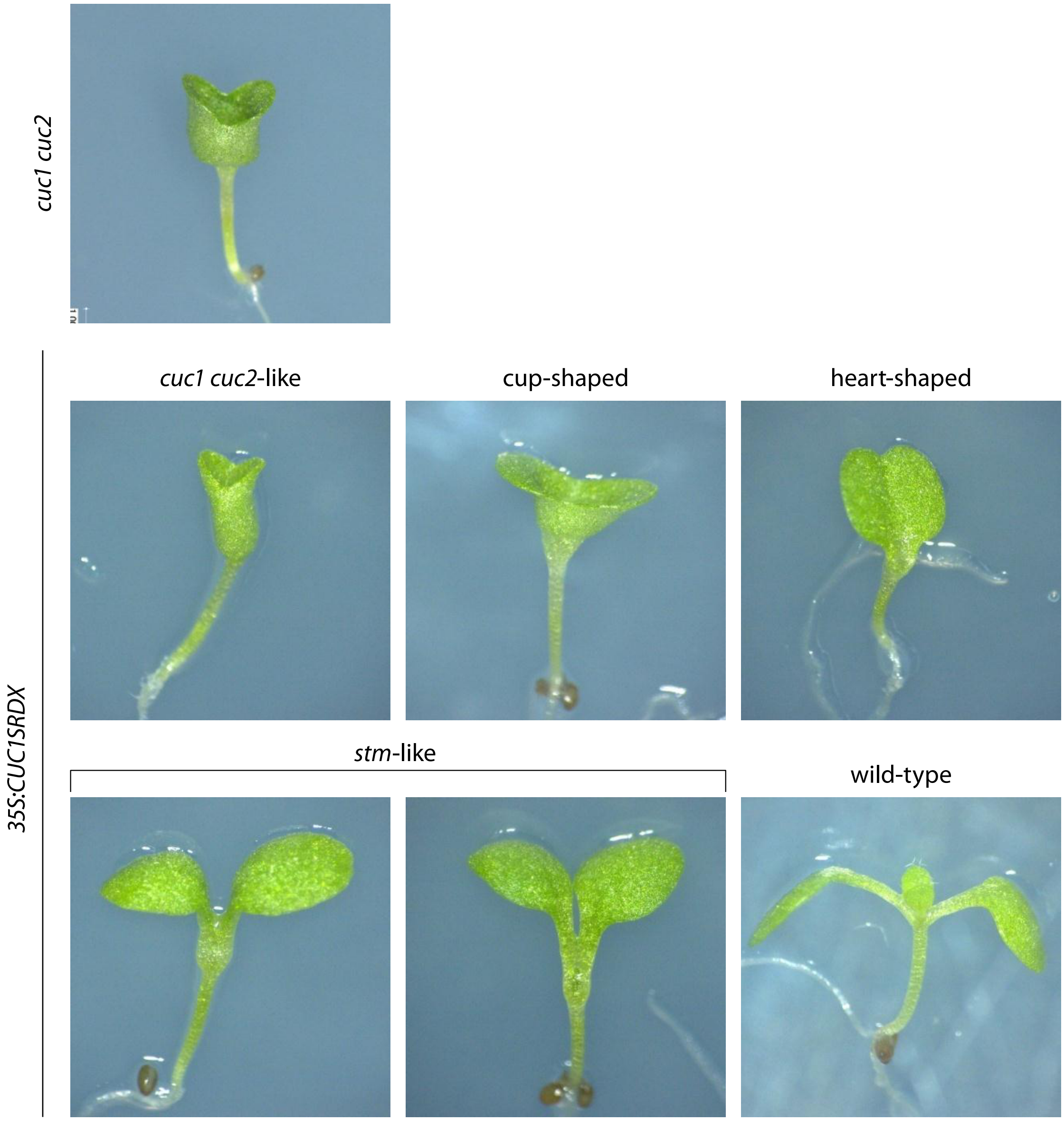
Novel vector systems to accelerate functional analysis of transcription factors using chimeric repressor gene-silencing technology (CRES-T)
[Plant Biotechnol. 28(2): 201-210 (2011)]



Supplemental Figure 1. Classification of the *35S:CUC1SRDX* phenotypes.

