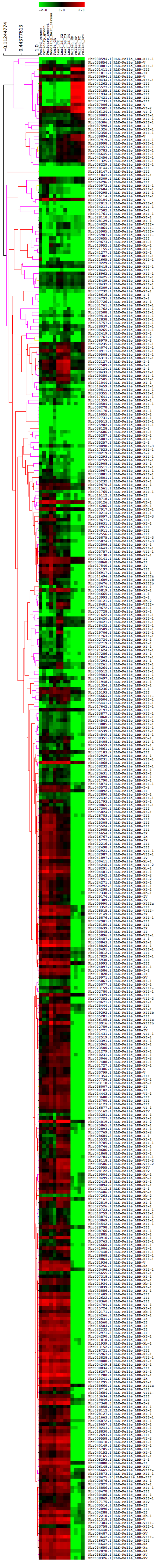
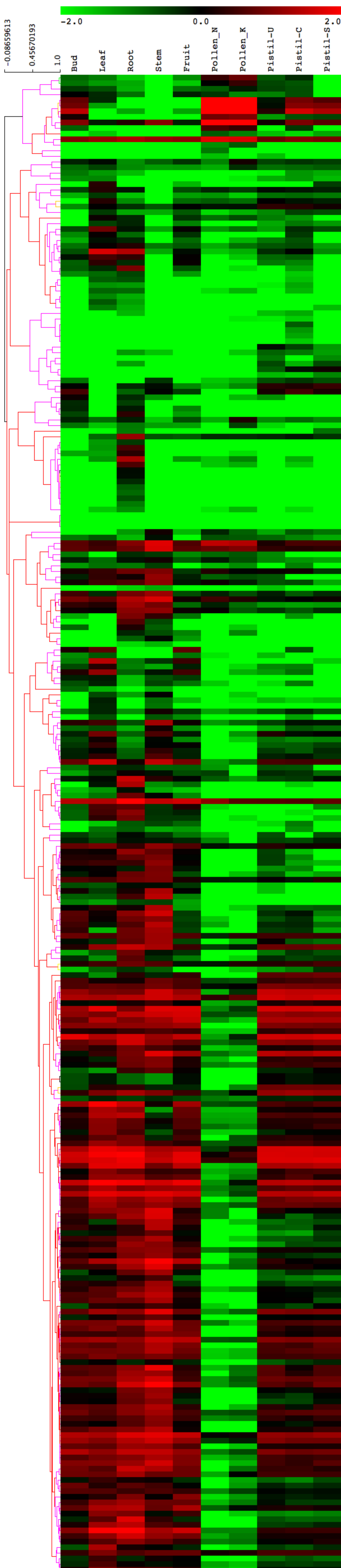


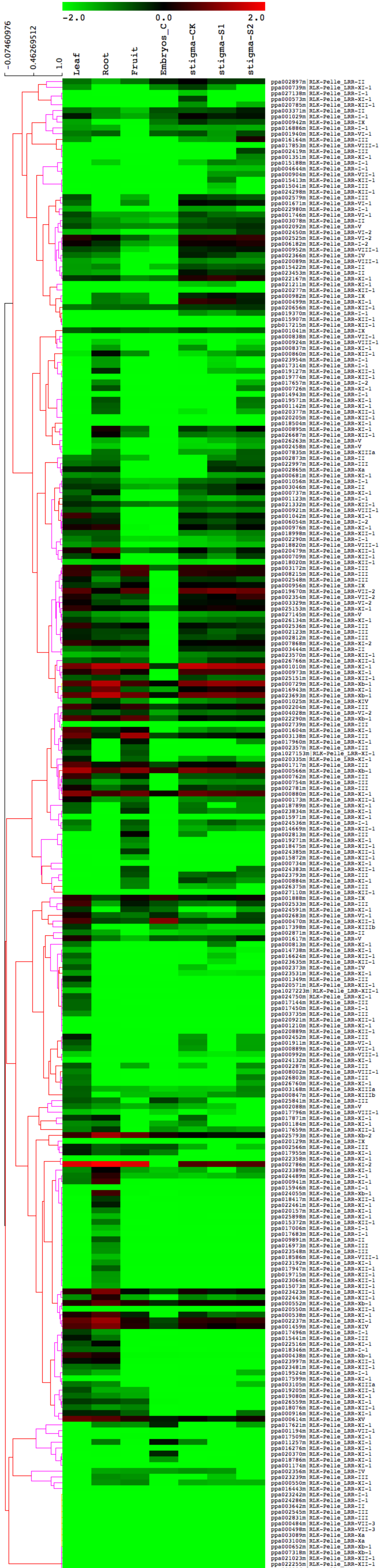
Supplementary Figure 2. Heat map of the expression patterns of 244 apple LRR-RLK genes in different tissues. Red and green colors correspond to up-regulation and down-regulation, respectively. Normalized gene expression values are provided in Supplementary Table 11



