**Supplementary figure 1** The boxplot distribution of gene expression the two tissues of each species. The X-axis shows the sample name; the Y-axis represents log10(FPKM+1). The boxplot of each area shows five statistics (from top to bottom are the upper limit, upper quartile, median, lower quartile, respectively).

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**Supplementary figure 2** Individual species tissue-specific and common DEGs among the leaf-less control and leaf samples.

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**Supplementary figure 3** Overview of GO enrichments for C. ensifolium (a), C. goeringii (b) and C. sinense (c)

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**Supplementary figure 4** Overview of KEGG enrichments for C. ensifolium (a), C. goeringii (b) and C. sinense (c)

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