Supplemental Material

Supplemental Figure 1

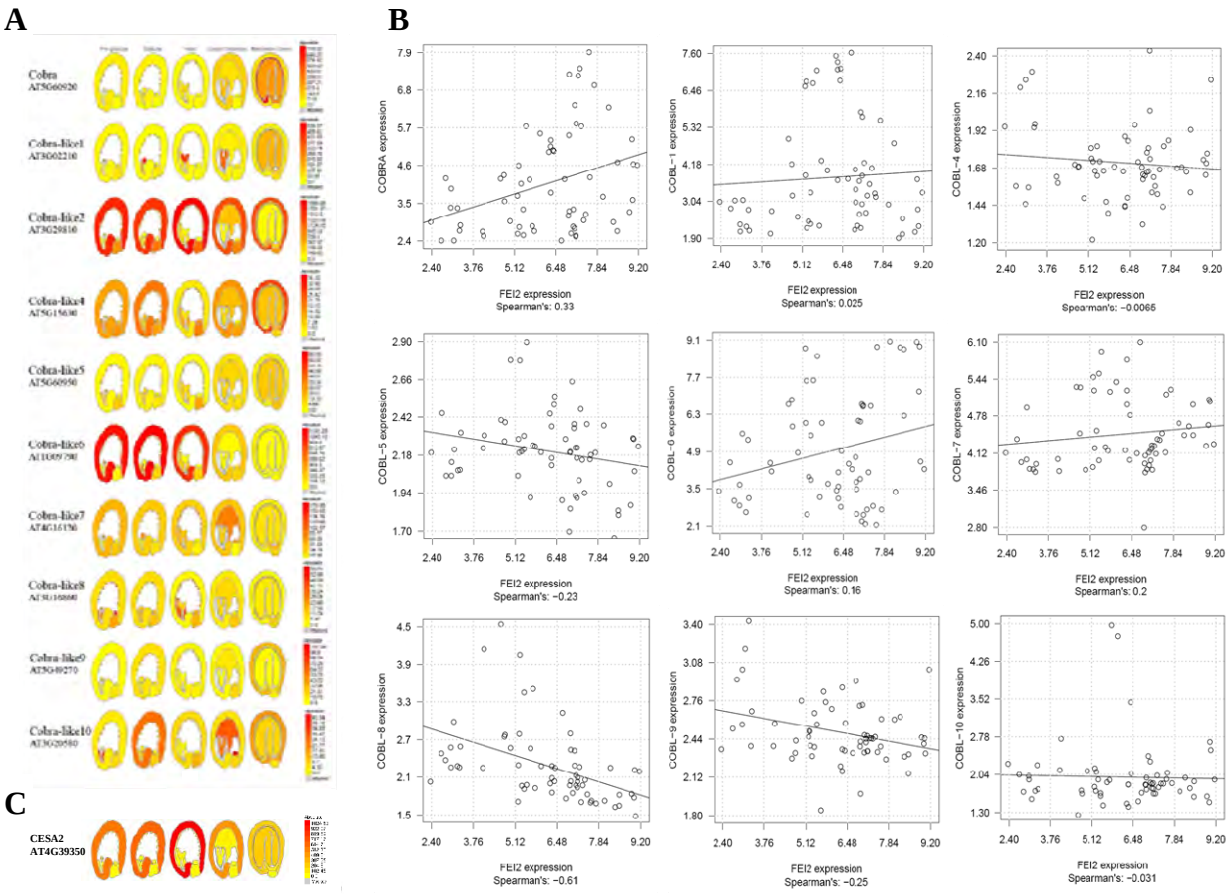

Fig. S1. **Expression analysis of the *COBRA-LIKE* gene family during seed development** Gene expression profiles during the course of seed development based on the Goldberg and Harada dataset for gene expression profile in seven seed sub-tissues sampled in five defined stages during the course of seed development (as described in Le et al., 2010) as illustrated by the web based eFP browser (Winter et al., 2007): A) expression of the *COB-LIKE* gene family C) expression of *CELLULOSE SYNTHASE 2*. B) The coexpression relationship between FEI2 and members of the *COBRA-LIKE* gene family during the course of seed development as demonstrated by Spearman correlation coefficient.

