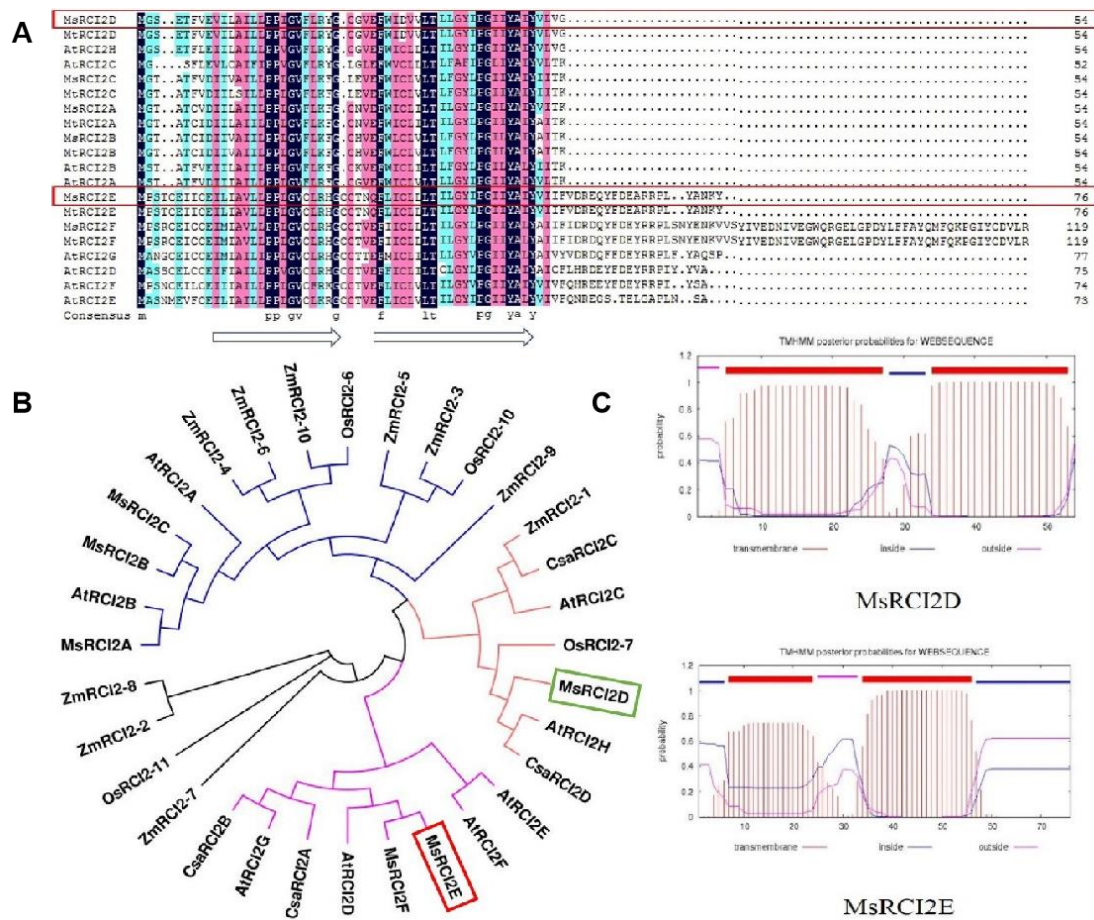


Supplementary Table S1

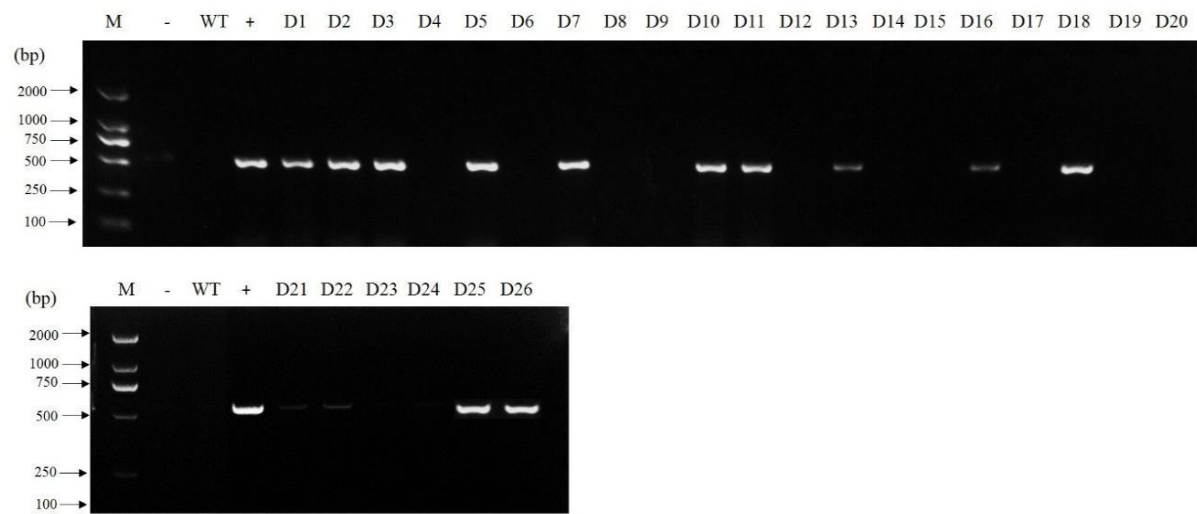
Gene Primer	Sequence of primer (5'-3')	Use for
<i>MsRCI2D</i>	S: ATGGGTTCTGAAACATTTGTGG AS: GGTCATCCAACATAACATAAATGGC	amplification and qPCR
<i>MsRCI2E</i>	S: ATGCCTTCAACTTGTGAAATTATCTGTGAG AS: CTAGTATTTGTTTGCATACAAAGGACGCC	amplification and qPCR
<i>MsRCI2A</i> -qPCR	S: ATATTGAAAATGGGCACTGCTAC AS: TGGAAGATGATGATATGGATCACT	qPCR
<i>MsRCI2B</i> -qPCR	S: ATGGGCACAGCTACATGCATC AS: TCACTTGGTAATAGCATAGATAGCATAGA	qPCR
<i>MsRCI2C</i> -qPCR	S: ATGGGCACAGCTACCTTCG AS: TCACTTAGTGATAATATAGATAGCATAGAT	qPCR
<i>MsRCI2F</i> -qPCR	S: ATGCCTTCACGTTGTGAAAT AS: CTAGTATTGTGATTGTGCATACAAA	qPCR
