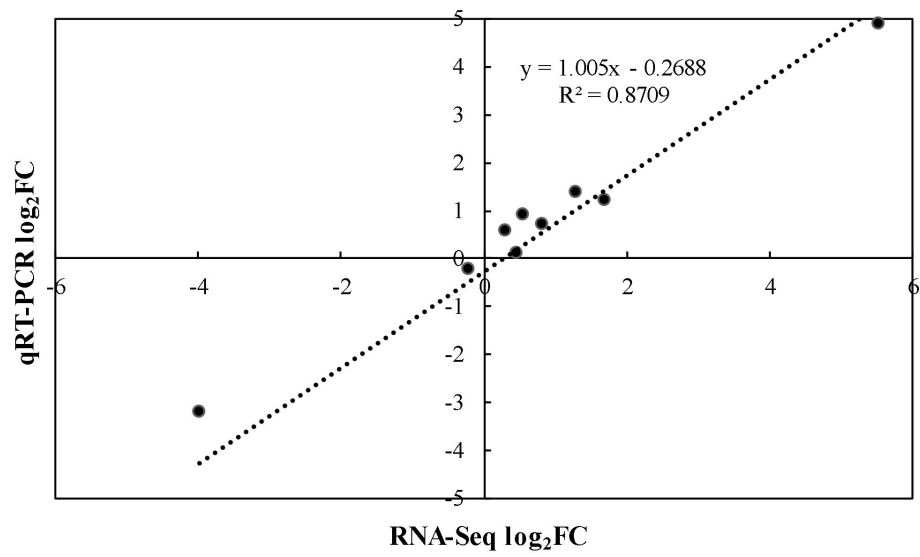
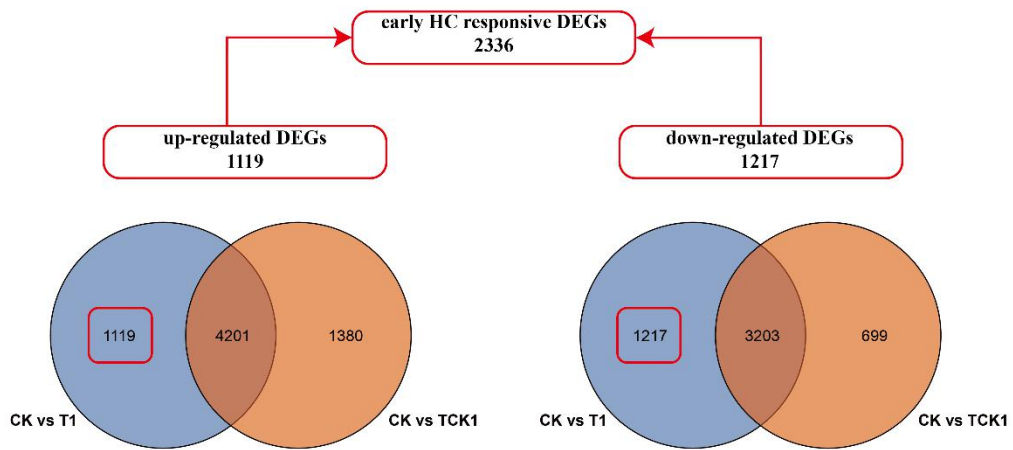


