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## Supplementary Material

### **NAC transcription factor involves in regulating bacterial wilt resistance in potato**

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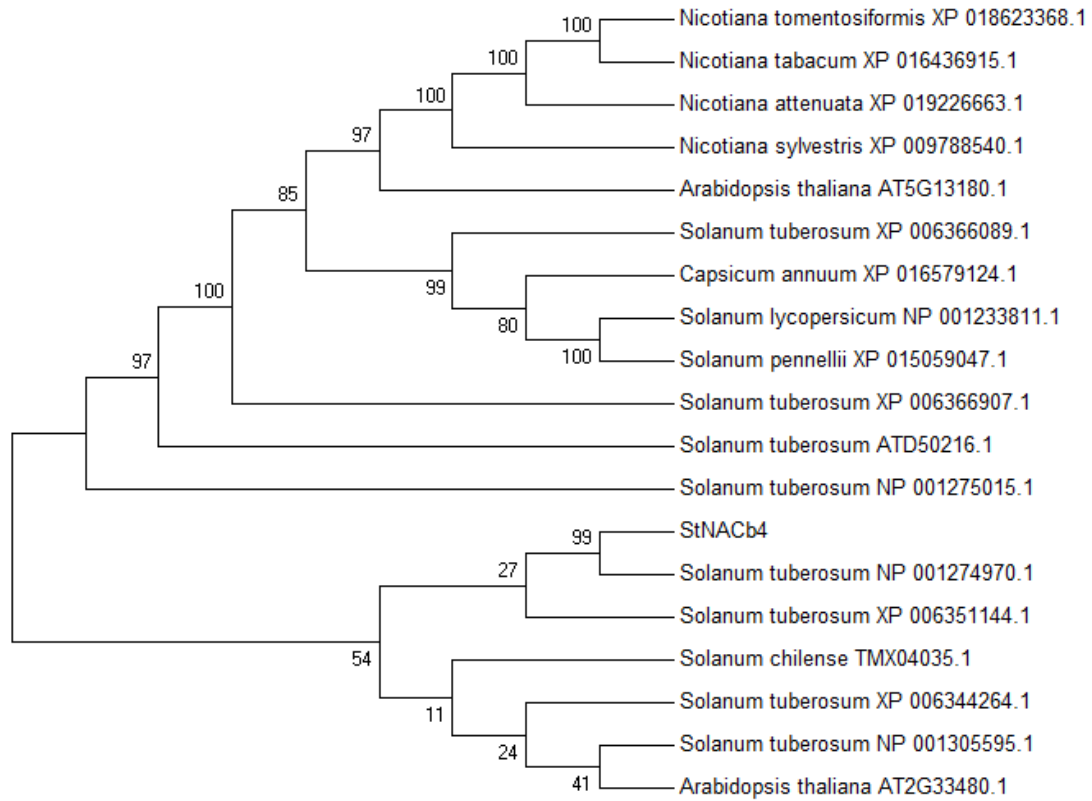
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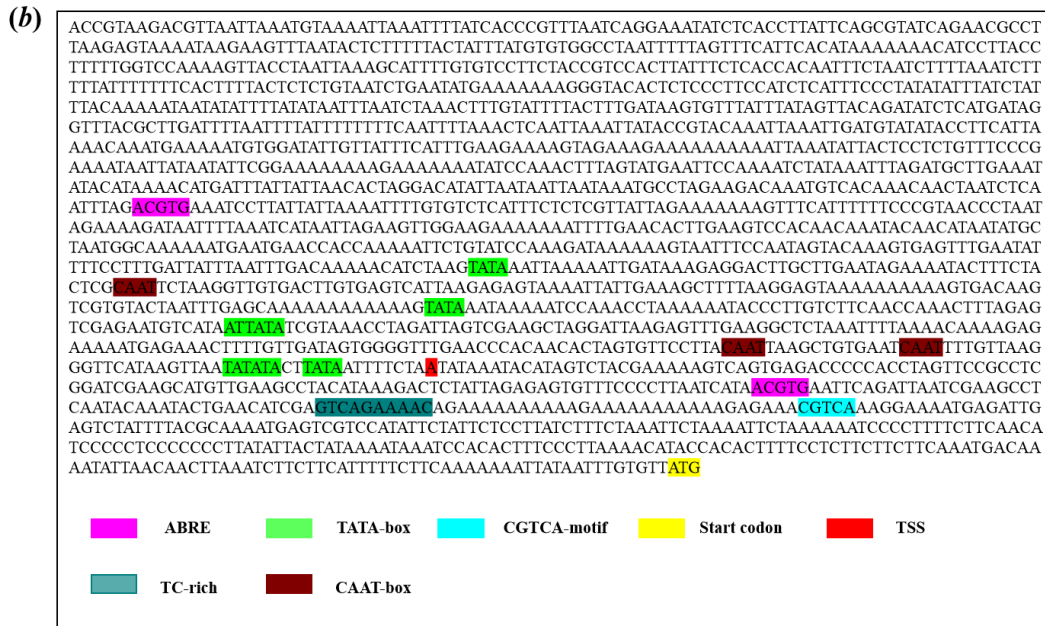
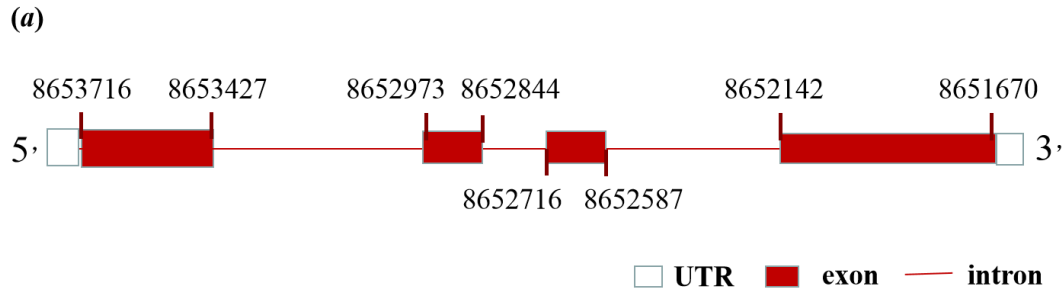
      10      20      30      40      50      60
....|....|....|....|....|....|....|....|....|....|....|....|
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                                     M K A
CCGAAATCAGCAATTGGAGTTACCGGCGGGATTCAGATTCATCCGACAGACGACGAAT 120
T G N Q Q L E L P A G F R F H P T D D E
