

Expanded View Figures

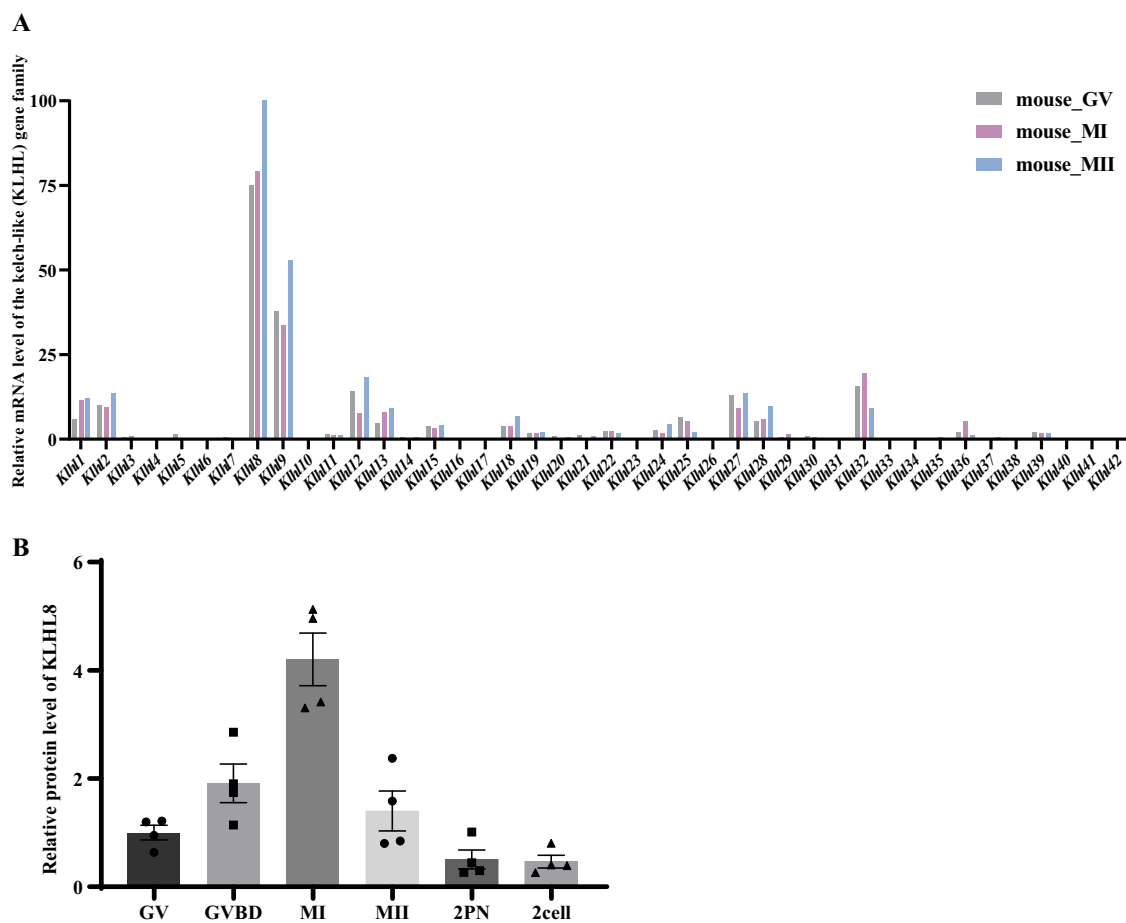


Figure EV1. The transcription level and protein abundance of KLHL8 during oocyte maturation.

(A) In-house database qRT-PCR results for KLHL family mRNA expression in GV, MI, and MII oocytes. (B) Quantification of KLHL8 protein abundance during oocyte maturation. Data are presented as mean $\pm$ SEM ($n = 4$).

