



**Figure 6 – figure supplement 1\_Related to Figure 6. SMC singleness is progressively resolved during primordium growth.**

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(A) Canalization of SMC fate in different *katanin* (*kat*) alleles (*lue1*, *bot1-7*) and respective wild-type (WT) backgrounds (*Col*, *Ws-4*). Percentages of class A and B primordia based on cleared tissue preparations as shown [Figure 6A](#). The proportion of primordia with several SMC candidates at stage 0-II gradually decreases with developmental progression while the proportion of ovules with a single SMC increases, suggesting canalization. A significant delay in canalization (dashed red line) in *kat* mutants was confirmed by a two-tailed Fischer's exact test (see also [Figure 2 - Source Data 1](#)). Related to [Figure 6B-C](#).

(B-C) Ectopic expression of SMC fate in *kat* primordia (*mad5* allele) compared to WT (*Col*). Percentage of ovule primordia showing H1.1-GFP eviction (B) and KNU-nlsYFP expression (C) in more than one SMC candidate at all developmental stages. Two-tailed Fischer's exact test was used to assess differences between genotypes. Related to [Figure 6B-C](#) and [Figure 6D-E](#).

(D-E) Nuclear area as a marker of SMC candidates. Illustration of the cells selected for nuclear area measurements in representative class A and B ovules (D). Nuclei areas were measured in two L1 cells types (L1a, apical position and L1b, closer to the placenta), in cSMC: candidate SMC; L2b: a neighbouring L2 cell. Dashed circles mark the nuclei of these cells used in the measurements. Related to [Figure 6D](#). Quantification of nuclear area as shown in (D) for class A and B in WT (*Col*) and *kat* (*mad5* allele) ovule primordia at stage 0-III (E). Box plot representations include jittered points to visualize data variability. Red lines represent the median of cSMC nuclear area for comparison with the other cells. Wilcoxon signed rank test was used to assess difference between SMC and the other cell types. Related to [Figure 6D](#).

(F-H) Frequency of SMCs showing an S-phase pattern in *kat* and Class B primordia. F: Representative images; green, PCNA-GFP, magenta: Renaissance SR2200 cell wall label. Scale bar 10µm. Related to [Figure 6F](#), [6H](#). G: Quantification of S-phase occurrence in SMCs (salmon bars) and neighbors cells (dashed bars) of class A and class B *katanin* (*mad5*) ovule primordia in Phase I (stages 0-II and 0-III). H: Quantification of S-phase occurrence within the L2 apical domain of class B WT (*Col*) and *kat* (*mad5* allele) ovule primordia in Phase II (stages 1-I to 2-II). The plotted frequencies refer to the number of primordia showing a speckled PCNA-GFP pattern in SMC candidates. Two-tailed Fischer's exact test was used to assess differences between genotypes. Related to [Figure 6H](#).

All graphs: n= number of ovules scored. Error bar: standard error of the mean. P values: \*p≤0.05, \*\*p≤0.01, \*\*\*p≤0.001. See also [Figure 6 - Source Data 1](#).