

Figure S1 Positive transgenic lines identified by PCR (A). Relative expression levels of *rcnA* in various *35S::rcnA* transgenic lines (B).

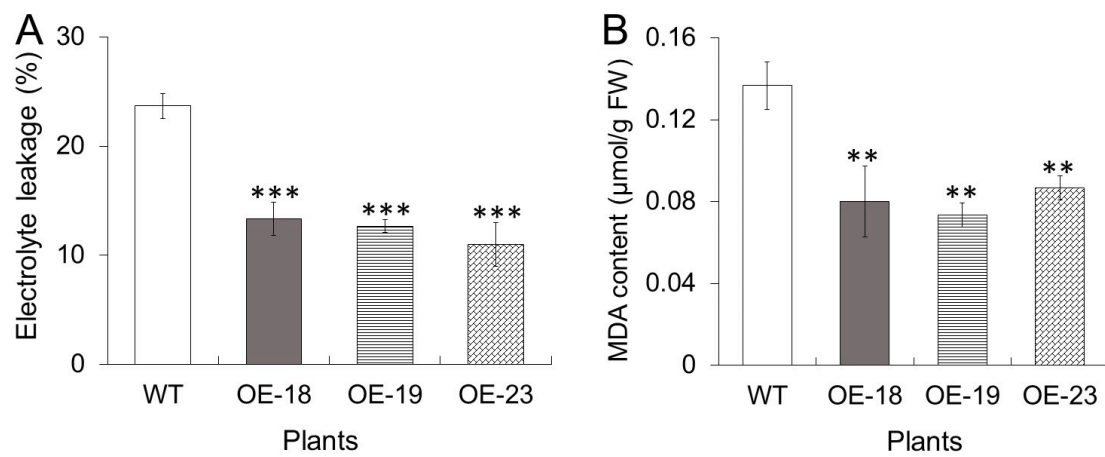


Figure S2 The electrolyte leakage (A) and malondialdehyde (MDA) content (B) in shoots of wildtype and *rcnA*-OE transgenic plants grown for two weeks in nutrient solution containing 5 mM NiCl_2 . Values were means \pm SD. Asterisk *, **, and *** indicate a significant difference between a transgenic line and WT at $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively, using the Student's t-test in Microsoft Excel.

Table S1 Primer sequences used in this study

Name	sequence (5'→3')	Application	Note
rA-F1	TCAGATCTATGACCGAATTTACAACCTCTTCTT	amplifying coding sequence of <i>rcnA</i> for constructing 35S:: <i>rcnA</i>	BglII site as underlined
rA-R1	TTCACGTGTTATCGCATTATGCCCATG	amplifying coding sequence of <i>rcnA</i> for constructing 35S:: <i>rcnA</i>	PmlI site as underlined
rA-F2	acgggggactcttgaccatggGAATGACCGAATTTACAACCTCTTCTTCA	amplifying coding sequence of <i>rcnA</i> for constructing 35S:: <i>rcnA-GFP</i>	nucleotides in lower case being homologous recombination arm
rA-R2	aagttcttctctttactagtTCGCATTATGCCCATGAAGC	amplifying coding sequence of <i>rcnA</i> for constructing 35S:: <i>rcnA-GFP</i>	nucleotides in lower case being homologous recombination arm
qrA-F	GCTGGAGCGGATTTAACACT	qPCR measuring expression of <i>rcnA</i> in transgenic 35S:: <i>rcnA</i> Arabidopsis lines	
qrA-R	CCATGTACGCCCATATACACA	qPCR measuring expression of <i>rcnA</i> in transgenic 35S:: <i>rcnA</i> Arabidopsis lines	
qUBQ10-F	CACACTCCACTTGGTCTTGCGT	<i>AtUBQ10</i> (At4g05320) as qPCR internal control	
qUBQ10-R	TGGTCTTTCCGGTGAGAGTCTTCA	<i>AtUBQ10</i> (At4g05320) as qPCR internal control	