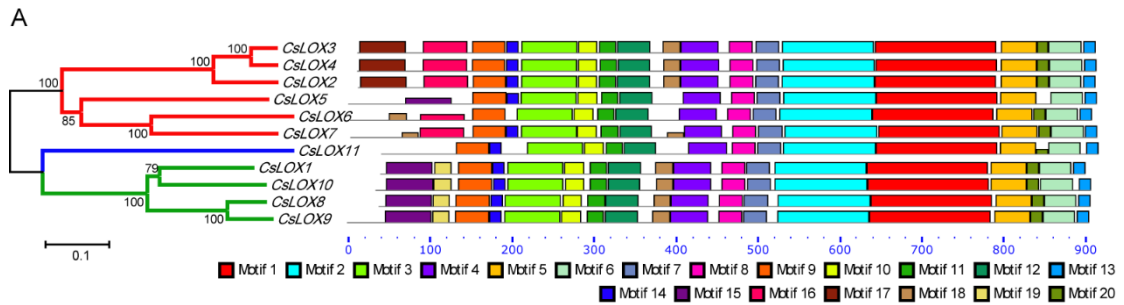


1 **Supplementary Data**

2

3



4

5 **Supplementary Fig. S1** Motifs of *CsLOX* genes in tea plant. A. Phylogenetic relationship and

6 conserved motifs within eleven *CsLOX* proteins. The phylogenetic tree among eleven *CsLOX*

7 are constructed using the NJ method, which shows different colors for each corresponding

8 subfamily. Twenty conserved motifs are set to different colors and the motif numbers are

9 arranged below the motifs. B. A 38-residue motif conserved among tea plant *CsLOX* sequences.

10 The logo of motifs in *CsLOX* genes of tea plant is created using amino acid sequences. The

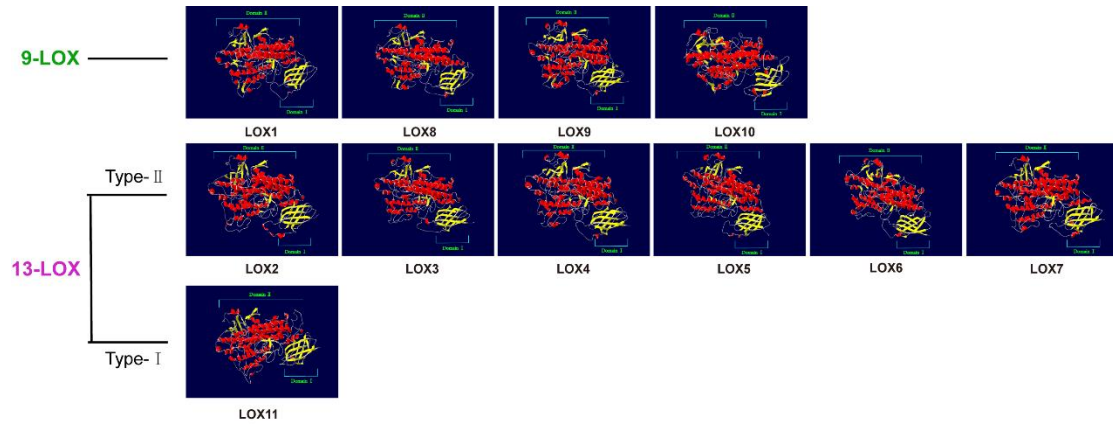
11 sequence conservation at the position are shown by means of overall height in each stack.

12 Height of each residue letter indicates relative frequency of the corresponding amino acid

13 residue and the width is the length of the motif. The five conserved histidines (H) are marked

14 with pink "H" letters.

15



16

17 **Supplementary Fig. S2** Prediction of the 3-dimensional structure of CsLOX proteins. The

18 yellow ribbons indicate the  $\beta$ -barrel, and the red ribbons indicate the bundle of helices.

CsLOX1 .....MLHRVVEGKGNQDKRIGTVLMMKKNVLDNFNFASIL 41  
CsLOX2 .....MLGQTTHSHVFNLLFRFPFSSLSLRKQVCFYVNSHHTIKAISSSSSTSDQTTISVTVVTVVQVAGLLSNLGL 90  
CsLOX3 .....MINSQTQSHVQLLIPWHPFSGTASFPSSLSLRKQVCFYVNSHHTIKAISSSSSTSDQTTISVTVVTVVQVAGLLSNLGL 90  
CsLOX4 .....MINSQTHSHVQLLIPWHPFSGTASFPSSLSLRKQVCFYVNSHHTIKAISSSSSTSDQTTISVTVVTVVQVAGLLSNLGL 90  
CsLOX5 MGNLSLDAAGLTAASAGTNGRSLRAIQVVFQVTVGNRNGSVRAVIGSDGNKTVTVEKDYNGSVLSSSSRGVDRVAVITIRKMKREKISDRIE 100  
CsLOX6 .....MSSFTVNHSLTSSSSQFLDVLVQLQKRNLSFSLIFQSHKSLYLRKRVTFEALVEAQSIVKVFVFLMNRKAVTVVNSRFRVGMIMDL 100  
CsLOX7 .....MLAKREMGSSVHERCSFVASSVNLNHRGQVQLVIFLEARRVQVQKVVGVGLVTVARISDVVAVRFAVFRVAVTVVNSRFRVGMIMDL 100  
CsLOX8 .....MLFTLHSSSTPLSLIERIFFGCFNLFWKDKSPENNMDHTDENSMSKSHDKRIRKGTIVLMMKSNLDFDGLSLPLV 96  
CsLOX9 .....MLFTLHSSSTPLSLIERIFFGCFNLFWKDKSPENNMDHTDENSMSKSHDKRIRKGTIVLMMKSNLDFDGLSLPLV 96  
CsLOX10 .....MFKMCKGNQKRSRDNMNSGSRKIRKGTIVLMMKSNLDFDGLSLPLV 96  
CsLOX11 .....MEQRGGGFCSSLQCNVAIKHAKHTSHSTHRIKQIIVQSRGSEVFGSAASVQLFSCSQVDFNTGK 69  
Consensus .....

