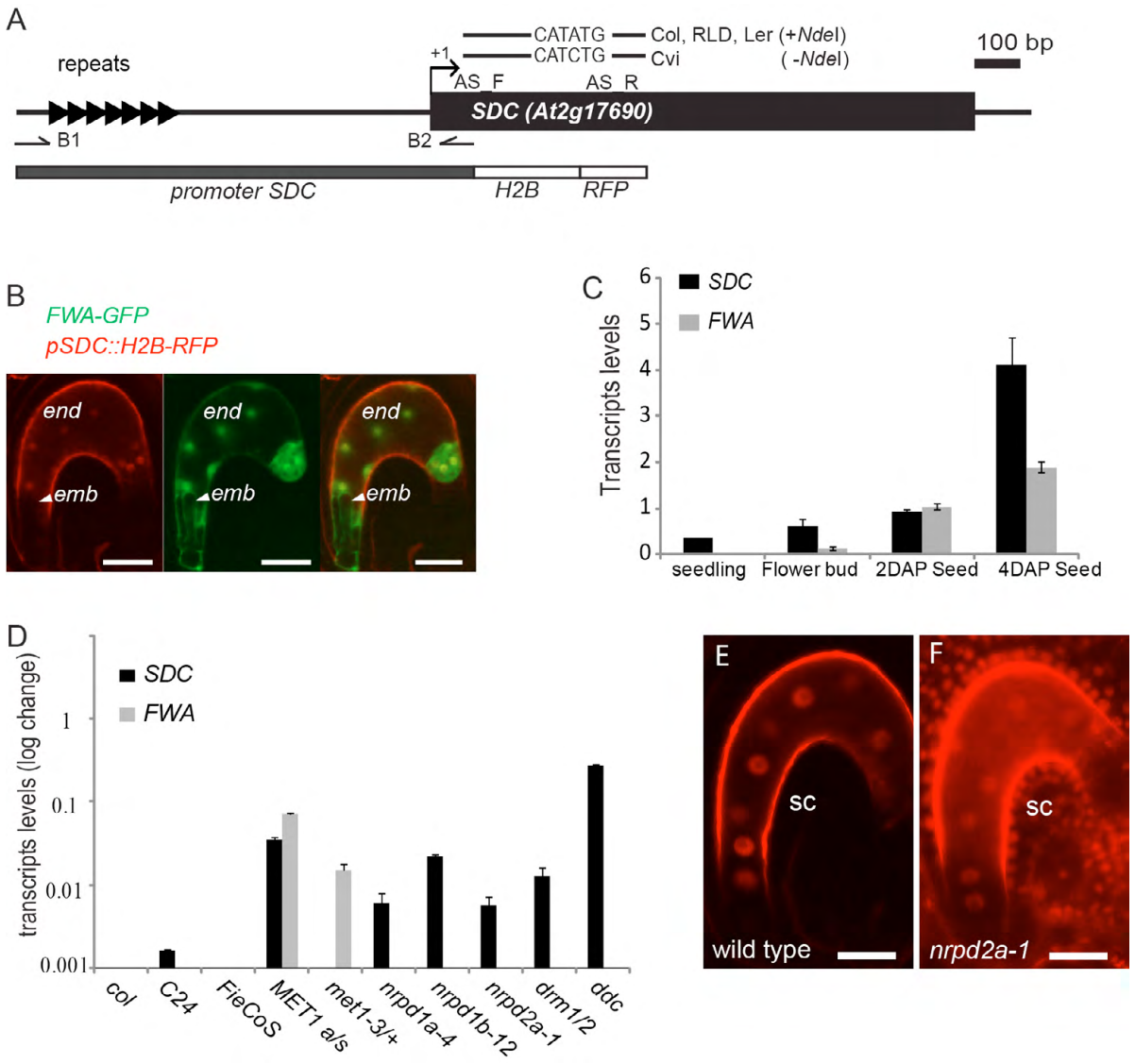

Fig. S1. *SDC* is expressed in endosperm specifically and silenced in vegetative tissues by RdDM. This figure relates to Fig. 2. (**A**) The *SDC* locus indicating sites of polymorphisms and primers. Seven black arrowheads indicate the tandem repeats. The polymorphism introduces a recognition site for *Nde*I in Col, RLD and L*er* but not in Cvi. (**B**) Confocal analysis of *pSDC::H2B-RFP* with the marker for endosperm (end) *pFWA-GFP*, which also provides outlines of the embryo (emb). Scale bars: 50 µm. (**C**) qRT-PCR analysis of parental expression of *SDC* and *FWA* in seeds at different developmental stages. (**D**) qRT-PCR analysis of *SDC* expression in somatic tissues in different mutants for Polycomb group genes (FieCoS), maintenance DNA methylation genes (MET1 antisense MET1 a/s and *met1-3*/+) and RdDM pathway genes (*nrpd1a-4*, *nrpd1b-12*, *nrpd2a-1* and *drm1,drm2* double mutant), and in the triple mutant *ddc* (*drm1-2*, *drm2-2, cmt3-11t*). RNA was extracted from 10-day-old seedlings. The *y*-axis is