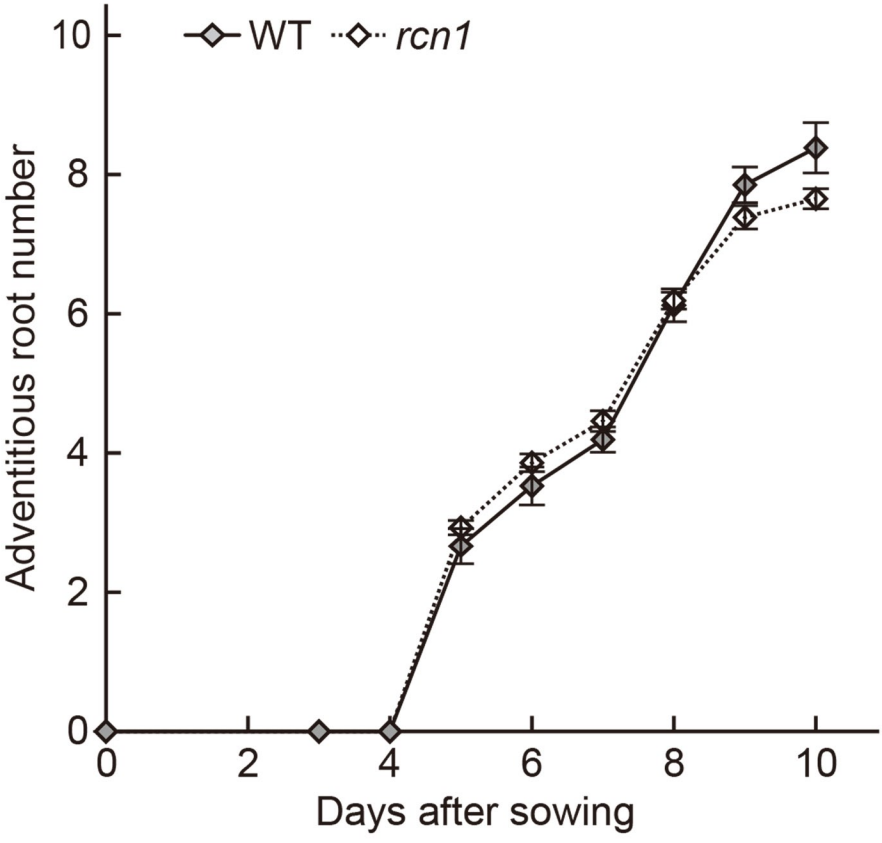
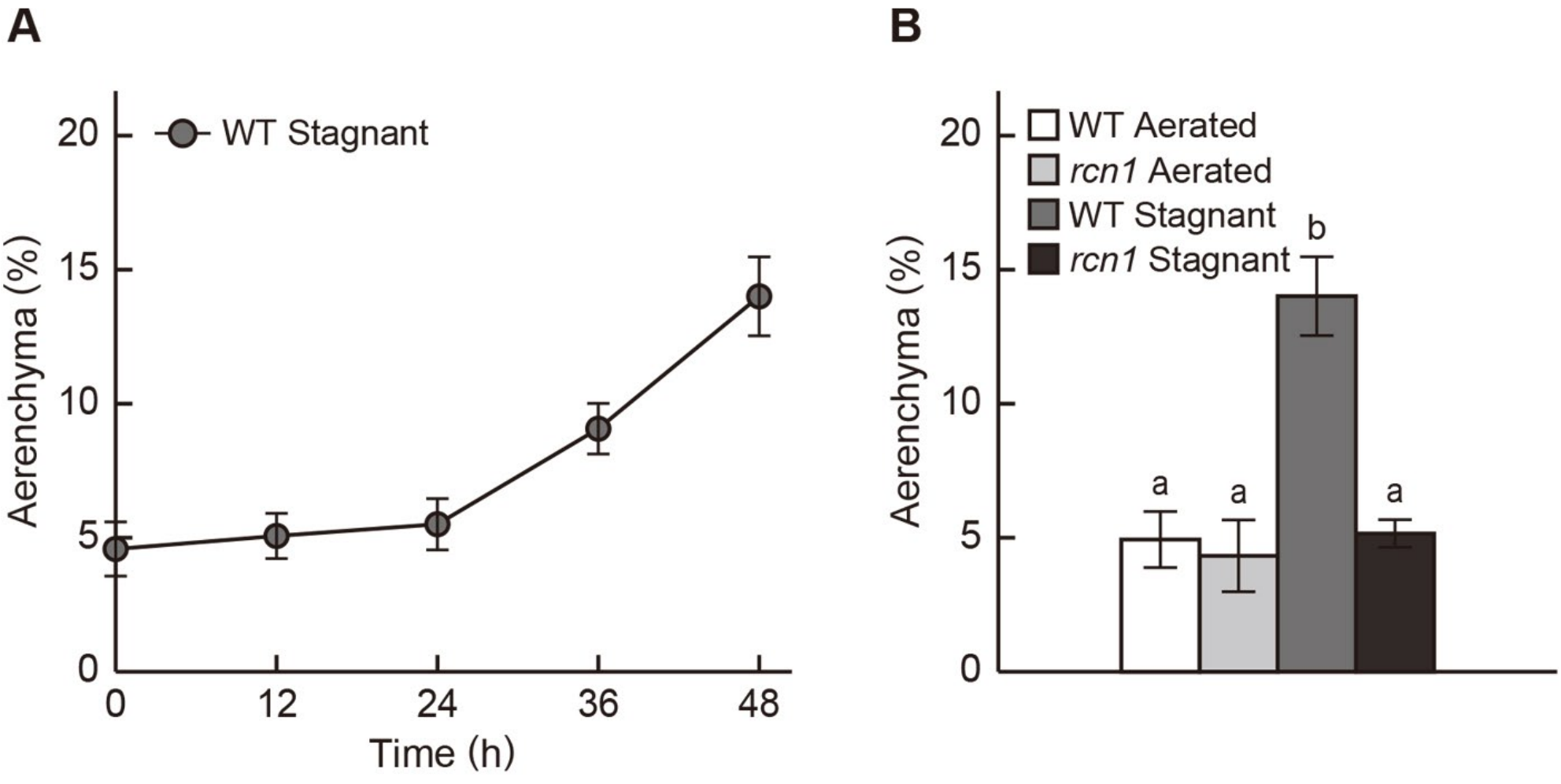
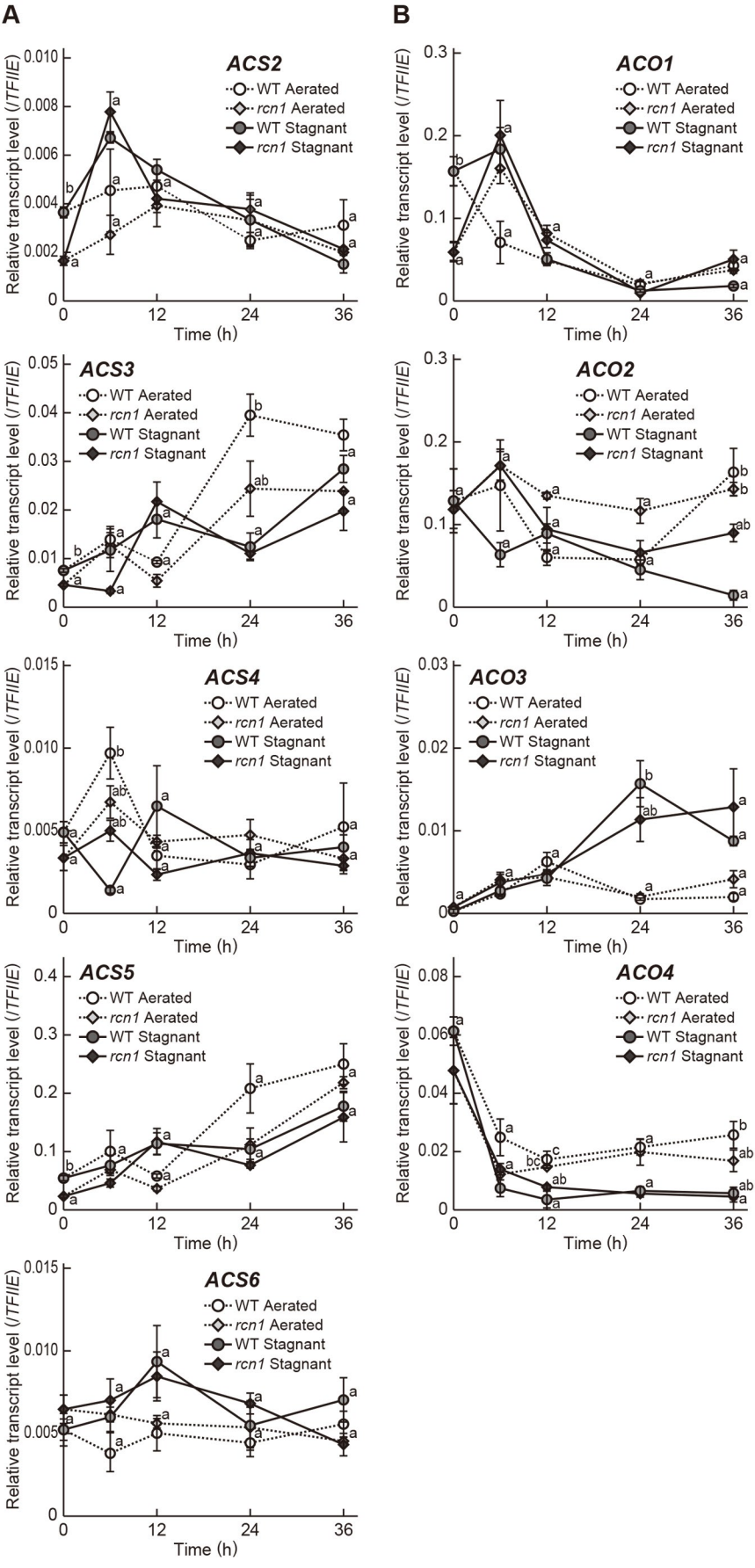


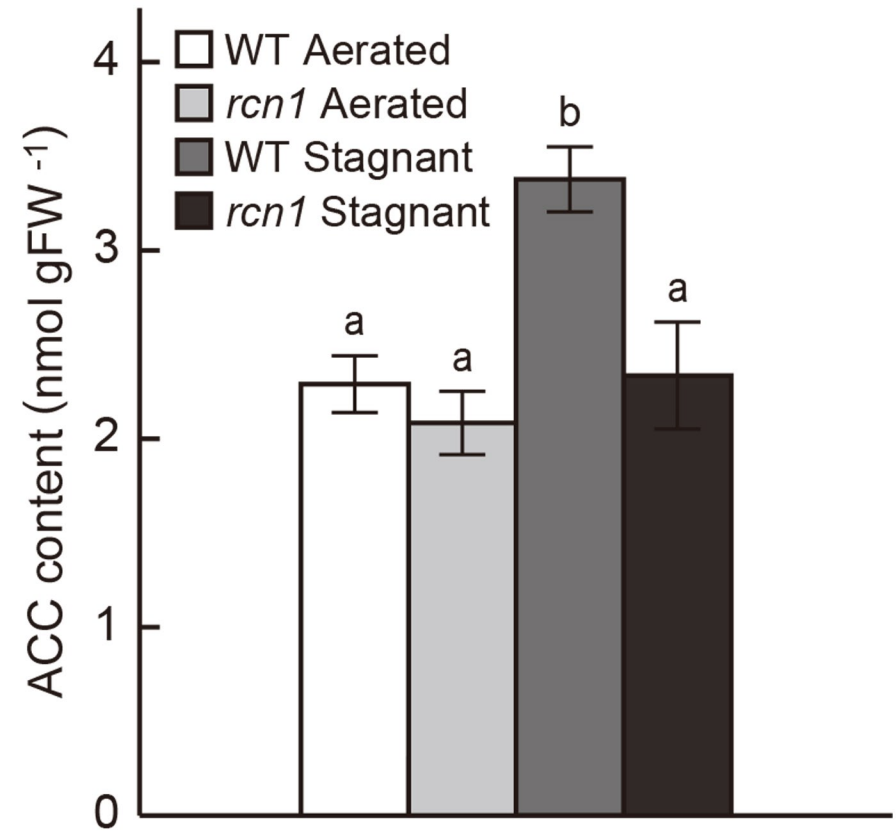
Supplemental Figure S1. Emergence of adventitious roots of the wild type and the *rcn1* mutant grown under aerated conditions. Emerged adventitious root numbers of the wild type and the *rcn1* mutant grown under aerated conditions were counted every day until day 10. Values are means (n = 15) ± SE. No Significant differences were observed between the wild type and the *rcn1* mutant at $P < 0.01$ (two sample *t* test).



