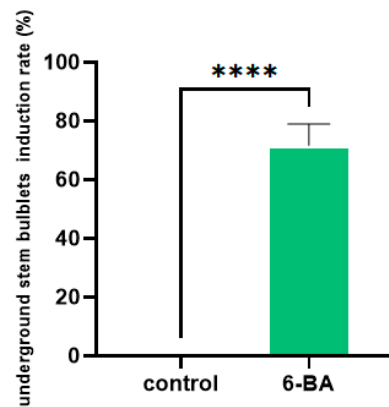
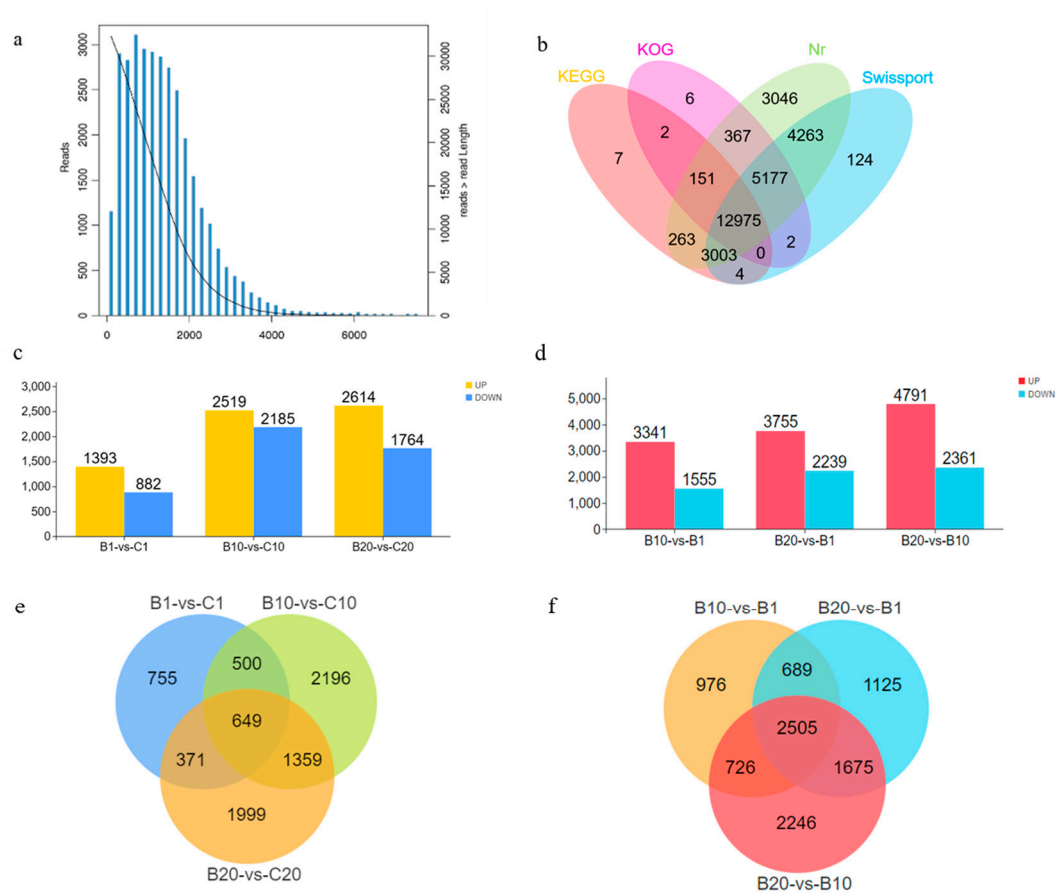


