416	$< 10^{-5}$
9	0.26306783	0.03539109	0.04476182	$< 10^{-5}$
10	0.11657907	0.03440147	0.04239688	$< 10^{-5}$
11	0.04351963	0.03179076	0.03609683	$< 10^{-5}$
12	0.08102435	0.03258770	0.03830303	$< 10^{-5}$
13	0.11766000	0.03433284	0.04294189	$< 10^{-5}$
14	0.14466003	0.03906574	0.05298123	$< 10^{-5}$
15	0.05718379	0.03269729	0.03842810	$< 10^{-5}$
16	0.10289539	0.03315041	0.04010339	$< 10^{-5}$
17	0.11984522	0.03364567	0.04121327	$< 10^{-5}$
18	0.07067248	0.03197153	0.03666547	$< 10^{-5}$

[a] the average TO for the genes in an observed module.

[b] the average TO of 100,000 iterations.

[c] the maximum of the average TO for the 100,000 iterations.

[d] the empirical probability of finding an average TO greater than or equal to the observed TO in 100, 000 collections of modules comprised of randomly selected genes.

Supplemental Table 8. Allele-biased genes enriched in the endosperm-associated co-expression modules M10, M15, M17, and M18.

Gene ID	Module	Allelic Expression Pattern	Stringency[a]	TF Family	Functional Annotation
GRMZM2G014119	10	MEG	High	-	Uncharacterized protein
GRMZM2G170099	10	MEG	High	-	Uncharacterized protein
GRMZM2G169695	10	MEG	High	-	AT-rich element binding factor 3
GRMZM2G124708	10	MEG	High	-	-
GRMZM2G121546	10	MEG	Low	-	Uncharacterized protein
GRMZM2G072174	10	MEG	Low	-	Uncharacterized protein
GRMZM2G154182	10	MEG	Low	NAC	Putative NAC domain transcription factor superfamily protein; Uncharacterized protein
GRMZM2G500698	10	MEG	Low	-	-
GRMZM2G170201	10	PEG	High	Orphans	Paired amphipathic helix repeat family protein
GRMZM2G043417	10	PEG	High	-	-
GRMZM2G059102	10	PEG	Low	MADS	MADS-box transcription factor 47; Uncharacterized protein
GRMZM2G359589	15	MEG	High	C2H2	Uncharacterized protein
GRMZM2G370991	15	MEG	High	-	Uncharacterized protein
GRMZM2G343972	15	MEG	High	-	Uncharacterized protein
GRMZM2G130580	15	MEG	High	Orphans	Uncharacterized protein
GRMZM2G024468	15	MEG	High	MYB	Uncharacterized protein
GRMZM2G150680	15	MEG	High	MYB	Putative MYB DNA-binding domain superfamily protein; Uncharacterized protein
GRMZM2G069840	15	MEG	High	-	-
GRMZM2G476175	15	MEG	High	-	-
GRMZM2G120085	15	MEG	Low	-	Uncharacterized protein
GRMZM2G474602	15	MEG	Low	-	-
GRMZM2G092101	15	PEG	High	-	Uncharacterized protein
GRMZM2G103164	15	PEG	High	-	Putative leucine-rich repeat receptor-like protein kinase family protein
GRMZM2G324131	15	PEG	High	C2C2-GATA	Putative GATA transcription factor family protein
GRMZM5G830365	15	PEG	High	-	Putative AP2/EREBP transcription factor superfamily protein
GRMZM2G089562	15	PEG	High	-	DNA-binding protein; Uncharacterized protein
AC209624.2_FG001	15	PEG	High	-	-
AC209624.2_FG003	15	PEG	High	-	-
GRMZM2G028366	15	PEG	High	-	-
GRMZM2G093947	15	PEG	High	-	-
GRMZM2G374169	15	PEG	High	-	-
GRMZM2G494808	15	PEG	High	-	-
GRMZM2G099353	15	PEG	Low	-	Uncharacterized protein
GRMZM2G110531	15	PEG	Low	Orphans	Speckle-type POZ protein
GRMZM2G004334	15	PEG	Low	Homeobox	Putative homeobox/lipid-binding domain family protein
GRMZM2G450822	15	PEG	Low	-	-
GRMZM2G062650	17	MEG	High	NAC	NAM-related protein 1
GRMZM2G063498	17	MEG	High	-	-