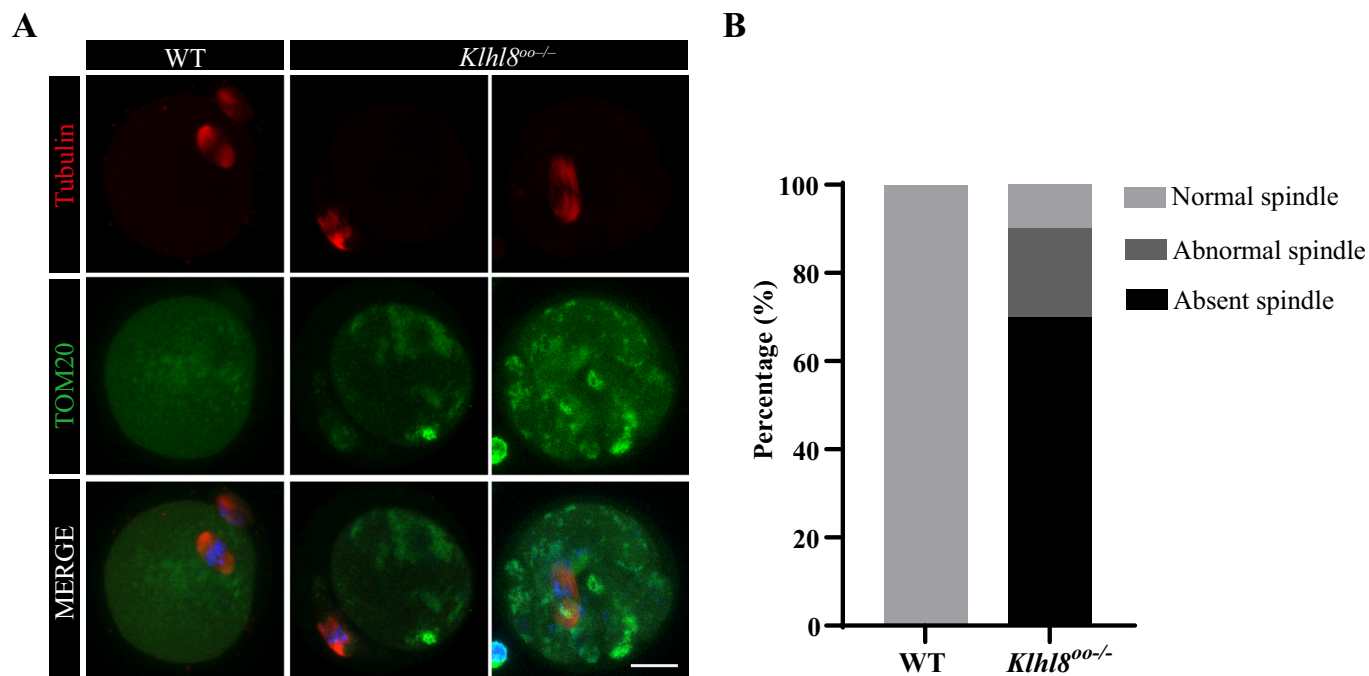


Figure EV2. *Klhl8* deletion causes abnormal spindle in MII oocytes.

(A) The spindle morphology in few oocytes that manage to extrude PB1 in vivo. Red, β -Tubulin; Green, mitochondria (TOM20). Scale bar, 20 μ m. (B) The percentage of oocytes with different spindle morphologies in WT and *Klhl8^{oo-/-}* MII oocytes (WT, $n = 8$; *Klhl8^{oo-/-}*, $n = 10$).

