

Supplementary Figure S4. *FaNPR3.2* nucleotide coding sequence (A) and its corresponding amino acid sequence (B). (A) The start codon (ATG) and the stop codon (TGA) are in italics, underlined 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 underlined. (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)

GGGGACAAGTTTGTACAAAAAGCAGGCTTAACAATGGATCATATGAATGACCTTTCGTCATCTTTGAGCTTTGC
CTTTCTTATGTATCAATGGATCAAGTGGTAACCATGTGTCTGCTCGGCCAATTCTCAAAGTACGGAGCATTGGA
GTCTAAGCAGACTCAGTGATAACCTGGAGAGGCTGTTGCTTGATTCTCAATATGACTATAGTGATGCGGACATAGT
TGTTGAGGGTGTCCCAGTTGGTGTCAATCGGTGTGTATTGGCTGCCCGCAGCCAGTTTTTTCATGAGCATTTTAA
GAAGGGAAATGATGATTCCAAGAAGGAAGGCAAACCACAGTATATGATGTCTGAATTGGTTCCTTATGGTGGAG
TTGGCTGTGAAGCATTCAAGGTAGTCTTGAAGTATTGTATACTGGAAAACCTTAAGCCACCACCTCTGAAGTATC
AACTGTATCAACATGTGTTGATGATGGTTGTGCACATGATTCATGTGGACCTGCAATTAATTACGCTGTGGAATTGT
TGATGCTGCTGCCACTTCCAGATGAAGGAAGTGTCAAGTTGTGCAGCGCCGTCTACCAACTTTGTCGAGA
AAGCTCTGTTGAAGATGTGATCCCAATTCTGTAGCCTCTTCCACTGCAAACAGAGTCAGCTGTTTTACACTG
CATCCAGAGGGTAGAAAGGTCAGATCTTGACAATGTGGTTCTAGAGAAAGAGCTTCTCATGAAGTTTTTATTAA
TATCAAATCACTCCGTCTAGAATATCAGAAAATGGCTGATCAATTATGGTGGAAATGGAACCGGTGGAGGATAAG
AGGCTTAAAAGCATAAGAAATATCCACATGGCATTAGATACTGATGATGTTGAACTGGTCACTCGTCTTCTAGATG
AGTCTGGTTCTAGTACATTAGATGATGCTTGTGCTCTCCACTATGCTGTTGCATACTGTGATCCGAAGATTGTTAAG
GAAGTCTTGGTCTACGCTGGGCAATACAAACCTTCGGAATGCCCGAGGACATACTGTACTTCATGTGGCTGCA
AGGCGTAAGGACCCAGCAGTCTAGTTCTCTTCTGAACAGTGGAGCCTCTGCCTTAGAAATTACATCAGATGGT
CAAAGTCTGTTGCAATTTGCCGGAGTTGACTAGACCAAAGGATTATTATGAGAACACAAAGCAGGGAGAGGT
GTCTAACAAAGATCGAATATGCATAGATCTTCTAGAGAGAGAGATGCAAAGAAATTCTATGGCTGTGAACATGTCA
AACACATCATATGTGATGGCCGATGATTTGCATGTGAGGCTGGACTATTTTGAAAATAGAGTGGCATTGTCACGGT
TGTTGTTTCTGCTGAAGCCAAGCTTGCTATGGAAGTGGCAGATCATCCAACAACCGGGCACACTGGCCTACCAT
CAAAGGATCTAGTGGAACTTACGAGAGTTGATTGAAATGAAACACCTTCTGTACGATCCAAAAGACTTCAA
GAAAATTGCAAGCCCTTATGAAAACAGTGGAAATGGGTCGACGCTTCTTCTCATTGTTCAAAGTTCTCGAT
AAGTTTCTGGATGATGAGATGGATATGGCTGATTATTTCTTGAGAAAGGCACTCCTGAAGAGCAGAAAAACAA
GAAGATGCGCTTCTTGGAACTTAAAGATGATGTGCAGAAGGCATTTTGCAGGGATGTGGCTGCAAAAACAGGGG
TCAGTCTTGACAGCCTCATCATCCTCATCGTCTCAAAGGAGGGGTTAATCGTAAGGTTAGGAAAAGGCCA
AGCTGAGACCCAGCTTCTTGTACAAAGTGGTCCCC

(B)

MDHMNDLSSSLSFASSYVSNSSGNHVSASANSQSTEHLSLRLSDNLERLLLDSDYDSDADIVVEGVPVGVNRCV
LAARSQFFHEHFKKGNDDSKKEGKPQYMMSELVPYGGVGCFAFKVVLNLYTGKLPPEVSTVSTCVDDGCAHD
SCGPAINYAVELLYAAATFQMKELVQVVRRLTNFVEKALVEVPIPVASFHCKQSQLFSHCIQRVERSOLDNVLEKEL
PHEVFINIKSLRLEYQKMADSIMVEMEPVEDKRLKSIRNIHMALDIDDVELVTRLLDESGSSTLDDACALHYAVAYCD
PKIVKEVLGLRLGNTNLRNARGHTVLHVAARRKDPVLPVLLNSGASALEITSDGQTAVAICRRLTRPKDYENTKQGE
VSNKDRIIDLLEREMQRNSMAVNMSNTSYVMADDLHVRLDY**FENRV**AFARLLFPAEAKLAMEVADHPPTGHTG
LPSKGSNGNLEVDLNETPSVRSKRLQEKLQALMKTIVEMGRRFFPHCSKVLDKFLDDEMDMADYFLEKGTPEEQKN
KKMRFLLEKDDVQKAFCDVAAKQGSVLTASSSSSSSPKEGVNRKVRKRP