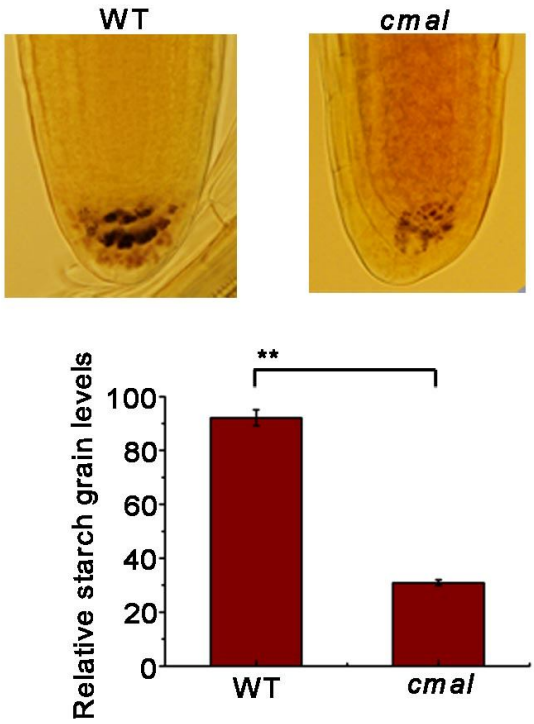
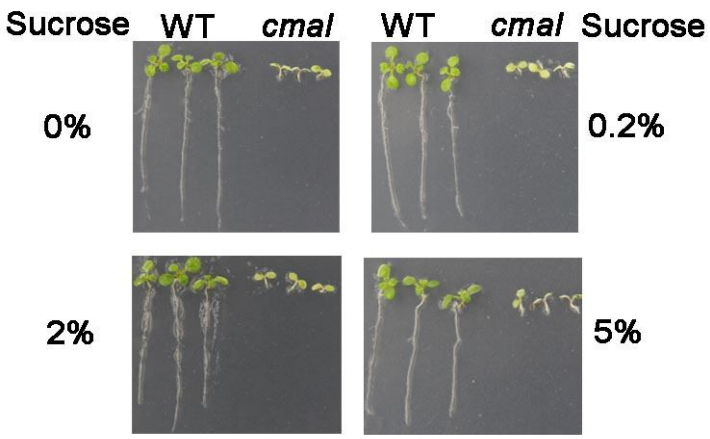
SUPPLEMENTAL FIGURES



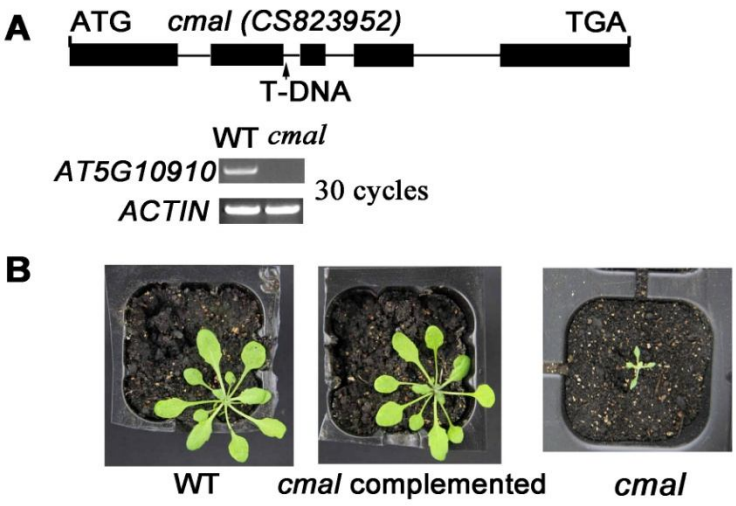
Supplemental Figure 1: Light microscopy of iodine-stained root tips of WT and *cmal* plants

Pictures of root tips of four-week-old old WT and *cmal* seedlings following decolorization and iodine staining for starch (upper panel). Quantification of starch grain levels (lower panel).



