**Methods**

**Sequence data**

The rice miRNA data including sequence data and genomic location of both precursor miRNAs as well as mature miRNAs were obtained from miRBase database (release 21, in June 2014). A small fraction of pre-miRNAs whose genomic locations were not provided were used as query to search against the MSU7 rice genomic sequence using BLASTN with E value cutoff 10-10 and only those miRNAs that could be exactly mapped to reference genome were recorded, in which osa-miR1882bl whose precursor was mapped to a sequence on MSU7 with only one mismatch, was also recorded considering that it could be perfectly mapped to indica genome(ASM165v1). Totally, 585 pre-miRNAs along with 703 mature were recorded for further use. SNPs were downloaded from SNP-Seek Database (<http://snp-seek.irri.org/)> and then loaded to local MySQL database. After that, genomic coordination of miRNAs were used as query against the local SNP database and we’ve got 7193 SNPs fallen on pre-miRNAs and 1270 SNPs on mature miRNAs.

**MiRNA target identification**

Because in this study, we focused on analyzing targets of conserved miRNAs. We classified the miRNAs according to their conservation aided by miRNA family classification downloaded from miRBase (miFAM.dat file). Those miRNAs who had at least one member from other plant species at the same miRNA family were classified to be conserved miRNAs. PsRNATarget web server was employed with default prediction parameter using sequences of mature miRNAs to predict the target genes. In addition, some targets were collected from Liu Q. et al paper, and these sequences were used as target transcript candidates to predict which miRNA could target it in psRNATarget web server to obtain its miRNA binding sites. In turn, 823 target genes were recorded with their binding sites’ genomic coordination. Then, they were queried against local SNP database and 1169 SNPs were found fallen within the miRNA binding sites of these target genes.

**Identification and analysis of SNPs involved in miRNA-mediated regulation**

To compare the SNP density of pre-miRNAs and that of exons as well as intergenic regions, we randomly selected 600 sequence fragments with the length of 150nt from exon regions and intergenic regions across all rice genomes using in-house Python script, respectively. The SNP density was calculated as SNP numbers per base and they were plotted using R package “ggplot”. Then, SNP frequency that is assessed as the division of number of miRNAs that has SNP at the given position by total miRNA number, was calculated for each position along mature miRNAs for conserved miRNAs and non-conserved miRNAs as well as binding sites of cognate target genes. And SNP frequency distribution was plotted using R package “ggplot” as well.

**Expression correlation analysis**

The expression data of both miRNAs along with their degradome validated target genes, was downloaded from EMBL-EBI database with accession number E-GEOD-21396 (packed data derived from RiceFREND). The expression level of both pre-miRNAs and their cognate target genes were used to do Pearson correlation test with 27 day-after-transplanting seedlings as samples.

**Combined complementarity pattern analysis**

Detailed description of CCPA was stated in the result part. After CCPA was applied to some well-studied miRNAs including osa-miR156, osa-miR172, osa-miR444 and osa-miR397, 7 non-reference combined haplotype patterns were generated for osa-miR156 and 2 non-reference combined haplotype patterns were generated for osa-miR172. The phenotype data were downloaded from SNP-Seek database, including 100-grain size, grain length, grain width, secondary branching, heading date and spikelet fertility. The cultivars belonging to these non-reference combined haplotype patterns were extracted from the local MySQL database. Then phenotypes of different rice cultivars belonging to these combined haplotype patterns were compared.