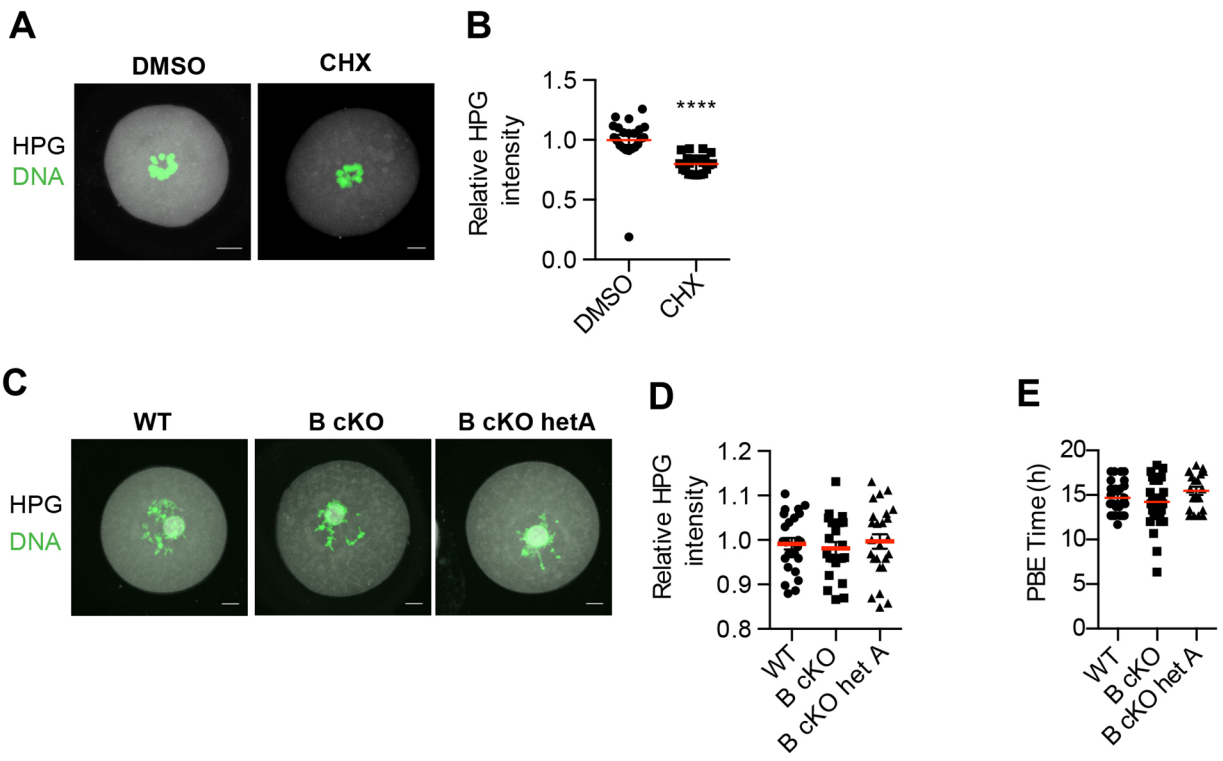

Fig. S1. Experimental controls. A) Prophase I oocytes from WT mice were collected and *in vitro* matured with DMSO or cycloheximide (CHX, 20μM) for 7 h. B) Relative pixel intensity of HPG from A. (Number of oocytes, DMSO: 22 and CHX is 22, Unpaired student's t-test, two tailed, ****p <0.001). C) Prophase I oocytes from WT, B cKO and B cKO/hetA were collected and stained with anti-HPG (Gray) and with DAPI (DNA, green). D) Relative pixel intensity of HPG from C. (Number of oocytes, WT: 25; B cKO: 22, B cKO het A: 25, One-Way ANOVA). E) Time required for completion of meiotic maturation via polar body extrusion (PBE) in WT, B cKO and B cKO hetA oocytes (Number of oocytes, WT: 25; B cKO: 32 and B cKO hetA: 20 One-way ANOVA, non-significant p=0.1628). These experiments were repeated 3 times with total of 3-4 mice/ genotype.