<i>Cu/Zn-SOD</i>	S: TAATTGCTGATGCCAACG AS: ACCACAGGCTAATCTTCCAC	qPCR
<i>CAT</i>	S: TTCTTCTTCTCCACCGTCCTCA AS: TCCAAGAGAATTGGACCTCTGG	qPCR
<i>GS</i>	S: CTGTCAAATGCCCTTCAATA AS: TGTTTCCTCCTCCTTCTCTC	qPCR
<i>GRI</i>	S: TGTGTCATTTCGTGGTTGTG AS: ACCCGCTATCTTTCCCTC	qPCR
<i>ATPase</i>	S:TTTGTTAATCAGGTAAAGCGATGTG AS: TCCAAGTCAATGTCCGGTTG	qPCR
<i>SOS1</i>	S:TTGCTTACTACACTGCTCAAGA AS: GCGATATAAGCAATCATTTCCCAA	qPCR
<i>NHX1</i>	S:CAATGCCGGGTTTCAAGTAAAG AS:AGTAGCACCCGTGGTTATAATG	qPCR
<i>HKT1</i>	S:TTCATTGTCATGATGTATCTTCCAC AS: CTGAGAGAATATAATACGATCCACTAGG	qPCR
<i>GAPDH</i>	S: GGCTGCATCAAGGAGGAAT AS: TCCAAGCTCAGCCTCATCAAG	qPCR
<i>Bar</i>	S: ATGAGCCCAGAACGACGC AS: TCAAATCTCGGTGACGGGC	PCR selection

