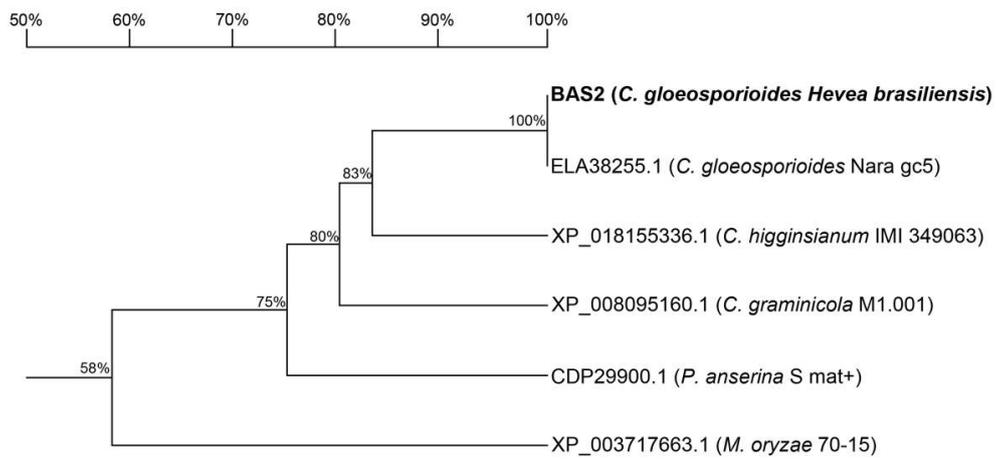
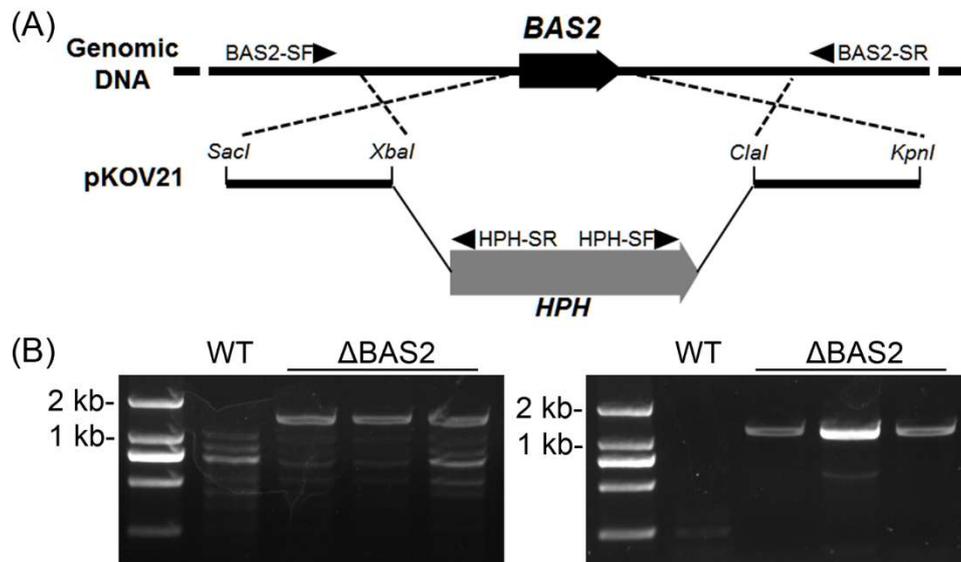