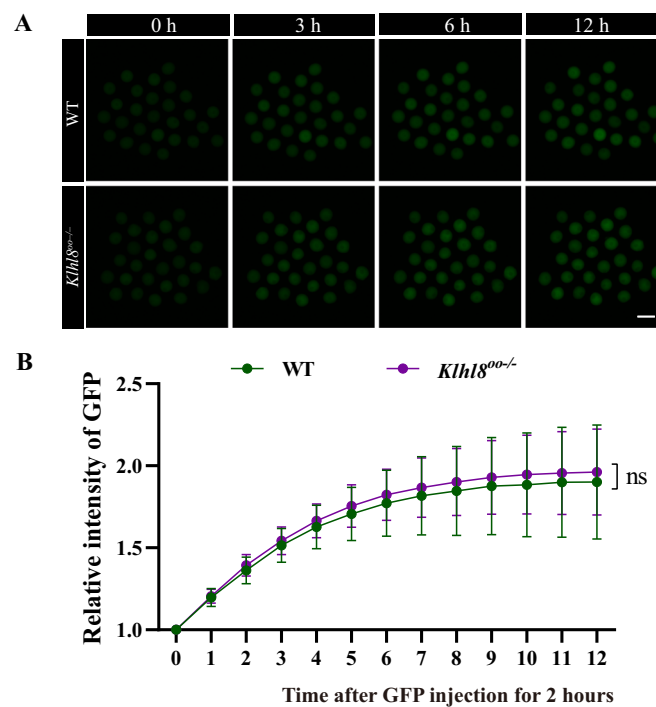
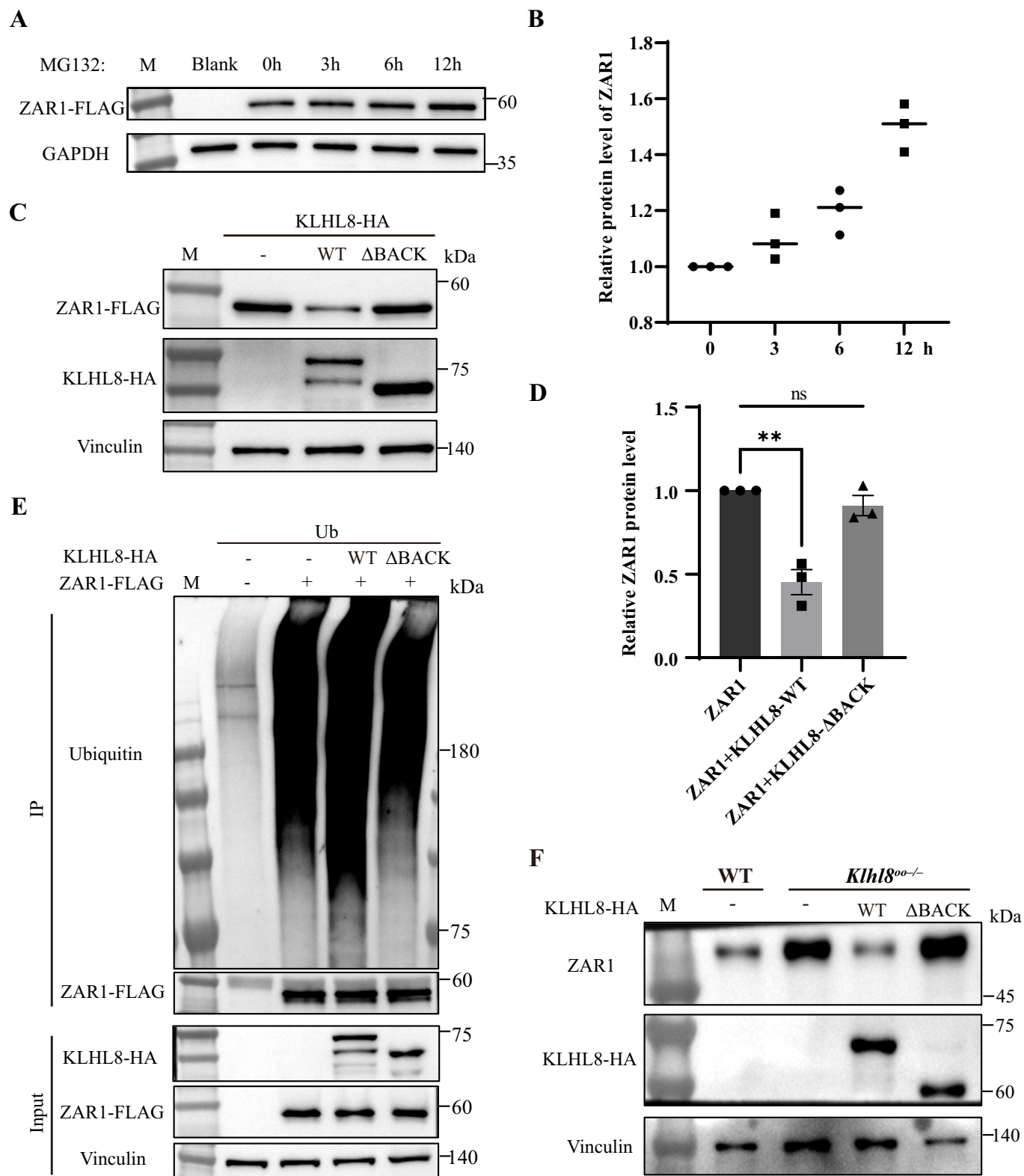


