Table S1 The disease index analysis in Jinyou 38 and Xintaimici in cucumber

Cucumber cultivars	Numbers	Days post-inoculation (dpi)	Disease index
Jinyou 38	77	7	14.85
Xintaimici	75	7	72.33

Note: High resistance (HR), 0＜DI≤15; Moderate resistance (R), 15＜DI≤35; Resistance(MR), 35＜DI≤55; Susceptible (S), 55＜DI≤75; High susceptible (HS), DI＞75.

Table S2 The primers of qRT-RCR used in this study

Analysis	**Primer name**	**Sequence(5′-3′)**
CsPR1-1a for qRT-RCR in transgenic cucumber	*CsPR1-1a* -F *CsPR1-1a* -R	GGCAGCCCAGACTTCTCAGC GCATCTCACTTTGGCACATCCTA
CsPR2 for qRT-RCR in transgenic cucumber	*CsPR2*-F *CsPR2*-R	AAGACAACATCCTCAACTTTGC CTGCTGAAAGAATTCCAGTGTG
CsPR3 for qRT-RCR in transgenic cucumber	*CsPR3*-F *CsPR3*-R	CATTTCTCTCATCCTTTGGCAG GATATCGAAATCAACGCCATCC
CsPYL2 for qRT-RCR in transgenic cucumber	*CsPYL2*-F *CsPYL2*-R	CAGAAATCATTGATGGACGACC TGAAACATCAGCAAGTGACTTG
CsPP2C2 for qRT-RCR in transgenic cucumber	*CsPP2C2*-F *CsPP2C2*-R	TATTCCCGATCCAGAAGTCATG CAAGCATTGAGAGGTAATCTGC
CsSnRK2.2 for qRT-RCR in transgenic cucumber	*CsSnRK2.2*-F *CsSnRK2.2*-R	GCAGATCCAGAGACGAGAATAA TCAATACTCTGTGTTGCCTCAT
CsABI5 for qRT-RCR in transgenic cucumber	*CsABI5*-F *CsABI5*-R	GAATCGCCATTACAGTCTGAAC AACTCATCCAATGTGAGTGAGT
CsRbohD for qRT-RCR in transgenic cucumber	*CsRbohD*-F *CsRbohD*-R	GCGTAACATTACTGGTGATTCC ATTCTTCCATCAGCATCCGTAT
CsRbohF for qRT-RCR in transgenic cucumber	*CsRbohF*-F *CsRbohF*-R	ATCGGACGATATTACACAGCTT ACAATCACCAGAACGAATACCT
Cucumber *CsActin* gene for and qRT-PCR	Actin-F Actin-R	TCGTGCTGGATTCTGGTG GGCAGTGGTGGTGAACAT

Table S3 List of primers used in the study

Analysis	**Primer name**	**Sequence(5′-3′)**
Sequencing of the cDNA of *CsMLO1*	*CsMLO1*-F	GATATCATGGCGGGGGCAGCCGGTGGCAA
	CsMLO1-R	GCGGCCGCTCATTCAACTCTATCAAATGAAAAGTC
Sequencing of the cDNA of *CsMLO2*	*CsMLO2*-F	GGATCCATGGCTGAATGTGGAACAGAG
	CsMLO2-R	CTCGAGTCATTTGGCAAATGAGAAGTCTGAG
qRT-PCR for *CsMLO1*	*RTCsMLO1*-F	ATGCGTTGGCTAGAGCTAAGATG
	RTCsMLO1-R	AGGTGTCTCTTGCAAACCTAAACC
qRT-PCR for *CsMLO2*	*RTCsMLO2*-F	GTCATTCACCTCACTGGAAAGTGG
	RTCsMLO2-R	AGTGACAGCATCTTGGCCTATCG
CsMLO1-silencing vector	*TRVCsMLO1*-F	GAATTCGTGGCAGAGGCCCTTCGCAAC
	TRVCsMLO1-R	GAGCTC TCATTCAACTCTATCAAATGA
CsMLO2-silencing vector	*TRVCsMLO2*-F	gtgagtaaggttaccgaattcCACCACTCAGCCAAGAAG
	TRVCsMLO2-R	ggcctcgagacgcgtgagctcTCATTTGGCAAATGAGAA
CsMLO1-overexpression vector	*LucCsMLO1*-F	tctgagctctctagaATGGCGGGGGCAGCCGGTGG
	LucCsMLO1-R	cataagcttctgcagTTCAACTCTATCAAATGAAA
CsMLO2-overexpression vector	*LucCsMLO2*-F	ctgagctctcagaATGGCTGAATGTGGAACAGA
	LucCsMLO2-R	cataagcttctgcagTTTGGCAAATGAGAAGTCTG
Chimeric primer for *CsMLO1*-nLuc	*CsMLO1-nLuc*-F	ACAACGATTCGCCCTCTCCATCTC
	CsMLO1-nLuc-R	CCTCGATATGTGCATCTGTAAAAGC
Chimeric primer for *CsMLO2*-nLuc	*CsMLO2-nLuc*-F	GTTGCCTCCTTCTTCACACCATAGC
	CsMLO2-nLuc-R	CCTCGATATGTGCATCTGTAAAGC