Phenotypes of *35S:CUC1SRDX* transgenic plants were classified according to the extent of fusion of the two cotyledons; *cuc1 cuc2*-like, cup-shaped, heart-shaped, *stm*-like and wild-type-like. Both margins of cotyledons were almost completely fused in *cuc1 cuc2*-like plants, while they were partially fused in cup-shaped plants. Only one side of the cotyledon was fused in the heart-shaped phenotype, while only cotyledonary petioles were fused in the *stm*-like phenotype.

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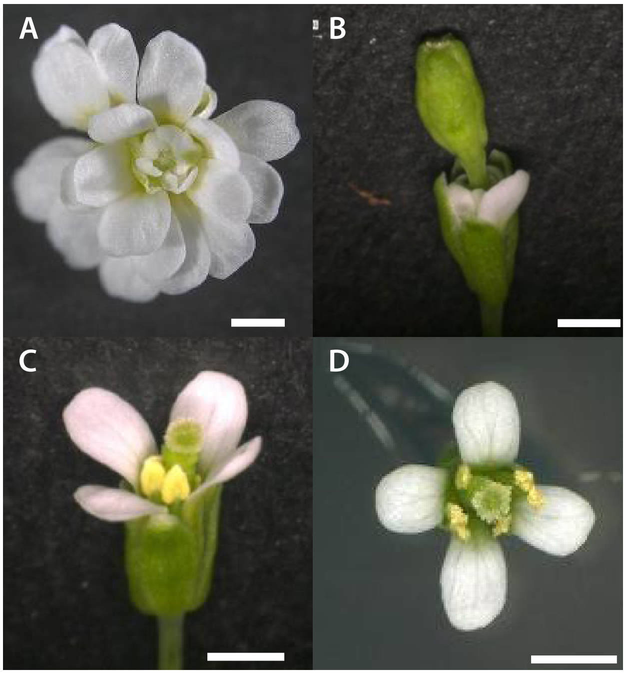
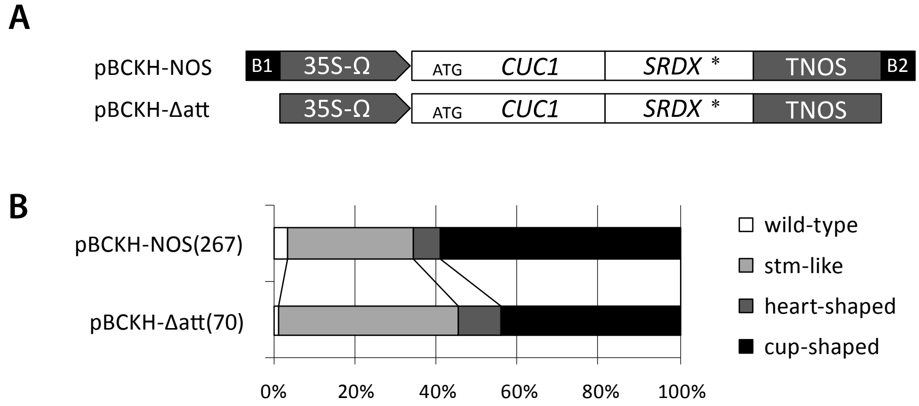


Supplemental Figure 2. Classification of the *35S:AGSRDX* phenotypes.

Phenotypes of *35S:AGSRDX* transgenic plants were classified into *ag*-like (A), double flower (B), mild (C) and wild-type-like (D). Ectopic carpel, stamens and petals appeared in the carpel of double flower (B). Bars indicate 1 mm.



Supplemental Figure 3. The efficiency of CRES-T for constructs lacking Gateway sequences.

