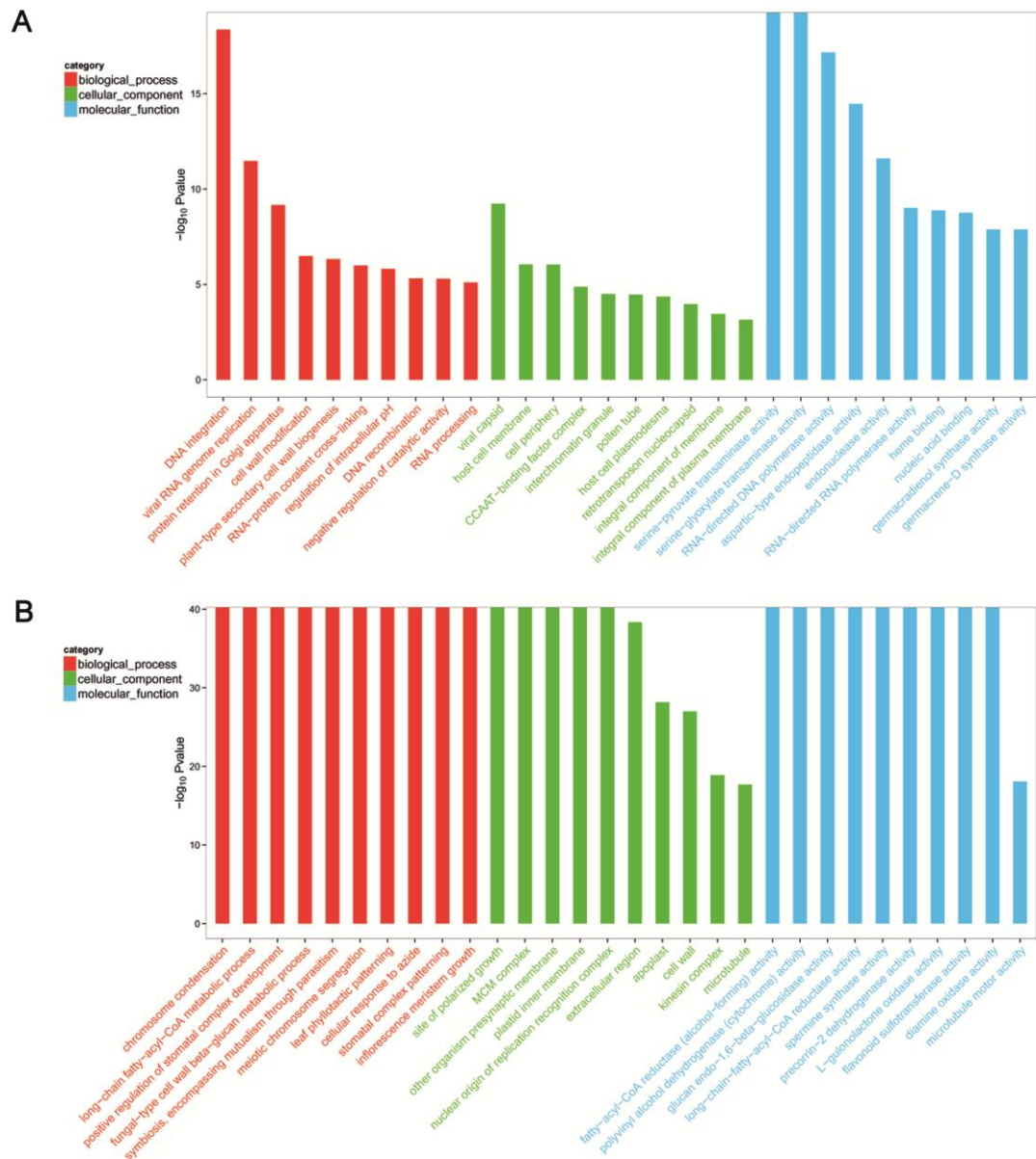
