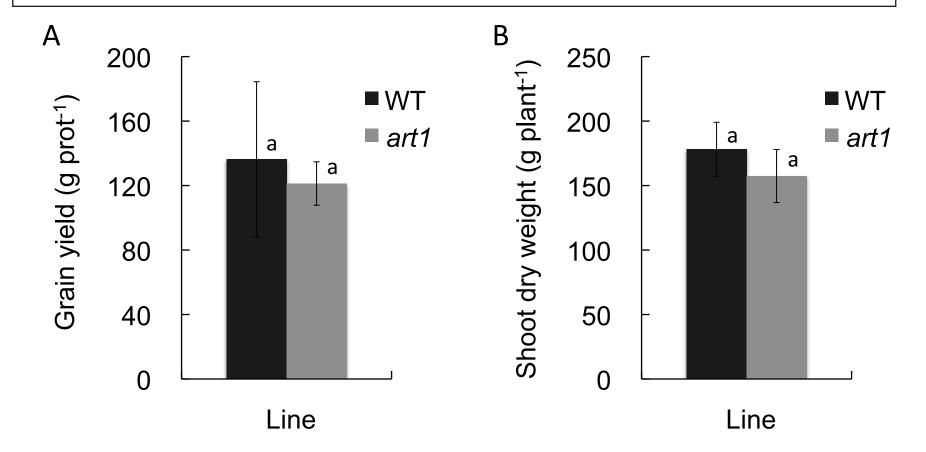
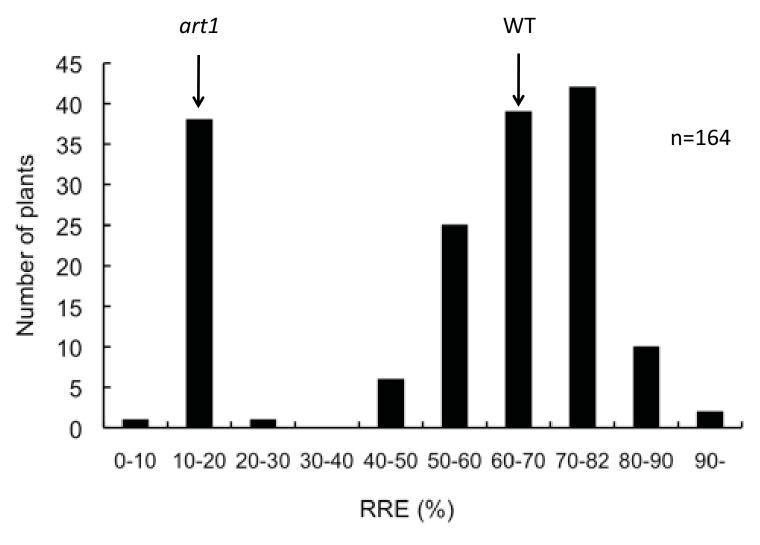
Supplemental Data. Yamaji et al. (2009). A Zn-finger transcription factor ART1 regulates multiple genes implicated in aluminum tolerance in rice.

