

**Supplementary Figure S4.** *Fa*NPR3.2 nucleotide coding sequence (A) and its corresponding amino acid sequence (B). (A) The start codon (ATG) and the stop codon (TGA) are in italics, underlaid and colored in blue; primers for cDNA cloning are red-dark green (forward) and red-light green (reverse); attB sequences are in red; the position of primers for gene expression analyses are underlaid. (B) amino acid residues corresponding to NPR conserved domains are labelled in different colors as follow, BTB superfamily domain, in green; DUF3420 domain, in pink; superfamily “NPR1-like-C”, in red; ANK superfamily domain is boxed in blue. The putative hinge region (FENRV) in the SA- binding core is highlighted in yellow box with larger, bolder font size.

(A)

GGGGACAAGTTTGTACAAAAAGCAGGCTTAACAATGGATCATATGAATGACCTTCGTCATCTTTGAGCTTTGC  
CTCTTCTTATGTATCAAATGGATCAAGTGGTAACCATGTGTCTGCCTCGGCCAATTCTCAAAGTACGGAGCATTGGA  
GTCTAAGCAGACTCAGTGATAACCTGGAGAGGCTGTTGCTTGATTCTCAATATGACTATAGTGATGCGGACATAGT  
TGTTGAGGGTGTCCCAGTTGGTGTCAATCGGTGTGTATTGGCTGCCCCGAGCCAGTTTTTTCATGAGCATTTTAA  
GAAGGGAAATGATGATTCAAGAAGGAAGGCAAACCACAGTATATGATGTCTGAATTGGTTCCTTATGGTGGAG  
TTGGCTGTGAAGCATTCAAGGTAGTCTTGAAGTATTTGTATACTGGAAAACTTAAGCCACCACCTCCTGAAGTATC  
AACTGTATCAACATGTGTTGATGATGGTTGTGCACATGATTCATGTGGACCTGCAATTAATTACGCTGTGGAATTGT  
TGTATGCTGCTGCCACTTTCCAGATGAAGGAACTTGTCAAGTTGTGCAGCGCCGTCTTACCAACTTTGTCGAGA  
AAGCTCTTGTGAAGATGTGATCCCAATTCTGTAGCCTCTTCCACTGCAAACAGAGTCAGCTGTTTTACACTG  
CATCCAGAGGGTAGAAAGGTCAGATCTTGACAATGTGGTTCTAGAGAAAGAGCTTCCTCATGAAGTTTTATTAA  
TATCAAATCACTCCGTCTAGAATATCAGAAAATGGCTGATTCAATTATGGTGGAAATGGAACCGGTGGAGGATAAG  
AGGCTTAAAAGCATAAGAAATATCCACATGGCATTAGATACTGATGATGTTGAACTGGTCACTCGTCTTCTAGATG  
AGTCTGGTTCTAGTACATTAGATGATGCTTGTGCTCTCCACTATGCTGTTGCATACTGTGATCCGAAGATTGTTAAG  
GAAGTTCTTGGTCTACGTCTGGGCAATACAAACCTTCGGAATGCCCCGAGGACATACTGTACTTCATGTGGCTGCA  
AGGCGTAAGGACCCAGCAGTCCTAGTTTCTCTTCTGAACAGTGGAGCCTCTGCCTTAGAAATTACATCAGATGGT  
CAAAGTCTGTTGCAATTTGCCGGAGTTGACTAGACCAAAGGATTATTATGAGAACACAAAGCAGGGAGAGGT  
GTCTAACAAAGATCGAATATGCATAGATCTTCTAGAGAGAGAGATGCAAAGAAATTCTATGGCTGTGAACATGTCA  
AACACATCATATGTGATGGCCGATGATTTGCATGTGAGGCTGGACTATTTTGAAAATAGAGTGGCATTGTCACGGT  
TGTTGTTTCTGCTGAAGCCAAGCTTGCTATGGAAGTGGCAGATCATCCAACAACCGGGCACACTGGCCTACCAT  
CAAAAGGATCTAGTGGGAACCTTACGAGAGGTTGATTGAAATGAAACACCTTCTGTACGATCCAAAAGACTTCAA  
GAAAATTGCAAGCCCTTATGAAAACAGTGGAAATGGGTGACGCTTCTTCTCCTCATTGTTCAAAAGTTCTCGAT  
AAGTTTCTGGATGATGAGATGGATATGGCTGATTATTTCTTGAGAAAGGCACTCCTGAAGAGCAGAAAAACAA  
GAAGATGCGCTTCTTGGAACCTAAAGATGATGTGCAGAAGGCATTTTGCAAGGATGTGGCTGCAAAAACAGGGG  
TCAGTCTTGACAGCCTCATCATCCTCATCGTCTCCAAAGGAGGGGTTAATCGTAAGGTTAGGAAAAGGCCA  
AGCTGAGACCCAGCTTTCTTGACAAAGTGGTCCCC

(B)

MDHIMNDLSSSLFASSYVSNSSGNHVSASANSQSTEHLSSLRLSDNLERLLDSQYDYSADIVVEGVPVGVNRCV  
LAARSQFFHEHFKKGNDDSKKEGKPQYMMSELVPYGGVGCEAFKVVNLNYLTGKLKPPPEVSTVSTCVDDGCAHD  
SCGPAINYAVELLYAAATFQMKELVQVQRRLTNFVEKALVEVPIPVASFHCKQSQLFSHCIQRVERSDLDNVLEKEL  
PHEVFINIKSLRLEYQKMADSIMVEMEPVEDKRLKSIRNIHMALDIDDVELVTRLLDESGSSTLDDACALHYAVAYCD  
PKIVKEVLGLRLGNTNLRNARGHTVLHVAARRKDPVPLVPLNSGASALEITSDGQTAVAICRRLTRPKDYENTKQGE  
VSNKDRIIDLLEREMQRNSMAVNMSNTSYVMADDLHVRLDYFENRVAFARLLFPAEAKLAMEVADHPTTGHTG  
LPSKGSSGNLREVDLNETPSVRSKRLQEKQLQALMKTVMGRRFFPHCSKVLDKFLDDEMDMADYFLEKGTPEEQKN  
KKMRFLLELKDDVQKAFCDVAAKQGSVLTAASSSSSSPKEGVNRKVRKRP