CsLOX1 DRVHELLQKVSLLQISAVNALDVLVGLKGLKGFAYLEDWITITPLTAG.DSAYDVTWDEEIGVPGAIIIRNFHSSFYRSLTLDHVGGRVHF 140  
CsLOX2 DRGLD.DITDILFGSILHLSVADLDFPTGLERETIRGVARRM...SQDENEVYELNFWAEFGEIGAVLVNENHHRMVKMIAFDGFG.NGVFCV 184  
CsLOX3 SHGLD.DIADLIGSISQELVSAELDFPTGLERETIRGVARRM...SQDENEVYELNFWAEFGEIGAVLVNENHHRMVKMIAFDGFG.NGVFCV 185  
CsLOX4 SHGLD.DIADLIGSISQELVSAELDFPTGLERETIRGVARRM...SQDENEVYELNFWAEFGEIGAVLVNENHHRMVKMIAFDGFG.NGVFCV 185  
CsLOX5 DQWGG...FIMGQGIILQLISEIDFVMSGRCIESYVGMFLP.FSSHRIEYAAHNVHDFPCGPAIYITNFBSSYHMLIEVHVGNEG.PVFF 196  
CsLOX6 SFRDGEIVAAERQVGLQVSTDEPMTMEFLSREAVLLEL.SKLVGTQNTYQVEFVESDFVGPVATVYNYVPEFVLSISFERFVH...F 189  
CsLOX7 RHL.D..ALTIMIGRNVVLQVSTDEPMTMEFLSREAVLLEL.SKLVGTQNTYQVEFVESDFVGPVATVYNYVPEFVLSISFERFVH...F 193  
CsLOX8 DRVDELLGHVSLQLISAVNGDQK.D.FGKIGKFAVLEDWITITLTPESA..DVSFNVTWEDEAVGPGAETIKRHHNFVYKRTVLELIPGHAQICF 139  
CsLOX9 DRIEEVIGQVSLQLISAVNGDQK.D.FGKIGKFAVLEDWITITLTPESA..DVSFNVTWEDEAVGPGAETIKRHHNFVYKRTVLELIPGHAQICF 177  
CsLOX10 DRVDELLGHVSLQLISAVNGDQK.D.FGKIGKFAVLEDWITITLTPESA..DVSFNVTWEDEAVGPGAETIKRHHNFVYKRTVLELIPGHAQICF 146  
CsLOX11 MSGIARLDGKTKNLSHSDGIPANG.EHGVKGFAYLEKWIITISVASASEAFNVTEDEAVGPGAETIKRHHNFVYKRTVLELIPGHAQICF 146  
Consensus .....

CsLOX1 VCSNSWYPAKNTKTRVFSSTQVYLSLTFAPLLENVQVNLGDKGILEEMVNDLVANNHGGDKGSRVYRIFDGGSTEYVPRRRTGTF 240  
CsLOX2 TCNSWASFDNDFEPRFFETKSKVYGGDGLKRLREDEENICDQGERKTHRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 283  
CsLOX3 TCNSWASFDNDFEPRFFETKSKVYGGDGLKRLREDEENICDQGERKTHRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 284  
CsLOX4 TCNSWASFDNDFEPRFFETKSKVYGGDGLKRLREDEENICDQGERKTHRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 284  
CsLOX5 FADTWHSRRKNDPQRRIIFKQVLSQTEPGKLDLHEGRCIRGKGRKRLRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 295  
CsLOX6 ACNSWQVQANVNSKRIIFKQVLSQTEPGKLDLHEGRCIRGKGRKRLRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 292  
CsLOX7 FCNSWQVQANVNSKRIIFKQVLSQTEPGKLDLHEGRCIRGKGRKRLRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 288  
CsLOX8 VCSNSWYPAKNTKTRVFSSTQVYLSLTFAPLLENVQVNLGDKGILEEMVNDLVANNHGGDKGSRVYRIFDGGSTEYVPRRRTGTF 239  
CsLOX9 TCNSWASFDNDFEPRFFETKSKVYGGDGLKRLREDEENICDQGERKTHRVDVYNDLIGDSDNSLQVNLGDKGSRVYRIFDGGSTEYVPRRRTGTF 277  
CsLOX10 VCSNSWYPAKNTKTRVFSSTQVYLSLTFAPLLENVQVNLGDKGILEEMVNDLVANNHGGDKGSRVYRIFDGGSTEYVPRRRTGTF 246  
CsLOX11 WFCFSVFCVSKLQSMLLCCLSLVYVNLGDKGILEEMVNDLVANNHGGDKGSRVYRIFDGGSTEYVPRRRTGTF 263  
Consensus .....

CsLOX1 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 340  
CsLOX2 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 376  
CsLOX3 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 377  
CsLOX4 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 378  
CsLOX5 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 392  
CsLOX6 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 395  
CsLOX7 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 389  
CsLOX8 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 339  
CsLOX9 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 377  
CsLOX10 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 345  
CsLOX11 KDFECSRLALLMSFNIVHEDRSHMSDFLAVLKSQVQVFLGALCDKTPNEISFDQILKIEGKILPEGLLDIKRINPIEMLEKELVR 358  
Consensus .....

CsLOX1 TGD.EGYLRFEMQVIREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 438  
CsLOX2 TDEARREFT.EALVREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 475  
CsLOX3 DAEGLLRFET.EALVREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 476  
CsLOX4 DAEGLLRFET.EALVREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 477  
CsLOX5 TAG..QKLYLDEIIRRRRTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 489  
CsLOX6 ELEEEVTRR..FFKSTDTDTTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 482  
CsLOX7 ESSGDLKLYNFKVIRKQVYRTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 488  
CsLOX8 TGD.ERLTFEVPVQVIREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 437  
CsLOX9 TGD.ERFCHFPVQVIREKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 475  
CsLOX10 SDGGERFHFEMFEMDEKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 444  
CsLOX11 QASREKTFEFP.LPIAEMLEKTRARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 450  
Consensus .....

CsLOX1 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 530  
CsLOX2 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 566  
CsLOX3 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 567  
CsLOX4 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 568  
CsLOX5 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 580  
CsLOX6 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 573  
CsLOX7 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 579  
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CsLOX9 VYVRRIN.AISTRTARRRDEARERMLGVRVVRVSRQCEFRSFDLRLYGMQNSITEDRPNNLD.FTIEEYFNRRRRTDDEHARM 574  
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Consensus .....

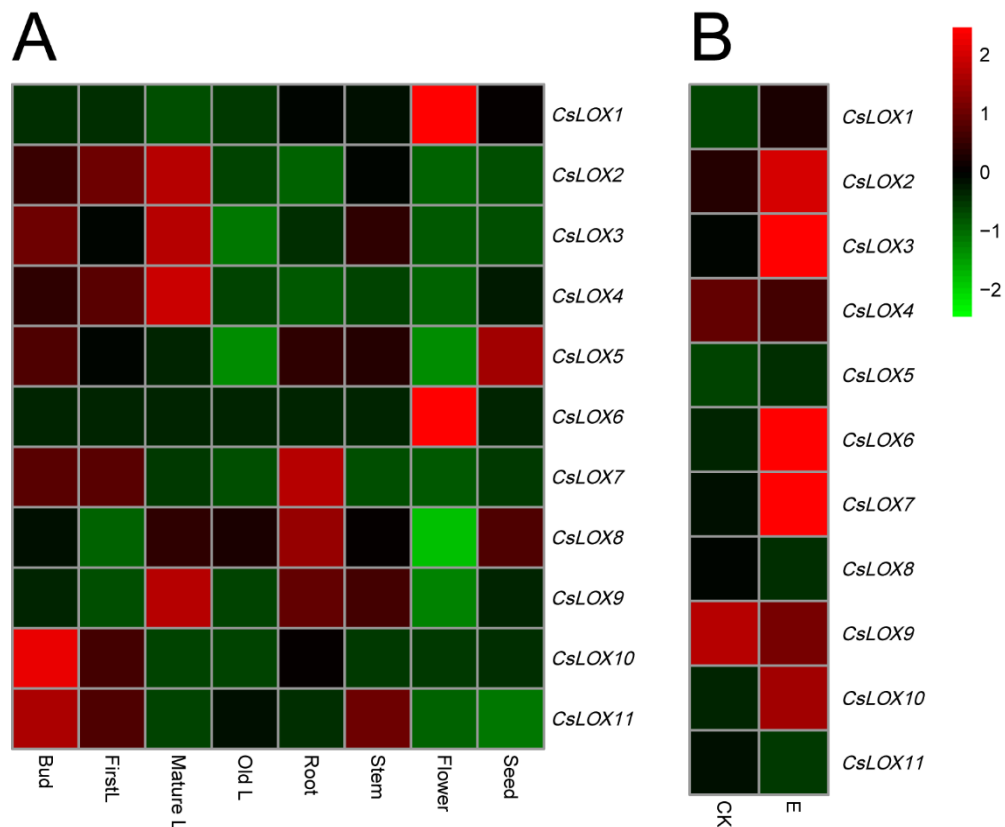
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CsLOX3 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 667  
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CsLOX5 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 680  
CsLOX6 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 673  
CsLOX7 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 679  
CsLOX8 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 635  
CsLOX9 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 673  
CsLOX10 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 635  
CsLOX11 EYVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 639  
Consensus .....

