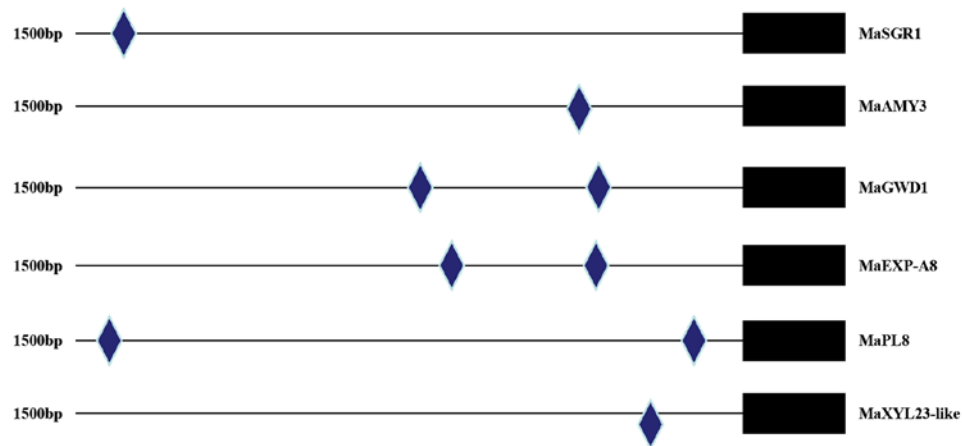
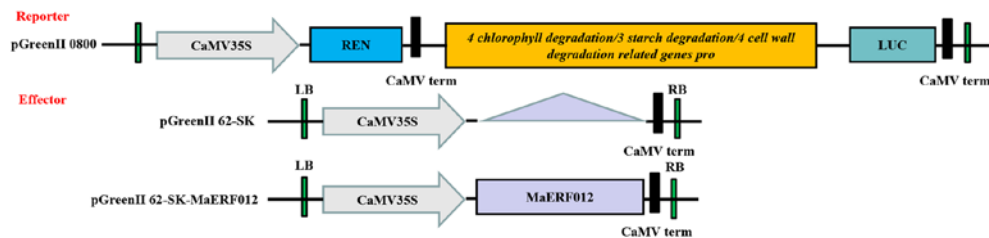


## Supplementary Materials



**Figure S1.** Multiple alignment of MaERF012 (XM\_009415777.2) protein with other ERF proteins. Other plants ERF proteins including banana MaERF003 (XP\_009417483.2) and MaERF113 (XP\_018683838.1), tomato SIERF003 (XP\_004242199.1), SIERF014 (XP\_010312777.1), SIERF017 (XP\_004251702.1) and SIERF021 (XP\_004250714.1), papaya CpERF003 (XP\_021906523.1), CpERF113 (XP\_021900277.1), CpERF020 (XP\_021903568.1), CpERF023 (XP\_021893066.1), CpERF024 (XP\_021908529.1), CpERF036 (XP\_021891938.1) and CpERF039 (XP\_021893663.1). The multiple alignments were made using DNAMAN.



**Figure S2.** Phylogenetic analysis of MaERF012 and other ERF proteins. The phylogenetic tree was performed by MEGA 5.0 with a default parameters, minimum evolution test and bootstrap test of phylogeny. The numbers indicate the bootstrap values.