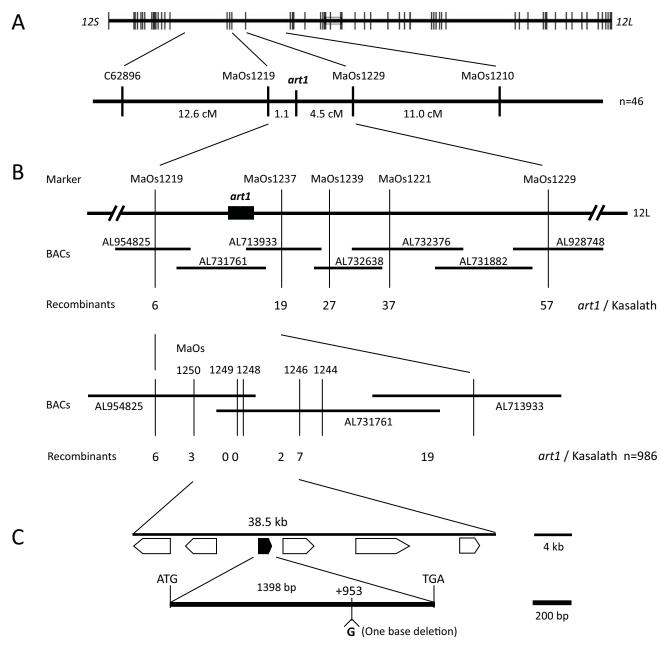


Supplemental Figure 1. Air-dried weight of shoot and grain yield of both WT rice and art1 grown in a field. Both WT rice (cv. Koshihikari) and art1 mutant were cultivated in a field (soil pH 6.5) at an experimental farm of Okayama University in 2006. Three replicates of a plot (1 m × 0.4 m) were made for each line. Plant growth and yield were investigated at harvest. (A) Grain yield. (B) Shoot dry weight. Data are means \pm SD (n = 3 biological replicates). Same letters indicate no significant differences at P > 0.05 by Student t test.



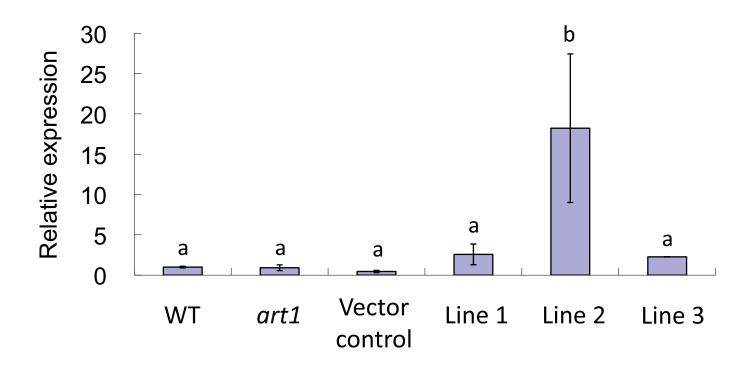
Supplemental Figure 2. Frequency distributions of Al sensitivities in an F_2 population from a backcross between the mutant (art1) and WT.

Four-day-old seedlings were exposed to a 0.5 mM $CaCl_2$ solution (pH 4.5) for 24 h and then transferred to 20 μ M Al solution containing 0.5 mM $CaCl_2$ (pH 4.5) for a further 24 h. Relative root elongation (RRE) used for evaluation of their sensitivities to Al was calculated as: root elongation with Al / root elongation without Al×100.

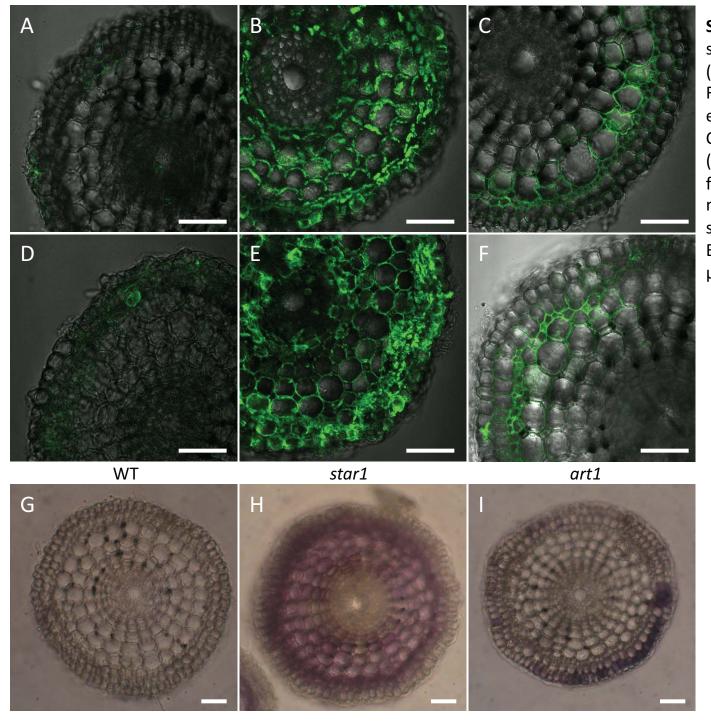


Supplemental Figure 3. Map-based cloning of ART1.