A, Schematic representation of *35S:CUC1SRDX* constructs. The filled boxes indicate attB1 (B1) and attB2 (B2) sequences. B, The frequency of each *35S:CUC1SRDX* phenotype class. Phenotype class was defined as indicated in Supplemental Figure 1. The number of T_1 plants examined is given in parentheses in each case.

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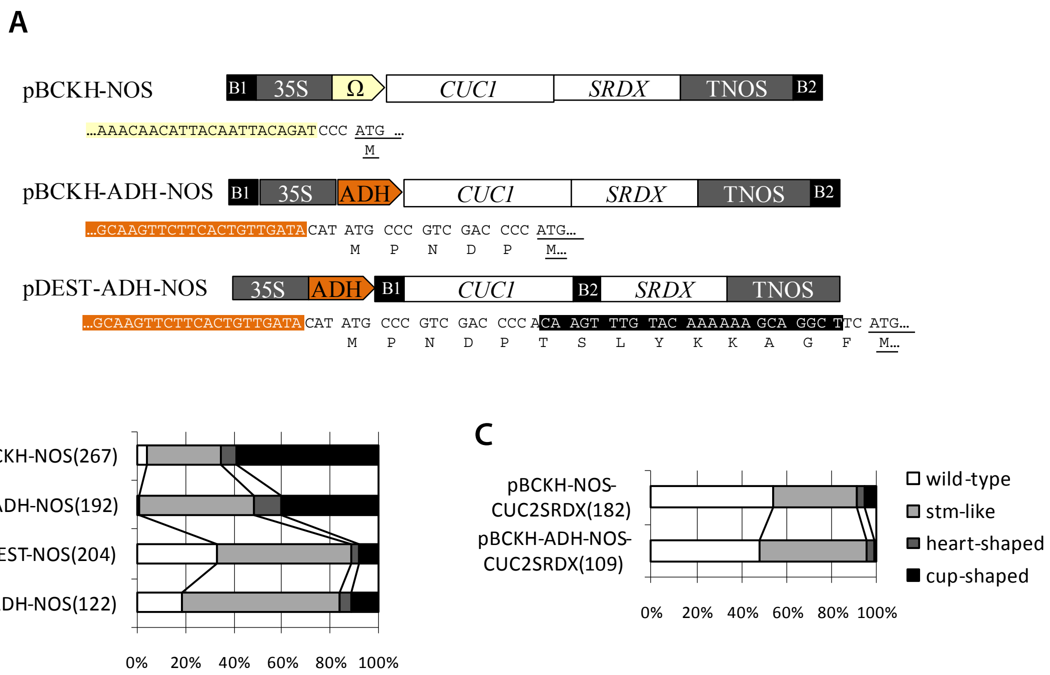

Supplemental Figure 4. The efficiency of CRES-T for constructs with the *AtADH* 5′-UTR.

A, Schematic representation of *35S:CUC1SRDX* constructs using pBCKH/p35SSRDXG (pBCKH-NOS), pBCKH/p35AASRDXG (pBCKH-ADH-NOS) and pDEST_35AA_SRDX_HSPH (pDEST-ADH-NOS). The DNA and the amino-acid sequences around the initiation codon are shown. The filled boxes indicate attB1 (B1) and attB2 (B2) sequences. The yellow box, orange box and underlined sequence indicate omega sequence, *AtADH* 5'-UTR (ADH) and *CUC1*, respectively. B, The frequency of each *35S:CUC1SRDX* phenotype class. C, The frequency of each *35S:CUC2SRDX* phenotype class constructed by insertion of *CUC2* instead of *CUC1* in A. Phenotype class was defined as indicated in Supplemental Figure 1, except that "cup-shaped" includes the *cuc1 cuc2*-like phenotype in this case. The number of examined T1 plants is given in parentheses in each case. The data for pBCKH-NOS and pDEST-NOS are also shown in Figure 3.