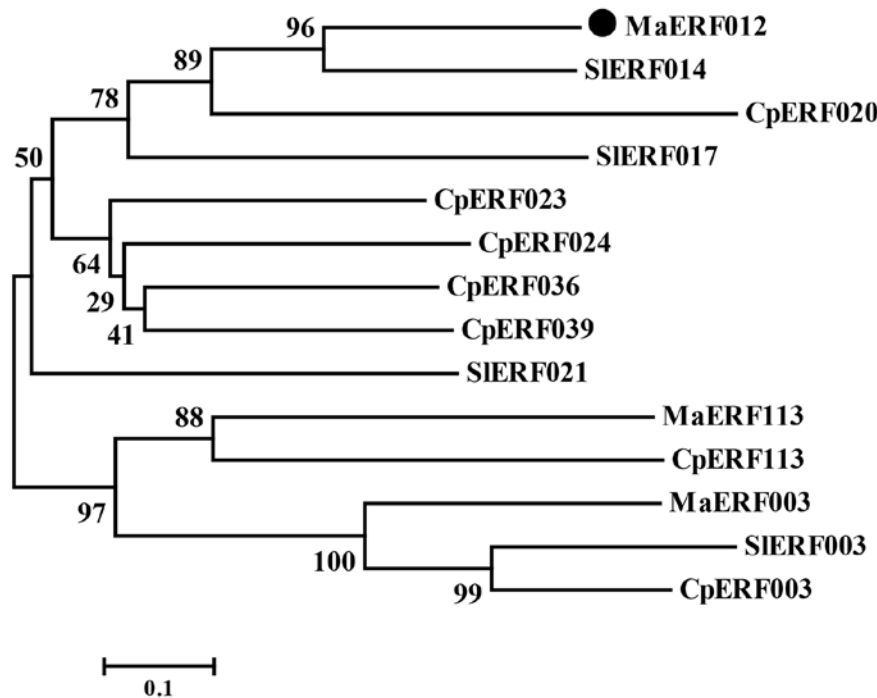
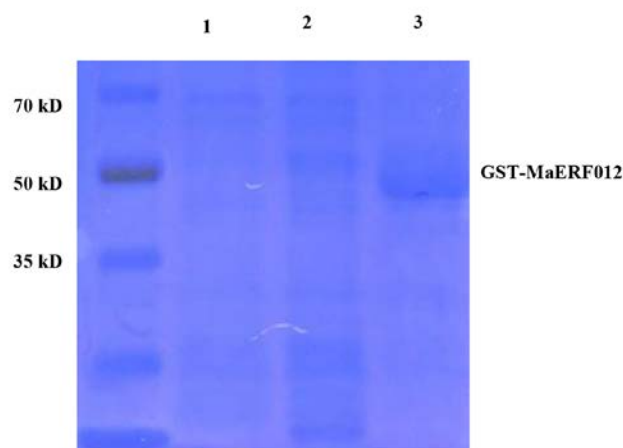


Figure S3. Picture of the effector and reporter vectors.