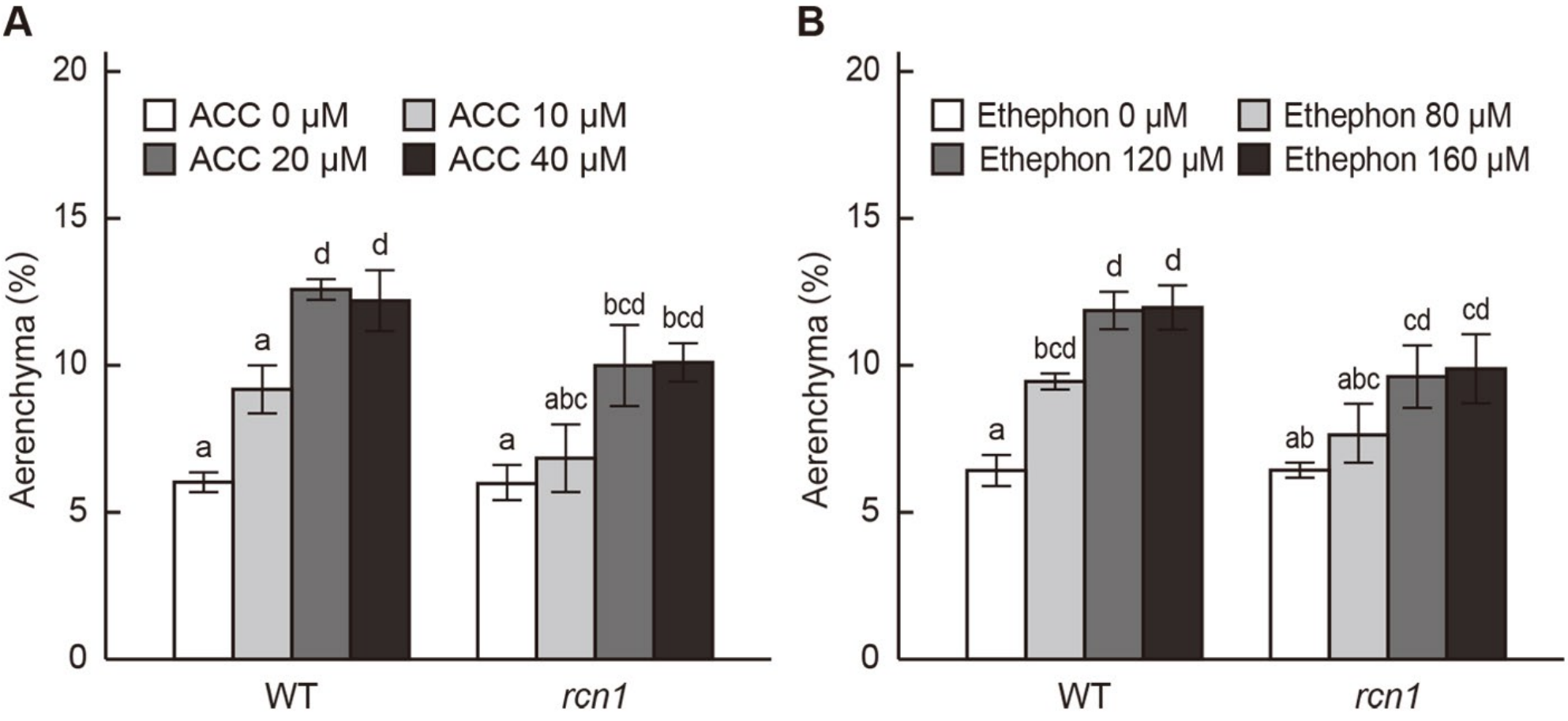
Supplemental Figure S2. Aerenchyma formation at 20 mm from the tips of adventitious roots in the wild type and the *rcn1* mutant. Twenty-d-old aerobically grown rice seedlings were transfered to aerated or stagnant conditions. Time-course of aerenchyma formation at 20 mm from the tips of adventitious roots in the wild type under stagnant conditions (A). The percentage of aerenchyma of root-cross-sectional area at 20 mm from the tips grown under aerated or stagnant conditions for 48 h (B). Values are means (n = 6) ± SE. Different lower-case letters denote significant differences between the wild type and the *rcn1* mutant in each condition ($P < 0.01$, one-way ANOVA and then Tukey's test for multiple comparisons).