Supplemental Figure 2

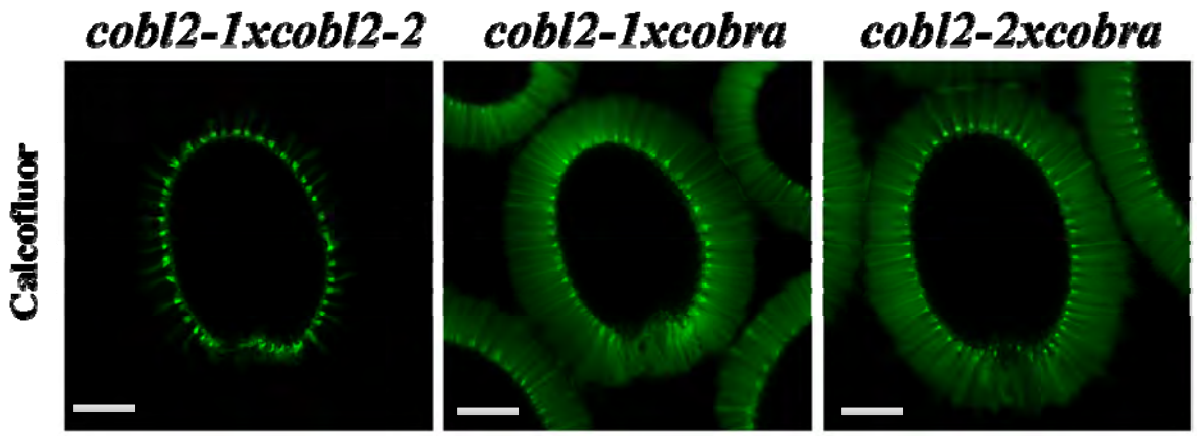

Fig. S2. Allelism tests between *cobl2-1* and *cobl2-2* demonstrate that both carry a mutation in the same gene. Allelism tests were conducted between *cobl2-1*, *cobl2-2* and *cob-1*. The last of which served as a negative control. F2 seeds were examined and photographed. Scale bars: 0.25mm

Supplemental Figure 3

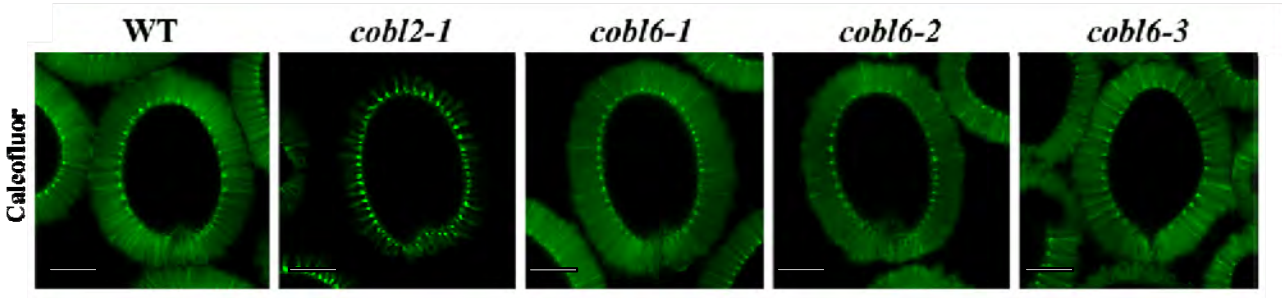

Fig. S3. Mutants in *cobl6* did not display seed mucilage phenotypes. For three different insertion alleles of *cobl6* homozygous plants were identified and examined for perturbation in seed mucilage rays formation by calcofluor stain for β-glucans. The phenotype of all three alleles was indistinguishable from the wild type. Scale bars: 0.25mm

Supplemental Figure 4

Fig. S4. Expression of COBL2 promoter driven GUS in seeds. pCOBL2::GUS expression pattern was observed along the course of seed development. Siliques were harvested 12 days post-anthesis and stained for GUS activity as compared to wild type. Scale bars: 1.5mm (upper panel); 0.5 mm (lower panel).

