



Supplementary Figure 9. UPF2 is essential for oocyte growth. **a**, Schematic representation of oocyte growth and maturation. *Zp3* starts to be expressed at the early stage of growing oocyte in primordial follicles. **b**, Number of pups born per plug from *Upf2^{CTL}* (*Upf2^{+/fl}; Zp3Cre Tg⁺*) and *Upf2^{cKO}* (*Upf2^{fl/fl}; Zp3Cre Tg⁺*) mice. The number of mice and plugs examined are indicated. Horizontal bars represent the mean, and the error bars the standard deviation. (**P* < 0.05; t-test two-sided). **c**, Frequency of non-surrounded nucleolus and surrounded nucleolus states in *Upf2^{CTL}* and *Upf2^{cKO}* GV oocytes. (**P* < 0.05, Fisher's exact test. *Upf2^{CTL}*, *n* = 74 oocytes, *n* = 3 mice; and *Upf2^{cKO}*, *n* = 68 oocytes, *n* = 3 mice). **d**, Left, representative confocal immunofluorescence micrographs showing *Upf2^{CTL}* (top) and abnormal *Upf2^{cKO}* (bottom) MII oocytes stained with anti-tubulin antibody (green) and Hoechst 33342 (red). Scale bars, 20 μ m. Right, the frequency of abnormal MII oocytes is presented for the respective genotypes. (**P* < 0.05, Fisher's exact test. *Upf2^{cKO}*, *n* = 43 oocytes, *n* = 2 mice; *Upf2^{CTL}*, *n* = 21 oocytes, *n* = 2 mice). **e**, Expression scatter plot showing relative average expression of transcripts between control and *Upf2^{cKO}* GV oocytes. Significantly deregulated (*P* < 0.01, moderated *t*-statistic adjusted) genes with a fold change greater than two

are highlighted in red. (*Upf2^{CTL}*, $n = 3$; *Upf2^{ckO}*, $n = 3$). **f**, Venn diagram showing the common genes upregulated in *Tut4/7^{ckO}* (*Tut4^{fl/fl}*; *Tut7^{fl/fl}*; *Zp3Cre Tg⁺*) and *Upf2^{ckO}* GV oocytes. **g**, Gene ontology analysis of upregulated genes in *Upf2^{ckO}* GV oocytes.