SUPPLEMENTSAL DATA

Coordinated activation of cellulose and repression of lignin biosynthesis pathways in rice

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Supplemental Figure S1
**Supplemental Figure S1. Overview of monolignol biosynthesis pathway.**

The boxed scheme showing the proposed pathways leading to the biosynthesis of guaiacyl (G) and syringyl (S) phenylpropanoid units in angiosperms. All the enzymatic reactions presented in the pathway have been demonstrated at least *in vitro* studies in several different plant species, and may not represent the actual *in vivo* pathway in any specific species because of the variety of isoenzymes and kinetic properties causing several alternative routes through the metabolic pathway to exist. For reactions with a question mark, either the respective enzyme is unknown or obscure alternative enzymatic steps exist. For a more extensive pathway description, the reader is referred to references (Boerjan et al., 2003; Ralph et al., 2004; Vanholme et al., 2008). Enzymes are indicated for each reaction step as PAL, phenylalanine ammonia-lyase; C4H, cinnamate 4-hydroxylase; C3H, 4-coumarate 3-hydroxylase; COMT, caffeate O-methyltransferase; F5H, ferulate 5-hydroxylase; 4CL, 4-coumarate:coenzyme A ligase; CCoAOMT, caffeoyl CoA O-methyltransferase; CCR, cinnamoyl-CoA reductase; CAD, cinnamyl alcohol dehydrogenase.
Supplemental Figure S2

Supplemental Figure S2. qRT-PCR expression analysis of cell wall related genes in SHN leaf and culm.

Data are expressed as the mean relative transcript levels in SHN lines compared to that of WT (log2 ratio) at each tissue (leaf and culm). Error bars represent ± s.e.m. (n=3) (three WT and three SHN lines). Asterisks indicate levels of significance of differential expression (t-test, *, P ≤ 0.05; **, P ≤ 0.01).
Supplemental Figure S3. Gene expression and regulation of lignin biosynthetic pathway genes.

WT absolute expression levels of SHN-regulated lignin biosynthetic genes obtained from the microarray are plotted in \( \log_2 \) scale with the 40th percentile of genome-wide gene expression values (marking the level above which genes can be considered to be 'expressed') indicated by a dashed line. The differential expression values of specified genes in SHN lines are shown alongside. The rice AC element sequences identified in the promoters (1 Kb upstream of start site) of the SHN-regulated lignin pathway genes, are shown with the number of occurrences of the element in each promoter given in brackets. The sequence logo of the rice AC element identified in the promoter regions of rice lignin biosynthetic genes is given below, with the height of a character at a particular position representing the fraction of occurrences of the corresponding nucleotide in that position.
SUPPLEMENTAL REFERENCES