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ATGGCGGGGGCAGCCGGTGGCAAGTCGCTGGAGCAAACACCGACATGGGCCGTTGCCGTTGTTTGCTTTGTTTTGCTCGTCATCTCTATT   90
M  A  G  A  A  G  G  K  S  L  E  Q  T  P  T  W  A  V  A  V  V  C  F  V  L  L  V  I  S  I     30
TTCATCGAATATAGTCTCCATCTTATCGGACATTGGCTAAAGAAGAGACACAAACGGGCGTTGTTTGAAGCATTAGAGAAGATCAAATCA   180
F  I  E  Y  S  L  H  L  I  G  H  W  L  K  K  R  H  K  R  A  L  F  E  A  L  E  K  I  K  S     60
GAGCTTATGTTATTGGGGTTTATATCATTGCTACTAACGGTGGGGCAAGGACCAATAACGGAGATATGTATTCCACAACATGTAGCTGCA   270
E  L  M  L  L  G  F  I  S  L  L  L  T  V  G  Q  G  P  I  T  E  I  C  I  P  Q  H  V  A  A     90
ACGTGGCATCCATGTACAAAGGAAAGAGAAGATGAGATGAACAAAGAGGTGGAGAAATCTGTGGAACATTTGGGTCTTAATCGCCGGAGA   360
T  W  H  P  C  T  K  E  R  E  D  E  M  N  K  E  V  E  K  S  V  E  H  L  G  L  N  R  R  R     120
CTCCTTCATCTCCTCGGAAATGGTGAAAGTTTCCGGCGGAGTTTGGCCGCTGCGGGAGGAGAGGATAAATGTGCCGCCAAGGGTAAAGCT   450
L  L  H  L  L  G  N  G  E  S  F  R  R  S  L  A  A  A  G  G  E  D  K  C  A  A  K  G  K  A     150
TCCTTTATTTCAGCAGATGGAATTCATCAACTTCATATCTTCATTTTTGTGTTGGCTGTTTTTCATGTTTTGTATTGTGTTCTAACTTAT   540
S  F  I  S  A  D  G  I  H  Q  L  H  I  F  I  F  V  L  A  V  F  H  V  L  Y  C  V  L  T  Y     180
GCGTTGGCTAGAGCTAAGATGAGGAGTTGGAAAACATGGGAAAAAGAGACCAAAACTGCTGAATACCAATTCTCACATGATCCAGAGAGG   630
A  L  A  R  A  K  M  R  S  W  K  T  W  E  K  E  T  K  T  A  E  Y  Q  F  S  H  D  P  E  R     210
TTTAGGTTTGCAAGAGACACCTCATTTGGGAGAAGACATTTGAGCTTTTGGACCAAAAATCCTGCCTTGATGTGGATCGTTTGTTTCTTC   720
F  R  F  A  R  D  T  S  F  G  R  R  H  L  S  F  W  T  K  N  P  A  L  M  W  I  V  C  F  F     240
AGACAATTTGTAAGATCTGTTCCAAAAGTTGATTACTTGACATTAAGACATGGGTTTATAATGGCACATTTAGCACCTCAAAGTCATACA   810
R  Q  F  V  R  S  V  P  K  V  D  Y  L  T  L  R  H  G  F  I  M  A  H  L  A  P  Q  S  H  T     270
CAATTTGATTTTCAAAAATACATTAATAGATCCCTTGAAGAAGACTTCAAAGTTGTTGTGGGAATCAGCCCACCAATTTGGTTCTTTGCT   900
Q  F  D  F  Q  K  Y  I  N  R  S  L  E  E  D  F  K  V  V  V  G  I  S  P  P  I  W  F  F  A     300
GTTCTATTTCTCCTCTCAAACACTCACGGTTGGAGGGCGTATCTATGGCTGCCATTCATCCCACTAATCATTTTGCTGTTGATTGGAACA   990
