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	CsPR1-1a -F	GGCAGCCCAGACTTCTCAGC		
transgenic cucumber	CsPR1-1a -R	GCATCTCACTTTGGCACATCCTA		
CsPR2 for qRT-RCR in	CsPR2-F	AAGACAACATCCTCAACTTTGC		
transgenic cucumber	CsPR2-R	CTGCTGAAAGAATTCCAGTGTG		
CsPR3 for qRT-RCR in	CsPR3-F	CATTTCTCTCATCCTTTGGCAG		
transgenic cucumber	CsPR3-R	GATATCGAAATCAACGCCATCC		
CsPYL2 for qRT-RCR in	<i>CsPYL2-</i> F	CAGAAATCATTGATGGACGACC		
transgenic cucumber	<i>CsPYL2-</i> R	TGAAACATCAGCAAGTGACTTG		
CsPP2C2 for qRT-RCR in	CsPP2C2-F	TATTCCCGATCCAGAAGTCATG		
transgenic cucumber	CsPP2C2-R	CAAGCATTGAGAGGTAATCTGC		
CsSnRK2.2 for qRT-RCR in	CsSnRK2.2-F	GCAGATCCAGAGACGAGAATAA		
transgenic cucumber	CsSnRK2.2-R	TCAATACTCTGTGTTGCCTCAT		
CsABI5 for qRT-RCR in	CsABI5-F	GAATCGCCATTACAGTCTGAAC		
transgenic cucumber	CsABI5-R	AACTCATCCAATGTGAGTGAGT		
CsRbohD for qRT-RCR in	CsRbohD-F	GCGTAACATTACTGGTGATTCC		
transgenic cucumber	CsRbohD-R	ATTCTTCCATCAGCATCCGTAT		
CsRbohF for qRT-RCR in	CsRbohF-F	ATCGGACGATATTACACAGCTT		
transgenic cucumber	CsRbohF-R	ACAATCACCAGAACGAATACCT		
Cucumber CsActin gene for	Actin-F	TCGTGCTGGATTCTGGTG		
and qRT-PCR	Actin-R	GGCAGTGGTGGTGAACAT		

Table S3 List of primers used in the study

Analysis	Primer name	Sequence(5'-3')	
Sequencing of the cDNA	CsMLO1-F	GATATCATGGCGGGGGGCAGCCGGTGGCAA	
of CsMLO1	CsMLO1-R	GCGGCCGCTCATTCAACTCTATCAAATGAAAAGTC	
Sequencing of the cDNA	CsMLO2-F	GGATCCATGGCTGAATGTGGAACAGAG	
of CsMLO2	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	TRVCsMLO1-F	GAATTCGTGGCAGAGGCCCTTCGCAAC	
vector	TRVCsMLO1-R	GAGCTC TCATTCAACTCTATCAAATGA	
CsMLO2-silencing	TRVCsMLO2-F	gtgagtaaggttaccgaattcCACCACTCAGCCAAGAAG	
vector	TRVCsMLO2-R	ggcctcgagacgcgtgagctcTCATTTGGCAAATGAGAA	
CsMLO1-overexpression	LucCsMLO1-F	tctgagctctctagaATGGCGGGGGGCAGCCGGTGG	
vector	LucCsMLO1-R	cataagcttctgcagTTCAACTCTATCAAATGAAA	
CsMLO2-overexpression	LucCsMLO2-F	ctgagctctcagaATGGCTGAATGTGGAACAGA	
vector	LucCsMLO2-R	cataagcttctgcagTTTGGCAAATGAGAAGTCTG	
Chimeric primer for	<i>CsMLO1-nLuc-</i> F	ACAACGATTCGCCCTCTCCATCTC	
CsMLO1-nLuc	<i>CsMLO1-nLuc-</i> R	CCTCGATATGTGCATCTGTAAAAGC	
Chimeric primer for	CsMLO2-nLuc-F	GTTGCCTCCTTCTTCACACCATAGC	
CsMLO2-nLuc	<i>CsMLO2-nLuc-</i> R	CCTCGATATGTGCATCTGTAAAGC	

gccgggggcagccggtggcaagtcgctggagcaaacaccgacatgggccgttgccgttgtttgctttgttttgctcgtcatctcta	т 90
$ \begin{tabular}{cccccccccccccccccccccccccccccccccccc$	30
CATCGAATATAGTCTCCATCTTATCGGACATTGGCTAAAGAAGAGACACAAACGGGCGTTGTTTGAAGCATTAGAGAAGATCAAAT	A 180
