**Supplementary Figure S1.** A phylogenetic tree of the identified NLR proteins. A neighbor-joining tree was constructed with NGPhylogeny software using the full-length protein sequence of CbAR9 (CB.CBv1.2.scaffold1468.5) and CB.CBv1.2.scaffold1022.13/1022.20/2141.4/778.4/778.11/-778.13/778.14/778.16/778.21/778.26. The scale bar represents the proportion of site changes along each branch.
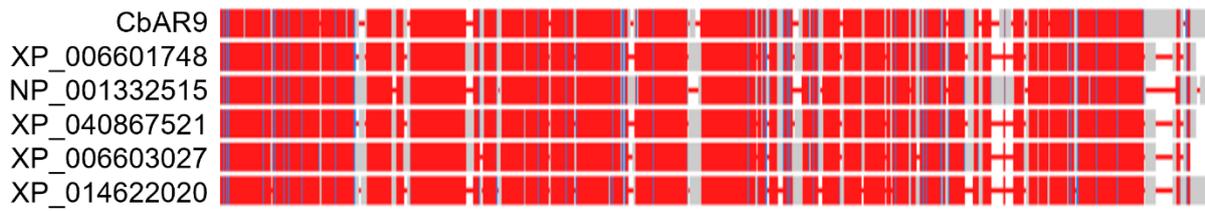
Accession	Organism	Description
XP_006601748	*Glycine max*	NBS-LRR disease-resistance protein scn3r1 isoform X2
NP_001332515	*Arabidopsis thaliana*	Disease resistance protein RPP8L3
XP_040867521	*Glycine max*	NBS-LRR disease-resistance protein scn3r1 isoform X1
XP_006603027	*Glycine max*	Disease resistance protein RPP13
XP_014622020	*Glycine max*	Disease resistance protein RPP13

Supplementary Figure S2. Identification of proteins with a similar NLR domain as CbAR9 in various plant species. The proteins were identified using the SmartBLAST program.

A
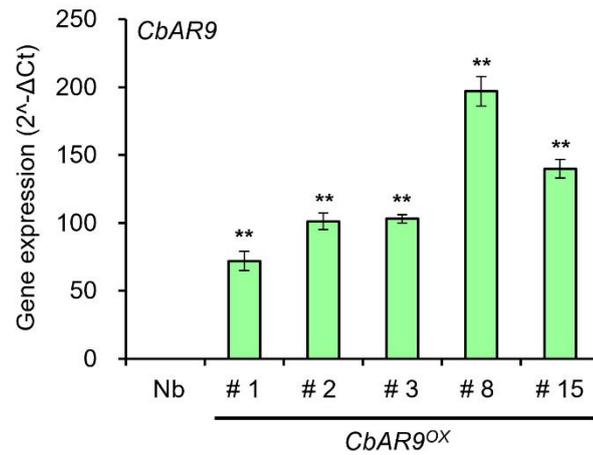
B

Supplementary Figure S3. Verification and phenotype of *CbAR9*-overexpressing plant lines. (A) Analysis of *CbAR9* expression in *CbAR9*^{OX} and the wild-type *Nicotiana benthamiana* plants, as determined by RT-qPCR. *NbActin* served as the internal reference. Data are shown as means ± SD. Asterisks indicate statistically significant differences from controls (** $P < 0.01$). The experiments were repeated at least three times, with similar results. (B) Growth phenotype of *CbAR9*^{OX} without biotic stress. Plants were grown in pots containing soil in a greenhouse under a programmed 16-h light/8-h dark photoperiod at 28 °C. The humidity was adjusted to 50%.