Supplemental Table 8 Continued

GRMZM2G041065	17	MEG	High	-	Pyrophosphate-energized vacuolar membrane proton pump
GRMZM2G179777	17	MEG	Low	-	Triacylglycerol lipase
GRMZM2G085078	17	MEG	Low	-	-
GRMZM2G047104	17	PEG	High	-	Putative homeodomain-like transcription factor superfamily protein
AC191534.3_FG003	17	PEG	High	-	-
GRMZM2G006732	17	PEG	High	-	-
GRMZM2G339663	17	PEG	High	-	-
GRMZM5G897856	17	PEG	High	-	-
GRMZM2G112925	18	MEG	High	Orphans	-
GRMZM2G103247	18	MEG	Low	Orphans	Uncharacterized protein
GRMZM2G147226	18	MEG	Low	-	Uncharacterized protein
GRMZM2G012071	18	MEG	Low	-	-
GRMZM2G152764	18	MEG	Low	-	-
GRMZM2G459363	18	MEG	Low	-	-
GRMZM2G447406	18	PEG	High	-	Uncharacterized protein
GRMZM2G449489	18	PEG	High	-	Uncharacterized protein
GRMZM2G007736	18	PEG	High	-	Uncharacterized protein
GRMZM2G139406	18	PEG	High	-	Uncharacterized protein
GRMZM2G048850	18	PEG	High	C2C2-GATA	Uncharacterized protein
GRMZM2G145123	18	PEG	High	-	Putative RING/U-box superfamily protein; Uncharacterized protein
GRMZM2G104866	18	PEG	High	AP2-EREBP	Putative AP2/EREBP transcription factor superfamily protein; Uncharacterized protein
GRMZM2G121570	18	PEG	High	MYB	MYB-type transcription factor
GRMZM2G084462	18	PEG	High	-	Isopentenyl transferase IPT2
GRMZM2G037469	18	PEG	High	-	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1
GRMZM2G136465	18	PEG	High	-	-
GRMZM2G164314	18	PEG	High	-	-
GRMZM2G366435	18	PEG	High	-	-
GRMZM2G479318	18	PEG	High	-	-
GRMZM5G871454	18	PEG	High	-	-
GRMZM2G156794	18	PEG	Low	-	Uncharacterized protein
GRMZM2G046686	18	PEG	Low	-	Hexokinase-1; Uncharacterized protein
GRMZM2G131165	18	PEG	Low	-	Anthranilate N-benzoyltransferase protein 1
GRMZM2G480434	18	PEG	Low	AP2-EREBP	-
GRMZM2G311401	18	PEG	Low	-	-
GRMZM2G345189	18	PEG	Low	-	-
GRMZM2G474620	18	PEG	Low	-	-

[a] Stringency of criteria used for defining imprinted/allele-biased gene expression patterns. High indicates genes identified by applying the relatively stringent criteria used by Xin et al. (2013); Low indicates additional genes identified by applying the less stringent criteria used in this study.

Supplemental Table 9. Motif analysis of the endosperm compartment-correlated modules M10, M12, M15, M17, and M18.

Module	Motif	E-value	Motif Sequence	Matching TF[a]
10	1	1.30E-136	[CG]CGCCGCCGCCG	abi4
	2	4.40E-62	AAA[AT]AAA[AT]A[AT]A[AT]	SOC1
	3	2.50E-56	[GA][GA][AG]GAG[AG][AG][GA]GAG	-
	4	2.20E-54	CAGC[AG]GCAGC	-
	5	1.50E-41	AA[AG]AAAAAAAAA	SOC1
	6	4.60E-39	C[GT]CC[GAT]CC[GT]CC	-
	7	2.70E-39	[GC]C[GC][GC]CG[CG][CG][CG]GC[GC]	-
	8	2.40E-33	[AT][AT]A[TA][TA]TAT[AT]T[AT][TA]	-
	9	5.10E-28	GG[AG]GG[AG][GA]G[AG][AG]G[GA]	-
	10	3.00E-25	C[GC]TCG[TG]CG[CTG]C	bZIP911
12	1	7.70E-196	CGCCGCCGCCGC	abi4
	2	4.10E-92	CG[CG]CGCCGCC	abi4
	3	1.20E-76	[GA][GA]AGAG[AG][GA]AGAG	-
	4	9.30E-83	AAAAAAAA[AT]A	SOC1
	5	2.10E-78	C[TG]CCTCC[TG]CC[TG]C	-
	6	4.30E-65	[TA]A[TA]ATATA[TA][AT]TA	-
	7	4.40E-55	C[GC][GC]CG[GC]CGGC	ERF1
	8	3.10E-53	CG[TC]CGTCG[CT]C	-
	9	8.70E-51	C[TC]GC[TC]GC[TG]GC	-
	10	1.30E-37	[AT]TTTTT[AT]TTT	-
15	1	7.00E-178	CACTCGGCAAAG	-
	2	7.10E-175	GCCGCCGCCGCC	abi4
	3	4.30E-86	GAGAG[AG][GA]AGA[GA][AG]	-
	4	1.00E-68	C[GC]GCG[GC]CG[GC]C	ERF1
	5	3.00E-64	AAAAA[AT]AAAA	SOC1
	6	2.70E-43	G[CG][GC]G[CA]GG[CA][GC]G[CG]G	abi4
	7	8.30E-48	C[AG]GCAGC[AG]GC	-
	8	3.70E-46	C[CT][CT]C[CT][CT]C[CT]CC[CT]C	-
	9	9.60E-43	[CT]C[GC][TCG]CG[CT]CG[GCT]CG	-
	10	5.10E-30	A[AT]A[TA]A[AT]A[TA][AT]AA[AT]	-
17	1	1.20E-154	[GC][CG]CGCCGCCGCC	abi4
	2	3.70E-88	ATATA[TA]A[TA]A[TA]AT	-
	3	1.50E-83	A[AG]AAAAAAAA	SOC1
	4	7.40E-97	[AG]GAGA[GA][AG]GAGAG	-
	5	7.30E-48	CCGCCGCCGC	ERF1
	6	3.40E-50	CG[CT]CG[TCG]CGCC	abi4
	7	3.10E-44	AAA[AT][AT][AT]AA[TA]AAA	SOC1
	8	6.40E-34	CTCC[TG]CCTCC	-
	9	7.40E-34	C[AG]GC[AG]GC[AG]GC	
	10	1.90E-37	CC[GC]C[GC]C[GC]C[CG][GC][CG]C	
18	1	1.80E-203	[CG]CGCCGCCGCCG	abi4
	2	2.40E-182	ATATATATATAT	
	3	1.00E-174	TAGATAGATAGA	--
	4	1.90E-101	CACTCGGCAAAG	--
	5	2.00E-99	CG[CG]CGCCGCC	abi4
	6	9.20E-81	TA[GA]ATATA[GTA]A[TA]A	
	7	1.90E-81	[AT]AAA[TA]AAA[TA]AAA	SOC1
	8	1.80E-104	TAGATA[GT]A[GT]A[GT]A	--
	9	2.80E-115	[GA]GAGAG[AG]GAGAG	--
	10	1.40E-74	C[GC]GCG[GC]CGGC	ERF1

