Figure S1 Multiple sequence alignment of CmbHLH family proteins. The four-color modules at the top of the figure are represented respectively: red represents the N-terminal basic region of bHLH, yellow and green represents two amphiphilic regions, blue represents variable length loop. Process the data into pictures by using Clustal W.
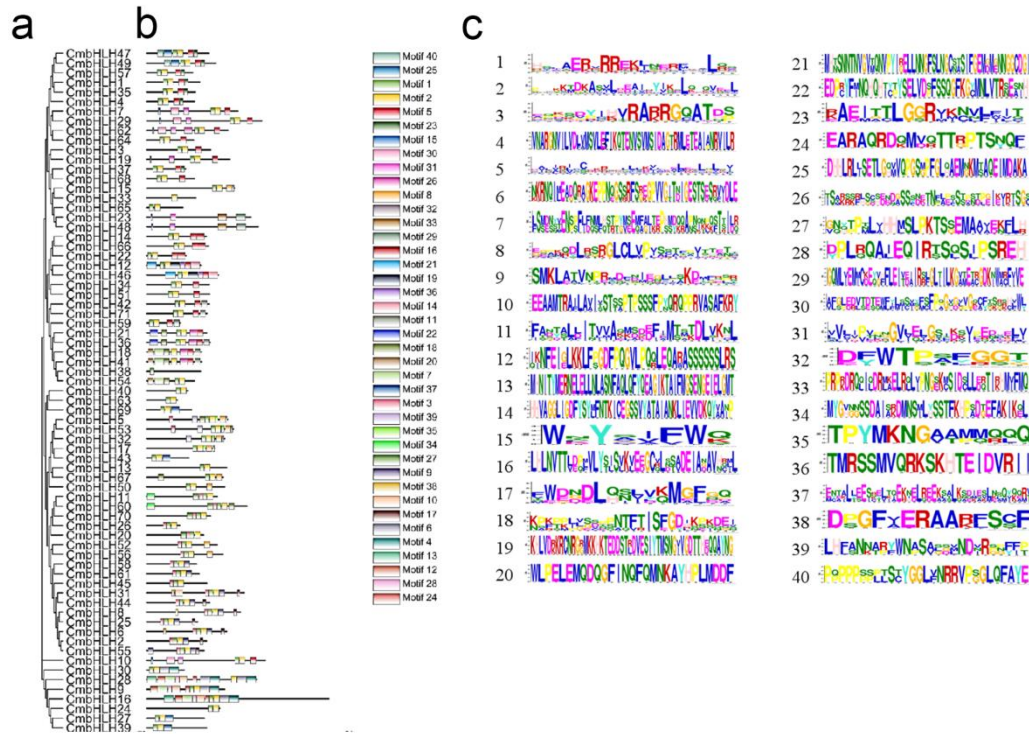
Figure S2 Motif composition of CmbHLH TF family. (**a**) Phylogenetic tree of CmbHLHs; (**b**) Conserved motifs of the CmbHLHs; (**c**) The sequence composition of each motif in CmbHLHs.
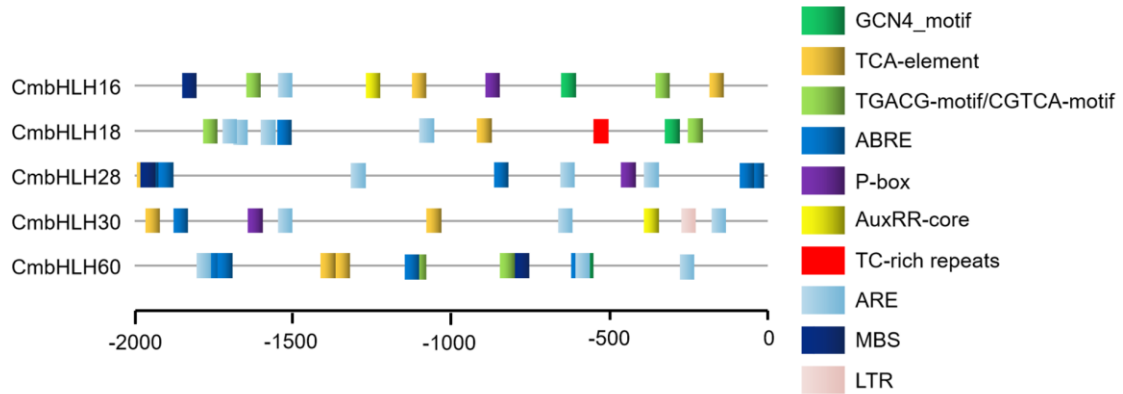