CsLOX1 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 729  
CsLOX2 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 766  
CsLOX3 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 767  
CsLOX4 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 768  
CsLOX5 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 780  
CsLOX6 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 773  
CsLOX7 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 779  
CsLOX8 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 735  
CsLOX9 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 773  
CsLOX10 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 735  
CsLOX11 DQVYDASRLGSLAMPHPYLDLPEFRDMMNNAARQDINAGGLDRTVFEVAVRNSAVVVD.NVFEQALPADIIRGVAVEDTASRSGVRLDIO 739  
Consensus .....

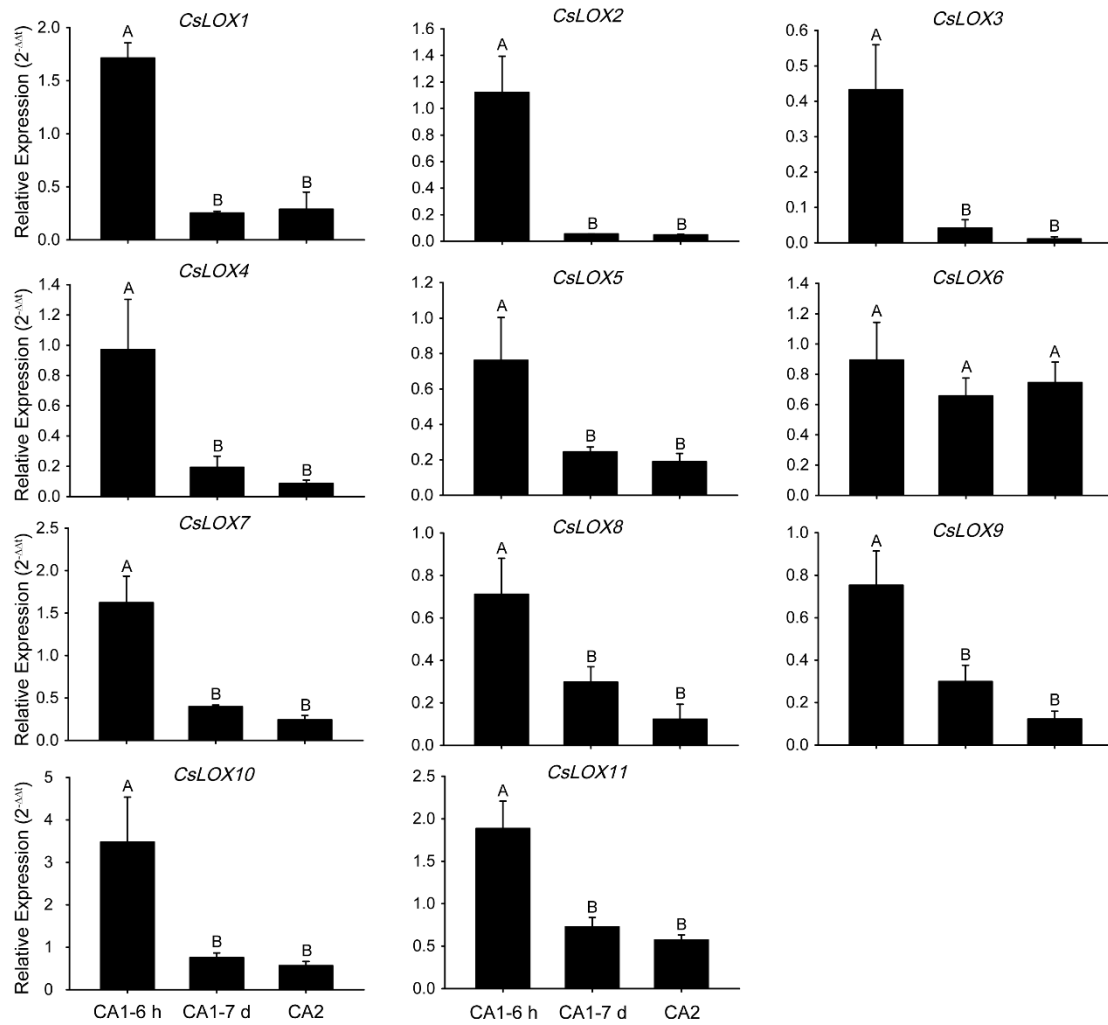
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CsLOX3 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 865  
CsLOX4 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 866  
CsLOX5 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 878  
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CsLOX8 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 833  
CsLOX9 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 830  
CsLOX10 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 871  
CsLOX11 RTILSRNREPEGT..FEYEFKSSDRAEKTITIAQLTLLGVSLIEIISHSDEWVHC..QRSDADTIDDEPLEGSGKREGEIDEMENRND 835  
Consensus .....

CsLOX1 EN.LRNRVGVKVFV...TSEGLHGHG... 860  
CsLOX2 EN.LRNRVGVKVFV...TSEGLHGHG... 899  
CsLOX3 EN.LRNRVGVKVFV...TSEGLHGHG... 900  
CsLOX4 EN.LRNRVGVKVFV...TSEGLHGHG... 901  
CsLOX5 EN.LRNRVGVKVFV...TSEGLHGHG... 913  
CsLOX6 EN.LRNRVGVKVFV...TSEGLHGHG... 905  
CsLOX7 EN.LRNRVGVKVFV...TSEGLHGHG... 911  
CsLOX8 EN.LRNRVGVKVFV...TSEGLHGHG... 868  
CsLOX9 EN.LRNRVGVKVFV...TSEGLHGHG... 905  
CsLOX10 EN.LRNRVGVKVFV...TSEGLHGHG... 872  
CsLOX11 EN.LRNRVGVKVFV...TSEGLHGHG... 875  
Consensus .....

