Supplementary data

Supplementary Table S1. Primers used for RACE.

Supplementary Table S2. Primers used for quantitative real-time PCR analysis.

Supplementary Table S3. Primers used for fusing GFP.

Supplementary Table S4. Primers used for Y1H assay.

Supplementary Table S5. Primers used for transient expression assay.

Supplementary Table S6. Primers used for Y2H analysis.

Supplementary Table S7. Primers used for BiFC assays.

Supplementary Table S8. Sequence similarities among the different *MaERFs* genes.

Supplementary Figure S1. Schematic analysis of MaERFs with ERF domains and EAR repressor domains.

Supplementary Figure S2. Amino acid sequence alignment of the MaERFs proteins.

Supplementary Figure S3. Phylogenetic tree of ERFs.

Supplementary Figure S4. Subcellular localization of MaERFs in tobacco leaves.

Supplementary Figure S5. Expressions of *MaERFs* genes in banana fruit peel with four different ripening treatments.

Supplementary Figure S6. Expressions of *MaERFs* genes in banana fruit pulp with four different ripening treatments.

Supplementary Table S1. Primers used for RACE.

Name	Sequences(5'-3')
MaERF4-3RACE1	GGCGGATTGCGACGAATTGAAG
MaERF4-3RACE2	CCCCAACGAGATCGGGTGCT
MaERF6-3RACE1	CACCTTCGACACCGCCGAG
MaERF6-3RACE2	TTCCTCCGTCTTCTCCGCTC
MaERF7-3RACE1	CCGACTTCATTCCTCAACGC
MaERF7-3RACE2	CTTCATTCCTCAACGCAACCATC
MaERF8-3RACE1	ATGTCAATCCTTGCTCCTATCG
MaERF8-3RACE2	GTTCCTCCCTACCCCATACTTT
MaERF11-3RACE1	TCTCCGAGGGCGAAGAACAG
MaERF11-3RACE2	AAGGCTAAGACCAACTTCCCAATC
MaERF13-3RACE1	GAAACAAGCAAAGCGGTCAAGTCT
MaERF13-3RACE2	CTGTTCTTCCTCGTCCTTGGTG
MaERF14-3RACE1	AGACCAATTTTCCCTCCTTACC
MaERF14-3RACE2	CTATCACCAACATCAGCACCAC
MaERF2-5RACE1	TCACTCTCCTTTGCTTTCTTGC
MaERF2-5RACE2	CTCCTCCAAATACTCTGTTCCC
MaERF5-5RACE1	ACGGAGTTGATGATGAAGATACA
MaERF5-5RACE2	CGTTCTCGGGGAAGTTGAGTTTG
MaERF10-5RACE1	CACTCGGAGACATCGCAAGAAC
MaERF10-5RACE2	CAACCCTCGCTACTGCTTTCCCA
MaERF11-5RACE1	GCGGTGAAGATTGGGAAGTTGG
MaERF11-5RACE2	CGGTGAAGATTGGGAAGTTGGTC
MaERF14-5RACE1	GGGGGTTGACCTGCTTCCTA
MaERF14-5RACE2	GCGGACGGTAAGGAGGGAAAAT
MaERF15-5RACE1	CGAGGACAGGTAAATACTACAGGAC
MaERF15-5RACE2	GCTCTCCACCGCCAAACCC

Supplementary Table S2. Primers used for quantitative real-time PCR analysis.

Name	Forward primer(5'-3')	Reverse primer(5'-3')
MaERF1	GGAGAGTGTGGTGGAGTTGG	CGAGGATTGAGAGTTGCGGTT
MaERF2	GCAAGAAAGCAAAGGAGAGT	GAGAAGGATTGGAAGAAGTC
MaERF3	CTACAGCCCCCGAGACAAC	TGGTCACTCCTTCCACAAAAAC
MaERF4	TCGGTTTGCCCCTTGACGC	GGTGACTTGAGCACATCCCAG
MaERF5	GACGGAGCAGCAGACGAACT	GGCGAGAAAGAACACTGGAGC
MaERF6	TTCCTCCGTCTTCTCCGCTC	GGGGATTTGGTCAACTCTGC
MaERF7	AGGAGGGGACAGCAGCAGAT	CGGTCAAGGAGACGAATGGG
MaERF8	TGTCAATCCTTGCTCCTATCG	CAGTCCTCCAAAATCCTTCATC
MaERF9	AGACCTTCTTCCAGTCACCCA	GAGCAATCTACTTGACTTCCACC
MaERF10	CGTTTACAGAGTGCGTCGGA	CTCGGATGGAGGAGACAGGT
MaERF11	TGGGTTCAAGGGAATCGGG	TGTTCGTGGGTTCTGTCAAG
MaERF12	CCACCAGCCGACGATGACT	ATAGAACGGAACGACCAAAAGG
MaERF13	CAGCACCTCCCTCCCTTCA	CTGTGGCAGTCGCTTTCGC
MaERF14	GGACGACCTCCACGATACG	TGAGAGTAGATAGGCGAAACGG
MaERF15	GAAGCGGTGAAGATGGTGGT	GCGAGGAAAGGGCATAATAG

Supplementary Table S3. Primers used for fusing GFP.

Name	Sequences(5'-3')	Restriction Site
MaERF1-GFPFor	GGACTCTAGAggatccGATGGATTACTCTCTCCTTTC	*BamH* I
MaERF1-GFPRev	TGCTCACCATaagcttCCACGGCCTGGCAAACCC	*Hind* Ⅲ
MaERF4-GFPFor	GGACTCTAGAggatccGATGGAGGCATCCATCGGCTT	*BamH* I
MaERF4-GFPRev	TGCTCACCATaagcttGCTCACGGTGACTTGAGC	*Hind* Ⅲ
MaERF5-GFPFor	GGACTCTAGAggatccGATGTGTCACAACGTGGCGAA	*BamH* I
MaERF5-GFPRev	TGCTCACCATaagcttGCTGCCTGAAGAAGATGGAGG	*Hind* Ⅲ
MaERF9-GFPFor	GGACTCTAGAggatccGATGGTGAAGAGCAAGATCAGAGGG	*BamH* I
MaERF9-GFPRev	TGCTCACCATaagcttGCAGAAGCTCCACAGATGGAT	*Hind* Ⅲ
MaERF11-GFPFor	GGACTCTAGAggatccGATGTCTCCGAGGGCGAAGAACA	*BamH* I
MaERF11-GFPRev	TGCTCACCATaagcttAGCCACCTCCGGCGGC	*Hind* Ⅲ
MaACO1-GFPFor	GGACTCTAGAggatccGATGGCGATTCCGGTCATCGATTT	*BamH* I
MaACO1-GFPRev	TGCTCACCATaagcttAATAGCTCTGACTGCCTCAAATC	*Hind* Ⅲ
MaACS1-GFPFor	GGACTCTAGAggatccGATGAGGATCTACGGCGATGA	*BamH* I
MaACS1-GFPRev	TGCTCACCATaagcttGGTGGCGGCTTGAACGAGA	*Hind* Ⅲ

Supplementary Table S4. Primers used for Y1H assay.

