


WoLF PSORT
Protein Subcellular Localization Prediction

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















Original Website: 

Interface Designed by Genscript Corporation. All rights reserved.

InterProScan (version: 4.8) Launched Mon, Jun 11, 2012 at 15:23:11
Finished Mon, Jun 11, 2012 at 15:29:11

Sequence: Sequence_1
Length: 207
CRC64: 07510AAE48E578BE

InterPro Match	Query Sequence	Description
IPR001005 PF00249 SM00717	SANT/Myb domain	Myb_DNA-binding SANT SWI3, ADA2, N-CoR and TFIIB [®] DNA-bin
IPR009057 G3DSA:1.10.10.60 SSF46689	Homeodomain-like	no description Homeodomain-like
IPR015495 PTHR10641	Myb transcription factor	MYB-LIKE DNA-BINDING PROTEIN MYB
IPR017930 PSS1294	Myb domain, DNA-binding	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 →

```

1  MDKKP  - - - - - CN - - - S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  AaMYB305
1  MDKKP  - - - - - CN - - - S  HDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  AaMYB340
1  MEKRRG  G G S S  SAEAEVRKGPMTMEEDLILINNYIANHGE  DCVWNSLAKSAGLKRRTGKS  AcMYB21
1  MEKRR  - - - - - S S G G S G  GAAEVRKGPMTMEEDLILINNYIANHGE  CVWNSLAKSAGLKRRTGKS  AcMYB24
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTMEEDLILINNYIANHGE  CVWNSLAKSAGLKRRTGKS  CaMYB305
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTMEEDLILINNYIANHGE  CVWNSLAKSAGLKRRTGKS  FaEOBII
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTMEEDLILINNYIANHGE  CVWNSLAKSAGLKRRTGKS  gene28435
1  HSKRP  - - - - - M S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  GhMYB8
1  MDKKP  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  GhMYB24
1  MDKKQL  - - - - - C K T - - S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  GhMYB181
1  MDKKQL  - - - - - C K T - - S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  GhMYB182
1  MDKKP  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  NaMYB305
1  MDKKP  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  NlxNsMYB305
1  MDKRT  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  PhEOBI
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  PhEOBII
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  PhNOM1
1  MDKKP  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  PsMYB26
1  MDK-I  - - - - - CN S S S S  QDVEVRKGPMTMEEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  SlMYB305
1  MDKKP  - - - - - CN S S S S  QDAEVRKGPMTLGEDLILINNYIANHGE  GVUNSLAKSAGLKRRTGKS  VvMYB24

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← R3 →

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54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  AaMYB305