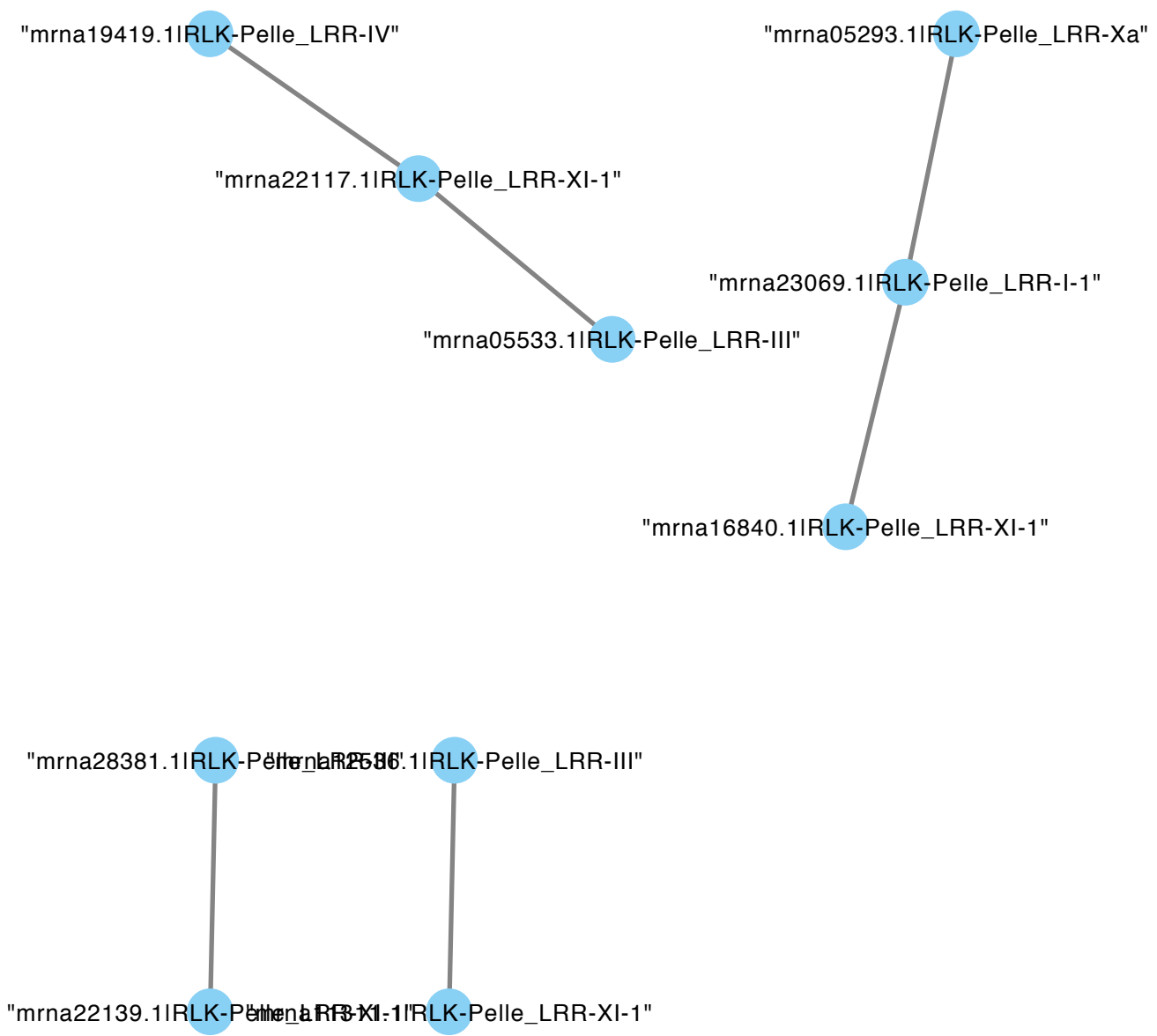
Supplementary Figure 3. Heat map of the expression patterns of 427 Chinese white pear LRR-RLK genes in different tissues. Red and green colors correspond to up-regulation and down-regulation, respectively. Normalized gene expression values are provided in Supplementary Table 2.



