

Figure S1. Phylogenetic tree of banana LOX genes family.

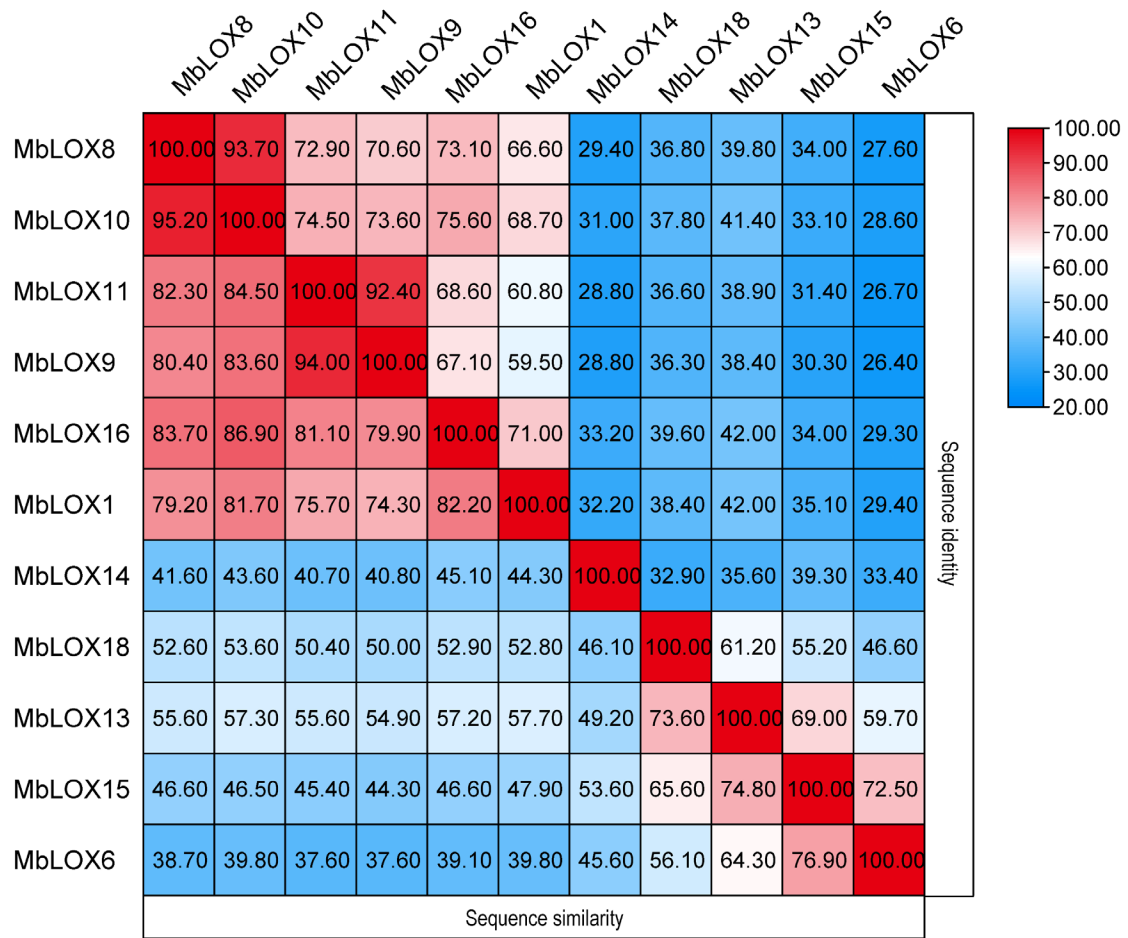


Figure S2. Sequence identities and similarities (%) among the *MbLOXs*.

