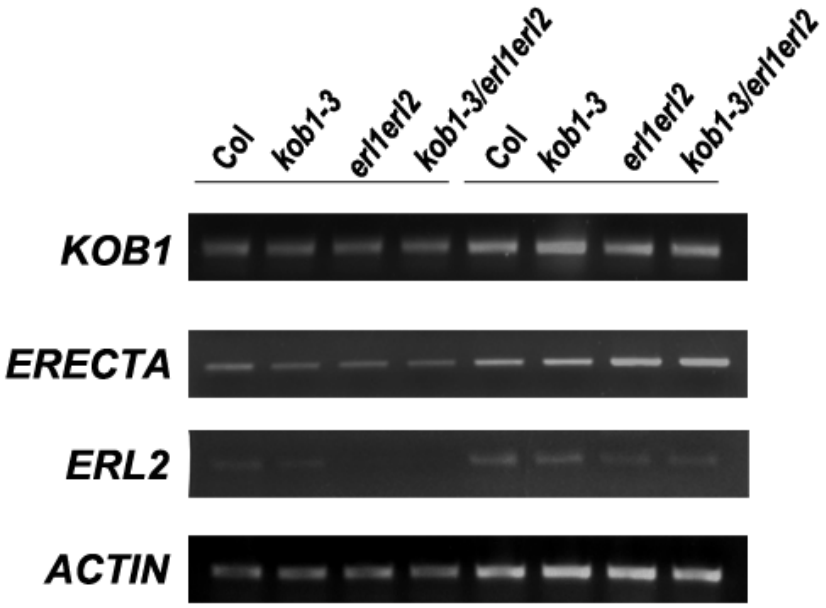

Fig. S1. **Semi-quantitative RT-PCR analysis of *KOBITO1, ERECTA, ERL2* and actin transcripts in 15-day-old seedlings.** Expression of *KOBITO1* is not changed in either *kob1-3* or *erl1 erl2* mutants. The *kob1-3* mutation does not lead to a change in *ERECTA* or *ERL2* expression. At an increased number of cycles *ERL2* transcript can be detected in the *erl1 erl2* mutant. *KOBITO1, ERECTA and ERL2* were amplified for 34 (the first 4 lanes) and 36 cycles (the last 4 lanes); Actin was amplified for 24 (the first 4 lanes) and 26 (the last 4 lanes) cycles.

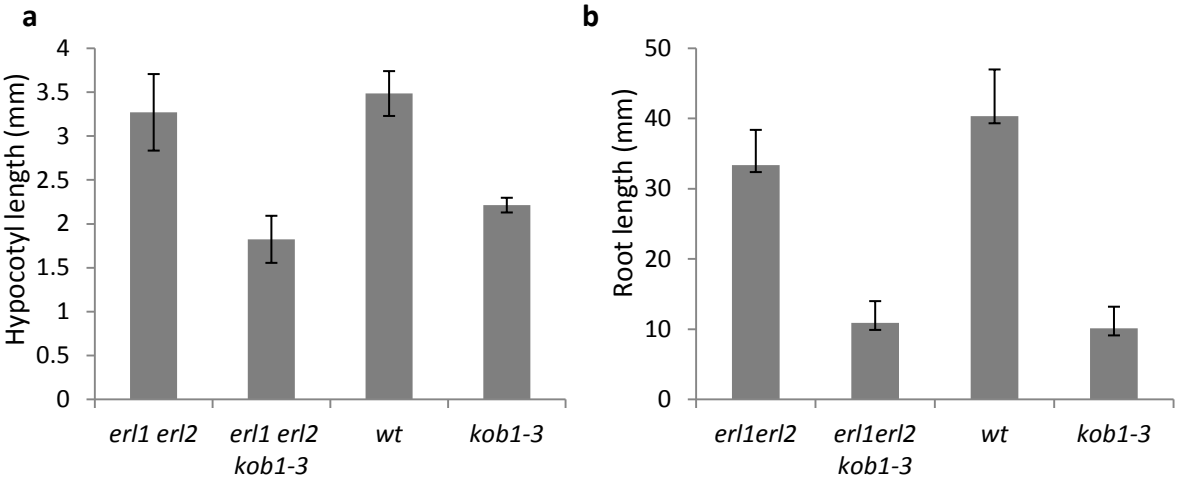

Fig S2. The effect of *kob1-3* on elongation of hypocotyls and roots. The *kob1-3* mutation results in reduced elongation of hypocotyl (a) and root (b). This phenotype is not dependent on the *erl1 erl2* background. Values are mean ± SD for 7 to 10 fifteen-day-old seedlings.