$ \begin{tabular}{cccccccccccccccccccccccccccccccccccc$	60
GCTTATGTTATTGGGGGTTTATATCATGGCTACGGGGGCAAGGAGGGGGGATATGGGGGGATATGGGGGGGAGGAGGGGGGGGGG	A 270
$            L \  \   M \  \   L \  \   G \  \   G \  \   F \  \   I \  \   G \  \   G \  \   G \  \   G \  \   G \  \   F \  \   I \  \   C \  \   I \  \   P \  \   Q \  \   H \  \   V \  \   A \  \   A$	90
GTGGCATCCATGTACAAAGGAAAGAGAAGATGAGATGAACAAAGAGGTGGAGAAATCTGTGGAACATTTGGGTCTTAATCGCCGGA	A 360
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
ccttcatctcctcggaaatggtgaaagtttccggcggagtttggccgctgcggaggaggaggataaatgtgccgccaagggtaaagg	т 450
L H L L G N G E S F R R S L A A G G E D K C A A K G K A	150
ctttatttcagcagatggaattcatcaacttcatatcttcatttttgtgttggctgtttttcatgttttgtattgtgttctaactti	т 540
$ \begin{tabular}{cccccccccccccccccccccccccccccccccccc$	180
GTTGGCTAGAGCTAAGATGAGGAGTTGGAAAACATGGGAAAAAGAGACCAAAACTGCTGAATACCAATTCTCACATGATCCAGAGAG	G 630
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
TAGGTTTGCAAGAGACACCTCATTTGGGAGAAGACATTTGAGCTTTTGGACCAAAAATCCTGCCTTGATGTGGATCGTTTGTTT	'C <b>720</b>
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
ACAATTTGTAAGATCTGTTCCAAAAGTTGATTACTTGACATTAAGACATGGGTTTATAATGGCACATTTAGCACCTCAAAGTCATA	A 810
	270
${\tt ATTTGATTTTCAAAAATACATTAATAGATCCCTTGAAGAAGACTTCAAAGTTGTTGTGGGAATCAGCCCACCAATTTGGTTCTTTGCTTTTGATTGA$	т 900
$ \begin{tabular}{cccccccccccccccccccccccccccccccccccc$	300
TCTATTTCTCCTCTCAAACACTCACGGTTGGAGGGCGTATCTATGGCTGCCATTCATCCCACTAATCATTTTGCTGTTGATTGGAA	A 990
L  F  L  S  N  T  H  G  W  R  A  Y  L  W  L  P  F  I  P  L  I  I  L  L  I  G  T	330
${\tt attgcaagtgatcataacgaaaatggcactaagaatacaagaagaggtgaagtagtgaagggcgtgccggtggtggagcctggcg}$	т 1080
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
cctcttttggtttaatcgacctcgccttattctttatctcatcaactttgttctctttcaaaatgccttccaagttgccttctttg	т 1170
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
${\tt Gacttggtatgagttgggttgaattcttgcttccatgagcatatagaagatgtggtgatcagaatttctatgggggtgcttgtacagaatttctatgggggtgcttgtacagagtggtgtgatgatgagagtgcttgtacagagtggtggtgatgatgagagtggtggtggtgatga$	.A 1260
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
CCTTTGCAGTTATGTTACTCTTCCTCTTTATGCACTAGTCACTCAGATGGGTTCAACAATGAAGCCAACTATATTCAATGAGAGAG	'G <b>1350</b>
$            L \ C \ S \ Y \ V \ T \ L \ P \ L \ P \ L \ Y \ A \ L \ V \ T \ Q \ M \ G \ S \ T \ M \ K \ P \ T \ I \ F \ N \ E \ R \ V $	450
AGAGGCCCTTCGCAATTGGTACCACTCGGCTCGAAAGCACATCAAACACAACCGCGGTTCGGTCACTCCAATGTCGAGCCGACCCG	C 1440