Supplemental Figure 5

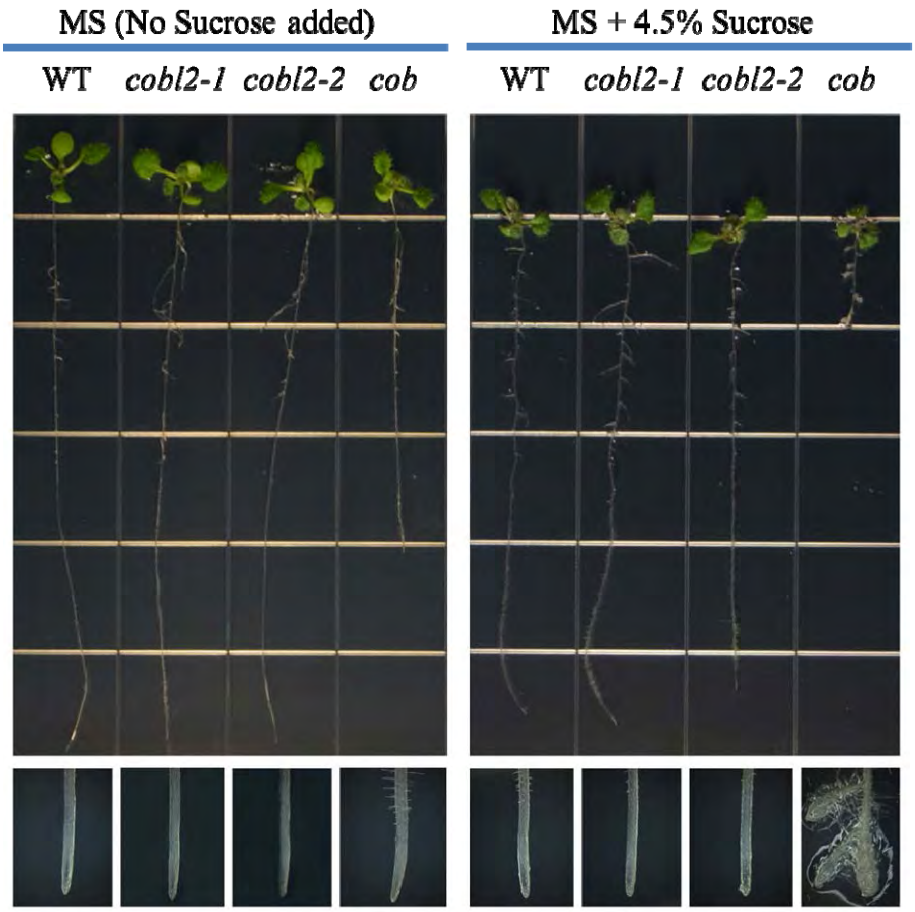

Fig. S5. ***cobl2*** **mutants display no root elongation phenotype.** Phenotypes of *cobl2* mutant seedlings during the course of root elongation. Seedlings were grown on MS medium with 0% sucrose for 4 days and then transferred to medium supplemented with either 0% or 4.5% sucrose for another 5 days.

