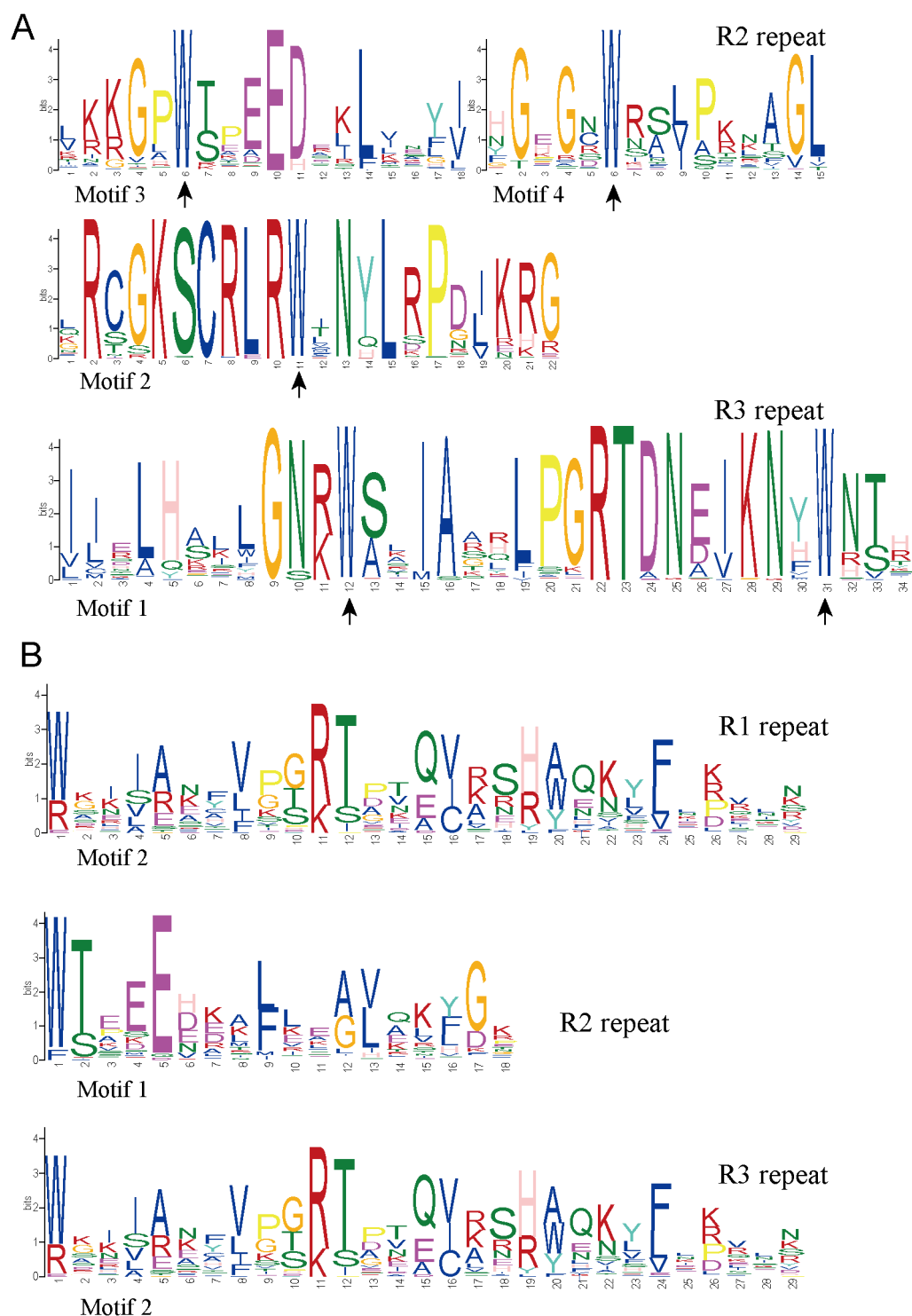


Figure S1. The location of *PebMYB* genes.

The *PebMYB* genes on the 18 chromosomes are represented in cyan color where the gene density was showed by heatmap in 18 chromosomes. The scale bar is 10 Mb.



