Full title: Petal-specific activity of the promoter of an anthocyanidin synthase gene of tobacco (*Nicotiana tabacum* L.)

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Supplementary Fig. 1 The genomic structure of *NtANS1* and *NtANS2* (a) and complete DNA sequences and the deduced amino acid sequences of the *NtANS1* and *NtANS2* genes (b). a Schematic representation of the structures of tobacco *ANS* genes. The black boxes and numbers represent exons and nucleotide sequence bp lengths of the *ANS* gene, respectively. b The exons are indicated in uppercase and the introns are indicated in lowercase. The start codon (ATG) is underlined and the stop codon (TAG) is indicated with an asterisk.
Supplementary Fig. 2 Multiple alignment of the amino acid sequences of anthocyanidin synthases (ANSs). Identical amino acid residues are marked with an asterisk (*); conserved substitution amino acids are marked with a colon (:); semi-conserved substitution amino acids are marked with a period (.). Accession numbers of ANS from different plants: *Arabidopsis thaliana*, AtANS, AAM13301; *Gerbera hybrida*, GhANS, AAY15743; *Malus sp.*, MdANS, X71360; *Nicotiana tabacum*, NtANS1, AFM52334; *Nicotiana tabacum*, NtANS2, AFM52335; *Oryza sativa*, OsANS, CAA69252; *Petunia hybrida*, PhANS, P51092; *Torenia fournieri*, TfANS, BAB21477. The iron-binding residues (H239, D241, and H295) are indicated with inverted black triangles. Residues involved in the binding of 2OG (Y224, R305, and S307) are highlighted with black dots.
Supplementary Fig. 3 Nucleotide sequence of the \textit{NtANS1} promoter. The putative transcription start site (T) is underlined. Several putative \textit{cis}-element related flower-specific expressions are indicated by different colors. The CArG-box is indicated by a purple box, G-boxes by dark blue boxes, H-boxes by yellow boxes, P-boxes by red boxes, and the TACPyAT motifs by green boxes.

\begin{verbatim}
-914 cccgtcaactcaaga\textcolor{orange}{acctacctata}tttaatatccccacctccaataataaacctcaactaatagcaca\textcolor{red}{aaaagttgcaataaagttgggaga}aagatttt
-814 aaaggcaagagaa\textcolor{green}{atat}taatctcatcagagatagttgtaagtttgcaaatataatgccccctcttttattactctccataaagtttgtatgatggttaaagtttgc
-714 ccaggcatcataatataattg\textcolor{orange}{gtgaa}aatcttacctcacatcagtatgacctgccgc\textcolor{purple}{cagctag}ctagttcaagtttagccacattttt
-614 taaaagtgctacaaaca\textcolor{green}{actttaac}ccctacctg\textcolor{blue}{cctagagagagatg}atcctgcctc\textcolor{blue}{caaaaaagaaga}aaataataagcaacgtaac
-514 aacaacatag\textcolor{green}{ttat}gtttcctctgttcaaat\textcolor{red}{at}taatggaat\textcolor{red}{htag}taaagttgaga\textcolor{green}{ctgtatagccagagatc}\textcolor{green}{aaggggtag}cctgc\textcolor{green}{taaaaaacacaatcagat}
-414 taaggctattatattttttaaaggagtgcga\textcolor{red}{aagaaaaactttaa}atattatcttgaggac\textcolor{red}{ctgcgtagataa}aagaataaacttaaagaag\textcolor{red}{agtata}\textcolor{red}{tagtcc}
-314 tga\textcolor{blue}{aacaaggtatagggaaaatac}atgagctg\textcolor{red}{cagctccacagcaggctggtttgttgcttacataga\textcolor{red}{atctgctc}}\textcolor{red}{caca}cacc\textcolor{red}{acaccattc}
-214 tagttccctggcatcgcagatttg\textcolor{red}{gagag}taa\textcolor{red}{aacta}a\textcolor{red}{acaataaacc\textcolor{red}{aaactt}aacc\textcolor{red}{aaacttaggtaagctag}\textcolor{red}{tacg}\textcolor{red}{tactgctttggttgtaatttata}
-114 caaaacatgc\textcolor{red}{tagatatac}tctcacaag\textcolor{red}{aatc}aagt\textcolor{red}{tacttcttctcctcagcacaac}ct\textcolor{red}{aagacccctcct}cttttgtgccc\textcolor{red}{atcctcataataacccatcacta}
-14 agagcat\textcolor{red}{cacaacta}TAAT\textcolor{red}{AAAGGGGAAAAGA}AAGA\textcolor{red}{AGCAAGAAATAATACAGAG}
\end{verbatim}
Supplementary Fig. 4 Genomic PCR analysis to verify the presence of transgenes in tobacco plants. DNA from non-transgenic wild-type (NT) and transgenic tobacco plants with a 35S promoter (35S-P) and NtANS1 promoter (NtANS1-P) was subjected to amplification reactions using primers specific for the Bar selective marker gene. The NtANS gene provided an internal control for tobacco genomic DNA.