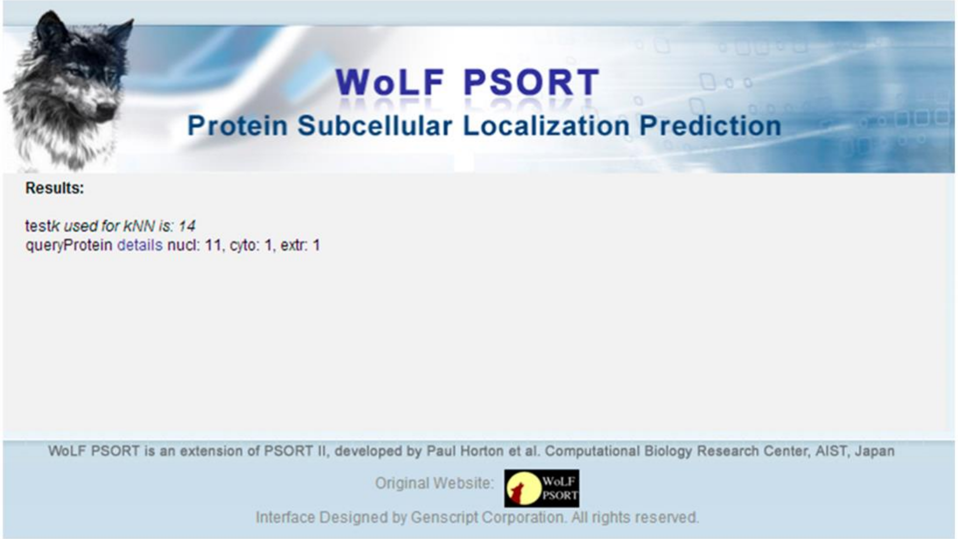
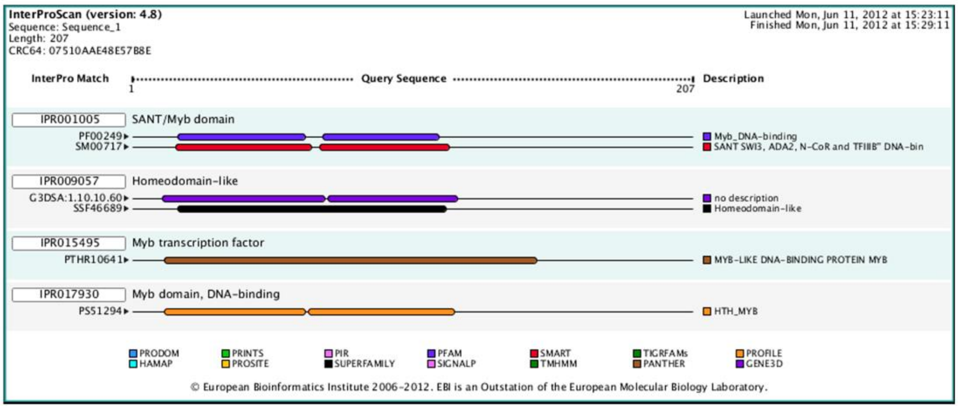


Results:

```
testk used for kNN is: 14
queryProtein details nucl: 11, cyto: 1, extr: 1
```

WoLF PSORT is an extension of PSORT II, developed by Paul Horton et al. Computational Biology Research Center, AIST, Japan

Interface Designed by Genscript Corporation. All rights reserved.



```
InterProScan (version: 4.8)                    Launched Mon, Jun 11, 2012 at 15:23:11
Sequence: Sequence_1                           Finished Mon, Jun 11, 2012 at 15:29:11
Length: 207
CRC64: 07510AAE48E57B8E
```

InterPro Match		Description
IPR001005	SANT/Myb domain	
	PF00249	Myb_DNA-binding
	SM00717	SANT SWI3, ADA2, N-CoR and TFIIIB" DNA-bin
IPR009057	Homeodomain-like	
	G3DSA:1.10.10.60	no description
	SSF46689	Homeodomain-like
IPR015495	Myb transcription factor	
	PTHR10641	MYB-LIKE DNA-BINDING PROTEIN MYB
IPR017930	Myb domain, DNA-binding	
	PS51294	HTH_MYB

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Figure S1: Screenshots corresponding to the results of prediction of domains and functional sites performed with InterProScan database (version 4.8) (www.ebi.ac.uk/Tools/pfa/iprscan/) and prediction of protein localization sites in cells performed with the WoLF PSORT computer program (http://www.genscript.com/psort/wolf_psort.html).