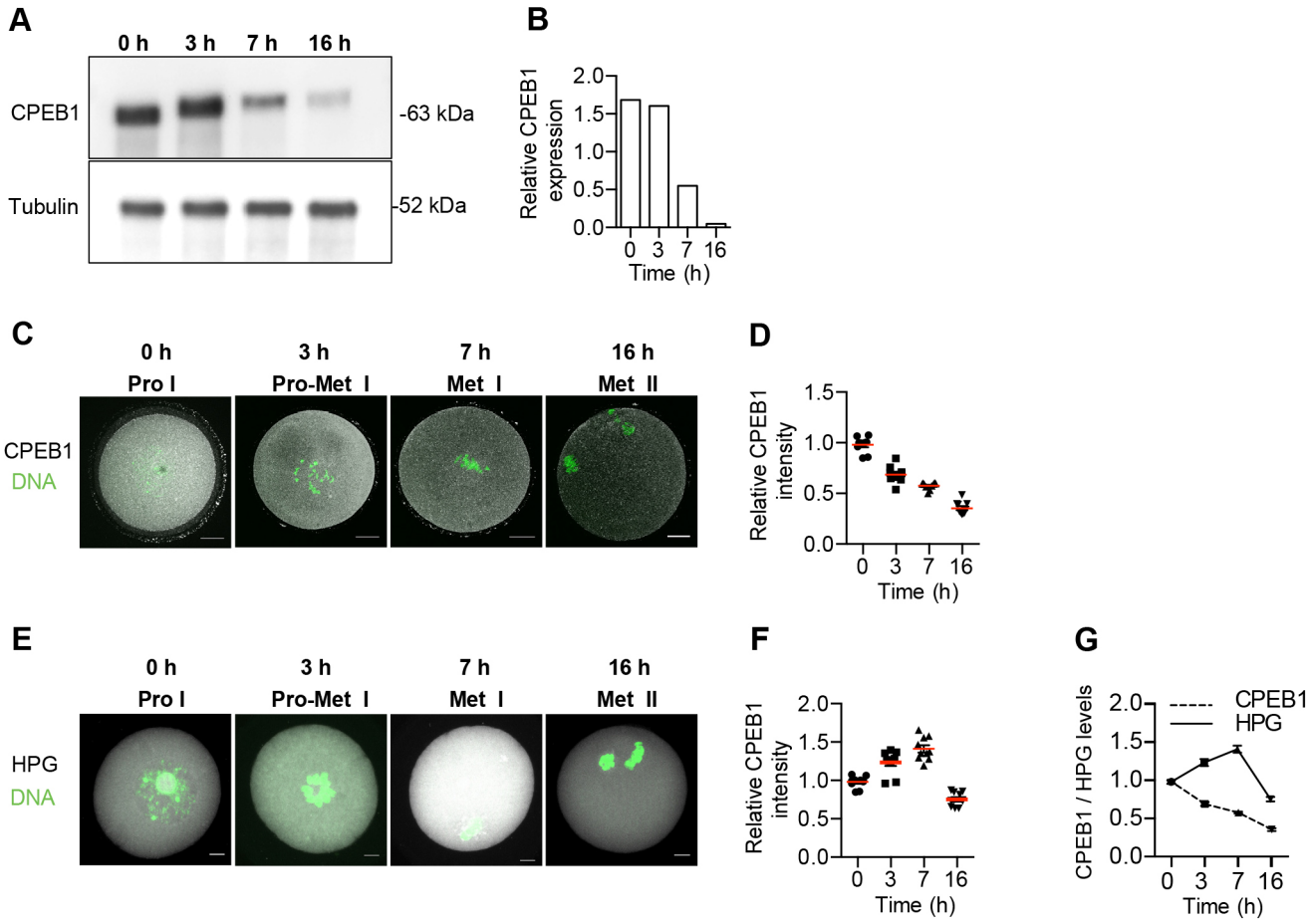

Fig. S2: CPEB1 stability and phosphorylation dynamics and translation levels during mouse oocyte meiotic maturation. A-G) Prophase I oocytes from WT mice were collected and *in vitro* matured. Oocytes were collected at the indicated time points to obtain oocytes at major cell cycle phases where translation dynamics differ: prophase I (0h), pro-Metaphase I (3h), Metaphase I (7h) and Metaphase II (16h). A) Prophase I oocytes from WT mice were collected and matured for the indicated time points prior to lysis and resolution by SDS-PAGE and membranes were probed with anti-CPEB1 (30 oocytes/lane). α-Tubulin served as a loading control. B) Relative CPEB1 expression from A. Values normalized to 0h. This experiment was conducted 3 times with a total of 3-5 WT mice. C) Oocytes matured *in vitro* for the indicated amount of time were stained with anti-CPEB1 (gray) and DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. D) Relative pixel intensity of CPEB1 from C. Values normalized to 0h. E) Oocytes matured in vitro for the indicated amount of time were labeled with HPG to detect translation and stained with anti-HPG (gray) and DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. F) Relative pixel intensity of HPG from E. G) Overlay of CPEB1 and HPG levels, values from E and F. Scale bar is 10μm.