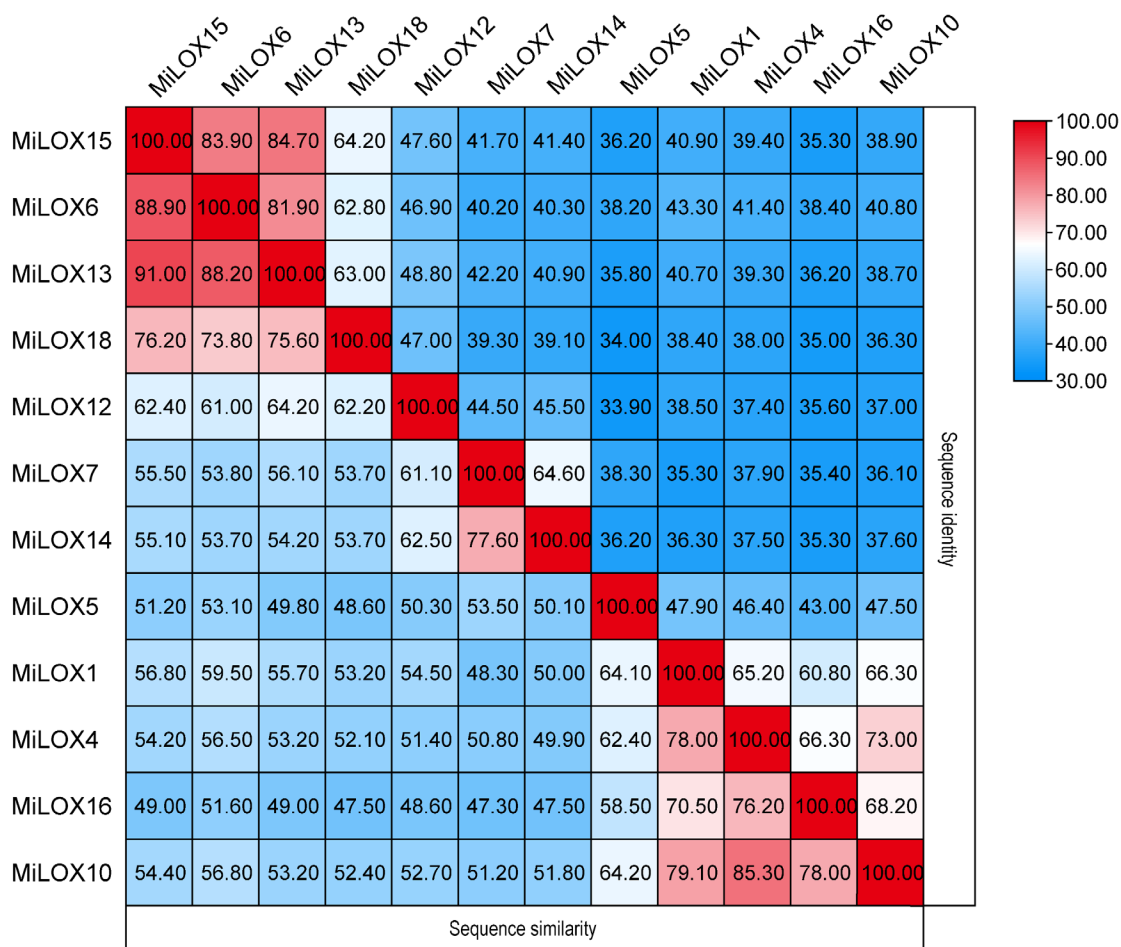


Figure S3. Sequence identities and similarities (%) among the *MiLOXs*.

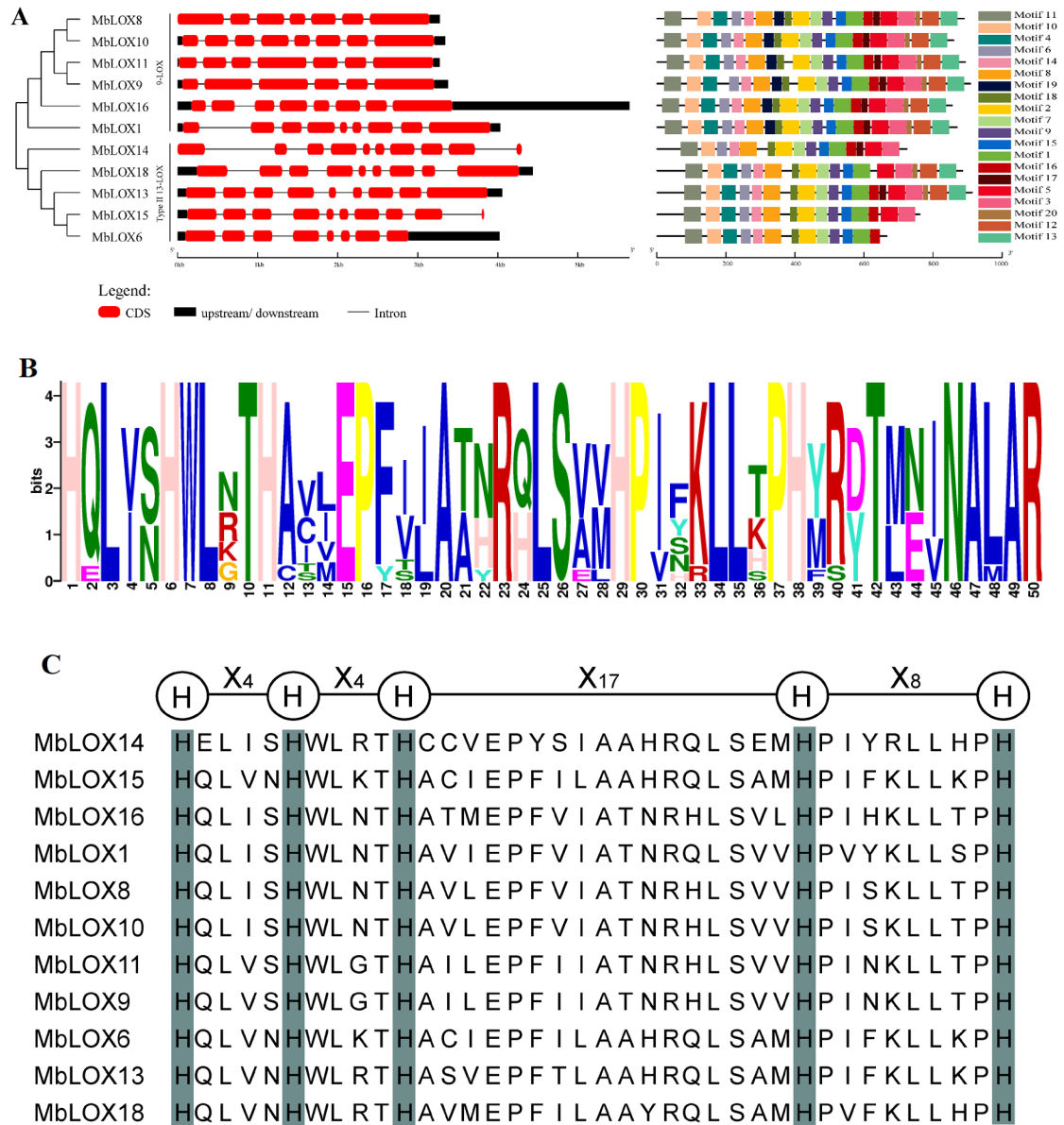


Figure S4. Gene structures and conserved motifs (A), Motif 1 sequence (B) and the 38 conserved residues of MbLOX proteins of *MbLOXs* or their encoded proteins. the dark color in C shows highly conserved histidine (His).