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  AaMYB340
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  AcMYB21
58  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  AcMYB24
55  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  CaMYB305
56  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  FaEOBII
56  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  gene28435
55  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  GhMYB8
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  GhMYB24
56  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  GhMYB181
56  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  GhMYB182
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  NaMYB305
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  NlxNsMYB305
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  PhEOBI
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  PhEOBII
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  PhNOM1
55  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  PsMYB26
53  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  SlMYB305
54  CRLRW  L N Y L R P D V R R G N I T P E E Q L L I M E L H A K U G N R U S K I A K H L P G R T D N E I K N Y W M R T R  VvMYB24

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113  IQKHME  Q G D Q S S S T T F N M G Q M N L D H - - - S C N D Q A S S - - - S Q M S A C G P V V D H T A V D - - Q  AaMYB305
114  IQKHIK  Q A E A S - - - - - T G H I N P E H - - - S - N E Q A S T - - - S L L S S - - C H A D H A V E - - - S  AaMYB340
120  IQKYIK  Q S D V T T T S - - - S V G S H H S S I - - - E I N D Q A A S T S S H N V F C T Q D Q A M E T Y S P T P T S  AcMYB21
117  IQKYI  I I K S G E T T T - - - V G S Q S S E - - - F I N H H A T T S - - - H V M N D T Q E T M D M Y S P T T S  AcMYB24
114  IQKHIK  Q V D H - N Q Q N - S Q Q Q K S S S S - D H H Q T N T S Q A S N - - - - S T M V E F M E N Y S P T - S  CaMYB305
115  IQKHIK  Q G D Q - - - - - N M S Q G Q S S D - - - G T A D Q A S T - - - S Q V S S A T V G L D A M E T - T  FaEOBII
115  IQKHIK  Q G D Q - - - - - S M S Q G Q S S D - - - G T A D Q A S T - - - S K V G S S T V G L D A M E T - T  gene28435
114  IQKHIK  Q V E M - - - - - S G O T S S G - - - Q N D Q A T M S S - - - T O T C H V V N M E T Y S P P - Y  GhMYB8
113  IQKH  M N K Y A E V C - - - - - Y S N Q S D C E L - - - L - - D Q Q A S S - - - S Q L P C N - - S T N T T A D - S  GhMYB24
115  IQKHIK  Q A E M - - - - - F Q Q Q I S N N S - - - E I N D H Q A S T - - - S H V S T H A E F P H E T Y S P P - F  CaMYB181
115  IQKHIK  Q A E M - - - - - F Q Q Q S N N S - - - E I N D H Q A S T - - - S H V S T H A E F P H E T Y S P P - C  CaMYB182