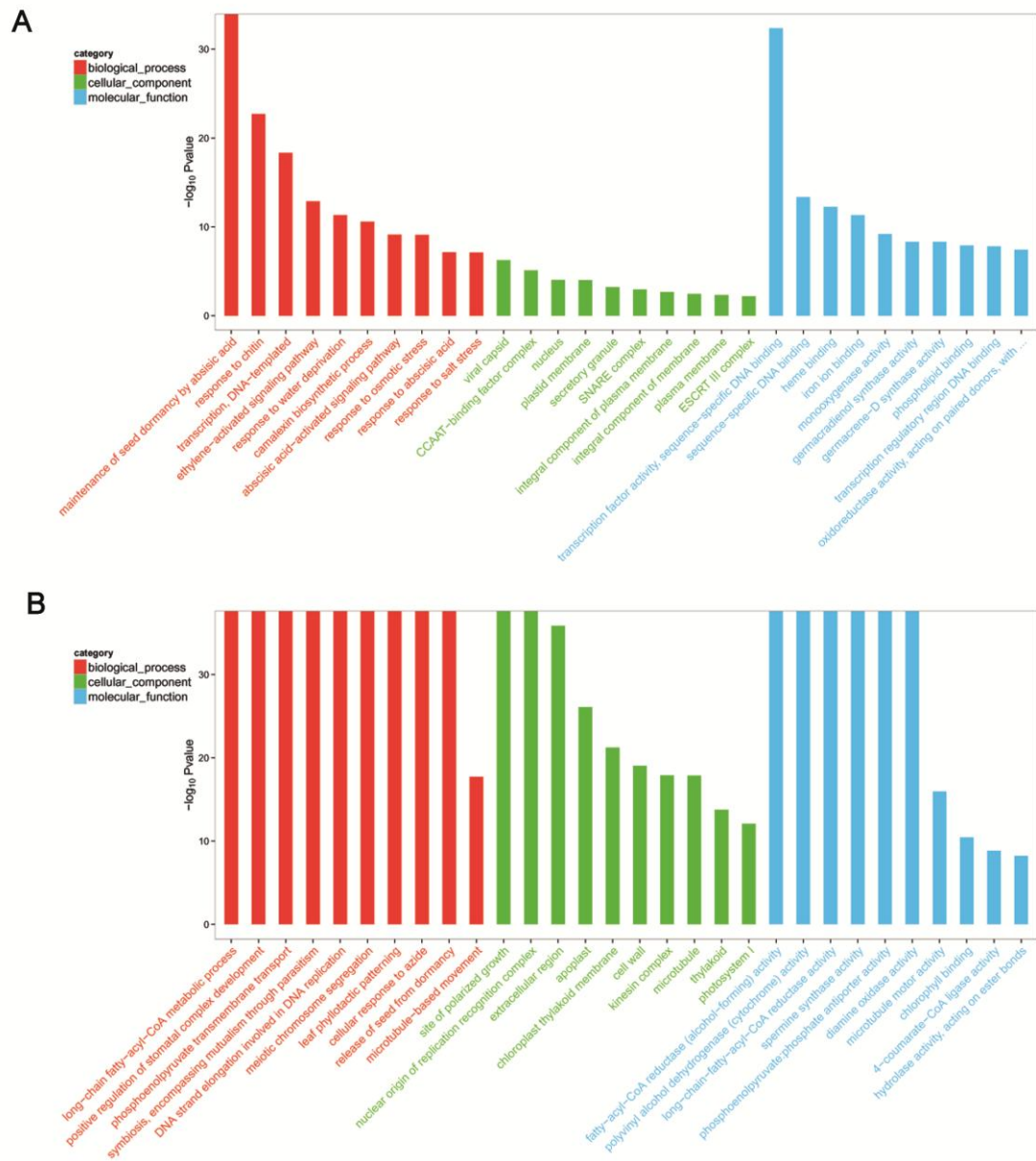