displayed in log scale. (**E, F**) Confocal section of a developing seed at 1 DAP expressing the *pSDC::H2B-RFP* construct in wild-type and the *nrpd2a-1* backgrounds. sc, seed coat. Scale bars: 50 µm

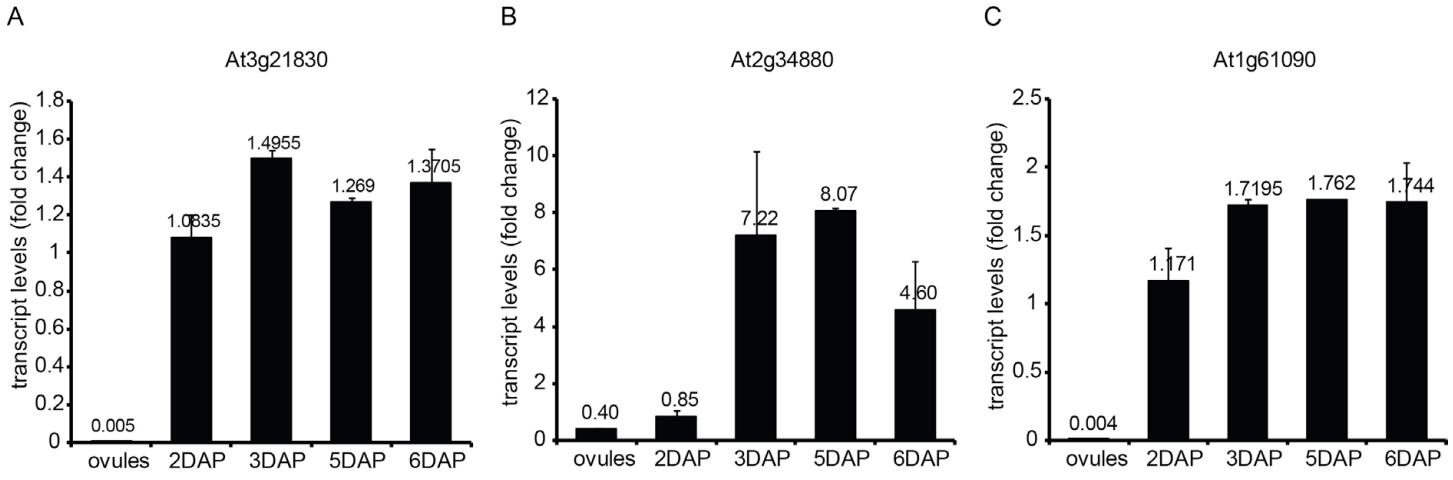

Fig. S2. Expression pattern of candidate imprinted genes during seed development. This figure relates to Fig. 3. Real-time PCR analysis of expression pattern of (**A**) At3g21830, (**B**) At2g34880 and (**C**) At1g61090 in ovule before fertilization and in seeds collected at different stages of development. The qPCR results were normalized with *UBQ10* expression levels in 2 DAP seeds. Three technical replicates and two biological replicates were performed; the *y*-axis is linear and the levels of expression are reported above each column. We observed a 200-fold increase of transcripts levels in 2 DAP seeds compared with unfertilized ovules for At3g21830 and At1g61090. Transcript levels of At2g34880 were multiplied by five from ovules to 2 DAP seeds and increased more than 20 times in 3 DAP seeds compared with ovules.

