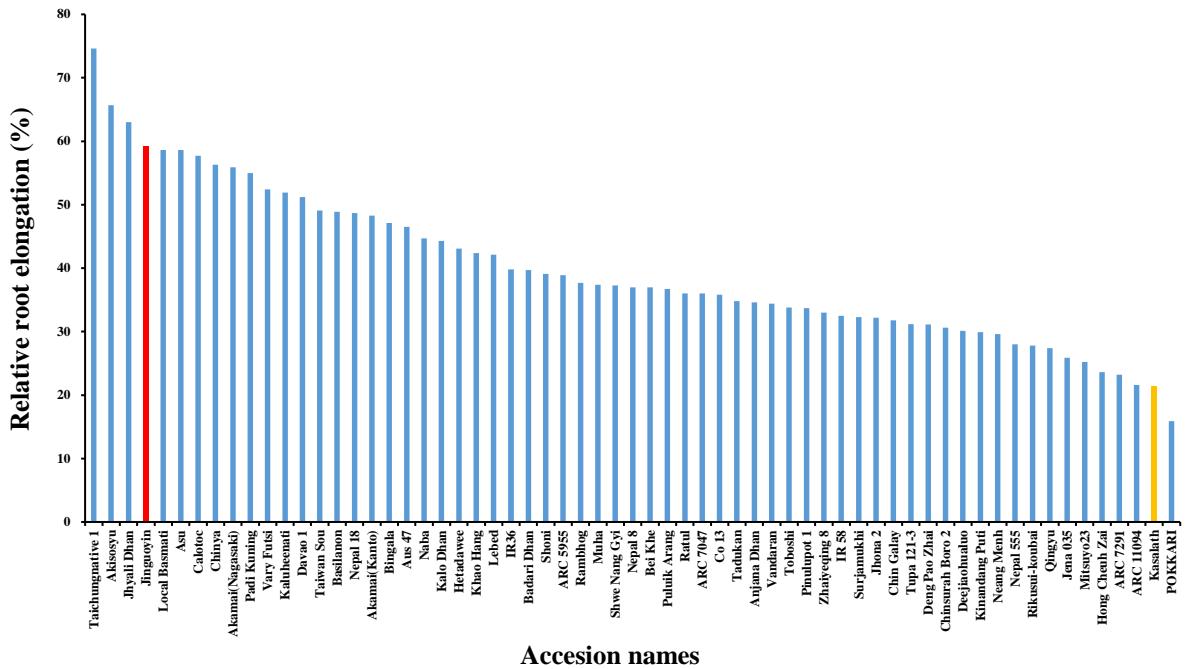
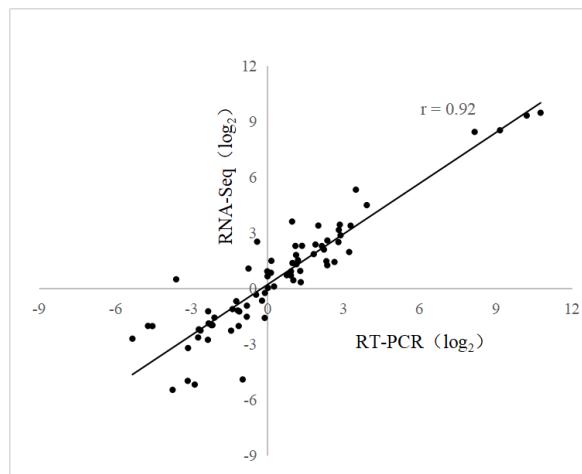


Supplementary Materials:



Supplementary Figure 1. Al tolerance of 65 *indica* rice varieties. Four-day-old seedlings were exposed to a 0.5 mM CaCl₂ (pH 4.5) solution containing 0 or 30 μM Al for 24 h. Relative root elongation was calculated as the following: root elongation with Al/root elongation without Al × 100.



Supplementary Figure 2. Correlation of the gene expression ratio between RNA-seq data and quantitative real-time PCR (qRT-PCR) results. There were 17 genes randomly selected and subjected to qRT-PCR analysis. *Histone H3* was used as an internal standard. qRT-PCR data (fold change of the gene expression in response to Al) were plotted against data (fold change of the gene expression in response to Al) from RNA-seq. Both x and y-axes are shown in a log₂ scale. r indicates the correlation coefficient.

(a)

```

ART1-promoter_([Jinguoyin]).seq
ART1-promoter_([Kasalath]).seq
ART1-promoter_([Nipponbare]).seq
Consensus

```

(b)

```

ART1-CDS_([Jinguoyin]).seq
ART1-CDS_([Kasalath]).seq
ART1-CDS_([Nipponbare]).seq
Consensus

```

Supplementary Figure 3. Sequence comparison of the promoter (a) and coding sequence (CDS) regions (b) of *ART1* between Kasalath and Jinguoyin. The promoter and coding region sequences of Kasalath and Jinguoyin data were taken from the genome resequencing data, while the reference sequence of Nipponbare was taken from RAP-DB (<https://rapdb.dna.affrc.go.jp/>) and aligned by ClustalW.

