

Title: NHX1 participates in tobacco disease defense against *Phytophthora parasitica* var. *nicotianae* by affecting vacuolar pH and priming the anti-oxidative system

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Supplementary Figure S1. Screening distinctive sequence of *NbNHX1* for gene silencing. A, EST information of *NbNHX3* cloned from *N. benthamiana*. The yellow mark indicates the same sequence between unigene of SGN-U521516 and the EST of *NbNHX3*; red mark presents the same sequence between unigene of SGN-U518331 and the EST of *NbNHX3*. B-C, The sequence alignment among *NbNHX1* (Nb1), unigene *NbNHX2* (Nb2, ID: SGN-U515339), and unigene *NbNHX3* (Nb3, ID: SGN-U518331). The underline sequence indicates the distinctive 263 bp sequence from *NbNHX1* used for gene silencing.

Supplementary Figure S2. Virus inducing gene silencing and ectopic expression in *N. benthamiana*. A, TRV inducing gene silencing in *N. benthamiana*. Diagrams illustrate the pTRV2 derivative clone vectors used in this study. B, Phenotypes of *N. benthamiana* at 28 days post inoculation with TRV carrying a conserved fragment of a phytoene desaturase gene. C, Expression of *NbNHX1* in *NbNHX1* silenced tobaccos (N1-N30). D, Wilt spot area in *NbNHX1* silenced tobaccos (N1-N30). E, PEBV mediating ectopic gene expression in *N. benthamiana*. Diagrams illustrate the pCAPE2 derivative clone vectors used in this study. F, Phenotypes of *N. benthamiana* at 28 days post inoculation with PEBV carrying a conserved fragment of a phytoene desaturase gene. G, Expression of *NHX1* in *SeNHX1* transgenic tobaccos (S1-S30) and *AtNHX1* transgenic tobaccos (A1-A30). H, Wilt spot area in *SeNHX1* transgenic tobaccos (S1-S30) and *AtNHX1* transgenic tobaccos (A1-A30).

Supplementary Figure S3. *In situ* calibration curve and pH quantification test. A, The calibration curve was performed by plotting the ratio of emission fluorescence (505-550 nm) excited with 458 or 488 nm, against the pH of equilibration buffers. B,

Vacuolar pH quantification under TEST1 (pH 5.1) and TEST (pH 5.4) treatment. Data are means \pm SE ($n = 60$ cells from 6 leaves).