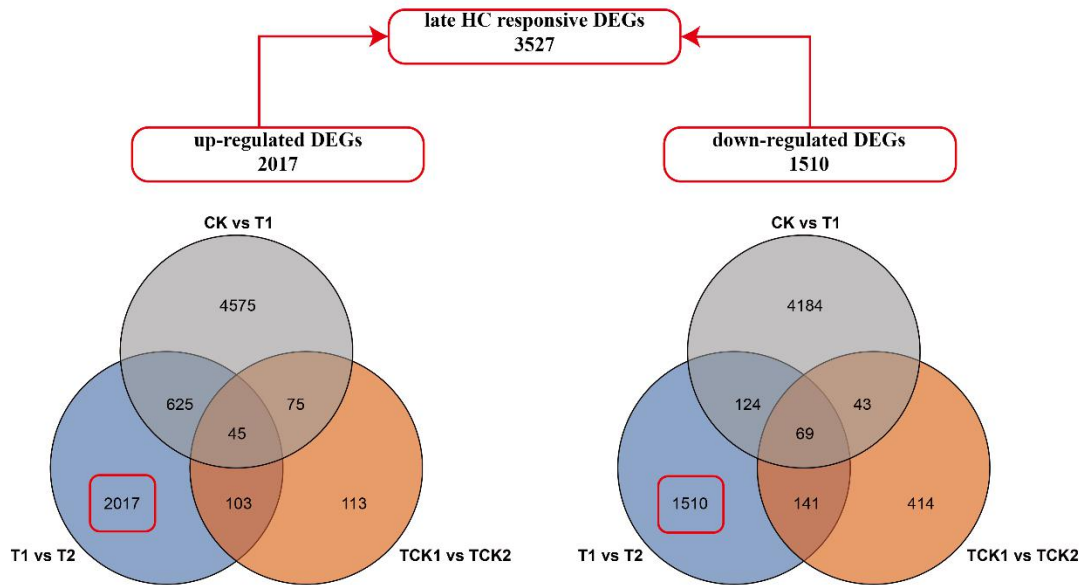
**Figure S1.** Experimental flow charts. One-year-old shoots (approximately 50-80 cm long and bearing 8-15 lateral floral buds) of *pyrus pyrifolia* 'Huanghua' trees were collected on 27 November 2019. Then, the shoots were placed in water in vials in a cold store (temperature:  $4 \pm 1^\circ\text{C}$ , relative humidity: 75%). The water in the vials was changed every 7 days. After 15 days, 30 days and 45 days, the shoots were removed from cold store in batches and placed in a phytotron (kept under a day/night: 14 h/10 h, temperature:  $25 \pm 1/20 \pm 1^\circ\text{C}$ , relative humidity 75%) for estimating the dormancy status of lateral floral buds. Meanwhile, 1% w/v HC solution or water (defined as the H-CK group) was applied to endodormant floral buds (cultivated in cold store for 15 days). 150 mg/L ABA or water (defined as the A-CK group) was applied to ecodormant floral buds (cultivated in cold store for 45 days). After treatments, the shoots were placed in water in a phytotron. Lateral floral buds were collected from each treatments at 0 day, 0.5 days, 3 days and 9 days after treatment. .



**Figure S2.** Coefficient analysis between gene expression ratios (log<sub>2</sub>FC) obtained from qRT-PCR and RNA-Seq data (compared with CK and C1 samples). \*\*indicates a significant correlation at  $p < 0.01$ .

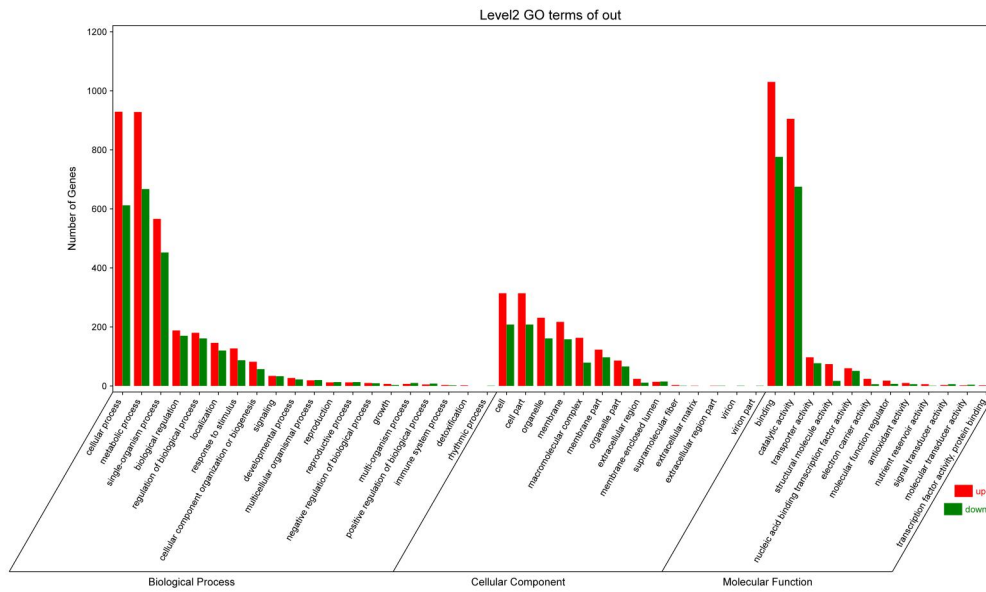


(a)