Figure S3 Visualization of *cis*-elements in the promoter sequences of *CmbHLH* genes. Different colors represent different *cis*-acting elements in the promoter sequences of *CmbHLH* genes.

Table S1 Promoter sequences of the candidate resistant genes to necrotrophic fungus.

Promoter sequences of the candidate genes
>*CmbHLH16*
TAGTCTTGGTTAGTAAACTTGGCTATTTAAATATGTTGTAAAAGTTGATTAAATATATACACAAG
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CTTTCCTTAAGTACTAAATGTATTCTCTTTTTGCCACATATAAAATAATGGAGTAGAACTAAAAG
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GAACATAATTGACAAAGAGGACCCAATGATGTGATAAAGAAGATTCAATGGTGGTGTTCTATT
GTTGACCTTCCTGACTCATTATCTCAAGACCATGATTGGGGACTAAATTAAATTGCGTTTTGCA
GCATATATGTATACAAACATATTCGTAAACATTTTTTTTTTAAACATAGCCCTAAAAGTTGTGTT
CAAAGTATTCACACATGAAATAATTGTTTGTATCTTTACCGTTTACTCTCTATAAATTACCTTTAC
TCTCAGTAAATTACCTCTTTCAATCGACTTTATTTATGACCAGATGAACATCTTTTTACATTTTAA
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GTACTATTTGAAAGGGTTTTAACTATGTCTTTTTACCAGAAATAACTTATGTAAAAAGTCGTAC
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CAAATGGGCCTCTATACATGTCTTTTTTTATAACTTGCTTTATGATTAAAACCCTATTTGAAAAA
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ACACTTCAT

>*CmbHLH18*

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>*CmbHLH28*

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AAACATACGAATATTTGTTCAAATCCGTTAAATTGCGTACATATCTGTCACTAGAGGTACAAAT
TTGTACGATTCTGATA

Table S2 Number of bHLH TF in each subfamily of chrysanthemum and *Arabidopsis.*

Subgroup	Chrysanthemum	*Arabidopsis*	Rate (Chrysanthemum/*Arabidopsis*)
Ia	3	10	0.30
Ib	0	10	0.00
II	2	4	0.50
IIIa+c	3	5	0.60
IIIb	1	4	0.25
IIIe+d+f	5	12	0.42
IVa	8	4	2.00
IVb+c	4	6	0.67
IVd	4	1	4.00
Va	0	3	0.00
Vb	6	5	1.20
VIIa(1)	0	5	0.00
VIIa(2)	2	8	0.25
VIIa(3)+b	0	5	0.00
VIIIa	3	3	1.00
VIIIb	2	6	0.33
VIIIc	0	6	0.00
IX	5	5	1.00
X	4	5	0.80
XI	2	5	0.40
XII	10	17	0.59
XIII	2	3	0.67
XIV	0	5	0.00
XV	0	3	0.00
Orphans	5	16	0.31
Total	71	156	0.46

Table S3 Proportion of conserved amino acids at each point of CmbHLH protein.

Amino acid location	Conserved amino acids >50%	Ratio (%)
5	His，H	55
8	Ala，A	59
9	Glu，E	77
10	Arg，R	68
12	Arg，R	77
13	Arg，R	92
14	Glu，E	52
23	Leu，L	83
26	Leu，L	61
27	Val，V	51
28	Pro，P	76
35	Lys，K	56
37	Asp，D	65
38	Lys，K	59
39	Ala，A	79
40	Ser，S	52
42	Leu，L	82
45	Ala，A	56
46	Ile，I	63
48	Tyr，Y	70
49	Ile，I	54
50	Lys，K	52
52	Leu，L	92
56	Val，V	55
59	Leu，L	75

Table S4 Selection criteria for differential genes.