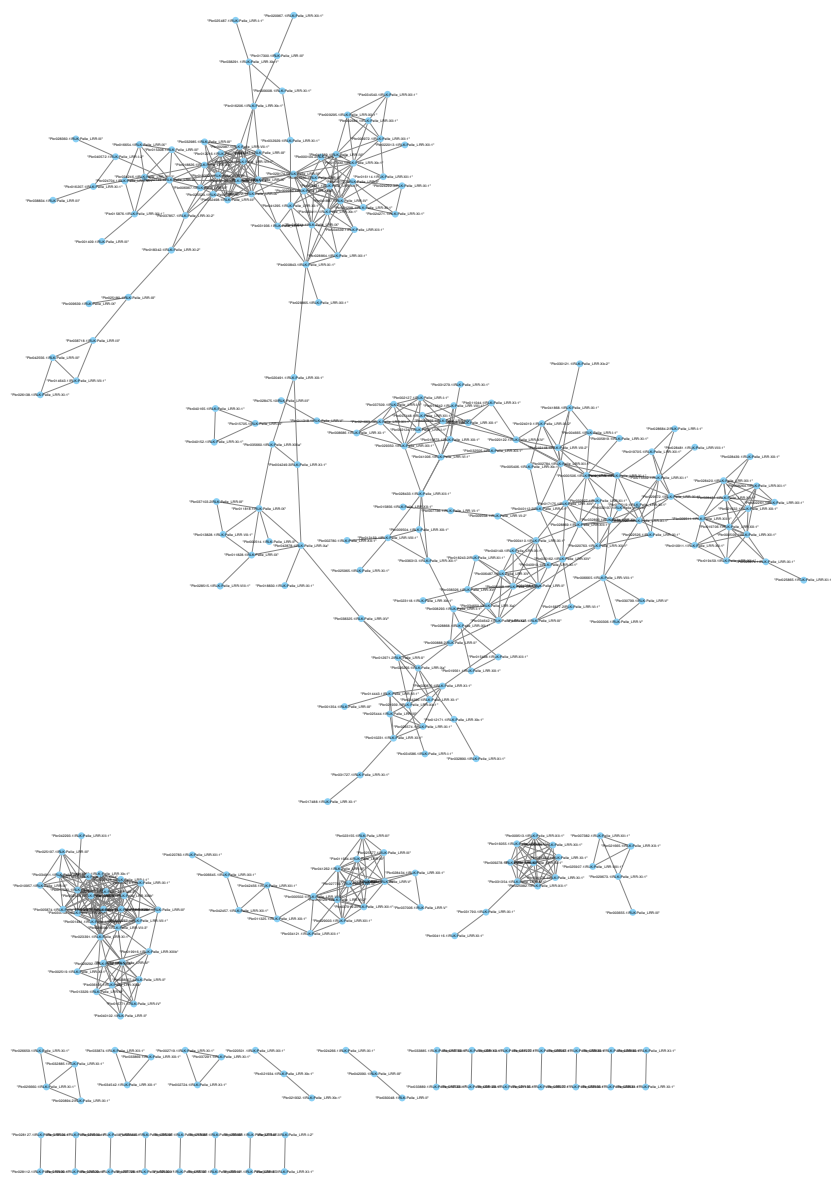
Supplementary Figure 4. Heat map of the expression patterns of 267 mei LRR-RLK genes in different tissues. Red and green colours correspond to up-regulation and down-regulation, respectively. Normalized gene expression values are provided in Supplementary Table 14.