20 **Supplementary Fig. S3** Multiple sequence alignments of eleven CsLOX proteins. The protein  
 21 sequences were aligned using the DNAMAN software. The consensus amino acid residues are  
 22 marked with letters at the bottom. The conserved domains are involved in substrate binding  
 23 (Domain I) and oxygen binding (Domain II), which are indicated with a solid red box. The red  
 24 triangle and solid blue box indicate a conserved amino acid sequence proposed to be essential  
 25 for iron binding (His522, His527, His713, Asn717 and Ile861).  
 26



27 **Supplementary Fig. S4** Heat map analysis of CsLOX gene expression data based on RNA-  
 28 Seq. Green and red colors represent low and high levels of transcript abundance, respectively.  
 29 A. Expression patterns of CsLOX genes across different tissues (bud, first leaf, mature leaf in  
 30 summer, old leaf in winter, root, stem, flower, seed). B. Expression patterns of CsLOX genes  
 31 under insect feeding treatment (CK for control leaf collected at five time points (3, 6, 9, 12 and  
 32 24 h) and E for leaf partially consumed by *Ectropis oblique*, sampled at five time points (3, 6, 9,  
 33 12 and 24 h).  
 34

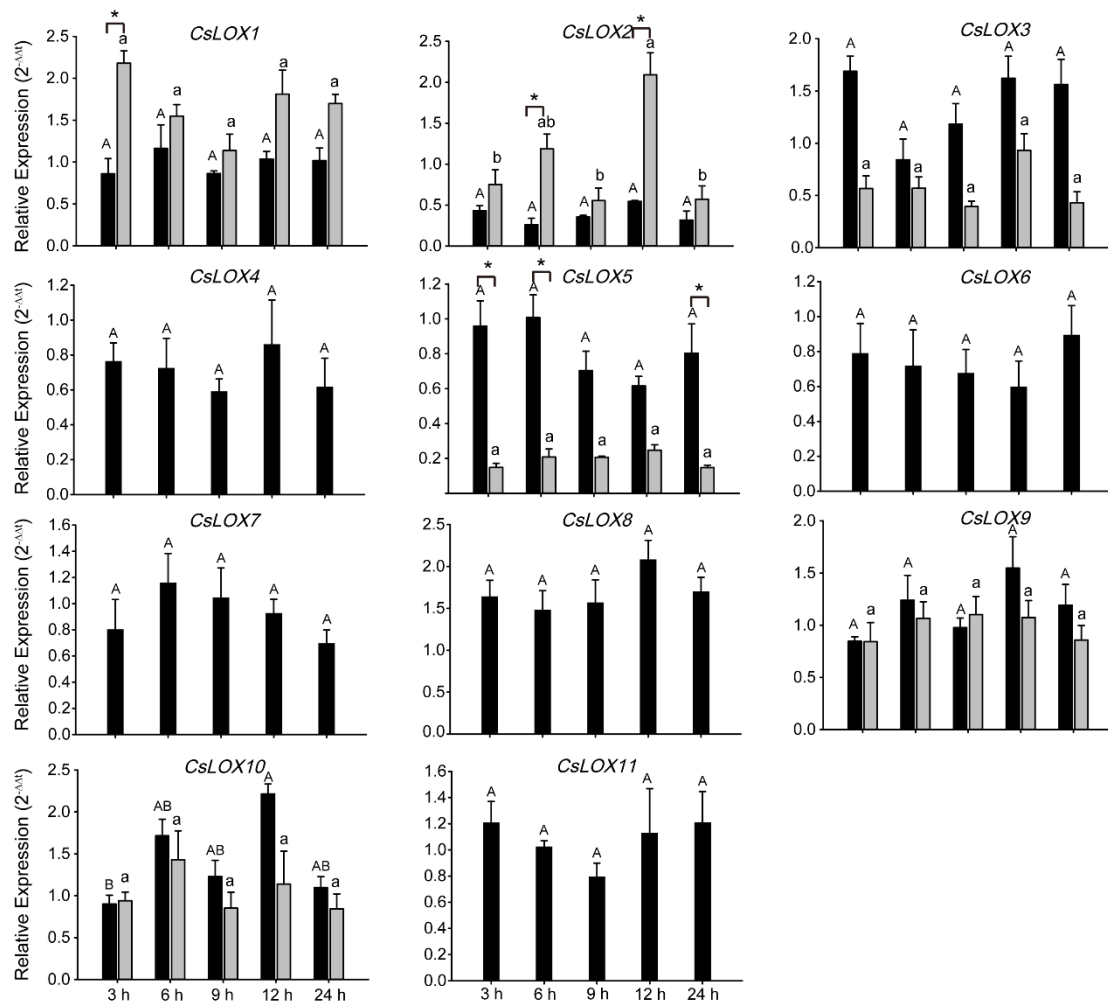


35

36 **Supplementary Fig. S5** qRT-PCR analysis of CsLOX genes under cold-acclimation treatment

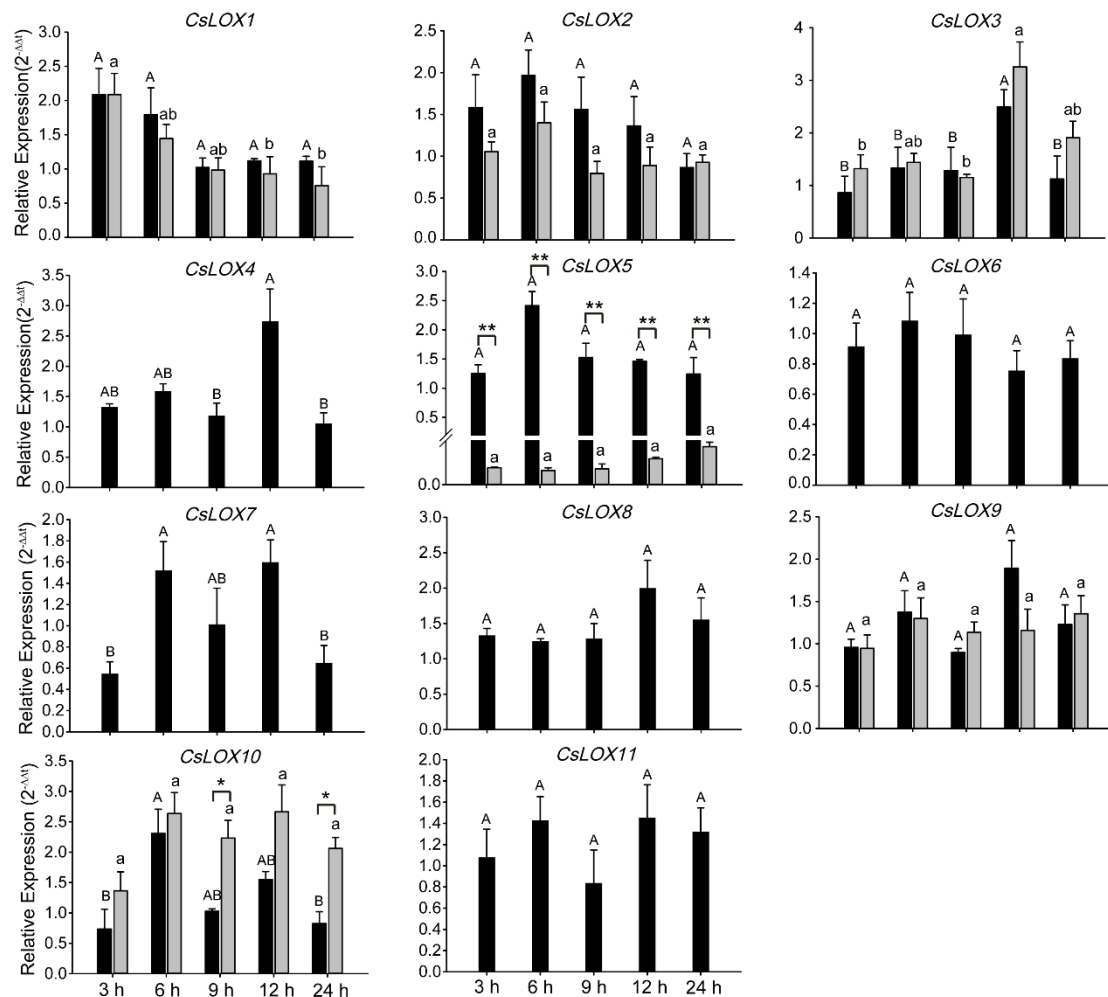
37 (CA1-6h, CA1-7d, CA2, see Materials and Methods). Bars show the mean  $\pm$  SD (n= 3) of three