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
cccgactcacagcatgtcacctgtccaccttctccgacactacaagagtgaagtcgatagcttccacacctcaccgagaaggtcaccectaccgagaaggtcaccectaccgagaaggtcaccectaccgagaaggtcaccectaccectaccgagaaggtcaccectaccegagaaggtcaccectacectaccectaccectaccectaccectaccectaccectacectaccectacectaccectaccectaccectaccectacectacectacectaccectacectacectacectacectacectacect	G 1530
PTHSMSPVHLLRHYKSEVDSFHTSPRRSP	510
CGACACCGATCGTTGGGACAACGATTCGCCCTCTCCATCTCGCCATGTTGATGGTTCGTCTTCGTCACAACCCCACGTTGAGATGG	A 1620
D T D R W D N D S P S P S R H V D G S S S Q P H V E M G	540
TTATGAAAAAGATCCCGTTGAATCAAGTTCGTCTCAAGTTGATCCGGTTCAACCATCTCGAAACCGCAATCAACATGAGATTCATA	т 1710
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
AGGCCCCAAAGACTTTTCATTTGATAGAGTTGAA <b>TGA</b>	1749
	=
G P K D F S F D R V E *	582

**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.

ATGGCTGAATGTGGAACAGAGCAGCGTACTTTGGAAGATACCTCAACTTGGGCTGTTGCGGTTGTTTGT	'TCA 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 <b>30</b>		
atcttcattgaacatgtcattcacctcactggaaagtggctggagaaaaggcacaagccagctcttgttgaagctctagaaaaggt	'AAA 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	к 60		
${\tt G}{\tt C}{\tt A}{\tt G}{\tt G}{\tt G}{\tt C}{\tt A}{\tt T}{\tt G}{\tt G}{\tt G}{\tt A}{\tt T}{\tt C}{\tt G}{\tt A}{\tt A}{\tt G}{\tt G}{\tt C}{\tt A}{\tt G}{\tt G}{\tt G}{\tt C}{\tt A}{\tt G}{\tt G}{\tt C}{\tt G}{\tt C}{\tt A}{\tt G}{\tt G}{\tt C}{\tt G}{\tt C}{\tt A}{\tt G}{\tt G}{\tt C}{\tt C}{\tt C}{\tt C}{\tt A}{\tt A}{\tt C}{\tt C}{\tt C}{\tt C}{\tt A}{\tt G}{\tt G}{\tt C}{\tt C}{\tt C}{\tt C}{\tt C}{\tt A}{\tt C}{\tt C}{\tt C}{\tt C}{\tt C}{\tt C}{\tt C}{\tt C$	GCA 270		
A E L M L L G F I S L L T I G Q D A V T Q I C V S K E L	A 90		
GCAACTTGGCTTCCCTGTGCAGCAAGAGCTAAAACAGGAGTAAAAGTTGCGAAGAACAGTCGTCTTAGACTTCTTGAATTTTTAGAT	CCT 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 <b>120</b>		
GACTATGGTTCGAGGCGTATTTTAGCCTCGAAAGGAGATGATGCATGC	ATC 450		
DYGSRRILASKGDDACAKRGQLAFVSAYG	I 150		
catcagctccatattttcatcttcgtattggctgtcttccatgtcctatactgcatcataactttggcttttggcagaacgaagatcgaaggatcgaa	GAGC 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 <b>180</b>		
aaatggaaggcctgggaggatgaaaccaagacaattgaataccagtactataatgatccagcaagatttagatttgctagagatac	ACG 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	Г <b>210</b>		
${\tt TTTGGACGCCGACACTTGAGCTTCTGGAGTCGTACACCAATTTCCCTCTGGATTGTTTGT$	ACC 720		
FGRRHLSFWSRTPISLWIVCFFKQFFGSV	Г 240		
