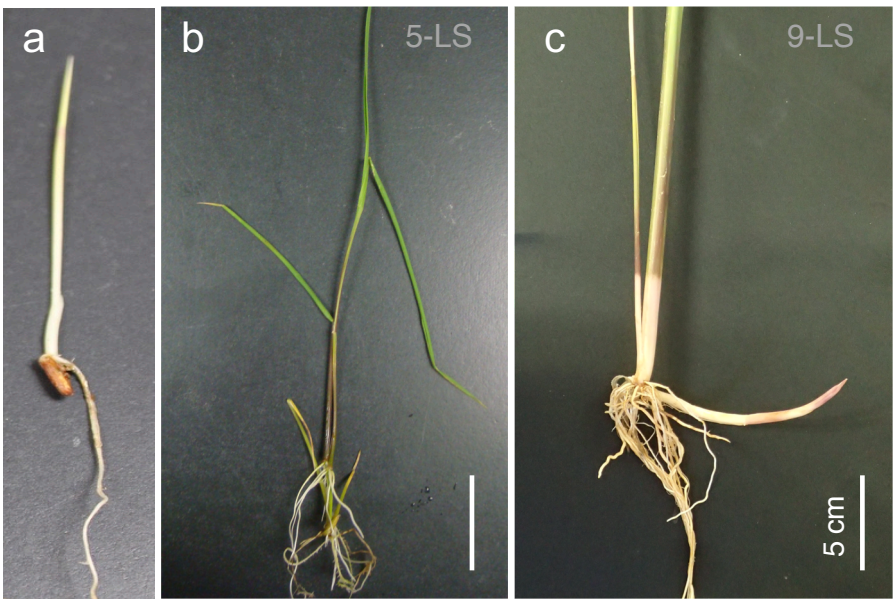

Figure S1. Rhizome development of samples growing from seeds of *O. longistaminata*. (a) A 5-day-old seedling of *O. longistaminata*. (b,c) Rhizome development of *O. longistaminata* growing from seed at the 5-leaf stage (b) and 9-leaf stage (c).