Figure EV3. Translation efficiency in WT and *Klh18^{oo/-}* oocytes.

(A) GFP expression in WT and *Klh18^{oo/-}* GV oocytes after mRNA injection for 2 h. Scale bar, 100 μ m. (B) The quantification of GFP intensity in WT and *Klh18^{oo/-}* GV oocytes (WT, $n = 28$; *Klh18^{oo/-}*, $n = 29$). Data are presented as mean $\pm$ SD. Statistical significance was determined using Multiple unpaired t test: ns not significant.



◀ **Figure EV4. BACK domain of KLHL8 is necessary for ZAR1 ubiquitination and proteasome degradation.**

(A) Western blot result showing ZAR1 protein level after adding MG132. (B) Quantification of the ZAR1 protein level after adding MG132 for different duration. Data are presented as mean $\pm$ SEM ($n = 3$). (C) Immunoblotting for ZAR1 with *Klhl8*-WT or *Klhl8*- Δ BACK overexpression in cultured HeLa cells. (D) Quantitative analysis of ZAR1 protein level with *Klhl8*-WT or *Klhl8*- Δ BACK overexpression in cultured HeLa cells. Data are presented as mean $\pm$ SEM ($n = 3$). Statistical significance was determined using an unpaired two-tailed *t* test: ns not significant, $**P = 0.0018$. (E) The ubiquitination of ZAR1 with *Klhl8*-WT or *Klhl8*- Δ BACK overexpression in cultured HeLa cells. (F) Immunoblotting for ZAR1 in WT and *Klhl8*^{ko/ko} GV oocytes with *Klhl8*-WT or *Klhl8*- Δ BACK mRNA injection. Vinculin was used as the protein loading control.