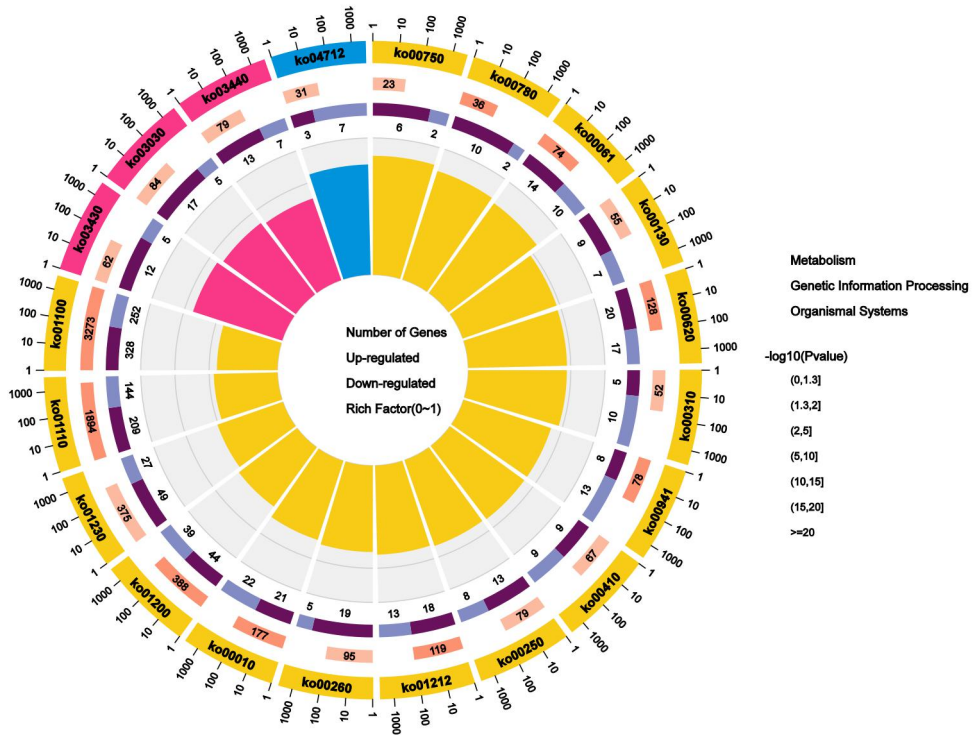


(b)

**Figure S3.** Venn diagrams of HC-regulated genes. **(a)** Venn diagrams of early HC responsive genes; **(b)** Venn diagrams of late HC responsive genes. The red box indicates the candidate DEGs.