Name	Sequences(5'-3')	Restriction Site
MaACO1-pAbAiFor	TTGAATTCGAGCTCggtaccTATAGATTATTAGCTTTAAGGAT	*Kpn* I
MaACO1-pAbAiRev	ATGCCTCGAGgtcgacGTCAACTAAGAAATTAATGGACAG	*Sal* I
MaACS1-pAbAiFor	TTGAATTCGAGCTCggtaccCTCGAAAGTGGACCTCCGTT	*Kpn* I
MaACS1-pAbAiRev	ATGCCTCGAGgtcgacGTGACCCGTTATCTCAGGTAC	*Sal* I

Supplementary Table S5. Primers used for transient expression assay.

Name	Sequences(5'-3')	Restriction Site
MaACO1-101For	ATGCCTGCAGgtcgacTATAGATTATTAGCTTTAAGGAT	*Sal* I
MaACO1-101Rev	GACCACCCGGggatccGTCAACTAAGAAATTAATGG	*BamH* I
MaACS1-101For	ATGCCTGCAGgtcgacCTCGAAAGTGGACCTCCGTT	*Sal* I
MaACS1-101Rev	GACCACCCGGggatccGTGACCCGTTATCTCAGGTAC	*BamH* I
MaERF9-1300For	ggatccATGGTGAAGAGCAAGATCAGAG	*BamH* I
MaERF9-1300Rev	GgtcgacGCAGAAGCTCCACAGATGGAT	*Sal* I
MaERF11-1300For	ggatccATGTCTCCGAGGGCGAAGAAC	*BamH* I
MaERF11-1300Rev	GgtcgacAGCCACCTCCGGCGGCG	*Sal* I

Supplementary Table S6. Primers used for Y2H assay.

Name	Sequences(5'-3')	Restriction Site
MaERF9-ADFor	GGAGGCCAGTgaattcATGGTGAAGAGCAAGATCAGAG	*EcoR* I
MaERF9-ADRev	CGAGCTCGATggatccGCAGAAGCTCCACAGATGGA	*BamH* I
MaERF11-ADFor	GGAGGCCAGTgaattcATGTCTCCGAGGGCGAAGAA	*EcoR* I
MaERF11-ADRev	CGAGCTCGATggatccTCAAGCCACCTCCGGCG	*BamH* I
MaACO1-DBDFor	CATGGAGGCCgaattcATGGCGATTCCGGTCATCGATTT	*EcoR* I
MaACO1-DBDRev	GCCGCTGCAGgtcgacGTCAAATAGCTCTGACTGCCTCAA	*Sal* I
MaACS1-DBDFor	CATGGAGGCCgaattcATGAGGATCTACGGCGAGGA	*EcoR* I
MaACS1-DBDRev	GCCGCTGCAGgtcgacGTCAGGTGGCGGCTTGAACG	*Sal* I

Supplementary Table S7. Primers used for BiFC assays.

Name	Sequences(5'-3')	Restriction Site
MaACO1-BiFCFor	CGCCACTAGTggatccATGGCGATTCCGGTCATCG	*BamH* I
MaACO1-BiFCRev	TAGCCTCGAggtcgaCAATAGCTCTGACTGCCTCAAATC	*Sal* I
MaACS1-BiFCFor	CGCCACTAGTggatccATGAGGATCTACGGCGATGAG	*BamH* I
MaACS1-BiFCRev	TAGCCTCGAggtcgaCGGTGGCGGCTTGAACGAGA	*Sal* I
MaERF9-BiFCFor	CGCCACTAGTggatccATGGTGAAGAGCAAGATCAGAG	*BamH* I
MaERF9-BiFCRev	TAGCCTCGAggtcgaCGCAGAAGCTCCACAGATGGAT	*Sal* I
MaERF11-BiFCFor	CGCCACTAGTggatccATGTCTCCGAGGGCGAAGAAC	*BamH* I
MaERF11-BiFCRev	TAGCCTCGAggtcgaCAGCCACCTCCGGCGGCG	*Sal* I

Supplementary Table S8. Sequence similarities among the different *MaERFs* genes. Numbers indicate percentage homology at the amino acid level.

