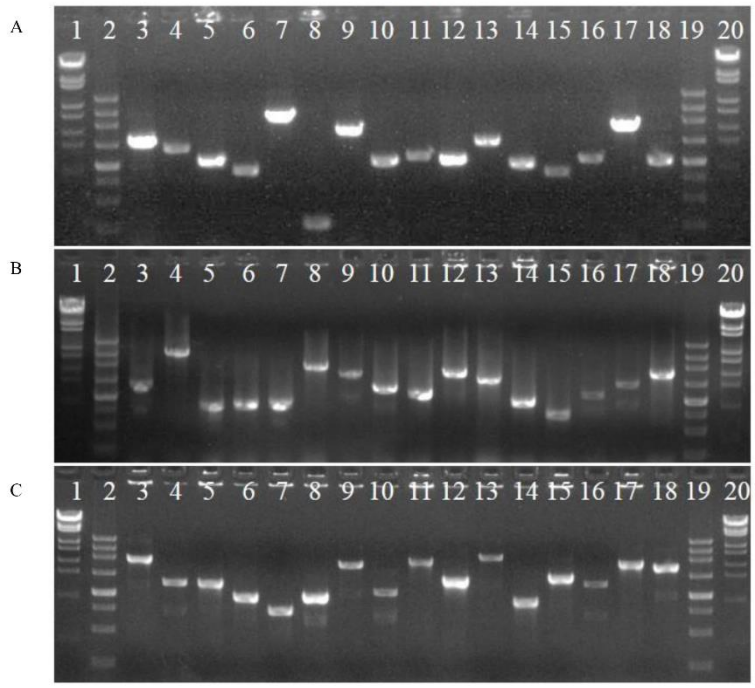

Figure S1. The test of PCR amplification of three reading frames libraries. (A) Reading frame 1. (B) Reading frame 2. (C) Reading frame 3. 1, 2, 19, 20, DNA Marker DL2000. 3~18, the detection of insert size. The capacity of libraries are greater than 1.5 x 10^6 cfu and the insert sizes are 0.5~3kb. The recombinant frequency is 97.9% and the redundancy rate is less than 3%. Therefore, the quality of libraries are good.