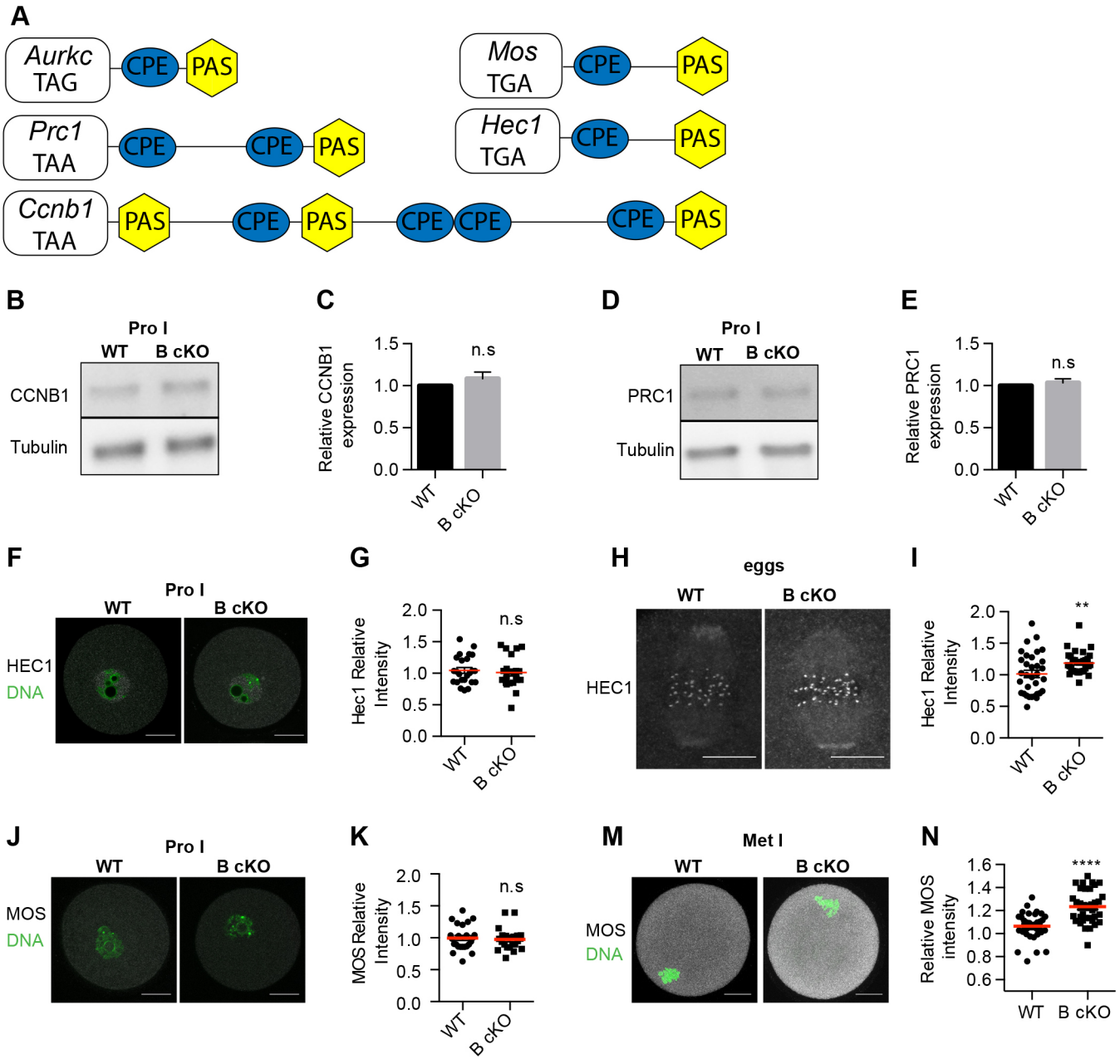

Fig. S3. CPE-containing candidate genes in WT and B cKO oocytes

A) Schematic representation of the 3′ UTR present in the mouse *Aurkc*, *Ccnb1*, *Hec1*, *Mos* and *Prc1*. Polyadenylation sequences (PAS) are in yellow. Consensus CPEs are in blue. (B) Prophase I oocytes from WT and B cKO were lysed and resolved by SDS-PAGE prior to western blotting to detect CCNB1 (25 oocytes/lane). C) Relative CCNB1 expression from B (Unpaired student's t-test, two tailed, n.s: not-significant). (D) Prophase I oocytes from WT and B cKO were lysed and resolved by SDS-PAGE prior to western blotting to detect PRC1 (25 oocytes/lane). E) Relative PRC1 expression from D. Values normalized to α-tubulin (Unpaired student's t-test, two tailed, n.s: not-significant). F) Prophase I oocytes from WT and B cKO were stained with anti-HEC1 (gray) and DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. G) Relative pixel intensity of HEC1 from F (Number of oocytes; WT-24 and B cKO-22, (Unpaired student's t-test, two tailed,n.s: not-significant). H) Met II eggs from WT and B cKO were stained with anti-HEC1 (gray). Shown are representative confocal z-projections. I) Relative pixel intensity of HEC1 from F (Number of oocytes; WT-33 and B cKO-34, Unpaired student's t-test, two tailed **p <0.01). J) Prophase I oocytes from WT and B cKO were stained with anti-MOS (gray) and DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. K) Relative pixel intensity of MOS from J (Number of oocytes; WT-24 and B cKO-22, Unpaired student's t-test, two tailed, n.s: not-significant). M) Confocal images of Met I oocytes from WT and B cKO stained with anti-MOS (gray) and DAPI (green). N) Relative intensity of MOS from M. Values normalized to WT (Number of oocytes: WT-32; B cKO-35).

