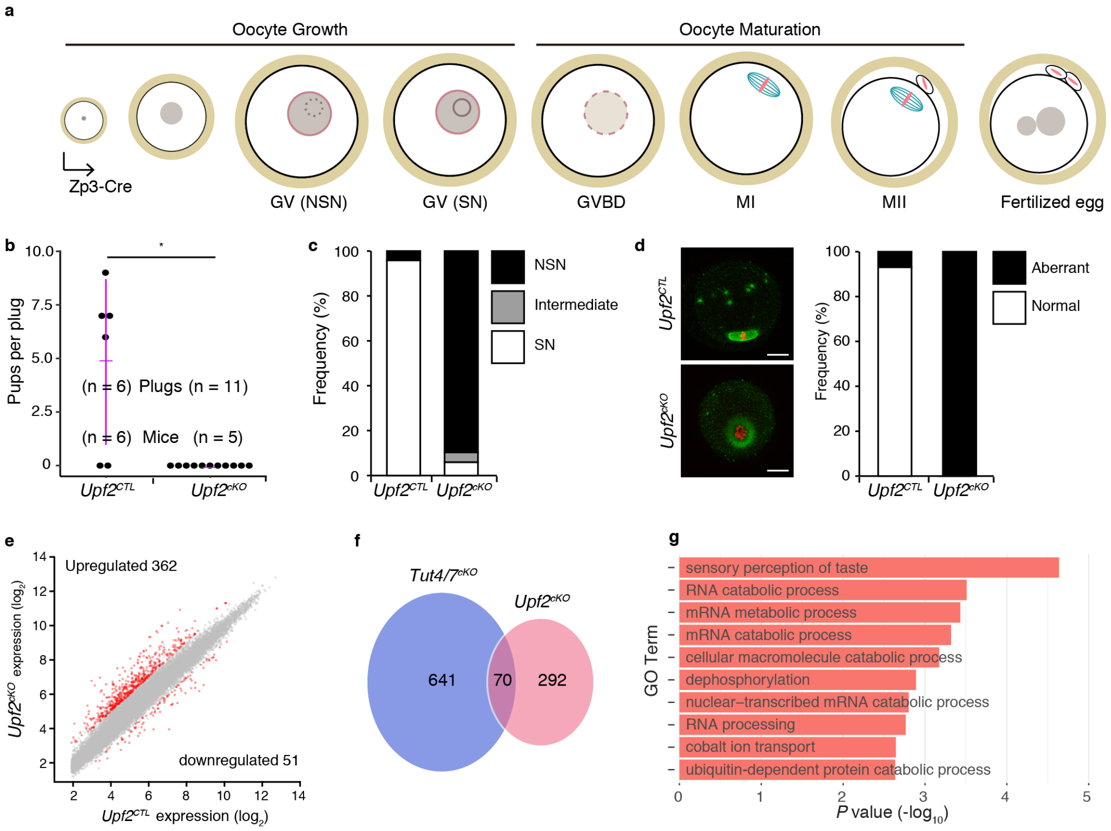

Supplementary Figure 9. UPF2 is essential for oocyte growth. a, Schematic representation of oocyte growth and maturation. *Zp3* starts to be expressed at the early stage of growing oocyte in primordial follicles. **b**, Number of pups born per plug from *Upf2*^{CTL} (*Upf2*$^{+/fl}$; *Zp3Cre Tg*$^{+}$) 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 µm. Right, the frequency of abnormal MII oocytes is presented for the respective genotypes. (*$P < 0.05$, Fisher's exact test. *Upf2*^{CTL}, n = 43 oocytes, n = 2 mice; *Upf2*^{cKO}, 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.