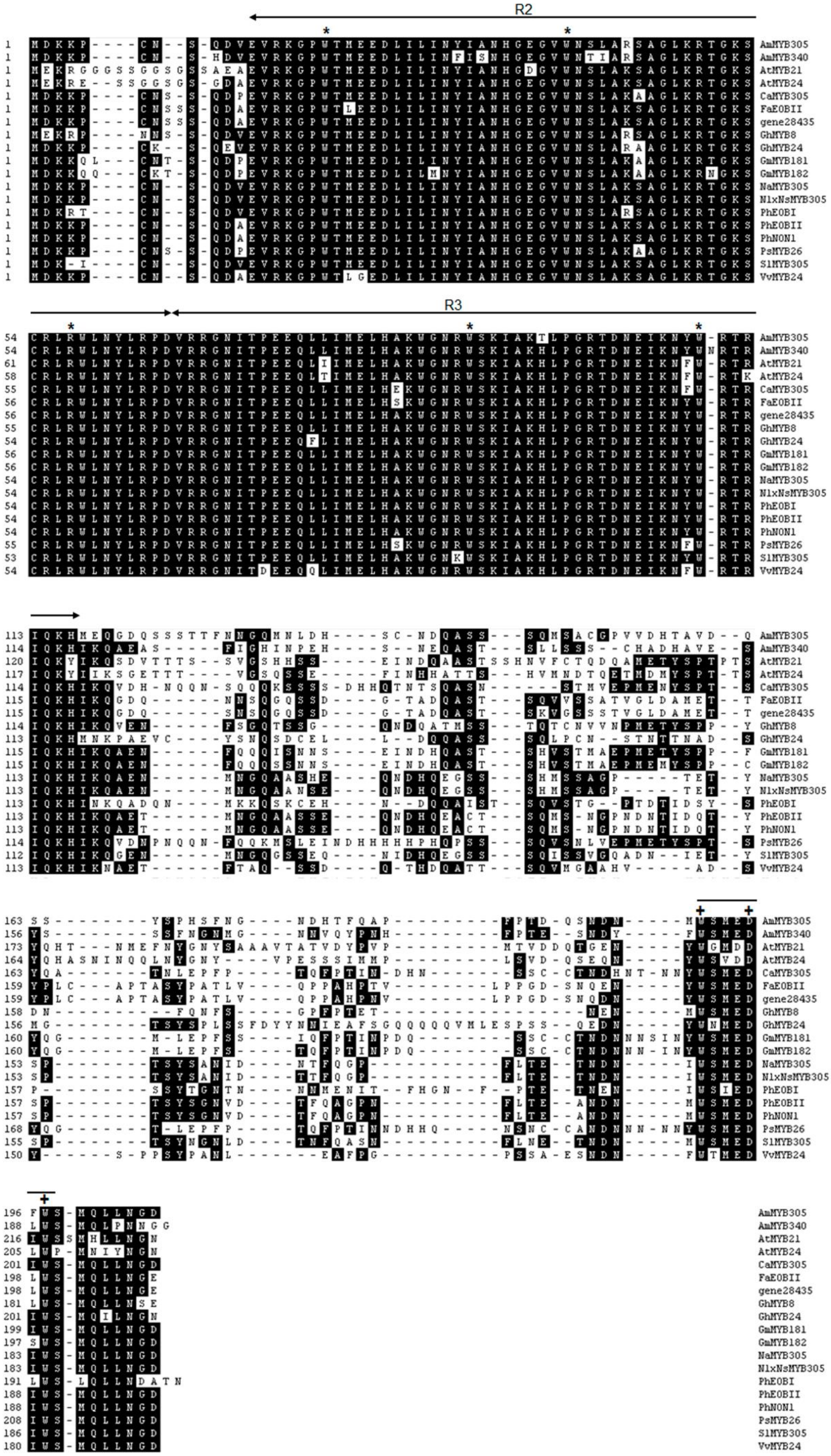

R2
R3
AmMYB305
AmMYB340
AtMYB21
AtMYB24
CaMYB305
FaEOBII
gene28435
GhMYB8
GhMYB24
GmMYB181
GmMYB182
NaMYB305
NlxNsMYB305
PhEOBI
PhEOBII
PhNON1
PsMYB26
SlMYB305
VvMYB24

