

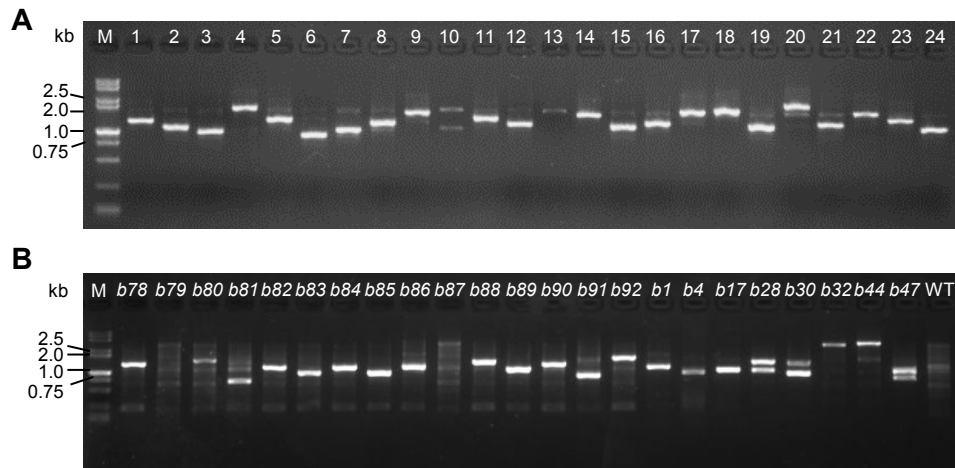


Figure S1. PCR analysis of cDNA clones and inserted fragments in TKS SARE transgenic lines

(A) The PCR products of 24 cDNA clones randomly chosen from the SARE cDNA library. Lanes 1-24 show the PCR products of different clones, respectively. **(B)** An example of the size distribution of the inserted fragments in TKS transgenic lines. M, DNA marker.