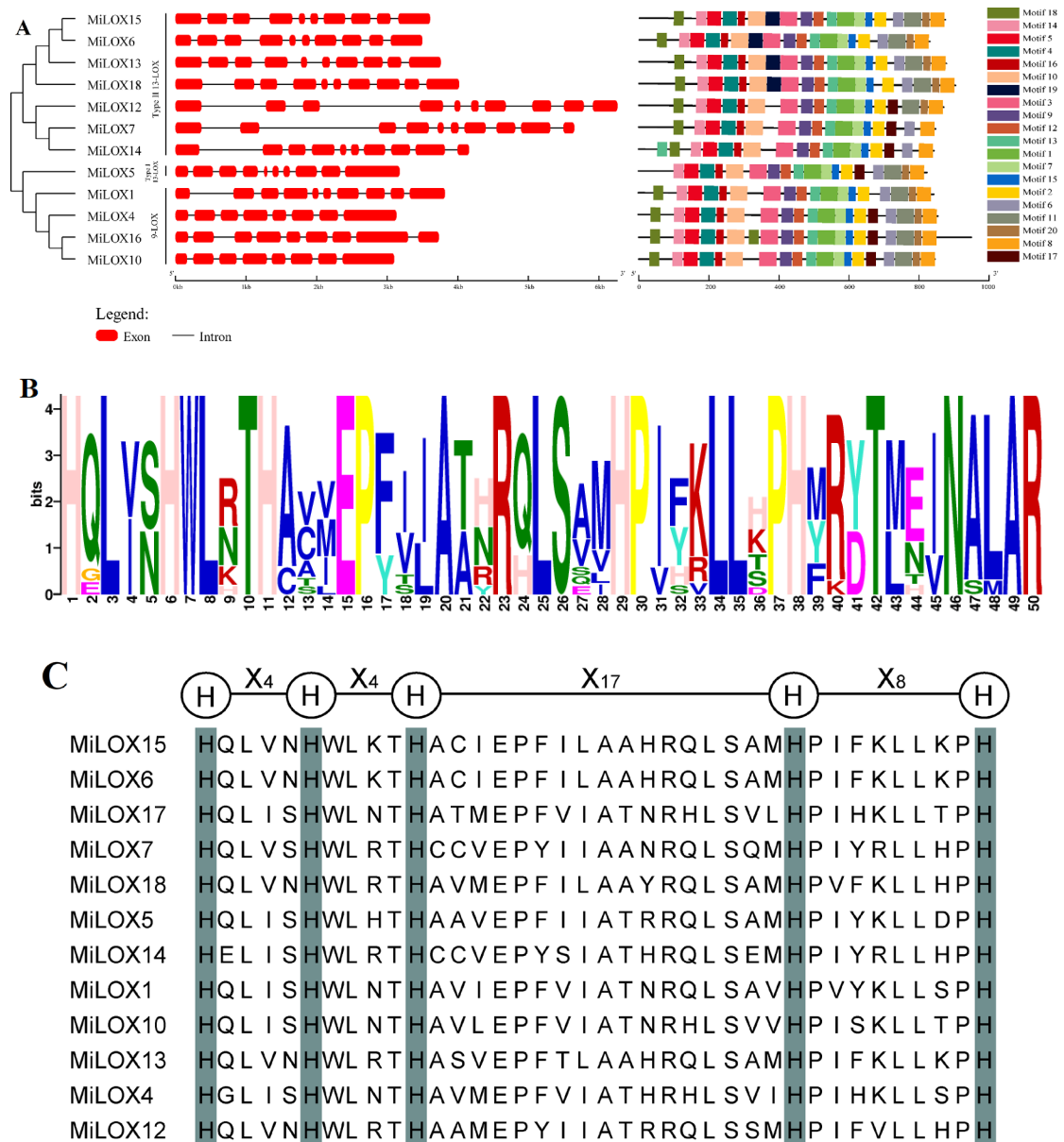


Figure S5. Gene structures and conserved motifs (A), Motif 1 sequence (B) and the 38 conserved residues of MiLOX proteins of *MiLOXs* or their encoded proteins. the dark color in C shows highly conserved histidine (His).

