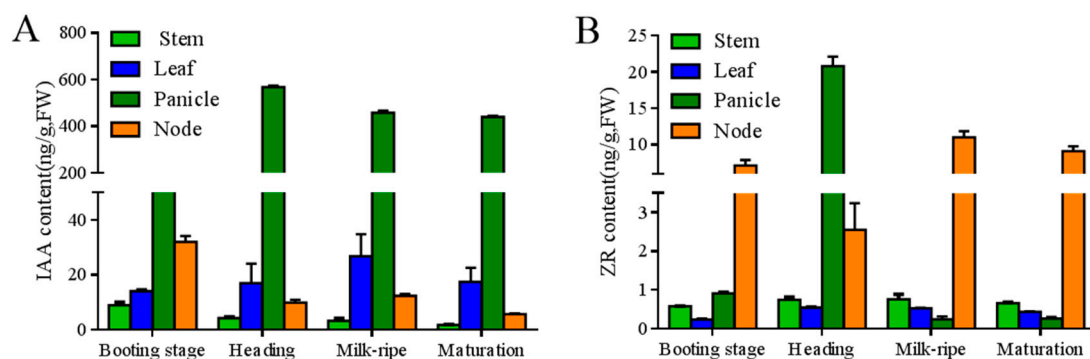
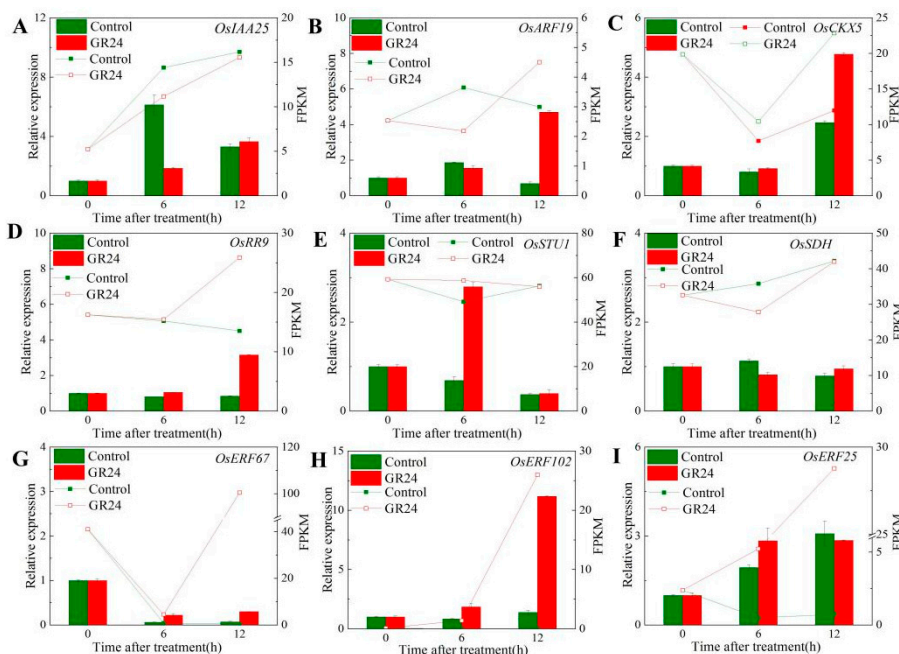


## Supplementary Figures

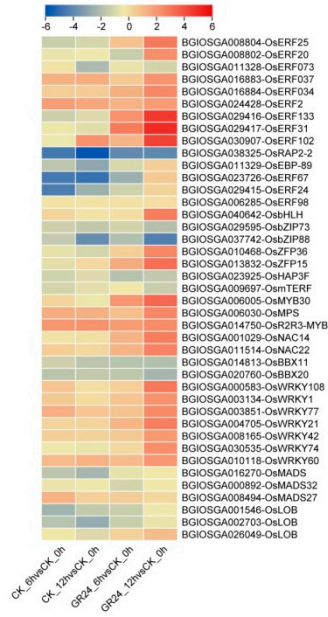


**Figure S1. Changes of phytohormone contents in different organs of HHZ first seasonal rice.**

**A**, The IAA contents of first cropping HHZ rice in different periods. **B**, The contents of ZR of first cropping HHZ rice in different periods. Data represent means  $\pm$  SE ( $n=3$ ).



**Figure S2. qRT-PCR validation for transcriptome data.** Panels **A-I** represent the relative expression levels of *OsIAA25*, *OsARF19*, *OsCKX5*, *OsRR9*, *OsSUT1*, *OsSDH*, *OsERF67*, *OsERF102* and *OsERF25*, respectively. Data represent means  $\pm$  SE ( $n=3$ ). The histogram shows the relative expression level of qRT-PCR; Broken lines show the FPKM values of genes obtained by transcriptional sequencing. Expression value of 1 indicated that the gene expression level of 0 h as a control and convert the qPCR value of 0 h to 1. Symbols “\*”, “\*\*\*” and “ns” indicated significant difference ( $P<0.05$ ), extremely significant difference ( $P<0.01$ ) and no significant difference, between GR24 treatment and control at the same treatment time, respectively.



**Figure S3. Analysis of differentially expressed genes annotated as transcription factors. A** heatmap representing the relative expression of genes annotated as transcription factors. The relative expression levels are shown as log<sub>2</sub>Foldchange levels. Blue cells indicate down-regulation and red cells indicate up-regulation.