[a] Transcription factors of which the known binding motif most significantly matches the identified motif (q-value < 0.05).

Supplemental Table 10. Occurrences of sub-motifs of each motif enriched in upstream sequences of M18 genes as identified by MEME.

Motif	Sub-motifs	Sites	Motif	Sub-motifs	Sites	Motif	Sub-motifs	Sites
1	CCGCCGCCGCCG	63	5	CGCCGCCGCC	65	8	TAGATAGATAGA	36
	GCGCCGCCGCCG	18		CGGCGCCGCC	32		TAGATATAGATA	31
	TCGCCGCCGCCG	13		CGCCGCCGGC	3		TAGATAGAGATA	10
	CCGCCGCCGCCC	3	6	TAGATATAGATA	24		TAGAGAGAGAGA	8
	GCGCCGCCGCCC	3		TAGATATATATA	13		TAGATATAGAGA	7
2	ATATATATATAT	90		TAAATATAAATA	11		TAGATAGATATA	6
	ATATATATAGAT	10		TAGATATAGAAA	10		AAGATAGAGAGA	1
3	TAGATAGATAGA	72		TAGATATAAATA	8		TAGATAGAGAGA	1
	TAGATATATAGA	18		TAAATATAAAAA	7	9	AGAGAGAGAGAG	40
	TAGATAAATAGA	10		TAAATATATAAA	6		GGAGAGAGAGAG	21
4	CACTCGGCAAAG	45		TATATATATATA	6		AGAGAGGGAGAG	6
	CACTCGACAAAG	4		TAAATATATATA	4		GGAGAGGGAGAG	6
	CACTCGGCACAG	3		TAGATAAAAAAA	4		GGAGGAGGAGAG	6
	CACTCGGTAAAG	3		TAAATATAGAAA	3		GGAGAAGGAGAA	4
	CTCTCGGCAAAG	3		TAGATATATAAA	3		GGAGAAGGAGAG	4
	CTCTCGGCACAG	3		TAGATATAAAAA	1		GGAGAGAGAGAA	3
	CACCCGGCAAAG	2	7	AAAATAAATAAA	23		GGAGAAAGAGAG	2
	CACTCAGCAAAG	2		AAAATAAAAAAA	12		GGAGGGAGAGAG	2
	CACTCGGCAAAA	2		AAAAAAAAAAAA	11		GGAGGGAGAGGG	2
	CACTCGGCAAAC	2		TAAAAAAATAAA	10		GGAGAGAGAGGG	1
	CACTCGGCAAAT	2		AAAAAAAATAAA	8		GGAGAGGGAGGG	1
	CACTTGGCAAAG	2		TAAATAAATAAA	8		GGAGGGGGAGAG	1
	CGCTCGGCAAAG	2		TAGAAAAATAAA	7		GGAGGGGGAGGG	1
	CTCTCGACAAAG	2		AAGAAAAATAAA	5	10	CGGCGGCGGC	40
	TACTCGGCAAAG	2		TAAAAAAAAAAA	4		CGGCGCCGGC	31
	AACTCGGCAAAG	1		TAAATAAAAAAA	4		CCGCGGCGGC	26
	CACTCGGCGAAG	1		AATATAAATAAA	3		CGGCGGCGCC	3
	CACTCGGTACAG	1		AAGATAAATAAA	2			
	CATTCGGCAAAG	1		TATATAAATAAA	2			
	CCCTCGGCAAAG	1		AAAATATATAAA	1			
	CTCTCAGCAAAG	1						