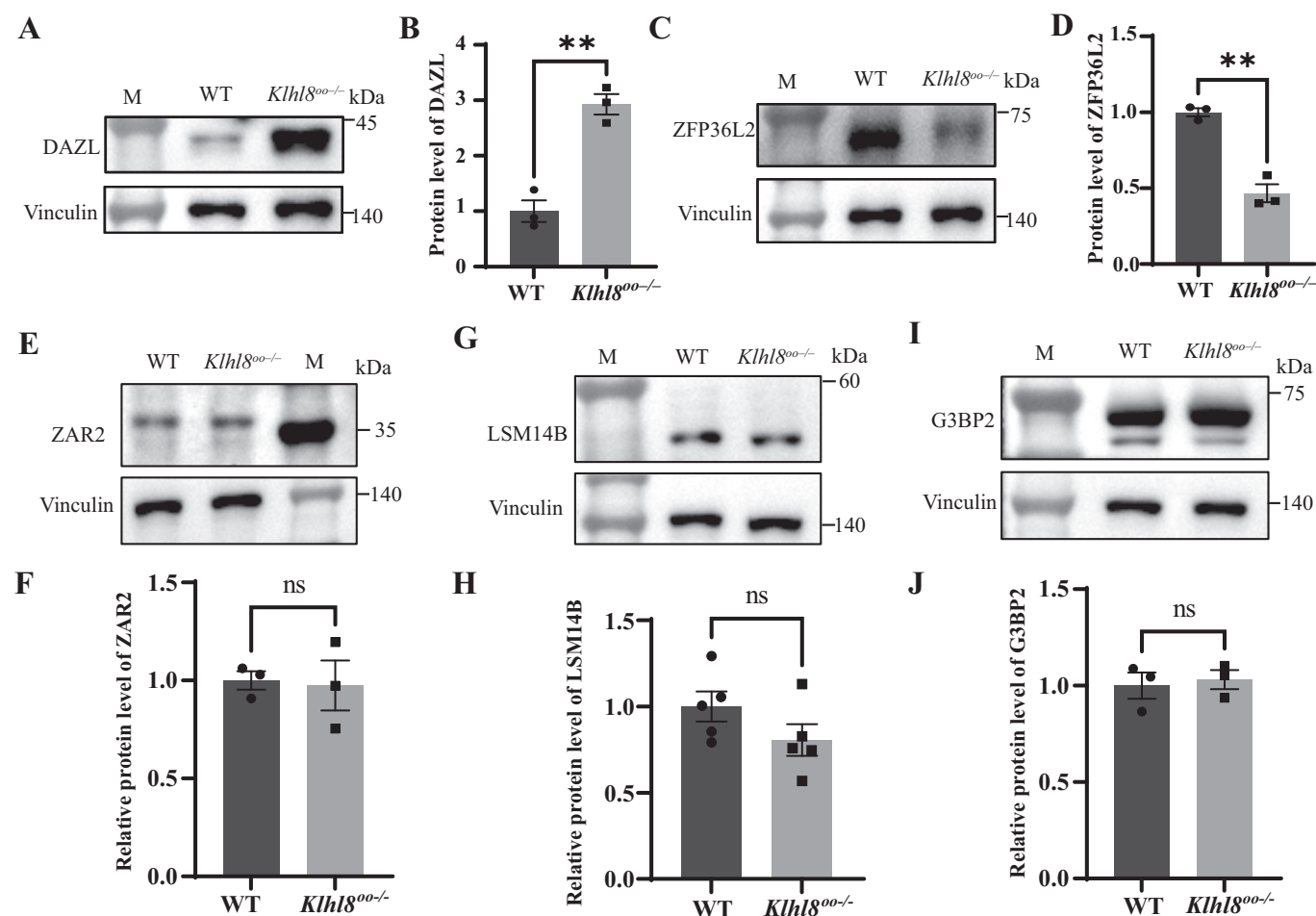


Figure EV5. Effects of *Khlh8* deletion on other RNA binding proteins.

(A, B) Western blot result and quantitative analysis of DAZL protein level in WT and *Khlh8*^{00-/-} oocytes. Vinculin was used as the protein loading control. Data are presented as mean $\pm$ SEM ($n = 3$). Statistical significance was determined using an unpaired two-tailed t test: $^{**}P = 0.002$. (C, D) Western blot result and quantitative analysis of ZFP36L2 protein level in WT and *Khlh8*^{00-/-} oocytes. Vinculin was used as the protein loading control. Data are presented as mean $\pm$ SEM ($n = 3$). Statistical significance was determined using an unpaired two-tailed t test: $^{**}P = 0.0012$. (E, F) Western blot result and quantitative analysis of ZAR2 protein level in WT and *Khlh8*^{00-/-} oocytes. Vinculin was used as the protein loading control, $n = 3$. (G, H) Western blot result and quantitative analysis of LSM14B protein level in WT and *Khlh8*^{00-/-} oocytes. Vinculin was used as the protein loading control, $n = 5$. (I, J) Western blot result and quantitative analysis of G3BP2 protein level in WT and *Khlh8*^{00-/-} oocytes. Vinculin was used as the protein loading control, $n = 3$. In (F, H, J), data are presented as mean $\pm$ SEM. Statistical significance was determined using an unpaired two-tailed t test: ns not significant.