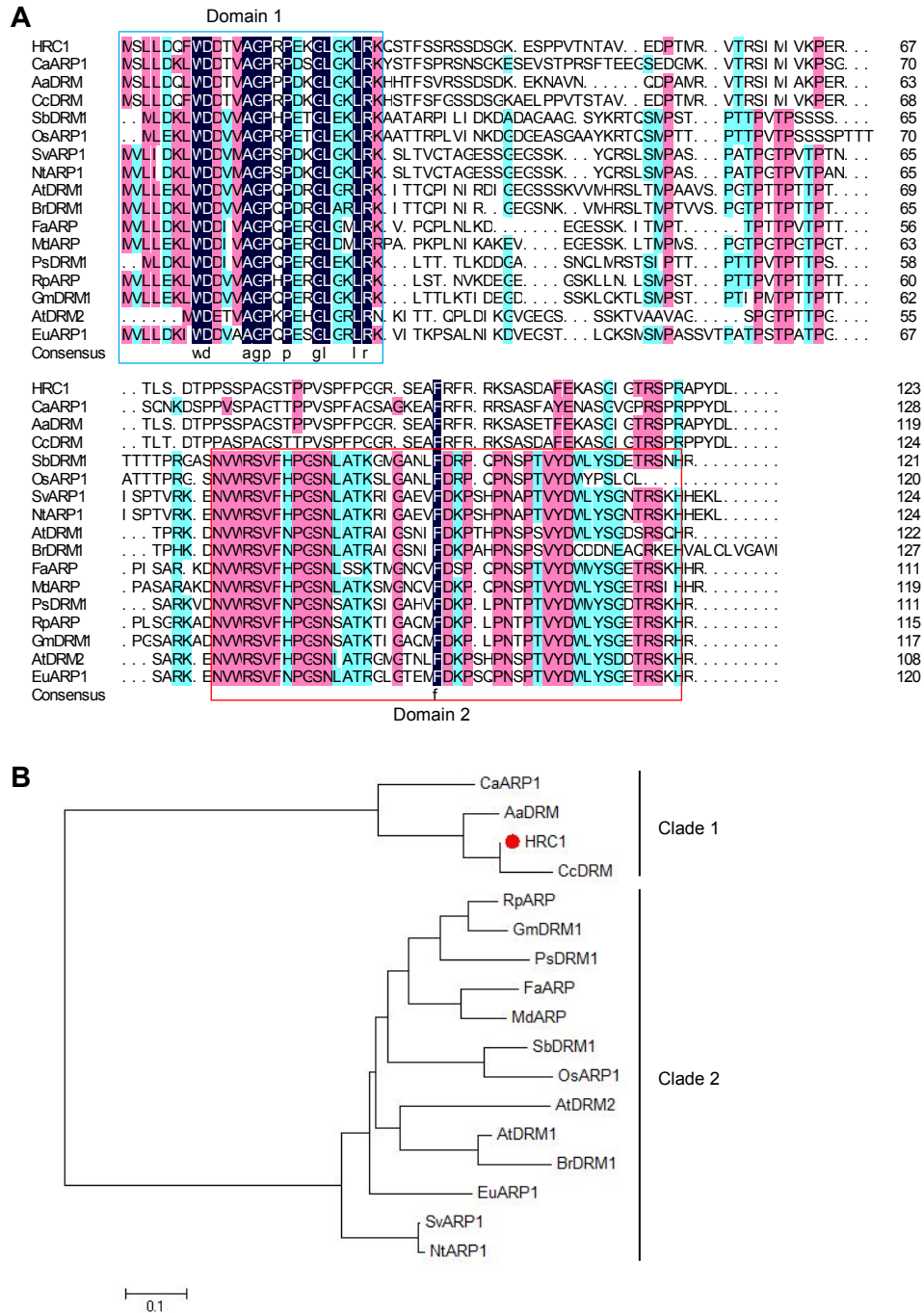


Figure S2. Multiple sequence alignment and a phylogenetic tree of HRC1 and previously reported DRM1/ARP family proteins

(A) The sequence alignment and conserved residues were displayed using the DNAMAN version 8.0 software (Lynnon Biosoft). Identical amino acid residues are highlighted in black, and similar amino acid residues in pink ($\geq 75\%$) or blue ($\geq 50\%$). The blue box indicates the conserved domain at the N-terminal end of ARP/DRM proteins, and the red box indicates the conserved domain at the C-terminal end. The ARP/DRM family proteins used in this alignment are HRC1, *Taraxacum kok-saghyz* Rodin

(in this study, UTG29897.2); AaDRM, *Artemisia annua* (PWA57077); AtDRM1, *Arabidopsis thaliana* (AT1G28330; NP_564305); AtDRM2, *A. thaliana* (AT2G33830; NP_850220); BrDRM1, *Brassica rapa* (ACQ90305); CaARP1, *Capsicum annuum* (XP_016538690); CcDRM, *Cynara cardunculus* (KVH87709); EuARP1, *Elaeagnus umbellata* (AAC62104); FaARP, *Fragaria × ananassa* (AAA73872); GmDRM1, *Glycine max* (NP_001241246); MdARP, *Malus × domestica* (AAA71994); NtARP1, *Nicotiana tabacum* (AAS76635); OsARP1, *Oryza sativa* (ABA95234); PsDRM1, *Pisum sativum* (AAB84193); RpARP, *Robinia pseudoacacia* (AAG33924); SbDRM1, *Sorghum bicolor* (XP_021311495); SvARP, *Solanum virginianum* (AAS75891). **(B)** A Neighbor-Joining tree based on the amino acid sequences of the ARP/DRM family proteins in **(A)**. Evolutionary analyses were conducted using MEGA version 7.0 software (Kumar S et al., 2016).

REFERENCES

Kumar, S., Stecher, G., and Tamura, K. (2016). MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol. Biol. Evol.* **33**: 1870-1874.

