

Figure S1. The enriched KEGG pathways between 20 and 80 DAFB (A), between 80 and 140 DAFB (B) and between 20 and 140 DAFB (C).

The X-axis represents the percentage of genes identified in this study. The same gene can be included in more than one category.

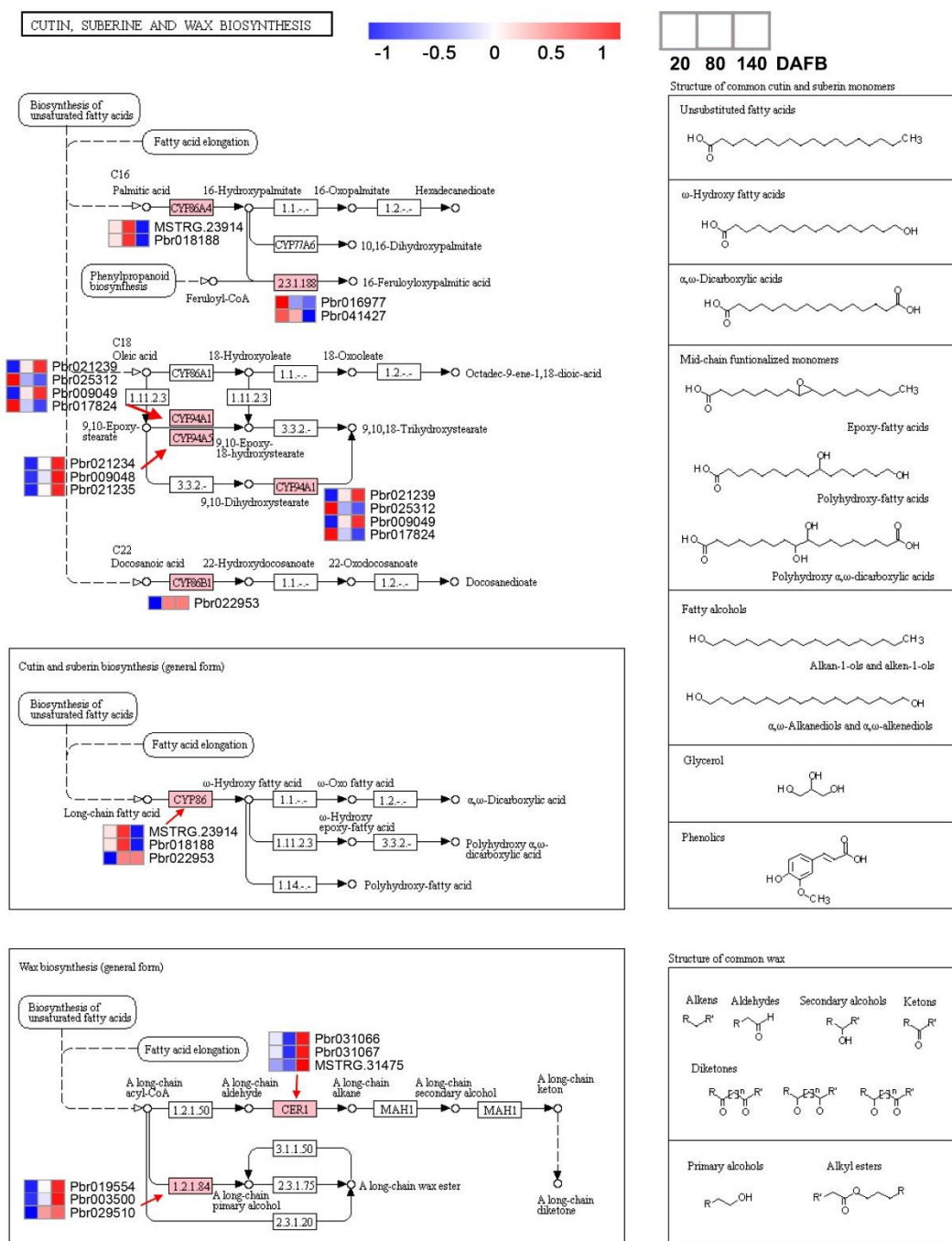


Figure S3. Cutin, suberin and wax biosynthesis from the KEGG database.

The three columns represent developmental stages at 20, 80 and 140 DAFB, respectively. The prefix of newly assembled genes used is “MSTRG”, and the sequence is presented in Table S10.