Gene ID (name)	Cm_A3 vs Cm_CK0		Cm_A5 vs Cm_CK0	
	log2FC	Padj	log2FC	Padj
c60363_g1(*CmbHLH16*)	3.9	8.29E-12	3.7	4.40E-16
c61229_g1(*CmbHLH18*)	2.4	0.00023616	1.6	0.0050347
c93607_g1(*CmbHLH28*)	3.5	4.53E-19	2.7	2.4474E-23
c93607_g2(*CmbHLH30*)	4.1	3.06E-14	3.7	1.1979E-20
c77068_g1(*CmbHLH60*)	3.8	2.27E-43	2.7	1.3631E-21

Note: Cm_A3 vs Cm_CK0 represents the ratio of the expression of this gene at day 3 of inoculation to that at day 0 of inoculation by *Alternaria* sp.; Cm_A5 vs Cm_CK0 represents the ratio of the expression of this gene at day 5 of inoculation to that at day 0 of inoculation by *Alternaria* sp. The screening criterion for differential genes is the default value of log2FC is greater than 1 and Padj less than or equal to 0.05.

Table S5 Relative activity of leaf cells of WT and transgenic chrysanthemum.

Lines	A_{600nm}	Relative cell activity/ %
WT	1.237±0.178[a]	54.93[a]
35S::*CmbHLH18–5–1*	0.525±0.067[b]	80.86[b]
35S::*CmbHLH18–32–9*	0.370±0.040[bc]	86.53[bc]
35S::*CmbHLH18–14–4*	0.276±0.008[c]	89.95[c]

Note: The different letters signified significant differences at $p < 0.05$ by one-way ANOVA.

Table S6 Primers used in this study.

Primer codes	Forword primer (5′-3′)	Reverse primer (5′-3′)	Purpose
qCmbHLH16	CTTCAAATGACACCAAC GAGGAT	GAGGCGGGCGGAATACA	For RT-qPCR in Chrysanthemum.
qCmbHLH18	GGCTGCAATTCAAAGGA TGTTC	GTCATGCAGAAGTCGTCCG CC	
qCmbHLH28	TTCTGAGATGGCGGTAG	CGTGGCACATCCTCTTT	
qCmbHLH30	TGTAGTTGGCATCACCG	CAAATCCACCAGTATCACA T	

qCmbHLH60	CTTCTGATGGCGAGTTT	GGTTTGTCCACCTATGTTAG	
CiUBI	AGCTGAGCAGACTCCCGATG	AGGCGAATCATCAGTACCAAGT	For RT-qPCR.
CmbHLH18	GGTGTCCAAATCATCCCAGAA	GGATCGGACAAGCAACCGTA	For isolation and transformation of *CmbHLH18* into vector.
Super1300	GCCATTTCGCCTTTTCAG	TGATAATCATCGCAAGACCG	
CmbHLH18-V	CTAGTCTAGAATGGGAAAGGTATCGAACACGATT	CGGGGTACCAAGAACTTGTTGCAGATTCTTCGA	
CmbHLH18-At	TGAAGTGCAAATGTCAGGGAA	TACTTCCTACTCCCACCAA	For identification of transgenic *Arabidopsis.*
AtActin	CTAAGCTCTCAAGATCAAAGGC	AACATTGCAAAGAGTTTCAAGG	For RT-qPCR in *Arabidopsis.*
AtSOD	TGGAACTGCCACCTTCACAAT	GATGCCGCAAGCAACACG	
AtCAT	ACGCCGATTTGCGAGATACA	CAGACAGGAGCACCCGAGTTT	
AtPAL	AAGCCTGAGTTCACCGATCATC	TACGAGCTTCCGTCGAGGAT	
AtPOD	TGCGAGAGACGGTATTGTCA	TCTCCCAAGTAGCTCCCTCT	
AtCHT	CGGAAACTGGAAACCTACA	CAGTTGAAGGGTTGAAAGG	
AtGLU	GCAATGCAGAACATCGAGAA	TCATCCCTGAACCTTCCTTG	