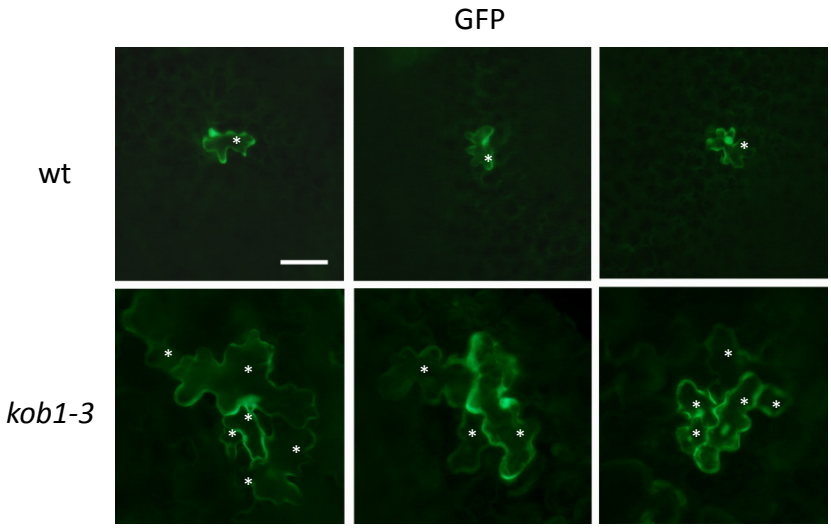

Fig S3. **Increased plasmodesmata conductivity in *kob1-3* does not correlate with decrease in cell size.** Selected images of adaxial epidermis of cotyledons of 10-day-old seedlings expressing bombarded GFP. Cells with a GFP signal labeled with an asterisk.