	MaERF1	MaERF2	MaERF3	MaERF4	MaERF5	MaERF6	MaERF7	MaERF8	MaERF9	MaERF10	MaERF11	MaERF12	MaERF13	MaERF14	MaERF15
MaERF1	100%														
MaERF2	69.9%	100%													
MaERF3	23.6%	21.5%	100%												
MaERF4	31.5%	32.0%	24.7%	100%											
MaERF5	23.4%	22.9%	20.9%	25.9%	100%										
MaERF6	26.2%	24.6%	18.0%	26.3%	42.2%	100%									
MaERF7	27.1%	25.8%	22.7%	28.4%	26.4%	24.3%	100%								
MaERF8	23.5%	22.6%	19.9%	27.0%	24.2%	23.2%	48.6%	100%							
MaERF9	24.1%	23.6%	25.5%	24.0%	24.5%	23.4%	22.5%	24.4%	100%						
MaERF10	30.3%	28.9%	27.2%	28.7%	32.8%	30.0%	31.5%	31.7%	21.4%	100%					
MaERF11	32.0%	31.5%	26.8%	31.5%	31.8%	33.0%	30.1%	29.9%	23.0%	61.7%	100%				
MaERF12	29.4%	29.3%	21.7%	30.0%	30.1%	28.9%	24.7%	26.5%	22.6%	38.9%	40.8%	100%			
MaERF13	32.4%	29.6%	21.6%	28.9%	30.2%	30.9%	25.0%	27.6%	24.4%	39.7%	40.9%	75.9%	100%		
MaERF14	29.0%	27.7%	22.4%	26.7%	29.6%	27.0%	24.7%	24.5%	27.0%	39.7%	39.9%	69.2%	72.6%	100%	
MaERF15	29.0%	28.5%	23.2%	29.0%	27.3%	27.0%	26.9%	28.5%	22.2%	36.5%	39.9%	45.3%	45.6%	44.3%	100%
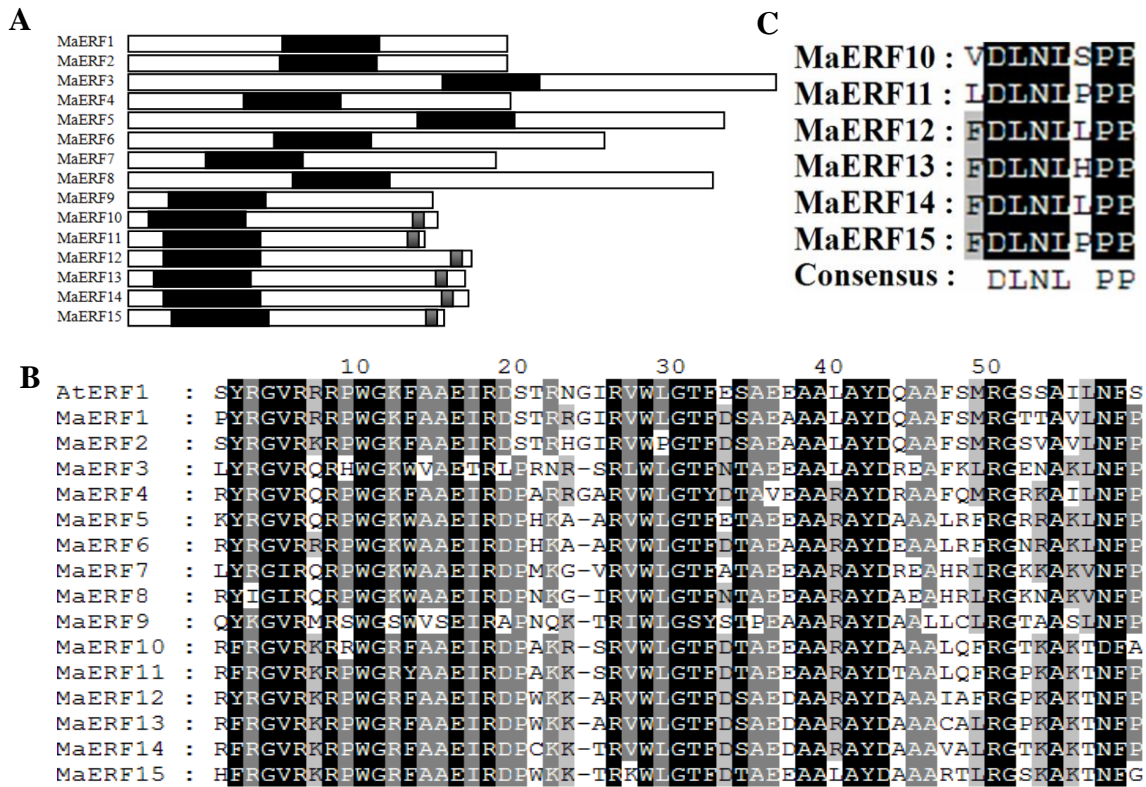
Figure S1. Schematic analysis of MaERFs with ERF domains and EAR repressor domains. (A) Location of ERF domains (black bars) and EAR repressor domains (gray bars). (B) Comparison of ERF domains by deduced amino acids. Identical and similar amino acids are indicated by black and grey shading, respectively. (C) Comparison of EAR repressor domains by deduced amino acids. Identical and similar amino acids are indicated by black and grey shading, respectively.

```
MaERF1  : ---------------------------------------------------------------------------------------MDYSLSFHSHNQEHSSESSTYSPRS :  25
MaERF2  : ----------------------------------------------------------------------------------------MDYYL-FDSLNHEHSPESSTGSPEP :  24
MaERF3  : MEGSDGGGRQKGVQRTSVQPRPLKKIRSPDRRHQYSSTSTSSSSSSSQCSSNSNPVSSSFSGPPVSSSSTLYSKPIFPFASAGSSRAVVDLTLSPPARSSLHHQPPPWQQQQMISFGRHHPHQIR : 125