Supplemental Table 11. Putative functions of the 93 M18 genes that contain at least one MRP-1-binding sub-motifs (Motifs 3a/8a, 6a/8b, 8c, and 8f).

Gene ID	MM	TF Family	Locus/ TF Name	Functional Annotation
AC196417.3_FG008	0.997666935	-	-	-
AC204876.3_FG006	0.995274098	-	-	-
AC233883.1_FG006	0.98545352	-	-	Uncharacterized protein
GRMZM2G002903	0.980405318	-	-	Uncharacterized protein
GRMZM2G003493	0.709293417	-	-	Uncharacterized protein
GRMZM2G005710	0.925096716	-	-	Uncharacterized protein
GRMZM2G007784	0.97271802	-	-	-
GRMZM2G008271	0.998357469	-	BAP-1A	Basal layer antifungal peptide
GRMZM2G008403	0.997103295	-	BAP-1B	Basal layer antifungal peptide
GRMZM2G009427	0.995625792	-	-	-
GRMZM2G010762	0.994304527	-	-	Early nodulin-like protein 3
GRMZM2G011896	0.988628322	-	-	Putative leucine-rich repeat receptor-like protein kinase family protein; Uncharacterized protein
GRMZM2G017869	0.995815117	-	-	Uncharacterized protein
GRMZM2G024350	0.995946537	-	-	Uncharacterized protein
GRMZM2G027472	0.995775449	-	-	Uncharacterized protein
GRMZM2G028386	0.995641682	AP2-EREBP	EREB137	-
GRMZM2G034862	0.995837595	-	-	Uncharacterized protein
GRMZM2G045082	0.995397205	-	-	Putative uncharacterized protein
GRMZM2G045638	0.978759996	-	-	Uncharacterized protein
GRMZM2G047833	0.995274098	-	-	-
GRMZM2G048850	0.697116411	C2C2-GATA	GATA33	Uncharacterized protein
GRMZM2G049695	0.930118941	MYB-related	MYBR24	Putative MYB DNA-binding domain superfamily protein
GRMZM2G049912	0.950990813	-	-	Uncharacterized protein
GRMZM2G050407	0.966973351	-	-	Uncharacterized protein
GRMZM2G054359	0.996226267	-	-	Uncharacterized protein
GRMZM2G054632	0.977265787	-	-	Uncharacterized protein
GRMZM2G058703	0.998757072	-	-	Uncharacterized protein
GRMZM2G060991	0.984451944	-	-	-
GRMZM2G066546	0.982044708	-	-	Uncharacterized protein
GRMZM2G076370	0.997249693	-	-	Uncharacterized protein
GRMZM2G079547	0.994976509	-	-	Uncharacterized protein
GRMZM2G082785	0.991592203	-	BETL-1	BET1 protein
GRMZM2G082799	0.978839534	-	-	BET1 protein
GRMZM2G086827	0.998053357	-	MEG-10	-
GRMZM2G086835	0.923876737	-	-	Zinc finger protein 7
GRMZM2G088896	0.998693431	-	MEG-9	-
GRMZM2G091445	0.999221086	-	BETL-10	Putative defensin
GRMZM2G094054	0.997047242	-	MEG-6	Putative uncharacterized protein
GRMZM2G095337	0.885645943	-	-	Uncharacterized protein
GRMZM2G103526	0.7672607	-	-	Acid phosphatase 1; Uncharacterized protein
GRMZM2G106655	0.99900411	-	-	-
GRMZM2G107302	0.999258566	-	-	Uncharacterized protein
GRMZM2G107754	0.99443088	-	-	Uncharacterized protein
GRMZM2G110395	0.833343634	-	-	-
GRMZM2G110816	0.987045749	-	-	Uncharacterized protein
GRMZM2G115574	0.993363479	-	-	Uncharacterized protein
GRMZM2G128531	0.995574221	-	-	Blue copper protein
GRMZM2G131982	0.99682921	DBB	-	-