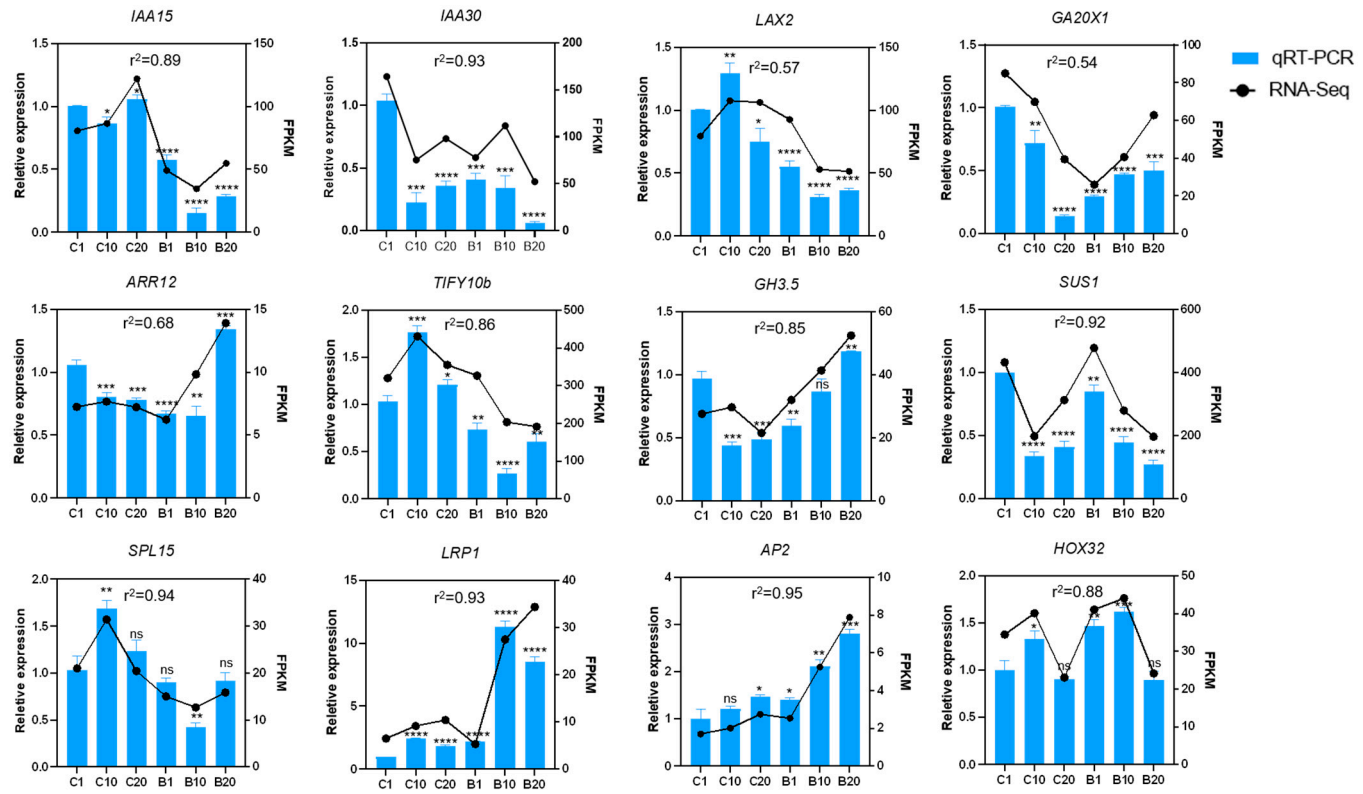
**Figure S1.** Morphology and anatomy of leaf axils at C1(a, d), C10 (b, e) and C20 (c, f) stages under the influence of distilled water. Scale bar for sample images a, b, c = 5 mm; scale bar for microscope images d, e, f = 200 μm. P, Petiole; S, stem; black circle, leaf axil.