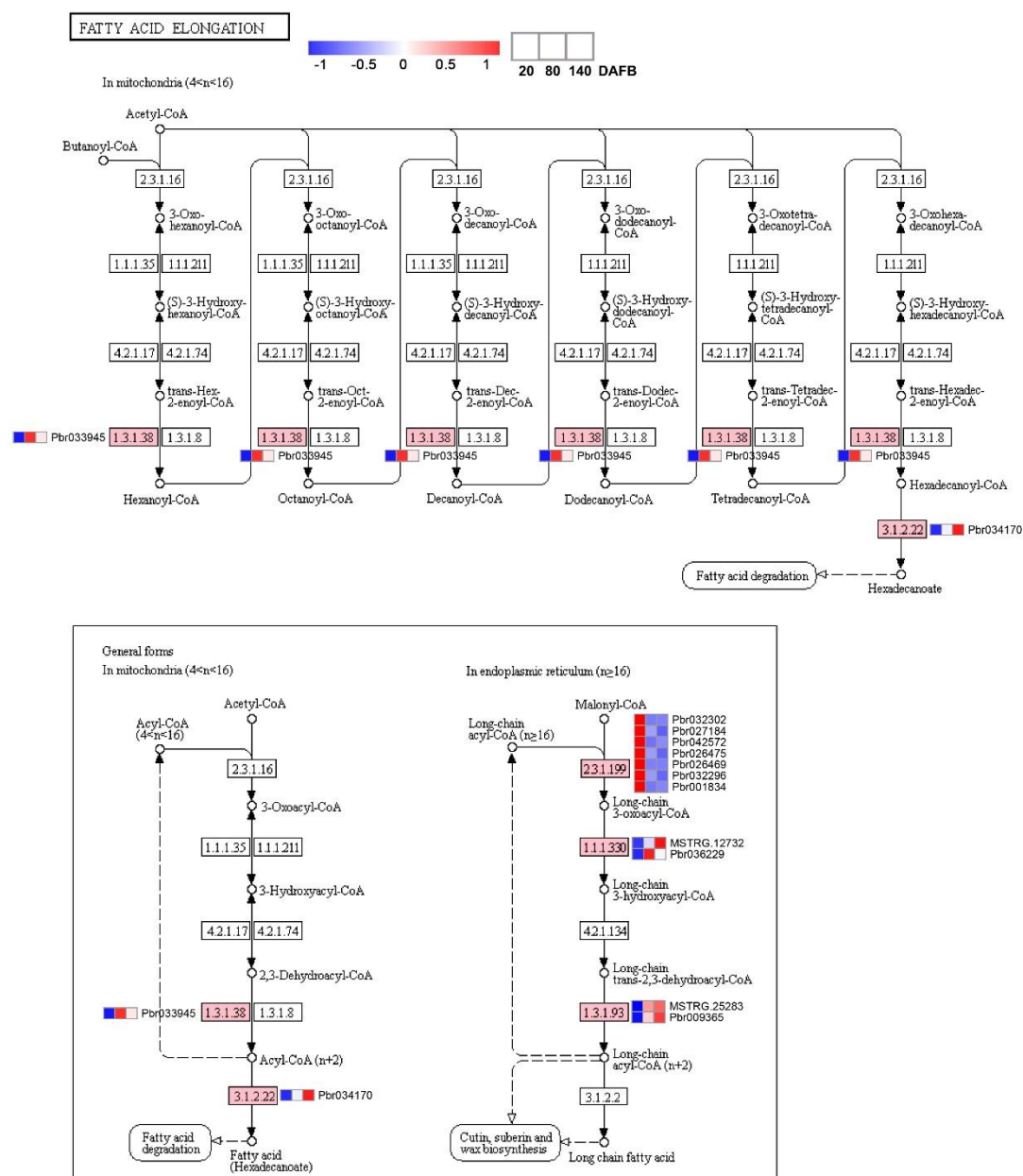


Figure S6. Fatty acid elongation from the KEGG database.

The three columns represent developmental stages at 20, 80 and 140 DAFB, respectively. The prefix of newly assembled genes used is “MSTRG”, and the sequence is presented in Table S10.

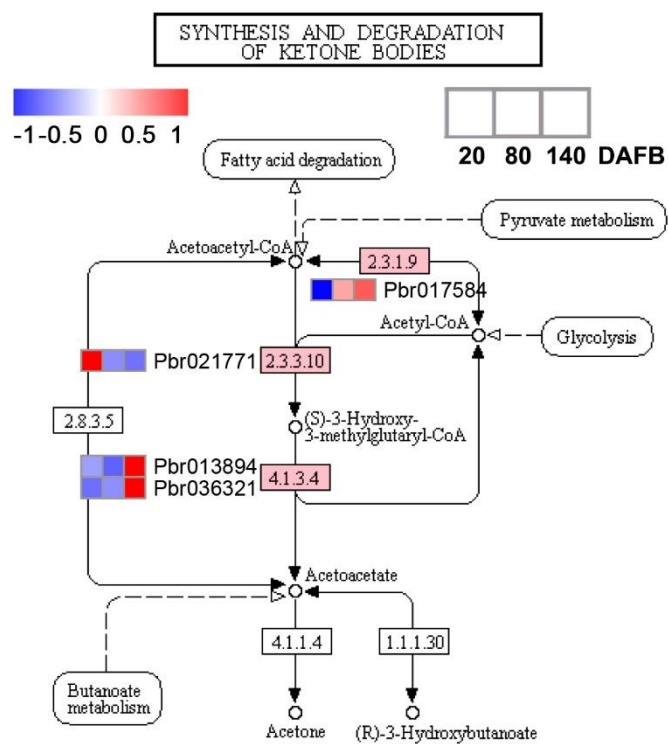


Figure S7. Synthesis and degradation of ketone bodies from the KEGG database.