Supplemental Table 11 Continued				
GRMZM2G118214	0.789535171	C2C2-GATA	GATA7	Putative GATA transcription factor family protein; Uncharacterized protein
GRMZM2G122437	0.970709069	-	-	Uncharacterized protein
GRMZM2G126055	0.972985678	-	-	Putative cytochrome P450 superfamily protein; Uncharacterized protein
GRMZM2G133370	0.998120923	-	BAP-3B	Basal layer antifungal peptide
GRMZM2G133382	0.996008427	-	BAP-3A	Basal layer antifungal peptide
GRMZM2G133407	0.966870998	-	-	Uncharacterized protein
GRMZM2G136771	0.995682732	-	-	Uncharacterized protein
GRMZM2G137959	0.998934848	-	MEG-4	MEG4
GRMZM2G141574	0.950302131	-	-	-
GRMZM2G147226	0.968661535	-	-	Uncharacterized protein
GRMZM2G148270	0.984627461	-	-	Putative uncharacterized protein
GRMZM2G152655	0.999157709	-	BAP-2	Basal layer antifungal protein2; Uncharacterized protein
GRMZM2G156794	0.995986927	-	-	Uncharacterized protein
GRMZM2G158400	0.997452659	-	-	Uncharacterized protein
GRMZM2G158407	0.999145715	-	-	-
GRMZM2G165535	0.986253278	-	-	Uncharacterized protein
GRMZM2G170181	0.695195223	-	-	-
GRMZM2G172596	0.998045775	-	-	GAST1 protein
GRMZM2G175250	0.994699115	-	-	Putative cytochrome P450 superfamily protein
GRMZM2G175896	0.997778567	-	MEG-12	-
GRMZM2G175912	0.999396321	-	MEG-13	-
GRMZM2G181051	0.998899063	-	MEG-11	-
GRMZM2G332483	0.99739216	-	-	Uncharacterized protein
GRMZM2G332703	0.983249958	-	-	-
GRMZM2G341010	0.998049519	-	-	Uncharacterized protein
GRMZM2G342246	0.99535502	-	-	Beta-expansin 7
GRMZM2G347956	0.843165264	-	-	Plastid-specific 30S ribosomal protein 1
GRMZM2G354335	0.998651579	-	MEG-1	Putative uncharacterized protein
GRMZM2G383937	0.995865784	-	-	-
GRMZM2G406552	0.791376554	-	-	Nonspecific lipid-transfer protein
GRMZM2G409309	0.996479121	-	-	-
GRMZM2G422083	0.995972492	MYB-related	MYBR33	Putative MYB DNA-binding domain superfamily protein
GRMZM2G426158	0.995470482	-	-	-
GRMZM2G466545	0.964270672	-	-	Uncharacterized protein
GRMZM2G487702	0.993630476	-	-	-
GRMZM2G502035	0.998543642	-	MEG-2	MEG2; Maternally expressed gene 2; Uncharacterized protein
GRMZM5G800473	0.996024857	-	-	-
GRMZM5G802585	0.808982972	-	-	Uncharacterized protein
GRMZM5G803611	0.922753269	-	-	Uncharacterized protein
GRMZM5G812796	0.999152	-	-	Uncharacterized protein
GRMZM5G836886	0.93249873	-	-	-
GRMZM5G864689	0.623012716	-	-	Uncharacterized protein
GRMZM5G888860	0.957073782	-	-	-
GRMZM5G890815	0.954454282	-	-	-
GRMZM5G897740	0.998634244	-	-	Uncharacterized protein

Supplemental Table 12. Results of Y1H assays for binding of MRP-1 to the promoters of genes within M18.

Gene ID	Locus/TF Name	Sub-motifs Contained in Promoter[a]	Y1H Results[b]
AC184794.2_FG003	-	None	–
GRMZM2G009854	-	None	+
GRMZM2G016145	TCRR-1	None	(+)
GRMZM2G027472	-	3a/8a (3), 6a/8b (2), 8c (1), 8f (1)	+
GRMZM2G030403	MYBR9	None	–
GRMZM2G034862	-	3a/8a (1), 8f (1)	+
GRMZM2G054359	-	3a/8a (5), 6a/8b (1), 8f (3)	+
GRMZM2G055621	-	None	–
GRMZM2G058703	-	3a/8a (2)	+
GRMZM2G062565	-	None	+
GRMZM2G063042	-	None	+
GRMZM2G070399	-	None	–
GRMZM2G072219	-	None	–
GRMZM2G082799	-	6a/8b (1), 8c (1)	+
GRMZM2G084462	-	None	–
GRMZM2G087413	-	None	+
GRMZM2G091445	-	6a/8b (1)	+
GRMZM2G107302	-	3a/8a (6)	+
GRMZM2G111306	MRP-1	None	–
GRMZM2G112925	-	None	–
GRMZM2G121111	MYBR81	None	–
GRMZM2G123411	-	None	+
GRMZM2G125386	-	None	–
GRMZM2G133370	-	3a/8a (1), 6a/8b (1), 8c (1)	+
GRMZM2G133382	-	3a/8a (5), 8c (1)	+
GRMZM2G136771	-	3a/8a (5), 6a/8b (1)	+
GRMZM2G138392	-	None	(+)
GRMZM2G141574	-	6a/8b (2), 8f (1)	+
GRMZM2G152655	BETL-2	3a/8a (4), 8c	+
GRMZM2G158407	-	3a/8a (2)	+
GRMZM2G175912	-	6a/8b (3)	(+)
GRMZM2G175976	BETL-3	None	–
GRMZM2G181051	-	8f (1)	+
GRMZM2G332483	-	3a/8a (1), 8c (1), 8f (1)	+
GRMZM2G354335	MEG-1	6a/8b (2), 8f (1)	+
GRMZM2G386276	-	None	–
GRMZM2G402156	MYBR19	None	–
GRMZM2G422083	MYBR33	6a/8b (2)	+
GRMZM2G426158	-	3a/8a (2)	+
GRMZM5G800473	-	6a/8b (1)	+
GRMZM5G812796	-	6a/8b (1)	+
GRMZM5G897740	-	8f (1)	+