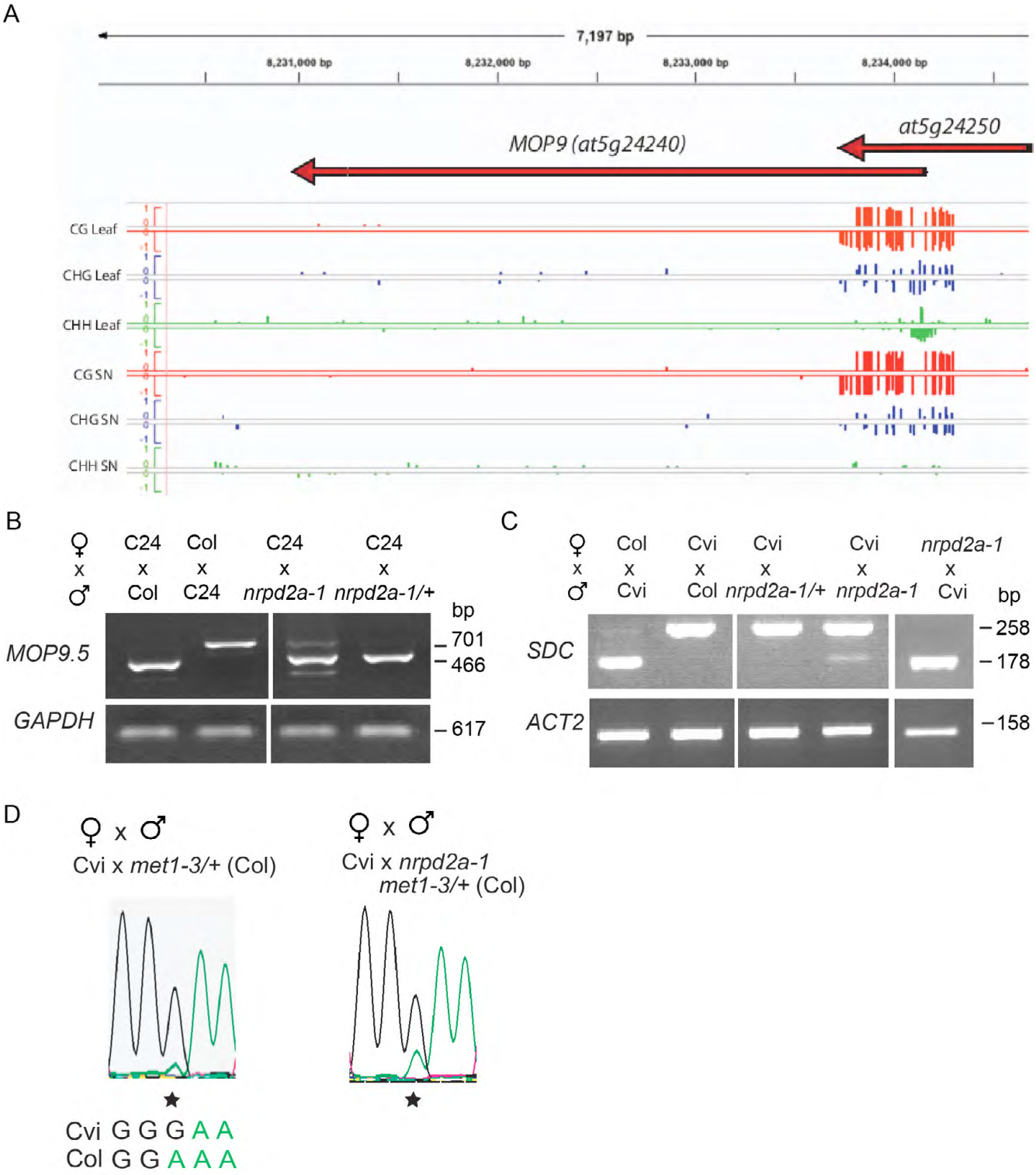

Fig. S3. Regulation of paternal expression of imprinted genes. This figure relates to Fig. 4. (**A**) DNA methylation analysis of the *MOP9.5* locus in leaf and sperm cells (SN). (**B**) Allele-specific RT-PCR analysis of *MOP9.5* in seeds produced by crosses between wild-type mother and *nrpd2a-1* homozygous and *nrpd2a-1*+/– fathers (Col background). GAPDH is used as loading control. (**C**) Allele-specific RT-PCR analysis of *SDC* in seeds produced by crosses between wild-type mother and *nrpd2a-1* homozygous and *nrpd2a-1*+/– fathers (Col background). ACT2 is used as loading control. (**D**) Allele-specific RT-PCR analysis of *SDC* expression in the seeds produced by the reciprocal crosses between Cvi wild-type ovules and pollen from *met1-3*/+ and double mutant *nrpd2a-1*, *met1-3*/+ (Col background). We used RT-PCR sequencing chromatographs at selected SNP present in different accessions.

