

NAC047/052/104 synergistically regulate the dark-induced leaf senescence in non-heading Chinese cabbage

Bing Yang^{1,2,†}, **Dingyu Zhang^{2,†}**, Zitong Meng^{1,2}, Yijiang Yin², Xiao Yang², Mengqin Cao^{1,2}, Ruixin Li², Yishan Song^{1,*}, and Hongfang Zhu^{2,*}

¹College of Food Science and Technology, Shanghai Ocean University, Shanghai 201306, China

²Shanghai Key Laboratory of Protected Horticultural Technology, Horticultural Research Institute, Shanghai Academy of Agricultural Sciences, Shanghai, 201403, China

*Corresponding author: yssong@shou.edu.cn (Yishan Song);
zhuhongfang@saas.sh.cn (Hongfang Zhu);

[†] These authors contributed equally to this work.

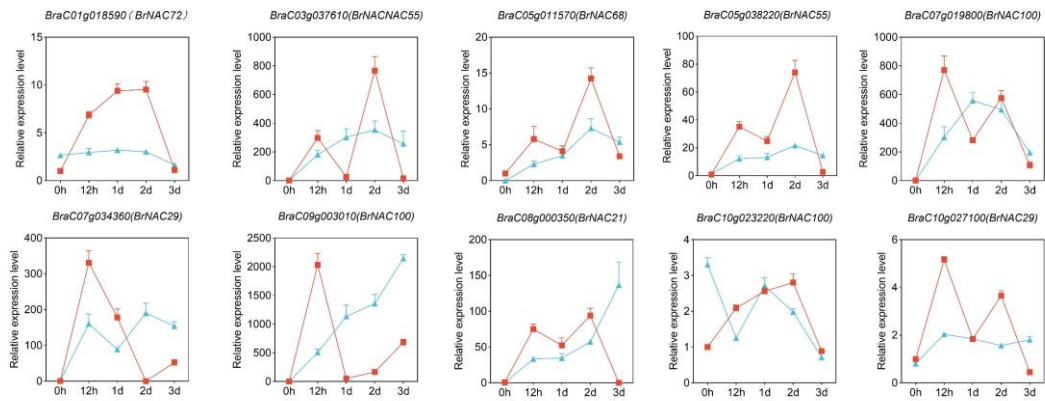