MaERF003.seq	.....ARRCSLPI LCI GSPAVI SLSSLSSLSLTHTRSCSHVTDAPR.....	45
MaERF012.seq	.....VVKSKI RG.....ALDHCD..PRSSAAAVGKK.....	26
MaERF113.seq	.....VVSALAHVI SSSSSVVDTRGCEPAST CCGI KLEEAAGRGDTAAQVSEI CQNV.....	53
PaERF003.seq	.....MARP.....	4
PaERF020.seq	.....M.....SNVCAYELADSAHGDHDK.....	21
PaERF023.seq	.....MEGPP.....YIEDDS.....TTITITNTIAAEI HSKSSS.....RN	33
PaERF024.seq	.....M.....CYYSKPT.....NKASSSSSSSSRSNVSS.....	25
PaERF036.seq	AKII FTLLTNEKNHTI QI SI KPETPT CNSASSSPPSPSSLPCHDCSPLQI SI I PETAT CNSASSPSPSPSSNPLPKLSEEPKLPRIH	90
PaERF039.seq	.....MEASF.....HQKCEARS.....IGATSPSSSSSSSTLSSSSI NKSCCKFCFEESIIN	48
PaERF113.seq	.....VVSALTQVI GTAG.....AHNQAPG.....SSSSSGKEI PCSCPDCS.....	38
SIERF003.seq	.....MARP.....	4
SIERF014.seq	.....VVKTECKS.....LSMSI SSI ATSNNNNAKTKN.....	29
SIERF017.seq	.....MVKPNSKDTEFSCSSSS.....	17
SIERF021.seq	.....MCGIT S.....	6
MaERF003.seq	.....LCRYGVRGRVGSVSEIRHFLKTRVLGTFGTATDAARANDAAARLACGSKAR..TNFVDPN...C	110
MaERF012.seq	.....CYNGVNRSGVSVSEIRAPNCKTRVLGYSYTFEAAARANDALLCLRGTAAS..LNFP..ASLLQ	90
MaERF113.seq	.....RRRHYGVNRGSPVGVSEIRAPNCKTRVLGTFDTATDAARANDAAARLACGSKAR..LNFPERVQGR..	120
PaERF003.seq	.....CCRYGVRGRVGSVSEIRHFLKTRVLGTFGTATDAARANDAAARLACGSKAR..TNFVDPN...SSS	72
PaERF020.seq	.....KYLGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..TNFVDPN...SSS	88
PaERF023.seq	SGTR.....HPVYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..EEVED	102
PaERF024.seq	VTGR.....HPVYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..NSASS	94
PaERF036.seq	HRSRK.....HPVYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..RLVNL	160
PaERF039.seq	VI NKSKRVKI NKNEEDGKNYSAYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..ELAHQ	133
PaERF113.seq	.....MRRHYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..ELVQAG..	105
SIERF003.seq	.....CCRYGVRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..TNFVDPN...SSS	72
SIERF014.seq	.....CYNGVNRSGVSVSEIRAPNCKTRVLGYSYTFEAAARANDALLCLRGTAAS..LNFP..ASLLQ	90
SIERF017.seq	.....SLRYGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..ELVQAG..	81
SIERF021.seq	.....KYLGVNRGRVGSVSEIRHFLKTRVLGYSYTFEAAARANDAAARLACGSKAR..LNFP..ELVQAG..	69
AP2/ERF		
