

Figure S1. Graft-induced transcripts grouped according to temporal expression profiles. Each of the profiles is represented as a different plot.

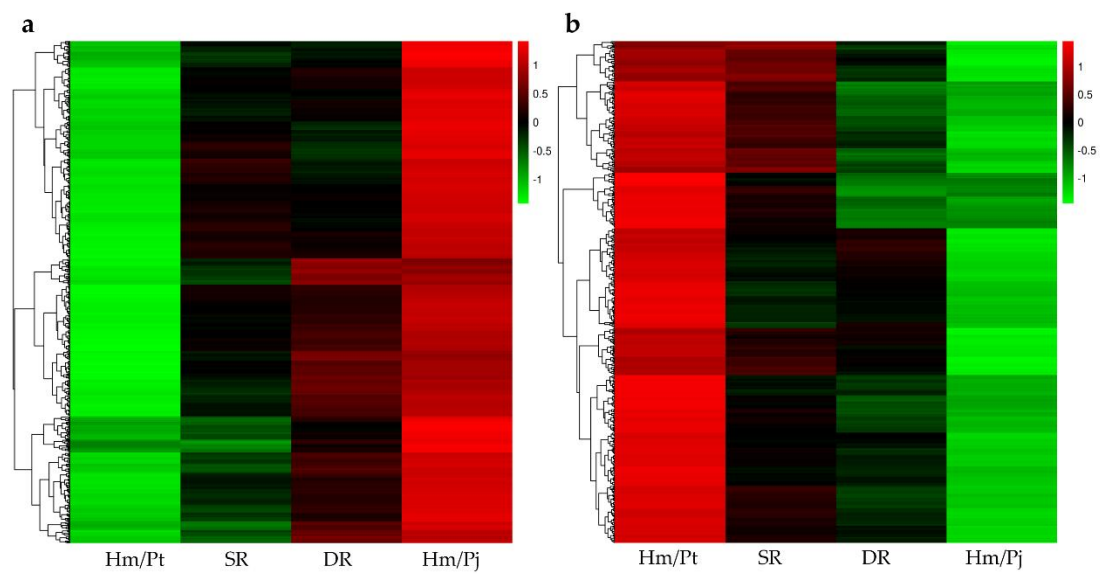


Figure S2. Heatmap of genes in upregulated and downregulated expression profiles. Heatmap color indicates $\log_{10}(\text{FPKM}+0.01)$ value. **a** Heatmap of genes in profile 19, **b** Heatmap of genes in profile 0.

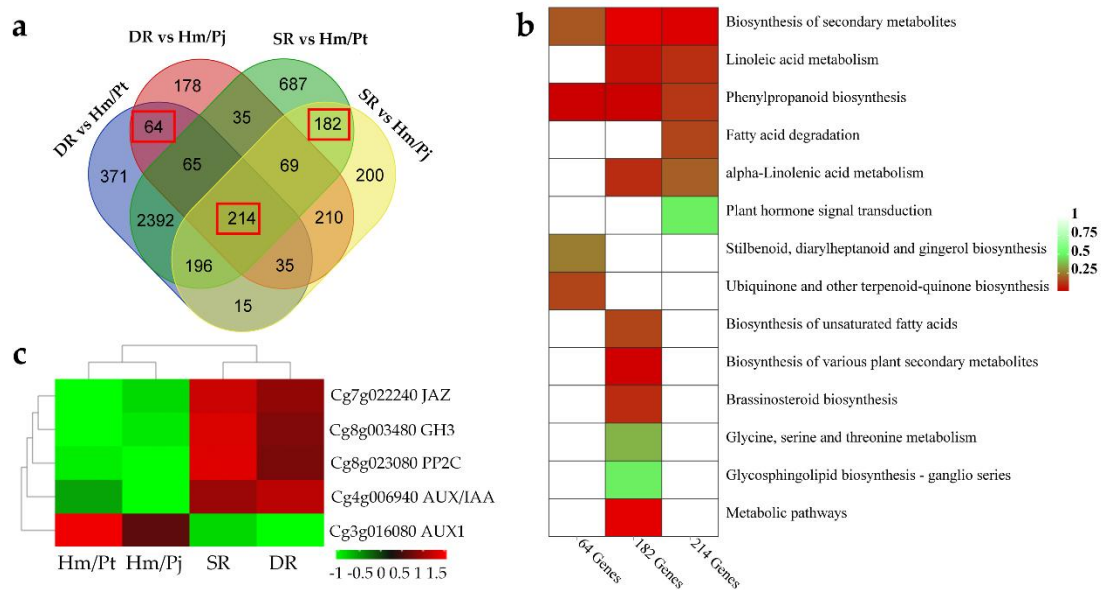


Figure S3. DEG analysis between different graft combinations. **a** Venn diagram of DEGs in each graft combinations. **b** KEGG pathways for different compare groups. **c** heatmap of DEGs between DR and SR vs Hm/Pt and Hm/Pj.

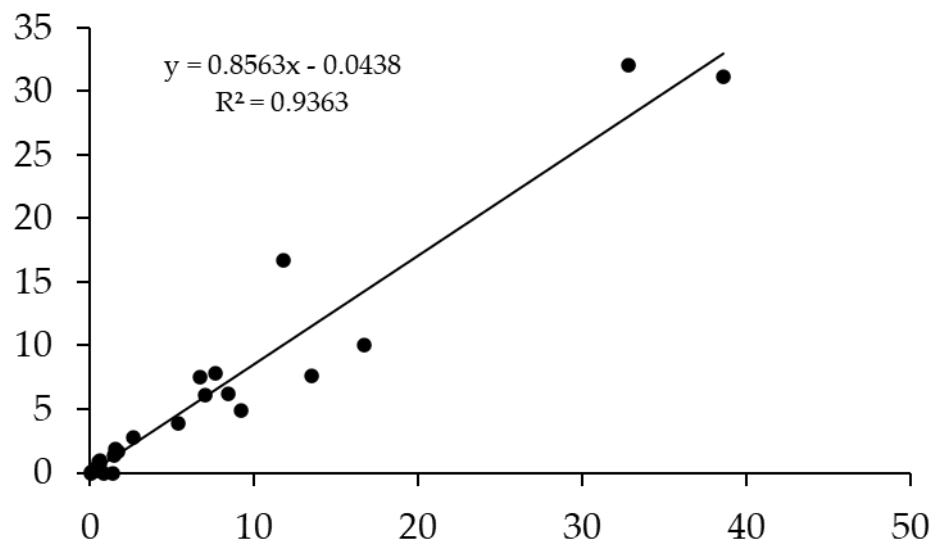


Figure S4. Pearson's correlation of RNA-seq and qRT-PCR results.

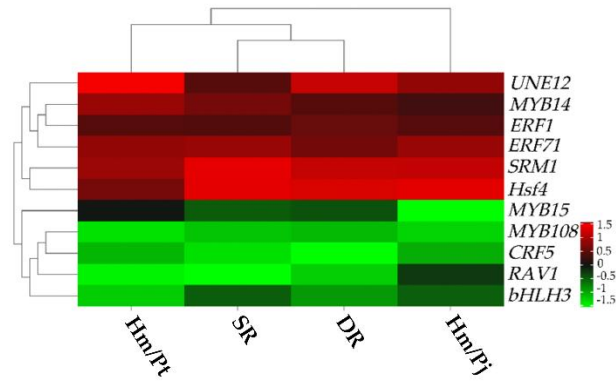


Figure S5. The expression of important graft compatibility related transcription factors.

Heatmap color indicates $\log_{10}(\text{FPKM}+0.01)$ value.