Figure S2: Sequence alignment of R2R3-MYB proteins. Identical amino acids are shaded in black. The two MYB repeats (R2 and R3) are indicated with sets of arrows, and the critical Trp (W) residues are indicated by asterisks. The W/Y-MDDIW motif region is indicated with a line (+ indicates conserved amino acids). Numbers indicate amino acid positions.

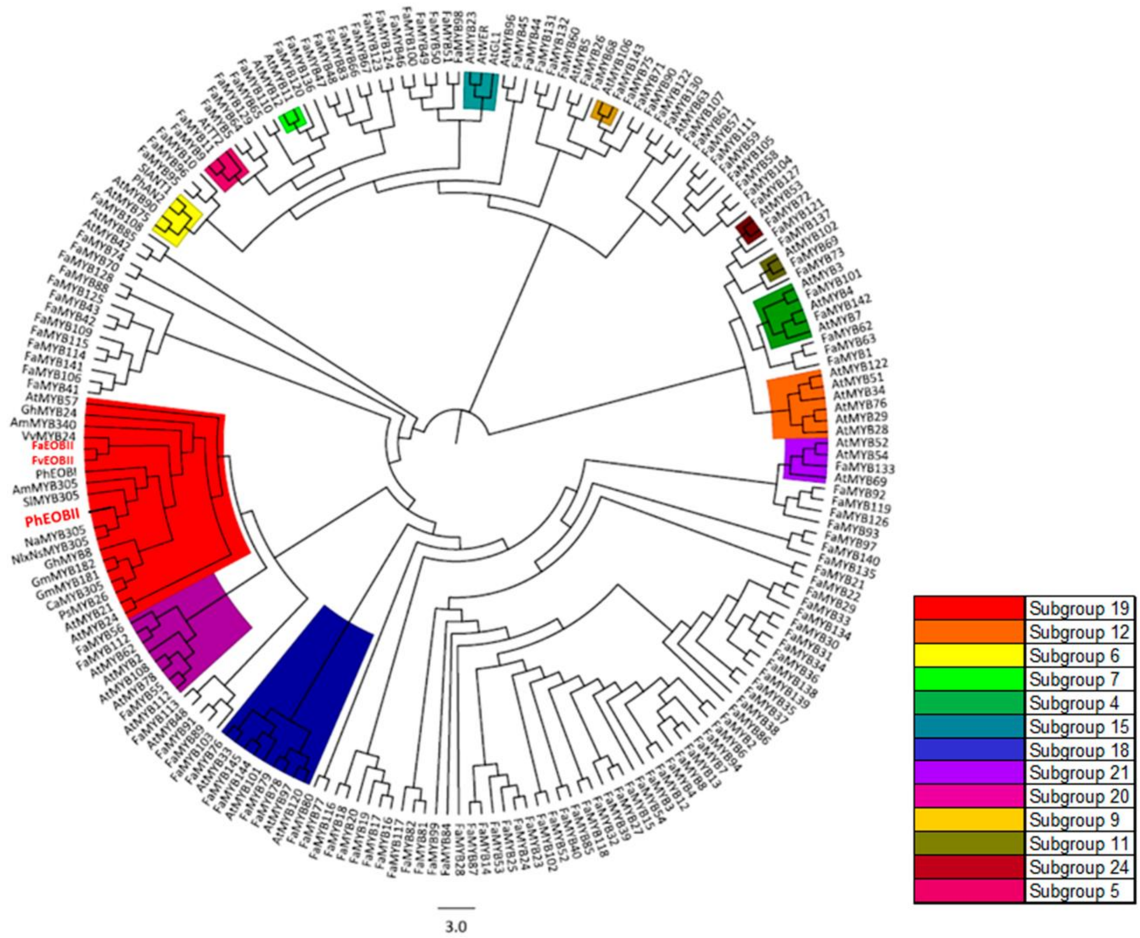
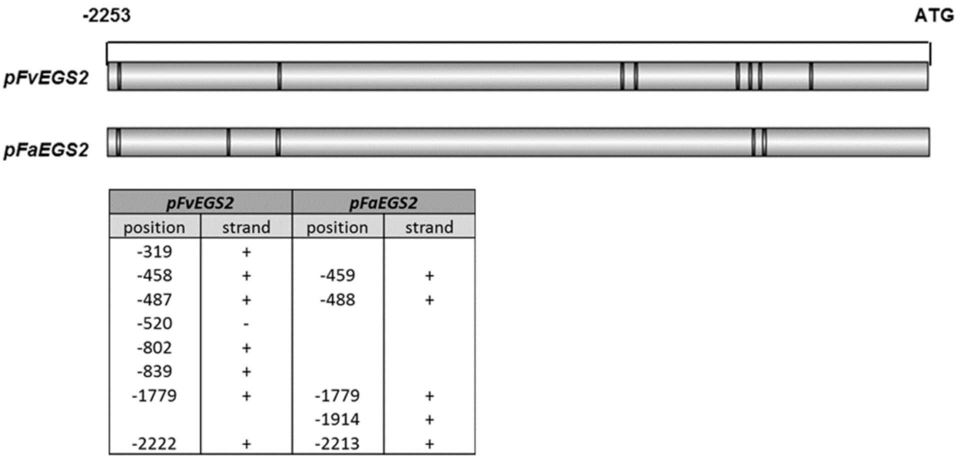