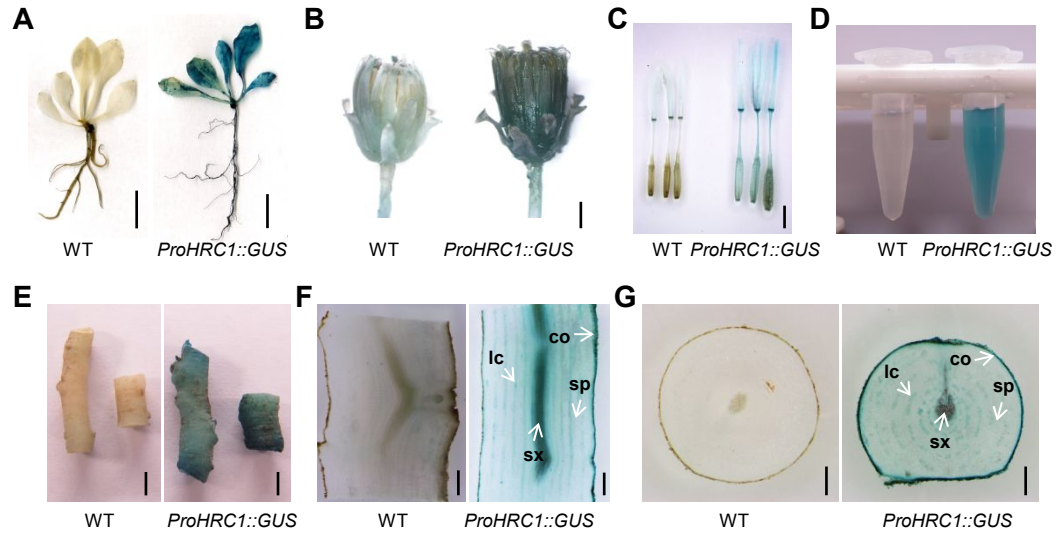


Figure S3. Tissue-specific expression analysis of *HRC1*

Activities of the *HRC1* promoter assayed by GUS staining in seedlings (A), flower buds (B), seeds (C), root latex (D), roots (E), longitudinally sectioned roots (F), and cross-sectioned roots (G) of WT and *ProHRC1::GUS* transgenic T_0 plants. Scale bars in (A) are 1 cm, (B–C, E) are 2 mm, (F–G) are 500 μ m, respectively. co, cork; lc, laticifer cell; sp, secondary phloem; sx, secondary xylem.

Table S1. Analysis of cDNA inserts isolated from TKS SARE mutants

Mutants	Insertion direction	Gene size	Phenotypes	Gene ID	<i>Arabidopsis</i> homolog	Gene function annotation in <i>Arabidopsis</i>
<i>b51</i>	Antisense	Non-full length	More leaves, less rubber threads	cds.evm.model.utg26511.5	<i>AT5G13810.1</i>	Glutaredoxin family protein
<i>b70</i>	Sense	Full length	Large leaves	cds.evm.model.utg7179.2	<i>AT4G39900.1</i>	Unknown protein
<i>b95</i>	Sense	Full length	The leaf surface was not smooth	cds.evm.model.utg10998.7	<i>AT3G53740.4</i>	Ribosomal protein L36e family protein
<i>b127</i>	Sense	Non-full length	Small plant, more rubber threads	cds.evm.model.utg8512.2	<i>AT1G11840.6</i>	Glyoxalase I homolog
<i>b194</i>	Sense	Full length	Large leaves and light green in color	cds.evm.model.utg9618.7	<i>AT2G44080.1</i>	ARGOS-like protein
<i>b248</i>	Sense	Non-full length	The leaf color was yellow and green	cds.evm.model.utg9816.11	<i>AT3G01690.1</i>	Alpha/beta-Hydrolases superfamily protein
<i>b317</i>	Antisense	Non-full length	Early flowering	cds.evm.model.utg7926.7	<i>AT1G19610.1</i>	<i>Arabidopsis</i> defensin-like protein
<i>b322</i>	Antisense	Non-full length	The leaf edge was not smooth	cds.evm.model.utg29063.3	<i>AT5G19130.1</i>	GPI transamidase component family protein
<i>b325</i>	Antisense	Non-full length	More rubber threads	cds.evm.model.utg14388.24	<i>AT5G22250.1</i>	Ribonuclease H-like superfamily protein
<i>c33</i>	Sense	Full length	Single short root	cds.evm.model.utg12289.10	<i>AT2G41430.5</i>	Dehydration-induced protein
<i>c97</i>	Sense	Non-full length	Single long root	cds.evm.model.utg2191.19	<i>AT3G07740.4</i>	Transcriptional adapter
<i>c112</i>	Sense	Full length	More rubber threads	cds.evm.model.utg29897.2	<i>AT1G56220.1</i>	Dormancy/auxin associated family protein
<i>c219</i>	Sense	Full length	Many lateral roots	cds.evm.model.utg29561.2	<i>AT3G02800.1</i>	Tyrosine phosphatase family protein
<i>c670</i>	Sense	Full length	Many branches of root	cds.evm.model.utg36768.2	<i>AT3G12630.1</i>	A20/AN1-like zinc finger family protein
<i>c1196</i>	Sense	Full length	Single short root	cds.evm.model.utg35750.2	<i>AT4G08950.1</i>	Phosphate-responsive 1 family protein