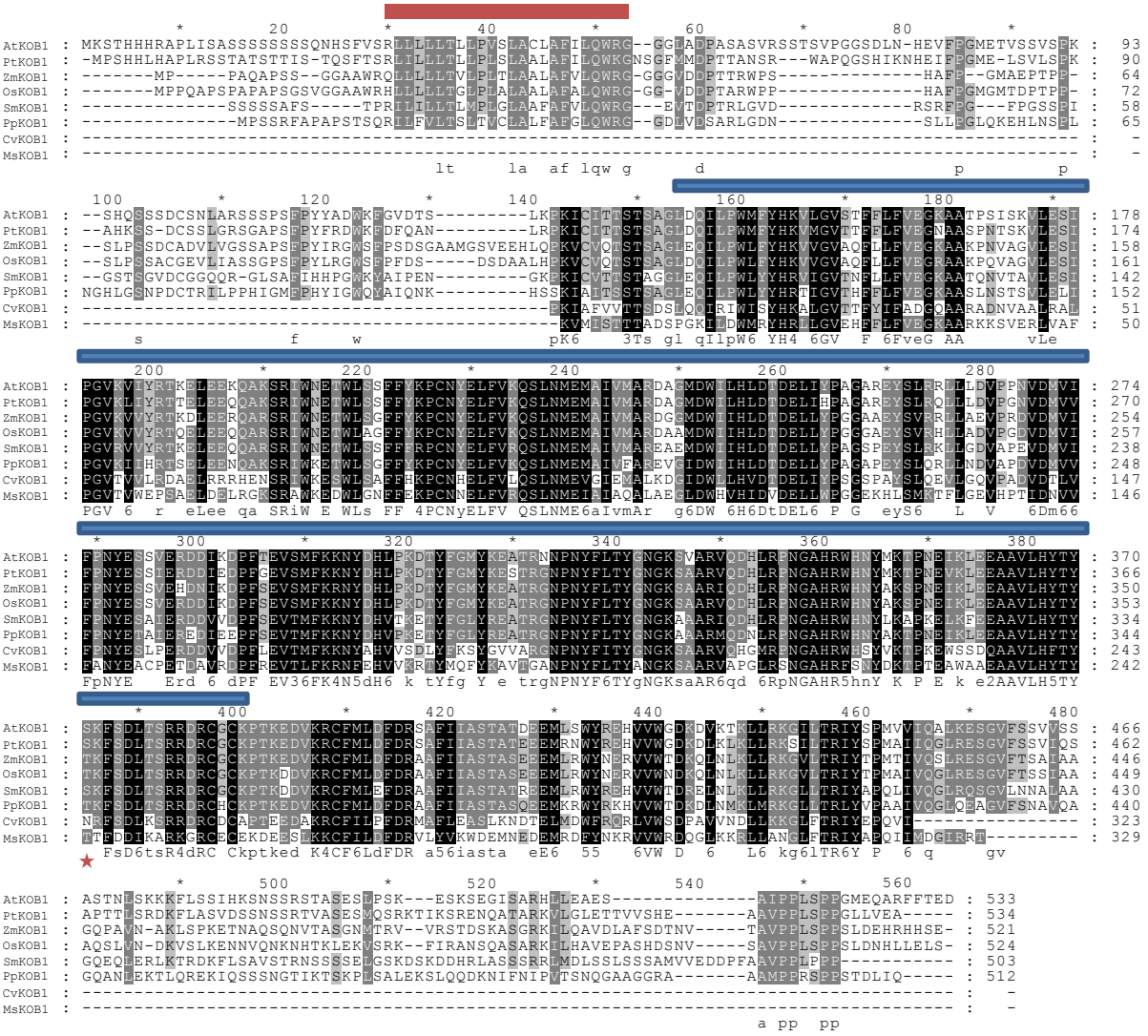

Fig S4. CLUSTAL W alignment of the predicted amino acid sequences for KOBITO1 from *Arabidopsis thaliana*, *Populus trichocarpa*, *Zea mays*, *Oryza sativa*, *Selaginella moellendorffii*, *Physcomitrella patens*, *Chlorella variabilis,* and *Micromonas* strain RCC299.
Residues shaded black are identical or conserved in all eight sequences, those shaded in dark grey are identical in at least six sequences, and those shaded in light gray are identical in five sequences. The serine residue that is mutated in *kob1-3* is labeled with a star below the sequence. A putative glycosyltransferase domain is marked on top with a blue box and a putative transmembrane domain is labeled on top with a red box. The consensus residues are given below the alignment.

Table S1. Primer sequences used in map based cloning of kob1-3

Marker	Primer-1	Primer-2	Fragment Length(Col/Ler)
KDY43	GACGTGGACGGAATCTCCTCG	CGAGTGTAGTGGCCGTTGG	123bp/98bp
KDY42	GTGGCACCATCCTAATTAG	CTTTTTATACGTTTTCCCTTCC	166bp/144bp
KDY19	GCAAGAGAGTCATATGACG	CGTGAATGAACACATGGTGTG	137bp/120bp
KDY48	CCCAAGAAGTATAGACAGTTTCG	ACCTTTGGTCAATACCCACC	267bp/263bp
KDY20	CGTCCCTAGACACACATTATTC	ATAGAGGTGGGCAATGTGAG	167bp/153bp
KDY8	ACTCGGAGCTACTCAATAC	GCAAAAGATGCATCGCTG	125bp/107bp
KDY7	CCGCGTGTCCAACGAGTG	ATCGGGCAACGATATTCG	124bp/114bp
*F17O14b (3-AC012562-1121)	GTGCCCTGAATCATATGTGT	AGACCGGACCGTCTCGTT	99bp/92bp
*F17O14a (3-AC012562-1108)	TTTGGTCCTATTGTGATTAC	ATAGATGCGAGTCAGAATAC	141bp/121bp

* Markers were download from http://amp.genomics.org.cn/. Marker ID is shown in parentheses.

Table S2. Primer sequences used in RT-PCR

ERL2c1602.rc	AGAAAGATTATTGAAGGAGATG
ERL2c1455	CGATGTGTCATTTAATTTTCTTG
ERg1761	GTATATCTAAAAACGCAGTCG
ERg2856.rc	AGCTGCTCAAGTTGCTTCAACTT
kdt550-470	GGTGTTGATACTAGCTTAAAGCC
kdy550g-4240.rc	CAGGTCTCATTCCAAATCCGG
Act2-1	GCCATCCAAGCTGTTCTCTC
Act2-2	GCTCGTAGTCAACAGCAACAA