MaERF003.seq	SI PAPALSPGLAAKLEKCCSASR.....EEGERVEVVAPVG.....EE.....EEAEVTRVDEEYIEE	163
MaERF012.seq	LPDC...VNSPKSI CRVAAAAT.....NAASPSYSSDTAEETLASSAGDGLAME.....DS.PI DDSI NFEA..	181
MaERF113.seq	TDLGFLVSPGVRCPRPVPLQLPATSYDPLLQVACLLCSREEDLQNVASGLYGGFTIPVSSCTPTTS.....ALGSSCHFLDFSSCS	204
PaERF003.seq	SSSSKLLSATLAAKLHKCHMASLCPNKK.....HEEPRYTRFANN.....GNAGKS...SEKNGREESCS...NSCVCLAELEEDHVQ	149
PaERF020.seq	CANG...ELSPRSVCRAASDAAMAVDAR.....MNVNGLAPSTITELVVDDESSRNLSYEAASEE.....CVTVGREALSI SVED	160
PaERF023.seq	LPRPS...TCTPRDI CAAAAAAS.....VILS...KSDVVSVDGDDDFVREIELP.....ELANGGYRNSCG	163
PaERF024.seq	LPVPE...SNSPRDI CAAAAAALGAA.....NDALSAENARNDENVTITAERSSAVNEFVTEDL.....IFDMNLLVMAELGM	169
PaERF036.seq	FPRPS...SLAPRDI CAAAAAAM.....AEFTNLPSSSSSSNDSEIELLEI VCLPNI DG.....SYELCELI MEIER	230
PaERF039.seq	LPRPS...SANDRDI CAAAAAAM.....LHCKSGCDEKNRLVNAAPPSPASTVASSDDA.....FADLPDLADVTRCI	200
PaERF113.seq	NTELAFIP...VADITTTATTVYANCNPVDVAD..SCEPVSCVYCCDLLR...YACLLTGVDVLSVYTS.....NIADCPPLPHLS..	182
SIERF003.seq	SSSTKYLAAALI AKLCRCQKSLNANNRPDTAKLEDGNDRLSSCGNRGDHGI TRRTVQASVEXPVYKESCTENNNCTEKSLEDHGI EQ	162
SIERF014.seq	IDHHTCTTLPKAI CRVAAAATPE CQNVGLV...LSDNNNSTNPTI SS..PPCSSTSSSEDI NDGCLLS.....NI NTFDCESMI EQV	178
SIERF017.seq	IRNGR...TATPSEI CAAACFANNTEPELI RVGPBENSLLSSSSSEI FRAEPPSVSVSDRVESEKTEI TLGNDFI DVYRVE SRVESEKTE	169
SIERF021.seq	FPPKA...SSSPEDI RLAAQCAAI T.....VQNTNSASSSBGCGAPVTVGLSPTIEI QAI N..DF.....PADSPHMTTEEDIN	139
MaERF003.seq	MEELLI YNGSLIEI TSSSSSSS.....SSSSSSSSYL.....	194
MaERF012.seq	FFCSPECRDYMNLPLFAF...CAEIVGEE...ADIHLVSFC.....	188
MaERF113.seq	CYTNFSSSSSSSSSSSVHCE...CKDKGSRPP.....	235
PaERF003.seq	MEELLDVGSNELCVTST.....	168
PaERF020.seq	VF...VSFGVSVLDGDNCPN.....YSACL.....	162
PaERF023.seq	LVSPPLRDI ADDDAAT.....ADHDLVKFP.....	187
PaERF024.seq	VVYPPLDF CREFSCEIM.....AAERLIRSDFF.....	194
PaERF036.seq	DEFVGPSSVCVTDGPGI DI G.....FNYHDEELFPVVCYCH.....	259
PaERF039.seq	.....SSSSSSCHNCDCGCK.....SFDDDNPAH.....	237
PaERF113.seq	MEELLDVGSIELSSVLCE.....	208
SIERF003.seq	YNFDPKYNL..ALHGTI FDDPPSAEEVYVESSADI PLVSFC.....	181
SIERF014.seq	NSLDNGFVDAFSSSLGTUNDSDFI FPGFDDLSCEFFI PPPSSPQSPICQPNLESLEENLYNDVGCSCQTSFLVN	219
SIERF017.seq	YTYENSVDYEMDDCLVDY.....SSTNSF.....	247
SIERF021.seq	.....	163