MaERF4  : ----------------------------------------------------------------------------------------------------MEASIGFDDS :  10
MaERF5  : ------------------MCHNVANPHQLPDDSFAAEGSDGAPLSSYHRAQEISTIVSALAHVMASERRPRQVGMAVDSVSVVSSSSSSSSSSSSLSCISSSYSSPSLGGQGGGASSQNRTR : 105
MaERF6  : ---------------------------------------------MEYERSVMVSALVHVVAGGR-------------------------------GTEAPPGGGNGQTRWNEGFVH :  41
MaERF7  : -----------------------------------------------------------MCGGAIISDFIP------------------------QRNHHRHCP :  21
MaERF8  : ---------------------------------------------MCGGAIISDFIPLATVASRRVMAEHLWPGLEKSKQTTGRRRRGVEVP :  47
MaERF9  : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF10 : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF11 : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF12 : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF13 : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF14 : ------------------------------------------------------------------------------------------------------------------- :   -
MaERF15 : ------------------------------------------------------------------------------------------------------------------- :   -


MaERF1  : SATDGFGLVCPDKPLPFDENDFEEMLLLSMLAEASGKAASSSSSEVLDSRSSPRPKEEEVESRSKVGHDTKGEKPYRGVRRRPWGKFAAEIRDSTRRGIRVWLGTFDSABAAALAYDQAAFSMRG : 150
MaERF2  : FPWTGVGLFYPDVPLPFNIDDSEEMLLLGMLAEASGKASSS--SEACD-RSVIRAKEEEVDSRSKAADEPK-EKSYRGVRKRPWGKFAAEIRDSTPHGIRVWEGTFDSABAAALAYDQAAFSMRG : 145
MaERF3  : TYPPSPPFMTTEEAAATQQQLQHRVYQEQYLLRYWSEALNLNPRARMVMAMSRPLHPSSLCPRPLLPPIPTPAKLYRGVRQRHWGKWVAETRDLRNR-SRLWLGTFNTABBAAALAYDREAFKLRG : 249
MaERF4  : TLDLIRQCLLGDLPQPDSPGLAPAFPCDGACRPPEP-----------ALGRRPSLTISVPPRPVGAAADCDELKRYRGVRQRPWGKWAAEIRDPARGARVWLGTYDTAVBAAARAYDRAAFQMRG : 124
MaERF5  : RVPSPPDLALRHHQGLGEFARYRGDASPDVAVTEQYPQGGPLPILGYPVPAAAMEEPSPASSNPEEAERSEPRRKYRGVRQRPWGKWAAEIRDPHRA-ARVWLGTFETABBAAARAYDAAALRFRG : 229