<b>BAS2</b> ( <i>C. gloeosporioides</i> ( <i>H. brasiliensis</i> ))	MVRI . TLF T T L A L A N T A F A Q I K P N N A G A S K V G K G D G S C F I I T G G C V S D A D C S	50
ELA38255.1 ( <i>C. gloeosporioides</i> Nara gc5)	MVRI . TLF T T L A L A N T A F A Q I K P N N A G A S K V G K G D G S C F I I T G G C V S D A D C S	50
XP_018155336.1 ( <i>C. higginsianum</i> IMI 349063)	MVRV . T L L A T L A F A A T A F A Q I T P N K A G S S N V G K G D G S C F I I T G G C V D D S D C S	50
XP_008095160.1 ( <i>C. graminicola</i> M1.001)	MVRI . T L F A T I A F A A T A F S . L S P N N A G A R N V G K G D G S C F I I T G G C V D N A D C S	49
XP_003717663.1 ( <i>M. oryzae</i> 70-15)	MVRV S T F A A I L A M A L S V T A N V T P N D A G A K N V G T G N G C C F I I T G G C V N G T D C Q	51
CDP29900.1 ( <i>P. anserina</i> S mat+)	MVRI . T V T A L L A F V V T A M A Q I T P N N A G A R N V G C G N G S C F I I T G G C V N N A D C A	50
<b>BAS2</b> ( <i>C. gloeosporioides</i> ( <i>H. brasiliensis</i> ))	S A C C A . N A S G V G V C S A E A A C F C N G K N G C G F D D P N A A A T I A A A C A Q A K K C G	99
ELA38255.1 ( <i>C. gloeosporioides</i> Nara gc5)	S A C C A . N A S G V G V C S A E A A C F C N G K N G C G F D D P N A A A T I A A A C A Q A K K C G	99
XP_018155336.1 ( <i>C. higginsianum</i> IMI 349063)	S A C C A . D A S G V G V C S A E A A C F C N G K N G C N F V D P N R E A T I A A A C A Q A E K C G	99
XP_008095160.1 ( <i>C. graminicola</i> M1.001)	S A C C A . N L S G V G I C S A E A A C F C N G K K G C N F V D P N K D A T I A A A K A Q V K K C G	98
XP_003717663.1 ( <i>M. oryzae</i> 70-15)	S R C C A G N G E N K G V C S N E V A A N C N G K T G C G F E D P N K A C T V K E A K E Q V K K C G	101
CDP29900.1 ( <i>P. anserina</i> S mat+)	S G C C A . D A S G V G V C S A E A A C F C N G K N G C G F V D P N A C C T I A A A C A Q V A R C G	99

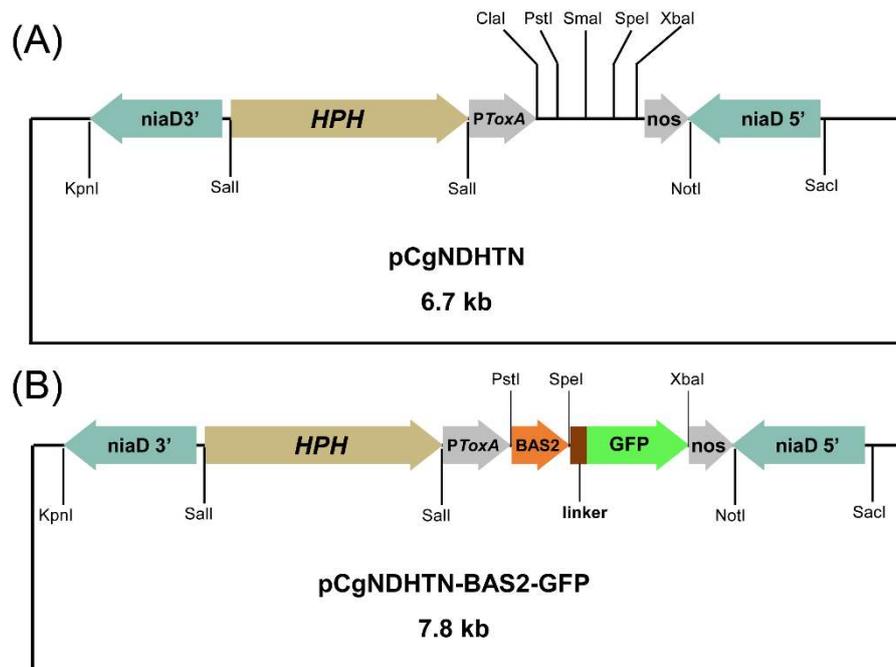
**Figure S1.** Alignment of amino acid sequences of BAS2 of *C. gloeosporioides* from *H. brasiliensis*, *C. gloeosporioides* Nara gc5, *C. higginsianum*, *C. graminicola*, *M. oryzae*, and *P. anserina*.