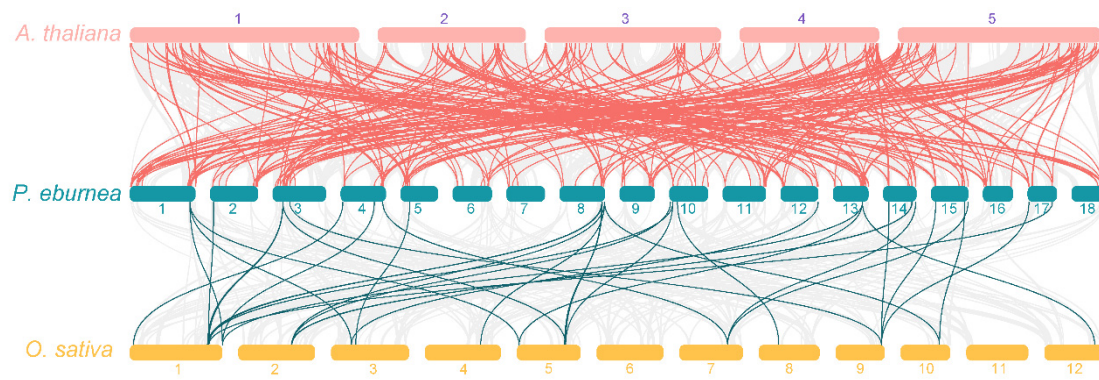


Figure S3. The synteny results of *PebMYB* genes.

Synteny analysis between *P. eburnea* and other two species. The collinear genes between species were marked in grey while the collinear *PebMYB* genes were marked in salmon or cyan color.

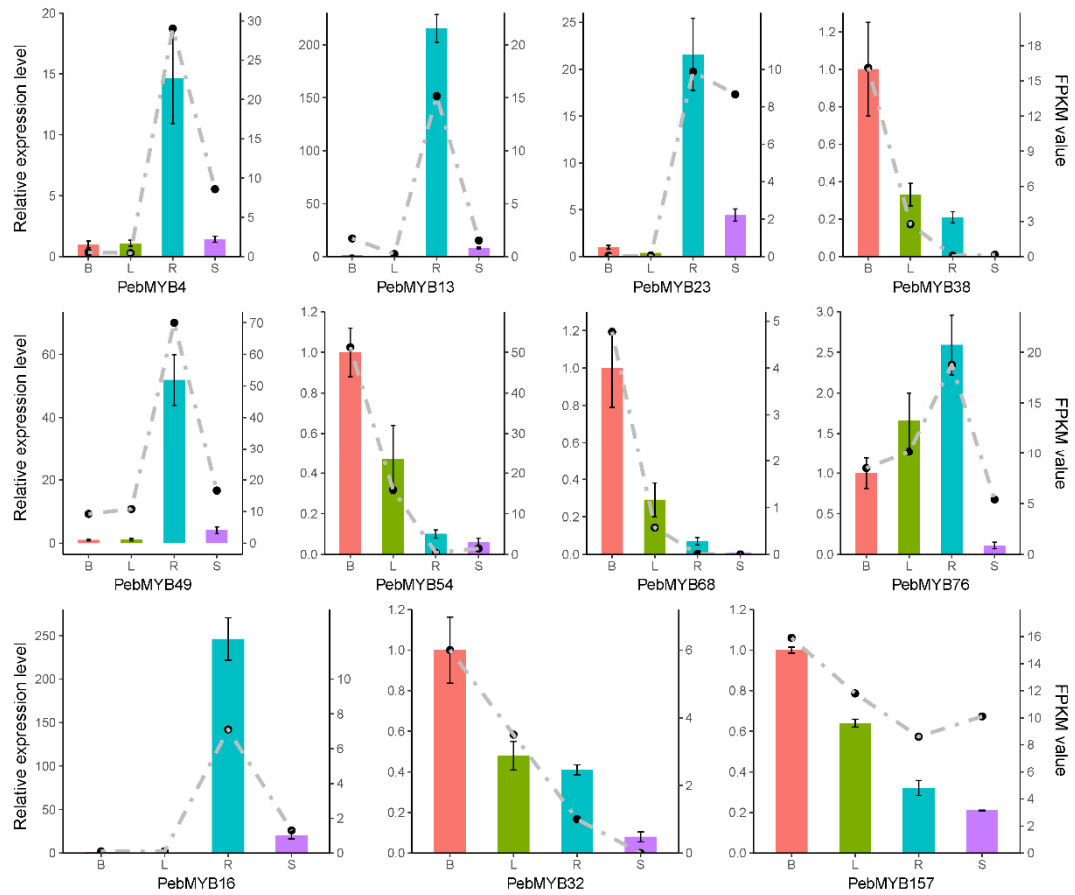


Figure S4. Validation of RNA-seq data by qRT-PCR

The left y-axis (corresponding to the columns) indicates the relative expression levels in qRT-PCR, whereas columns and bars indicate the mean value and standard error. The right y-axis (corresponding to the black dots and grey dotted lines) indicates FPKM value of RNA-seq.