MaERF6  : EAAS------ELHASFGDFGRSS-SSAASADATEQT-------------AAPAAEAAAAMAGTEQGER----VRYRGVRKRPWGKWAAEIRDPHRA-ARVWLGTFDTABBAAARAYDEAALRFRG : 140
MaERF7  : DPD-----------------------HL-LSASD-------------LWPDSFHPHSVSTQDKVPR--KRGRKNLYRGIRQRPWGKWAAEIRDPMRG-VRVWLGTFPATABBAAARAYDREAHRIRG : 106
MaERF8  : DDDDDDDDFEADFQEFSDETQVDEFDGVHFGFGSEA-----------PFPRDGSPKSVYLDGLATKSSKRKRKNRYIGIRQRPWGKWAAEIRDPNRG-IRVWLGTFNTABBAAARAYDAEAHRLRG : 160
MaERF9  : ------------------------------------MVKSKIRGDLDHSVPRSSAAAAKGKKCQYKGVRMRSWGSWVSEIRAPNQK-TRIWLGSYSTPEAAAARAYDAALLCLRG :  76
MaERF10 : ---------------------------------MSPSAAR-------GELRETRFRGVRKRRWGRFAAEIRDPAR-SRVWLGTFDTABBAAARAYDAAALQFRG :  63
MaERF11 : ---------------------------------MSPRAKNSEGGEGGGETKEMRFRGVRRRPWGRYAAEIRDPAIK-SRVWLGTFNTABBAAARAYDTAALQFRG :  70
MaERF12 : -----------------------------MRKGR-APAVAAAAA----AMTVEVRYRGVRKRPWGKFAAEIRDWKK-ARVWLGTFDSABDAAARAYDAAAIAFRG :  70
MaERF13 : -----------------------------MRKGR-VPAAAAA---------VETRFRGVRKRPWGKWK-ARVWLGTFDSABDAAARAYDAAACALRG :  65
MaERF14 : -----------------------------MRKGRGEAAHPPAEV----GGAAGTRFRGVRKRPWGRFAAEIRDPCKK-TRVWLGTFDSABDAAARAYDAAAVAIRG :  71
MaERF15 : ---------------------------MAVET----------LRLRKEGLGPPAAAAAVA----GGEKEAHFRGVRKRPWGRFAAEIRDPWKK-TRKWLGTFDTABBAAALAYDAAARTLRG :  78


MaERF1  : TTAVLNFE--------------VERVRESLRGVKYEEEEIGLSPVVALKRRN----------------------------TLRRKSTSKKAKGREVRT---------------------- : 206
MaERF2  : SVAVLNFP--------------VERVQESLNGIKCWKEEEKVSPAVALKRRH----------------------------SMRRKWMSKKAKESETSSSS------------------- : 203
MaERF3  : ENAKLNFEHLFLGTGGGSGDRGGASCSSSSSSPPATPEEARPQTIHHQLQPRPPP----------------------PVAFETAGVTATVIGSSSSGDGSASG----------------------L : 331
MaERF4  : RKAILNFE--------------HEIGSSEQWDAAMTTAAQVLSGKRKREEEE------------------------------EEAARAIKRERSPAMEKGG---------------------- : 181