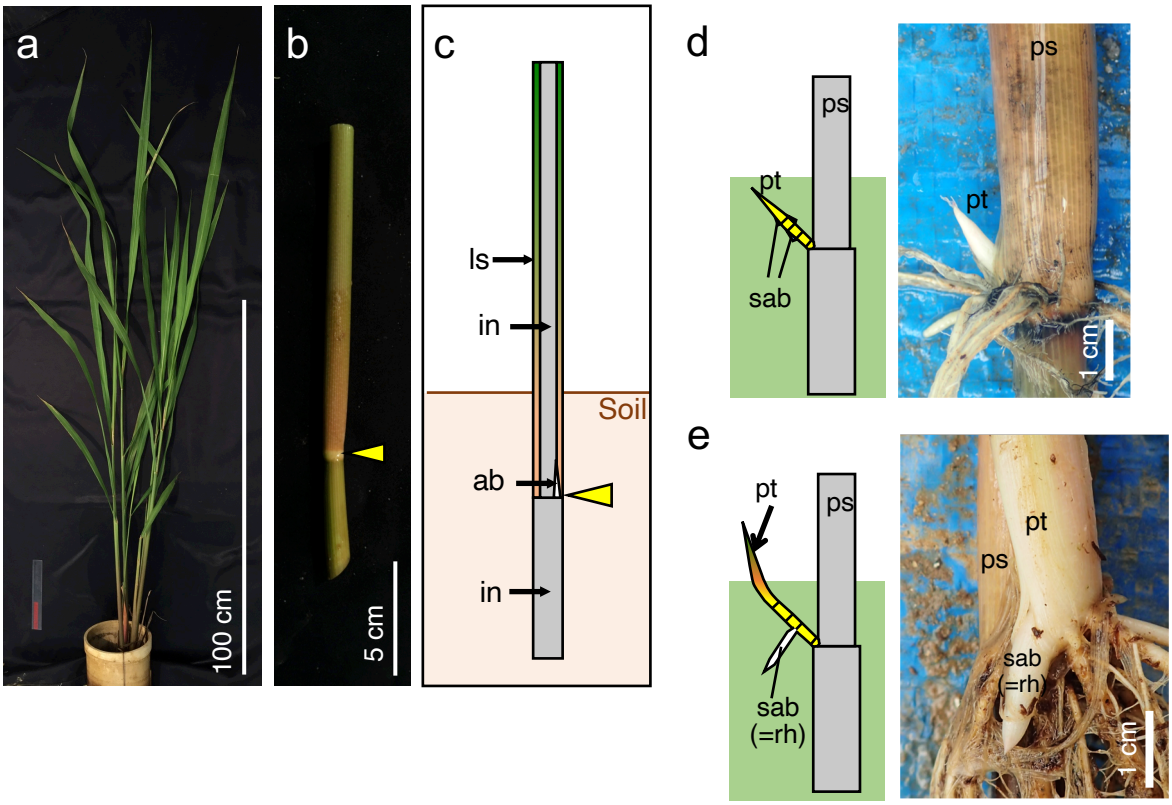

Figure S2. Establishment of the cutting system using *O. longistaminata* stem. (a) Photograph of the *O. longistaminata* plant used as the starting material for cuttings. The yellow arrowhead indicates the node position. (b) The cutting sample which has one node. (c) Longitudinal diagram of the elongated stem. (d,e) Cutting after one week (d) and four weeks (e). ls, leaf sheath; in, internode; ab, axillary bud; ps, parental shoot; pt, primary tiller; sab, secondary axillary bud; rh, rhizome. Scale bars (a) 100 cm, (b) 5 cm, (d,e) 1 cm.