[a] The number in parenthesis indicates the number of copies of that sub-motif.

[b] Scoring: + indicates strong positive, (+) indicates weak positive, – indicates negative. Images of the Y1H growth assays are shown in Supplemental Figure 16.

Supplemental Table 13. Sequences of the primers used to generate the clones for the *in situ* hybridization probes.

Gene ID	Forward Primer	Reverse Primer
GRMZM2G008271	TCTAGTTCATCACCCATGGC	GATCATGCATTAAGAGGGTC
GRMZM2G058703	CACATTGTTAGTATTAGACC	TAAAGCAGGAAGGGGAGAGG
GRMZM2G087413	TAAAGATCTCAGTGTCACAC	AGCCAGGTTGAAACGGCCTC
GRMZM2G089713	TACATTCTGGATCAGGTCCG	CCCTTCAACTTGTACTCGTC
GRMZM2G091774	GGAGGCCTCCTCAAGATTGG	AGCATAATAGCATCAGTTGG
GRMZM2G107302	AGTACACGACTCAGCCATTG	GACACCAAAATACTATATGC
GRMZM2G121137	TATCAGTATCTTCCACAAGC	CAAAACACCAACACAAATGC
GRMZM2G123411	CTCTAAACTCAAACAAATAC	CGAGTGCTTCAGACACTCGG
GRMZM2G132162	AGCATACTATTAGACATACC	GAGGCCACGTATGGAGAACC
GRMZM2G133370	GATCTTATCCATCACCTATG	CTAATATCATTGAAGACACAC
GRMZM2G149869	CGCCGACGCAAGACTACCAG	ACCTAACACCTGATGAATCC
GRMZM2G158400	GGAGAAGAAATTACAGATCC	TAGTAAAGATTTATGAGCAC
GRMZM2G158407	GAACATCGAAAGTATCATGC	AACAGTTTTGTTCATATCTC
GRMZM2G170400	AAAGCTTGTGGGGAAAATGG	GTGAAGGATGGTGTCACGGC
GRMZM2G175912	CATGTCACAAATGATATCGG	TGACTAAATTTCGCGAATCG
GRMZM2G332483	CAAGATCAGCCCCAAGCACG	ACTTATCTTATTGAGTTCAC
GRMZM2G426158	ATAGGCAATGTAAGAGTAGC	TTGAGACTGTTTCGAGATAG
GRMZM2G429899	GGCTACACAAATGCCTGAAG	ACATCCAGAGCTGACACGTG
GRMZM2G437435	TGGATGCTACACTCCTATCG	ATGGCTCCTCGTTGCTCAGC
GRMZM5G812796	CGATCGTCGTCGCAGAAAGG	GAAATACTCCACATGCATTG

Supplemental Table 14. Sequences of the primers used to generate the constructs to test the sub-motifs in Y1H assays. The sub-motif sequences are in bold red letters and are underlined. In all constructs, the sequence of the reverse primer was GATCCTCGAGGGACTAGCTAGACAAGCTCTC.

