Supplementary information

Supplementary Figure 1 (supporting Figure 2)**.** Subcellular localization, APC/C degradation assay and expression analysis of *S. pombe* Sor1. **a, b** Sor1 localizes to nucleus throughout the cell cycle. Cycling *S. pombe* cells expressing Sor1-GFP were fixed, stained with DAPI, and analyzed by fluorescence microscopy (**a**). Cycling *S. pombe* cells expressing Sor1-Flag were fixed and stained with antibodies against Flag and tubulin. Nuclei were visualized by DAPI staining (**b**). **c** *in vitro* assay shows no evidence that Sor1 is an APC/C substrate. **d** Mutating conserved Sor1 residues only slightly reduces Sor1 protein levels. Proteins extracted from cycling cells were analyzed by gel electrophoresis and Western blotting using anti-tubulin antibodies. The TAP epitope was detected using PAP antibodies (rabbit antiperoxidase antibody linked to peroxidase).

Supplementary Figure 2 (supporting Figures 3 and 4)**.** Meiotic and somatic *Atsororin* mutant phenotypes can be complemented with the wild type *AtSORORIN* gene. **a** Overall plant architecture and fertility are wild type-like in the complemented transgenic plant line, but not in the *Atsororin* mutant. **b** Seed counts demonstrate nearly wild type-like fertility of the complemented transgenic plant line, but sterility in the *Atsororin* mutant. Unpaired Mann-Whitney test has been applied (****$p<0.0001$). Somatic defects in *Atsororin* mutants are tissue-specific and WAPL-dependent. DNA was stained with DAPI (magenta) and fluorescence *in situ* hybridization (FISH) was performed to detect centromeric regions (green). **c** Spreads of cell nuclei from rosette leaf cells. Interphase stages were analyzed for wild type plants and *Atsororin*, *wapl1-1 wapl2* and *Atsororin wapl1-1 wapl2* mutants. The number of centromeric signals is indicated in the top left corner. Scale bar = 10µm. **d** Quantification of centromeric-FISH signals in interphase leaf nuclei. *Atsororin* mutants (n = 52) have a significantly higher number of cells that have more than 10 signals, when compared to wild type (n = 84), *wapl1-1 wapl2* (n = 68) and *Atsororin wapl1-1 wapl2* (n = 82). Chi-square test was performed (****$p<0.0001$).

Supplementary Figure 3 (supporting Figure 7)**.** Immunolocalization of the axis protein ASY1 and the meiosis-specific cohesin subunit REC8 in male meiocytes during late zygotene in wild type plants and *Atsororin*, *wapl1-1 wapl2* and *Atsororin wapl1-1 wapl2* mutants. Absence of AtSORORIN does not influence their time of deposition or their relative localisation on meiotic chromosomes. Scale bar = 10 µm.

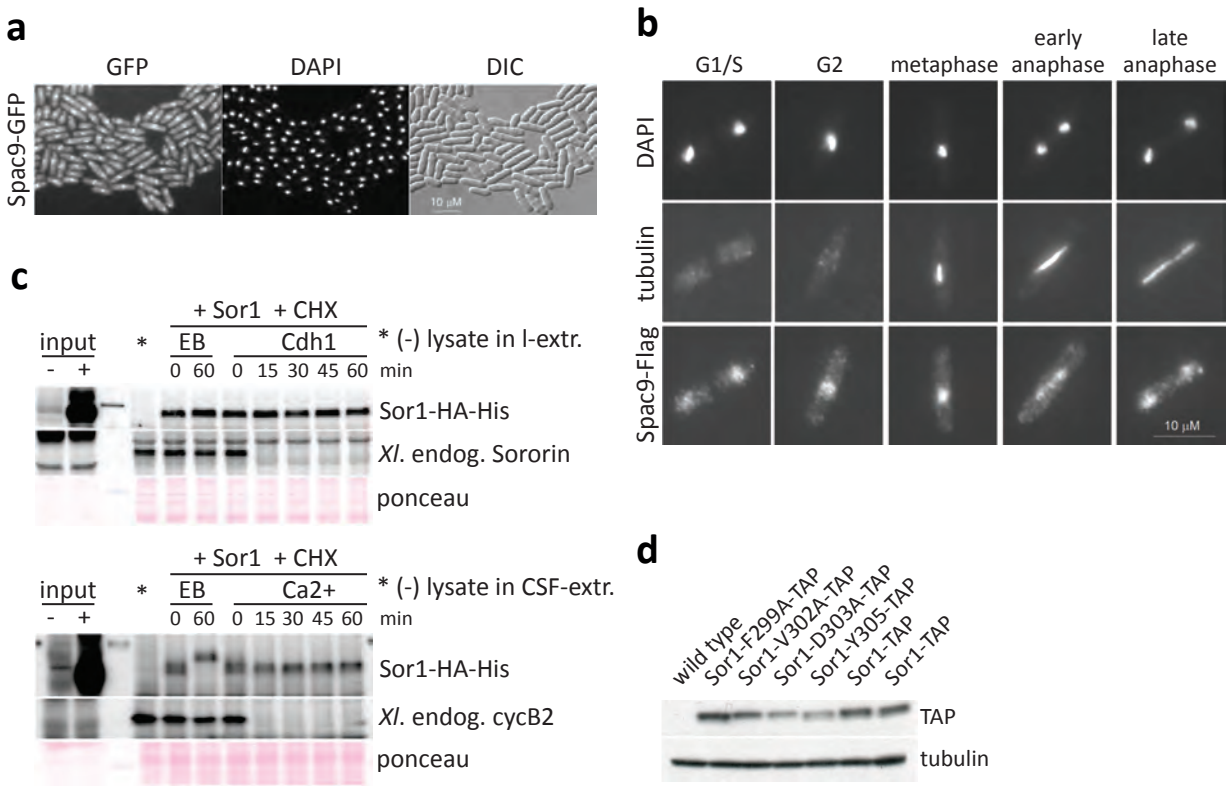
Supplementary Movie 1. Root tips from wild type plants display normal tissue organization and nucleus size.