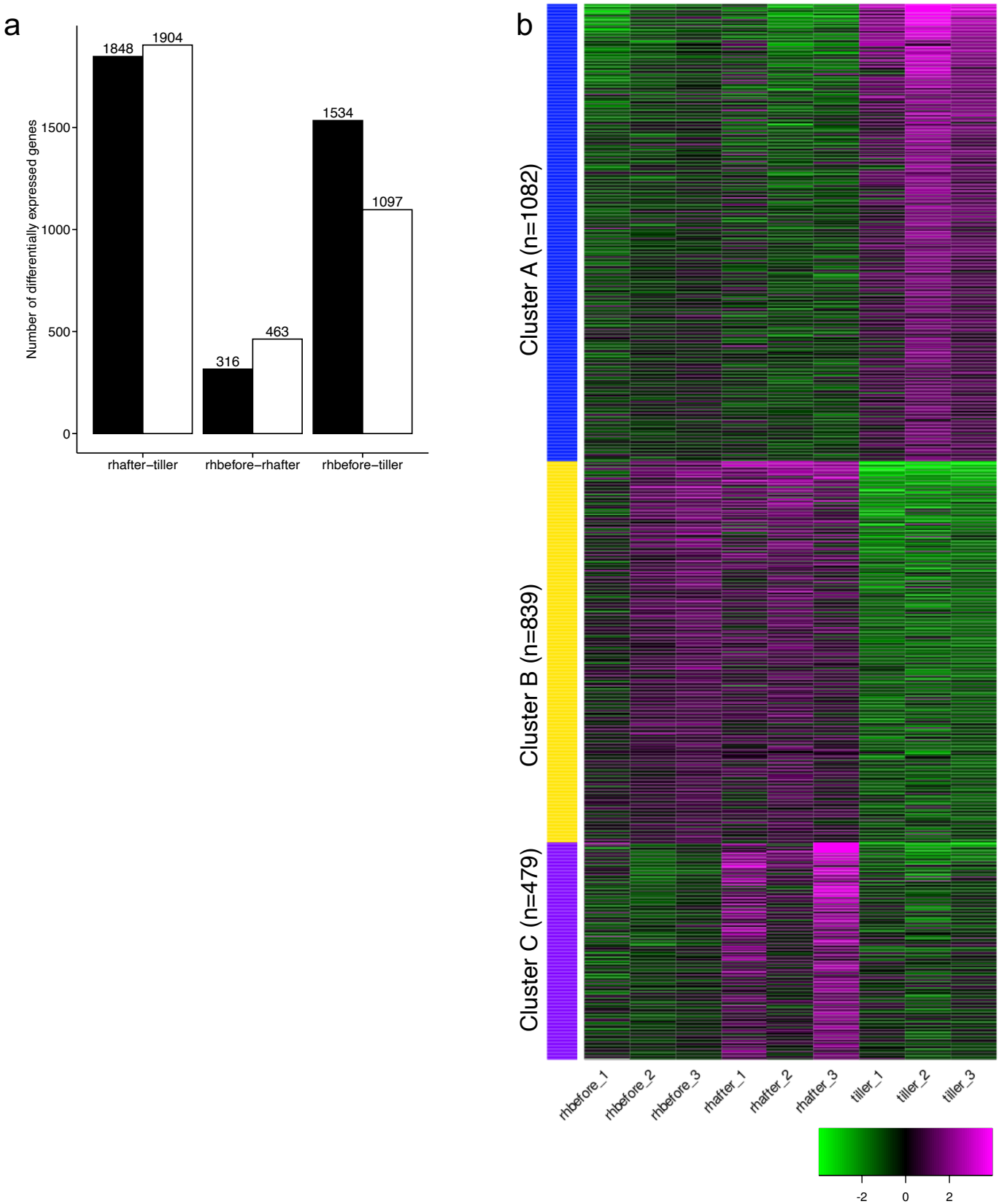

Figure S3. Clustering analysis of the genes expressed in tiller and rhizome buds from cuttings. (a) Number of differentially expressed genes for each pairwise comparison. Tiller, tiller; rhbefore, rhizome bud before bending; rhafter, rhizome bud after bending. Black and white bars represent upregulated and downregulated genes in each comparison. (b) Heatmap representation and clustering of the expression of 2,400 genes with specific expression patterns in each sample. Cluster k-mer was set to 3. Color key indicates log2FC values.