MaERF5  : RRAKLNFEENVR--------LQPSLSVPLATSN---------SPATTSDTIT------------------------------DYLAYTTLLQGGEEHPRIPPT-------------------- : 285
MaERF6  : NRAKLNFEEEAG--------LRKAPAVTPEAHMESQPFGRHGASGSTAAVAAR-----------------------------DYMEYSRLLRGEGEYQRMPPT-------------------- : 206
MaERF7  : KKAKVNFEN-----------EVEPEETDNSVP----------CNPVGNFIQPK----------------------------VEKSPVLAASNDCEG---------------------- : 153
MaERF8  : KNAKVNFETGAASLS----SRKRSSKPTASVIPKPKVLEKLDCNQNSNYLCDQDSELYSTFMEDQELTKPDHLNPVTTIKSSAPLEBAALNFHSDEGSNSLGYADFVWEFDAKTPEIMSILAPIE : 281
MaERF9  : TAASLNFE--------------ASLLLQLPDRVMSPKSIQRVAAAAATNAAS----------------------------------PSVSSDTAEDETLISS---------------------- : 130
MaERF10 : TKAKTNFAY---------PGPLYAPVVAGSVPSSPSNSNAESSTPSPKAGAV------------------------TALLPLDLELGHASARFSFPH---------------------- : 127
MaERF11 : PKAKTNFP------------IFTAAAGAGTAPSSPSSSGSGNTVESSTP-------------------------------SAPPPLELELGHAAARFPFLHA---------------------- : 129
MaERF12 : PKAKTNFP------------CSPSSPPPP-VPPFRSPSAARFAFGGRHPPPS--------------------------PPPPQRPTCSSLSSTVESFSGP---------------------- : 131
MaERF13 : PKAKTNFP------------LTSSSPTPQHLPPFR-PSATRFPLG--HRGHQ-------------------------PPPPTRPTSSSHSSTVESCNGP---------------------- : 124
MaERF14 : TKAKTNFP------------SLPSAFPPAPLP----AAAAHFPFYHQHQHHP--------------------------PPPPQRPTSSSHSSTVESFSGP---------------------- : 129
MaERF15 : SKAKTNFEG--------------YSAADVEIVPAAVPEPQIGLLSSSPWR-----------------------------SGFREPATALN---GRDLFLG---------------------- : 131


MaERF1  : --------------------------AESVVELEDLGAECLEELLSTSGFARPW---------------------------------------------------- : 234
MaERF2  : --------------------------SCGVESVLELEDLGTEYLEELLRTSEVANTC---------------------------------------------- : 234
MaERF3  : DESGGSEPTAPETTTPEMVWGNTAAAAEEWFSTWGPGSSIWDDIDGANSLLLHSRFTSFADMDPSNVAPPSSAATTTASPDADASSTAGPGPSSSVFLWKE : 432