TGGTGCAGCATTATCTCTGCAGGAAATGTCTTCTCTTTTCCCTTTGCCAGCATCAATTATCC 180
L V Q H Y L C R K C L L F P L P A S I I
CTGAAGTTGAAGTTTACAAATCTGATCCTTGGGATTTGCCAGGTGATATGGAGCAAGAAA 240
P E V E V Y K S D P W D L P G D M E Q E
AGTATTTTTTTTAGCACTAAGGAAGTGAAGTATCCAAATGGAAACGGGTCAAATAGAGCAA 300
K Y F F S T K E V K Y P N G N G S N R A
CAAATTCAGGATATTGGAAGGCAACTGGAATTGACAAGCAAATCGTATTAAGGGGCCAAC 360
T N S G Y W K A T G I D K Q I V L R G Q
AAGTAGGATTGAAGAAAACACTTGTCTTCTATAGAGGAAAATCTCCACATGGTTGTAGGA 420
Q V G L K K T L V F Y R G K S P H G C R
CCAATTGGATTATGCACGAATATCGACTTTCCAATCTCGAATCTAACCACCACCCAATCC 480
T N W I M H E Y R L S N L E S N H H P I
AGGAAAATTGGGTTATCTGTAGAATTTTCTTGAAAAAAGAGGCAATACTAAAAATAAGG 540