Supplemental Figure 6

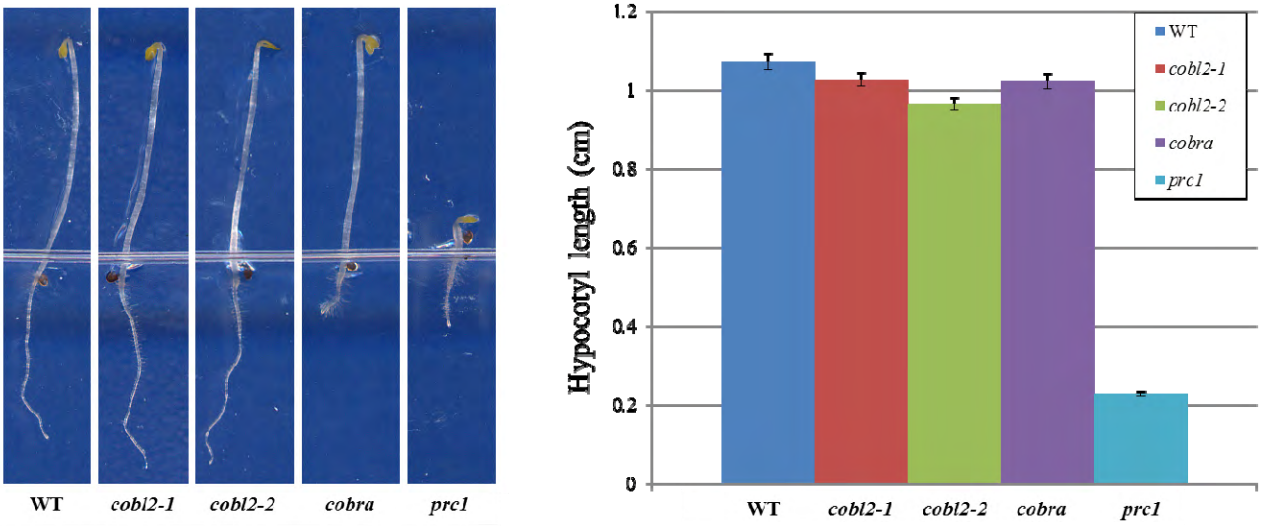

Fig. S6. Etiolated seedlings of *cobl2* mutants are indistinguishable from the wild type. Etiolated seedlings of wild-type, *cobl2-1*, *cobl2-2*, *cob1-1* and *cesa6*$^{prc1-1}$ mutants were examined after for 4 days of growing in the dark. The phenotype of both *cobl2* alleles was indistinguishable from the wild type.