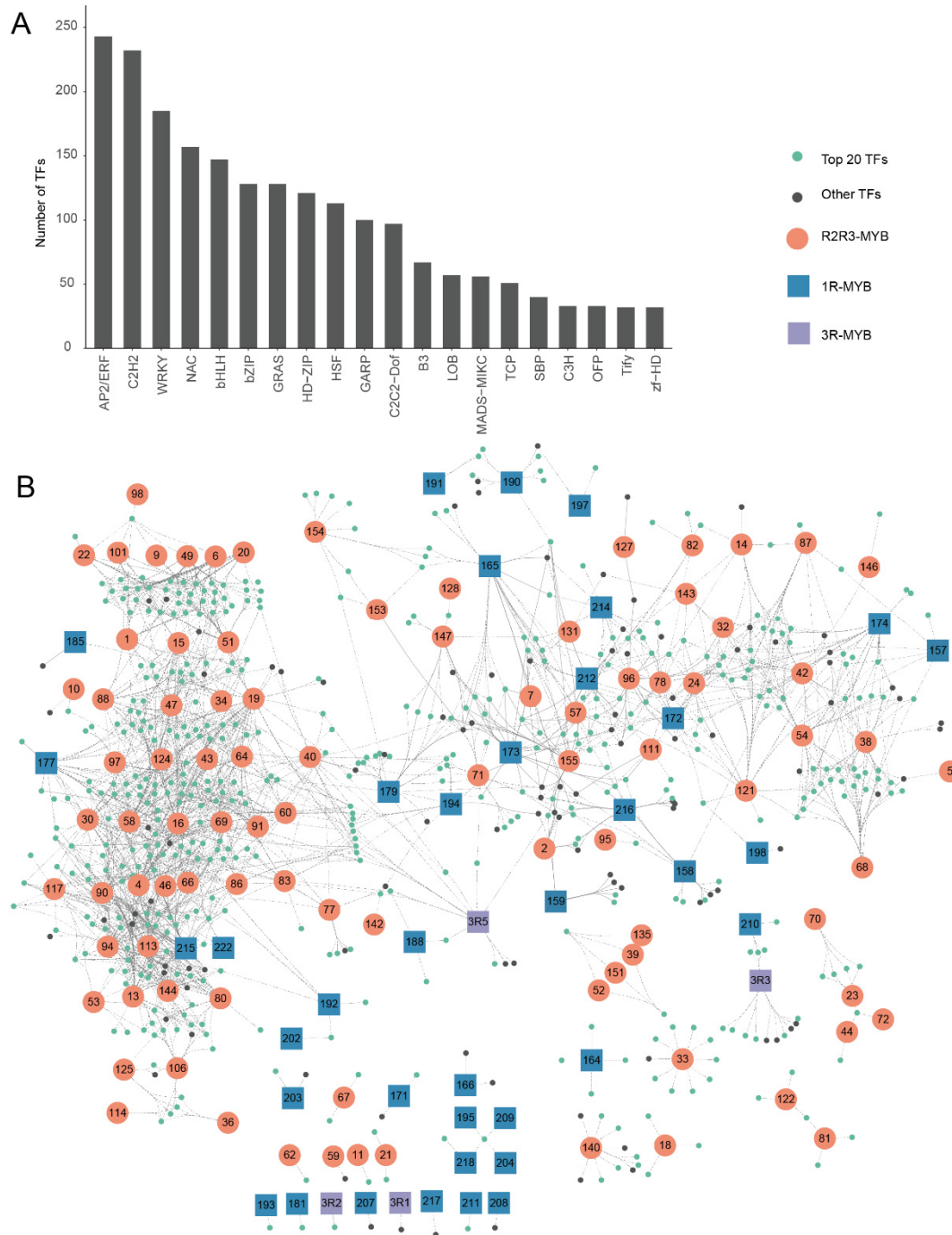


Figure S5. Interactions between *PebMYB* genes and other transcription factors (TFs).

**A.** The top 20 TF families with the highest number of members co-expressed with *PebMYB* genes. **B.** the potential interacting network between *PebMYB* genes and other TFs. Solid lines indicate positive interaction while dash lines indicate negative interaction. The corresponding *PebMYB* genes were indicated by character or number.