Q G N W V I C R I F L K K R G N T K N K
AGGAAAATATGACAACACATGATGAGGTTAGAAACAGAGAAGTTGGTAACGACTCGCCCC 600
E E N M T T H D E V R N R E V G N D S P
TTGTTTCAGTCAAACGAGTCCCTCGATATTCTGAGACATTGGCTTTTCGCCAACAGTGAAG 660
L V S V K T S P R Y S E T L A F A N S E
TGAAGAAGAAGACATCGATGATATTTTACGATTTTATGGGAGGGATAATTCAAATGGAGT 720
V K K K T S M I F Y D F M G G I I Q M E
TGCAGCTTCATCGTCAAGTAGTGGAATCACTGATTTGACAACACTACTAATGAAGAATCTGA 780
L Q L H R Q V V E S L I *
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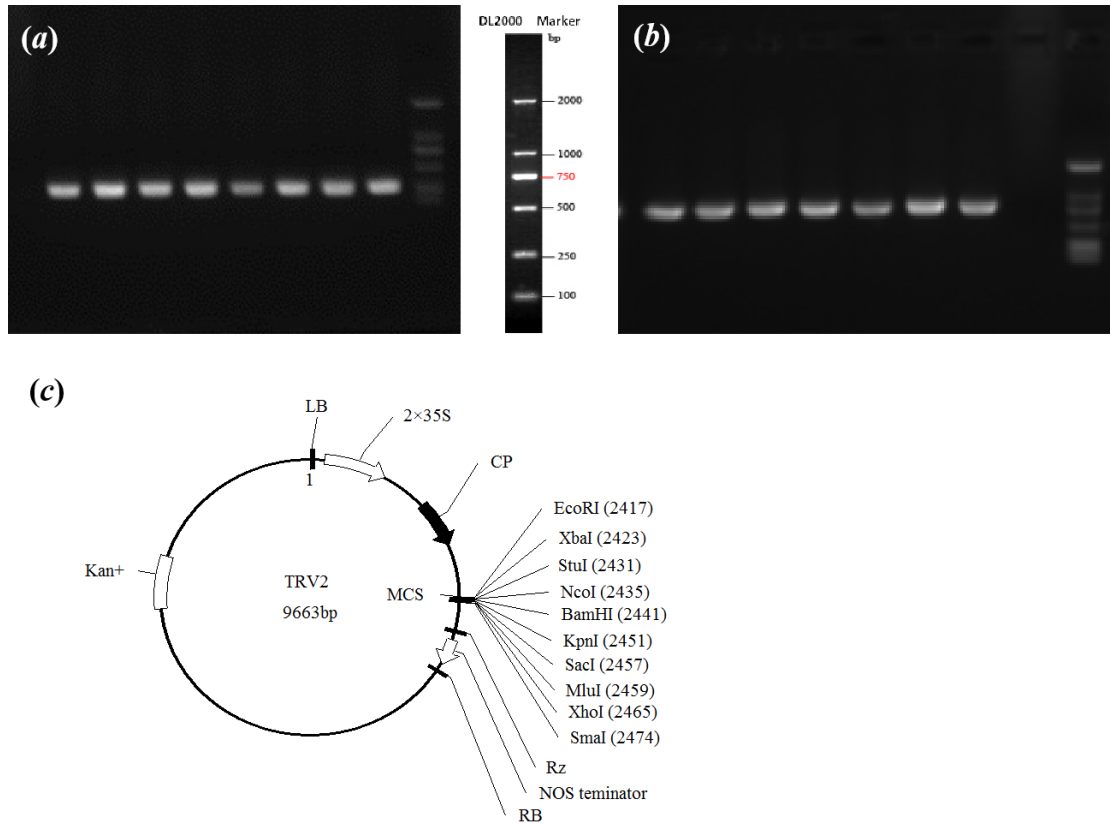
**Fig. S1.** The nucleic acid sequence and the encoded amino acid sequence of *StNACb4*. Note: Black underlined for the conservative domain NAM superfamily (12-133 aa).



