

Figure S1. Genes involved in cellulose biosynthesis and production (*COBRA*) were upregulated in the stem of *pPLAIIIγ*OE lines. Each data point represents the average \pm SE of three independent replicates at $P < 0.05$ (*) and $P < 0.01$ (**), respectively.

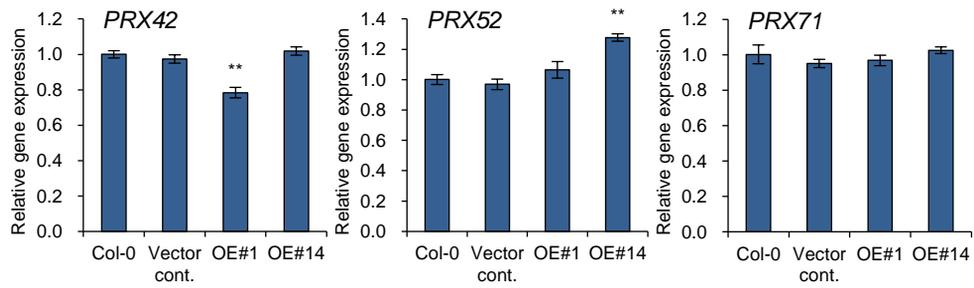
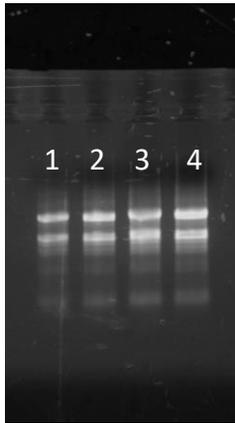


Figure S2. Expression levels of peroxidases in the stem of *pPLAIII*OE lines.

Each data point represents the average \pm SE of three independent replicates at $P < 0.05$ (*) and $P < 0.01$ (**), respectively.

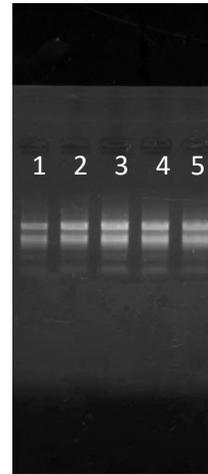
Total RNA from 2-week-old seedling
(In figure 2A)



- 1: Col-0
- 2: Vector control (35S:YFP)
- 3: pPLAIIIγOE#5
- 4: pPLAIIIγOE#14

1% agarose gel, 100 V, 20 mins
loading

Total RNA from 7-week-old stem
(In figure.3B, 4A, 4B, 5B, S1, S2)



- 1: Col-0
- 2: Vector control (35S:YFP)
- 3: pPLAIIIγOE#1
- 4: pPLAIIIγOE#5
- 5: pPLAIIIγOE#14

1% agarose gel, 100 V, 20 mins
loading

Figure S3. Agarose gel loading of total RNA used for qPCR. Total RNA isolated from 2- week-old seedling and 7-week-old stem was visualized in 1% of agarose gel