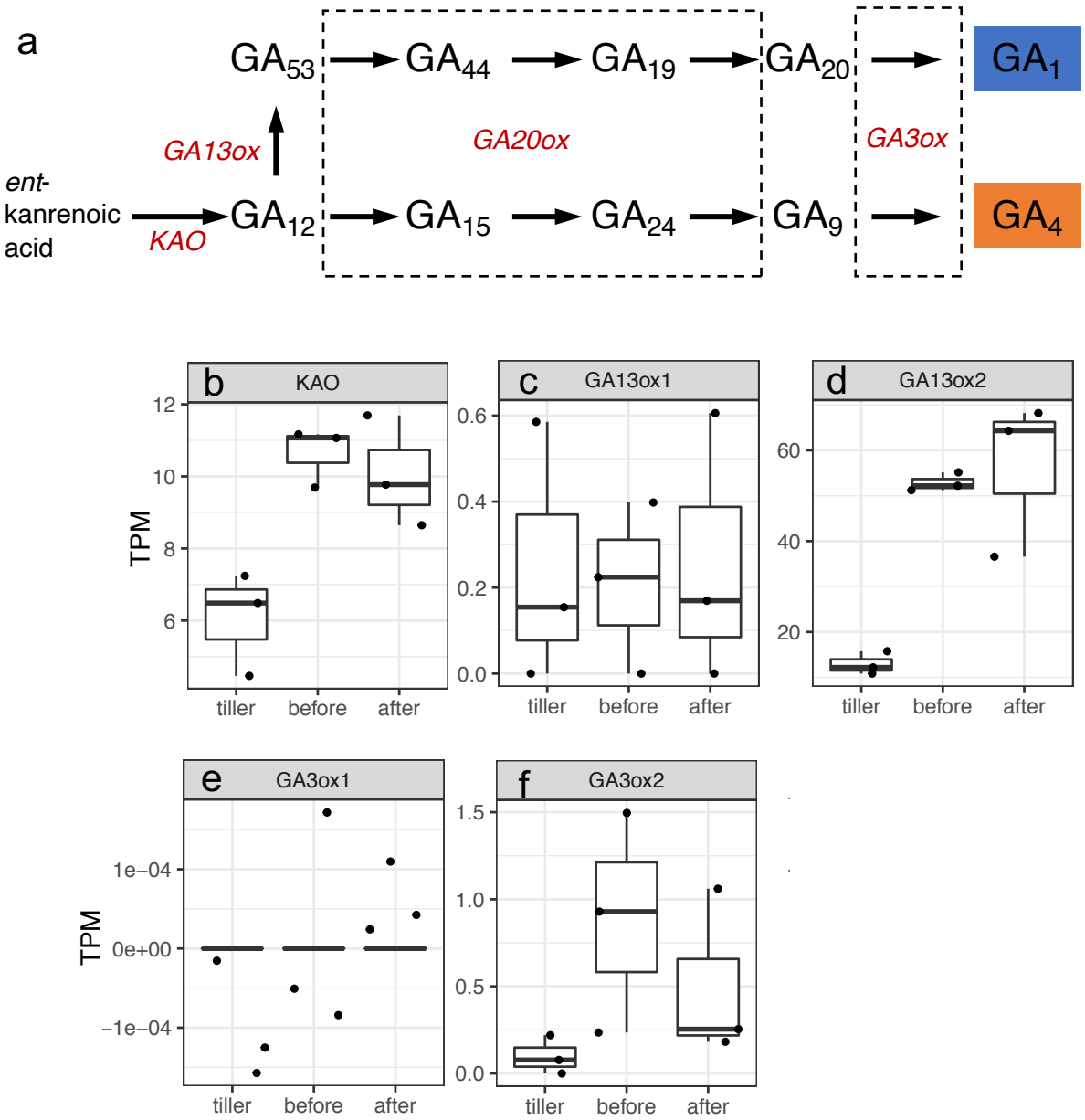

Figure S4. Expression levels of GA biosynthesis genes in tiller and rhizome buds from cuttings. (a) Simplified diagram of the GA biosynthetic pathway and related genes. Red color indicates the GA biosynthesis genes. (b–f) Expression of GA biosynthesis genes, indicated as transcripts per million (TPM) values from RNA-seq data: *KAO* (b), *GA13ox1* (c), *GA13ox2* (d), *GA3ox1* (e), and *GA3ox2* (f). Tiller, tiller bud; before, rhizome bud before bending; after, rhizome bud after bending.

