Supporting Information

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Schindler et al. 10.1073/pnas.1120517109



Fig. S1. (*A* and *B*) Fifty germinal visicle (GV)-intact oocytes from mice of the indicated genotypes were isolated, pooled, and used for mRNA purification and generation of cDNA. Gene-specific Taqman probes were used to detect *Aurkc* (*A*) and *Aurkb* (*B*) messages. The abundance in the wild-type sample was set to 1. These experiments were repeated twice. (C) Oocytes from the indicated genotypes (crossed into the CF1 genetic background) were collected, matured to meiosis I (MI), and processed with an anti-AURKC antibody. (Scale bar, 5 μ m.) AURKC, Aurora kinase isoform; HET, heterozygous; KO, knockout.



days between litters

Fig. S2. Aurkc^{-/-} mice are subfertile. The average number of days between the birth of new litters for each female in the 8-mo mating trial. The data are expressed as the mean \pm SEM. Student's t tests were used to analyze the data.

Ruffling



Fig. S3. Examples of membrane ruffling and blebbing. Representative images of one-cell embryos undergoing abnormal cytokinesis while being imaged live by differential interference contrast every 5–7 min. The time stamp is h:min after hCG injection. (Scale bar, 5 μm.)



Fig. S4. Destruction controls. (*A*) AURKB-GFP and AURKB-mCherry have the same destruction kinetics during meiotic maturation. (*B*) Nondegradable cyclinB-GFP signal does not diminish during a live imaging time course. GV-intact oocytes were injected with the indicated cRNAs and 1 h before the first time point cycloheximide was added. Fluorescent images were obtained at the indicated times. These time courses were conducted twice with at least 15 oocytes and the data are expressed as the mean \pm SEM.



AURKC

Fig. S5. AURKC levels in mouse oocytes and embryos. GV oocytes or one-cell embryos were collected and cultured in vitro and analyzed at the indicated stages by immunocytochemistry. Representative images are shown. (Scale bars, 5 μm.) MI, meiosis I; MII, meiosis II; 1C, one-cell embryo; 2C, two-cell embryo; 8C, eight-cell embryo; BL, blastocyst.



Fig. S6. Destruction of AURKB and AURKC is proteosome dependent. GV-intact oocytes were coinjected with the indicated cRNAs and imaged at the indicated time intervals. Cycloheximide was added to the cells to stop translation 1 h before the first time point and MG132 was added to one-half of the cells to inhibit the proteosome. These time courses were conducted twice, with at least 15 oocytes and the data are expressed as the mean \pm SEM.



Fig. S7. (*A*) The stability of the KEN and A-box mutant AURKB-GFP is not different from the stability of wild-type AURKB-mCherry during meiotic maturation. (*B*) The stability of AURKB-GFP lacking the N terminus is not different from the stability of wild-type AURKB-mCherry during meiotic maturation. (*C*) The stability of chimeric AURKC-GFP containing the N terminus of AURKB does not differ from the stability of wild-type AURKC-mCherry. GV-intact oocytes were coinjected with the indicated cRNAs and imaged at the indicated time intervals. Cycloheximide was added to the cells 1 h before the first time point. These time courses were conducted twice with at least 15 and the data are expressed as the mean \pm SEM.



Fig. S8. Female mice of the indicated genotype were hormonally primed and mated to wild-type males. Ninety-six hours after mating, embryos were flushed from uteri and counted. (A) The data are presented as the total number of blastocysts per mouse. The horizontal bar represents the mean. (B) The same data are presented as the total numbers of morulas and blastocysts per mouse. BL, blastocyst; Mor, morula.