The three columns represent developmental stages at 20, 80 and 140 DAFB, respectively.

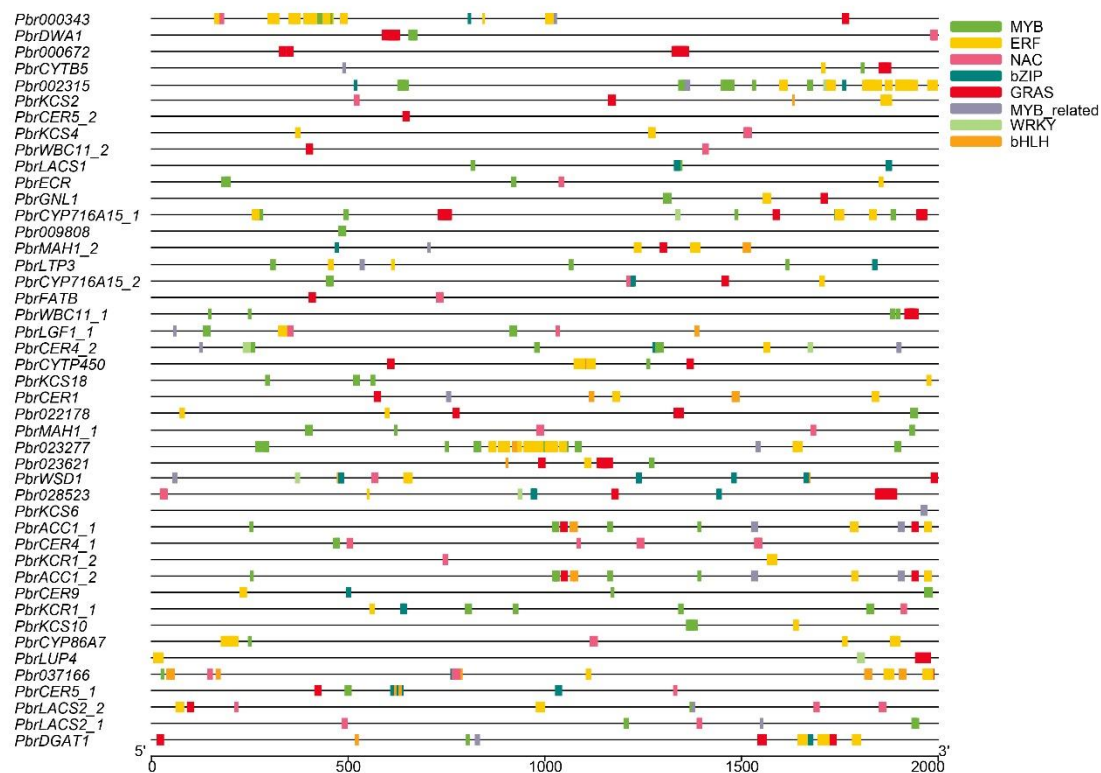


Figure S11. Prediction of the binding sites of TFs in the 2-kb upstream regulatory regions of genes

involved in cuticular wax. The different binding sites are represented by different colored boxes.

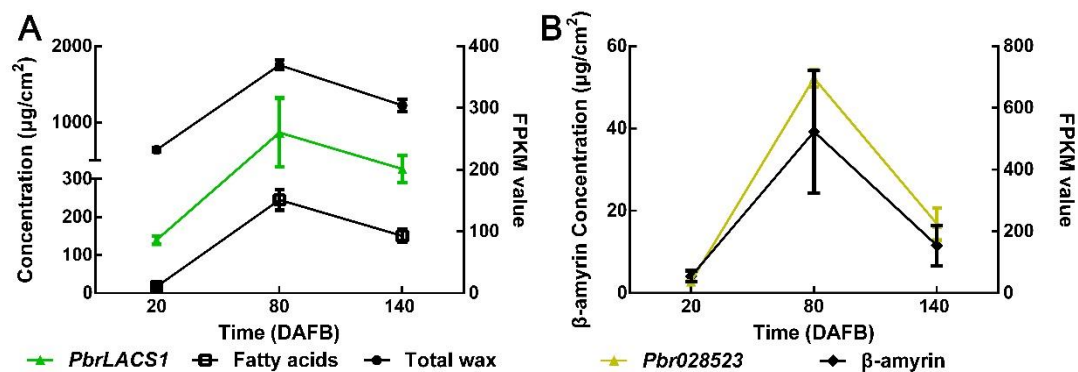


Figure S12. Wax concentrations and FPKM values of genes.

A. The total wax, fatty acid concentrations and FPKM values of *PbrLACS1* genes. B. The β-amyryn

concentrations and FPKM values of *Pbr028523* genes.