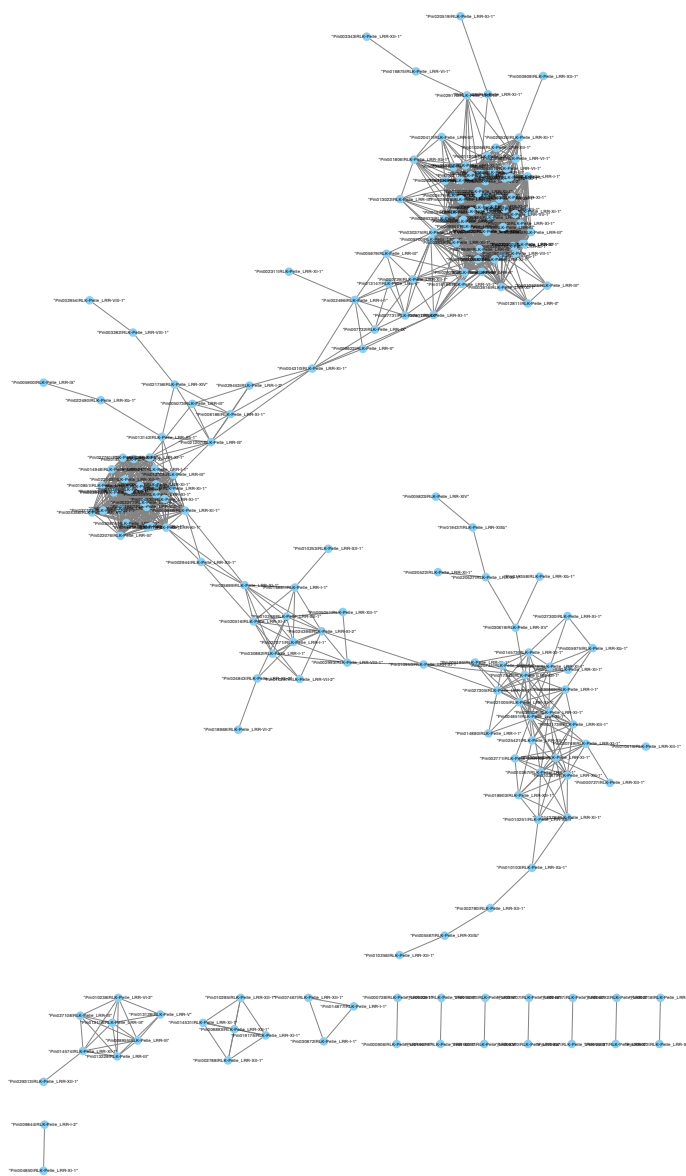
Supplementary Figure 5. Heat map of the expression patterns of 258 peach LRR-RLK genes in different tissues. Red and green colours correspond to up-regulation and down-regulation, respectively. Normalized gene expression values are provided in Supplementary Table 15.



