

Figure S2 Significantly expressed genes are involved in the circadian rhythm-plant pathway during the flower bud's differentiation phases. Color codes from blue to red indicate changes in transcriptional expression levels between -3 and 3. The boxes from left to right indicate the expression values of a unigene obtained in C1 vs C2, C2 vs C3, C3 vs C4, C4 vs C5; R1 vs R2, R2 vs R3, R3 vs R4, R4 vs R5, respectively. Each row represents a separate unigene.

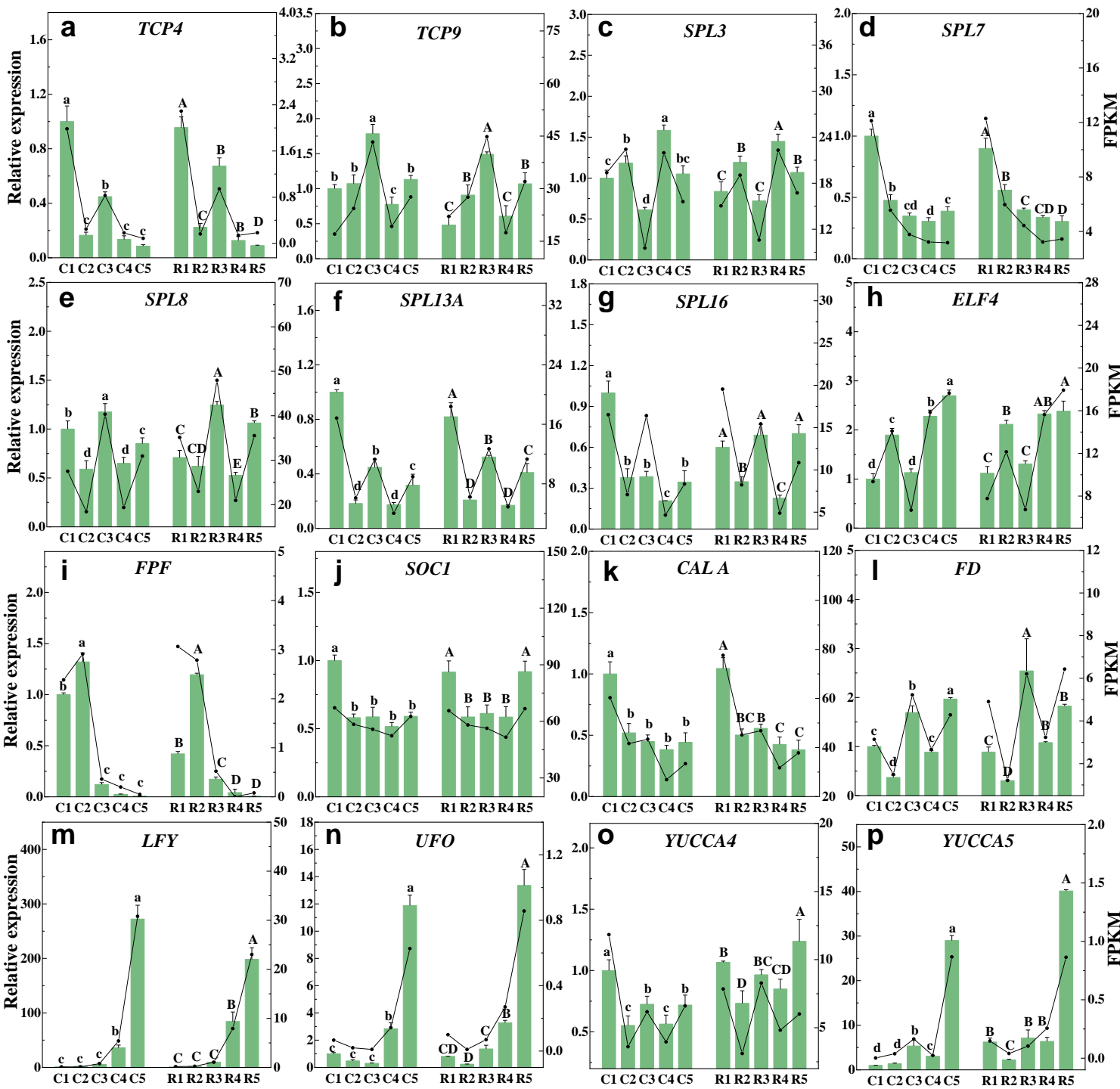


Figure S3 Expression of flowering related genes at different differentiation stages in two cultivation patterns, *TCP4* (a), *TCP9* (b), *SPL3* (c), *SPL7* (d), *SPL8* (e), *SPL13A* (f), *SPL16* (g), *ELF4* (h), *FPF* (i), *SOC1* (j), *CALA* (k), *FD* (l), *LFY* (m), *UFO* (n), *YUCCA4* (o), *YUCCA5* (p). The histogram and left axis are the relative expressions measured by qRT-PCR, and the dot-line and right axis are the FPKM value obtained by RNA-Seq. Error bars show the Mean \pm SD of the three biological replicates. Different capital letters on the bars indicate significant differences between different stages of rain-sheltered model at $p < 0.05$ determined by Duncan's tests, lowercase letters indicate significant differences of shelter-free model.