Supplemental Figure 2: Phenotype of *cmal* grown on MS medium supplied with different sucrose concentrations.

WT and *cmal* plants were grown on MS medium supplemented with different sucrose concentrations for 10 days.



Supplemental Figure 3: Cloning of *CMAL*.

(A) Schematic representation of the genomic organization of *CMAL* indicating the exons (black boxes), introns (lines between exons), and the position of the T-DNA insertion in the *cmal* mutant. *CMAL* expression in WT and *cmal* mutant plants was assayed using RT-PCR as indicated in the lower panel. The *Arabidopsis ACTIN* gene was used as an internal control.

(B) The phenotype of *cmal* plants complemented with WT *CMAL* and grown on soil for four weeks.

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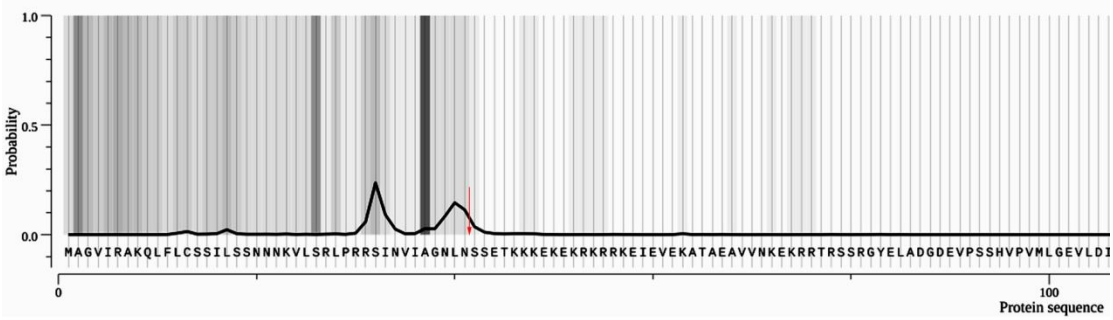
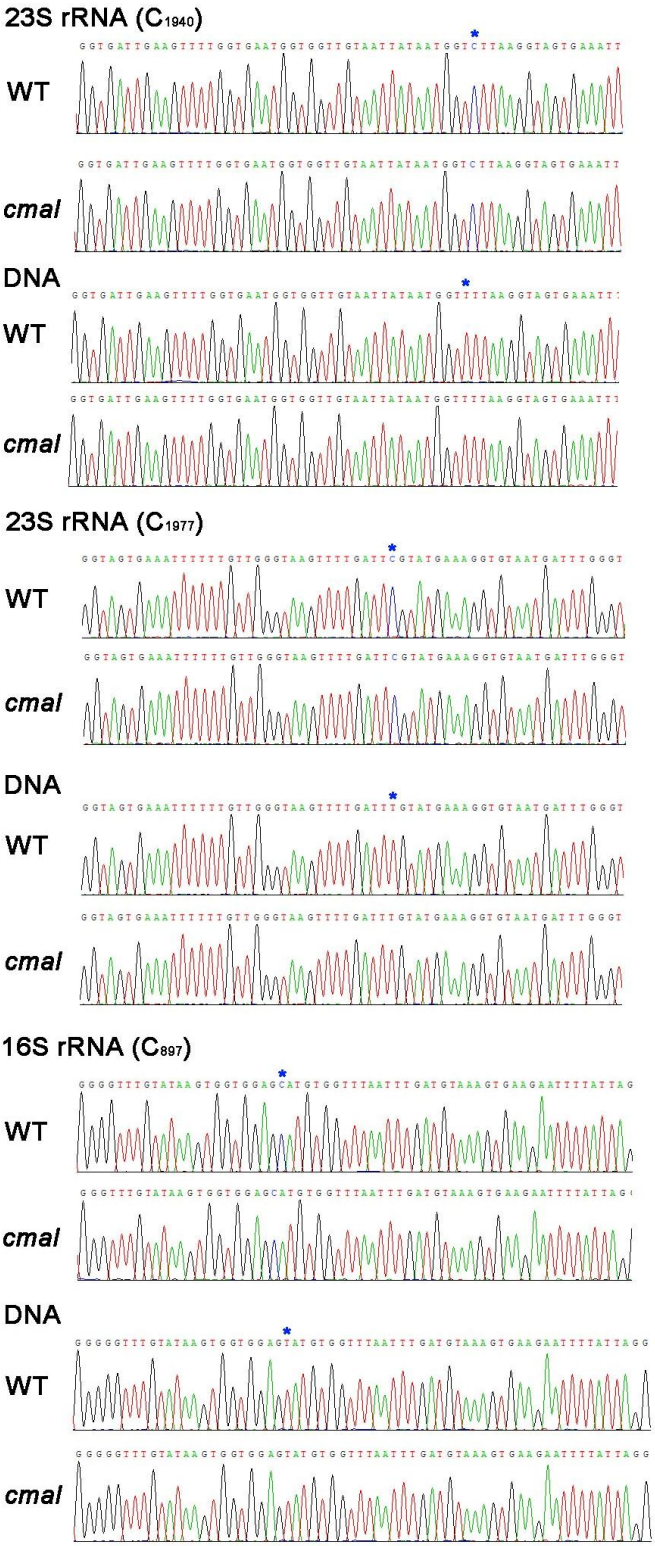
### targetp v1.1 prediction results ###################################
Number of query sequences:  1
Cleavage site predictions included.
Using PLANT networks.

Name                  Len     cTP    mTP     SP  other  Loc  RC  TPlen
----------------------------------------------------------------------
Sequence              434   0.672  0.320  0.074  0.005   C    4     41
----------------------------------------------------------------------
cutoff                      0.000  0.000  0.000  0.000
```



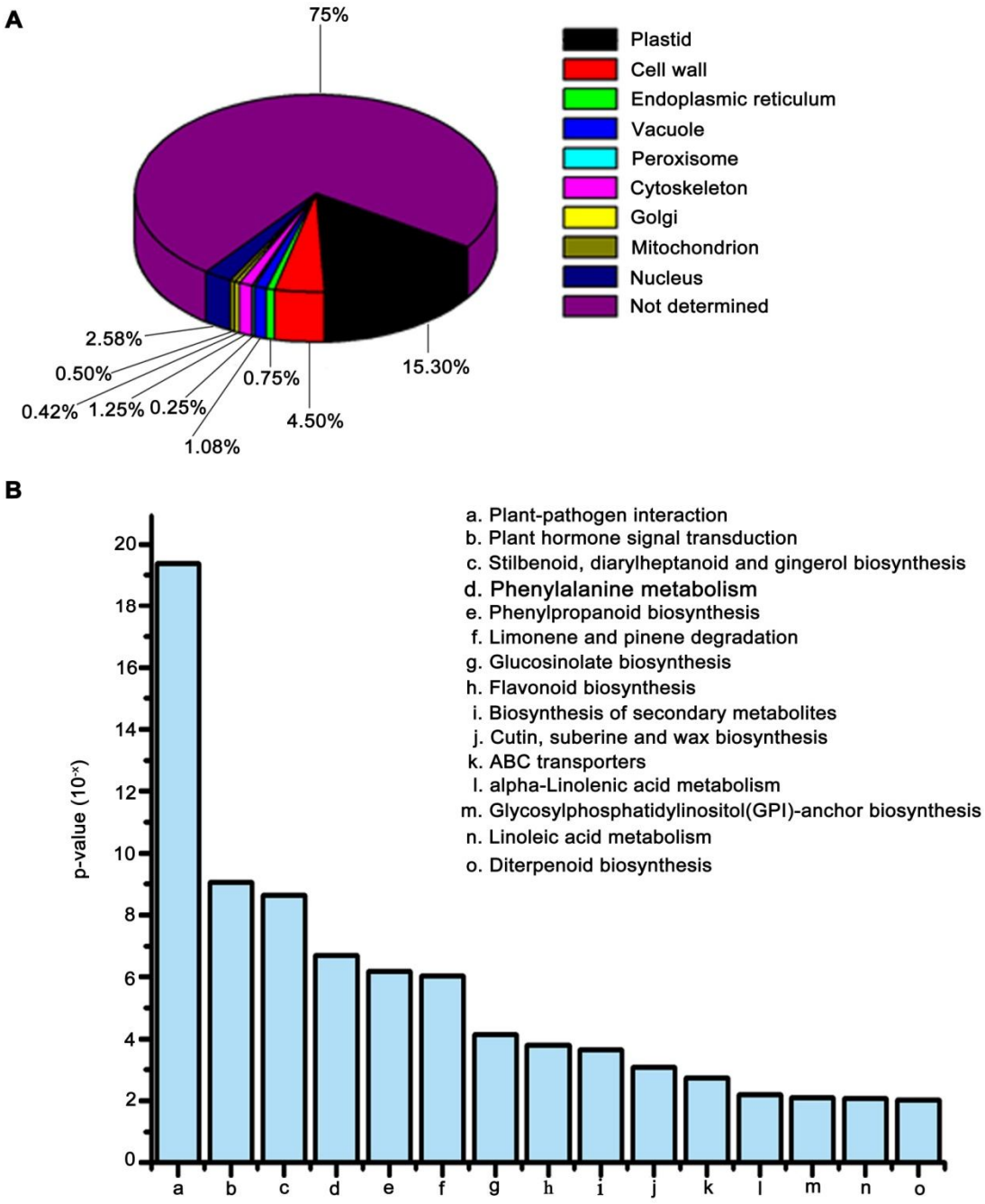
Supplemental Figure 4. Outputs of TargetP server for the subcellular localization prediction of CMAL protein.