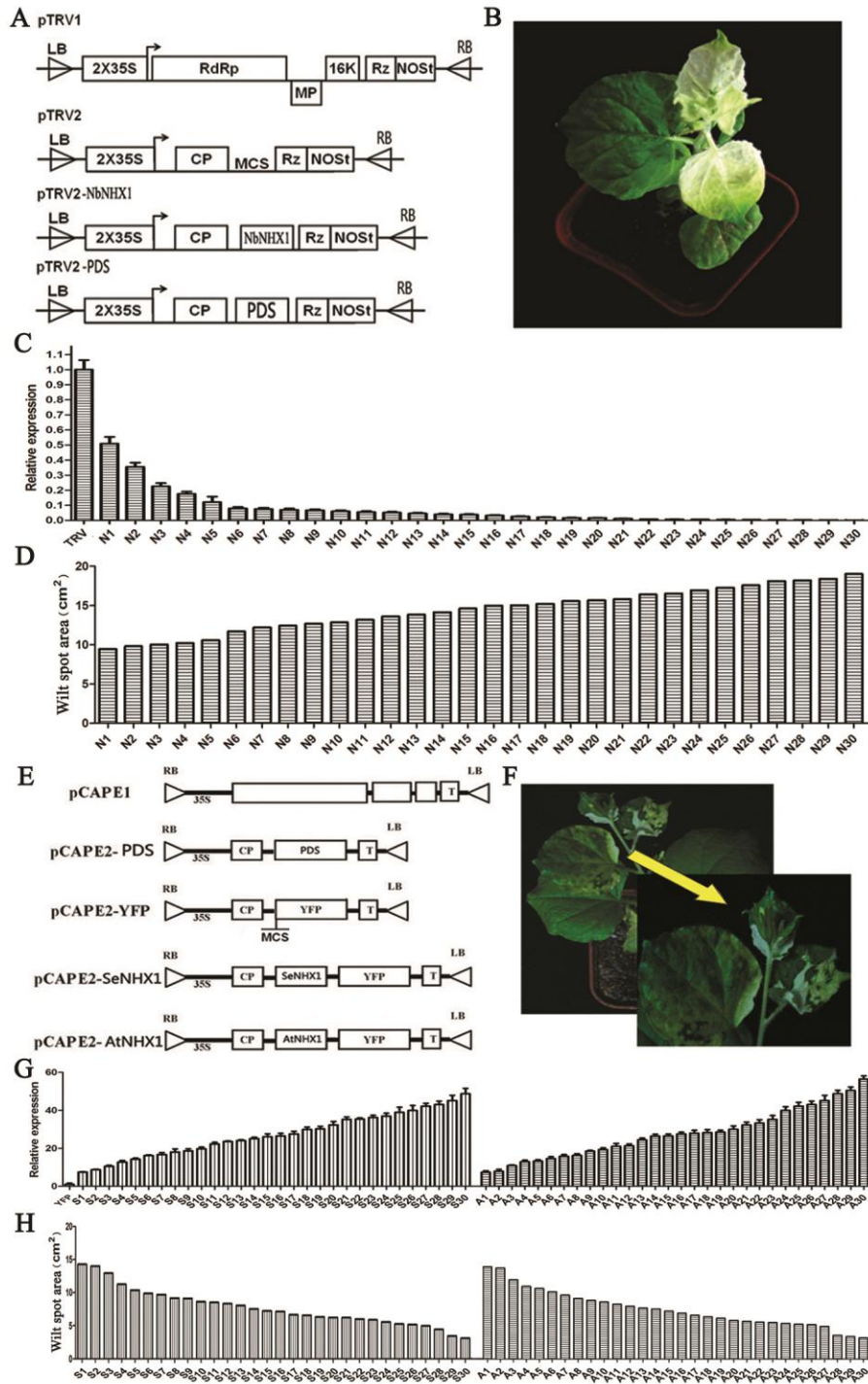
Supplementary Figure S4. The relative expression of *NHX1* in different genotype tobacco. A, The relative expression of *NbNHX1* at 0, 24, 36 and 48 hpi. B, The relationship between relative expression of *NbNHX1* and vacuole H⁺ net flux. C, The relative expression of *NbNHX1* in NS1-NS6. The relative expression of *NHX1* in S31-S36 (D), A31-A36 (E) and NOE1-NOE6 (F). G, The relative expression of *NbNHX1* in 6 Nb-GFP plants. The relative expression was calculated by actual expression of *NHX1* against that in untreated, or TRV plants or GFP plants.

Supplementary Figure S5. Vacuolar H⁺ net fluxes in *NbNHX1* silenced *N. benthamiana* under 0 and 1.5 mM ATP or *PPi* treatment. Dynamic curves of transient H⁺ net fluxes: normal condition plus supply of ATP (A) or *PPi* (B). C-D, Mean of vacuolar H⁺ net fluxes corresponding to (A-B) during the measuring periods. E, The changes of vacuolar H⁺ flux (Δ H⁺ flux) after ATP or *PPi* supply in TRV or TRV-Nb plants. The value obtained from NMT indicates net ion flux; the positive values of H⁺ flux in the figures represent cation efflux or anion influx, and *vice versa*. TRV represents pTRV2 empty vector transformed tobaccos (control plants). TRV-Nb represents pTRV2-NbNHX1 vector transformed tobaccos (*NbNHX1* silenced plants). Data are means \pm SE ($n = 6$ vacuole per *NbNHX1* silenced line, 6 independent *NbNHX1* silenced lines). The asterisks on the bars indicate significant differences from the TRV plants in the same treatment at $P \leq 0.05$.