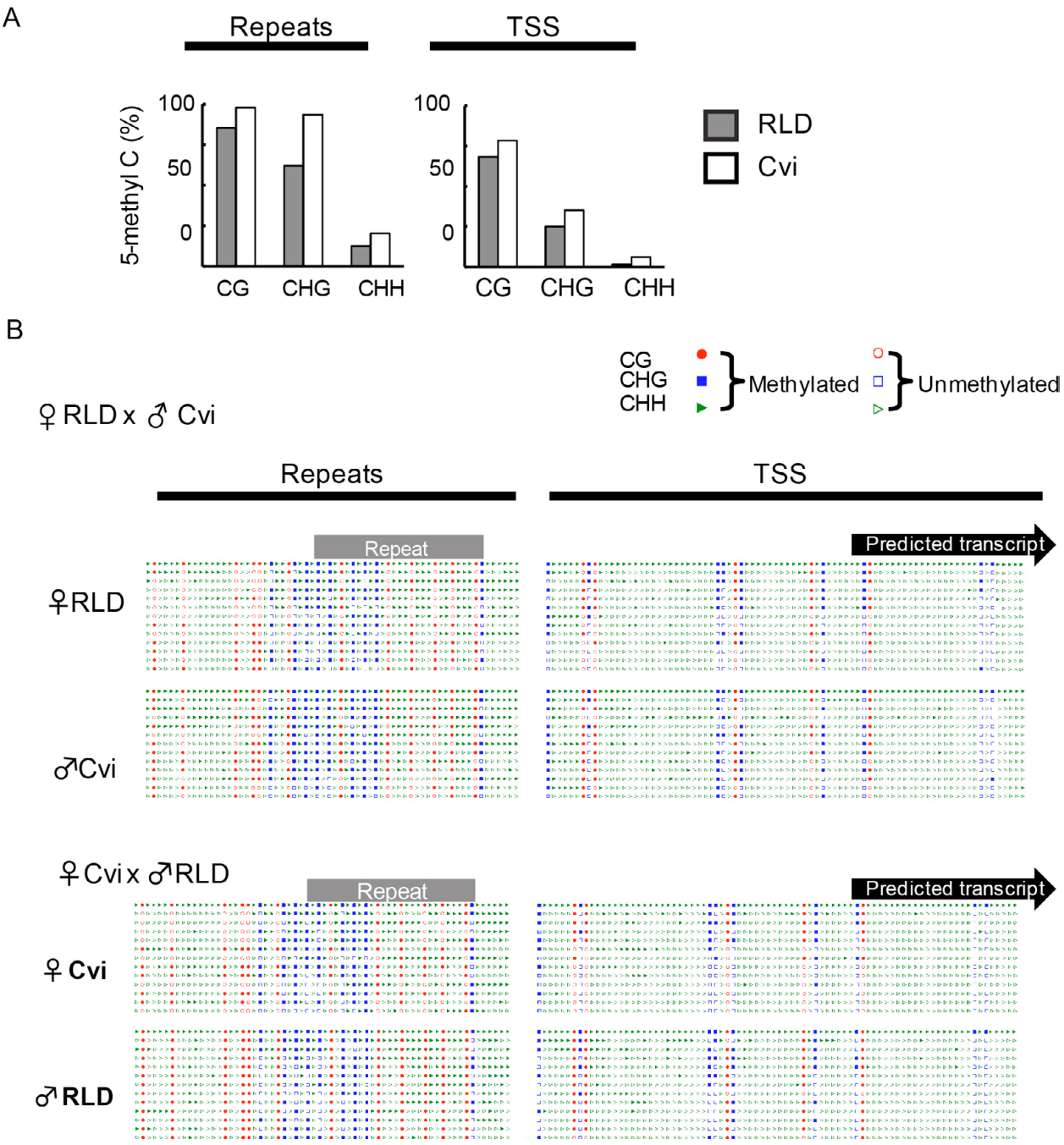

Fig. S4. Maternal control of *SDC* expression. This figure relates to Fig. 6. (**A**) Percent methylation at CG, CHG and CHH sites on the 32 bp repeat region and TSS region of *SDC* in leaves. DNA was extracted from leaves. (**B**) Cytosine methylation patterns of the 32 bp repeat region and TSS are visualized graphically using CyMATE software. The data sets are same as in Fig. 6B. Each line represents the methylation pattern of an individual clone. First lines of all blocks are reference sequences. Empty symbols represent converted (unmethylated) cytosine residues. Filled symbols represent unconverted (methylated) cytosine residues. Red circles, blue squares and green triangles represent each 5-methylcytosine in CG, CHG and CHH contexts, respectively.