Sub-motif	Forward Primer
3a/8a	GATCAAGCTTA**TAGATAGATAGA**TTAAGCGTATCGCTAG
3b	GATCAAGCTT**TAGATATATAGA**TTAAGCGTATCGCTAG
3c	GATCAAGCTT**TAGATAAATAGA**TTAAGCGTATCGCTAG
6a/8b	GATCAAGCTTA**TAGATATAGATA**TTAAGCGTATCGCTAG
6b	GATCAAGCTTA**TAGATATATATA**TTAAGCGTATCGCTAG
6c	GATCAAGCTT**TAAATATAAATA**TTAAGCGTATCGCTAG
6d	GATCAAGCTT**TAGATATAGAAA**TTAAGCGTATCGCTAG
6e	GATCAAGCTT**TAGATATAAATA**TTAAGCGTATCGCTAG
6f	GATCAAGCTT**TAAATATAAAAA**TTAAGCGTATCGCTAG
6g	GATCAAGCTT**TAAATATATAAA**TTAAGCGTATCGCTAG
6h	GATCAAGCTT**TATATATATATA**TTAAGCGTATCGCTAG
6i	GATCAAGCTT**TAAATATATATA**TTAAGCGTATCGCTAG
6j	GATCAAGCTT**TAGATAAAAAAA**TTAAGCGTATCGCTAG
6k	GATCAAGCTT**TAAATATAGAAA**TTAAGCGTATCGCTAG
6l	GATCAAGCTT**TAGATATATAAA**TTAAGCGTATCGCTAG
6m	GATCAAGCTT**TAGATATAAAAA**TTAAGCGTATCGCTAG
8c	GATCAAGCTT**TAGATAGAGATA**TTAAGCGTATCGCTAG
8d	GATCAAGCTT**TAGAGAGAGAGA**TTAAGCGTATCGCTAG
8e	GATCAAGCTT**TAGATATAGAGA**TTAAGCGTATCGCTAG
8f	GATCAAGCTT**TAGATAGATATA**TTAAGCGTATCGCTAG
8g	GATCAAGCTT**AAGATAGAGAGA**TTAAGCGTATCGCTAG
8h	GATCAAGCTT**TAGATAGAGAGA**TTAAGCGTATCGCTAG

Supplemental Table 15. Sequences of the primers used to generate the constructs to test the promoters in Y1H assays.

Gene ID	Forward Primer	Reverse Primer
AC184794.2_FG003	GATCAAGCTTGTCTAGAATGGTTTAGTGTAG	GATCCTCGAGGCACTTTCCGCAGATCCCATATG
GRMZM2G009854	GATCAAGCTTCAGCTACACCTGAAAACCTAAAC	GATCCTCGAGCTTTTTGATGATTTAGCAGGTGG
GRMZM2G016145	GATCAAGCTTCGTCTACTTCTTGCTCTAGATC	GATCCTCGAGGGACTAGCTAGACAAGCTCTC
GRMZM2G027472	GATCGGTACCATGGTGTGGAACGACCGTTG	GATCCTCGAGATGGATGACCGATAAGAGC
GRMZM2G030403	GATCAAGCTTGAATAGTGGTATGAACTATGC	GATCCTCGAGGAGAGTTGAGGATTGAGTAC
GRMZM2G034862	GATCAAGCTTGGCCTCTAACGTAATGGTTAAGG	GATCCTCGAGGGGTGATTAGAAAATACTAATGCC
GRMZM2G046532	GATCAAGCTTGGCATGTACATAGGGCTCTG	GATCCTCGAGTATTCTATCCTTTGAGATGGAATG
GRMZM2G054359	GATCAAGCTTGGTGTTGGTTAGTCACAAGTC	GATCCTCGAGGGGTGCTAGATGAGAGCTAATACC
GRMZM2G055621	GATCAAGCTTGATGGGGAGAGGCATGTAAC	GATCCTCGAGGTCGTATGAACAGGAGTGC
GRMZM2G058703	GATCAAGCTTATCAGGATACAATCGTTCTG	GATCCTCGAGGGGTGATGAACTAGAAAGTG
GRMZM2G062565	GATCGGTACCGGTTTGTGCTGAACCTTTGG	GATCCTCGAGGGACAGTGAGTGACCTAACTATG
GRMZM2G063042	GATCGGTACCGACCGAAGGGGAAAAAGAC	GATCCTCGAGGGTTTGTTTATATTTGCTAG
GRMZM2G070399	GATCAAGCTTCATGGGTTGCACGTGAAC	GATCCTCGAGCGACGATCTACACTGCTGTC
GRMZM2G072219	GATCAAGCTTCTATCTTCTACATTCTTTGCC	GATCCTCGAGTTTGTAGTGCTATATGTGGATTGG
GRMZM2G082799	GATCAAGCTTCCTTTTCTTTATACCACATGCC	GATCCTCGAGAAGGAAAGATGATCAAGCTTC
GRMZM2G084462	GATCAAGCTTGGATCGATGACGTGATCAAG	GATCCTCGAGGTCTTGATGATCTTGATTATTGTAGCC
GRMZM2G087413	GATCAAGCTTGGGATTTTGTAGGAATCATC	GATCCTCGAGGGGTATAACTTCAACTGTTG
GRMZM2G091445	GATCAAGCTTACCACTGCTTGCTAGTGATTTC	GATCCTCGAGTGAGGAGAACAGCATACACATG
GRMZM2G107302	GATCAAGCTTGTAGTTCAGCAGAAAACAGCACGC	GATCCTCGAGCGAGCGTGTACTGCACGCACAT
GRMZM2G111306	GATCAAGCTTATATCACAAGGAAAGATATG	GATCCTCGAGGAGGTGCGAGGGATTAAGTAC
GRMZM2G112925	GATCAAGCTTGCCTTTACGGGCTTTTTAGG	GATCCTCGAGGTTTCCTTGGGCTTTGG
GRMZM2G115340	GATCGGTACCAAAAGAGGTGGGATCACCC	GATCCTCGAGCCATCAGCAACTAACGTTTC
GRMZM2G121111	GATCAAGCTTAGAGGAGCGGTTGAACACTG	GATCCTCGAGCGGCCGGGGTTAGCTAAGCTAG
GRMZM2G123411	GATCAAGCTTGCCCGTCCTGTCCTACAACG	GATCCTCGAGGGGTGAAAAGGGTAAGAGC
GRMZM2G125386	GATCAAGCTTCTTGGTTTTGGTGAATTGTGCC	GATCCTCGAGAGAGGAAACAATTGTTCTTGC
GRMZM2G133370	GATCGGTACCGCGGTTGGTAGACAGGTAGG	GATCCTCGAGAGGTGATGGATAAGATCTAATA