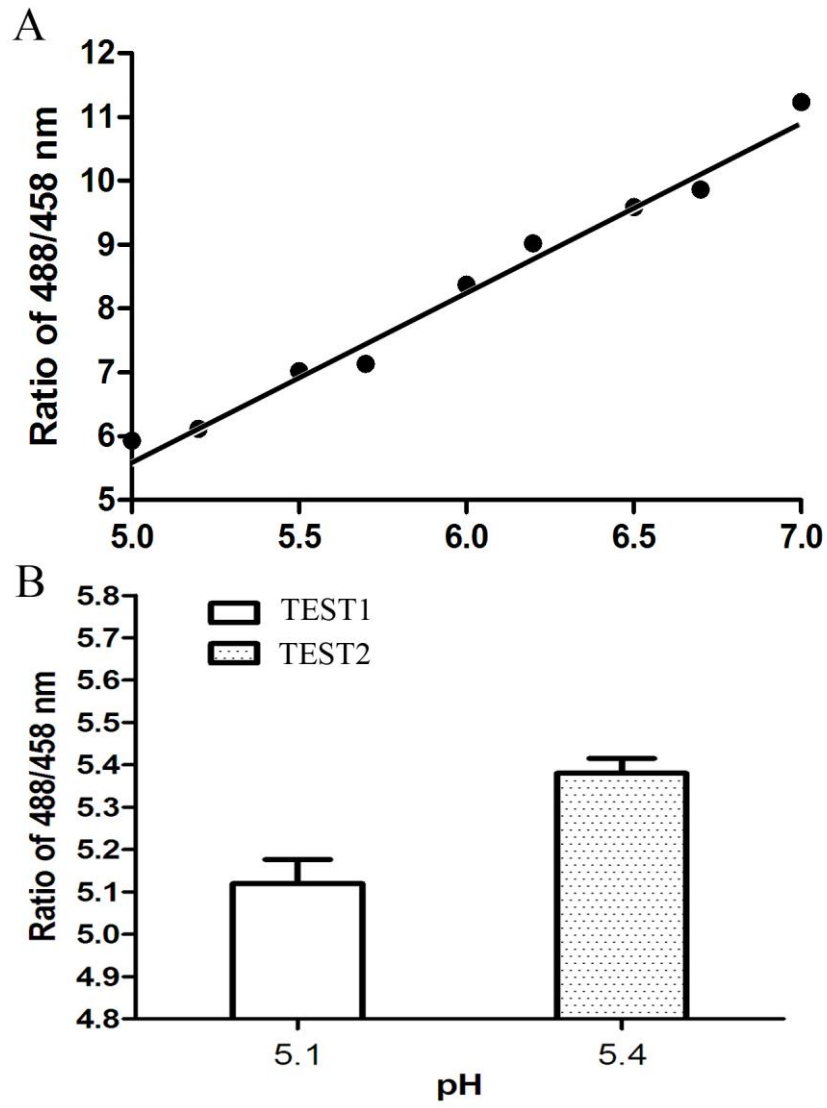
Supplementary Figure S6. Responses of *NHX1* transgenic tobaccos to ES4326. Infection experiments were performed with 6-week-old plants of Se/At-YFP transgenic and YFP plants mediated by PEBV. 30 leaves were collected to examine the growth of the pathogen at 0, 72, and 96 hpi. YFP means pCAPE2-YFP vector transformed tobaccos. Se/At-YFP represents pCAPE2-At/SeNHX1-YFP vector transformed tobaccos. Data are means \pm SE ($n = 30$ leaves from 30 independent transgenic lines). The asterisks on the bars indicate significant differences from the YFP plants in the same treatment at $P \leq 0.05$.

Supplementary Table S1. The primers of ROS responsive genes used in real-time PCR.

