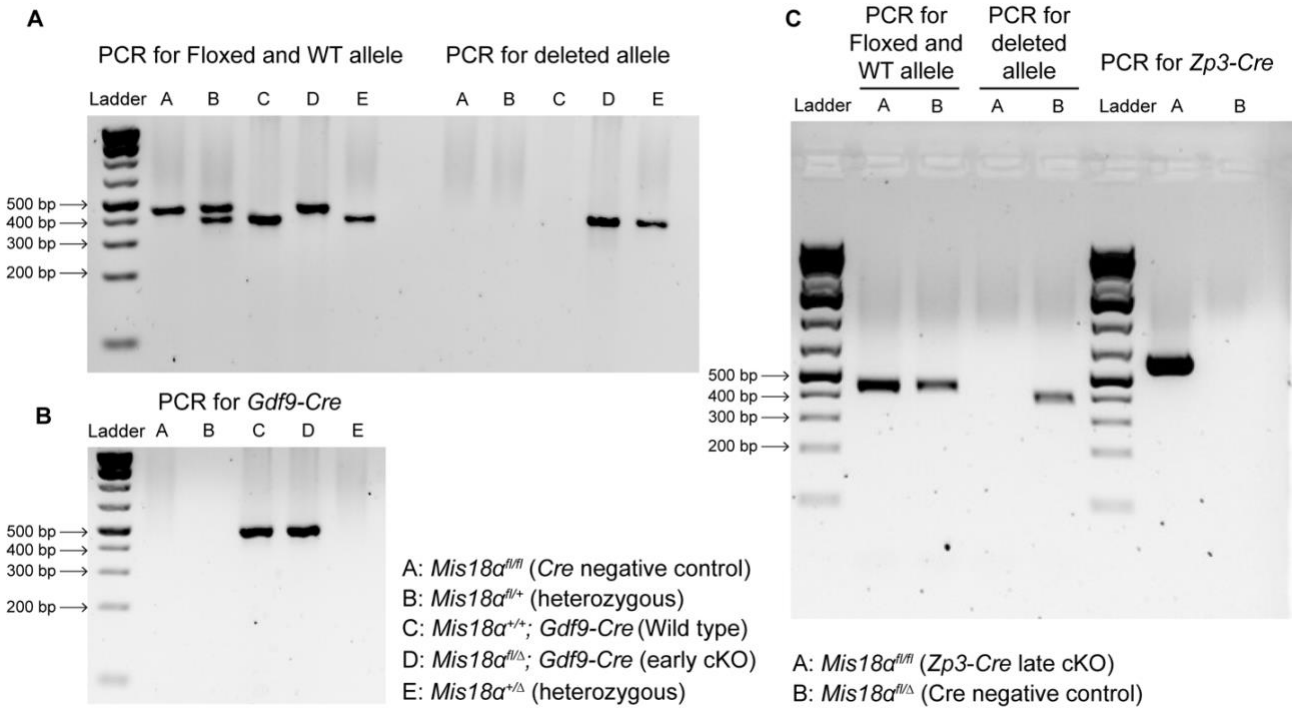

Figure S1: Genotyping of mice used in this study. Related to Figure 1.

(A-C) Genotyping gels for *Mis18α*$^{fl/fl}$ mice for both *Cre* drivers.