<i>c1198</i>	Antisense	Full length	Anthers color changed	cds.evm.model.utg1316.12	<i>AT3G51030.1</i>	Thioredoxin H-type 1
<i>c1199</i>	Sense	Full length	Flower traits changed	cds.evm.model.utg2370.9	<i>AT5G27700.1</i>	Ribosomal protein
<i>c1528</i>	Sense	Full length	Many lateral roots	cds.evm.model.utg5051.6	<i>AT4G28190.1</i>	Developmental regulator
<i>c1714</i>	Sense	Non-full length	More rubber threads	cds.evm.model.utg23863.10	<i>AT1G15780.1</i>	Unknown protein
<i>c1829</i>	Sense	Non-full length	More rubber threads	cds.evm.model.utg19620.1	<i>AT2G05380.1</i>	Glycine-rich protein 3 short isoform
<i>c2284</i>	Antisense	Non-full length	More rubber threads	cds.evm.model.utg16440.3	<i>AT4G37760.1</i>	Squalene epoxidase
<i>c2349</i>	Sense	Non-full length	More rubber threads	cds.evm.model.utg4192.21	<i>AT2G22780.1</i>	Peroxisomal NAD-malate dehydrogenase
<i>c3304</i>	Antisense	Non-full length	Less rubber threads	cds.evm.model.utg35301.5	<i>AT3G23660.1</i>	Sec23/Sec24 protein transport family protein
<i>c5740</i>	Antisense	Non-full length	Less rubber threads	cds.evm.model.utg8856.6	<i>AT2G42590.2</i>	General regulatory factor
<i>d868</i>	Antisense	Full length	Less rubber threads	cds.evm.model.utg5124.7	<i>AT1G31812.1</i>	Acyl-CoA-binding protein
<i>d1031</i>	Antisense	Non-full length	Less rubber threads	cds.evm.model.utg11341.1	<i>AT2G17570.1</i>	Undecaprenyl pyrophosphate synthetase family protein