Figure S1 Transcriptional levels of NAC family genes

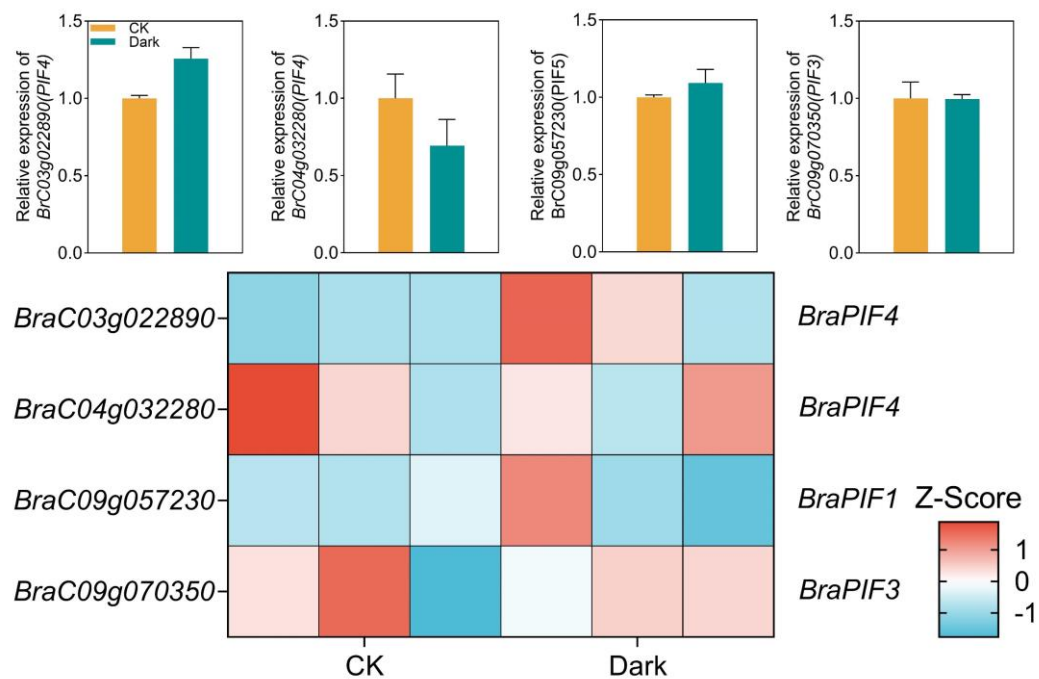


Figure S2 Relative expression levels of PIF3/4/5 genes in the dark

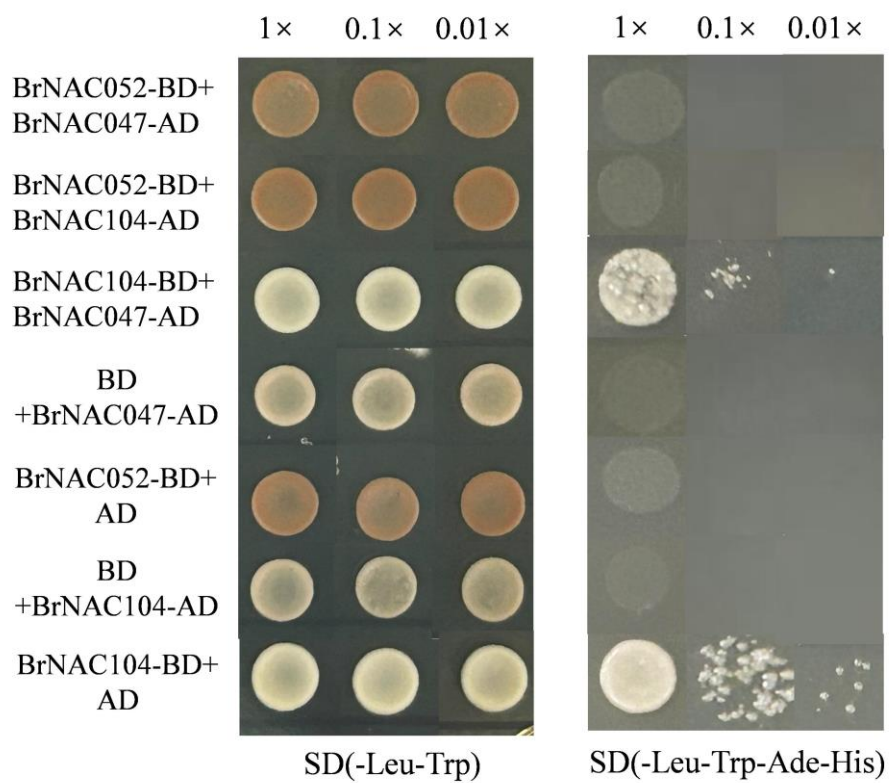


Figure S3 Proteins interacting with BrNAC047, BrNAC052, and BrNAC104 in yeast

<i>BraC07g019800</i>	<i>NAC100</i>	TCCGACCAAGAAACCGAAGA	TAAACCGGTGGAGTCAGGAC
<i>BraC07g034360</i>	<i>NAC29</i>	GCCCTGTCTCGATCATACCA	AATAACCGGAAACAGCTGCC
<i>BraC08g000350</i>	<i>NAC21</i>	AGAAAGGGCAAGCTTGTTGG	GGAAGAGAAGCGGAGACTGT
<i>BraC09g003010</i>	<i>NAC100</i>	CCAATTGGGTCATGCACGAA	TTGATCCCTGAACCGAGCTT
<i>BraC10g023220</i>	<i>NAC100</i>	ATCCTGCTACGACAACCCAA	AAGTCGTGTTGTTCGGGTTG
<i>BraC10g027100</i>	<i>NAC29</i>	GCACAAGGGAAGCCAAGTAC	CGTGCATGATCCAATCGGTT