Supplemental Table 15 Continued		
GRMZM2G133382	GATCAAGCTTCTCGAATAATCTAATGTATTC	GATCCTCGAGTGTGATGGATAAGAGCTAATAATA
GRMZM2G136771	GATCAAGCTTAAAGCAATGCTCATCTTTAACC	GATCCTCGAGGTGAAATGAAGAGGAGTGG
GRMZM2G138392	GATCAAGCTTCGGTTTTGAATGTGC	GATCCTCGAGGTCAGACACGATGAGAGAG
GRMZM2G141574	GATCAAGCTTATGCACTTTGGATATACC	GATCCTCGAGAAGAAGAGGATATATAGATC
GRMZM2G150680	GATCGGTACCCGTGGGTTTCGTACCCAC	GATCCTCGAGATCAGCACAAGATCCAAGG
GRMZM2G152655	GGCCGGTACCAGTTGATATAACTAGATAGG	GATCCTCGAGGGGTGACAGATGATATGAGC
GRMZM2G158407	GATCAAGCTT CTGTCTCGGATGGAAAAAC	GATCCTCGAGGGTTAATTATTTGGGTGAGGA
GRMZM2G175912	GATCGGTACCACGGTTAATAGTAGAGCCAG	GCCCTCGAGGACGCAAGAAAATCTAAAGAAC
GRMZM2G175976	GATCAAGCTTCAAATTACCCGCAGGGGTATG	GATCCTCGAGTGTAGTTTGCTATCACCCTT
GRMZM2G181051	GATCAAGCTTAACTTCTGCAGAGTGTTTTG	GATCCTCGAGGTCGCAAGAAAATTTAAGGAAC
GRMZM2G314094	GATCAAGCTTCGAGAGCCTAACTTCACCCAAC	GATCCTCGAGCACAAATTAAATGCATAGAAG
GRMZM2G332483	GATCGGTACCATACATAGATGGACAAACTG	GATCCTCGAGGAGATGAGAGCACAATATTAC
GRMZM2G354335	GGCCGGTACCTCTCGACACAGGTAGGTAG	GATCCTCGAGGTCGCAAGAAATGTTAAGGAAC
GRMZM2G386276	GATCCCCGGGGTAGGAACTCACATAAG	GATCCTCGAGCTTTAAGTTAAATATGGTACC
GRMZM2G402156	GATCAAGCTTGCCCTGGACGGTTCGCGATTAG	GATCCTCGAGGGGGTTGGGTACTACGATATATG
GRMZM2G422083	GATCAAGCTTCCATACAGATATAGGTATATG	GATCCTCGAGACATGGATGGAGAAAAGGGC
GRMZM2G426158	GATCAAGCTTCGAGCCTTCGCATCGTTGATC	GATCCTCGAGGGTCGTATGAACAGGAGTGCTAG
GRMZM2G846314	GATCAAGCTTCGGAAAGGACAGGACGTGTG	GATCCTCGAGGATGCAACAAATACCTCCTAC
GRMZM5G800473	GATCAAGCTTCGAGCGAGCCGGAAGTTTG	GATCCTCGAGATTGGAATGTATGTGAGTGAG
GRMZM5G812796	GATCAAGCTTCTTCTGACCATTGGCTCTG	GATCCTCGAGGAGGAAACGAGTATTCTTGC
GRMZM5G897740	GATCAAGCTTCAAGTTTCATACCAATATACG	GATCCTCGAGCGCCACCACTTCTTCTCTG

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