Table S2. Primers used in this work

Primer name	Primer sequence (5'-3')	Purpose
Biotin-		
3' Biotin-DSN-attB2-Oligo (dT)	GTTAAGCAGTGGATCAACGCAGAGTGGCCGC ACAACCTTTGTACAAGAAAGTTGGGT(T)19	cDNA library construction
5' DSN-attB1 adapter-F	TCGTCAAGCAGTGGATCAACGCAGAGTGGCC ACAACCTTTGTACAAAAAAGTTGG	cDNA library construction
5' DSN-attB1 adapter-R	pCCAACCTTTTTTGTACAAAGTTGTGGCCACTCT GCGTTGATCCACTGCTTGAC	cDNA library construction
P35S-F1	TCGCATGCCTGCAGGTCAC	Vector amplification
T35S-R1	CCAACCACGTCTTCAAAGC	Vector amplification
P35S-F2	GAGAGAGATAGATTTGTAGAGAG	Vector sequencing
T35S-R2	TCATTTGGAGAGGACTCCGGT	Vector sequencing
<i>c112</i> -Site-1D-F	GAATGCGGATATTTAATCGAAGTG	<i>c112</i> insertion site identification
<i>c112</i> -Site-1D-R	CGATAGAAAACAAAATATAGCGCGC	<i>c112</i> insertion site identification
<i>c112</i> -Site-2D-F	GTTGATGTAAATACGCGTGGAAG	<i>c112</i> insertion site identification
<i>c112</i> -Site-2D-R	TCTTATATGCTCAACACATGAGCG	<i>c112</i> insertion site identification
GW- <i>HRC1</i> -F	GGGGACAAGTTTGTACAAAAAGCAGGCTTA ATGAGCTTACTCGACCAATTCTG	35S:: <i>HRC1</i>
GW- <i>HRC1</i> -R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTC ACAGGTCGTAAGGAGCAC	35S:: <i>HRC1</i>
<i>ProHRC1</i> -F	GGGGACAAGTTTGTACAAAAAGCAGGCTTA GTAATCCAGGAAGCTGAGTGTGTG	<i>ProHRC1</i> :: <i>GUS</i>
<i>ProHRC1</i> -R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTA GCGCAGTAGACAGAAGATGATAAC	<i>ProHRC1</i> :: <i>GUS</i>
q <i>TkGAPDH</i> -Sense	AGTTGGTTTCGTGGTATGAC	qRT-PCR
q <i>TkGAPDH</i> -Anti	ACATGTCAGTGAACAGGTAGAC	qRT-PCR
q <i>HRC1</i> -Sense	CTACACCTCCGGTATCTCCT	qRT-PCR
q <i>HRC1</i> -Anti	GAGGGCTCCTGGTTCCAATC	qRT-PCR
q <i>c112</i> -insertion-sense	TAGCGGTCCACAAAGTCCAC	qRT-PCR
q <i>c112</i> -insertion-anti	CGGATTCAATTGAGCAGCCG	qRT-PCR
q <i>FPS1</i> -Sense	GGAACAAAAGAAAGTCCTAC	qRT-PCR
q <i>FPS1</i> -Anti	CAGCTTCTCATAACTCTTGC	qRT-PCR
q <i>FPS2</i> -Sense	GGAGTAAGGATCCAGGCAGC	qRT-PCR
q <i>FPS2</i> -Anti	CCAAGAAAGATTTTAACACG	qRT-PCR
q <i>GPS1</i> -Sense	GTCGTACTACTCTTCTCCGCATCAGA	qRT-PCR
q <i>GPS1</i> -Anti	GCATCATCAAGTACATCATCGTGAAGG	qRT-PCR
q <i>GPS2</i> -Sense	ATCTAAACCAGCATCAGAAGGGGTT	qRT-PCR
q <i>GPS2</i> -Anti	GCTCATTTGCATTGTTTCACCCGTC	qRT-PCR

qGPS3-Sense	CACTGAGGTGGTATCGCTAATAGCA	qRT-PCR
qGPS3-Anti	TCCATGACTTTTTCCAAGATACTCCAAAGCT	qRT-PCR
qGGPS1-Sense	GGAGGAATTGGGCAAACCG	qRT-PCR
qGGPS1-Anti	TCCGACAACTGTTCTTGAGCC	qRT-PCR
qGGPS2-Sense	ATTTCCGTTAAACGCCTCCCACA	qRT-PCR
qGGPS2-Anti	CGCGTGCAGGAGACGC	qRT-PCR
qGGPS3-Sense	CATGGCAATCCTCGCTGGAG	qRT-PCR
qGGPS3-Anti	CCCGACAGCCCTCCCATAC	qRT-PCR
qGGPS4-Sense	ATGGCGTTTGCAACAGCAATAACTTC	qRT-PCR
qGGPS4-Anti	TCAGATAAGTTCATCTAGAATCTTATCAATAC CGTAGAC	qRT-PCR
qGGPS5-Sense	TCCAAATCCGCACAGGTTTGGAAC	qRT-PCR
qGGPS5-Anti	GTTGTAACATCACTCGATTGGTCAGATTCAA	qRT-PCR

Table S3. Gene accession number used in this work

Gene name	Gene ID
<i>HRC1</i>	cds.evm.model.utg29897.2
<i>GAPDH</i>	cds.evm.model.utg9113.3
<i>FPS1</i>	cds.evm.model.utg4319.82
<i>FPS2</i>	cds.evm.model.utg8010.19
<i>GPS1</i>	cds.evm.model.utg24035.4
<i>GPS2</i>	cds.evm.model.utg10459.2
<i>GPS3</i>	cds.evm.model.utg6677.2
<i>GGPS1</i>	cds.evm.model.utg25318.4
<i>GGPS2</i>	cds.evm.model.utg5986.18
<i>GGPS3</i>	cds.evm.model.utg24832.5
<i>GGPS4</i>	cds.evm.model.utg25316.3
<i>GGPS5</i>	cds.evm.model.utg6181.22