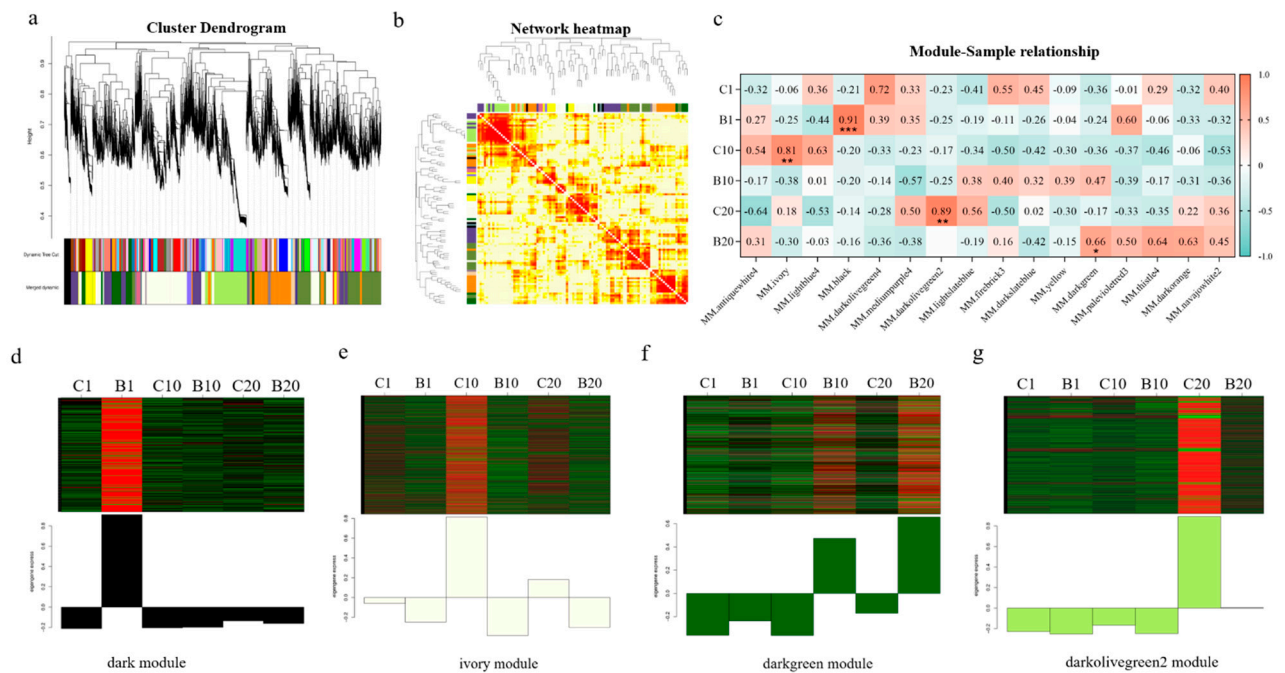
**Figure S2.** Induction rate of the control group and 6-BA treated group during in stem bulblet initiation. Induction rate = number of axils that produced axillary meristems/total number of underground axils. \*\*\*\*Differences significant at  $p < 0.0001$ .



**Figure S3.** PacBio Iso-Seq and expression profiles of *L. 'Aladdin'*. (a) Length distribution of transcripts obtained by PacBio IsoSeq. (b) Venn diagram of transcripts hits of KOG, Nr, KEGG and SwissProt. (c) Histogram displaying the number of DEGs that were up- or down-regulated between different groups (B1 vs C1, B10 vs C10, and B20 vs C20). (d) Histogram displaying the number of DEGs that were up- or down-regulated between different groups (B10 vs B1, B20 vs B1, and B20 vs B10). (e) Venn diagram of DEGs among the three comparisons (B1 vs C1, B10 vs C10, and B20 vs C20). (f) Venn diagram of DEGs among the three comparisons (B10 vs B1, B20 vs B1, and B20 vs B10).