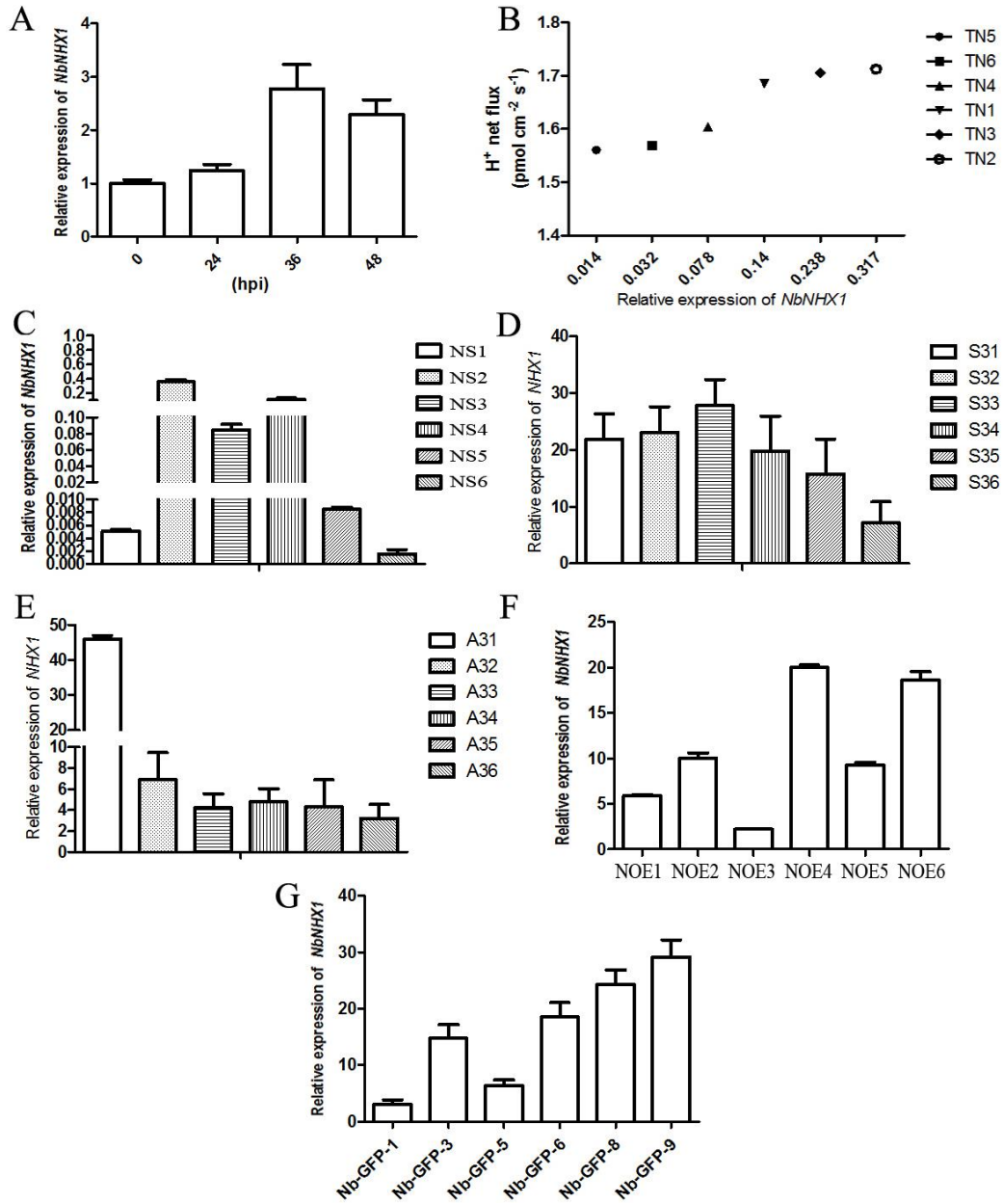
Supplementary Figure S2



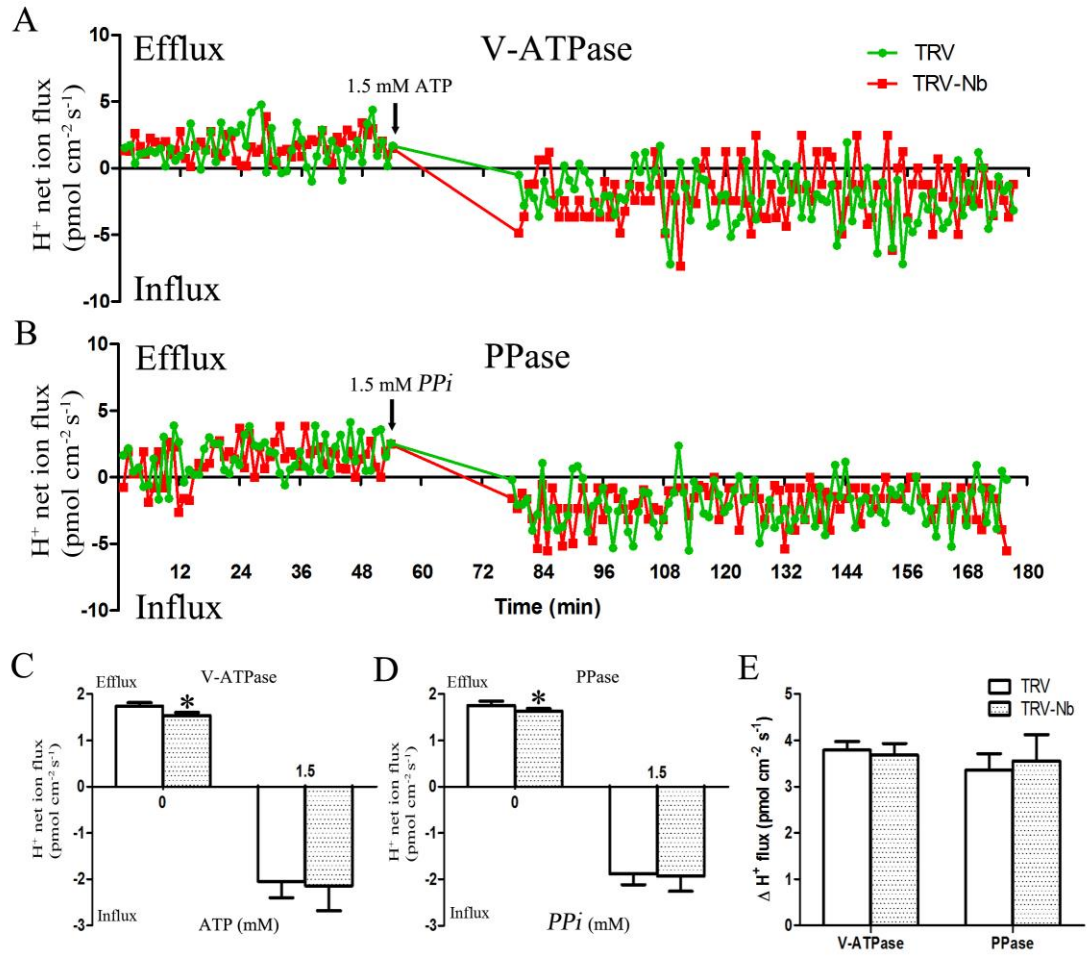
Supplementary Figure S3