AAGGTTGATTACATGACACTGAGACATGGATTCATCGTTGCACATCTTGCACCCGGAAGTGAAGTAAAATTTGATTTCCACAAATA	ATT 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		
agcagatctctggaagacgactttaaagttgttgtggggattagtcccgcaatgtggctatttgctgttctcttcatcctaaccaat	ACA 900		
S R S L E D D F K V V G I S P A M W L F A V L F I L T N	Г 300		
aatgggtggtattcatatctatggctgcctttcatctccttaattataattctattggtgggaacaaagctccatgttattataac	CAT 990		
N G W Y S Y L W L P F I S L I I I L V G T K L H V I I T	н 330		
${\tt atgggattgacaattcaagaaaggggtcatgttgtgaagggtgttccggtcgttcagcctcgggatgacctgttttggtttggacgtgacgtgacctgttttggtttggacgtgacgggacgtgacgacggacg$	CCA 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 <b>360</b>		
CAACTTATTCTCTTCCTGATCCACTTTGTTCTCTTTATGAATGCATTTCAGCTTGCCTTCTTTGCTTGGACCACTTATGCATTTAA	TGG 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	ฬ 390		
${\tt atgggttgtttccatcagcgagttgaagatattgtcatcagactctcaatgggggttatcatacaagttctctgcagttatgtcacAgttgtcacAgttatgtcacAgttgtcacAgttgtcatgtca$	ACTC 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		
CCACTCTATGCTTTGGTTACTCAGATGGGCTCTAACATGAGACCAACCA	GCAC 1350		
PLYALVTQMGSNMRPTIFNDRVATALKNW	H <b>450</b>		
CACTCCGCCAAGAAGAACATGAAGCAGCACCGCAACCCAGACAGTACCTCACCATTCTCAAGCAGGCCAGCTACTCCAACTCACGG	ATG 1440		
H S A K K N M <mark>K Q H R N P D S T S P F S S R P A T P T H G</mark>	M 480		
TCTCCTATTCACCTTCTGCACAAACATCAGCATGGCAGCACATCTCCCAGGCTATCCGATGCCGAACCCGATCGTTGGGAAGAGTTC	GCCT 1530		
<u>SPIHLLH</u> KHQHGSTSPRLSDAEPDRWEEL	P <b>510</b>		
${\tt ccttcttcacaccatagtagagccccccatcatgataatcatcaagatcaacaagaacaatctgagacaataattagagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaggacaagaacaggacaggacaagaacaggacaagaacaggacaggacaagaacaggacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaagaacaggacaggacaagaacaggacaagaacaggacaggacaggacaggacaggacaggacaagaacaggacaggacaggacaggacaggacaagagacaggacgac$	ATG <b>1620</b>		
P S S H H S R A P H H D N H Q D Q E Q S E T I I R E Q E	M 540		
a cagt t caagga c caagt t caagt g a a a c c g g t c c a t a c a c g t c c t g c c c t c a t c a g g a a t c a c t a g g a c c c a t c a g g a a t c a c t a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c c a t c a g g a c c c a t c a g g a c c c c c a t c a g g a c c c c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c a t c a g g a c c c c a t c a g g a c c c c c c c c c c c c c c c	TTC 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 <b>570</b>		
TCATTTGCCAAATGA 1			
SFAK*	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.