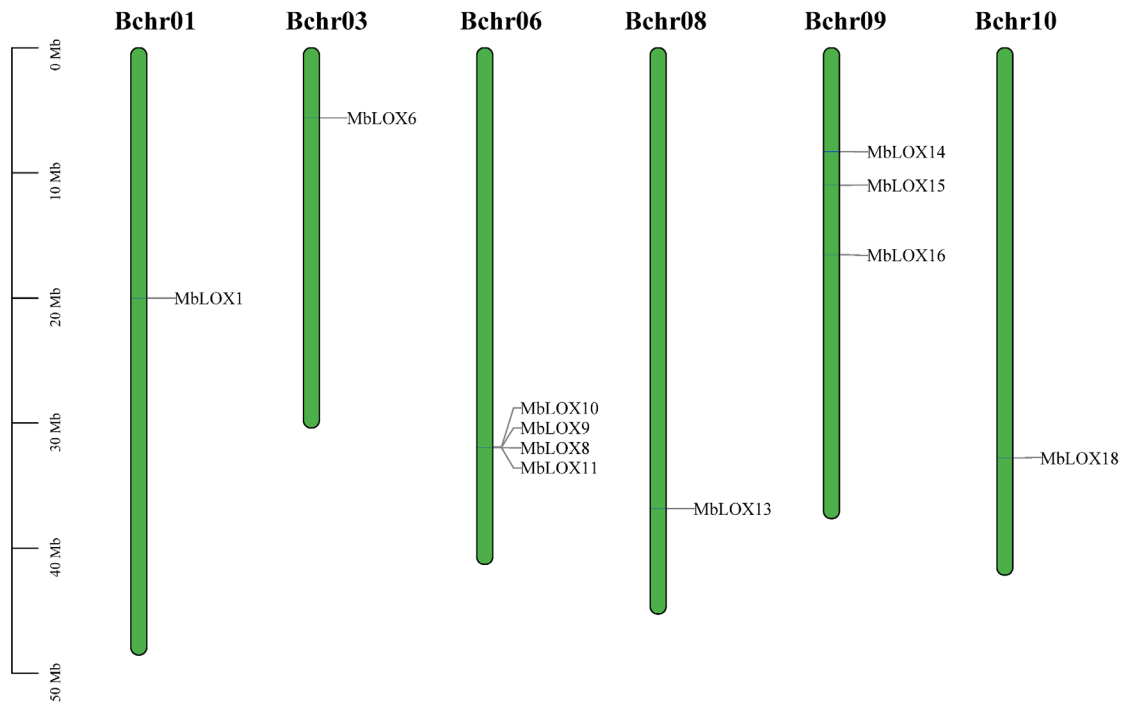


Figure S6. Chromosome localization of MbLOX genes.

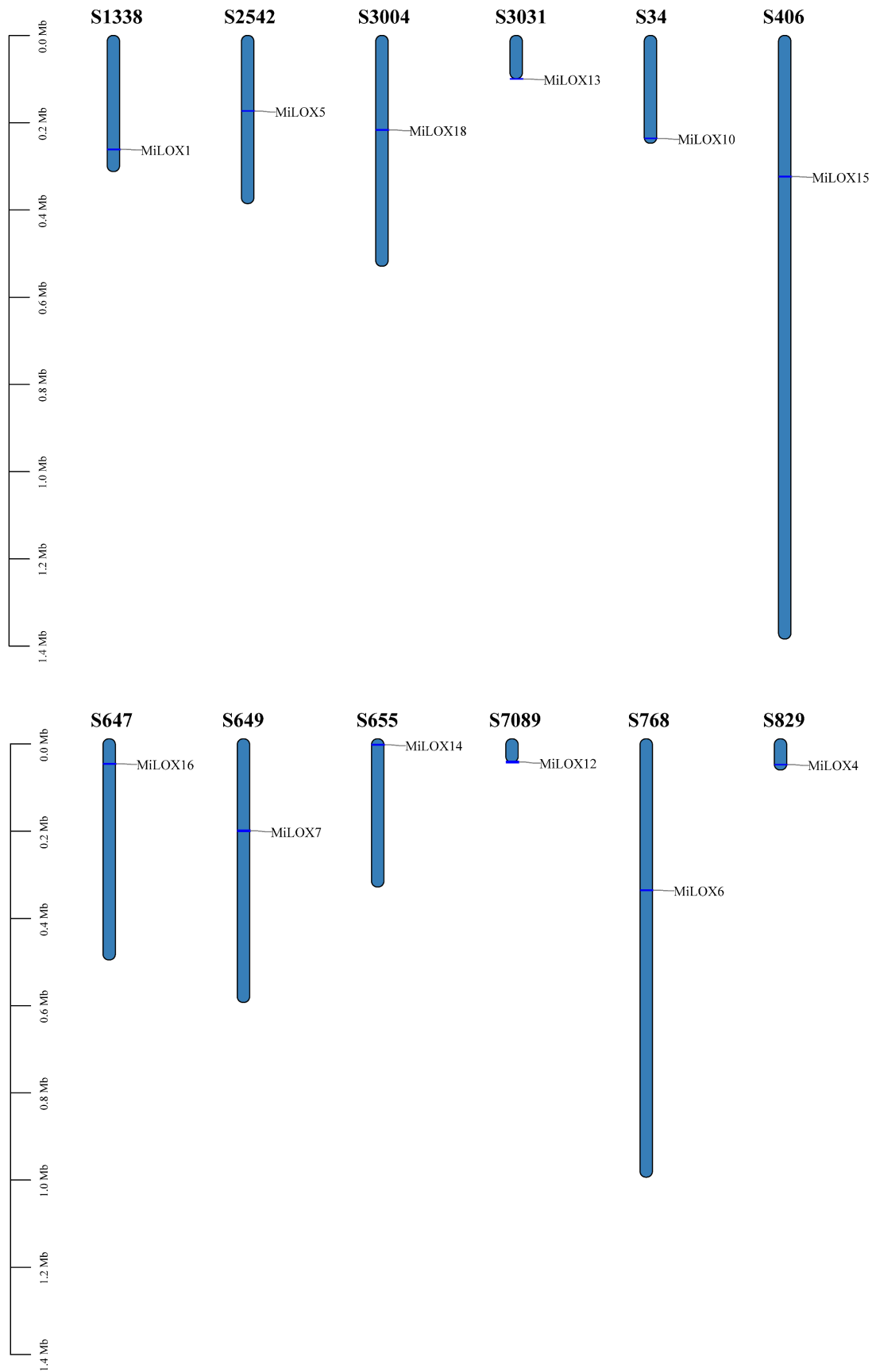


Figure S7. Chromosome localization of MiLOX genes.