V  L  F  L  L  S  N  T  H  G  W  R  A  Y  L  W  L  P  F  I  P  L  I  I  L  L  L  I  G  T     330
AAATTGCAAGTGATCATAACGAAAATGGCACTAAGAATACAAGAAAGAGGTGAAGTAGTGAAGGGCGTGCCGGTGGTGGAGCCTGGCGAT   1080
K  L  Q  V  I  I  T  K  M  A  L  R  I  Q  E  R  G  E  V  V  K  G  V  P  V  V  E  P  G  D     360
GACCTCTTTTGGTTTAATCGACCTCGCCTTATTCTTTATCTCATCAACTTTGTTCTCTTTCAAAATGCCTTCCAAGTTGCCTTCTTTGCT   1170
D  L  F  W  F  N  R  P  R  L  I  L  Y  L  I  N  F  V  L  F  Q  N  A  F  Q  V  A  F  F  A     390
TGGACTTGGTATGAGTTTGGGTTGAATTCTTGCTTCCATGAGCATATAGAAGATGTGGTGATCAGAATTTCTATGGGGGTGCTTGTACAA   1260
W  T  W  Y  E  F  G  L  N  S  C  F  H  E  H  I  E  D  V  V  I  R  I  S  M  G  V  L  V  Q     420
ATCCTTTGCAGTTATGTTACTCTTCCTCTTTATGCACTAGTCACTCAGATGGGTTCAACAATGAAGCCAACTATATTCAATGAGAGAGTG   1350
I  L  C  S  Y  V  T  L  P  L  Y  A  L  V  T  Q  M  G  S  T  M  K  P  T  I  F  N  E  R  V     450
GCAGAGGCCCTTCGCAATTGGTACCACTCGGCTCGAAAGCACATCAAACACAACCGCGGTTCGGTCACTCCAATGTCGAGCCGACCCGCC   1440
A  E  A  L  R  N  W  Y  H  S  A  R  K  H  I  K  H  N  R  G  S  V  T  P  M  S  S  R  P  A     480
ACCCCGACTCACAGCATGTCACCTGTCCACCTTCTCCGACACTACAAGAGTGAAGTCGATAGCTTCCACACCTCACCGAGAAGGTCACCG   1530
T  P  T  H  S  M  S  P  V  H  L  L  R  H  Y  K  S  E  V  D  S  F  H  T  S  P  R  R  S  P     510
TTCGACACCGATCGTTGGGACAACGATTCGCCCTCTCCATCTCGCCATGTTGATGGTTCGTCTTCGTCACAACCCCACGTTGAGATGGGA   1620
F  D  T  D  R  W  D  N  D  S  P  S  P  S  R  H  V  D  G  S  S  S  S  Q  P  H  V  E  M  G     540
GGTTATGAAAAAGATCCCGTTGAATCAAGTTCGTCTCAAGTTGATCCGGTTCAACCATCTCGAAACCGCAATCAACATGAGATTCATATT   1710
G  Y  E  K  D  P  V  E  S  S  S  S  Q  V  D  P  V  Q  P  S  R  N  R  N  Q  H  E  I  H  I     570
GGAGGCCCCAAAGACTTTTCATTTGATAGAGTTGAATGA                                                      1749
G  G  P  K  D  F  S  F  D  R  V  E  *                                                        582