Supplemental Figure 7

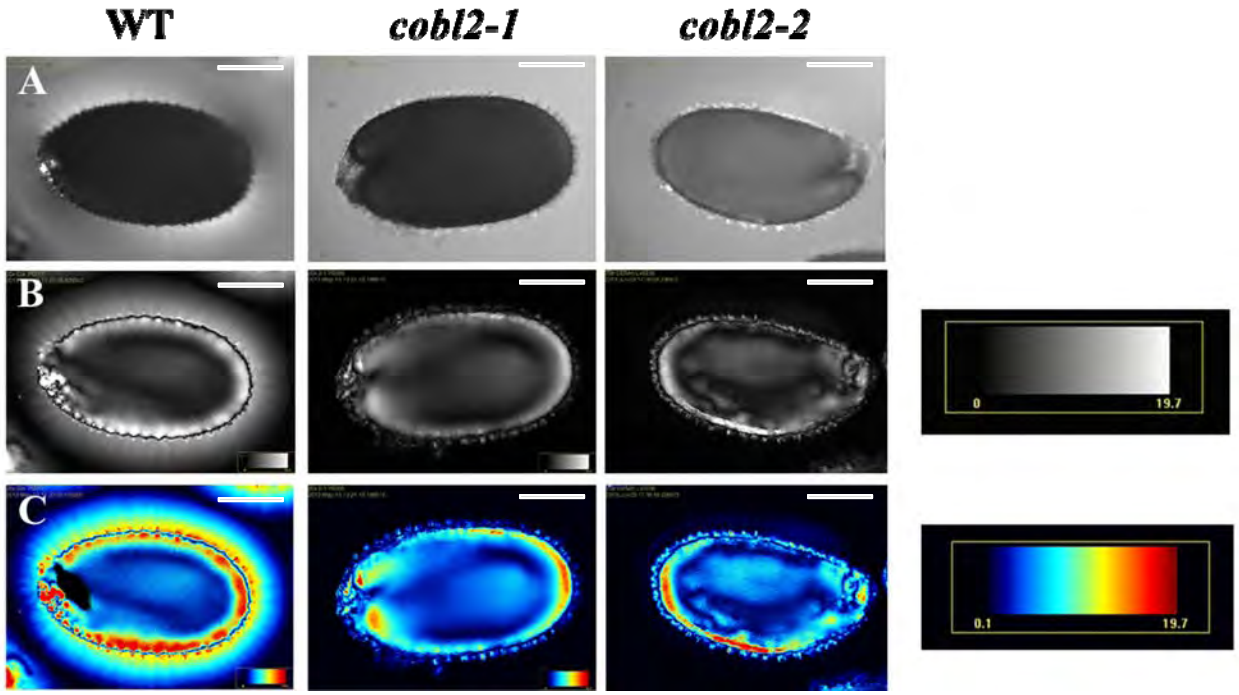

Fig. S7. Both *cobl2* mutant alleles display reduced crystalline cellulose levels in the rays of seed mucilage. Polarized light birefringence as visualized by LC-PolScope demonstrating reduced crystalline cellulose in seed mucilage rays of *cobl2-1* and *cobl2-2* mutants. Polarized light image (A). Retardance of polarized light as visualized by the LC-PolScope: in gray scale (B) and in color scale (C). Scale bars: 0.25 mm.

Supplemental Figure 8

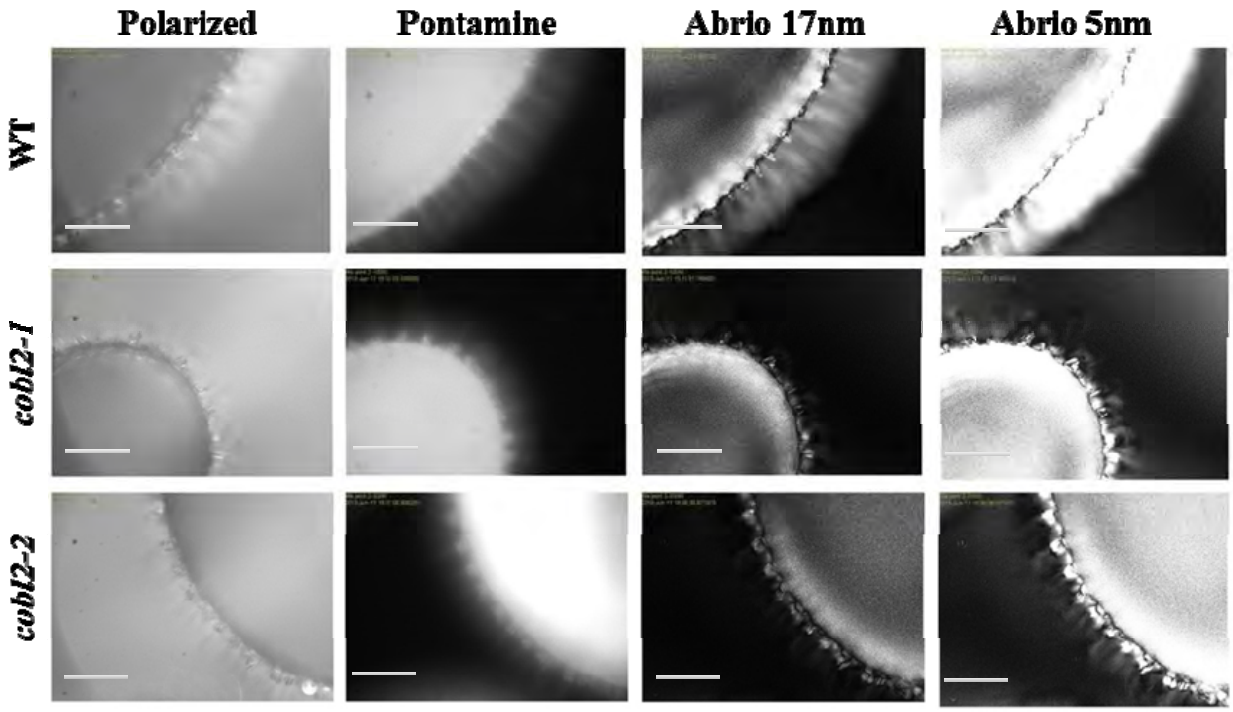

Fig. S8. Comparison of seed mucilage rays visualization by LC-PolScope and pontamine stain. Seeds of the indicated genotypes were pre-stained with pontamine fast scarlet S4B stain for cellulose and then examined by LC-PolScope. Seeds were visualized by: polarized light (Left panel); pontamine (middle-left panel); LC-PolScope low sensitivity (middle-right panel) and High sensitivity (right panel). Note that the residues of seed mucilage rays in the *cobl2* mutants can be visualized using the LC-PolScope only with the higher sensitivity. Scale bars: 0.1 mm