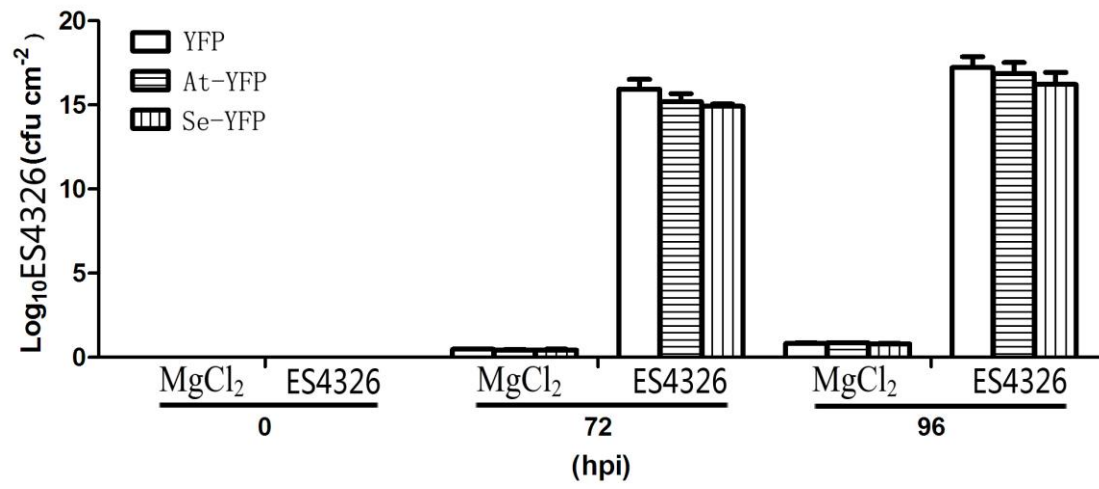
Supplementary Figure S4



Supplementary Figure S5



Supplementary Figure S6



Supplementary Table S1.