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Figure S1 Nucleotide and deduced amino acid sequences of cucumber *CsMLO1* cDNA encoding an MLO homolog protein. The deduced amino acid sequences are given below the nucleotide sequences. The transcriptional start site is shown in bold type and the termination codon is marked by an asterisk (*). The amino acids shown in a solid box reveal a domain of the MLO-related protein, a member of the plant integral membrane proteins.

```
ATGGCTGAATGTGGAACAGAGCAGCGTACTTTGGAAGATACCTCAACTTGGGCTGTTGCGGTTGTTTGTTTTTTCTTGGTTGTTATTTCA   90
M  A  E  C  G  T  E  Q  R  T  L  E  D  T  S  T  W  A  V  A  V  V  C  F  F  L  V  V  I  S     30
ATCTTCATTGAACATGTCATTCACCTCACTGGAAAGTGGCTGGAGAAAAGGCACAAGCCAGCTCTTGTTGAAGCTCTAGAAAAGGTTAAA  180
I  F  I  E  H  V  I  H  L  T  G  K  W  L  E  K  R  H  K  P  A  L  V  E  A  L  E  K  V  K     60
GCAGAGCTTATGCTATTGGGATTCATATCCCTACTTCTAACGATAGGCCAAGATGCTGTCACTCAAATTTGTGTTTCGAAAGAGCTTGCA  270
A  E  L  M  L  L  G  F  I  S  L  L  L  T  I  G  Q  D  A  V  T  Q  I  C  V  S  K  E  L  A     90
GCAACTTGGCTTCCCTGTGCAGCAAGAGCTAAAACAGGAGTAAAAGTTGCGAAGAACAGTCGTCTTAGACTTCTTGAATTTTTAGATCCT  360
A  T  W  L  P  C  A  A  R  A  K  T  G  V  K  V  A  K  N  S  R  L  R  L  L  E  F  L  D  P    120
GACTATGGTTCGAGGCGTATTTTAGCCTCGAAAGGAGATGATGCATGCGCTAAGAGGGGCCAACTCGCTTTCGTGTCGGCATATGGAATC  450
D  Y  G  S  R  R  I  L  A  S  K  G  D  D  A  C  A  K  R  G  Q  L  A  F  V  S  A  Y  G  I    150
CATCAGCTCCATATTTTCATCTTCGTATTGGCTGTCTTCCATGTCCTATACTGCATCATAACTTTGGCTTTTGGCAGAACGAAGATGAGC  540
H  Q  L  H  I  F  I  F  V  L  A  V  F  H  V  L  Y  C  I  I  T  L  A  F  G  R  T  K  M  S    180
AAATGGAAGGCCTGGGAGGATGAAACCAAGACAATTGAATACCAGTACTATAATGATCCAGCAAGATTTAGATTTGCTAGAGATACTACG  630
K  W  K  A  W  E  D  E  T  K  T  I  E  Y  Q  Y  Y  N  D  P  A  R  F  R  F  A  R  D  T  T    210
TTTGGACGCCGACACTTGAGCTTCTGGAGTCGTACACCAATTTCCCTCTGGATTGTTTGTTTCTTCAAACAGTTCTTTGGATCAGTTACC  720
F  G  R  R  H  L  S  F  W  S  R  T  P  I  S  L  W  I  V  C  F  F  K  Q  F  F  G  S  V  T    240
AAGGTTGATTACATGACACTGAGACATGGATTCATCGTTGCACATCTTGCACCCGGAAGTGAAGTAAAATTTGATTTCCACAAATACATT  810
K  V  D  Y  M  T  L  R  H  G  F  I  V  A  H  L  A  P  G  S  E  V  K  F  D  F  H  K  Y  I    270
AGCAGATCTCTGGAAGACGACTTTAAAGTTGTTGTGGGGATTAGTCCCGCAATGTGGCTATTTGCTGTTCTCTTCATCCTAACCAATACA  900