cTP: chloroplast transit peptide; mTP: mitochondrion transit peptide; SP: secretory protein; other: no signal peptide; TPlen: the length of signal peptide. The symbol "C" indicates that this protein is predicted to be localized in chloroplasts. The likelihood probabilities are reported on the plot.



Supplemental Figure 5: The methylation of other methylcytosine sites of plastid rRNAs.

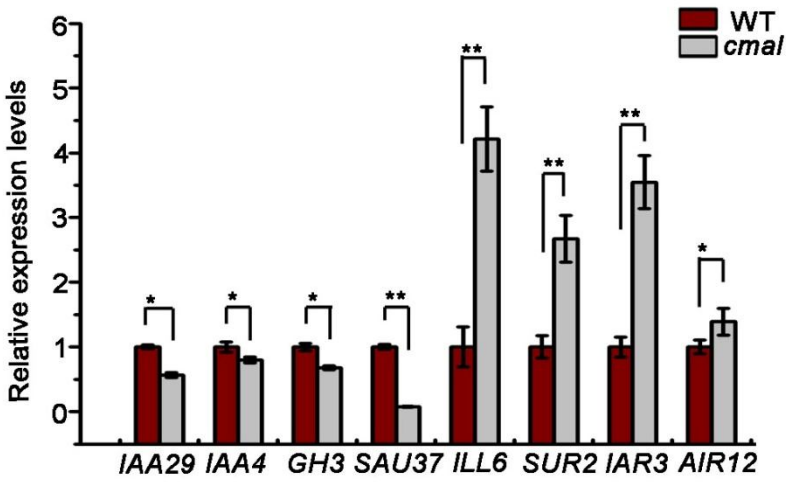
The excremental procedure was the same as that in Figure 3B except that different primers were used for RT-PCR. The sequences were assayed using the Chrosome software. Blue asterisks indicate the methylcytosine sites.



Supplemental Figure 6: Global gene expression assay of the WT and *cmal* plants.