MaERF4  : ----------------------DGGFVPSMSVCPLTPSSWKGVWDWEGADTKGIFN---------VPPLSPLSPHPSLGCAQVTVS-------------- : 236
MaERF5  : ------SLLDQYMYS--NYASPMCSTVNDGSSLPAPSIPTYSSVVSSSSTPYSPFYASSTTEQQTNWSGVSDIP-----ETSWMGSSQFPPSSSGS----- : 368
MaERF6  : ------ALLDQMMYSGASAASPFTDASLASSSFASAPFPPSSPLIYPPESEQQMDYLQPPPWKLYNLIRHQVTKPQYFEEPWLTVEVFLPKSI------- : 294
MaERF7  : -----DG----EVR------RLSEELMAYESYMNFFGIPYMEGGTPAAAAEEGTAADDEVVTGNGMEACNPPVSSGMEMLWIFDDILPA----------- : 227
MaERF8  : PELFEDGGPHKKLRSDISGVELSEELYANEPYMKFLPTPYFEG---SSDASMDSLFGGELLQG-GVDLWS---FDDLPMEAVFTEGI------------- : 361
MaERF9  : -----------------------SMGDGPAMEDSPIDDSINFETFFQSPKCRDYMLNPSLFFAPQAEEWGEEADILWSFC---------------- : 188
MaERF10 : --------RPASSAR---------EASVSHHCLALGRAAALTGMSVCDRLQSASDSVSPAEP-----TMRLPFDVDLNLSPPSEVV-------------- : 191
MaERF11 : --------RPFLFLG---------AAPRSD-------AAALTGFKGIG--TRVSPTVMAAQ------ARRLPFDLDLNLPPPPEVA-------------- : 183
MaERF12 : --------RITAAAA----PTHVRASHRRRQSNPPPQ-RVLVGEEDCHSDCGSSSSVVDDDNGDIASACPQPLPFDLNLLPPADDDFHAVALNL------- : 212
MaERF13 : --------RMPAAAATAATPIHLRTAHLGRQANPPPP-RVLAGENDCHSDCGSSCSVVDDD-ADVASAYRQPLPFDLNLHPPPEDDLHVTVLRL------- : 208
MaERF14 : --------RHPSAAA----PIHIRPRILRKQVNPPPPPRVLNGDDDCHSDCGSSSVVDDD-GDIVSLCRQPLAFDLNLLPPSEDDLHDTALRL------- : 210
MaERF15 : --------QPGLAVE---------SGSEFS-------GYRFEAVKMVVKGEQERRGTVAED------KKKPPFCFDLNLPPPFV--------------- : 185
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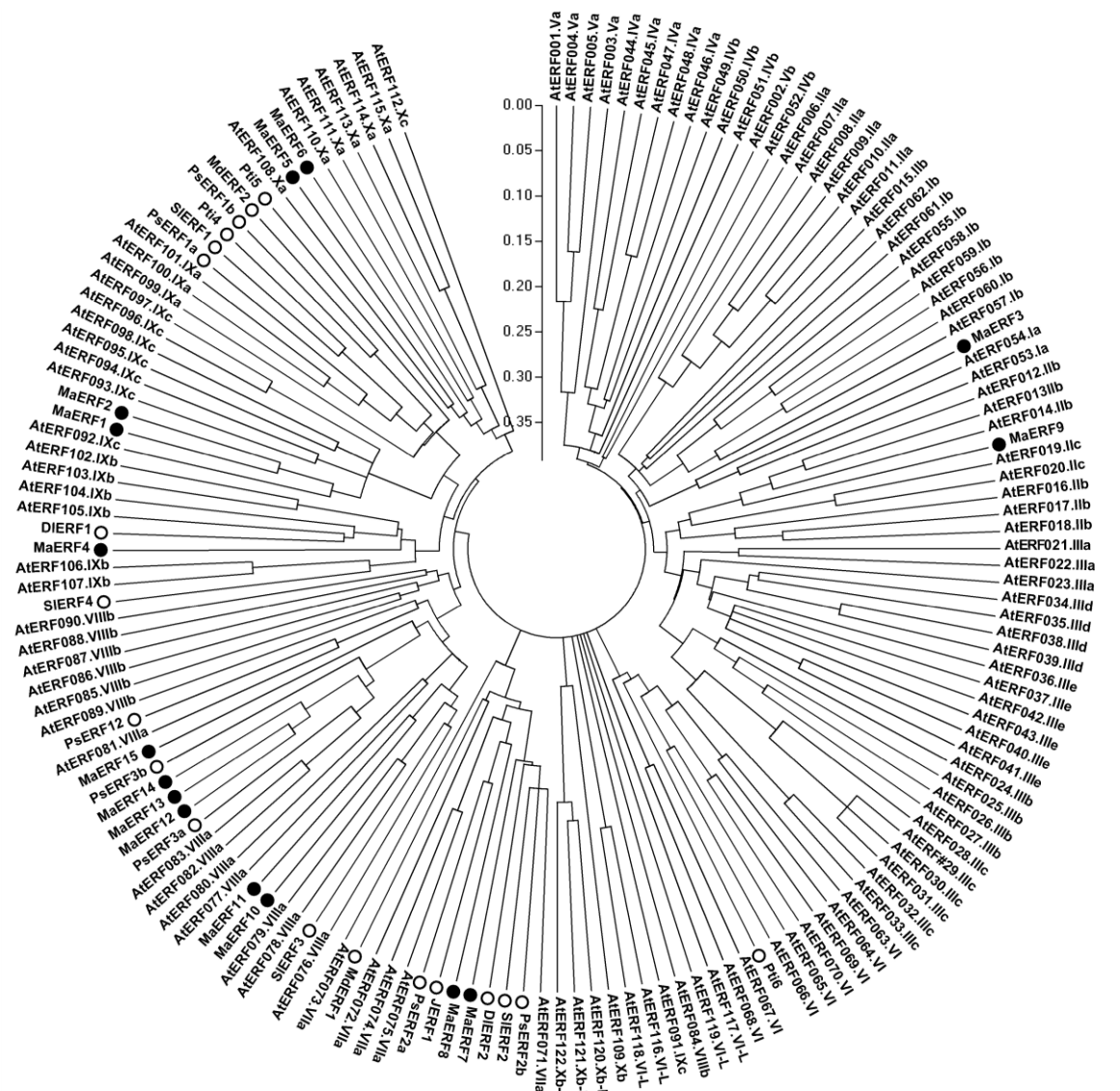
Figure S2. Amino acid sequence alignment of the MaERF proteins. Identical and similar amino acids

were presented by black and gray shading, respectively. Gaps were introduced to optimize alignment.
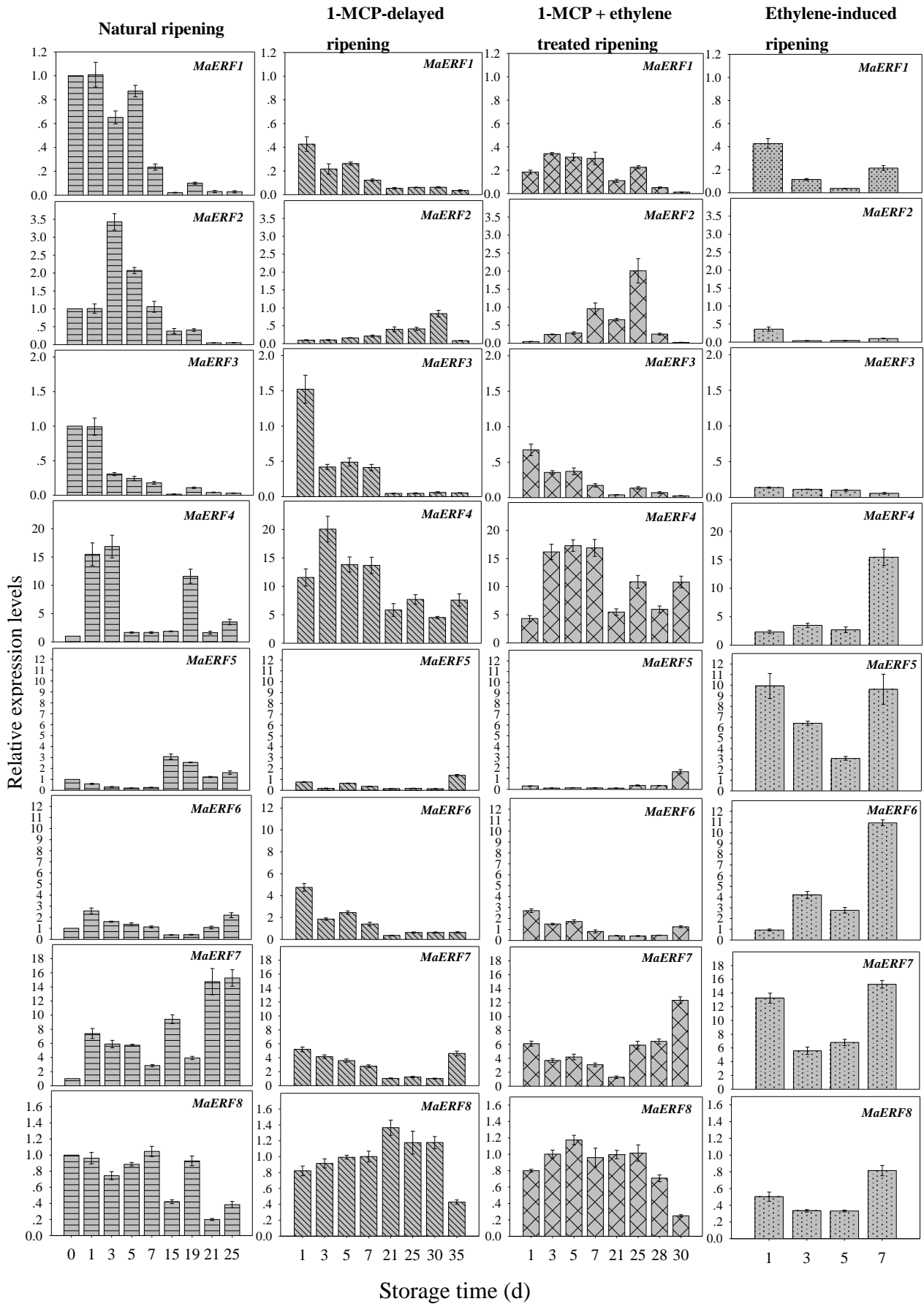