113  IQKHIK  Q A E M - - - - - N G Q A A S H E - - - Q N D H Q E G S S - - - S H S S A G P - - - - T E F - Y  NaMYB305
113  IQKHIK  Q A E M - - - - - N G Q A A N S E - - - Q N D H Q E G S S - - - S H S S A G P - - - - T E F - Y  NlxNsMYB305
113  IQKH  I N K Q A D Q N - - - - - H K K Q S K C E H - - - N - - D Q Q A I S T - - - S Q V S T G - - F T D T I D S Y - S  PhEOBI
113  IQKHIK  Q A E T - - - - - N G Q A A S S E - - - Q N D H Q E A C T - - - S Q H S - N G P N D N T I D Q T - Y  PhEOBII
113  IQKHIK  Q A E M - - - - - N G Q A A S S E - - - Q N D H Q E A C T - - - S Q H S - N G P N D N T I D Q T - Y  PhNOM1
114  IQKHIK  Q V D M P N Q Q N - F Q Q K M S L E I N D H H H H P H Q P P S S - - - S Q V S N L V E P H E T Y S P T - S  PsMYB26
112  IQKHIK  Q G E N - - - - - N M Q G S S E Q - - - N I D H Q E G S S - - - S Q T E S V G Q A D N - I E T - Y  SlMYB305
113  IQKH  I K N A E T - - - - - R T A Q - - S S D - - - Q - T H D Q A T T - - - S Q V H G A A H V - - - - A D - S  VvMYB24

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163  S S - - - - - Y S P H S F N G - - - N D H T F Q A P - - - - - F P P I D - Q S N D W - - - - - M S S M E D +  AaMYB305
176  Y S - - - - - S S F N G M N G - - - N M V Q Y P N H - - - - - F P P T E - S N D V - - - - - F W S M E D +  AaMYB340
173  Y Q H T - - - - - N M E F N Y G N Y S A A A V T A T V D Y P V P - - - - - M T V D D Q T G E N - - - - - V W G M D D  AcMYB21
164  Y Q H A S N I N Q Q L N Y G N Y - - - V P E S S I M M P - - - - - L S V D - Q S E Q N - - - - - Y W S V D D  AcMYB24
163  Y Q A - - - - - N L E P F P - - - - - T Q F P T I N - D H N - - - - - S S C C T N D N N T - N N Y W S M E D  CaMYB305
159  Y P L C - - - - - A P T A S Y P A T L V - - - Q P P A H P T V - - - - - L P P G D - S N Q E N - - - - - Y W S M E D  FaEOBII
159  Y P L C - - - - - A P T A S Y P A T L V - - - Q P P A H P N V - - - - - L P P G D - S N Q E N - - - - - Y W S M E D  gene28435
158  D N - - - - - F Q N F S - - - - - G P F P T E T - - - - - H E N - - - - - H S M E D  GhMYB8
156  M G - - - - - T S Y S P L S S F D Y Y N N I E A F S G Q Q Q Q V M L E S P S S - - - - - Q E D N - - - - - Y W N M E D  GhMYB24
160  Y Q G - - - - - M - L E P F S S - - - I Q Q F P T I N P D Q - - - - - S S C C T N D N N N S I N Y W S M E D  GhMYB181
160  Y Q G - - - - - M - L E P F S S - - - T O F P T I M P D Q - - - - - S S C C T N D N N N M I N Y W S M E D  GhMYB182
153  S P - - - - - T S Y S A M I D - - - N T F Q G P - - - - - F L T E - T N D N - - - - - I W S M E D  NaMYB305
153  S P - - - - - T S Y S A M I D - - - T F Q G P - - - - - F L T E - T N D N - - - - - I W S M E D  NlxNsMYB305