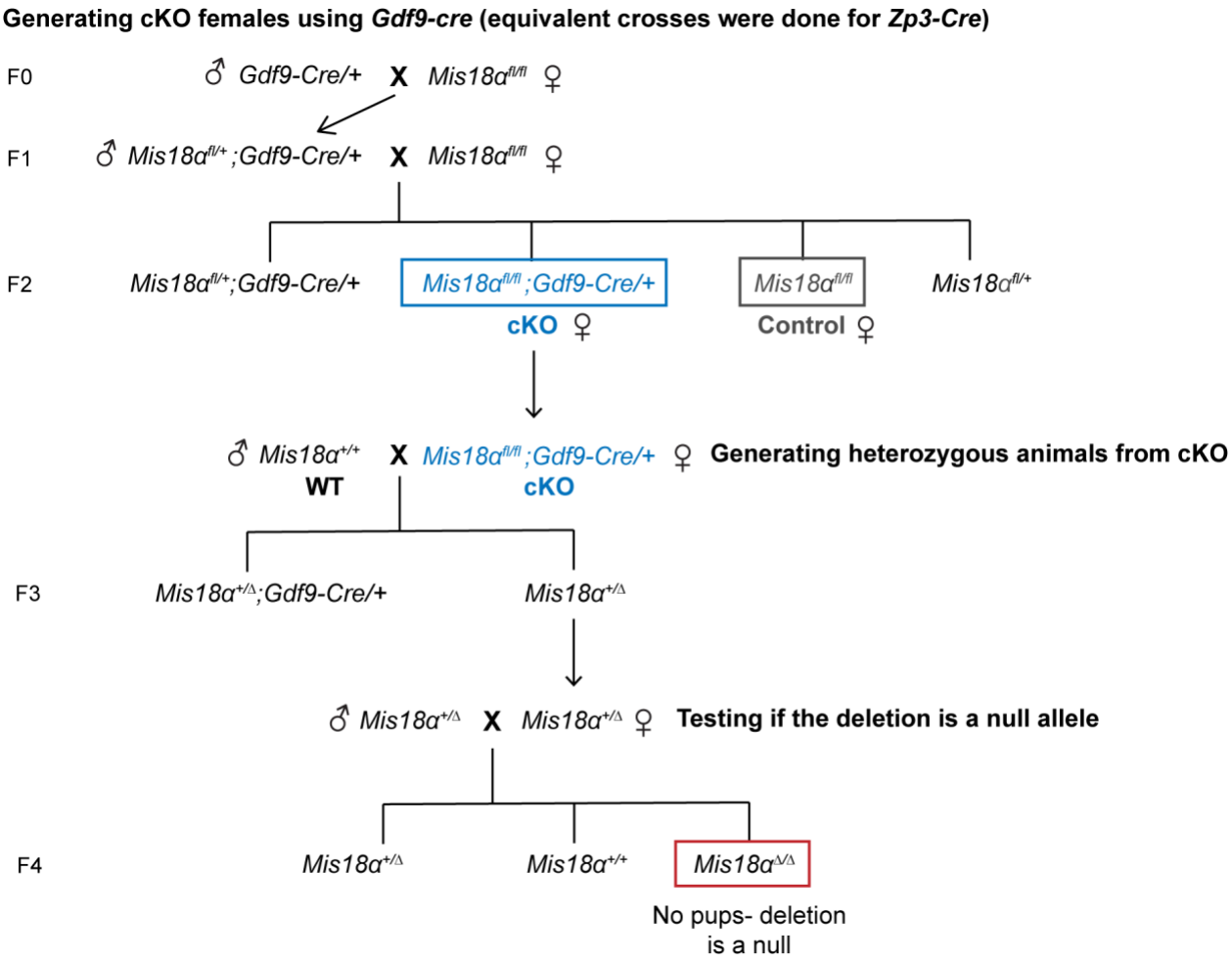

Figure S2 : Cross scheme to combine the *Cre* recombinases with the *Mis18α* floxed allele. Related to Figures 1- 4.

Crosses are shown for *Gdf9-Cre,* and equivalent crosses were done for *Zp3-Cre*. The blue and grey boxes designate cKO and control females used for CENP-A measurements in oocytes (Figure 4). The cKO mothers were also used to generate heterozygous animals, which were then utilized to confirm that *Mis18α* deletion is a null allele (also see Figure 1D).