Figure S3: Phylogenetic Tree of 206 MYB Transcription Factor.



pFvEGS2		*pFaEGS2*	
position	strand	position	strand
-319	+		
-458	+	-459	+
-487	+	-488	+
-520	-		
-802	+		
-839	+		
-1779	+	-1779	+
		-1914	+
-2222	+	-2213	+

Figure S4: Schematic diagram of *EGS2* promoter from *F.* × *ananassa* and *F. vesca* varieties using PLACE online database (www.dna.affrc.go.jp) and DOG 2.0.1 for Windows (Illustrator of Protein Domain Structures). The bar on top indicates the length of the promoter fragment relative to the ATG codon. The location of the MBSII boxes is shown using black lines in the diagram, and their exact position is indicated on the panel.

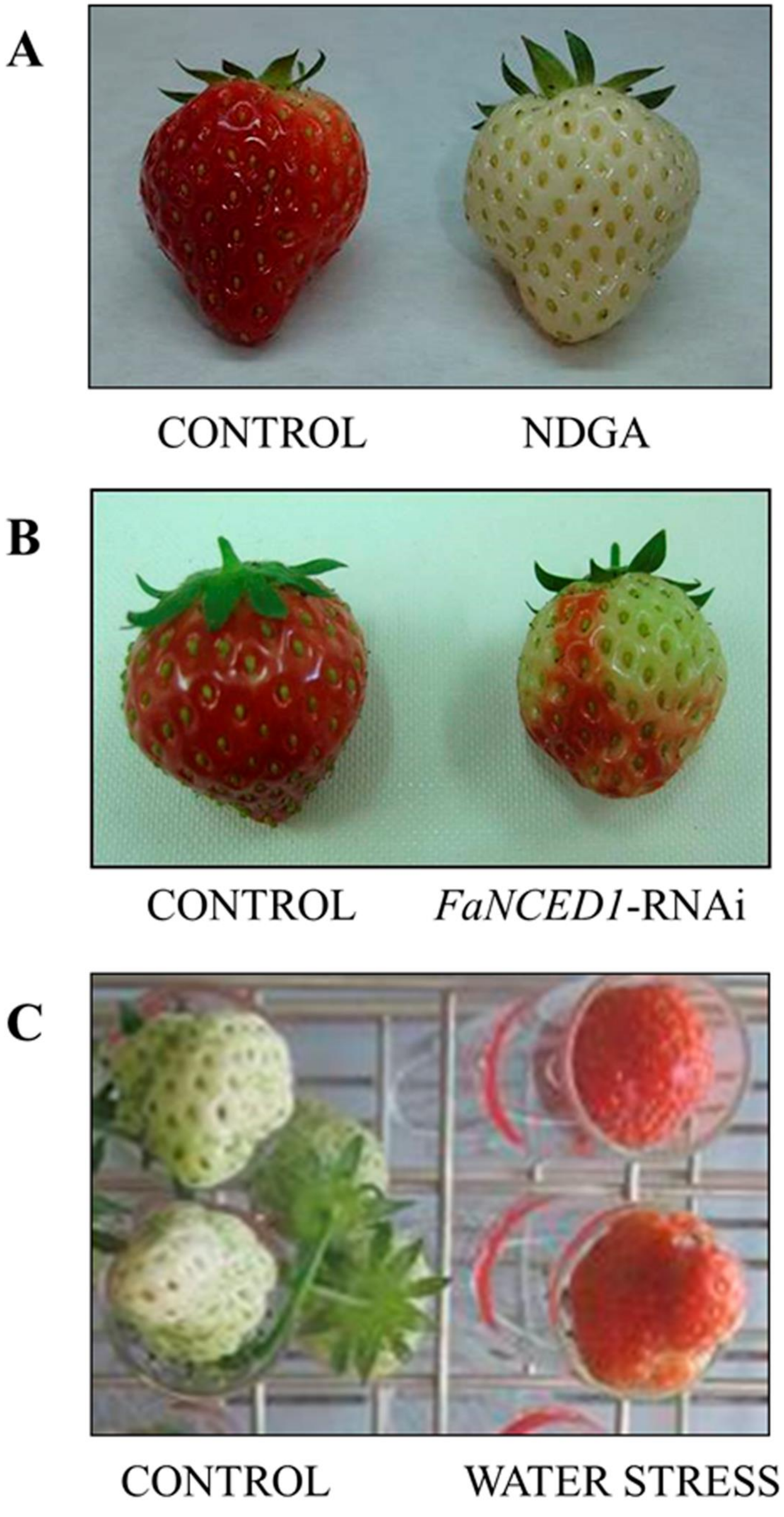

A
CONTROL
NDGA
B
CONTROL
FaNCED1-RNAi
C
CONTROL
WATER STRESS

Figure S5: Overview of the phenotype of fruits analyzed in studies of the regulation of gene expression regulated by ABA. (A) Strawberry fruits treated with NDGA (100 