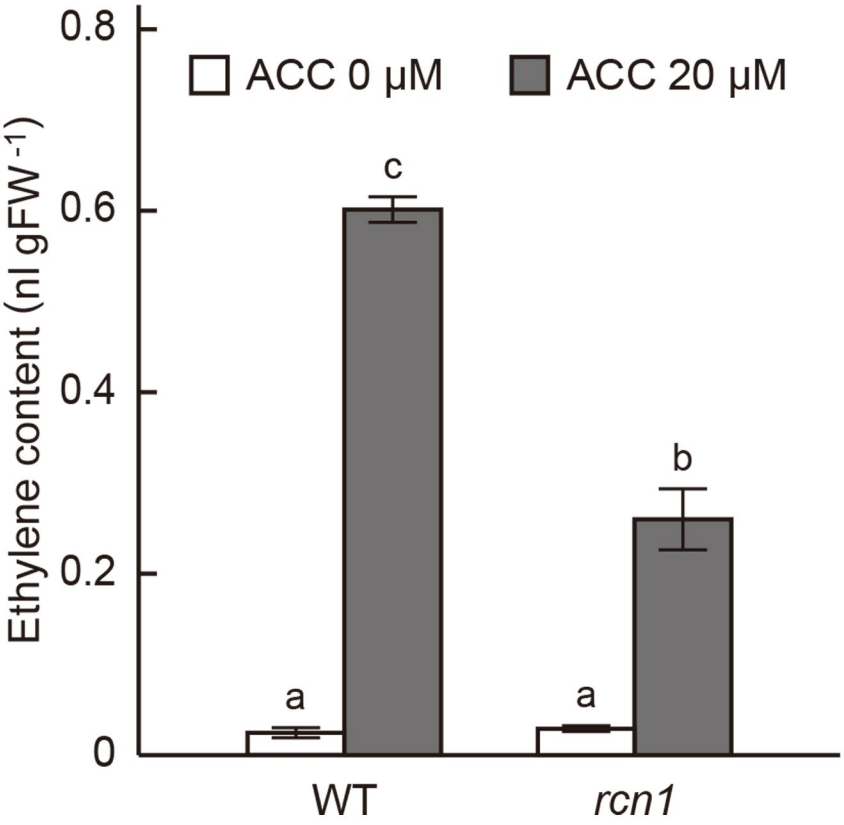
Supplemental Figure S3. Expression of genes encoding ethylene biosynthesis enzymes in adventitious roots of the wild type and the *rcn1* mutant grown under aerated or stagnant conditions. Time-course qRT-PCR analyses of the *ACS* genes (A) and the *ACO* genes (B) using RNAs extracted from adventitious roots at 10 mm (±2 mm) from the root tips grown under aerated or stagnant conditions. The transcription initiation factor *TFIIE* gene was used as a control. Values are means (n = 3) ± SE. Different lower-case letters denote significant differences between the wild type and the *rcn1* mutant in each condition ($P < 0.01$, one-way ANOVA and then Tukey's test for multiple comparisons).