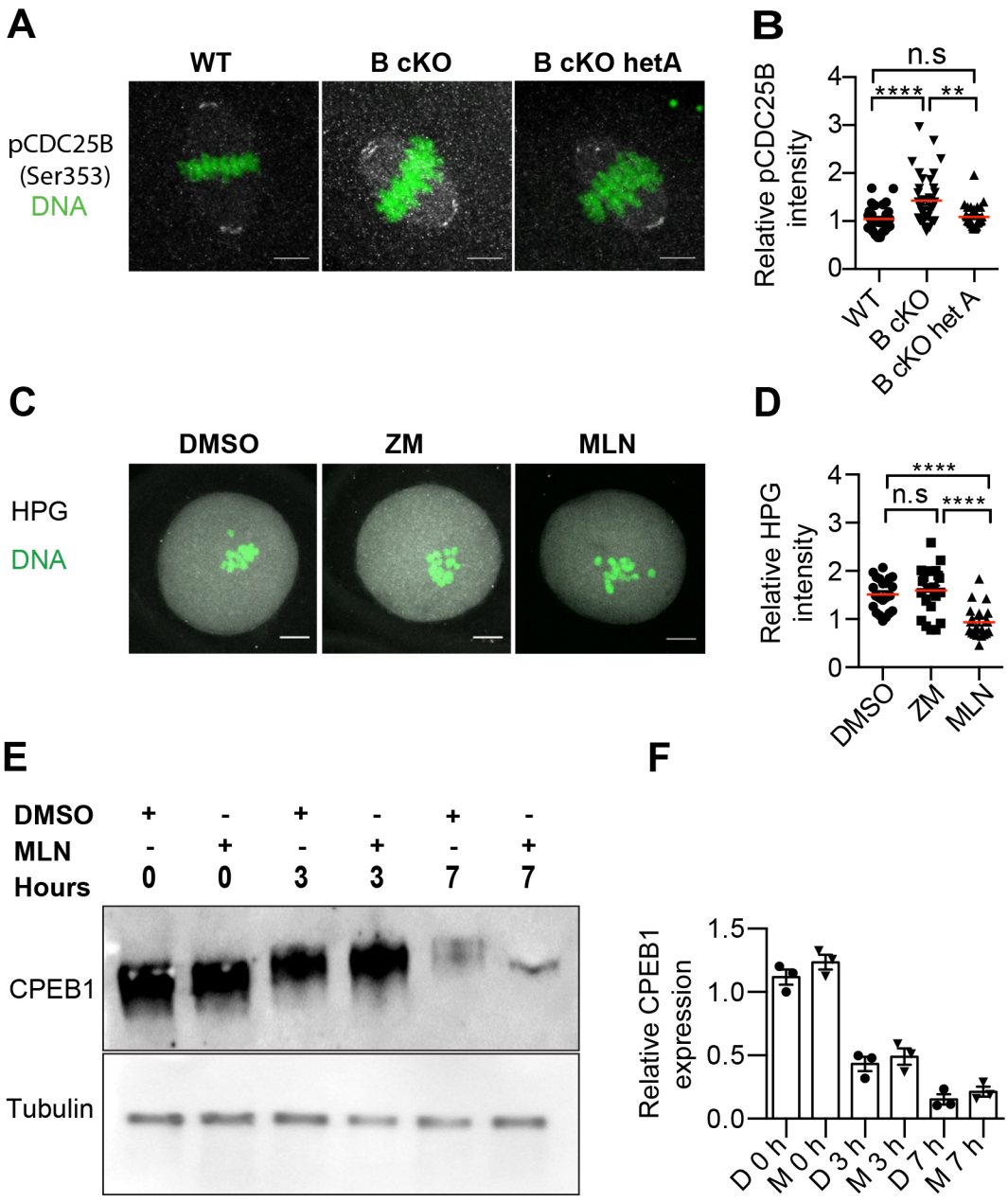

Fig. S4. AURKB/C inhibition does not affect translation. A) IVM Met II eggs from WT, B cKO and B cKO hetA were stained with anti-pCDC25B (Ser353) (gray) and DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. B) Relative pixel intensity of pCDC25B from A (Number of oocytes; WT-32, B cKO-36 and B cKO hetA -29, One-way ANOVA, n.s: not-significant, **p<0.01, ****p<0.0001). This experiment was repeated 3 times with total of 3 mice/genotype). C) Prophase I oocytes from WT mice were collected and matured to metaphase of meiosis I. Oocytes were matured in presence of DMSO, 5μM ZM447439 (ZM) or 1μM MLN8237 (MLN) and stained to detect HPG (gray) to assess translation DAPI (DNA, green) to confirm meiotic stage. Shown are representative confocal z-projections. D) Relative pixel intensity of HPG from C Number of oocytes: DMSO- 24; ZM-22; MLN- 21. One-way ANOVA, n.s. = not-significant, **** p<0.0001. E) WT oocytes were in vitro matured with or without MLN and 25 oocytes were collected per group after 0, 3 and 7 hours of maturation. Oocytes were lysed and resolved by SDS-PAGE, then membranes were probed with anti-CPEB1. F) Relative CPEB1 expression from E. Values normalized to a-tubulin. These experiments (C-E) were repeated 3 times with 2-3 mice per experimental replicate. Scale bar is 10 μm.