38 biological replicates. Letters above the bars represent significant differences at  $P < 0.05$ .



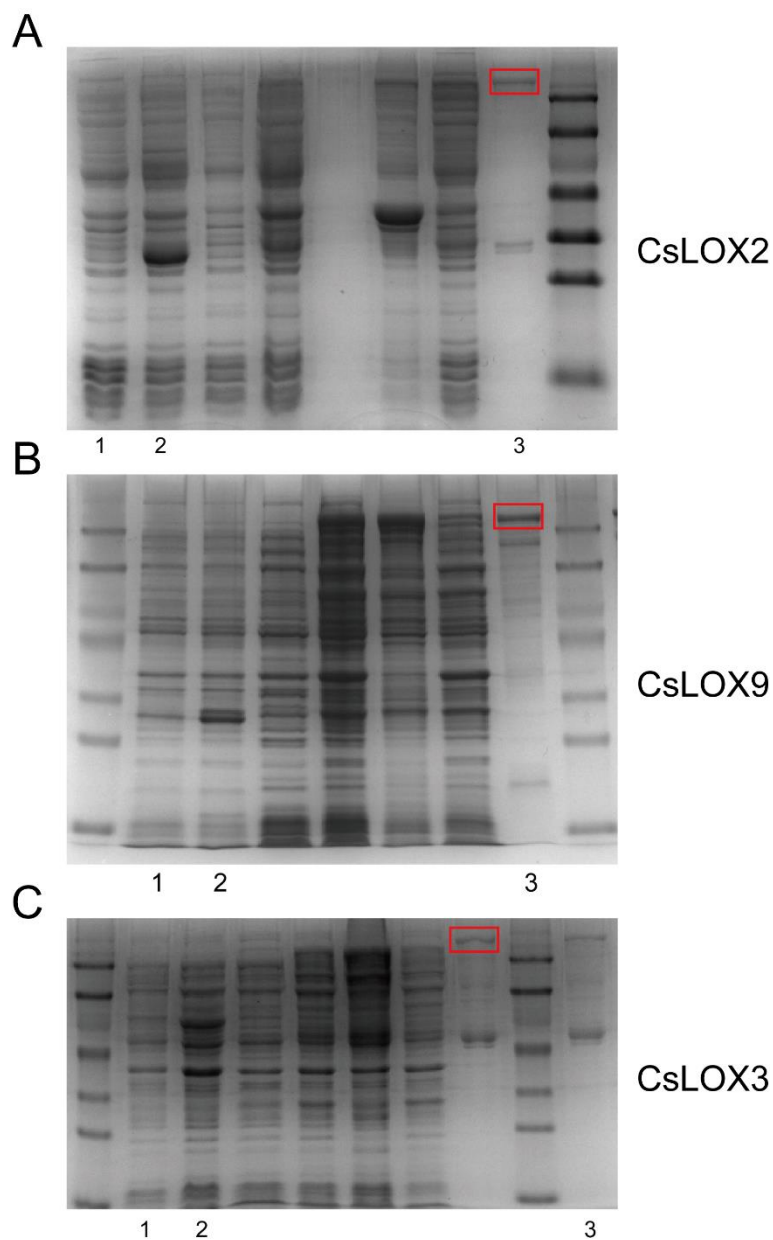
39

40 **Supplementary Fig. S6** Expression pattern of CsLOX genes under ABA phytohormone  
 41 treatments. qRT-PCR analysis of CsLOX genes at different time points. Black bars and grey  
 42 bars indicate full-length and AS transcripts, respectively. Data represent the means  $\pm$  SD (n= 3)  
 43 of three biological replicates. Different letters above the bars denote significant differences at  
 44  $P < 0.05$ . The asterisks indicate the significance level (\* $P < 0.05$ , \*\* $P < 0.01$ ) based on a Tukey's  
 45 honestly significant difference test.



46

47 **Supplementary Fig. S7** Expression pattern of *CsLOX* genes under SA phytohormone  
 48 treatments. qRT-PCR analysis of *CsLOX* genes at different time points. Black bars and grey  
 49 bars indicate the full-length and AS transcripts, respectively. Data represent the means  $\pm$  SD  
 50 ( $n = 3$ ) of three biological replicates. Different letters above the bars denote significant  
 51 differences at  $P < 0.05$ . The asterisks indicate significance level ( $*P < 0.05$ ,  $**P < 0.01$ ) based  
 52 on a Tukey's honestly significant difference test.



53

54 **Supplementary Fig. S8** Heterologous expression of CsLOX in *E. coli*. A. SDS-PAGE image  
 55 shows the purified CsLOX2 recombinant protein. 1, protein extracted from empty pGEX-4T-1  
 56 before induction. 2, protein extracted from empty pGEX-4T-1 after induction. 3, purified protein  
 57 of CsLOX2. B. SDS-PAGE image shows the purified CsLOX9 recombinant protein. 1, protein  
 58 extracted from empty pGEX-4T-1 before induction. 2, protein extracted from empty pGEX-4T-  
 59 1 after induction. 3, purified protein of CsLOX9. C. SDS-PAGE image shows the purified  
 60 CsLOX3 recombinant protein. 1, protein extracted from empty pMAL-C2X before induction. 2,  
 61 protein extracted from empty pMAL-C2X after induction. 3, purified protein of CsLOX3. The  
 62 solid box shows the position of expected protein.