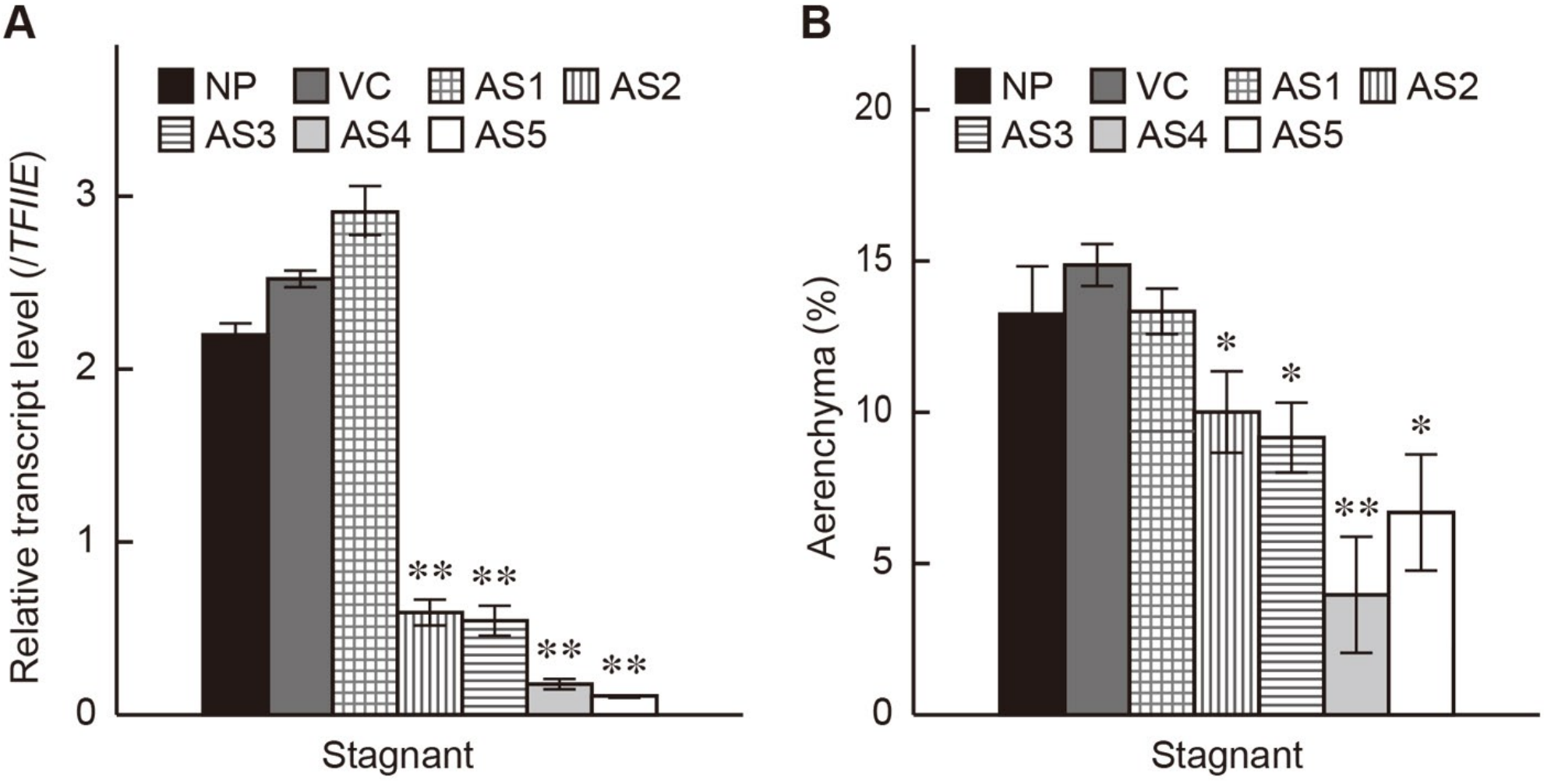
Supplemental Figure S4. ACC contents in adventitious roots of the wild type and the *rcn1* mutant. ACC content was measured at 10 to 30 mm from the root tips grown under aerated or stagnant conditions for 12 h. Values are means (n = 3) ± SE. Different lower-case letters denote significant differences between the wild type and the *rcn1* mutant in each condition ($P < 0.01$, one-way ANOVA and then Tukey's test for multiple comparisons).