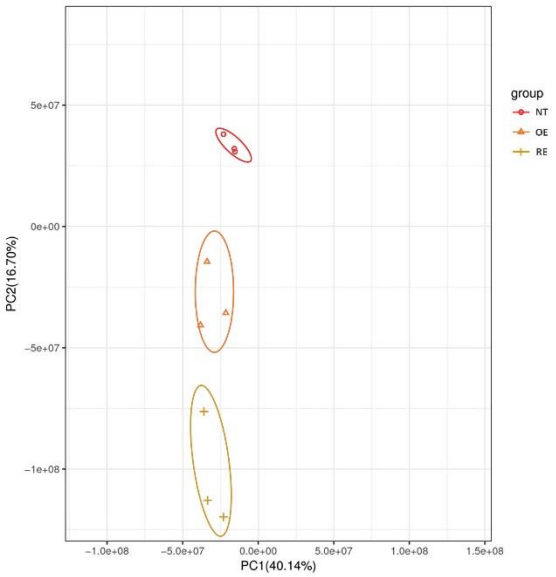

Figure S2. primary component analysis (PCA) of RNA-seq

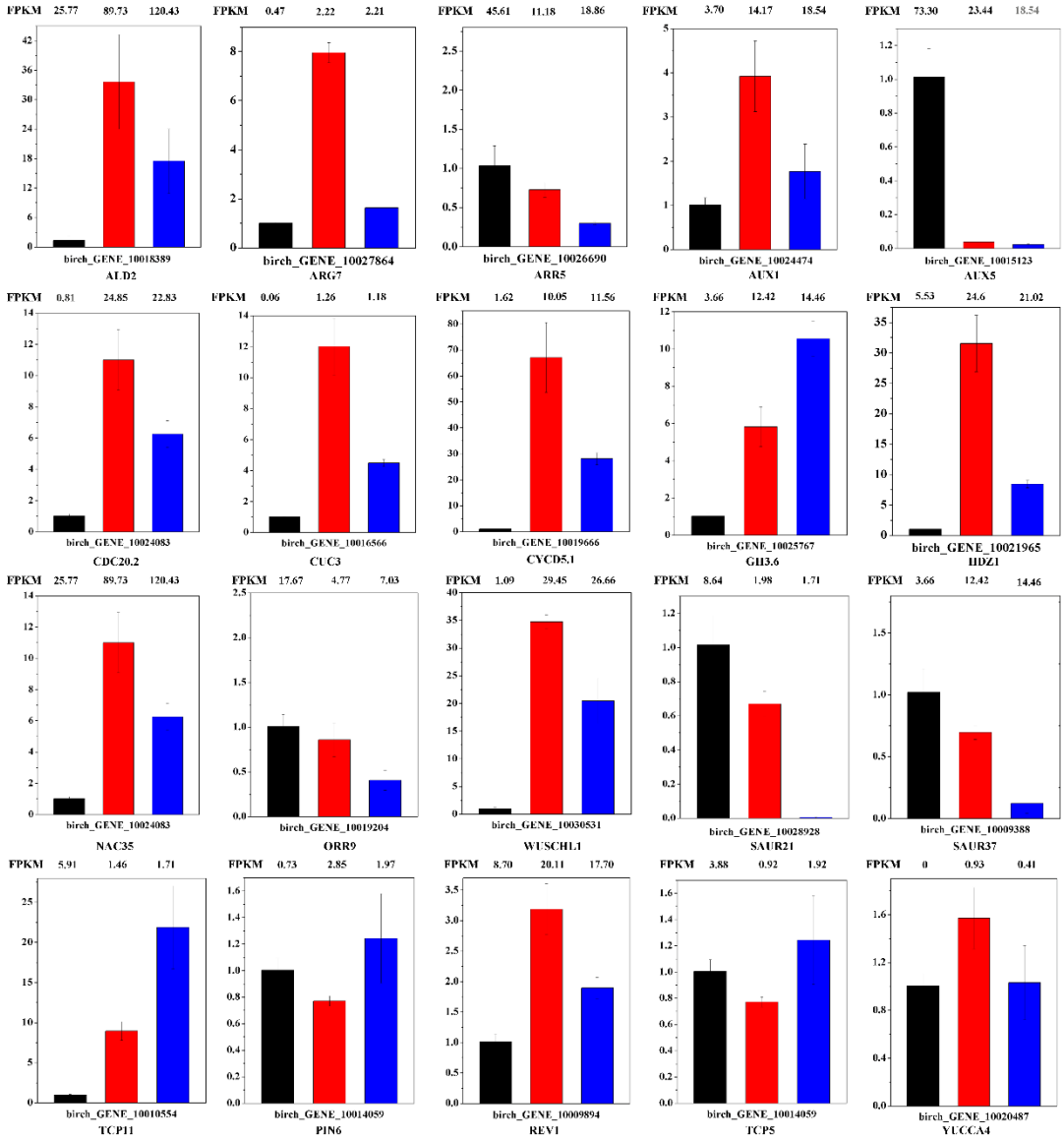

Figure S3. Quantitative real-time reverse transcription PCR (qRT-PCR) verification of RNA-seq. Differential expression among NT (black column), OE (red column) and RE (blue column). The Illumina sequencing results are indicated above each bar. The relative expression levels were determined by quantitative real-time qRT-PCR using 18s rRNA (Genbank accession No. GU476453.1) and α-tubulin for (Genbank accession No. FJ228477.1) internal controls. Each qRT-PCR was repeated three times and the error bars represent SD. Most expression of genes are coincident with RNA-seq, except *TCP11*.