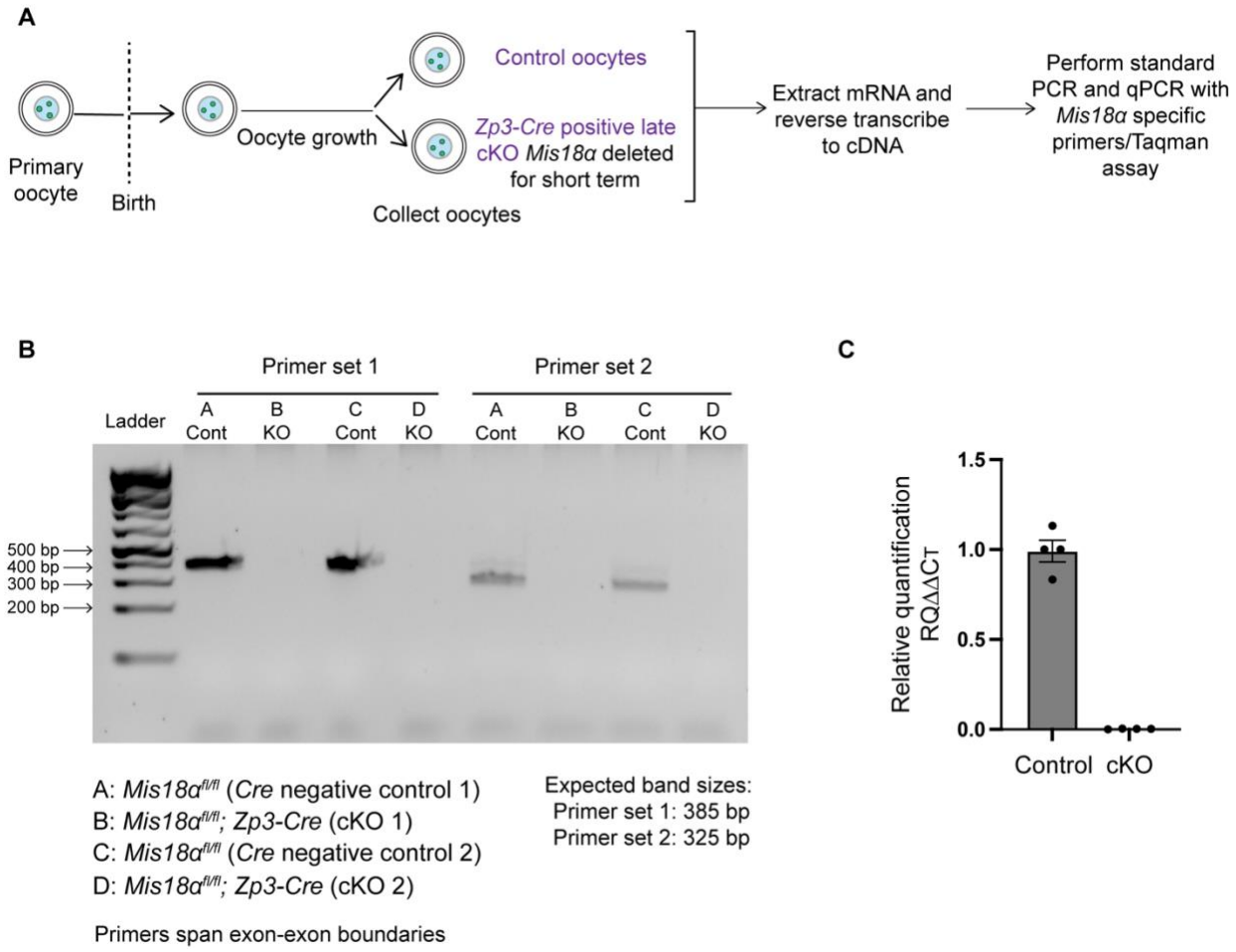

Figure S3: *Mis18α* gene expression in oocytes. Related to Figure 2.

(A) Schematic of *Mis18α* gene expression assay for control and late cKO oocytes. (B) Standard RT-PCR gives no amplification from late cKO oocytes compared to the control. (C) Quantification of real time PCR for *Mis18α* gene expression using a Taqman assay against *Mis18α*, with *H2A* as the endogenous control. Expression was quantified using the Livak method[S1]. *Mis18α* mRNA is undetectable by both methods. Error bars: S.E.M.

Supplemental Reference:

S1. Livak, K.J., and Schmittgen, T.D. (2001). Analysis of relative gene expression data using real-time quantitative PCR and the 2(-Delta Delta C(T)) Method. Methods *25*, 402–408. 10.1006/meth.2001.1262.