S  R  S  L  E  D  D  F  K  V  V  V  G  I  S  P  A  M  W  L  F  A  V  L  F  I  L  T  N  T    300
AATGGGTGGTATTCATATCTATGGCTGCCTTTCATCTCCTTAATTATAATTCTATTGGTGGGAACAAAGCTCCATGTTATTATAACTCAT  990
N  G  W  Y  S  Y  L  W  L  P  F  I  S  L  I  I  I  L  L  V  G  T  K  L  H  V  I  I  T  H    330
ATGGGATTGACAATTCAAGAAAGGGGTCATGTTGTGAAGGGTGTTCCGGTCGTTCAGCCTCGGGATGACCTGTTTTGGTTTGGACGTCCA 1080
M  G  L  T  I  Q  E  R  G  H  V  V  K  G  V  P  V  V  Q  P  R  D  D  L  F  W  F  G  R  P    360
CAACTTATTCTCTTCCTGATCCACTTTGTTCTCTTTATGAATGCATTTCAGCTTGCCTTCTTTGCTTGGACCACTTATGCATTTAAGTGG 1170
Q  L  I  L  F  L  I  H  F  V  L  F  M  N  A  F  Q  L  A  F  F  A  W  T  T  Y  A  F  K  W    390
ATGGGTTGTTTCCATCAGCGAGTTGAAGATATTGTCATCAGACTCTCAATGGGGGTTATCATACAAGTTCTCTGCAGTTATGTCACACTC 1260
M  G  C  F  H  Q  R  V  E  D  I  V  I  R  L  S  M  G  V  I  I  Q  V  L  C  S  Y  V  T  L    420
CCACTCTATGCTTTGGTTACTCAGATGGGCTCTAACATGAGACCAACCATTTTCAACGACCGAGTGGCAACGGCATTGAAGAACTGGCAC 1350
P  L  Y  A  L  V  T  Q  M  G  S  N  M  R  P  T  I  F  N  D  R  V  A  T  A  L  K  N  W  H    450
CACTCCGCCAAGAAGAACATGAAGCAGCACCGCAACCCAGACAGTACCTCACCATTCTCAAGCAGGCCAGCTACTCCAACTCACGGCATG 1440
H  S  A  K  K  N  M  K  Q  H  R  N  P  D  S  T  S  P  F  S  S  R  P  A  T  P  T  H  G  M    480
TCTCCTATTCACCTTCTGCACAAACATCAGCATGGCAGCACATCTCCCAGGCTATCCGATGCCGAACCCGATCGTTGGGAAGAGTTGCCT 1530
S  P  I  H  L  L  H  K  H  Q  H  G  S  T  S  P  R  L  S  D  A  E  P  D  R  W  E  E  L  P    510
CCTTCTTCACACCATAGTAGAGCCCCCCATCATGATAATCATCAAGATCAACAAGAACAATCTGAGACAATAATTAGAGAACAGGAGATG 1620
P  S  S  H  H  S  R  A  P  H  H  D  N  H  Q  D  Q  Q  E  Q  S  E  T  I  I  R  E  Q  E  M    540
ACAGTTCAAGGACCAAGTTCAAGTGAAACCGGTTCCATAACACGTCCTGCTCGCCCTCATCAGGAAATCACTAGGACTCCATCAGACTTC 1710
T  V  Q  G  P  S  S  S  E  T  G  S  I  T  R  P  A  R  P  H  Q  E  I  T  R  T  P  S  D  F    570
TCATTTGCCAAATGA                                                                            1725
S  F  A  K  *                                                                               574
```