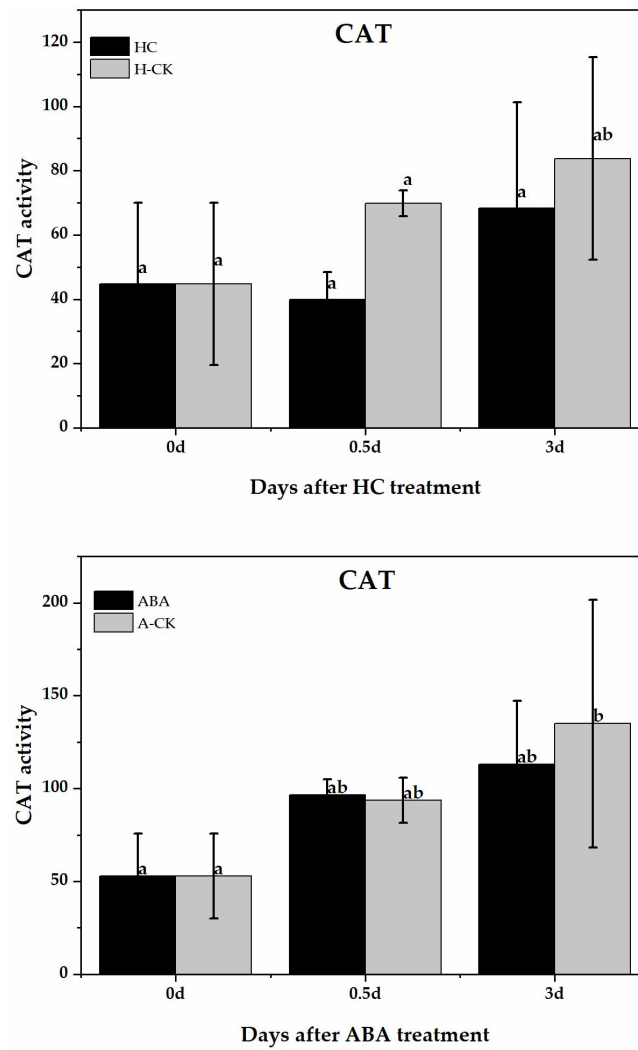


(a)

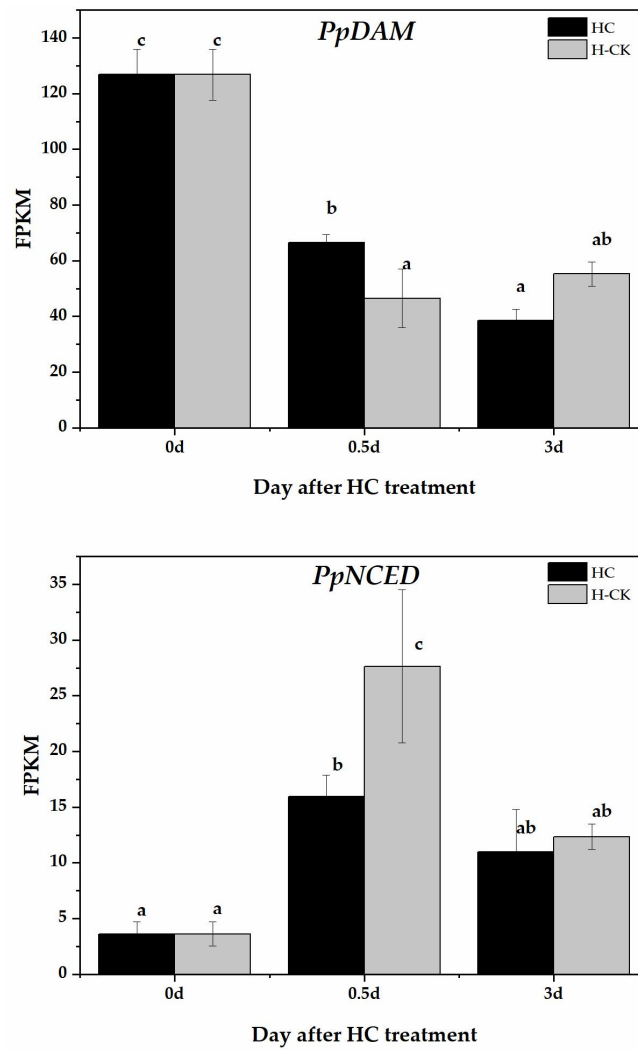


(b)

**Figure S4.** Venn diagrams of HC-regulated gens. **(a)** Gene Ontology enrichment analysis for DEGs in pear floral buds induced by HC treatment. The x-axis represents the second-order GO term, and y-axis represents the number of DEGs in this term; the red represents up- and the green represents down-regulation DEGs. **(b)** KEGG enrichment analysis for DEGs in pear floral buds induced by HC treatment. The first lap: pathways of top 20 enrichment, and different colors represents different KEGG A classes; the second lap: number and Q value of this pathway in background genes; the third lap: dark and light purple represents the proportion of up- and down-regulated genes, respectively; the innermost lap: RichFactor values of each pathway.



**Figure S5.** Changes in CAT activity after HC and ABA treatments in pear floral buds. Data are presented as the mean  $\pm$  standard error of three biological replicates; different letters indicate significant differences ( $P < 0.05$ , Tukey's test) between samples.