**Figure S1**



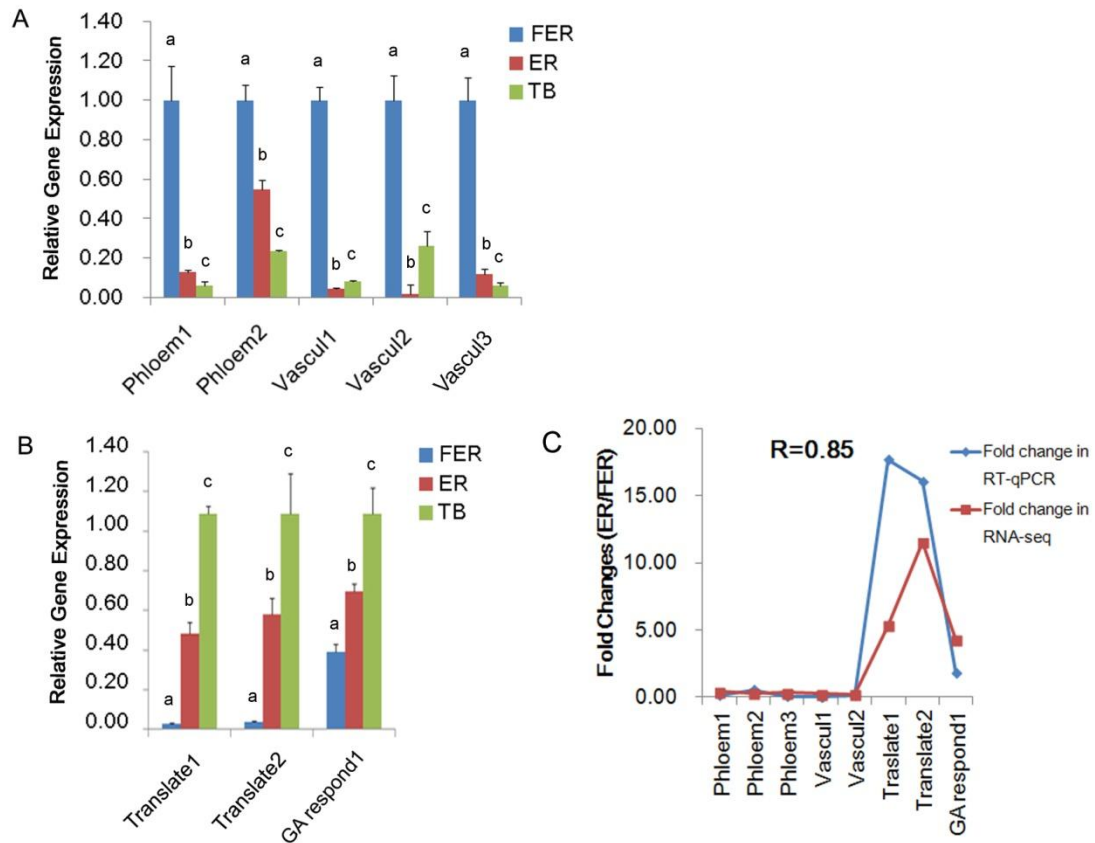
**Figure S1 GO analysis of the DEGs between TB and ER. A. Up-regulated DEGs in ER. B. Down-regulated DEGs in ER.**

**Figure S2**



**Figure S2 GO analysis of the DEGs between TB and FER. A. Up-regulated DEGs in FER. B. Down-regulated DEGs in FER.**

**Figure S3**



**Figure S3 RT-qPCR detection of the selected DEGs among TB, ER and FER. A.** Increased expression levels of some of the phloem and vasculature development related DEGs in the FER sample. **B.** Decreased expression levels of some of the translation and GA responsive factors in the FER sample. Error bars represent the value  $\pm$ SD (n=3). The lowercase letters above the columns indicate the differences among samples by significance test. **C.** Fold changes of DEG in both RT-qPCR and RNA-seq FPKM data. The correlation coefficient R=0.85.