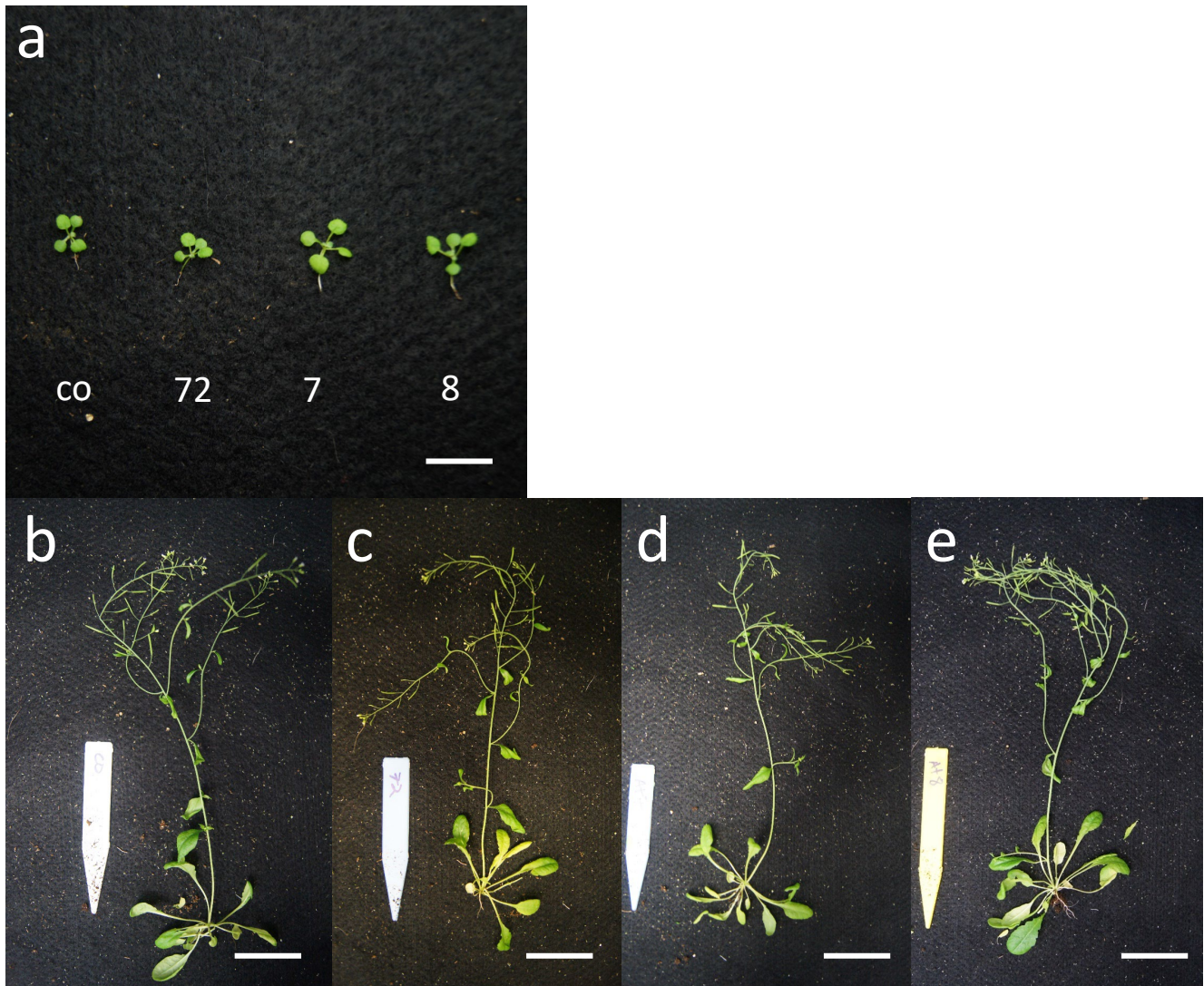