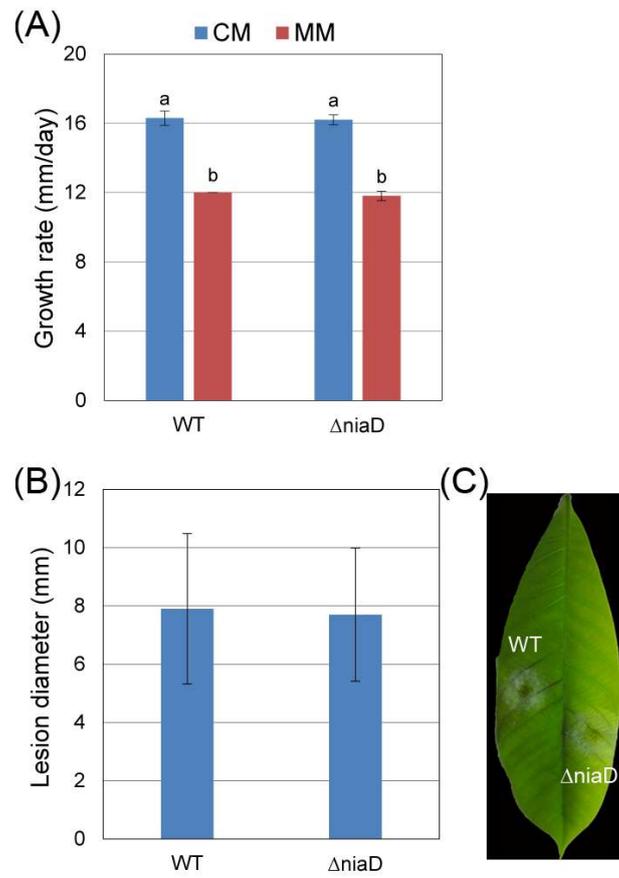
**Figure S2.** Phylogenetic analysis of BAS2 proteins. The neighbor joining phylogenetic tree was constructed by MEGA 7.0 according to the evolutionary relationship between BAS2 proteins in *C. gloeosporioides* from *H. brasiliensis*, *C. gloeosporioides* Nara gc5, *C. higginsianum*, *C. graminicola*, *M. oryzae*, and *P. anserina*.



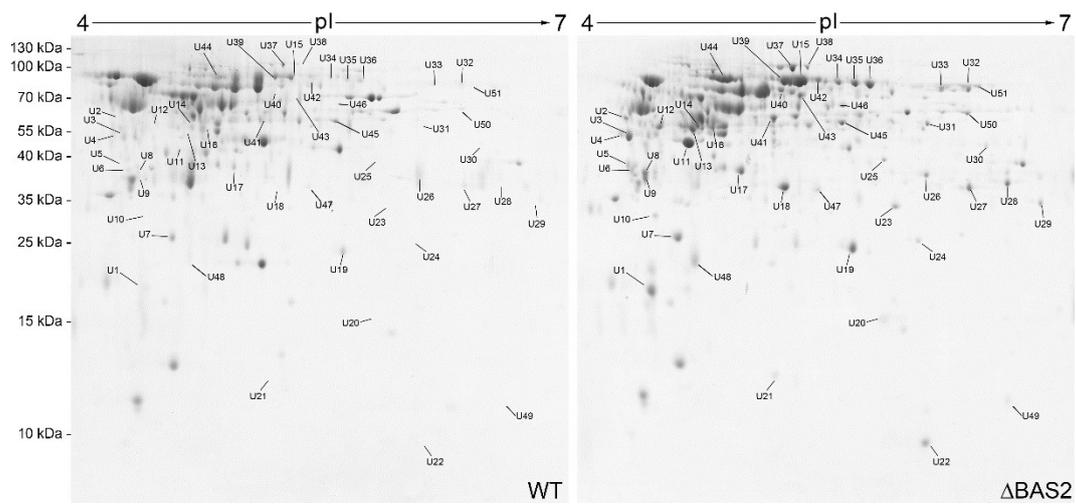
**Figure S3.** (A) The gene deletion strategy. Putative mutants were screened with diagnostic primers, indicated by black triangles. (B) Confirmation of the correct recombination of deletion cassettes with gene loci by Southern blot.



**Figure S4.** Strategy for generation of BAS2-GFP fusion overexpressing mutants. (A) Expression system using the gene loci of nitrate reductase (*niaD*). Promoter of ToxA and terminator *nos* were used for the gene expression; the Hygromycin phosphotransferase gene (*HPH*) was used for transformant selection. (B) The open reading frame of *BAS2* and the coding sequence of GFP with an N-terminal linker were linked together to construct the fusion expressing vector.