Figure S3. Phylogenetic tree of ERFs. Fifteen banana MaERFs (black circles) were aligned with the Arabidopsis ERF family and other fruit ERFs (white circles). The amino acid sequences were obtained from The Arabidopsis Information Resource or the National Center for Biotechnology Information database. Multiple alignment was carried using CLUSTALW and the phylogenetic tree was constructed with MEGA5.0 using a bootstrap test of phylogeny with minimum evolution test and default parameters.
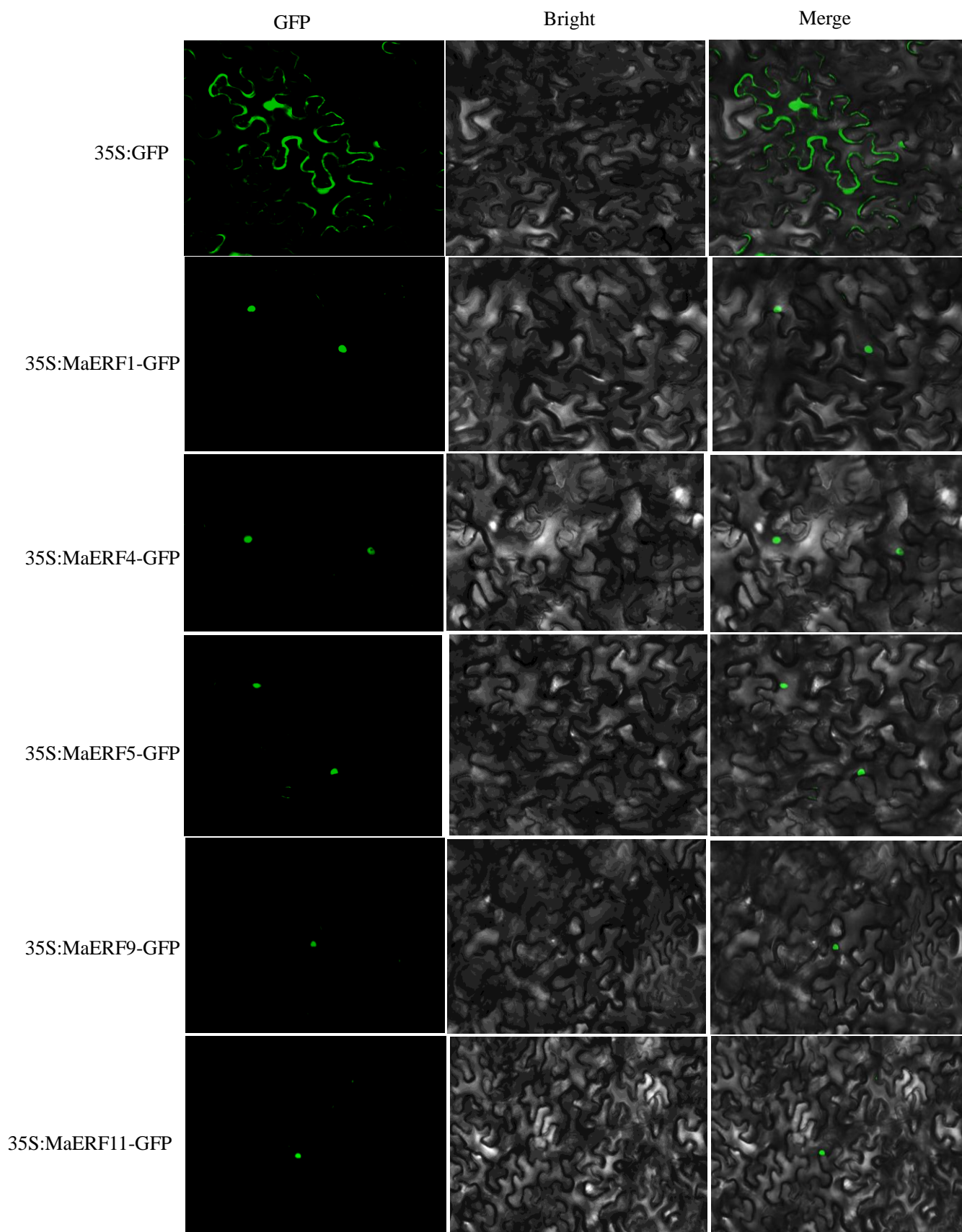
Figure S4. Subcellular localization of MaERFs in tobacco leaves. Leaves were transiently transformed with MaERF–GFP constructs or GFP vector through *Agrobacterium* transfection.

GFP fluorescence was observed with a fluorescence microscope. Images were taken in a dark field for green fluorescence, while the outline of the cell and the merged were photographed in a bright field.
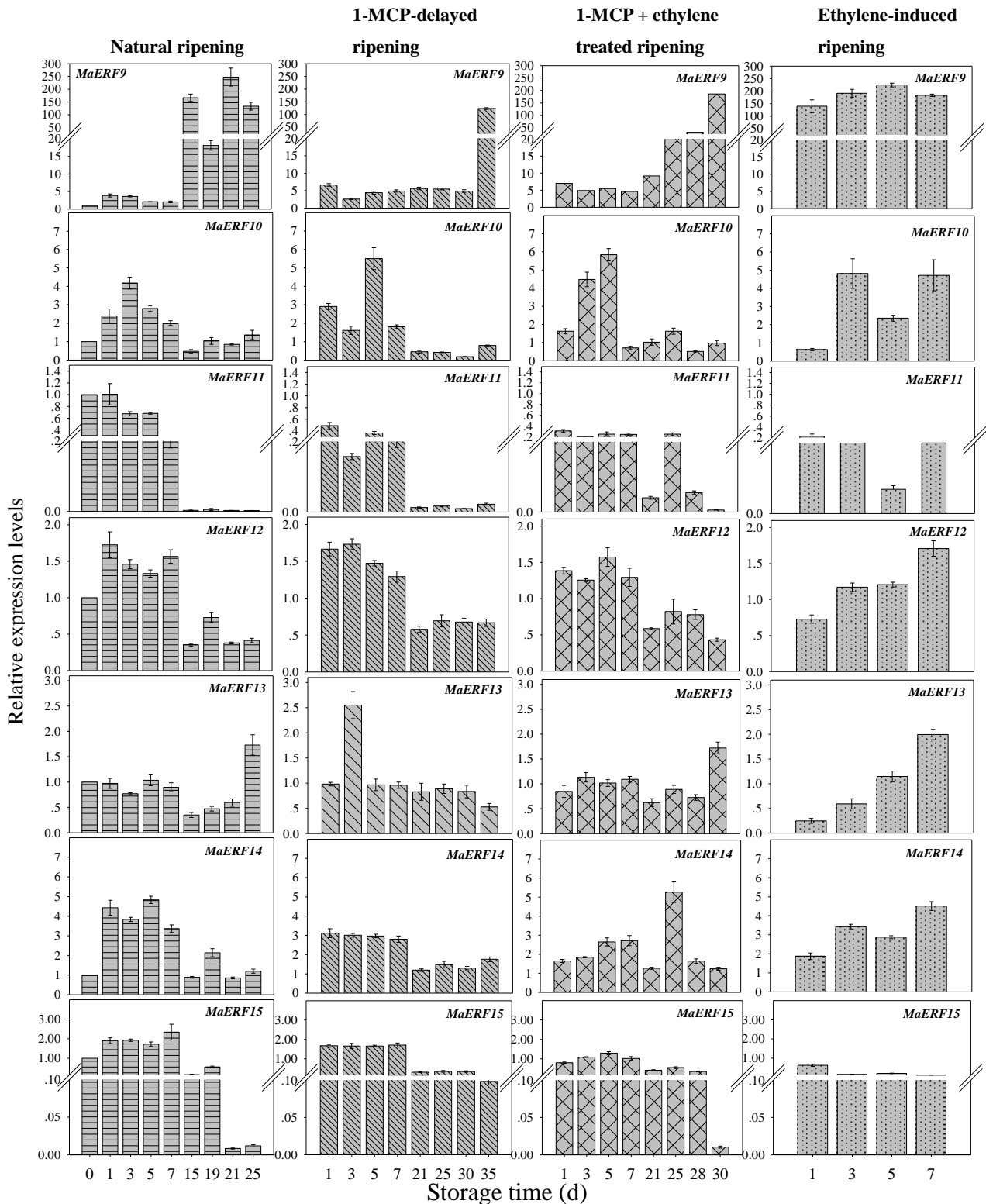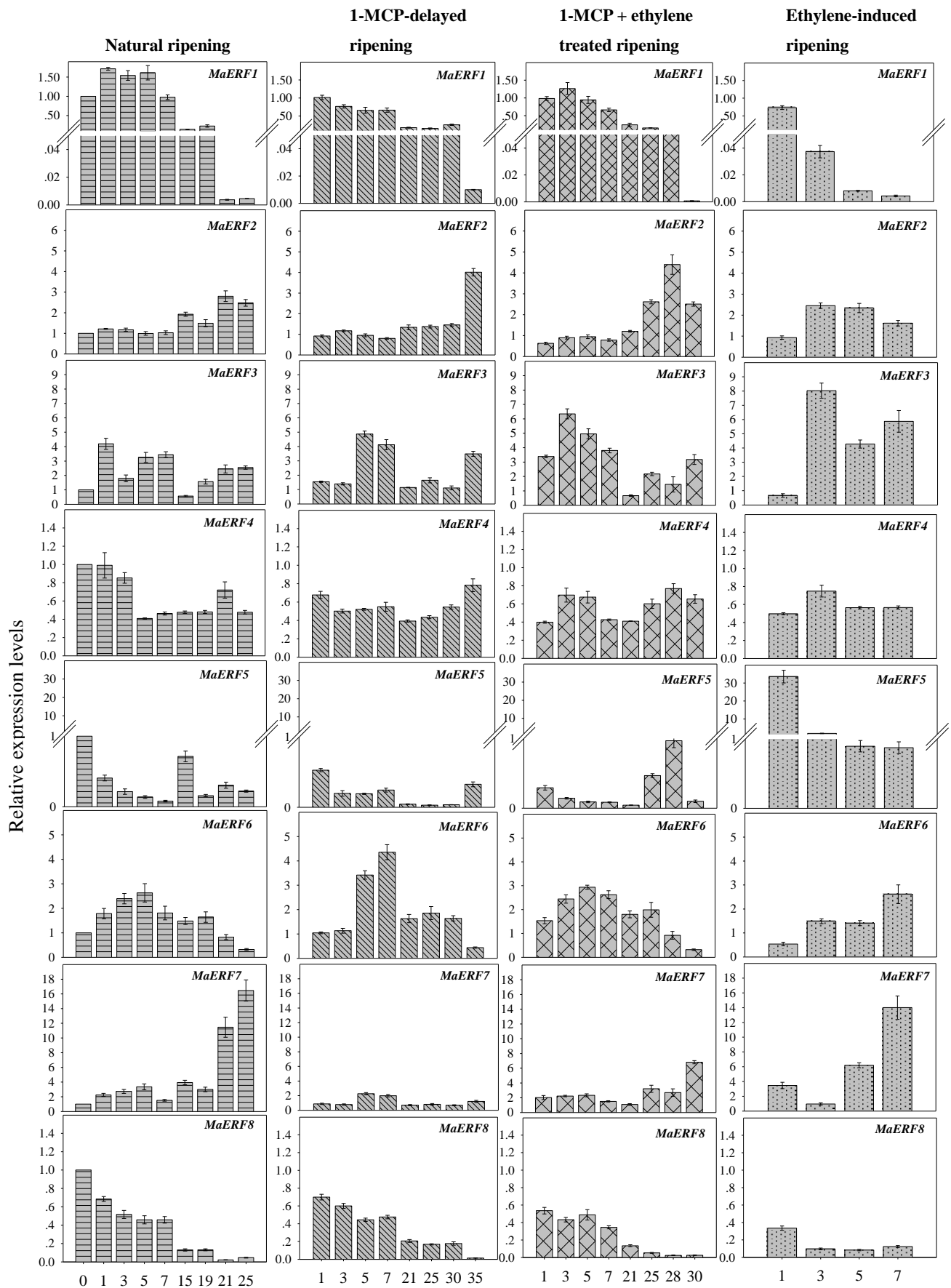
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Relative expression levels
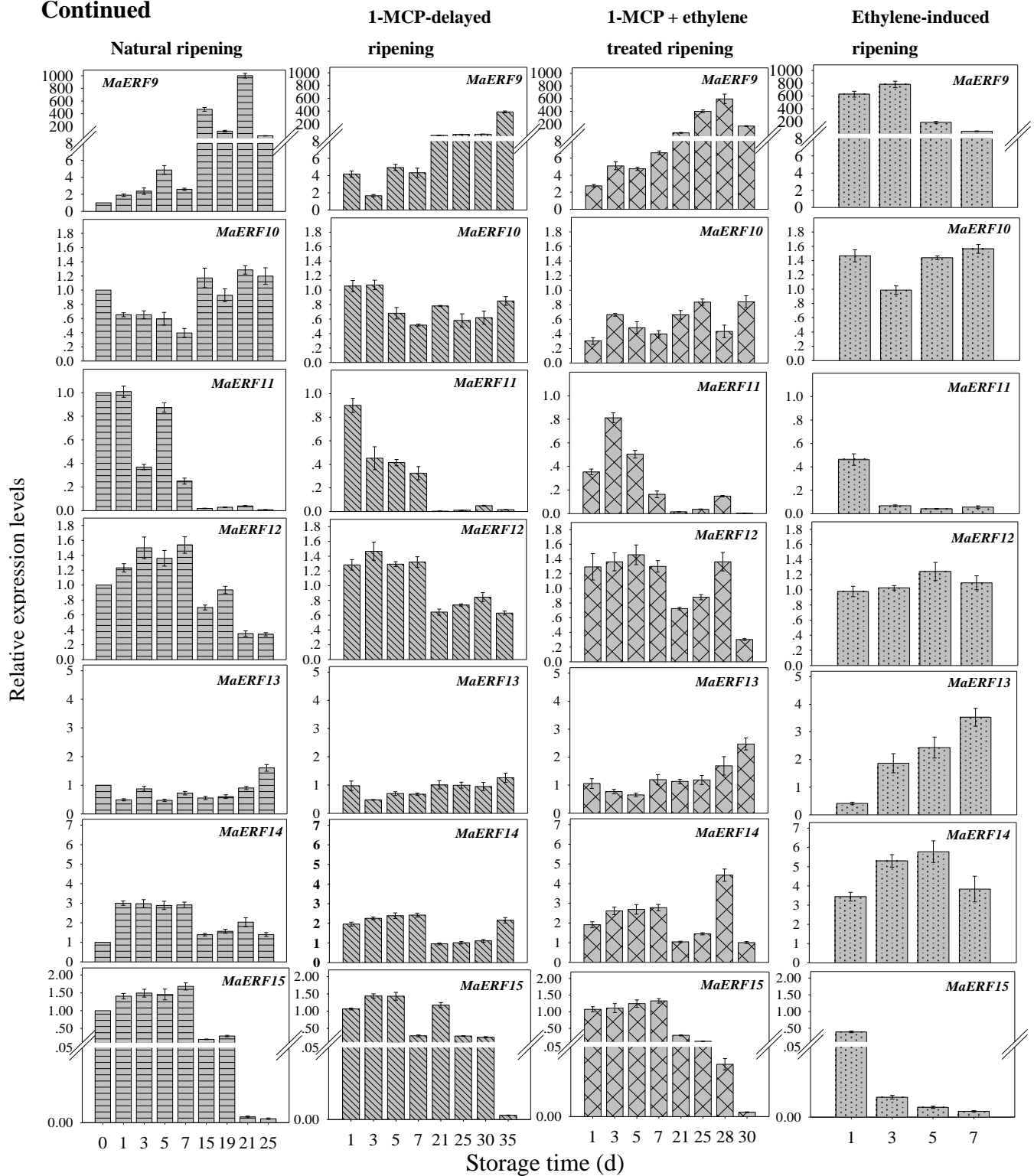
Storage time (d)

Continued

Figure S5. Expressions of *MaERFs* genes in banana fruit peel with four different ripening treatments, including natural (control), ethylene-induced, 1-MCP-delayed and combination of 1-MCP + ethylene treated ripening. Expression levels of each gene are expressed as a ratio relative to the harvest time (0 d of control), which was set at 1. Each value represents the means of three replicates, and vertical bars indicate the S.E.

Natural ripening   1-MCP-delayed ripening   1-MCP + ethylene treated ripening   Ethylene-induced ripening

Figure S6. Expression of *MaERFs* genes in banana fruit pulp with four different ripening treatments, including natural (control), ethylene-induced, 1-MCP-delayed and combination of 1-MCP + ethylene treated ripening. Expression levels of each gene are expressed as a ratio relative to the harvest time (0 d of control), which was set at 1. Each value represents the means of three replicates, and vertical bars indicate the S.E.