157  P - - - - - S Y T G H T N - - - N M M E N I T - F H G N - F - - - - - P T E - T N E N - - - - - I W S I F D  PhEOBI
157  S P - - - - - T S Y S G N V D - - - T F Q A G P N - - - - - F L T E - A N D N - - - - - I W S M E D  PhEOBII
157  S P - - - - - T S Y S G N V D - - - T F Q A G P N - - - - - F L T E - A N D N - - - - - I W S M E D  PhNOM1
168  Y Q G - - - - - T L E P F P - - - T O F P T I N D H H Q - - - - - N S N C - C A N D N N N - N N Y W S M E D  PsMYB26
155  S P - - - - - T S Y H G N I D - - - T H F Q A S M - - - - - F L M E - T N D N - - - - - H W S M E D  SlMYB305
150  Y - - - - - S - P P S Y P A M L - - - - - E A F P G - - - - - P S S A - E S N D N - - - - - F W T H E D  VvMYB24

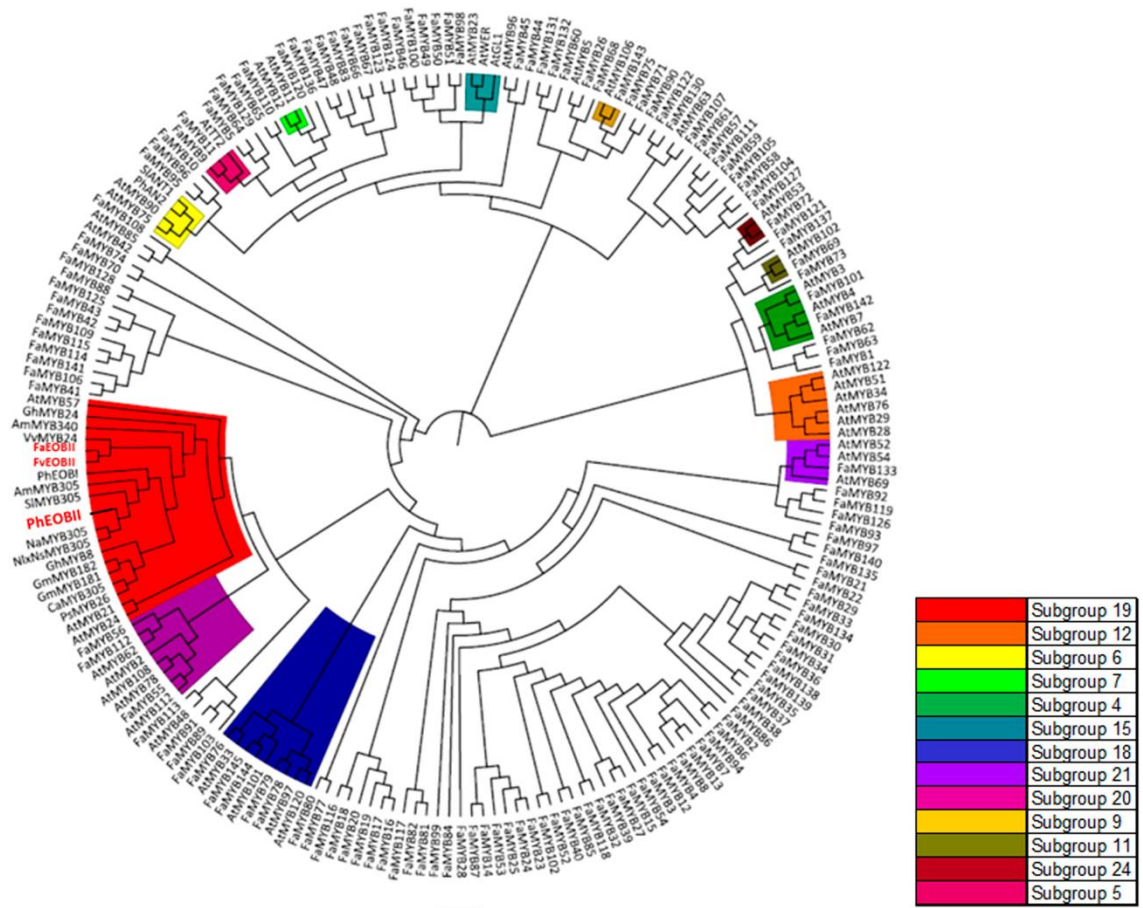
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196  F W S - M Q L L N G D  AaMYB305
188  L W S - M Q L P N N G G  AaMYB340
216  F W S M H L L N G N  AcMYB21
205  L W P - M N I Y N G N  AcMYB24
201  F W S - M Q L L N G D  CaMYB305
198  L W S - M Q L L N G E  FaEOBII
198  L W S - M Q L L N G E  gene28435
181  L W S - M Q L L N S E  GhMYB8
201  F W S - M Q L L N G H  GhMYB24
199  F W S - M Q L L N G D  GhMYB181
197  F W S - M Q L L N G D  GhMYB182
183  F W S - M Q L L N G D  NaMYB305
183  F W S - M Q L L N G D  NlxNsMYB305
191  L W S - L Q L L N D A T N  PhEOBI
188  F W S - M Q L L N G D  PhEOBII
188  F W S - M Q L L N G D  PhNOM1
208  F W S - M Q L L N G D  PsMYB26
186  F W S - M Q L L N G D  SlMYB305
180  F W S - M Q L L N G D  VvMYB24

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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.



3.0

Figure S3: Phylogenetic Tree of 206 MYB Transcription Factor.

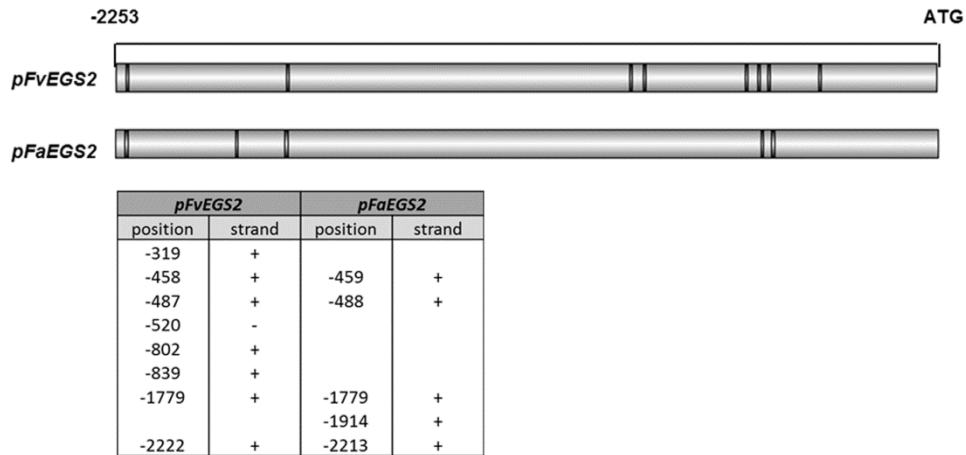
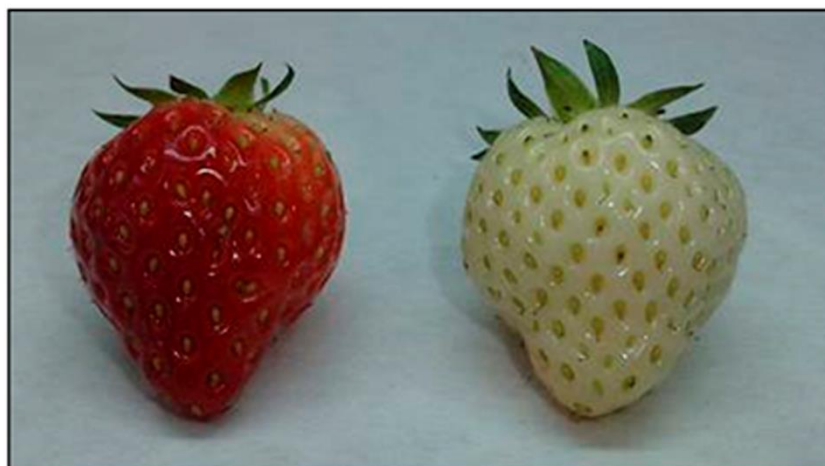


Figure S4: Schematic diagram of *EGS2* promoter from *F. × ananassa* and *F. vesca* varieties using PLACE online database (www.dna.affrc.go.jp) and DOG 2.0.1 for Windows (Illustrator of Protein Domain Structures). The bar on top indicates the length of the promoter fragment relative to the ATG codon. 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 μ M) and CONTROL fruits injected with H₂O, (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).

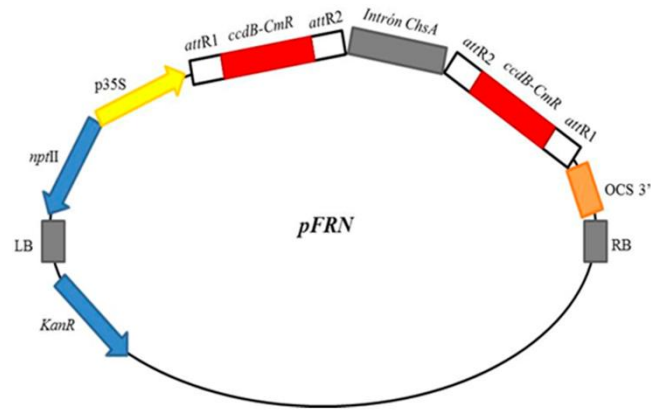


Figure S6: Structure of binary vector pFRN. RB: right border; LB: left border; attR1 and attR2: att sites where the Gateway LR recombination reaction occurs; ccdB: gene for negative selection of clones; CmR: chloramphenicol resistance gene; KanR:kanamycin resistance gene to select positive clones; nptII: 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.