Gomes et al., http://www.jcb.org/cgi/content/full/jcb.201304174/DC1

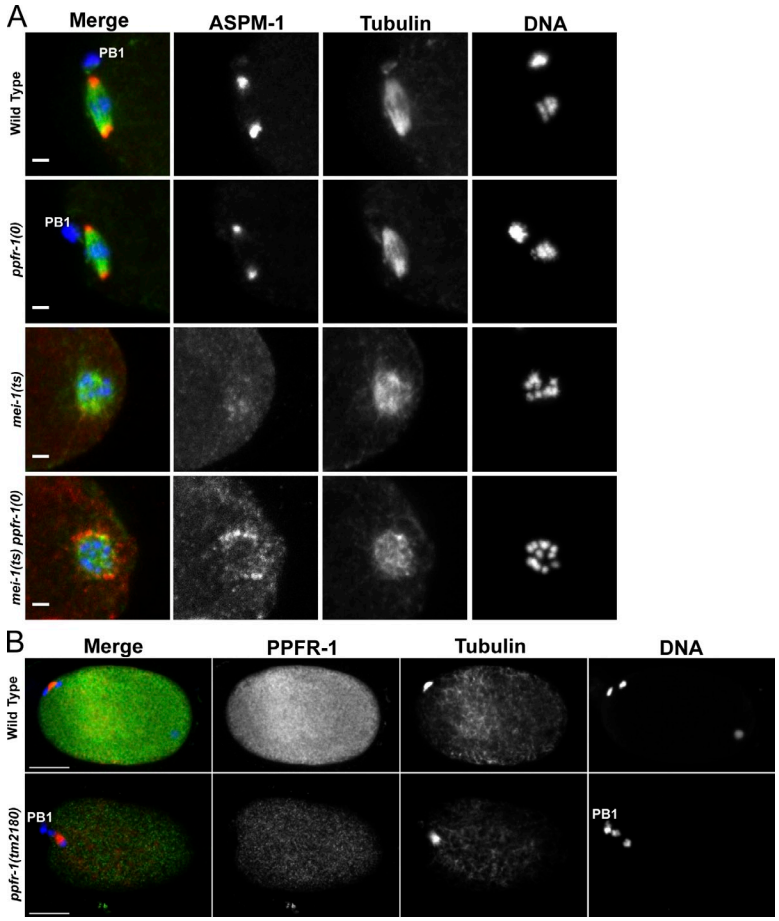

Figure S1. **ASPM-1 and PPFR-1 protein localization in meiotic embryos.** (A) Confocal micrographs of meiotic wild-type, *ppfr-1(0)*, *mei-1(ts)*, and *mei-1(ts) ppfr-1(0)* embryos at 20°C, stained for ASPM-1 (red), α-tubulin (green), and DNA (blue). In both wild type and *ppfr-1(0)* bipolar spindles form in metaphase with ASPM-1 localizing to the poles, whereas in *mei-1(ts)* neither spindle apparatus are bipolar nor ASPM-1 is detected. In *mei-1(ts) ppfr-1(0)* embryos, however, multiple discrete foci were present, although spindle morphology is indistinguishable from *mei-1(ts)*. Bars, 2 µm. (B) Confocal micrographs of meiotic wild-type and *ppfr-1(0)* embryos stained for PPFR-1 (green), α-tubulin (red), and DNA (blue). PPFR-1 localizes uniformly throughout the cytoplasm in wild-type embryos; lack of staining in *ppfr-1(0)* confirms antibody specificity. Bars, 10 µm.