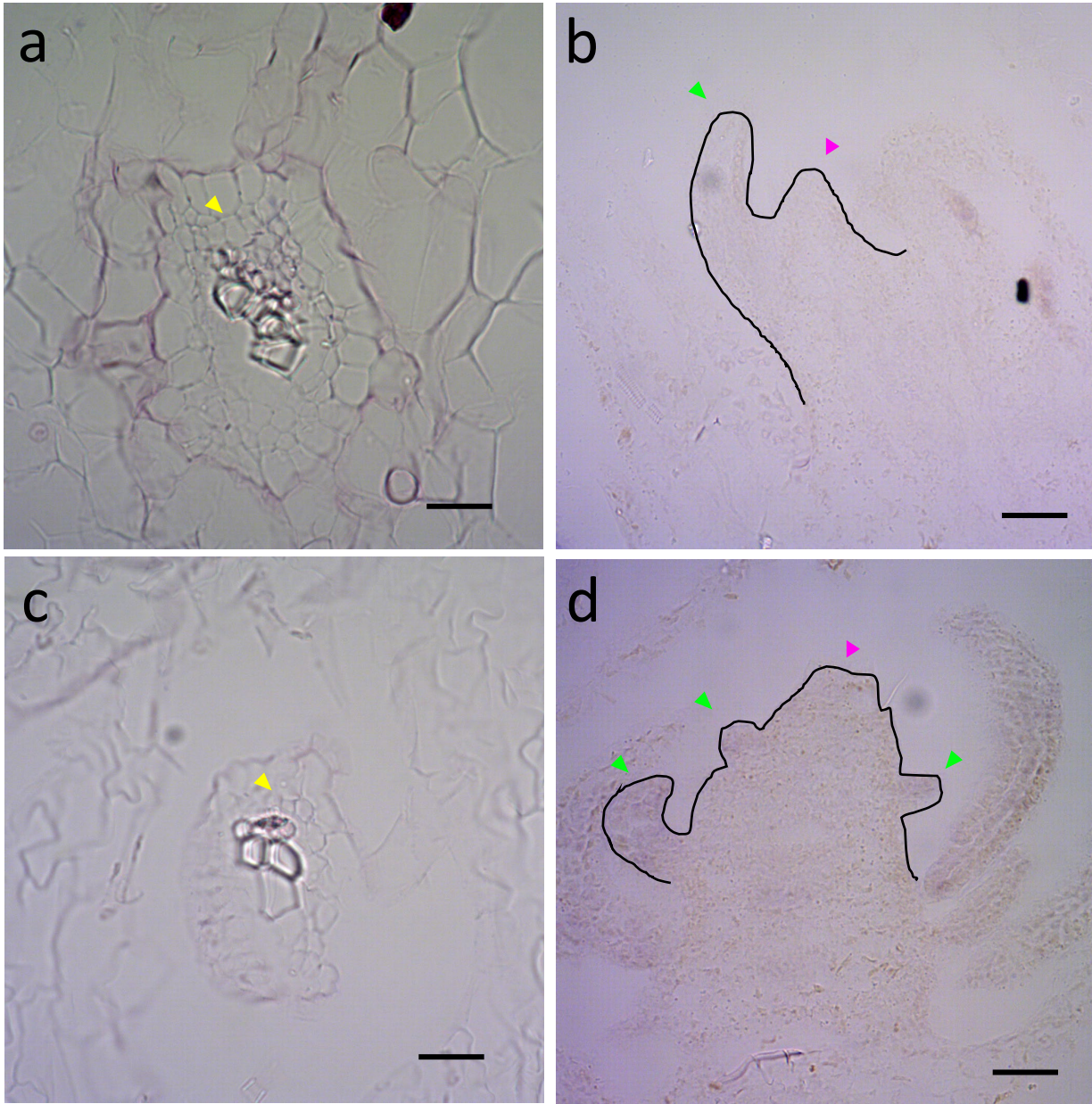