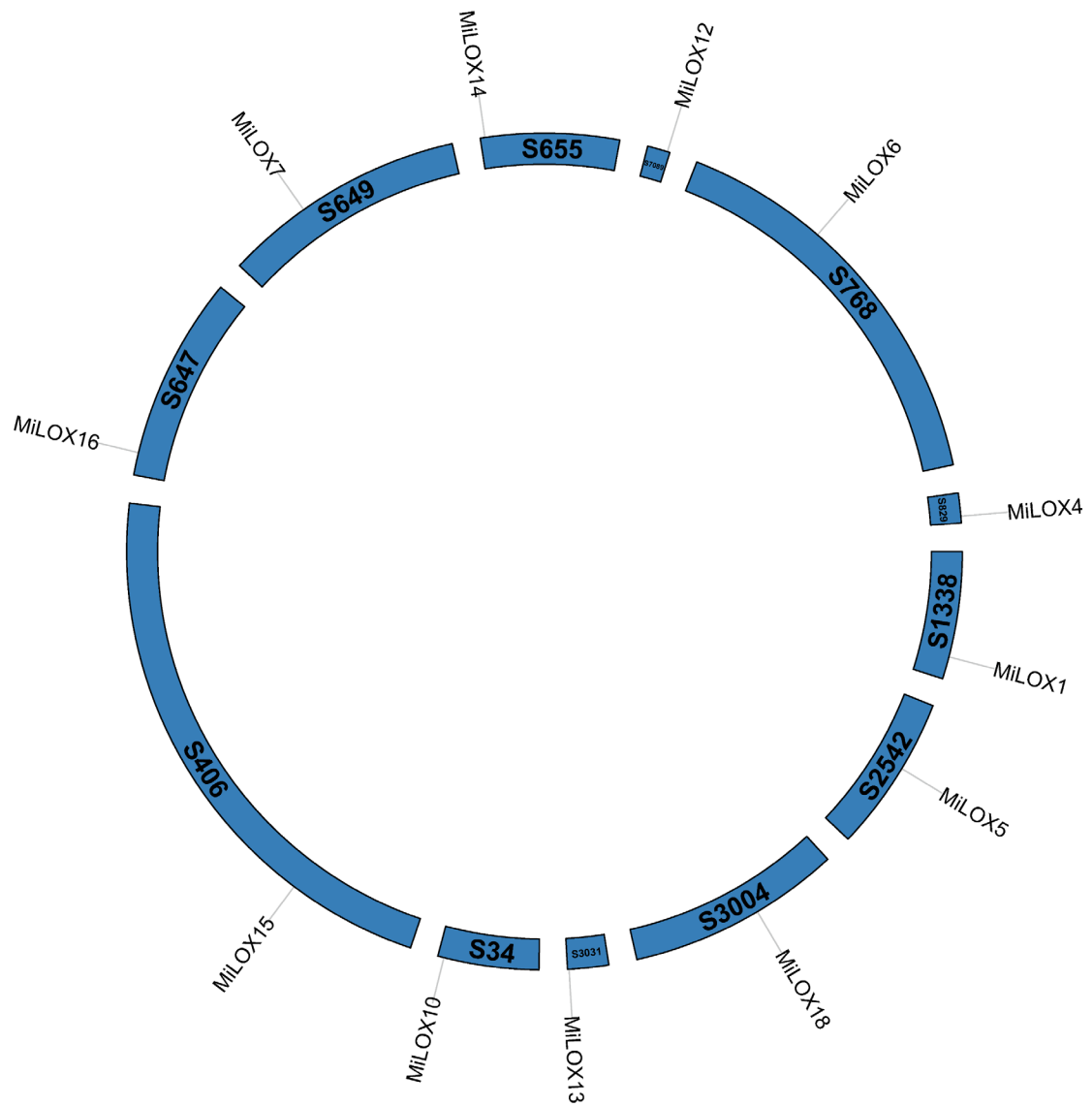


Figure S9. Collinear distribution of MiLOX genes.