Supplementary Figure S1



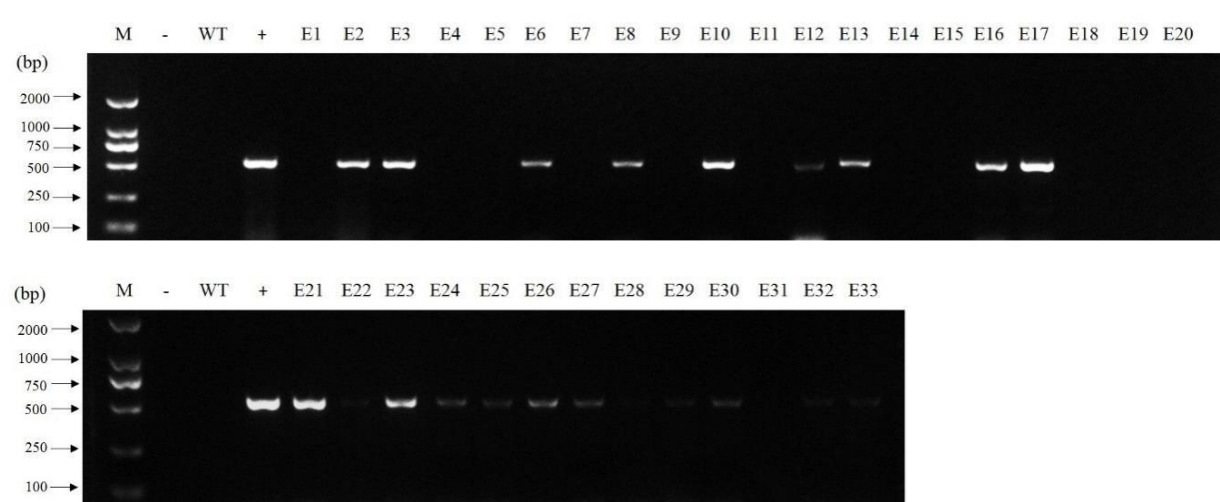
Sequence analysis of MsRCI2s proteins. (A) Amino acid sequence alignment of *RCI2s* genes in alfalfa and *Arabidopsis*; (B) Phylogenetic tree of RCI2 proteins in *Medicago sativa* L, *Arabidopsis thaliana*, *Zea mays*, rice and *Cucumis sativus* L. (C) Transmembrane domain analysis of MsRCI2D/E amino acid sequence.

Supplementary Figure S2



PCR detection of *MsRCI2D* transgenic hairy roots. M: Trans 2K DNA Marker; -: Negative control; +: Positive control; WT: Roots of non-transgenic lines; D1-D26: *MsRCI2D* transgenic hairy roots

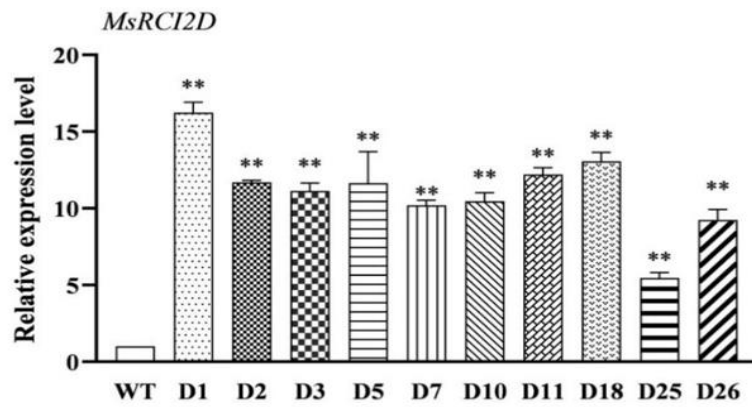
Supplementary Figure S3



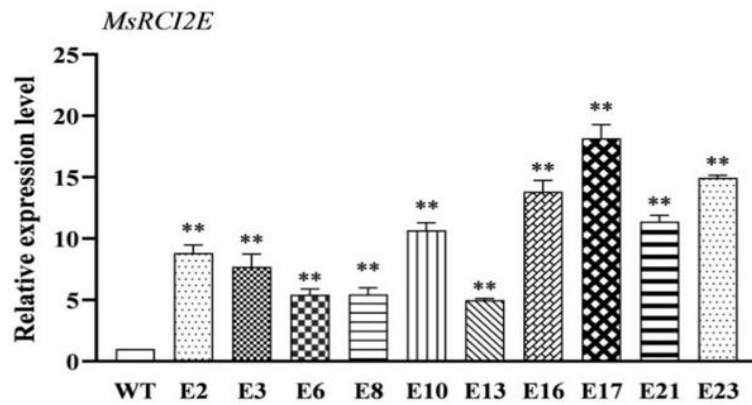
PCR detection of *MsRCI2E* transgenic hairy roots. M: Trans 2K DNA Marker; -: Negative control; +: Positive control; WT: Roots of non-transgenic lines; E1-E33: *MsRCI2E* transgenic hairy roots

Supplementary Figure S4

A



B



Relative expression levels of *MsRCI2D* (A) and *MsRCI2E* (B) in transgenic hairy roots. WT: Roots of non-transgenic lines; D1-D26: *MsRCI2D* transgenic hairy roots; E1-E35: *MsRCI2E* transgenic hairy roots. * indicates significant difference ($p < 0.05$), ** indicates extremely significant difference ($p < 0.01$)