(A) Rough mapping of ART1 on the short arm of chromosome 12. Forty-six F2 mutants from art1/ Kasalath population were used and genetic distances (cM) between two neighbor markers were shown. (B) Fine mapping of ART1 by using 986 F2 plants from art1/Kasalath population. Vertical lines represent molecular markers and the numbers below them indicate recombinants between each marker and the gene. lines Overlapped horizontal indicate the BAC clones. ART1 was finally mapped to a 38.5 kb candidate region between InDel MaOs1250 marker and MaOs1246. (C) Cloning of ART1. Six candidate genes are predicted to be located in the 38.5 kb region based on the pseudomolecules of genome annotation on TIGR website. Sequencing of the ORFs of the six candidate genes revealed that one gene (black box) had one-bp deletion in the mutant. The gene has no intron and is 1398 bp in length. The onebp (G) deletion in the mutant is indicated, 953 bp from the ATG.



Supplemental Figure 4. Expression levels of ART1/art1 in complementation lines and the control plants. Root of WT rice (cv. Koshihikari), art1 mutant, three independent transgenic complementation lines with genomic fragment of ART1 (Line 1 to 3) and vector control line of complementation test were used for quantitative RT-PCR to determine relative expression of ART1/art1. Histone H3 was used as an internal control. These expression levels include both endogenous ART1/art1 and transgenic ART1. Data are means \pm SD (n = 3 biological replicates). Different letters indicate significant differences at P < 0.05 by Tukey's test.



Supplemental Figure 5. Root Al staining in WT(A,D,G), star1 (B,E,H) and art1 (C,F,I). Four-day-old seedlings were exposed to 30 μ M Al in 0.5 mM CaCl₂ solution (pH 4.5) for 9 h (A-C) or 24 h (D-I) and then free-hand cross sections at 2 mm from the root tip were stained by Morin (A-F) or Eriochrome cyanine R. Bars = 50 μ m.

Supplemental Table 1. Primers for InDel markers used in mapping ART1

Primer Name	Forward (5'3')	Reverse (5'3')
C62896	GAGAAATCAAATCGGGCCAC	AAGGGCAAGATGCATTCGAC
MaOs1210	CGCAGGGAAGCAAAATTAAC	CACCTTATGGAGCATTCAGTTGTA
MaOs1219	CCCATGTAGAAGCCAAAGATAAG	CGTTGGATGATGGAAGG
MaOs1221	CTGCCTGCTGGATAGGACTTT	GTTTTCGCTGGATCTTTTGGTA
MaOs1229	TTCCTCATGGGATCACTTGC	TGGTGCATCAGCCATAAAACT
MaOs1237	GGCTACACTTATTTTGCGACG	ACCTCCAACTACCCACTCACC
MaOs1239	TGAGGGCACAAATGAATGG	AAATCTGACGAGCGACAAAAG
MaOs1244	TTATTCCACCAAAGATTAAGGG	GGTTCTGATTCCAAGTCACAGG
MaOs1246	TTACGGTCAACAATTCACCAA	CAAGAATTTAGAAACGAAAGGGAG
MaOs1248	GCCCGCTTCTTCTTGTGG	CCTCCGTCCTCTGGTGCTAC
MaOs1249	GAGCATTGCCCTTTTACACC	CCACTGGGATTCTCACTTCG
MaOs1250	GTTCATAGGGCAAAATGGTTAAG	TACCGAGCAGCGAGTAGG