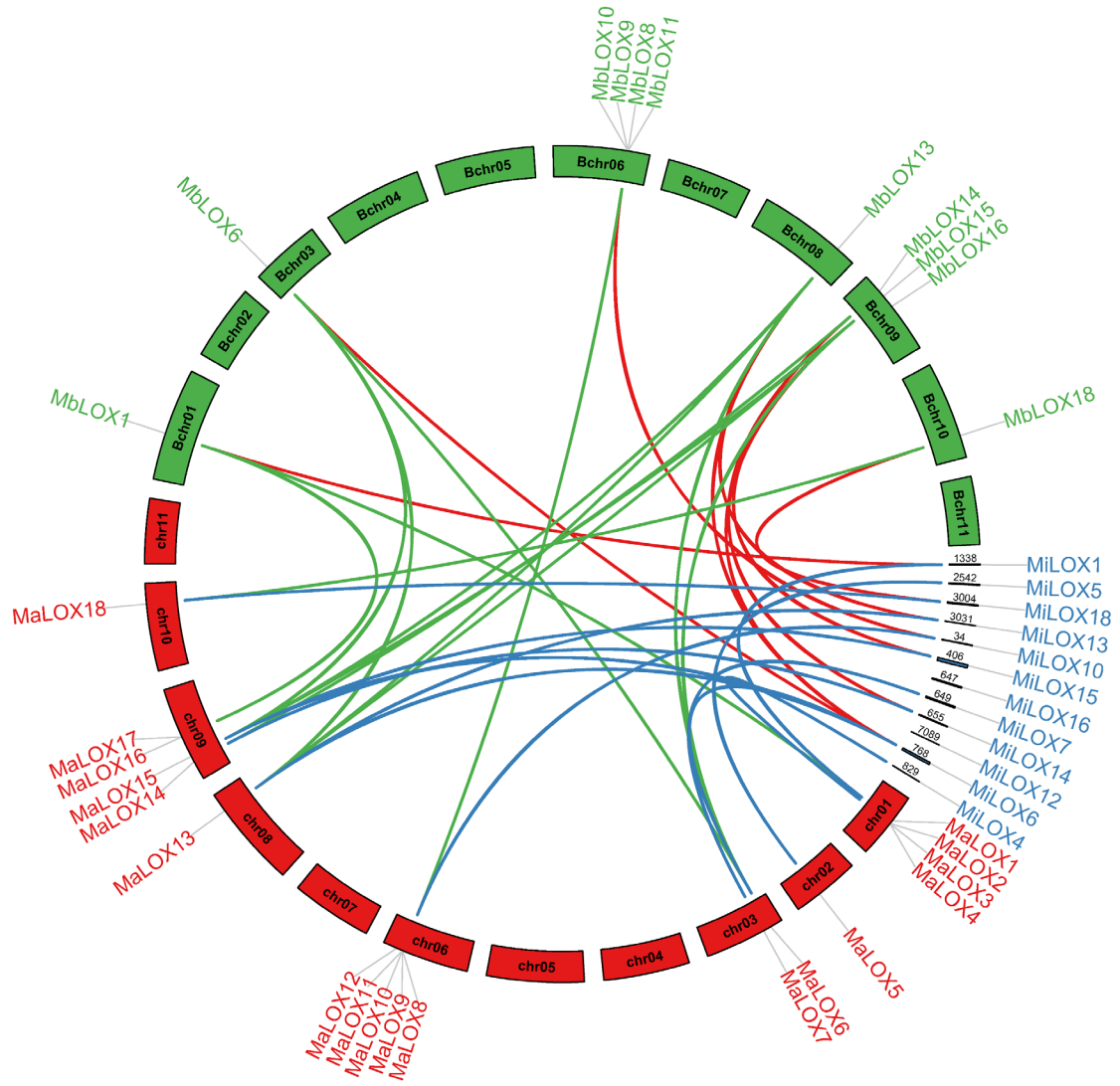


Figure S10. Orthologous among *M. acuminata*, *M. balbisiana* and *M. itinerans*.

		MbLOX8	MbLOX10	MbLOX11	MbLOX9	MbLOX16	MbLOX1	MbLOX14	MbLOX18	MbLOX15	MbLOX6	MbLOX13	
light responsive	Function												
	Element												
	G-Box	2		6		2	2	2	4	7	4	5	
	Box 4	1	1		1	3	3		1	1	4	1	
	TCCC-motif		1			2				1	2		
	GATA-motif		2			1			1	2	1		
	AE-box					2		6					
	GT1-motif					1		1	1		2	1	
Sp1							1	3			1		
I-box	1	1	1	1			1			2			
phytohormone responsive	Abscisic acid	ABRE	2		5		2	1	1	5	5	2	4
		AuxRR-core					1	3					
	Auxin	TGA-element		3		2	1		1	1		3	
	MeJA	CGTCA-motif	1	1		2	1		1	2	2		2
		TGACG-motif	1	1		2	1		1	2	2		2
	gibberellin	P-box								2		1	3
		GARE-motif											
		TATC-box							1				1
	salicylic acid	TCA-element		1		1					1		
	Ethylene	ERE		1		1			9			1	
stress responsive	anaerobic induction	ARE	1	1	1			3	1	2	1	1	
	anoxic specific inducibility	GC-motif							1			1	
	low-temperature	LTR	1		1				1	1	1		
	MYB-drought	MBS							1			1	
	defense and stress	TC-rich repeats				1		1			1		
	Wound	WUN-motif			1					1		1	
plant growth and development	meristem	CAT-box							1			1	
	circadian control	circadian					2	1					
	endosperm	GCN4_motif				1					1		
	zein metabolism	O2-site	1	1	1			2			1		

Figure S11. Analysis of *cis*-acting elements of MbLOX gene family promoter.