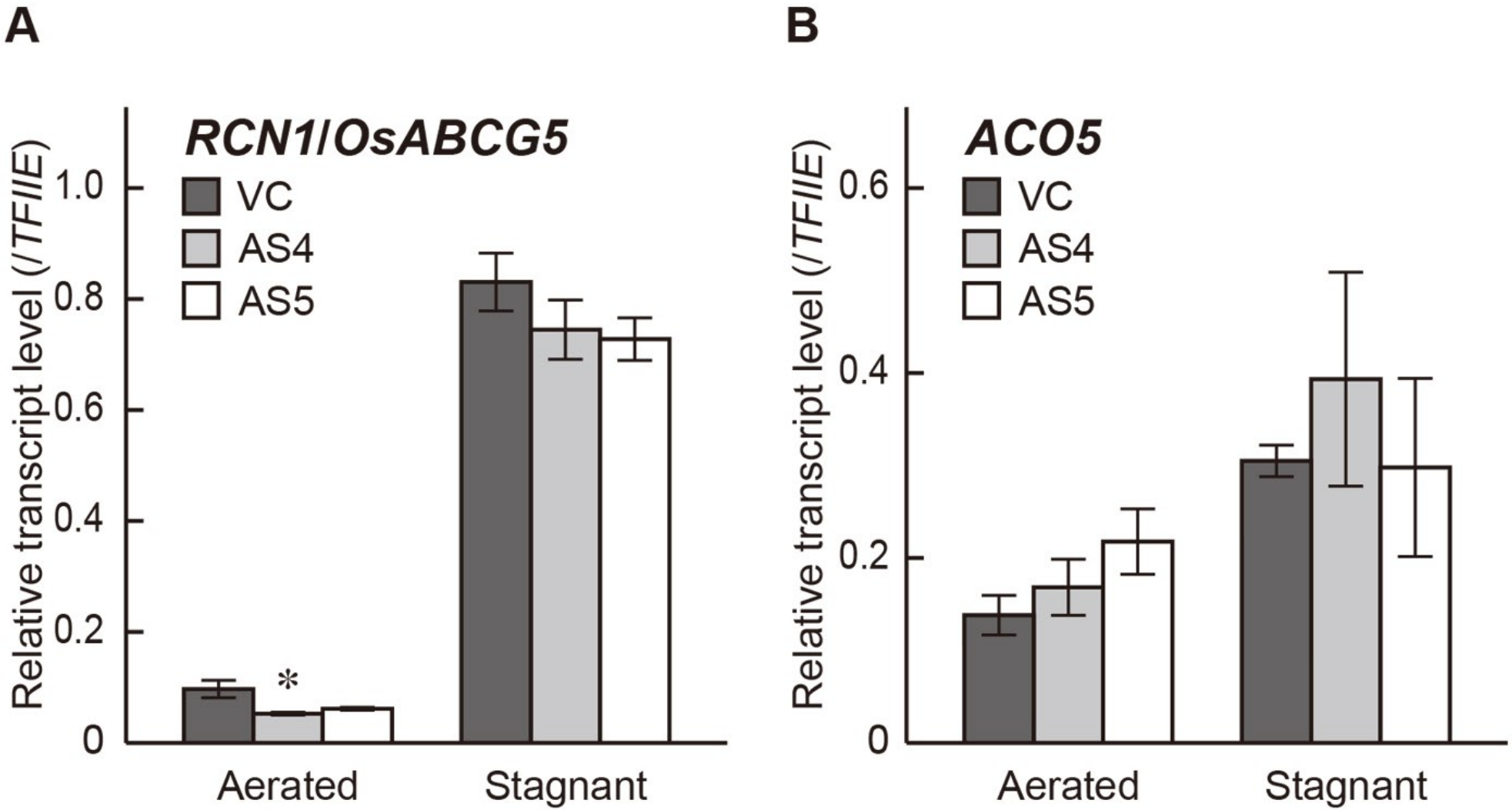
Supplemental Figure S5. Effects of an ethylene precursor and an ethylene-releasing compound on aerenchyma formation at 20 mm from the tips of adventitious roots of the wild type and the *rcn1* mutant. The percentage of aerenchyma of root-cross-sectional area at 20 mm from the tips of adventitious roots grown under aerated conditions for 48 h with 0, 10, 20 or 40 μM ACC treatment (A), and grown under aerated conditions for 48 h with 0 80, 120 or 160 μM ethephon treatment (B). Values are means (n = 6) ± SE. Different lower-case letters denote significant differences between the wild type and the *rcn1* mutant in each condition ($P < 0.01$, one-way ANOVA and then Tukey's test for multiple comparisons).



Supplemental Figure S6. Ethylene contents in roots of the wild type and the *rcn1* mutant grown under aerated conditions with or without 20 μM ACC treatment. Ethylene content was measured in roots at 24 h after initiation of growth under aerated conditions with or without 20 μM ACC treatment. Values are means (n = 3) ± SE. Different lower-case letters denote significant differences between the wild type and the *rcn1* mutant in each condition ($P < 0.01$, one-way ANOVA and then Tukey's test for multiple comparisons).