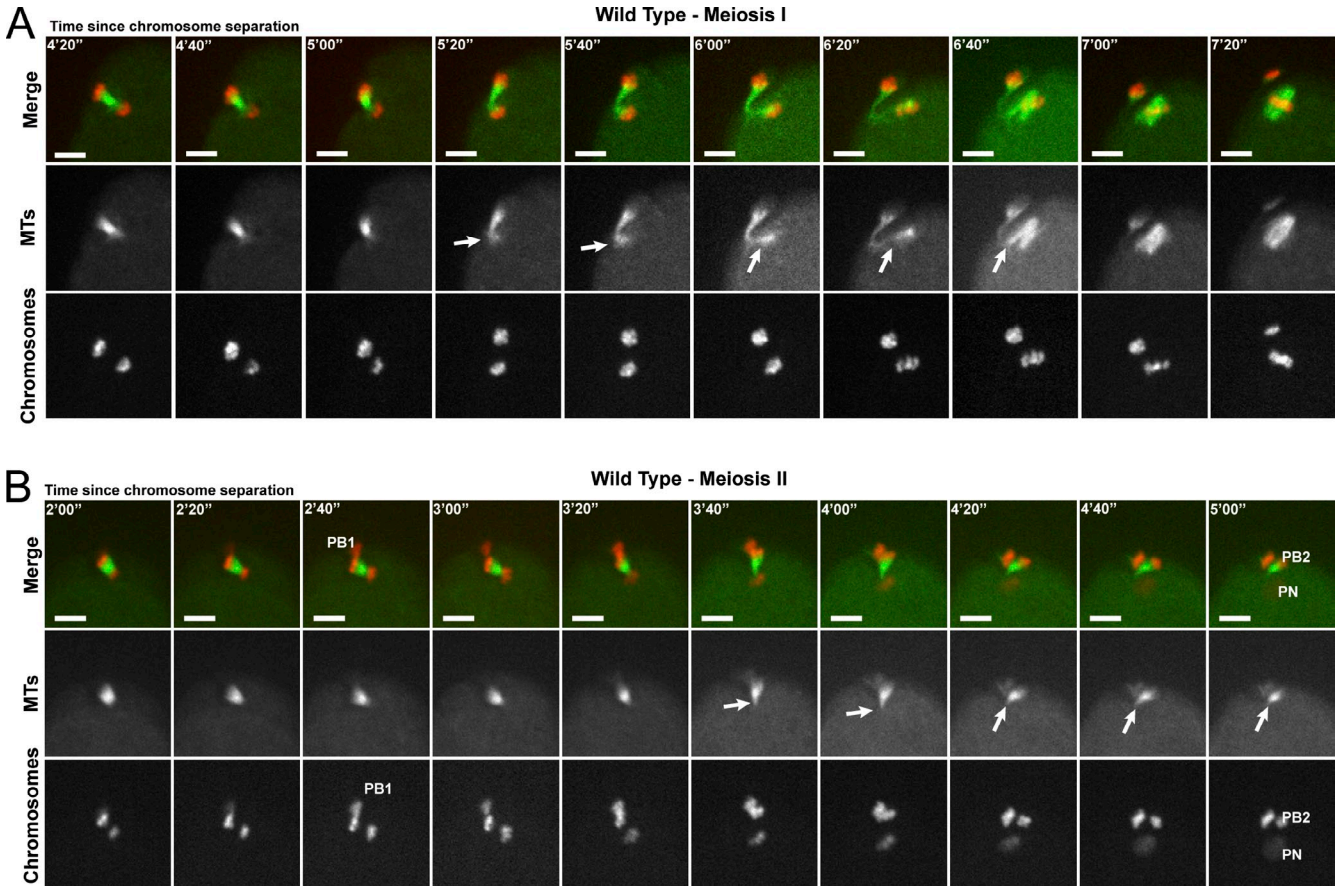

Figure S2. **Wild-type MI versus MII divisions.** Images taken from time-lapse sequences of embryos carrying α-Tubulin::GFP (green) and Histone2B::mCherry (red) transgenes progressing through the first and the second meiotic division. (A) During MI, the meiotic spindle is not fully disassembled and some MTs remain (arrows), serving as a seed for the nucleation of new MTs that are incorporated into the meiotic spindle during MII. (B) In contrast, during MII, the spindle is fully disassembled to remove the MT connections between the PB and the female PN (arrows). Bars, 5 μm.

Table S1 is a list of partners identified by the Y2H screens performed using MEL-26 as bait.