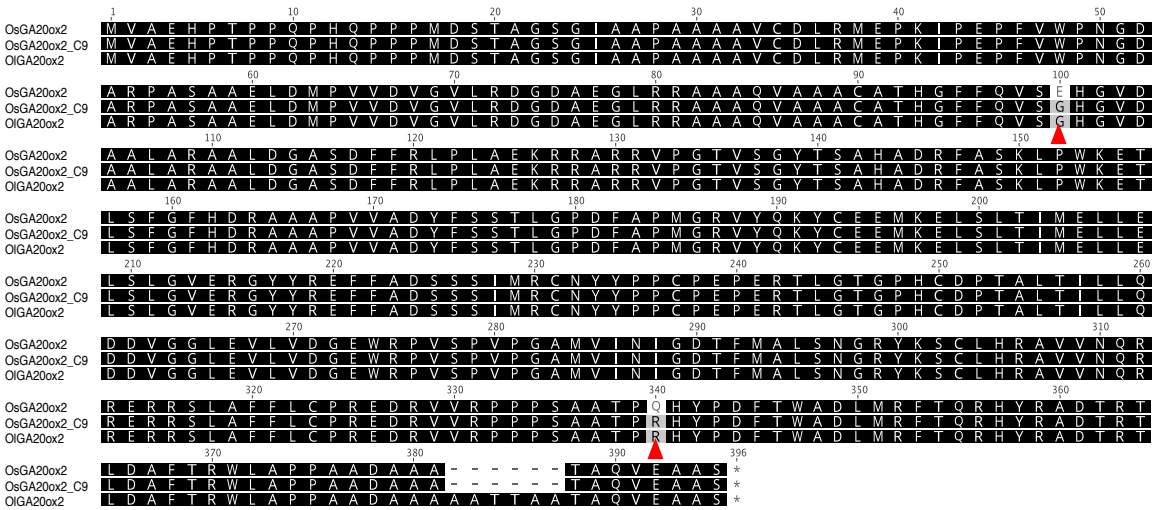

Figure S5. Alignment of GA20ox2 amino acid sequences. Multiple sequence alignment of the amino acid sequence of GA20ox2 from *O. sativa* (Os), deepwater rice (C9), and *O. longistaminata* (Ol). Red arrowheads indicate amino acid substitutions.

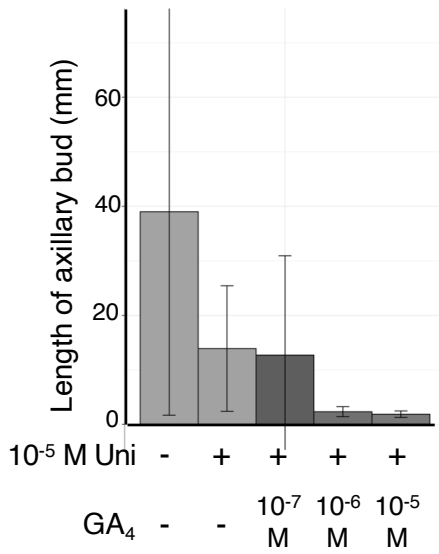

Figure S6. Effect of GA signaling on the length of rhizome buds. Length of the axillary buds whose angles were measured in **Figure 5**.

