Supplementary Figure S1. Expression of retro-transposases in callus and seedling in WT and RL.
Supplementary Figure S2. The Southern blot results of transposable element *pong* in WT and RL.
Supplementary Figure S3. The distribution of 24 nt siRNAs across rice genome in WT and RL.
Supplementary Figure S4. The specific location of sRNA expression variation between WT and RL. The specific region detected by bisulfite sequencing were marked with blue column.
Supplementary Figure S5. The secondary structures of predict novel miRNAs.
Supplementary Table S1. List of primers for MSAP amplification.
Supplementary Table S2. List of genes and their primers for qRT-PCR.
Supplementary Table S3. List of differentially expressed known miRNAs.
Supplementary Table S4. The stem-loop structure of precursor RNA of the novel miRNAs in WT and RL.
Supplementary Table S5. Target genes of miRNAs.
Supplementary Table S6. A summary of miRNAs and their target genes expression.