**Figure S5.** Phenotype assays of  $\Delta niaD$ . **(A)** Growth rate assay of WT and  $\Delta niaD$  cultured on complete medium (CM) and minimal medium (MM). **(B)** Mean lesion diameters after inoculation with conidia for 3 days. Bars represent standard deviation (SD). **(C)** Disease symptoms of rubber-tree leaves after inoculation with conidia suspension for 3 days.



**Figure S6.** Two-dimensional patterns of extracellular proteomes of WT and  $\Delta$ BAS2. Arrows indicate protein spots that were upregulated in abundance more than 1.5-fold between WT and  $\Delta$ BAS2.

**Table S1.** PCR primers used in this study. Lowercase letters indicate induced restriction sites.

Number	Primer	Sequence (5'→3')	Application
1	BAS2-5F	cgagctcTCGCAAAAATGTTCCAG	BAS2 deletion
2	BAS2-5R	gctctagaTTTCGCGGTAGTTGAGTG	BAS2 deletion
3	BAS2-3F	ccatcgatGCTGGAAAATGCAGAAACT	BAS2 deletion
4	BAS2-3R	gggggtaccAACATGGGGCAGGAGAC	BAS2 deletion
5	BAS2-JC5F	GCGCATTCTTTGAGGTTTCTTG	ΔBAS2 diagnosis
6	HYG-JCR	TGAGTTCAGGCTTTTTTCATTTGG	ΔBAS2 diagnosis
7	HYG-JCF	ACAGCGGTCATTGACTGGAGCGA	ΔBAS2 diagnosis
8	BAS2-JC3R	AAGGGCGGCGACAGTGAAGAGG	ΔBAS2 diagnosis
9	niaD-5F	gagctcAAGGAGTCCCGTTTGT	<i>niaD</i> deletion, expression system
10	niaD-5R	gcggccgcACTGACGACTGGCTTGTC	<i>niaD</i> deletion, expression system
11	niaD-3F	gtcgacACGAGCTGCCGTTTTTAG	<i>niaD</i> deletion, expression system
12	niaD-3R	ggtaccCGGTCACGACGCTGTAA	<i>niaD</i> deletion, expression system
13	niaD-JC5F	TGCCAGTAGCGTGGTTTAGGTC	ΔniaD diagnosis
14	niaD-JC5R	tctagaAATTTCCCGATCGTTC	ΔniaD diagnosis
15	niaD-JC3F	ACAGCGGTCATTGACTGGAGCGA	ΔniaD diagnosis
16	niaD-JC3R	AGTGTCACGATGTCGTGTTGC	ΔniaD diagnosis
17	Ptoxa-F	gtcgacTGGAATGCATGGAGGAG	Expression system of <i>C. gloeosporioides</i>
18	Ptoxa-R	atcgatGACCTATATTCATTCAT	Expression system of <i>C. gloeosporioides</i>
19	Tnos-F	tctagaAATTTCCCGATCGTTC	Expression system of <i>C. gloeosporioides</i>
20	Tnos-R	gcggccgcCCGATCTAGTAACATAG	Expression system of <i>C. gloeosporioides</i>
21	HPH-F	gtcgacAACTGATATTGAAGGAG	Expression system of <i>C. gloeosporioides</i>
22	HPH-R	gtcgacAACTGGTTCCCGGTCGG	Expression system of <i>C. gloeosporioides</i>
23	cBAS2-F1	ctgcagATGGTCCGCATCACTCT	BAS2-GFP fusion expressing mutant
24	cBAS2-R1	actagtGAAACCTTGCTTCTTGG	BAS2-GFP fusion expressing mutant
25	GFPlink-F	actagtGGAGCTGGTGCAGGCGCTGGAGC CGGTGCCATGGTGAGCAAGGGCGA	BAS2-GFP fusion expressing mutant

26	GFP-R	tctagaTTACTTGTACAGCTCGT	BAS2-GFP fusion expressing mutant
27	cBAS2-F2	tctagaATGGTCCGCATCACTCT	Transient expression in rubber-tree protoplasts
28	cBAS2-R2	gagctctGAAACCTTGCTTCTTGG	Transient expression in rubber-tree protoplasts

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