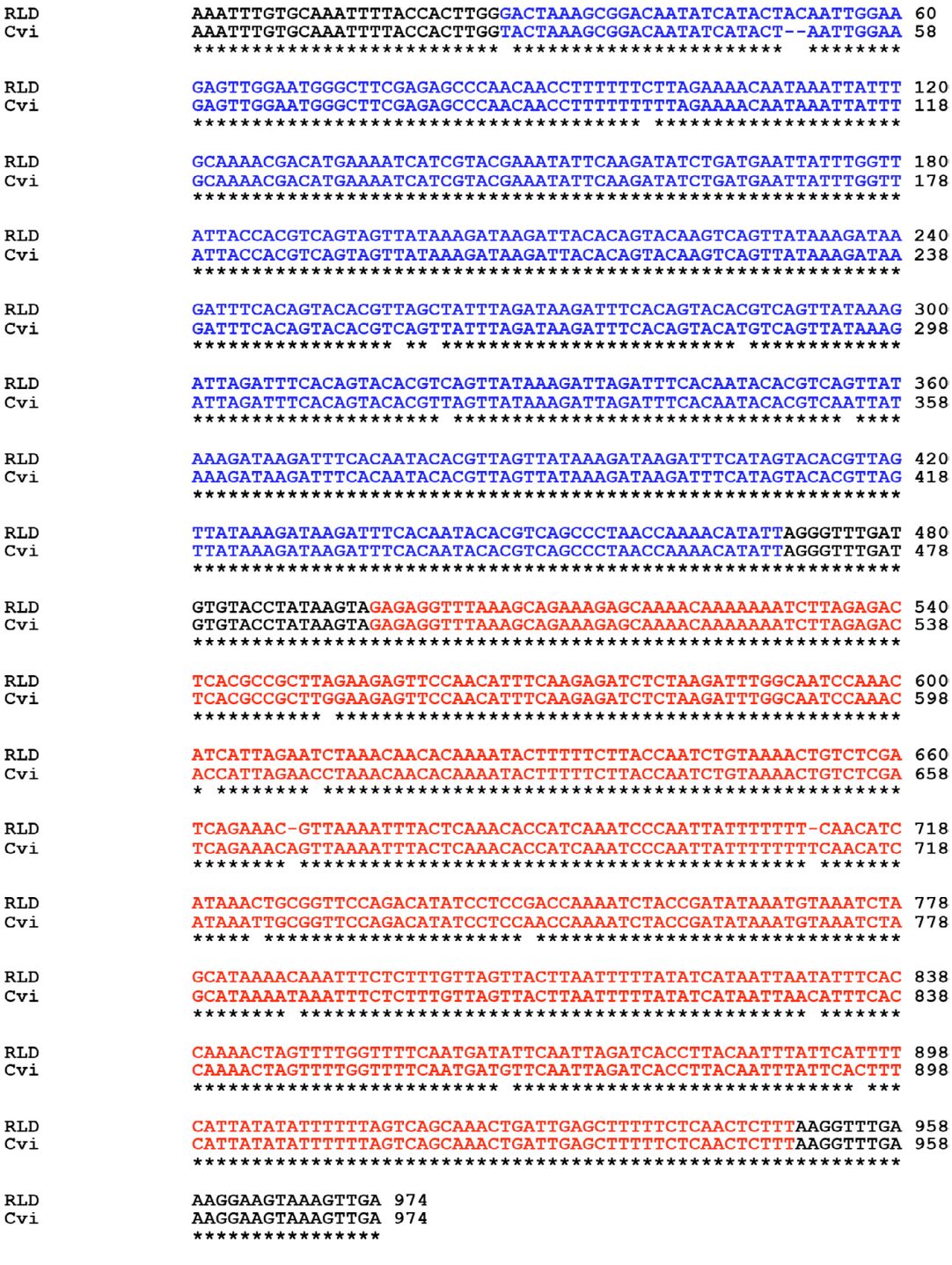

Fig. S5. Alignment between RLD and Cvi of the *SDC* promoter and 5′ UTR region, which were analyzed with bisulfite sequencing. Blue letters and red letters indicate repeats and the predicted *SDC* transcript, respectively. The sequence alignment was performed with ClustalW.

Table S1. Lists of primers used in this study

Primers for RT-PCR and RT-qPCR

Target	**Primers**	**Sequences (5′-3′)**
NRPD2a	NRPD2a-RTf	AACGGTAGATCAGGTGAGATGATGCG
	NRPD2a-RTr	CGGAACATAGACCCTAACCACATGGTC
	NRPD2a-qF	AAAGTTTGGAGTCTGTGGTG
	NRPD2a-qR	TTGATTTCCATCTCACGAGGT
FWA	FWA-RTf	GTGACTCTGGTCAAGACT
	FWA-RTr	TTGGTTCCACCAGAACCGGTA
FWA(qPCR)	FWA-qF	CTCTGGTCAAGACTCTTATGG
	FWA-qR	ATTCTGCTTGAATCTGTTG
MOP9.5	At5g24240-qF	GTGCTTACTCCAATAGACCA