**Fig. S2.** Evolutionary relationships of taxa. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 6.19541166 was shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) were shown next to the branches. The evolutionary distances were computed using the p-distance method and were in the units of the number of amino acid differences per site. The analysis involved 19 amino acid sequences. All positions with less than 50% site coverage were eliminated. That was, fewer than 50% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 268 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.



**Fig. S3.** Gene structure of *StNACb4* and cis-elements in the promoter sequence. (a) Gene structure of *StNACb4*; (b) cis-elements in the promoter sequence.



**Fig. S4.** Vector construction of VIGS-*NbNACb4* and VOX-*StNACb4*. (a) VIGS-*NbNACb4* colony PCR verification electrophoresis map, DL2000 Marker was used and the interference fragment size of *NbNACb4* gene was 249 bp; (b) VOX-*StNACb4* colony PCR verification electrophoresis map, DL2000 Marker was selected and *StNACb4* gene CDS fragment size was 708 bp; (c) pTRV2 vector map.

>*StPR10* promoter

TAATAAGATAATAAATAAAACAGGGGATAAAAAGTATTTTATTATAATTTATATATTTAAAGGGGC  
 ATTAAATGTGTATATAGTTCTACAAGCTTAAAAATTTAACGTTTTGATATGTAGTATAATATTTTAA  
 ATAAGGATTGGTTGATATAGTTTATATTATAATAAATATGTATTATATTATGAGGGAGATAGGTGAA  
 AATAAACAC**CACGACGCA**AAAAGTTTTAGTTAAATGATTAAAAATTTCAATTTAATCTATTGT  
 AATTAACCTATAAAATTTGTTTTTAAATCTATAAGTTTTTGATAAGTTTTTCATGATATTTAACGT  
 TAAAAAATGTATAGTTATATTACTTTTTTATGTAGTATTTTATAATCAGTTTTAAGAATAGTAAAG  
 TGAGATCTTTTCTTTTAGTACTATTGGTTTTAACCTGCCTTTCATAATTTAAAA**CGTA**TATTTCAA  
 TTAATAATTTAAACCCAATATAAATTTGAAACATCTTTAATGAAAAGAGCTTTACCAAAAAAGG  
 TTTCGT**CGTA**CTAGCTAAATTTCAAATTAGTTTATTTAATAACTATATTGATATTTGTTATAACT  
 TATATTTATATAIATAAATATATTTATTTTTGTGGATAGTACTATAAATTTTCGAGTTTGAGCACTTTA  
 ATCTATTAAACTTAAAGTTCGTTAATCATAACTAACTATTATATAGTCCTTTACTTGCAAGAAAA  
 CATGAAAGTCTGAATTATCTTGATAGTTATTTCCCAACAACATCTAACCATTTCATGAGGAAGTAGA  
 AATTAGTTGTCAACCTAACTCAATGAGTCTTATGTTTTAGTGGATACAATCTTATGGAAAATA  
 GGATTACATTCTGAAAAGACATGCTTAAACATAAATTAGCTTAAGATTATTCTTCTGTGACCTT  
 T**CGTG**ATGGTGCAACCATCCAAGGATGCCAGGTTAGTTGAATTATAGCACAGTCGTTCCGGAAT  
 AAAAAATAGCTGGTATTAC**CGTA**TTTTAAGAGTGT**TACG**GTGTTGATTGTTTTAATTAATAGTTTCT  
 ATCACTGTGTTGACATCTTTTTIATTTTTATTTTTTACCTGTGTTAACAGTTGTAA**CGTG**ACGAAA  
 CTTACAACCTTAAATTATGATTTTCGATTCCAACGAGTACTGTATCTTAAGATTTTAAAGTGGTTTAA  
 AAAGTTGATGAATATGTGGAAAATCTAATTCTAAATTGCTAAGTAGAATTAATTTTAAATATTT  
 AGTAATTTTTTATTAATAAAAAAAACAACTATATAAGCAGAAAAACCTAATACTCATTATCCTA  
 TTTAGGTTTTCTAACTTGTCAAAAATGAATATGACTTATGCTCATTAAACATTTGGTGAACAGGT  
 TTCTAAATATAAATATACTGAAAAGTCCATCCCTGTTTTGATTTTATTATTAGTTGGTTTAGAGTG  
 AGGTAAAAACAGGATATTTATGGTAGATTTTAAAAGTAATATAGTGTGTGTGA **ATG**

**Fig. S5.** Promoter sequence of *StPR10*. NAC recognition sequence (NACRS) or NAC binding sequences (NACBS) marked with red and borders were found in the promoter sequence of the *StPR10*. Translation Initiation site (ATG) was shown in a yellow box.

**Table S1. Primers used in this study**

Gene	Forward primer	Reverse primer	Function
<i>StNACb4</i>	F:ATGAAAGCAACCGGAAATCA	R:AATCAGTGATTCCACTACTTGA	Gene cloning of <i>StNACb4</i>
<i>StNACb4</i>	StNACb4-F: CAGGATATTGGAAGGCAACTGG	StNACb4-R: GATTGGGTGGTGGTTAGATTCCG	RT-qPCR in potato
<i>Actin</i>	Actin-F: TATAACGAGCTTCGTGTTGCAC	Actin-R: ACTGGCATAACGCGAAAGAACA	
<i>StPR10</i>	StPR10-F: AGACAACAACCTGAGTATCACAC	StPR10-R: GGTACGCTTCGATGGCCTTG	
<i>StNACb4</i>	Voxnac-F: <u>ATACGTCCTAATCCCGAGAAGGT</u> TAATTTTGTG (introduce homologous recombination)	Voxnac-R: <u>CACGTCCTTAAATCCTTAATTTTTTCTTC</u> TAAAAGTAG (introduce homologous recombination)	<i>StNACb4</i> overexpression transgenic vector
pTRV2	EXTRV-F: GGATTTAAGGACGTGAACTC	EXTRV-R: GGGATTAGGACGTATCGGACC	
<i>NbNACb4</i>	Xbanac-F: <b>CGGGATCCTGATCCTTGGGATTT</b> GCCAG (introduce XbaI enzyme site)	Bamnac-R: <b>GCTCTAGACGATATTCGTGCATAATCC</b> (introduce BamHI enzyme site)	VIGS of <i>NbNACb4</i>