Figure S2 Nucleotide and deduced amino acid sequences of cucumber *CsMLO2* cDNA encoding an MLO homolog protein. The deduced amino acid sequences are given below the nucleotide sequences. The transcriptional start site is shown in bold type and the termination codon is marked by an asterisk (*). The amino acids shown in a solid box reveal a domain of the MLO-related protein, a member of the plant integral membrane proteins.

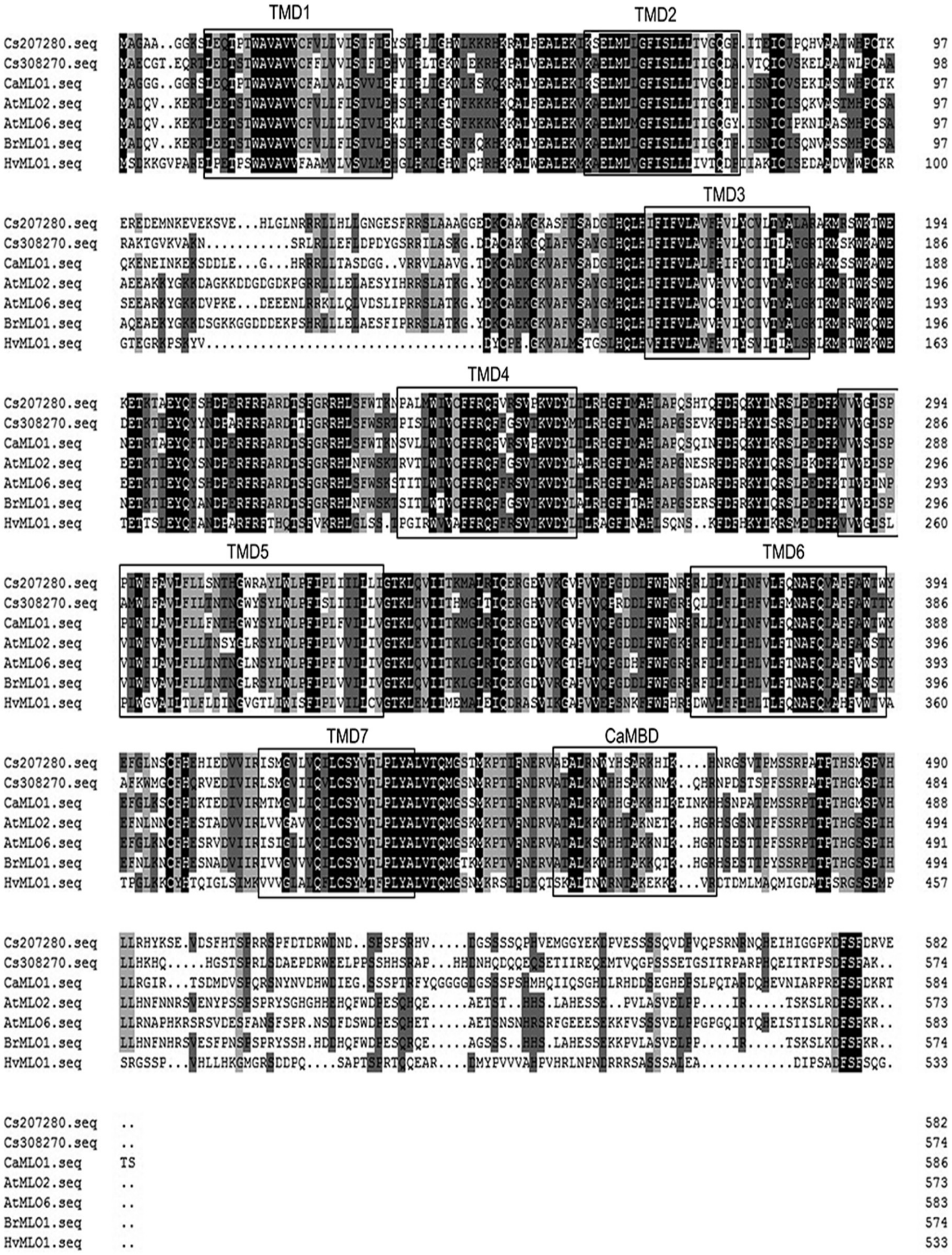

Figure.S3 Sequence analysis to *CsMLO1* and *CsMLO2* in cucumber. Comparison of the deduced amino acid sequence of *Cs207280* (*CsMLO1*) and *Cs308270* (*CsMLO2*) cDNA with other plant MLOs from pepper (*Capsicum annuum*, *MLO1*, accession no. AAX31277), Arabidopsis (*Arabidopsis thaliana*, *MLO2* and *MLO6*, accession no. Q9SXB6 and Q94KB7), turnip (*Brassica rapa*, *MLO1*, accession no. AAX77014) and barley (*Hordeum vulgare* subsp. *vulgare*, *MLO1*, accession no. P93766). The conserved seven transmembrane domains (TMD1 to TMD7) and the calmodulin-binding domain (CaMBD) of the MLO protein were shown in solid boxes.