(At5g24240)	At5g24240-qR	CATGGTTGAAATACGGAGGA
SDC	SDC-rtF	AATGTAAGTTGTAAACCATTTGAACGTGACC
	SDC-rtR	CAGGCATCCGTAGAACTCATGAGC
SDC (qPCR)	SDC-qF	TAGTCAGCAAACTGATTGAGC
	SDC-qR	AAGGTTTGTAAGATGTCGTGG
UBQ10	UBQ10-F	TTCTCTCAATTCTCTCTACCGT
	UBQ10-R	TGGCCTTAACGTTGTCGAT
ACT2	Act2-RT1	CTCAGGTATCGCTGACCGTATGAG
	Act2-RT2	CTTGGAGATCCACATCTGCTGGAATG
GAPDH	GAPDH5’	AGGGTGGTGCCAAGAAGGTTG
	GAPDH3’	GTAGCCCCACTCGTTGTCGTA
ACT11	Act11-qF	GAGATGATGCACCAAGAGCTGTA
(qPCR)	Act11-qR	CATACCAACCATGACACCAGTGT
RPS5A	AtRPS5A F	CTCTCATTCGCGCGACGCAAACG
	AtRPS5A R	GGGTTCAAGTCAGACAAGAGGTGG
DD31	DD31 +0F	ATGACAAAATCTCTACTCATGGTAAC
	DD31 +496R	CAATCTTGCTCCCTACTCTAAAG
DD65	DD65 +0F	ATGAAGTGTTTGTGTTTTGTCGTG
	DD65 +344R	GCAAAATCCAAACCCTGAAAAG
DD45	DD45 For	ATGGCTTCTAACACAAGTTTCCTCTTTGC
	DD45 Rev	TCAAAGTTTCACAGAGGAAGGCGCCGGAGAAGAACCACC