Function		Element	MiLOX15	MiLOX6	MiLOX13	MiLOX18	MiLOX12	MiLOX7	MiLOX14	MiLOX5	MiLOX1	MiLOX4	MiLOX16	MiLOX10
light responsive	light	Box 4	1	1	2	1	6			1	3		2	1
		GATA-motif	1	2				1	2	1		1	1	
		G-box	12	2	4	1	6	9	18		1	7	3	2
		GT1-motif		2	1	4					1	2	2	
		MRE	2					1	1	1	1	1		
		Sp1				1	1		1	1				4
		TCCC-motif	1	1		1		1		1			1	
		TCT-motif	1			1	4	1	1					
phytohormone responsive	Abscisic acid	ABRE	8	1	3	1	7	8	16			6	3	2
		AuxRR-core						1		1				
	Auxin	TGA-element	1		3			1						
		CGTCA-motif	1			1	1	3	1	1		1	1	1
	MeJA	TGACG-motif	1			1	1	3	1	1		1	1	1
		P-box		1	3									
	gibberellin	TATC-box		1	1							1		
		GARE-motif								1				
	salicylic acid	TCA-element					1		1					
	Ethylene	ERE				1	2	3	5					
stress responsive	anaerobic induction	ARE	3	1		1	1	2	1	2	2	1		2
	low-temperature	LTR	1			1		3	1	2				
	MYB-drought	MBS		1	1		1			2				
	defense and stress	TC-rich repeats							1		1		1	
	Wound	WUN-motif		1		1						1		2
plant growth and development	meristem	CAT-box			1	1	1				1			
	circadian control	circadian								1	2			
	endosperm	GCN4_motif		1		1		1		1				
	zein metabolism	O2-site			1		1			4	1	1		

Figure S12. Analysis of *cis*-acting elements of MiLOX gene family promoter.

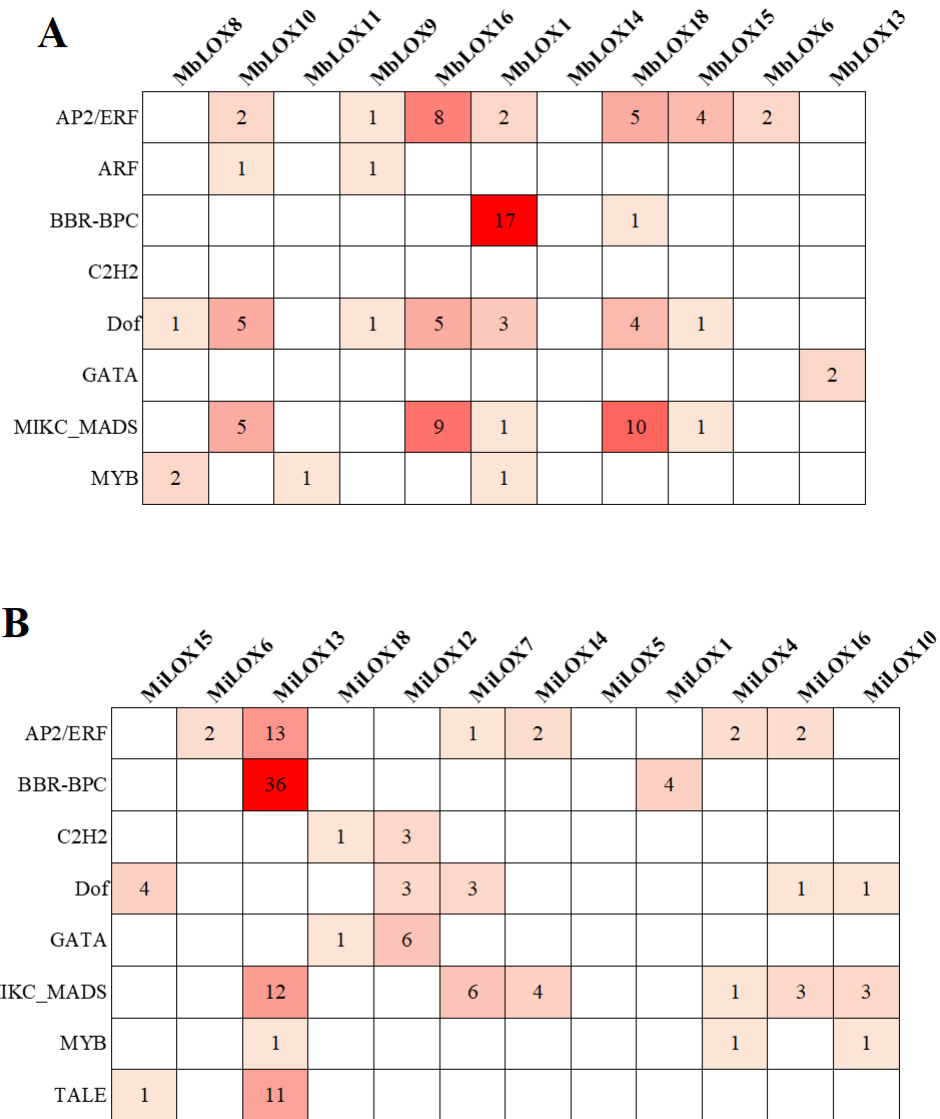


Figure S13. Transcription factor binding sites predicted in the promoters of *MbLOXs* (A) and *MiLOXs* (B).