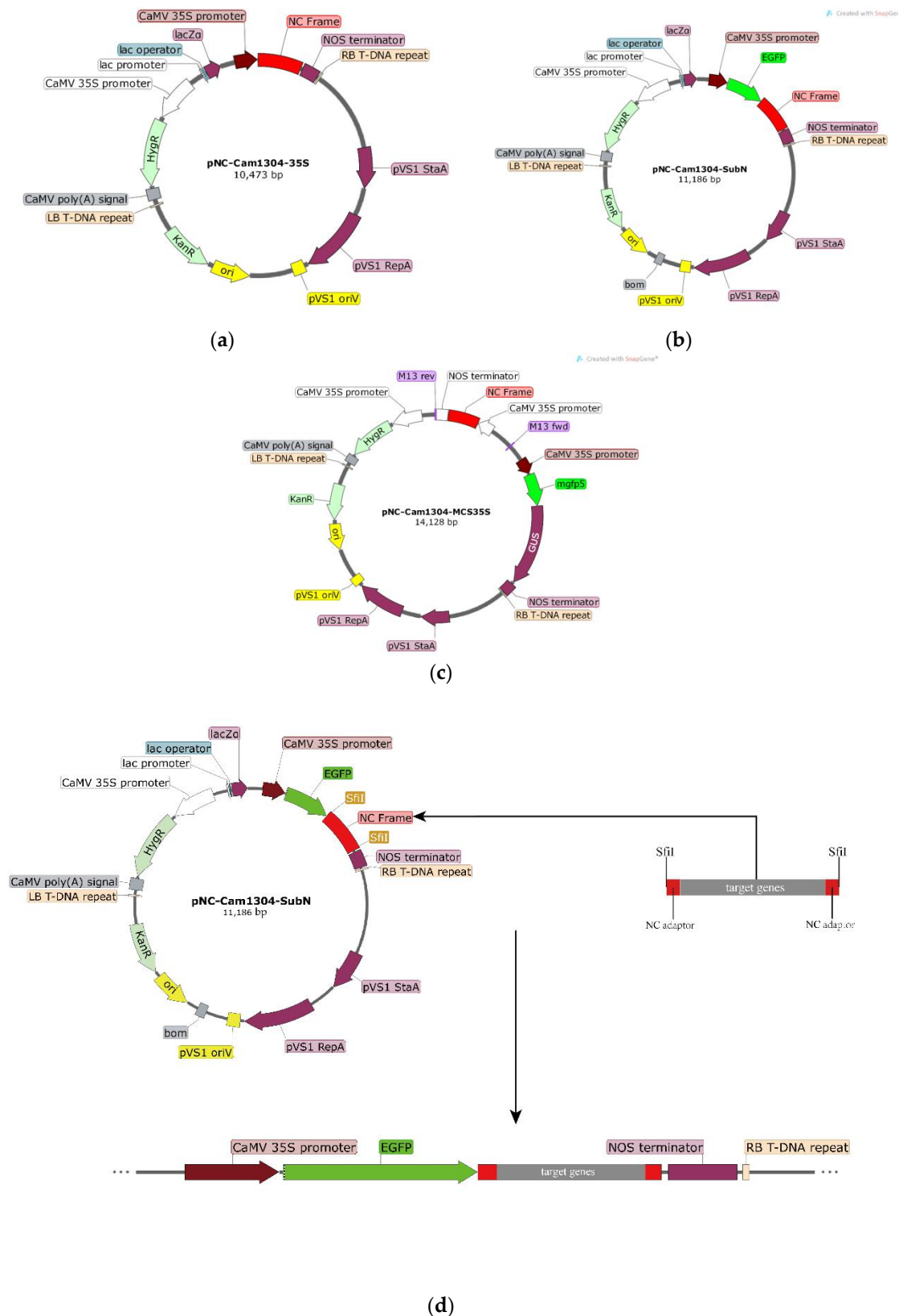


**Figure S6.** The relative expression of *PpDAM* and *PpNCED* in pear floral buds treated with HC. Data are presented as the mean  $\pm$  standard error of three biological replicates; different letters indicate significant differences ( $P < 0.05$ , Tukey's test) between samples.



**Figure S7.** The photo of typical floral bud break. The beginning of bud break was defined as green leaf tips enclosing visible flowers.





**Figure S8.** Structure diagram of vectors. **(a)** Structure diagram of pNC-Cam1304-35S vector. **(b)** Structure diagram of pNC-Cam1304-SubN vector. **(c)** Structure diagram of pNC-Cam1304-MCS35S vector. **(d)** Reconstruction diagram of pNC-Cam1304-SubN-target genes vector.