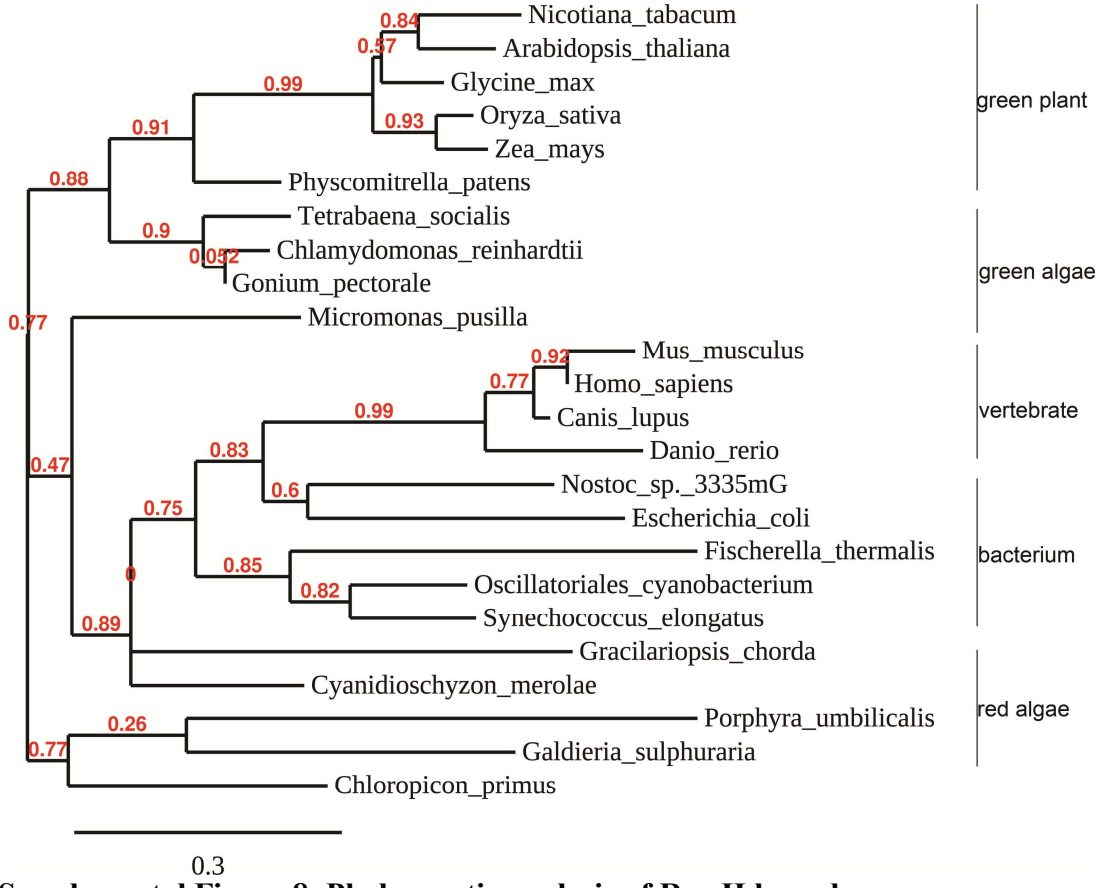
(A) Cellular component categorization of DEGs between *cmal* and the WT determined using RNA sequencing.

(B) Pathway enrichment analysis of DEGs based on the KEGG database. The pathways are sorted based on their associated *p* values.