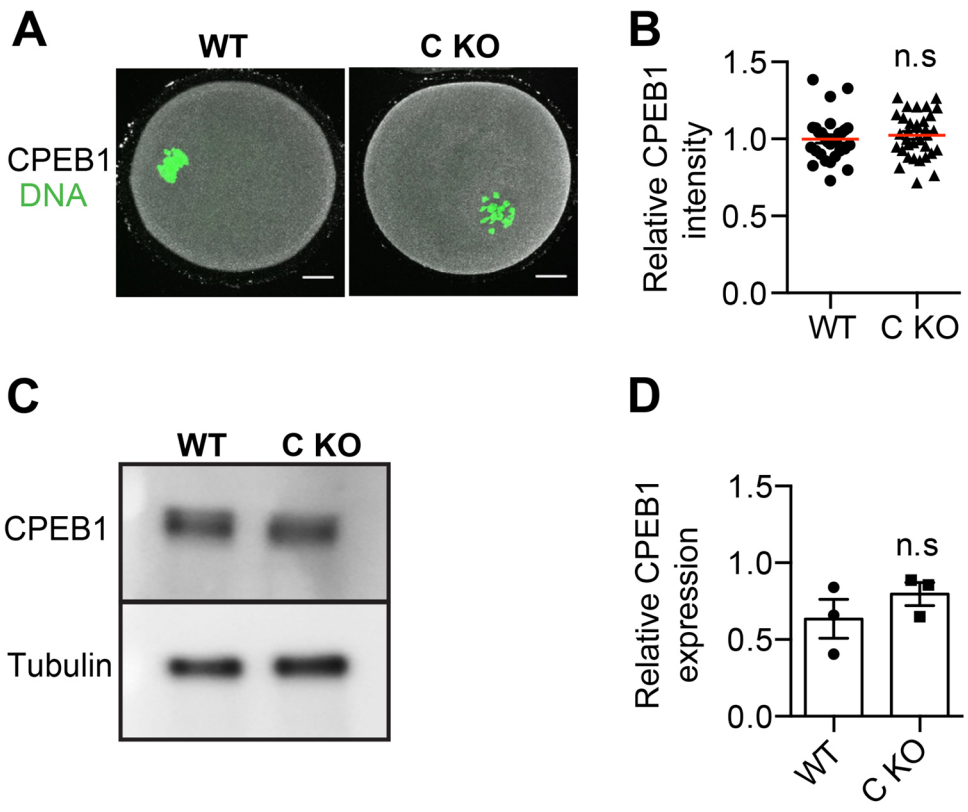

Fig. S5. Loss of AURKC does not affect CPEB1 function. A) Prophase I oocytes from WT and AURKC KO oocytes mice were collected and matured to metaphase of meiosis I and stained with anti-CPEB1 (gray) and DAPI (DNA, green). Shown are representative confocal z-projections. B) Relative pixel intensity of CPEB1 from A. Values normalized to WT (Number of oocytes: WT- 29; C KO- 33, (Unpaired student's t-test, two tailed, n.s. = not significant). Scale bar is 10 μm. C) Prophase I oocytes from WT and AURKC KO mice were matured to Metaphase I and prior to western blotting to detect CPEB1 (30 oocytes/lane). α-Tubulin served as a loading control. D) Quantification of CPEB1 expression after normalizing values from C to α-tubulin (Unpaired student's t-test, two tailed, n.s. = not significant). These experiments were repeated 3 times with 1 mouse per genotype for each experimental replicate.

Supplementary Materials and Methods

Sequence of Firefly-Luciferase-*AurkC*-3'UTR

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Sequence of Firefly-Luciferase-*Ccnb1*-3'UTR (Mutated)

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