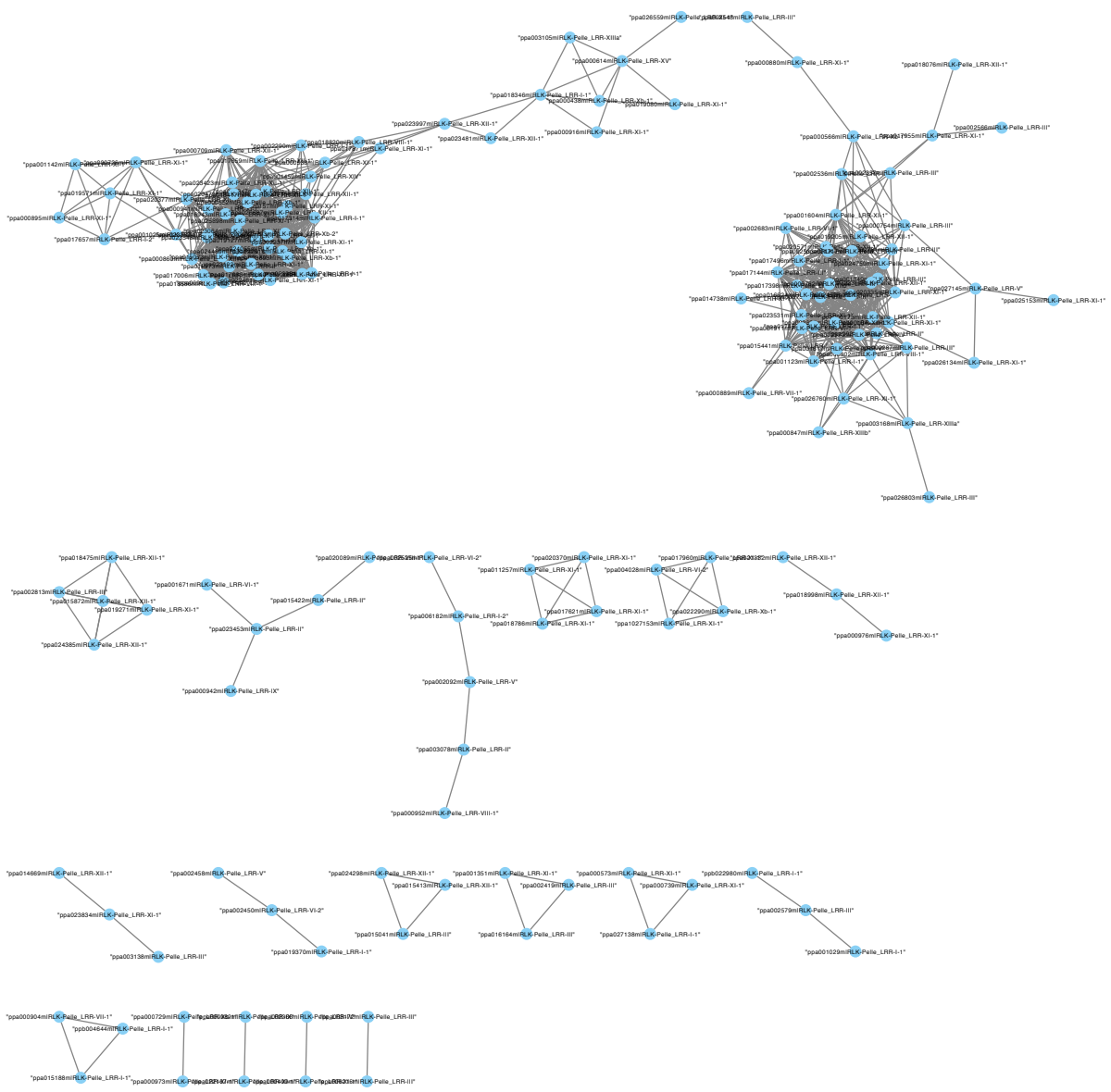
Supplementary Fig. 6. Co-expression network of strawberry LRR-RLK genes. Nodes indicate genes and edges indicate significant co-expression events between genes.



Supplementary Fig. 8. Co-expression network of Chinese white pear LRR-RLK genes. Nodes indicate genes and edges indicate significant co-expression events between genes.



Supplementary Fig. 9. Co-expression network of merL-RR-RLK genes. Nodes indicate genes and edges indicate significant co-expression events between genes.



Supplementary Fig. 10. Co-expression network of peach LRR-RLK genes. Nodes indicate genes and edges indicate significant co-expression events between genes.