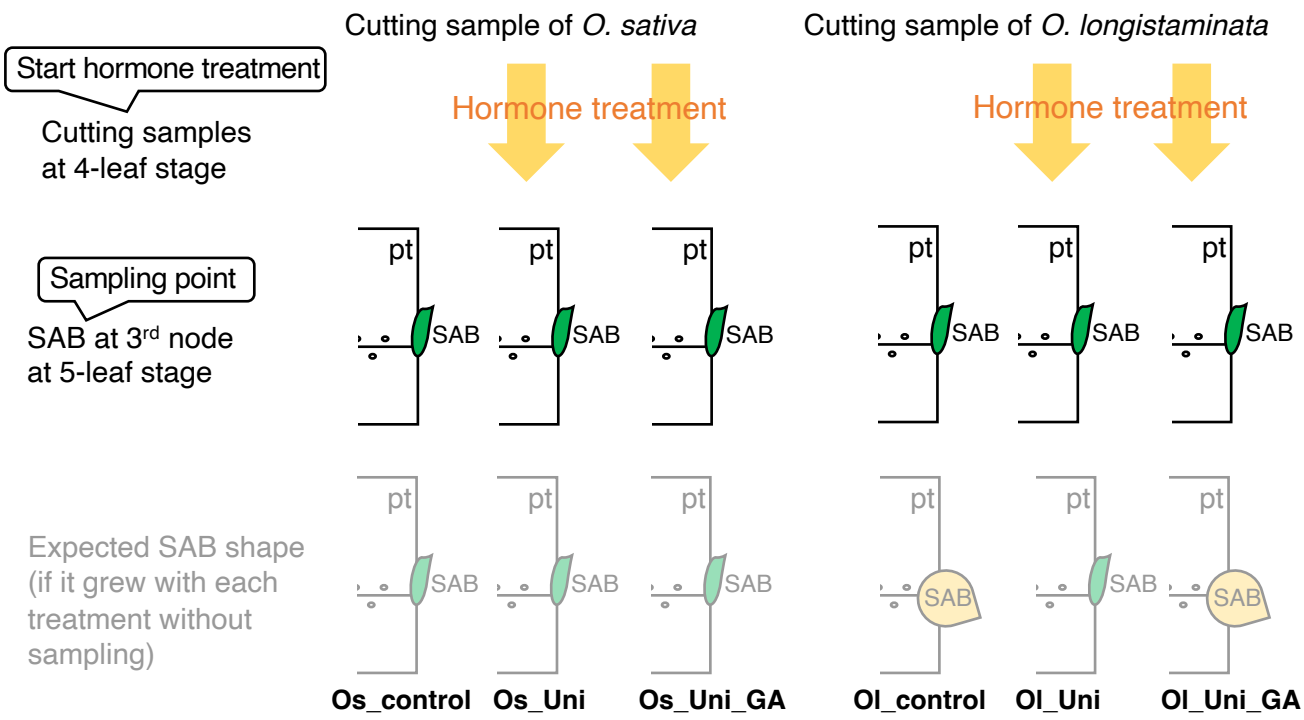

Figure S7. Timing of sample harvest and phytohormone treatment for RNA-seq analysis. Second axillary buds (SAB) from the third node at the 5-leaf stage of cuttings from *O. sativa* and *O. longistaminata* were collected after phytohormone treatment. The shape of SABs was similar to that of tiller buds at the harvest time point regardless of treatment (upper images). Lower images indicate the expected shape of the future bud following GA or uniconazole (UNI) treatment, shown in **Figure 5**. Control means mock-treatment with solvent only (0.1% [v/v] ethanol). Details are described in Methods.