**Figure S4.** The location of GCC box motifs in the promoters of 3 Chl degradation, 3 starch and 4 cell wall degradation genes.



**Figure S5.** The recombinant proteins of GST-MaERF012 was tested by SDS-PAGE gel stained. In lane 1-3: non-induced protein, before purification of the induced protein, after purification of the induced protein.

**Table S1.** Primers used in the present study.

Experiment	Gene	Forward primer (5'-3')
RT-qPCR	<i>MaERF012-F</i>	AGACCTTCTTCCAGTCACCCA
	<i>MaERF012-R</i>	GAGCAATCTACTTGACTTCCACC
	<i>MaSGR1-F</i>	GGAACAAGGTCCAAGGAAAGA
	<i>MaSGR1-R</i>	GGAGTTCATCGCAGAAGATGTA
	<i>MaGWD1-F</i>	GTGTAAAGGGAGAGGAGGAAATAC
	<i>MaGWD1-R</i>	CTCGCACAGAGACATGAGATAG
	<i>MaAMY3-F</i>	AGGAACAGGCTCTGGGTATG
	<i>MaAMY3-R</i>	AGACTCAGTGGGTGGTGGTA
	<i>MaPL8-F</i>	AGGTTCTCACAGGTTGTGT
	<i>MaPL8-R</i>	TCTCTTCCAAGGAAGCATCG
	<i>MaEXP-A8-F</i>	GCTCTGGGAGATGATTGGATT
	<i>MaEXP-A8-R</i>	CGTCGGTGATACAAGTTCTGATA
	<i>MaXYL23-like-F</i>	GTCACCGCTACTACCTATCT
	<i>MaXYL23-like-R</i>	TTGGTGTGCAGAGTGTAAAGG
Subcellular location	ERF012-like-GFP-F	ATCAAGCTTGGATCCATGGTGAAGAGCAAGATCAG
	ERF012-like-GFP-R	GCTCACCATGTCGACGCAGAAGCTCCACAG
Transient expression assay	MaERF012-like-sk-F	CGCTCTAGAACTAGTGGATCCATGGTGAAGAGCAAGATCAG
	MaERF012-like-sk-R	GATAAGCTTGATATCGAATTCTCAGCAGAAGCTCCACAG
	MaNOL-0800-F	CTATAGGGCGAATTGGGTACCATCTATTATTACACATGC
	MaNOL-0800-R	TGTTTTTGGCGTCTTCCATGGGACTAGAATAAGCTTATAT
	MaNYC1-0800-F	CTATAGGGCGAATTGGGTACCAACCGTGAACAATTTGGATGC
	MaNYC1-0800-R	TGTTTTTGGCGTCTTCCATGGGATGCTTGAAATCTGCGCATGT
	MaSGR1-0800-F	CTATAGGGCGAATTGGGTACCACTTCTCTTAGCATGAGC
	MaSGR1-0800-R	TGTTTTTGGCGTCTTCCATGGGTACTTAACTTCCGAGGGAT