**Figure S8: Genotyping *pAtWOX4:CrWUL* plants in *atwox4* null background.**

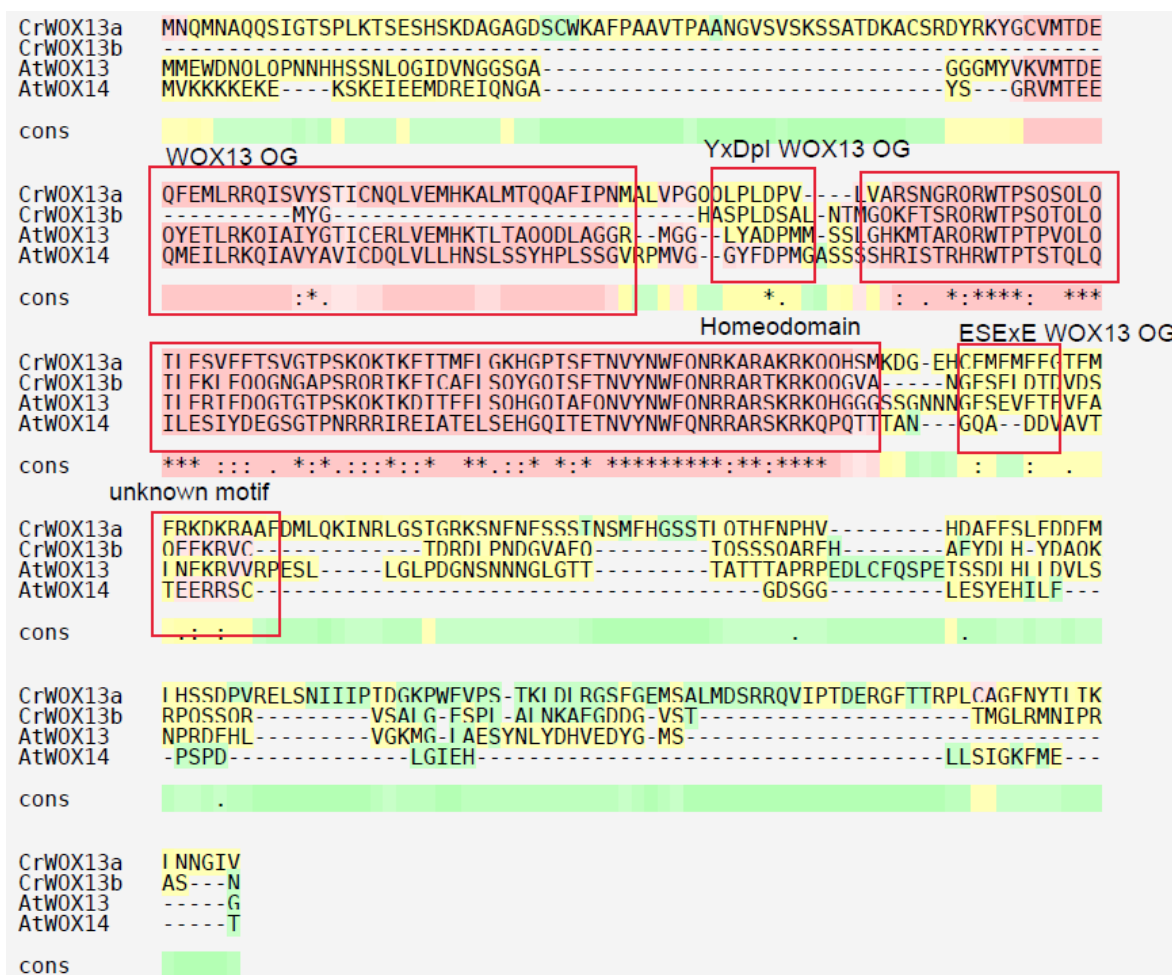
(a) Presence of TDNA insertion in Arabidopsis *atwox4* null-mutant seeds (GK\_462G01, N376572). 1, Primer Set 1; 2, Primer Set 2; 3, Primer Set 3. Primer sequences provided in Table S1. (b) Presence of *CrWUL* and Hygromycin-resistance gene in *atwox4* and *pAtWOX4:CrWUL* 3, 7 and 8 genomes. (c) Expression of *CrWUL* and Hygromycin-resistance genes in *atwox4* and *pAtWOX4:CrWUL* 3, 7 and 8 transcripts. +, positive control in (b, c) is expression vector used in transformation experiments.



**Figure S9: Whole plant morphology of *atwox4* null mutants and *pAtWOX4:CrWUL* lines.** (a) Young sporophytes. (b-d) Mature sporophytes of: Col, Colombia (a,b); 72, *atwox4* null (a,c); 7, 8 are two lines of *pAtWOX4:CrWUL* (d,e). Scale bars = 2cm (a), 4cm (b-e).

