Supplementary Figure 1: Heat map of the expression patterns of 281 rice barley 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 10.
Supplementary Figure 1. Heatmap of the expression profiles of top 100 DEG genes in different tissues. Red and green colors correspond to upregulation and downregulation, respectively. Normalized gene expression values are provided in Supplementary Table 12.
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. 7. Co-expression network of apple 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 necLRR-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.