**Supplementary Table. S1 Detailed information of *CsLOX* gene family was identified from tea plant genome.**

ID	Full-length (bp)	CDS length (bp)	Predicted Scaffold	Protein			Sub-cellular location		Predicted functionality
				Protein length (aa)	Mol.Wt (Da)	PI	TargetP	MultiLoc2	
<i>CsLOX1</i>	2796	2586	Scaffold1403	861	97915.63	5.8	Any other location	Cytoplasm	9-LOX
<i>CsLOX2</i>	3039	2703	Scaffold11162	900	102258.59	6.39	Chloroplast	Chloroplast	13-LOX
<i>CsLOX3</i>	2947	2706	Scaffold1936	901	101802.22	6.37	Chloroplast	Chloroplast	13-LOX
<i>CsLOX4</i>	2825	2712	Scaffold1939	902	101993.9	6.76	Chloroplast	Chloroplast	13-LOX
<i>CsLOX5</i>	2956	2745	Scaffold1275	914	103284.87	8.27	Chloroplast	Chloroplast	13-LOX
<i>CsLOX6</i>	2872	2721	Scaffold10095	906	102826.65	6.78	Chloroplast	Chloroplast	13-LOX
<i>CsLOX7</i>	3129	2739	Scaffold338	912	102809.89	8.28	Chloroplast	Chloroplast	13-LOX
<i>CsLOX8</i>	2610	2610	Scaffold5989	869	99648.72	5.82	Any other location	Cytoplasm	9-LOX
<i>CsLOX9</i>	2839	2721	Scaffold1291	906	104304.95	5.87	Secretory pathway	Cytoplasm	9-LOX
<i>CsLOX10</i>	2776	2622	Scaffold3698	873	100256.11	7.7	Any other location	Cytoplasm	9-LOX
<i>CsLOX11</i>	2674	2631	Scaffold844	876	99679.47	7.37	Chloroplast	Chloroplast	13-LOX

**Supplementary Table. S2 Analysis of secondary structure of CsLOX proteins**

ID	$\alpha$ -Helix	$\beta$ -sheet	Random coil
CsLOX1	309	127	425
CsLOX2	307	117	476
CsLOX3	307	117	476
CsLOX4	323	118	461
CsLOX5	336	122	456
CsLOX6	330	110	466
CsLOX7	323	125	464
CsLOX8	308	124	437
CsLOX9	317	129	460
CsLOX10	307	123	443
CsLOX11	306	111	459

**Supplementary Table. S3** Analysis of cis-acting regulatory elements in the promoter region of *CsLOX* genes.

Function (CsLOX1)	cis-regulatory element
light responsiveness	ACE,AE-box,ATCT-motif,Box 4,Box 1,CATT-motif,GA-motif,GAG-motif,GATA-motif,GT1-motif,I-box,MNF1,MRE,Sp1,TCCC-motif,as-2-box
auxin responsiveness	AuxRR-core
MeJA-responsiveness	CGTCA-motif,TGACG-motif
ethylene-responsive	ERE
abscisic acid responsiveness	
salicylic acid responsiveness	
gibberellin-responsive	GARE-motif,gibberellin-responsive
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	
anoxic specific inducibility	
drought-inducibility	
wound-responsive	

Function (CsLOX2)	cis-regulatory element
light responsiveness	AAAC-motif,AT1-motif,ATC-motif,ATCT-motif,Box 4,Box I,GA-motif,GAG-motif,GATA-motif,GT1-motif,I-box
auxin responsiveness	
MeJA-responsiveness	CGTCA-motif,TGACG-motif
ethylene-responsive	
abscisic acid responsiveness	
gibberellin-responsive	GARE-motif
heat stress responsiveness	HSE
defense and stress responsiveness	
salicylic acid responsiveness	
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	
wound-responsive	WUN-motif

Function (CsLOX3)	cis-regulatory element
light responsiveness	ATCC-motif,GAG-motif, Sp1
auxin responsiveness	
MeJA-responsiveness	CGTCA-motif,TGACG-motif
ethylene-responsive	
abscisic acid responsiveness	
salicylic acid responsiveness	TCA-element
gibberellin-responsive	
heat stress responsiveness	
defense and stress responsiveness	
anaerobic induction	
anoxic specific inducibility	
drought-inducibility	
wound-responsive	WUN-motif

Function (CsLOX4)	cis-regulatory element
light responsiveness	ACE,Box 4,Box I,G-Box,GATA-motif,I-box, Sp1,as-2-box,chs-Unit 1 m1
auxin responsiveness	
MeJA-responsiveness	
ethylene-responsive	
abscisic acid responsiveness	ABRE
salicylic acid responsiveness	TCA-element
gibberellin-responsive	GARE-motif
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	ARE
anoxic specific inducibility	GC-motif
drought-inducibility	
wound-responsive	WUN-motif

Function (CsLOX5)	cis-regulatory element
light responsiveness	4cl-CMA2a,AE-box,ATCT-motif,Box 4,Box I,G-box,LAMP-element,Sp1, TCT-motif,chs-CMA1a,chs-CMA2a,rbcS-CMA7a
auxin responsiveness	
MeJA-responsiveness	
ethylene-responsive	ERE
abscisic acid responsiveness	ABRE
salicylic acid responsiveness	
gibberellin-responsive	GARE-motif
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	
anoxic specific inducibility	
drought-inducibility	MBS
wound-responsive	

Function (CsLOX6)	cis-regulatory element
light responsiveness	AAAC-motif,AT1-motif,Box 4,Box I, Box II,G-Box,GA-motif,GAG-motif,GATA-motif,GT1-motif,MNF1,MRE,Sp1,TCCC-motif
auxin responsiveness	
MeJA-responsiveness	
ethylene-responsive	ERE
abscisic acid responsiveness	
salicylic acid responsiveness	
gibberellin-responsive	GARE-motif
heat stress responsiveness	HSE
defense and stress responsiveness	
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	MBS
wound-responsive	WUN-motif



Function (CsLOX7)	cis-regulatory element
light responsiveness	4cl-CMA2b,Box I,G-Box,GA-motif,GATA-motif, GT1-motif,I-box,L-box,LAMP-element,MRE,Sp1,TCCC-motif,as-2-box
auxin responsiveness	
MeJA-responsiveness	
ethylene-responsive	
abscisic acid responsiveness	
salicylic acid responsiveness	TCA-element
gibberellin-responsive	
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	
wound-responsive	WUN-motif

Function (CsLOX8)	cis-regulatory element
light responsiveness	4cl-CMA2b,ACE,AE-box,ATCT-motif,Box 4,Box I,GAG-motif,GT1-motif,Gap-box,L-box,MRE,chs-CMA1a
auxin responsiveness	
MeJA-responsiveness	
ethylene-responsive	ERE
abscisic acid responsiveness	
salicylic acid responsiveness	
gibberellin-responsive	GARE-motif
heat stress responsiveness	HSE
defense and stress responsiveness	
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	
wound-responsive	

Function (CsLOX9)	cis-regulatory element
light responsiveness	ACE,ATCC-motif,Box 4,G-Box,GATA-motif,I-box,Sp1,TCT-motif,as-2-box,chs-CMA1a
auxin responsiveness	AuxRR-core
MeJA-responsiveness	
ethylene-responsive	
abscisic acid responsiveness	ABRE
salicylic acid responsiveness	TCA-element
gibberellin-responsive	P-box
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	
wound-responsive	

Function (CsLOX10)	cis-regulatory element
light responsiveness	ACE,AE-box,Box 4,G-Box,GA-motif,GAG-motif,GT1-motif,I-box,Sp1,TCCC-motif,TCT-motif
auxin responsiveness	
MeJA-responsiveness	CGTCA-motif,TGACG-motif
ethylene-responsive	
abscisic acid responsiveness	
salicylic acid responsiveness	TCA-element
gibberellin-responsive	
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	MBS
wound-responsive	

