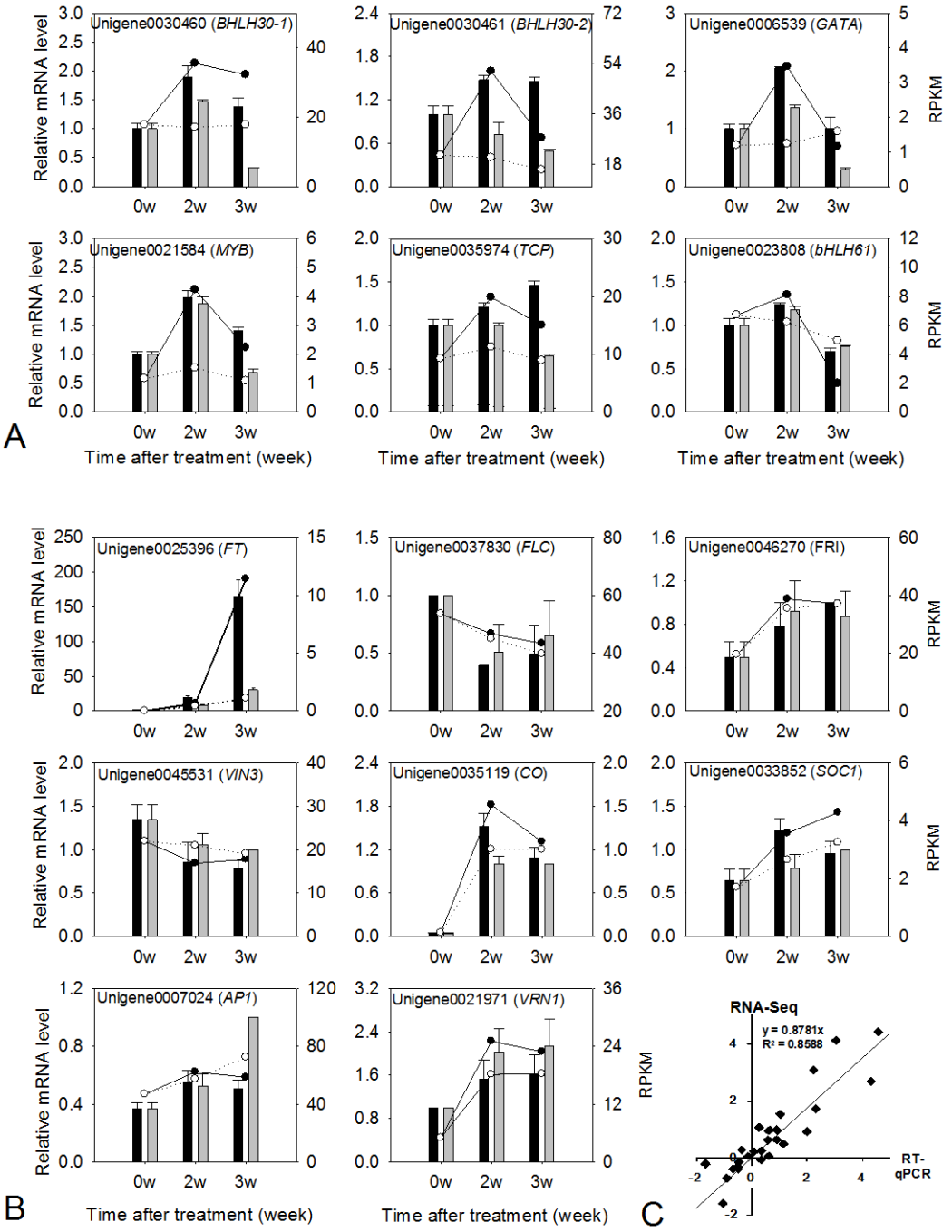

Additional file 14. RT-qPCR verification of differential expression.

The figure shows transcript levels of 14 genes, of which 6 probably associated with transcription factors (A) and 8 with flowering-related genes (B) under 15 ℃ (black) and 25 ℃ (white) treatment by comparing of RT-qPCR data (bar) with RNA-seq data (line). The relative RT-qPCR expression level is shown on the y-axis to the left, bars represent the standard error (n=3), and the normalized expression level (RPKM) of RNA-seq is indicated on the y-axis to the right. Actin was used as the internal control. (C) Coefficient analysis between gene expression ratios obtained from RNA-seq data and RT-qPCR. The RT-qPCR $\log_2$ expression ratios (x-axis) were plotted against RNA-seq data ratios (y-axis).