NRPD1a	NRPD1a-rtF	TAGCTGATAGTCTCTCTGTTACGGG
	NRPD1a-rtR	GGAGAATGCGTTTCAATGACTGG
NRPD1b	NRPD1b-rtF	ATGATGACAAGACGTTTGTCCTGG
	NRPD1b-rtR	GCCTGAGCCTGAGATGGAGACTGA
At2g34880 *(qPCR)*	At2g34880-qF	CCACTCTTCAAGGTTACTTTGG
	At2g34880-qR	CTCTTCCTTAACTCTAAGCAACAC
At1g61090 *(qPCR)*	At1g61090-qF	AAACTGCTACACTGAGAAGGA
	At1g61090-qR	TAAGGAACACAATACCCACTCT
At3g21830 *(qPCR)*	At3g21830-qF	CACGATCTTTGCTCTCACCA
	At3g21830-qR	AATCGCTGCTTCTTCCTCAG

Primers for cloning

Target	**Primers**	**Sequences (5′-3′)**
SDC	SDC-B1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTCCACAAGACCACAACTCC*
	SDC-B2	GGGACCACTTTGTACAAGAAAGCTGGGTCCGGCTTGAAGTAGATGAGAGG*

*Nucleotide sequences specific to the targets are underlined.

Primers for genotyping

Target	**Primers**	**Sequences (5′-3′)**
NRPD1a	Nrpd1a-4 LP	TGGGTTTGCCATTTTCATATC
	Nrpd1a-4 RP	CCACAAACTCTCCCGTAACAG
NRPD1a	Nrpd1b-12 LP	AGGCACCAAGAAAATGTTTTG
	Nrpd1b-12 RP	TTATTTTTGTCCCTGGAACCC
NRPD2a	Nrpd2a-1 LP	CATTGTCTCTTGGTTTTAGCTCG
	Nrpd2a-1 RP	TCATCAGTGGCTCGGTTTTAC
SDC	S_ 017593-LP	TCATAAACTGCGGTTCCAGAC
	S_ 017593-LP	CGTTCCATATTCCTCCTTTCC
mop9.5	508H08_LP	TCCTATGACTGGACCACGAAC
	508H08_RP	AATTTGCTGCAGGTTTTGATG
mop9.5	462F03_LP	AGCTCATGGGATTCATCAATG
	462F03_RP	TTGGAAGTTGCGAAGATATGG

Primers for genomic bisulfite sequencing

Target	**Primers**	**Sequences (5′-3′)**
SDC-repeat region	Forward	CCACAAACTCTCCCGTAACAG
	Reverse	TACTTATArrTACACATCAAACCCTA
SDC TSS region	Forward	TAGGGTTTGATGTGTAyyTATAAGTA
	Reverse	TAGGGTTTGATGTGTAyyTATAAGTA

Primers for allele specific RT-PCR

Target	**Primers**	**Sequences (5′-3′)**	Enzyme
FWA	FWA-Rtf2	GATCCAAAGGAGTATCAAAGATCT	*Nhe*I
	FWA-dNheI	GCCACTTTTGGTTCCACCAGAACCGGTAGCTA	
SDC	SDC_asF	GGTCAAAGCTACCAGAGGAG	*Nco*I
	SDC_asF	GTGTGACGCGAAAGAATGTG	
FIS2	FIS2_R5018	CCTGCATTGTTTGGGAGTGATAGAA	*180 bp deletion in Col-0*
	FIS2_F3412	GGATGATGTAGGAAATCCCCAATTGAGCCCTTTG	
MOP9.5	MOP9.5-asF	TGATGGATCAGGAGGAGCTT	*Bcl*I
	MOP9.5-asR	GGTGCATGAAGGTGGAATCT	
MINI3	MINI3-F2	GATTCTTCCCAGATTATCCCTC	*Mnl*I
	MINI3-R2	CATTGTACGGCTGATAAGGA	
At2g34880	At2g34880-asF	ATCATTCGGGTTTCAACTGC	*Pvu*II
	At2g34880-asR	CACGACCAAGAACCCAAGAT	
At1g61090	At1g61090F	CCCGGCTATGAAGTTGGTTA	*Mnl*I
	At1g61090R	CTGAAAGCCAATTCCCACAT	
At3g21830	At3g21830asF	CGACGAAAAAGATCATGTTGAA	*Mnl*I
	At3g21830asR	CAGCATTGGTGAGAGCAAAG	