Supplementary Movie 2. Root cellular organization and nucleus size are highly affected in *Atsororin* mutant plants.

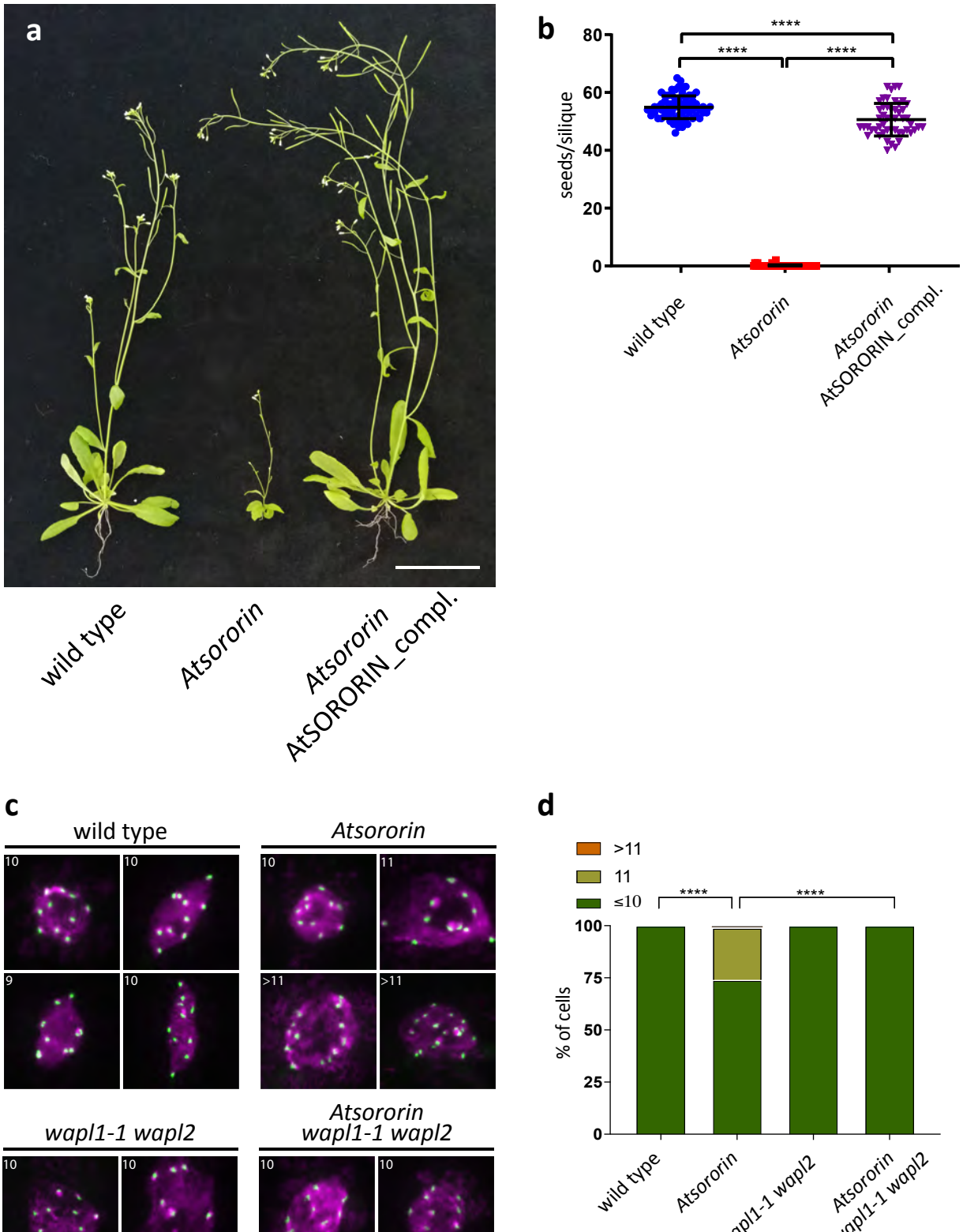
Supplementary Movie 3. Plants with mutations in both genes encoding WAPL (*wapl1-1 wapl2*) develop normal roots compared to wild type plants.

Supplementary Movie 4. *Atsororin wapl1-1 wapl2 triple* mutant plants develop normal roots, indicating that the *wapl1-1 wapl2* mutations suppress the effect of the *Atsororin* mutation with respect to root development.

Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3