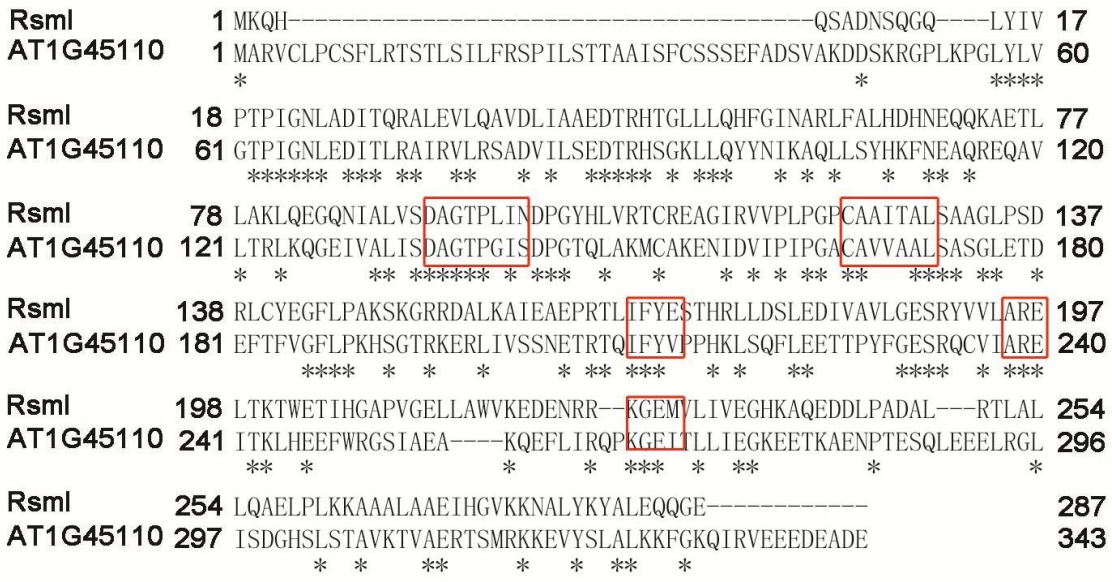
Supplemental Figure 7: RT-qPCR assay of auxin-responsive genes in *cmal* and WT plants.

Total RNAs from two-week-old Arabidopsis seedlings were subjected to qRT-PCR assays. Relative mRNA abundance was determined after normalization to the *TUBULIN6* gene. Data are means ± SD (n=3).



Supplemental Figure 8: **Phylogenetic analysis of RsmH homologs**.

Phylogenetic tree was constructed on the Phylogeny.fr web tool (http://www.phylogeny.fr). Posterior probabilities are indicated near nodes. The bar indicates the branch length that corresponds to 0.3 substitutions per position. Sequence data for phylogenetic tree construction can be found in the GenBank/EMBL library under the following accession numbers: *Arabidopsis thaliana* (AED91608.1), *Canis lupus* (XP_534100.3), *Chlamydomonas reinhardtii* (PNW73675.1), *Chloropicon primus* (QDZ19182.1), *Cyanidioschyzon merolae* (XP_005538735.1), *Danio rerio* (XP_689063.3), *Escherichia coli* (WP_148444004.1), *Fischerella thermalis* (PMB31361.1), *Galdieria sulphuraria* (XP_005707681.1), *Glycine max* (XP_003544633.1), *Gonium pectoral* (KXZ43589.1), *Gracilariopsis chorda* (PXF40402.1), *Homo sapiens* (NP_001107000.1), *Micromonas pusilla* (XP_003058985.1), *Mus musculus* (NP_084066.2), *Nicotiana tabacum* (XP_016433904.1), *Nostoc sp. 3335mG* (WP_110156463.1), *Oryza sativa* (XP_015624006.1), *Oscillatoriales cyanobacterium* (TAD77411.1), *Physcomitrella patens* (XP_024396154.1), *Porphyra umbilicalis* (OSX77860.1), *Synechococcus elongates* (AZB72509.1), *Tetrabaena socialis* (PNH04008.1), *Zea mays* (NP_001288454.1).



Supplemental Figure 9: The Arabidopsis ortholog of RsmI.

The sequence alignment of the RsmI and AT1G45110 proteins was assayed by ClustalW (https://www.ebi.ac.uk/Tools/msa/clustalo/). The putative SAM-binding sites are indicated by red boxes.