	TMD1	TMD2	
Cs207280.seq Cs308270.seq CaML01.seq AtML02.seq AtML06.seq BrML01.seq HvML01.seq	NAGAAGCKE <mark>IDET ET KAWAV VOOR VLIVIS IF IB VSIE LIIE HALKKE</mark> NA CGT.ECKTIDET ET MAVAV VOOR VLIVIS IF IB VOH DTEKA IEKK NA GGG.GGKEIDET FINAVAV VOOR VLISIS VUIB FIHTU EKKIKS NA GVKERTIDET SINAVAV VOOR VLISIS VUIB SIEKKIG TAKKK NA GVKERTIDET SINAVAV VOOR VLIJIS VVIB KLIKKIG SAKKK NA GV.KERTIDET SINAVAV VOOR VLIJIS VVID KLIKKIG SAKKK G NSIKKGV PA HE <mark>T PE SAAVAV VOOR VAN VOOR VLISVIDE</mark> HOLKKIG MUCH	HERALFEALEKI SELMI GEISLILTVGRGE IT IC POHVRA WHECIK HERALVEALEKI KIELMI GEISLILTUGO, VTGIC SKELAAIWIPOA GRALVEALEKI KIELMI GEISLILTUGO, ISI IC SKHPSTWHECK HEGALFEALEKI KIELMI GEISLILTUGO, ISI IC SKWPSTWHECS HERALVEALEKI KIELMI GEISLILTUGO, ISI IC FENTRASHECS HERALVEALEKI KIELMI GEISLILTUGO, ISI IC FENTRASHECS HERALVEALEKI KIELMI GEISLILTUGO, ISI IC SCHPSSHECS HERALVEALEKI KIELMI GEISLILTUGO, ISI IC SCHPSSHECS HERALVEALEKI KIELMI GEISLILTUGO, ISI IC SCHPSKA	97 98 97 97 97 97
Cs207280.seq Cs308270.seq CaML01.seq AtML02.seq AtML06.seq BrML01.seq HvML01.seq	EREDEMNKEVEKSVEHLGINRERIHL GNGESFRRSLAAAGGE RAKTGVKVANNSRLRIEFIDPDYGSRRLASKG.D QKENEINKESDDLEGHRRLIASDGG.VRRVLAAVG.T AEEAKYGKKDAGKKDGCOCKFGRRILELAESVIHRRSLATKG.Y SEEARYGKKDVFKEDEEENLRKLLQIVDSLIPRRSLATKG.Y AQEAEYGKKDSGKKGGDDEKFSRILLELAESFIFRRSLATKG.Y GTEGR FS YV	THES VGAARGEASTISADCIHOLE FIFEVERVERVLACHTALAAREVISSERTING AGARGCTAFVSANGIHOLFIFIEVERVERVLACHTALATSKWISSERANG VGADRGEVAFVSANGIHOLFIFIEVERVERVVERVLACHTALATSKNISSERANG VGAERGEVAFVSANGIHOLFIFIEVERVOEVVERVVERVTATATSKNIS NGAERGEVAFVSANGIHOLFIFIEVERVOEVVERVTATATSKNIS NGAERGEVAFVSANGIHOLFIFIEVERVOEVVERVTATATISKTEMERNE NGAERGEVAFVSANGIHOLFIFIEVERVUEVVERVTATATISKTEMERNE NGAERGEVAFVSANGIHOLFIFIEVERVUEVVERVTATISKTEMERNE NGAERGEVAFVSANGIHOLFIFIEVERVUEVVERVTASITEMELSE I EMITAMERNE	194 186 188 196 193 196
	TM	D4	
Cs207280.seq Cs308270.seq CaMLO1.seq AtMLO2.seq AtMLO6.seq BrMLO1.seq HvMLO1.seq	KET TÅ EYC I SE DE REREARD TSEGERHLSENT I NEAL WIV OFFRO DETKTI EYC IYN DE ARFBARD TO EGREHLSENT I NEV OFFRO NET TÆ YC IYN DE ARFBARD TSEGREHLSENT I NEV DE RO EET TI EYC IS DE REREARD TSEGREHLSENT I NEV DE RO EET TI EYC IS DE REREARD TSEGREHLSENST STIL NIVCERO DET TI EYC IS DE REREARD TSEGREHLSENST STIL NIVCERO TET TI EYC IA DE REREARD TSEGREHLNEN NST STIL NIVCERO TET TS EYC IA DE REREARD TSEGREHLNEN STIL NIVCERO TET TS EYC IA DE REREARD TSEGREHLNEN STIL NIVCERO TET TS EYC IA DE