μM) and CONTROL fruits injected with H_2O, (B) Transgenics strawberry fruits agroinfiltrated with the pFRN-*FaNCED1* construct (*FaNCED1*-RNAi) and CONTROL fruits agroinfiltrated with the empty pFRN vector and (C) water stressed strawberry fruits (control fruit: fruits with the pedicels immersed in MS medium with sucrose; fruits + water stress: fruits with the pedicels kept in the air).

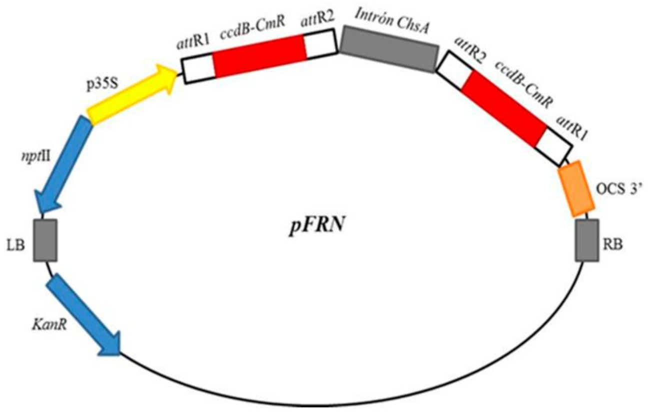


Figure S6: Structure of binary vector pFRN. RB: right border; LB: left border; attR1 and attR2: att sites where the Gateway LR recombination reaction occurs; ccdB: gene for negative selection of clones; CmR: chloramphenicol resistance gene; KanR:kanamycin resistance gene to select positive clones; nptII: kanamycin resistance gene to select transgenic plants; ChsA intron: intron of Chalcone isomerase gene; p35S: 35S promoter of virus cauliflower mosaic; OCS 3’: transcription termination sequence.