Supplemental Figure S7. Expression of the *CUT1L* gene and aerenchyma formation in adventitious roots of the *pACT1*::*CUT1L*-antisense T_0 transgenic lines. The percentage of aerenchyma of root-cross-sectional area at 10 mm (A) and at 20 mm (B) from the tips of adventitious roots of the wild type (Nipponbare; NP), the *pACT1*::*CUT1L*-antisense T_0 transgenic lines (AS1 to AS5) and the vector control (VC) grown under stagnant conditions for 48 h. All transgenic lines had a cv. Nipponbare background. Values are means (n = 3) ± SE. Significant differences between each of the transgenic lines and the vector control at $P < 0.01$ or at $P < 0.05$ (two sample *t* test) are denoted by ** or *, respectively.



Supplemental Figure S8. Expression of *RCN1*/*OsABCG5* and *ACO5* in adventitious roots of the *pACT1*::*CUT1L*-antisense T_1 transgenic lines. qRT-PCR analyses of the *RCN1*/*OsABCG5* gene (A) and the *ACO5* gene (B) using RNAs extracted from adventitious roots at 10 mm (±2 mm) from the root tips of the *pACT1*::*CUT1L*-antisense T_1 transgenic lines (AS4 and AS5) and the vector control (VC) grown under aerated or stagnant conditions for 36 h. All transgenic lines had a cv. Nipponbare background. The transcription initiation factor *TFIIE* gene was used as a control. Values are means (n = 3) ± SE. Significant differences between each of the transgenic lines and the vector control at $P < 0.05$ (two sample *t* test) are denoted by *.

Supplemental Table S1. List of primers used for qRT-PCR analysis

Gene Name	ID (RAP-DB)	Forward primer sequence	Reverse primer sequence
ACC synthase (ACS)			
ACS1	Os03g0727600	5’-ACAAAACCACACCATGTCCA-3’	5’-CGAAAGGAATCTGCTACTGCTGC-3’
ACS2	Os04g0578000	5’-CACCACCACCACCTCAGC-3’	5’-GACGTAGTAAGGCGCAGCAT-3’
ACS3	Os05g0196600	5’-GAGGCGAAGCTGAACATCTC-3’	5’-CATGTTGTTCTTGCTCCCATT-3’
ACS4	Os05g0319200	5’-AGCTGAGGCTGTGGGACA-3’	5’-GTGGCCAGGCTCATGTTC-3’
ACS5	Os01g0192900	5'-GCTTGGACACGCTGGATCTT-3'	5'-TTATTGCTGTTCTTGCTGCTG-3'
ACS6	Os06g0130400	5’-GGATGGTTCAGGTGTTGCTT-3’	5’-CCTGGCAAAGCAGTTATTCC-3’
ACC oxidase (ACO)			
ACO1	Os09g0451000	5'-GATAGCGTGTGTACCACAGCGACC-3'	5'-AGGTAGAAAACGCGAGCTGA-3'
ACO2	Os09g0451400	5'-AAGTCCATGGAAACCGAGAC-3'	5'-CCACAGTTCATGCACACACA-3'
ACO3	Os02g0771600	5'-GAGGTTCGTGTTCGAGGACT-3'	5'-CGCAGCCGTAGCTAGTGAAG-3'
ACO4	Os11g0186900	5'-GCATGGCCAACATTGCTC-3'	5'-GTTCGCCAGGGCTGCGAACC-3'
ACO5	Os05g0149400	5'-CGAGTACCCGGAGTACGTGTT-3'	5'-ATTTTGGCGCCTTGACGGCC-3'
ACO7	Os01g0580500	5'-GGACTACTACCAGGGCACCA-3'	5'-GATTAGCGCACGCGATTTTA-3'
G-type ABC transporter			
RCN1/*OsABCG5*	Os03g0281900	5'-AAGTGGGAGTGCCTCTGGAT-3'	5'-GGTGAGACGAGGTGACGAT-3'
Fatty acid elongase (β-ketoacyl-CoA synthase; KCS)			
CUT1L	Os03g0220100	5’-AAGTGCCTCCGCACAGTC-3’	5’-ACCATGGATTCGATCACAGC-3’
***CUT1L* 5'-UTR primers for the *CUT1L*- antisense transgenic lines**			
CUT1L5UTR	Os03g0220100	5'-CCATCACCAACACACCACTG-3'	5'-TCCTACGTACGACTTTAGTTTCTTC-3'
Control			
TFIIE	Os10g0397200	5’-GTGCAGCCCAAGGCTAAG-3’	5’-CGTCGAATAAGCGTAGAGCA-3’