REREARD TSEGREHLNEN STIL NIVCERO	EVESVERVUŠTI I REGETU AH LAPQSHTQPDG QYHNAS IDD DEž VVČTSP FEGSVERVUŠTI I REGETU AH LAPQSHTQPDG QYHNAS IDD DEž VVČTSP EVESVERVUŠTI I REGETU AH LAPQSQI I FERQXY I RSIDD DEž VVČTSP FEGSVERVUŠTI I REGETU AH LAPQSQI FERQXY I RSIDD DEŽ VVČTSP FERSVERVUŠTI I REGETU AH LAPQSDAREDER XY I QRSIDD DEŽ TI VD I SP FEGSVERVUŠTI I REGETU AH LAPQSDAREDER XY I QRSIDD DEŽ TI VD I SP FEGSVERVUŠTI I REGETU AH LAPGSDAREDER XY I QRSIDD DEŽ TI VD I SP FEGSVERVUŠTI I REGETU AH LAPGSDAREDER XY I QRSIDD DEŽ TI VD I SP FEGSVERVUŠTI I REGETU AH LAPGSDAREDER XY I QRSIDD DEŽ TI VD I SP FEGSVERVUŠTI I REGETU AH LAPGSDAREDER XY I QRSIDD DEŽ TI VD I SP	294 286 288 296 293 296 260
	TMD5	TMD6	
Cs207280.seq Cs308270.seq CaMLO1.seq AtMLO2.seq AtMLO6.seq BrMLO1.seq HvMLO1.seq	FIR FRAN FILSNIFGWRAYIRLEG PLITTE LIGTKLOVETKMAN RMR FRAN FILMNINGWYGYDLEG SLITTLUGTKLOVETKMAN RMR FRAN FILMNINGWYGYDLEG SLITTLUGTKLOVETKMG VIR YR YD FLLMNINGWYGYDLEG PLYND IVGTKLOVETKMG VIR YR YD FLLMNINGLNGYDLEG PFINT IVGTKLOVETKLOU VIR YR YD FLLMNINGLRGYDLEG PPINT IVGTKLOVETKLOU FLLGWETLENNINGLRGYDLEG SPELVIN IVGTKLOVETKLOU FLLGWETLENNINGLRGYDLEG SPELVIN IVGTKLOVETKLOU	IÇERGEVVKEVEVEVE BEDDI ƏNƏNRƏRLILIVLINEVLƏ ÇNAFƏ, PARƏNT MY IÇERGEVVKEVEVƏ FERDI ƏNƏGRƏ ÇILD TILƏ FVAƏVNAFƏ, PARƏNTIY IÇERGEVVEVEVƏ FERDI ƏNƏNRƏRLILIVLINA ÇONAFQ, PARƏNTIY IÇERGEVVEVEVƏ BEDDI ƏNƏGRƏRFILI VILƏ INAFƏ, PARƏNTIY IÇERGEVVETELVƏ BEDDI ƏNƏGRƏRFILI VILƏLINAFƏ PARƏNTIY IÇERGEVVETELVƏ BEDDI ƏNƏGRƏRFILI VILƏLINAFƏ PARƏNTIY IÇERGEVVEFARVƏ BEDDI ƏNƏGRƏRFILI VILƏLINAFƏ PARƏNTIY IÇERGEVVEFARVƏ BEDDI ƏNƏGRƏRFILI VILƏLINAFƏ PARƏNTIY IÇERGEVVEFARVƏ BEDDI ƏNƏGRƏRFILI VILƏLINAFƏ PARƏNTIY IÇERGEVVEFARVƏ BENKI ƏNƏHRƏ EDMILTINAFƏ PARƏNTIYA	394 386 388 396 393 396 360
	TMD7	CaMBD	
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**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<sup>453</sup> to Argine<sup>471</sup>) and CsMLO2 (Alanine<sup>443</sup> to Argine<sup>461</sup>) 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<sup>2+</sup>-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<sub>2</sub>O<sub>2</sub>, 10  $\mu$ M), abscisic acid (ABA, 100  $\mu$ M), salicylic acid (SA, 1 mmol·L<sup>-1</sup>), methyl jasmonate (MeJA, 100  $\mu$ mol·L<sup>-1</sup>) and CaCl<sub>2</sub> (10 mmol·L<sup>-1</sup>). (**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<sup>-ΔΔCt</sup> 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).