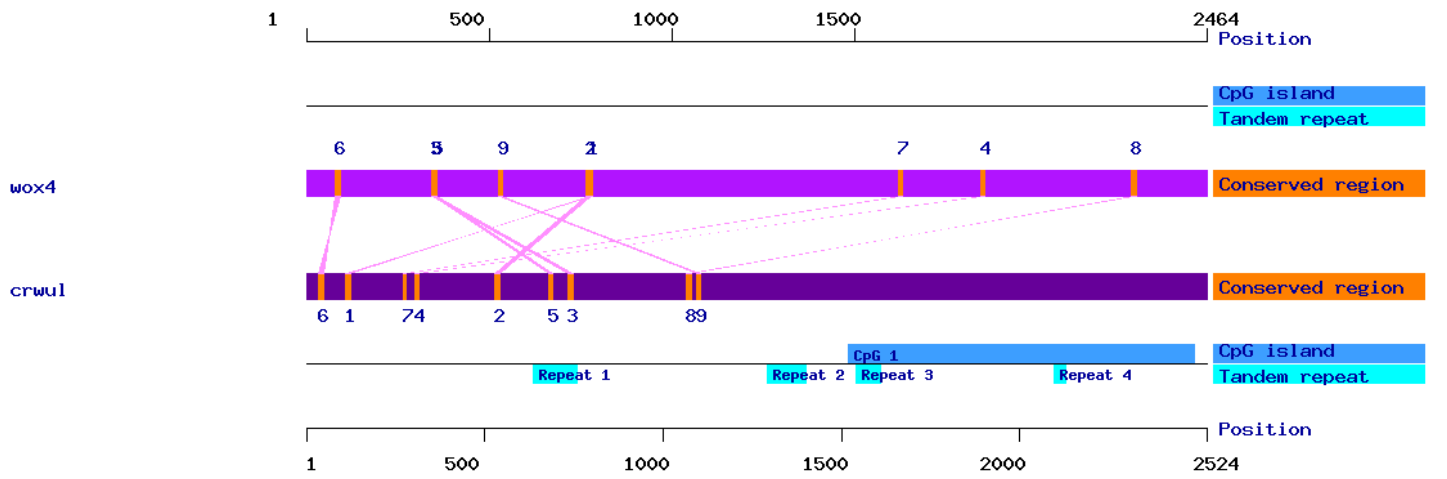


**Figure S10: *In situ* hybridization of sense probes in *S. kraussinia* sporophyte tissues. (a,b) *SkWOX11C*; vascular bundles (a), shoot (b). (c, d) *SkWOX11B*; vascular bundles (c), shoot (d). Green and purple arrows indicate leaf primordia and shoot, respectively. Yellow arrows denote phloem. Scale bars = 20 $\mu$ m (a, c), 100 $\mu$ m (c,d).**

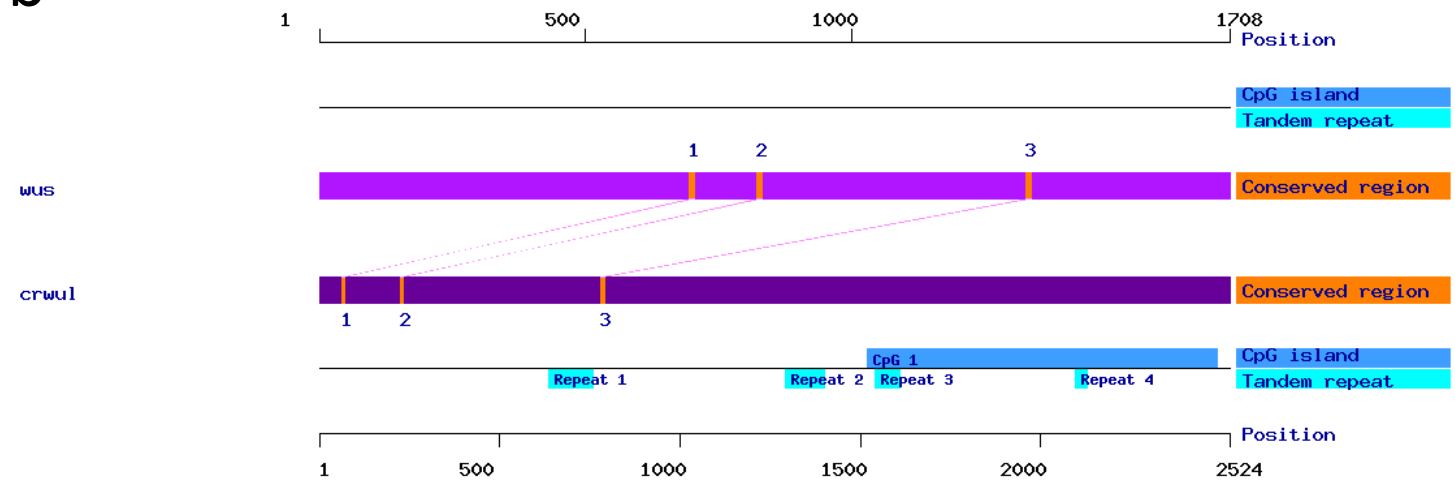


**Figure S11: Alignment of *C. richardii* and *A. thaliana* T1WOX/ancient clade.** Full length T1WOX/ancient clade sequences with known orthologous groups named and outlined.

a



b



**Figure S12: Upstream sequence comparison between *AtWUS*, *CrWUL* and *AtWOX4*.** (a) Comparison of *CrWUL* and *AtWOX4* ~2.5kb of upstream sequence. (b) Comparison of *CrWUL* and *AtWUS* ~2.5kb and 1.7kb respectively. Comparisons were made with PlantPAN3.0.