Function (CsLOX11)	cis-regulatory element
light responsiveness	ACE,Box 4,Box I,G-Box,GT1-motif,Sp1,TCCC-motif
auxin responsiveness	
MeJA-responsiveness	CGTCA-motif,TGACG-motif
ethylene-responsive	
abscisic acid responsiveness	ABRE
salicylic acid responsiveness	TCA-element
gibberellin-responsive	
heat stress responsiveness	HSE
defense and stress responsiveness	TC-rich repeats
anaerobic induction	ARE
anoxic specific inducibility	
drought-inducibility	
wound-responsive	

**Supplementary Table. S4 Plant lipoxygenase sequences used for phylogenetic tree construction**

Organism	Sequence ID	GeneBank Accession
<i>Arabidopsis thaliana</i>	<i>AtLOX1</i>	Q06327
	<i>AtLOX2</i>	P38418
	<i>AtLOX3</i>	Q9SMW1
	<i>AtLOX4</i>	Q9FNX8
	<i>AtLOX5</i>	Q9FNX7
	<i>AtLOX6</i>	Q9CAG3
<i>Glycine max</i>	<i>GmLOX1</i>	P08170
	<i>GmLOX2</i>	P09435
	<i>GmLOX3</i>	P09186
	<i>GmLOX4</i>	P38417
	<i>GmLOX6</i>	AAA96817
	<i>GmLOX7</i>	P24095
	<i>HvLOX1</i>	P93184
<i>Hordeum vulgare</i>	<i>HvLOX2</i>	Q8GSM3
	<i>HvLOX3</i>	Q8GSM2
	<i>HvLOX4</i>	CAI84707
	<i>HvLOXA</i>	P29114
	<i>HvLOXB</i>	AAB60715
<i>Lens culinaris</i>	<i>HvLOXC</i>	AAB70865
	<i>LcLOX1</i>	P38414
	<i>LeLOX1</i>	P38415
<i>Lycopersicon esculentum</i>	<i>LeLOX2</i>	P38416
	<i>LeLOX3</i>	AAG21691
	<i>LeLOX4</i>	Q96573
	<i>LeLOX5</i>	Q96574
<i>Nicotiana attenuata</i>	<i>NaLOX1</i>	AAP83136
	<i>NaLOX2</i>	AAP83137
	<i>NaLOX3</i>	AAP83138
<i>Nicotiana tabacum</i>	<i>NtLOX1</i>	CAA58859
	<i>OsLOX1</i>	Q76I22
	<i>OsLOX2</i>	P29250
	<i>OsLOX3</i>	Q7G794
	<i>OsLOX3b</i>	Q53RB0
	<i>OsLOX5</i>	Q7XV13
	<i>OsLOX6</i>	Q8H016
	<i>OsLOX7</i>	P38419
<i>OsLOX8</i>	Q84YK8	

	<i>OsLOXRC1</i>	Q9FSE5
	<i>PsLOX1</i>	AAB71759
	<i>PsLOX2</i>	P14856
	<i>PsLOX3</i>	P09918
<i>Pisum sativum</i>	<i>PsLOX7</i>	CAC04380
	<i>PsLOX8</i>	CAA75609
	<i>PsLOX9</i>	CAG44504
	<i>PsLOXG</i>	CAA53730
	<i>PvLOX1</i>	P27480
<i>Phaseolus vulgaris</i>	<i>PvLOX1b</i>	AAB18970
	<i>PvLOX2b</i>	AAG42354
	<i>PvLOX2c</i>	AAF15396
	<i>StLOX1</i>	CAA64765
	<i>StLOX2</i>	AAD09202
<i>Solanum tuberosum</i>	<i>StLOX3</i>	AAB67865
	<i>StLOX4</i>	CAA65268
	<i>StLOX5</i>	CAA65269
	<i>ZmLOX1</i>	AAL73499
<i>Zea mays</i>	<i>ZmLOX2</i>	AAF76207
	<i>TaLOX1</i>	GQ166692
<i>Triticum aestivum L.</i>	<i>TaLOX2</i>	GQ166691
<i>Actinidia deliciosa</i>	<i>AdLOX2</i>	DQ497797
	<i>VvLOXA</i>	XP_002285574
	<i>VvLOXC</i>	FJ858257
	<i>VvLOXG</i>	XP_002283147
	<i>VvLOXH</i>	XP_002283135
	<i>VvLOXI</i>	XP_002283123
<i>Vitis vinifera</i>	<i>VvLOXJ</i>	XP_002263854
	<i>VvLOXL</i>	XP_002278007
	<i>VvLOXP</i>	XP_002265505
	<i>VvLOXT</i>	XP_010651289.1
	<i>VvLOXU</i>	XP_010659819.1
	<i>VvLOXV</i>	XP_010659859.1
	<i>VvLOXW</i>	NP_001290017.1
	<i>PtLOX1</i>	XP_002299250.1
	<i>PtLOX2</i>	XP_002297796.2
<i>Populus trichocarpa</i>	<i>PtLOX3</i>	XP_006368564.1
	<i>PtLOX4</i>	XP_006388115.1
	<i>PtLOX5</i>	XP_006369132.1
	<i>PtLOX6</i>	XP_002304125.1

	<i>PtLOX7</i>	XP_006382593.1
	<i>PtLOX8</i>	XP_006382594.1
	<i>PtLOX9</i>	XP_011036799.1
	<i>PtLOX10</i>	XP_006382595.1
	<i>PtLOX11</i>	XP_002311617.1
	<i>PtLOX12</i>	XP_002311724.1
	<i>PtLOX13</i>	XP_002314229.2
	<i>PtLOX14</i>	XP_002314548.2
	<i>PtLOX15</i>	XP_002315780.1
	<i>PtLOX16</i>	XP_002319014.2
	<i>PtLOX17</i>	XP_002319015.2
	<i>PtLOX18</i>	XP_002320037.2
	<i>PtLOX19</i>	XP_002320571.2
	<i>PtLOX20</i>	XP_002323952.2
	<i>CsLOX1</i>	EU195885.2
	<i>CsLOX2</i>	FJ418174.1
	<i>CsLOX3</i>	FJ794853.1
	<i>CsLOX4</i>	MG708225
	<i>CsLOX5</i>	MG708226
<i>Camellia sinensis</i>	<i>CsLOX6</i>	MG708227
	<i>CsLOX7</i>	MG708228
	<i>CsLOX8</i>	MG708229
	<i>CsLOX9</i>	MG708230
	<i>CsLOX10</i>	MG708231
	<i>CsLOX11</i>	MG708232

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**Supplementary Table. S5 Primers used in this study (application details of primers are described in materials and methods)**