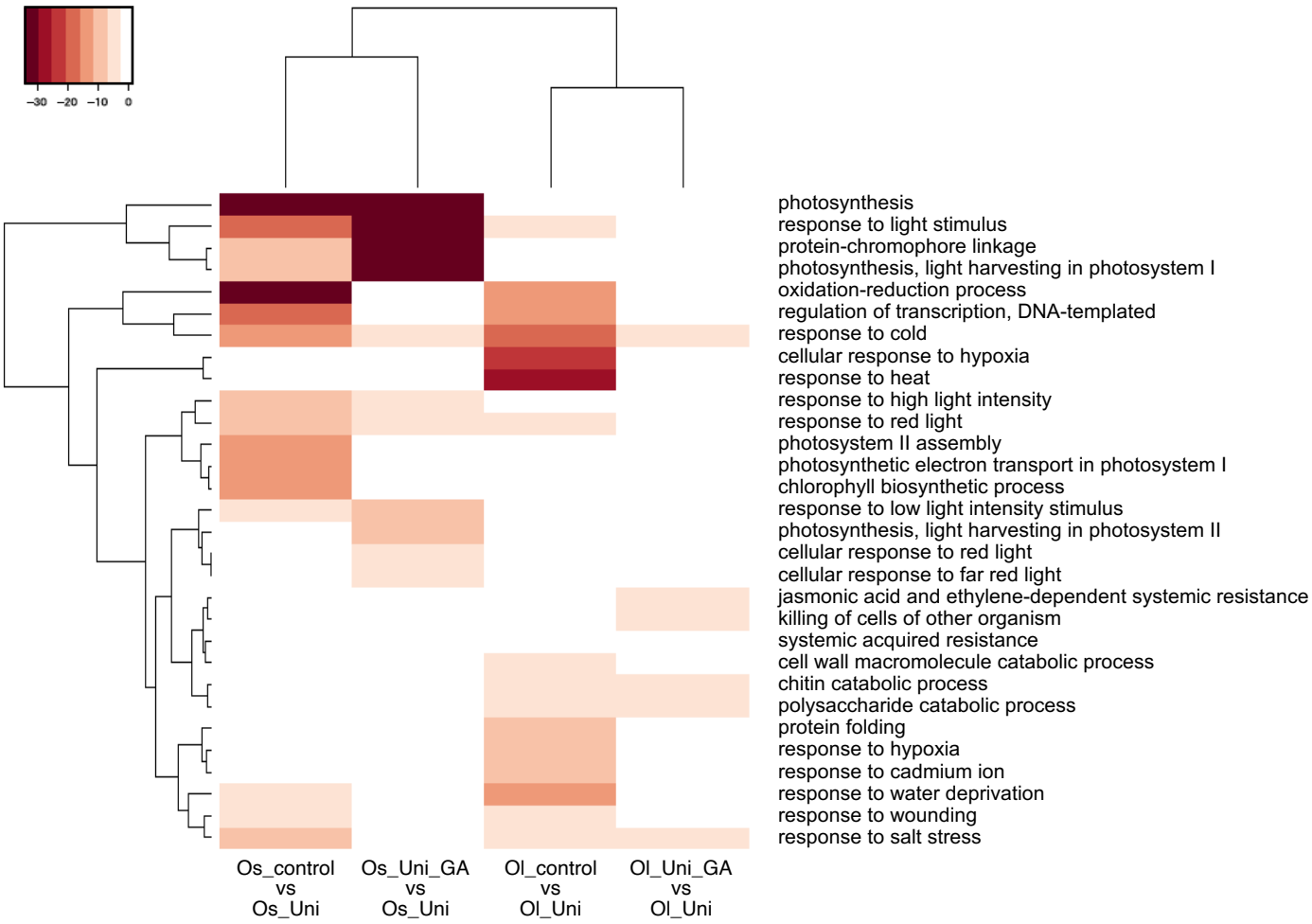

Figure S8. Heatmap showing the significance of GO terms. Top 10 GO terms related to biological process which are enriched in each category. The color scale indicates corrected $\log_{10}$(*P*-value).

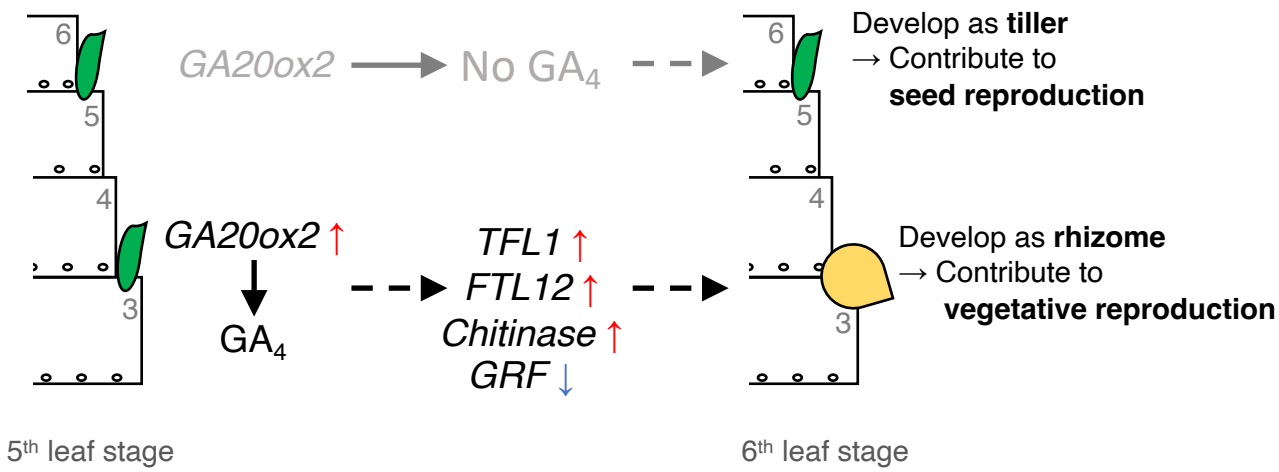

Figure S9. Model of the relationship between GA signaling and downstream genes affecting rhizome bud development. Red and blue arrows indicate upregulated and downregulated genes at the axillary bud of control (mock-treated) and GA_4-treated *O. longistaminata*, respectively. The numbers in the diagrams indicate node number.