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              ──────────
                VIGS
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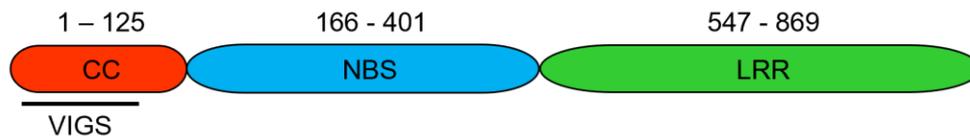
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CB.CBv1.2. Scaffold	Amino acid sequence
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CB.CBv1.2. Scaffold	Amino acid sequence
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778.14	MVVWCIKAPAKDRTTRPYHMQLYLEFCKLLFYPFIPEIPFELYLIITEQIWKP GEKILQISVKTIEFGLREAMIAEDEPQRGKAHEQLSDSVQQDIITKANVNIVD MAHANVASLLRTIESLLSSNSPMRSVSCDHREDFSALHEKISSLEVFLKNFEK NNVSRELTDLEVQIKEVANIVEQTIQLRVTEVVLKRHIMVGRDDQKERLLEDL TASYSGEPKVIPIVGMGGIGKTTLAKEVYNNESVLRRFDVHAWATVSQQHDRK EILLGLLRSTIKMEDRVKTRGEAELADMLQKSLKRKRYLIVLDDIWSCEVWDG VRQCFPTEDNAGSRILLTTRNNEVACYAGTENLSMQMDFMDQDESWNLFESAA FSNEASSSEFETIGKKIAEKCHGLPLTIVVVAGLLKSKREIEYWKSVAKDVTS FVTNDPDKQCSRVLGLSYDHLTSDLKTCLLHFGIFPEDSEIPVKKLMRSWMAE GFLKLENDLEGEAEKCLQDLVNRCLVLVCKKSRDETKIISCKVHDLIYELCLR EVERGSVFSMNDIELEVSYSRGLYLSMRKMQPFKHVTGDLSYFGLYRALLTPV HRQLRDHDNNDLSKRTRSIFSFHLKDSSFFLKSELIHFKLLKVLELRHIEIDN FPLQISSLIWLRYLSLVCNANFDVPPEICRLWNLQTFIVQGSQTVITITITIT FPEEIWGLMQLRHLKVKRVYLPNPPSVSADKGSHTRFSNIQTTSYLSSCCCTK EVISGIRNVKKLGFSGNNLSDSGLHSNLVYLQQLEILSFIRCSCILLPVTSAK VFPATLKKLKLESTYLDWSYMDIIAELPNLEVLKLIDDACDGEEWQQNVKGFT RLKLLFIHDNRLKCWKATNDNFPVLERLMLSKCSTLKEMPIEFAEIHSLQLIE LTSCLPGLGKYAARIQKEQQDLGNNPVDVRISNPFTEEVMANKDTELVVTNQI GSSGNENVGDNEEIRKLRRQIIEMHRAWANGLPPPPVPTDNLDYLSSLPPVSH AQLPIFVDMPQHASRSTPGQQYPTTSNIHFLTPQYKITTCSALPAIHAFAAPL PSEAPAFNVNPTVVIPHSTSNPILNIFSDQHYAPKPTFKSTGPYVFPQPPEFP PNTEKPVMTEEQEEIARKLRSLELTMKNLQGLGGYKSVSYKDLCMFPGVHLPL GFKMPKFEKYDGHGDPIAHLRRYCNQLRGAGGKEELLMAYFGESLSGLASEWF VDQDIDKWNSWDDLANEFVQQFQYNMELIPDEKSLTNMNKKSTETFREYAIRW REQAARVKPPMKESKIVEAFIQVQDETYYQHLLPALGKPFVEVPKMGEMIEDG IKTGRIVSFATLKATTQEIHKGLGSMGGRKNMEDASAIAVGQQAWARGPHHRY PRAQTHVYAQAPTNHYQNPLYPVPPPPYQVYNAQPYVQPPSYPHWRAPTLSSH PPTPHTY
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CB.CBv1.2. Scaffold	Amino acid sequence
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778.26	MADLEVQIKEVANVVEQTIQLRVTEVVLENDVKAQERLSDSLQQVAEDIDCIW TESTKIQDKGKHASKESTVQEFPSSSRSILNVENSMVGRDDQRKQLVEDLTRS YSGEATVIPIVGMGGNLVEPSVFYKGDKVFTESEAELAYILQKSLKVALYAGT KNSLPMRFMDQDESWNLFKSVAFSSEELPSDLETIGKQIADECHRLWNLQTFI VHGPMLSVITFPEEIWGLMQLRHLKLPRIYLPDCPSGSVDKGRHMDFSNLQTI SYLSSRCCTKEVIMGIQNVKKLRIRRDASSSGPLNNLVHLHQLETLNFTDSLS GLLPASAKAFPATLKKLKLKETGLSWPYLDIIAELPDLEVLKLMDNACLGNEW YPNVRGFTRWKVLLIKRNDLKYWKATDDNFPVLERLMIRSCYYLKEIPIEFAE IHTLQLIELIMCLPELGGFAARIQKEQEELGNNPVDVRISYQWSHSSSFTCYC GFQGDVISLNWKNVAGFVF

Supplementary Table S1. Amino acid sequence of the identified candidate NLR proteins.

Gene		Primer sequence	Purpose
CbAR9	F:	AAAAAGCAGGCTAAATGGCAGATGTAGCATTACAACTTGC	Cloning
	R:	AGAAAGCTGGGTATCAATGTTTGGGGTTGCAATCAG	Cloning
	R:	AGAAAGCTGGGTAATGTTTGGGGTTGCAATCAGC	Cloning
	F:	TCTAGAATGGCAGATGTAGCATTACAAC	VIGS
	R:	GGTACCTTTGTGATATTTAAGATCCACGAT	VIGS
	F:	CCATCCTCTACTACCCACAC	qRT-PCR
	R:	TGAAAGTTGTTGAACCCACC	qRT-PCR
778.14	F:	CCTGCATTAGGCAAGCCATTTG	qRT-PCR
	R:	CTGTTGTCCAACTGCAATGGC	qRT-PCR
778.16	F:	GGCTGAGGTACCTATCATTGC	qRT-PCR
	R:	TTGAAGAACCCACGCGACTC	qRT-PCR
1022.13	F:	ACTCTTCTGATGGGCCTCTC	qRT-PCR
	R:	CCGCTATGATGTCCAAGTACG	qRT-PCR
PR1	F:	GAGGACAACGTCCGTATGGT	qRT-PCR
	R:	AACTCCAGTTACTGCACCATTA	qRT-PCR
PR2	F:	CTACTTAAGCTTTGCAAGCACCA	qRT-PCR
	R:	AGATCTCTTTCCTCATCGTCACTT	qRT-PCR
ACT	F:	GTGCTGAGAGATTCCGTTGC	qRT-PCR
	R:	ATGGTTGAGCCACCACTGAG	qRT-PCR
NbPR1	F:	GTGCCCAAAATTCTCAACAAGACT	qRT-PCR
	R:	AAATCGCCACTTCCCTCAGC	qRT-PCR
NbPR2	F:	CAACATAACCTTCCACTCTTAGCCA	qRT-PCR
	R:	CATAGAATCCAAAAGGGCATCAAAAAGA	qRT-PCR
NbPR10	F:	TGAGATTGTTGAGGGTGATGGGG	qRT-PCR
	R:	TTGTCGCCTAAAACATCTCCTTCGA	qRT-PCR
NbACT	F:	CCCAGATGGGCAGGTGATCA	qRT-PCR
	R:	GAGTTGTATGTGGTCTCGTGGATTC	qRT-PCR

Supplementary Table S2. Sequence of primers used in this study.