Arg(R)	<u>CGC</u>	<u>AGG</u>	<u>CGG</u>	<u>AGA</u>	<u>CGA</u>	<u>CGU</u>
	1.30	1.61	1.08	0.82	0.68	0.51
Leu(L)	<u>CUG</u>	<u>CUC</u>	<u>UUG</u>	<u>CUU</u>	<u>CUA</u>	<u>UUA</u>
	2.00	1.98	0.97	0.69	0.25	0.11
Ser(S)	<u>AGC</u>	<u>UCC</u>	<u>UCG</u>	<u>AGU</u>	<u>UCU</u>	<u>UCA</u>
	2.07	1.46	1.18	0.50	0.50	0.30
Ala(A)	<u>GCC</u>	<u>GCG</u>	<u>GCU</u>	<u>GCA</u>	-	-
	1.61	1.27	0.57	0.55	0	0
Gly(G)	<u>GGC</u>	<u>GGG</u>	<u>GGA</u>	<u>GGU</u>	-	-
	1.99	0.91	0.71	0.39	0	0
Pro(P)	<u>CCG</u>	<u>CCC</u>	<u>CCU</u>	<u>CCA</u>	-	-
	1.35	1.21	0.81	0.63	0	0
Thr(T)	<u>ACC</u>	<u>ACG</u>	<u>ACA</u>	<u>ACU</u>	-	-
	1.71	1.38	0.49	0.42	0	0
Val(V)	<u>GUC</u>	<u>GUG</u>	<u>GUU</u>	<u>GUA</u>	-	-
	1.67	1.65	0.48	0.20	0	0
Ile(I)	<u>AUC</u>	<u>AUA</u>	<u>AUU</u>	-	-	-
	2.33	0.38	0.29	0	0	0
Asn(N)	<u>AAC</u>	<u>AAU</u>	-	-	-	-
	1.48	0.52	0	0	0	0
Asp(D)	<u>GAC</u>	<u>GAU</u>	-	-	-	-
	1.35	0.65	0	0	0	0
Cys(C)	<u>UGC</u>	<u>UGU</u>	-	-	-	-
	1.63	0.37	0	0	0	0
Gln(Q)	<u>CAG</u>	<u>CAA</u>	-	-	-	-
	1.43	0.58	0	0	0	0
Glu(E)	<u>GAG</u>	<u>GAA</u>	-	-	-	-
	1.60	0.40	0	0	0	0
His(H)	<u>CAC</u>	<u>CAU</u>	-	-	-	-
	1.44	0.56	0	0	0	0
Lys(K)	<u>AAG</u>	<u>AAA</u>	-	-	-	-
	1.72	0.28	0	0	0	0
Phe(F)	<u>UUC</u>	<u>UUU</u>	-	-	-	-
	1.75	0.25	0	0	0	0
Tyr(Y)	<u>UAC</u>	<u>UAU</u>	-	-	-	-
	1.63	0.37	0	0	0	0
Trp(W)	<u>UGG</u>	-	-	-	-	-
	1.00	0	0	0	0	0
Met(M)	<u>AUG</u>	-	-	-	-	-
	1.00	0	0	0	0	0

Figure S14. Relative usage of synonymous codons in MbLOX gene family members. The underlined data indicate that the MbLOX genes preferentially to use this codon.

Arg(R)	<u>AGG</u>	<u>CGC</u>	<u>CGG</u>	AGA	CGA	CGU		
	1.69	1.19	1.14	0.84	0.70	0.43		
Leu(L)	<u>CUG</u>	<u>CUC</u>	UUG	CUU	CUA	UUA		
	1.93	1.90	0.95	0.72	0.34	0.16		
Ser(S)	<u>AGC</u>	<u>UCC</u>	<u>UCG</u>	AGU	UCU	UCA		
	1.80	1.51	1.12	0.57	0.55	0.46		
Ala(A)	<u>GCC</u>	<u>GCG</u>	GCU	GCA	-	-		
	1.60	1.25	0.70	0.45	0	0		
Gly(G)	<u>GGC</u>	<u>GGG</u>	GGA	GGU	-	-		
	1.84	0.92	0.82	0.42	0	0		
Pro(P)	<u>CCG</u>	<u>CCC</u>	CCU	CCA	-	-		
	1.42	1.04	0.80	0.75	0	0		
Thr(T)	<u>ACC</u>	<u>ACG</u>	ACU	ACA	-	-		
	1.54	1.36	0.56	0.55	0	0		
Val(V)	<u>GUC</u>	<u>GUG</u>	GUU	GUA	-	-		
	1.68	1.65	0.43	0.24	0	0		
Ile(I)	<u>AUC</u>	AUA	AUU	-	-	-		
	2.23	0.45	0.32	0	0	0		
Asn(N)	AAC	AAU	-	-	-	-		
	1.42	0.58	0	0	0	0		
Asp(D)	GAC	GAU	-	-	-	-		
	1.33	0.67	0	0	0	0		
Cys(C)	<u>UGC</u>	UGU	-	-	-	-		
	1.67	0.33	0	0	0	0		
Gln(Q)	<u>CAG</u>	CAA	-	-	-	-		
	1.46	0.54	0	0	0	0		
Glu(E)	<u>GAG</u>	GAA	-	-	-	-		
	1.54	0.46	0	0	0	0		
His(H)	<u>CAC</u>	CAU	-	-	-	-		
	1.30	0.70	0	0	0	0		
Lys(K)	<u>AAG</u>	AAA	-	-	-	-		
	1.63	0.37	0	0	0	0		
Phe(F)	<u>UUC</u>	UUU	-	-	-	-		
	1.64	0.36	0	0	0	0		
Tyr(Y)	<u>UAC</u>	UAU	-	-	-	-		
	1.57	0.43	0	0	0	0		
Trp(W)	<u>UGG</u>	-	-	-	-	-		
	1.00	0	0	0	0	0		
Met(M)	<u>AUG</u>	-	-	-	-	-		
	1.00	0	0	0	0	0		

Figure S15. Relative usage of synonymous codons in MiLOX gene family members. The underlined data indicate that the MiLOX genes preferentially to use this codon.