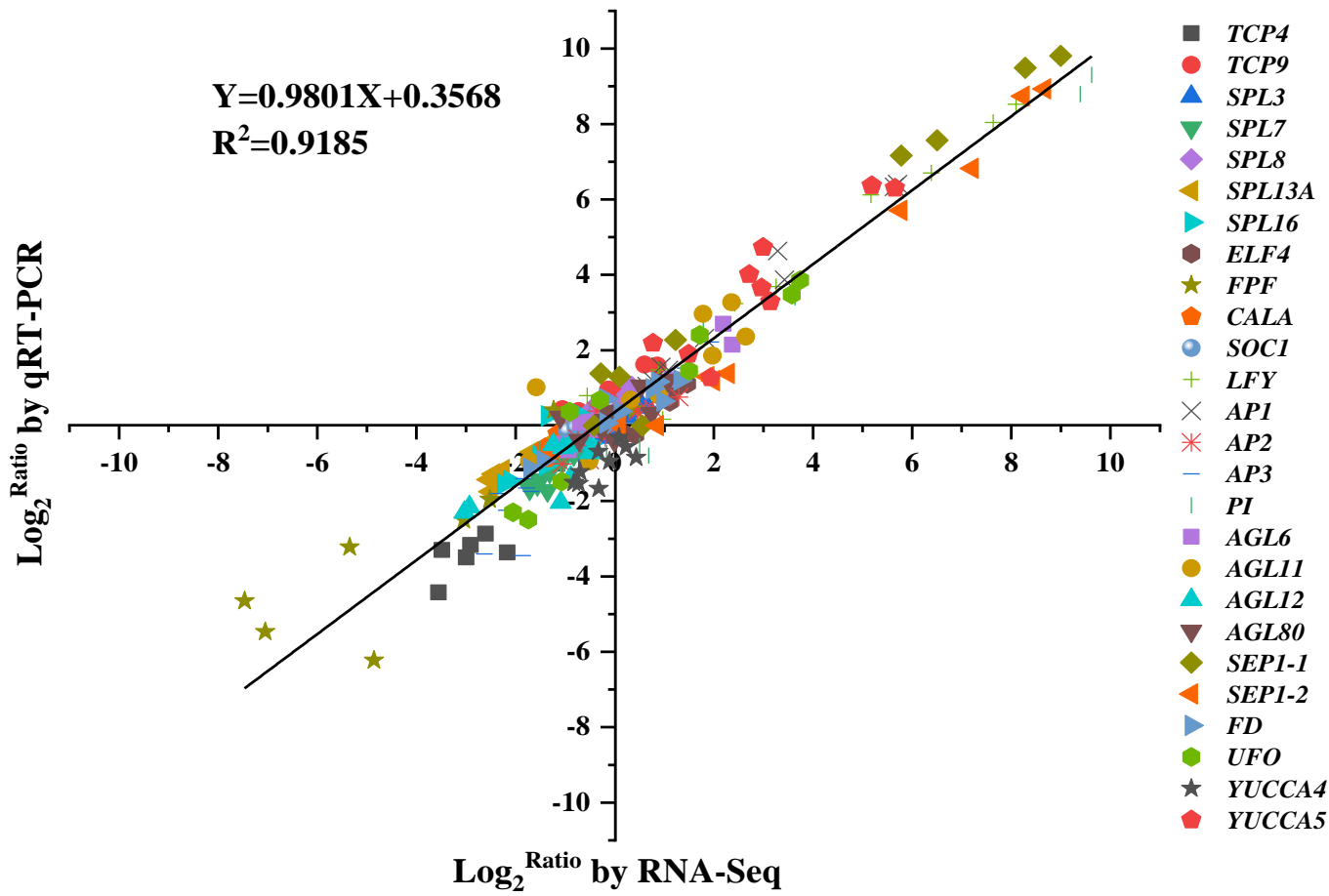


Figure S4 Correlation analysis between RNA-seq results and qRT-PCR data of ABCE model and flower bud differentiation genes.