Supplemental Figure 9

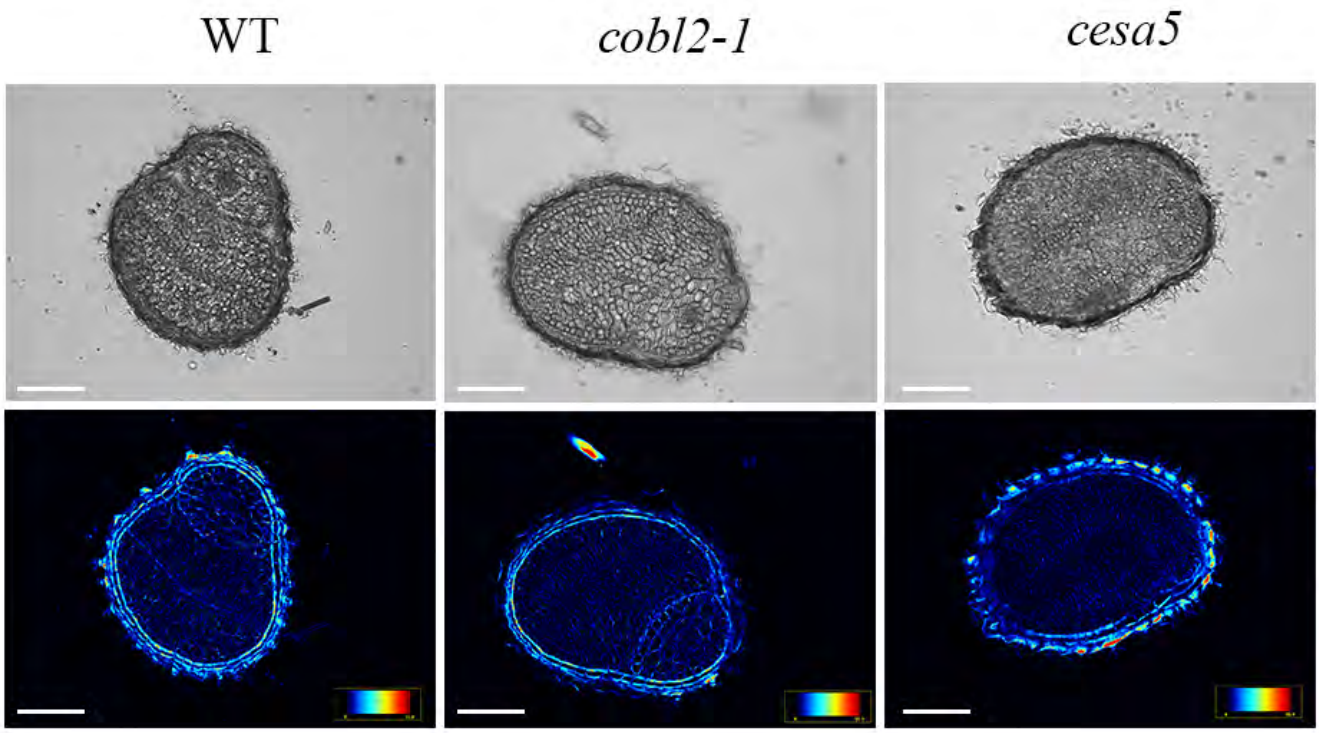

Fig. S9. Crystalline cellulose in whole seed section of *cobl2-1* and *cesa5* as compared to wild-type. Polarized light birefringence as visualized by LC-PolScope demonstrating reduced crystalline cellulose in seed sections of *cobl2-1* as compared to wild-type. Bright light image (upper panel); polarized light indicative of cellulose microfibril retardance (lower panel).