	MaPPH-0800-F:	CTATAGGGCGAATTGGGTACCTGTGAAGGTGCCCTACTG
	MaPPH-0800-R:	TGTTTTTGGCGTCTTCCATGGCATGATCGTGCGCCCTT
	MaBAM3-0800-F	CTATAGGGCGAATTGGGTACCATTGCCTCCAGTACCTAACATTACG
	MaBAM3-0800-R	TGTTTTTGGCGTCTTCCATGGCATACTGTCGGAGGCCGGCGA
	MaGWD1-0800-F	CTATAGGGCGAATTGGGTACCAATGACCCCATTAGATCGGATC
	MaGWD1-0800-R	TGTTTTTGGCGTCTTCCATGGACTTTCGTGGAGGGACATCC
	MaAMY3-0800-F	CTATAGGGCGAATTGGGTACCTCCTTCTGCGTTAGCCGTTG
	MaAMY3-0800-R	TGTTTTTGGCGTCTTCCATGGCGGCGAACGGTGGGGGAGAATC
	MaPL8-0800-F	CTATAGGGCGAATTGGGTACCTCGTATCACCATTTCGCACCTG
	MaPL8-0800-R	TGTTTTTGGCGTCTTCCATGGGATGGAGAATGCAGTTGCAAGG
	MaEXP-A8-0800-F	CTATAGGGCGAATTGGGTACCTAGGACCACTTTCATGCCTACAG
	MaEXP-A8-0800-R	TGTTTTTGGCGTCTTCCATGGGCTGTGAATATTAATGCATACCATC
	MaSUR14-like-0800-F	CTATAGGGCGAATTGGGTACCTTAATGGGCCATTAAACCTTGACAG
	MaSUR14-like-0800-R	TGTTTTTGGCGTCTTCCATGGCTCTTCTTCTCCTCTCTTCAAG
	MaXYL23-like-0800-F	CTATAGGGCGAATTGGGTACCTCTGGTGTGCGCAAACCTACC
	MaXYL23-like-0800-R	TGTTTTTGGCGTCTTCCATGGAGGAGAGGAGATGGCAGAAGC
Y1H	MAERF012-LIKE-AD-F	ATGGCCATGGAGGCCAGTGAATTCATGGTGAAGGCAAGATCAG
	MAERF012-LIKE-AD-R	TGCAGCTCGAGCTCGATGGATCCCTCAGCAGAAGCTCCACAG
	MASGR1-PABAI-F	TTGAATTCGAGCTCGGTACCTACTGGCGGCACATACTGGCGGCACATACTGGCGGCACA
	MASGR1-PABAI-R:	TGCCTCGAGGTCGACTGTGCCGCCAGTATGTGCCGCCAGTATGTGCCGCCAGTA
	MaAMY3-PAbAi-F	TTGAATTCGAGCTCGGTACCCACAGCCGCCCTCACAGCCGCCCTCACAGCCGCCCT
	MaAMY3-PAbAi-R	ATGCCTCGAGGTCGACAGGGGCGGCTGTGAGGGGCGGCTGTGAGGGGCGGCTGTG
	MaGWD1-PAbAi-F	TTGAATTCGAGCTCGGTACCTGTGGCCGCCATCTGTGGCCGCCATCTGTGGCCGCCATC
	MaGWD1-PAbAi-R	ATGCCTCGAGGTCGACGATGGCGGCCACAGATGGCGGCCACAGATGGCGGCCACA
	MaEXP-A8-PAbAi-F	TTGAATTCGAGCTCGGTACCTCCGCGGCATGTTCCGCGGCATGTTCCGCGGCATGT
	MaEXP-A8-PAbAi-R	ATGCCTCGAGGTCGACACATGCCGCCGAACATGCCGCCGAACATGCCGCCGA
	MaPL8-PAbAi-F	TTGAATTCGAGCTCGGTACCCGAGGCGGCTGGACGAGGCGGCTGGACGAGGCGGCTGGA
	MaPL8-PAbAi-R	ATGCCTCGAGGTCGACTCCAGCCGCTCGTCCAGCCGCTCGTCCAGCCGCTCG
	MaXYL23-like-PAbAi-F	TTGAATTCGAGCTCGGTACCAGGAGCCGCCGAAGGAGCCGCCGAAGGAGCCGCCGA
	MaXYL23-like-PAbAi-R	ATGCCTCGAGGTCGACTCGGGCGGCTCCTTCGGGCGGCTCCTTCGGGCGGCTCCT
EMSA	MaERF012-like-GST-F	GGTTCGCGTGGATCCATGGTGAAGAGCAAGATCAG
	MaERF012-like-GST-R	AGTCACGATGCGGCGCGCAGAAGCTCCACAG
	MaSGR1-probe-F	ATCATATTTCTGAATTAAGGTACTGGCGGCACATCGATATGGTATC
	MaSGR1-probe-R	GATACCATATCGATGTGCCGCCAGTACCTTAATTCAGAAATATGAT
	MaAMY3-probe-F	CGGACTCACGCCACACCACAGCCGCCCTGACGCAATTAGCGTCGA
	MaAMY3-probe-R	TCGACGCTAATTGCGTCAGGGGCGGCTGTGGTGTGGCGTGAGTCCG
	MaGWD1-probe-F	CTAATCACATGATGGTGTGTGGCCGCCATATTCTCTCCAAGCAACC
	MaGWD1-probe-R	GGTTGCTTGGGAGAGAATGATGGCGGCCACACACCATCATGTGATTAG
	MaEXP-A8-probe-F	GTTGGTTTATAAGGTGCTCCGCGGCATGTGCTGCAGACACGAAGT
	MaEXP-A8- probe -R	ACTTCGTGTCTGCAGCACATGCCGCCGAGCACCTTATGAACCAAC
	MaPL8-probe-F	ATATCTGTGTGCTCTTGCGAGGCGGCTGGACTTTCTCTGCACGCAAT
	MaPL8-probe-R	ATTGCGTGCAGGAAAGTCCAGCCGCTCGCAAGAGCACACAGATAT
	MaXYL23-like-probe-F	GGCAATCAGTCGGAGGAGGAGCCGCCGATTTGGTGCATATCATC
	MaXYL23-like-probe-R	GATGATAGTGACCAAATCGGGCGGCTCCTCCTCCGACTGATTGCC
Transgenic	MaERF012-Pdnor-F	AAAAAGCAGGCTTCATGGTGAAGAGCAAGATCAG
Fenjiao banana fruit	MaERF012-Pdnor-R	CAAGAAAGCTGGGTCTCAGCAGAAGCTCCACAG