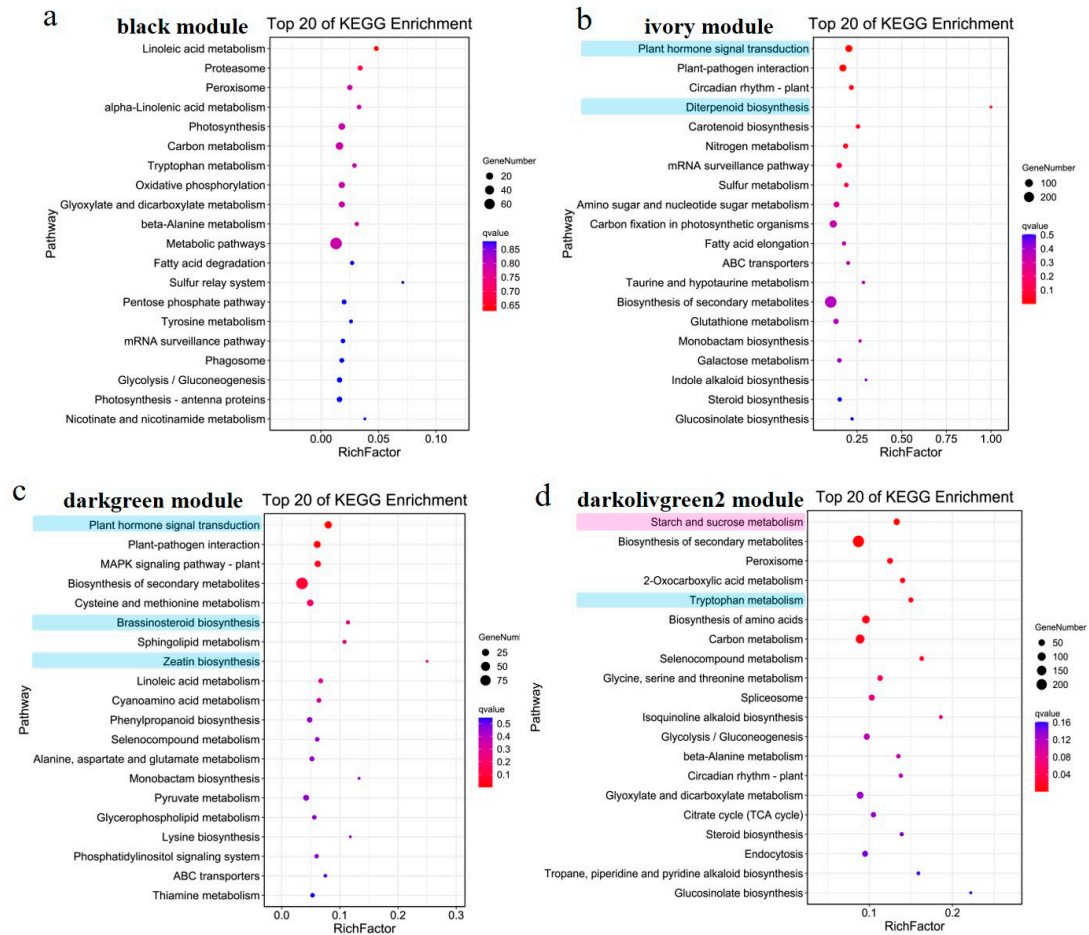


**Figure S4.** Expression of representative genes determined by RNA-seq and qRT-PCR. qRT-PCR expression data are shown in columns (left y-axis). As shown by RNA-seq, lines show FPKM values (right y-axis). Values represent the means  $\pm$  SD of 3 biological replicates. For statistical analyses, unpaired Student's t-test (two tailed) was used in Figure S4 (\* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ , \*\*\*\* $P < 0.0001$ ; ns indicates no significant difference). Correlations between qRT-PCR and RNA-seq expressions were indicated.



**Figure S5.** WGCNA network of axil samples. (a) Module level clustering diagram. (b) Network heatmap

plot. (c) Module-sample relationship. (d-g) Heatmaps depicting gene expression patterns for each module.



**Figure S6.** Top 20 KEGG pathways in each relevant module. The phytohormone signaling pathway is highlighted in blue, while the starch and sucrose pathway is highlighted in red.