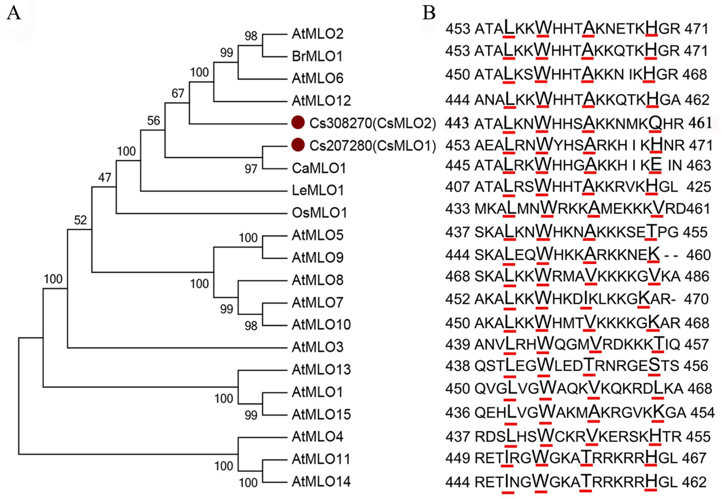

Figure S4. Phylogenetic analysis of CsMLO1/CsMLO2 and analysis of the CaM-binding domain (CaMBD) sequences of CsMLO1/CsMLO2. (**A**) Phylogenetic analysis of plant mildew resistance locus O (MLO) proteins. (**B**) Alignment of the putative CaMBD sequence of CsMLO1 (Alanine^{453} to Argine^{471}) and CsMLO2 (Alanine^{443} to Argine^{461}) with the corresponding regions of MLO families. The names of MLO families listed in (**A**) and their putative CaMBD sequences are aligned in the same order. The hydrophobic amino acids corresponding to a Ca^{2+}-dependent CaM-binding motif and the highly conserved tryptophan (W) residues were the capital letters.

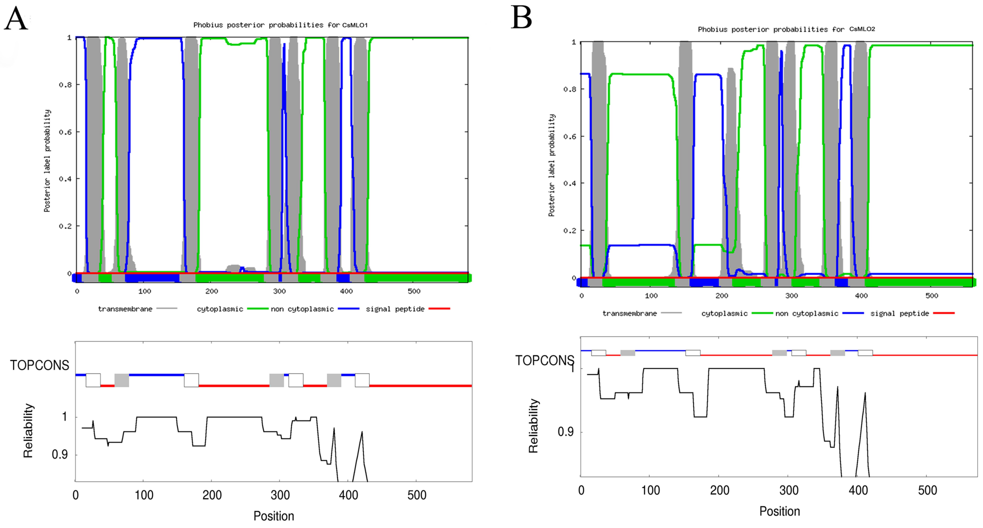

Figure S5. The predicted transmembrane topology of the CsMLO1 and CsMLO2 proteins analyzed. Cytoplasmic and non-cytoplasmic represented the intracellular and extracellular locations, respectively, using the online tools Phobius (http://phobius.sbc.su.se/) and TOPCONS (http://topcons.cbr.su.se/).