Primer name	Sequence (5' - 3')	Target gene
P1 (5' RACE, GSP1)	CCATGATGCCTCCATGTCCTTACCGAG	<i>CsLOX3</i>
P2 (5' RACE, GSP2)	TCAAGAGTGCAACTTCGGGCTTGTTG	
P3 (3' RACE, GSP2)	GTGGAGCTGGTGTGGTTCCTTATGAGC	<i>CsLOX3</i>
P4 (3' RACE, GSP2)	GACAGGAAAGGGAGTTCCAAAGAGC	
P5 (5' RACE, GSP1)	ATCTGTTGCACGAATTCCTCATCATCC	<i>CsLOX11</i>
P6 (5' RACE, GSP2)	TGTTTCTGTCTGGTTATCTTGGTTGCGAC	
P7 - F	AAACACATTATGAGAGCCAC	<i>CsLOX3</i>
P8 - R	CACAAATGCATTCACTTCTC	
P9 - F	GGGGATTGAGCAAAAACCC	<i>CsLOX11</i>
P10 - R	GATACCTAATAGCATATCAATTTGA	
P11 - F	ATCTGGTTCGCGTGGATCCATGTTGCAGACTCAAACGCA	<i>CsLOX2</i>
P12 - R	TCACGATGCGGCCGCTCGAGTCAAATTGAGATGCTATTAGGAA	
P13 - F	AGGATTTCAGAATTCGGATCCATGTTGAATAGTCAAACCCAC	<i>CsLOX3</i>
P14 - R	CAAGCTTGCCTGCAGGTCGACTCAAATTGAGATGCTCTTTGG	
P15 - F	ATCTGGTTCGCGTGGATCCATGCTACCAACCCTCTTCC	<i>CsLOX9</i>
P16 - R	TCACGATGCGGCCGCTCGAGTTAGATTGAGACACTATTAGGAATT	
P19 - F	TCTTGATTAATGCCGATGG	<i>α-CsLOX1</i>
P20 - F	TATCAAGAGTGGATGGAC	<i>β-CsLOX1</i>
P21 - R	AAATGCCTCCAATGGTTC	<i>α, β-CsLOX1</i>
P22 - F	CAACAAGTCATACTTGCCAG	<i>α-CsLOX2</i>
P23 - F	AATGCAAGACAGTGTTCAC	<i>β-CsLOX2</i>
P24 - R	GCCTGTTACTCGCTATTATG	<i>α, β-CsLOX2</i>

P25 - F	ATCCAGACAGTAGTCCTAC	$\alpha$ -CsLOX3
P26 - F	AACATTTTCAGGTGTTAACC	$\beta$ -CsLOX3
P27 - R	ATGTAAGGCTCTGTCACG	$\alpha, \beta$ -CsLOX3
P28 - F	ATTCTCAGCAAAGTAGATCCTG	$\alpha$ -CsLOX5
P29 - F	GTCAAAGAGAGTTTGATAAATGG	$\beta$ -CsLOX5
P30 - R	GTGTCTTGAACGGCCATTAC	$\alpha, \beta$ -CsLOX5
P31 - F	TGGCTGCTTCAACTTCTTATTCTG	$\alpha$ -CsLOX9
P32 - F	ATGGTGACCCTGGGGCTTTC	$\beta$ -CsLOX9
P33 - R	TGTAGTGACATAGTGGAGCTGG	$\alpha, \beta$ -CsLOX9
P34 - F	TTCCAGCTAGATATGCAATGG	$\alpha$ -CsLOX10
P35 - F	CATGGTCTTGGTGGATAGAG	$\beta$ -CsLOX10
P36 - R	GGTTGGGTATCCGCAGTC	$\alpha, \beta$ -CsLOX10
P37 - F	GAACCATTGGAGGCATTTG	CsLOX1
P38 - R	ATTCAAATTGAAACACTATTAGG	
P39 - F	TTTGAAGAATAGGGTTGGAGC	CsLOX2
P40 - R	TCACTGTTAATCTCTTAGCCC	
P41 - F	CTAAACACATTATGAGAGCCAC	CsLOX3
P42 - R	TAGGATTTGGACAGTATGAGAC	
P43 - F	ACTTGAAGAATAGATGTGGAGC	CsLOX4
P44 - R	TCTTACAAATGCATTCACCTTCTC	
P45 - F	GTTCCCTAACAGCATCTCTATC	CsLOX5
P46 - R	GTAGCCATTACAATCACTCTC	
P47 - F	GACCCAAGCCTCACAAATAG	CsLOX6

P48 - R	GCTTCATTTATGCTACTCACAC	
P49 - F	ATTTCTCTTCTCTCACTCTCAC	
P50 - R	GAACACCTCTCCATCACACT	<i>CsLOX7</i>
P51 - F	GGACTATTGCTCCTTCTACTAT	
P52 - R	GGTACATGTTTCGACTAGCTC	<i>CsLOX8</i>
P53 - F	TTTGAGAGATTTGGAAAGACGC	
P54 - R	ACCATTAGATTGAGACACTATTAG	<i>CsLOX9</i>
P55 - F	AGTGCCTTATACCTTGCTCT	
P56 - R	TTCTAGATTGAGATACTGTTGG	<i>CsLOX10</i>
P57 - F	AGGATAATCATGGAACAACGTG	
P58 - R	GCTCCGTTGAACGATAATTTG	<i>CsLOX11</i>
P59 - F	TATCAAGAGTGGATGGAC	
P60 - R	CCATTTTCGTCATTCTTGTA	<i><math>\beta</math>-CsLOX1</i>
P61 - F	ATGCAAGACAGTGTTCAC	
P62 - R	GTGGAAGGTTTACTCCTTC	<i><math>\beta</math>-CsLOX2</i>
P63 - F	AACATTTTCAGGTGTTAACC	
P64 - R	AAAGACCTTCTTCAGCATC	<i><math>\beta</math>-CsLOX3</i>
P65 - F	GTCAAAGAGAGTTTGATAAATGG	
P66 - R	GGATCCTCAACAGCCATAC	<i><math>\beta</math>-CsLOX5</i>
P67 - F	ATGGTGACCCTGGGGCTTTC	
P68 - R	TGTAGTGACATAGTGGAGCTGG	<i><math>\beta</math>-CsLOX9</i>
P69 - F	CATGGTCTTGGTGGATAGAG	
P70 - R	ACCCATATAACAATGGTGCATG	<i><math>\beta</math>-CsLOX10</i>
P71 - F	TTGGCATCGTTGAGGGTCT	<i>GADPH</i>

P72 - R	CAGTGGGAACACGGAAAGC	
P73 - F	CTAAACACATTATGAGAGCCAC	
P74 - R	GGCTCTTCCGATGTGCATAT	<i>CsLOX3</i>
P75 - F	CTCAACTTTGGGCAGTATCC	
P76 - R	GCTTCATTTATGCTACTCACAC	<i>CsLOX6</i>
P77 - F	ATTTCTTTCTCTCACTCTCAC	
P78 - R	GCAACACAACATTCCTTCCG	<i>CsLOX7</i>
P79 - F	GGTTGATCCTGCCAGTAGTC	
P80- R	CTACGGAAACCTTGTTACGAC	<i>18S rRNA</i>
P81 - F	GGGGACAAGTTTGTACAAAAAGCAGGCTATGTTGCAGACTCAAACGCA	
P82- R	GGGGACCACTTTGTACAAGAAAGCTGGGTAATTGAGATGCTATTAGGAACTC	<i>CsLOX2</i>
P83 - F	GGGGACAAGTTTGTACAAAAAGCAGGCTATGCTACCAACCCTCTTCC	
P84- R	GGGGACCACTTTGTACAAGAAAGCTGGGTGATTGAGACACTATTAGGAATTC	<i>CsLOX9</i>

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