Supplementary Methods

Method S1. Plant tissues sampled for transcriptome analysis.

Floral buds were sampled in natural populations in Guangxi Zhuang Autonomous Region, China, in mid-April (April 15–17), and sample information is shown in Table S1. Those samples were snap-frozen in liquid nitrogen and stored at -80 ℃ until RNA isolation for transcriptome sequencing.

Method S2. RNA isolation, quantification, and qualification.

RNA was isolated using an RNeasy Plant Mini kit (QianGen). Extracted RNA was checked for degradation and contamination using 1% agarose gels and a NanoPhotometer spectrophotometer (Implen, CA, USA), respectively, and then quantified with a Qubit RNA Assay kit on a Qubit 2.0 fluorometer (Life Technologies). RNA integrity was assessed on a Bioanalyzer 2100 system (Agilent) using the supplied RNA Nano 6000 assay kit.

Method S3. Library preparation and sequencing.

Three μg of total RNA per sample was used as input material for the RNA library preparations. Firstly, ribosomal RNA was removed by Epicentre Ribo-zero™ rRNA Removal kit (Epicentre, USA), and the rRNA-free residue was cleaned up by ethanol precipitation. Subsequently, sequencing libraries were generated using the rRNA-depleted RNA by NEBNext Ultra™ Directional RNA Library Prep kit for Illumina (NEB, USA) following the manufacturer's recommendations. Briefly, fragmentation was carried out using divalent cations under elevated temperature in NEBNext First Strand Synthesis Reaction Buffer (5×). First-strand cDNA was synthesized using random hexamer primer and M-MuLV Reverse Transcriptase, RNaseH minus (Promega). Second strand cDNA synthesis was subsequently performed using DNA Polymerase I and RNase H. In the reaction buffer, dNTPs with dTTP were replaced by dUTP. The remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure was ligated to prepare for hybridization. In order to select cDNA fragments preferentially 250–300 bp in length, the library fragments were purified with the AMPure XP system (Beckman Coulter, Beverly, USA). Then, 3 μl USER Enzyme (NEB, USA) was used with size-selected, adaptor-ligated cDNA at 37°C for 15 min followed by 5 min at 95°C before PCR. Then PCR was

performed with Phusion High-Fidelity DNA polymerase, Universal PCR primers, and Index (X) Primer. At last, products were purified (AMPure XP system) and library quality was assessed on the Agilent Bioanalyzer 2100 system. The libraries were sequenced on an Illumina NovaSeq 6000 platform and 150 bp paired-end reads were generated.

Method S4. Bioinformatics identification of mRNAs.

Clean data were obtained by removing reads containing adapters, reads containing poly-N, and low-quality reads from the raw data. The clean data of high quality were mapped to the reference genome. An index of the reference genome was built using Bowtie v2.0.6 (Langmead *et al*., 2009) and paired-end clean reads were aligned to the reference genome using TopHat v2.0.9 (Trapnell *et al*., 2009). After the alignment, the mapped reads of each sample were assembled by both Scripture (beta2) (Guttman *et al*., 2010) and Cufflinks (v2.1.1) (Trapnell *et al*., 2010) in a reference-based approach. Both methods use spliced reads to determine exon connectivity, but with two different approaches. Next, transcripts predicted to have coding potential by either one of the four tools (CNCI (v2) (Sun *et al*., 2013), CPC (Kong *et al*. 2007), Pfam Scan (v1.3) (Bateman *et al*., 2004), and PhyloCSF (v20121028) (Lin *et al*., 2011)) were coding genes.

Cuffdiff (v2.1.1) (Trapnell, *et al*., 2010) was used to calculate the FPKMs of mRNAs in each sample. Cuffdiff provides statistical routines for determining differential expression in digital transcript or gene expression data using a model based on the negative binomial distribution. The resulting *P*-values were adjusted using Benjamini and Hochberg's approach for controlling the false discovery rate. The corrected *P*-value < 0.05 were defined as differentially expressed.

Data Availability

The transcriptomic raw data have been deposited in NGDC database (https://ngdc.cncb.ac.cn/) with an accession number of CRA007610.