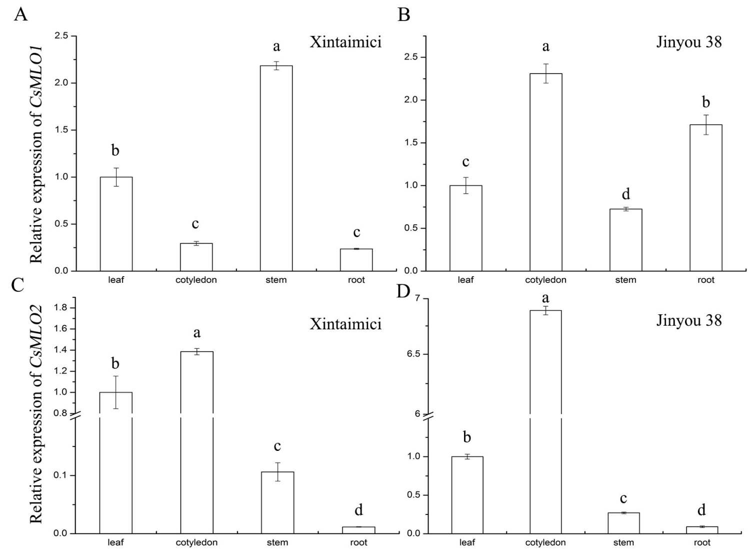

Figure S6. Expression pattern of *CsMLO1* and *CsMLO2* in cucumber. Spatial expression patterns of *CsMLO1* and *CsMLO2* in leaves, cotyledons, stems and roots according to reverse-transcription quantitative PCR (RT-qPCR). Expression analysis of candidate genes using the $2^{-\Delta\Delta Ct}$ method. Data are means ± standard deviations from three biological replicates per cultivar. The lowercase letters indicate significant differences according to Duncan's multiple range test ($P < 0.05$). (**A**) Expression pattern of *CsMLO1* in susceptible cultivar. (**B**) Expression pattern of *CsMLO1* in resistant cultivar. (**C**) Expression pattern of *CsMLO2* in susceptible cultivar. (**D**) Expression pattern of *CsMLO2* in resistant cultivar. The expression level in the leaf was normalized as 1. Data represent means ± SE of three biological replicates. Letters indicate significant differences at $P < 0.05$ compared with the leaf by Student's *t*-test.

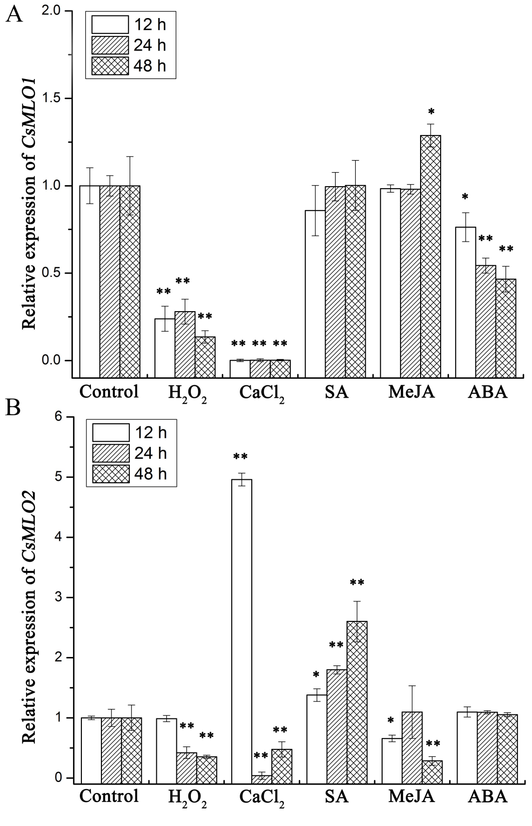

Figure S7. Expression patterns of *CsMLO1* and *CsMLO2* genes in response to plant hormones. (**A**) RT-qPCR analyses of *CsMLO1* transcripts in resistant variety under plant hormones treatments such as hydrogen peroxide (H_2O_2, 10 μM), abscisic acid (ABA, 100 μM), salicylic acid (SA, 1 $mmol \cdot L^{-1}$), methyl jasmonate (MeJA, 100 $\mu mol \cdot L^{-1}$) and $CaCl_2$ (10 $mmol \cdot L^{-1}$). (**B**) RT-qPCR analyses of *CsMLO2* transcripts in resistant varieties under plant hormones treatments. The relative expression levels of *CsMLO1* and *CsMLO2* in cucumber plants at variety time points were compared with the mock control, which was set to 1. Expression analysis of candidate genes using the $2^{-\Delta\Delta Ct}$ method. Data are means ± standard deviations from three biological replicates per cultivar. The asterisks indicated a significant difference (Student's *t*-test, $^*P < 0.05$ or $^{**}P < 0.01$).