Gene name	Unigene No.	Primers
TPX1	SGN-U505985	F 5' GCCGTTGGTGACATCATTCCC 3' R 5' CCTTTAGATTTCAACTCGTCAGC 3'
COX6B	SGN-U511126	F 5' CAGGTTCCCAACAACCAATCAAA 3' R 5' CCCATTCTCCCTCTGCTCGTT 3'
CSD1	SGN-U514519	F 5' GCAGCAGTGAAGGTGTTAGTGGCA 3' R 5' GGATTGTGGACCAGCAAGAGGAAT 3'
CAT1	SGN-U518840	F 5' CATACAAGTACCGTCCGTCAAGTGC 3' R 5' GAAAAACCCCTTGGCACTAGCACCTC 3'
TAPX	SGN-U506407	F 5' TCCCTCAAATGCCTCCAATCCT 3' R 5' GCATTTGCGCGAGGCTAACG 3'
PER21	SGN-U506123	F 5' TTGACAATGAAGCCCAGGTGA 3' R 5' CTCCTCCGCAGATTGATTGG 3'
PER12	SGN-U515270	F 5' CTGCTAGGGACTCTGTTGTCTTGACT 3' R 5' CGACGGAGGACGACTGTGGTATT 3'
NOS	SGN-U518155	F 5' TAAGACAACACGCCTTGGATT 3' R 5' GCCTGCCTTACTATTTGCCTC 3'
APX6	SGN-U521022	F 5' GGGTTTGGGAATCCAGTTGTC 3' R 5' TGCAACAAGTTTGGTATAGGCATT 3'
PRXR1	SGN-U509102	F 5' TTTGCGGAGGACAATTCTGGC 3' R 5' CCTGGACTCCCTTTCAACAG 3'

APX3	SGN-U515717	F 5' GGAAGGACGGTTGCCCGATGCT 3'
		R 5' TGTCTGTGGGAAGTTTCAGTAGGC 3'
FSD2	SGN-U508368	F 5' CTGGTTCTGGCACAATAACGGCT 3'
		R 5' TCCTCCTCCGTTGGGCTTCA 3'
FSD1	SGN-U508369	F 5' TGGCTCGCATACAAACCTGAA 3'
		R 5' CCACGACACGAGCTTCTCCATAA 3'
MSD1	SGN-U508400	F 5' GTGAGCAGACGGACCTTAGCAACA 3'
		R 5' CGTGACCTCCGCCGTTGAATT 3'
GST8	SGN-U513459	F 5' GCAGTATGTATGGGATGAGGGC 3'
		R 5' TTCACTGCATATTCATGTACGGTATT 3'
GST21	SGN-U513460	F 5' GGTTCCTGGGCTGATTACACTGAC 3'
		R 5' CCAAAGTAAGGTTTGTCTCCAAT 3'
GST29	SGN-U511196	F 5' CAGCCAAGGGCAATGTCCAAGTA 3'
		R 5' GTTCTGGTCCATCTATTCTCCCTTCT 3'
PR1	SGN-U512904	F 5' TCAACTCAACGCCGCTGGTG 3'
		R 5' GAATCAAAGGGCTGTTGCTCTTCA 3'
PR4	SGN-U508784	F 5' TTTCTGTGATGCTGCTGGACC 3'
		R 5' GCCTTGCTGATAGCCCACTCC 3'
Gns1	SGN-U515120	F 5' GAAAGCCTGGACCTATTGAAACC 3'
		R 5' GCAGTAGCATTAGTTTCAACCGAAC 3'
