RESEARCH ARTICLE

Starvation induces FoxO-dependent mitotic-to-endocycle switch pausing during Drosophila oogenesis

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ABSTRACT

When exposed to nutrient challenge, organisms have to adapt their physiology in order to balance reproduction with adult fitness. In mammals, ovarian follicles enter a massive growth phase during which they become highly dependent on gonadotrophic factors and nutrients. Somatic tissues play a crucial role in integrating these signals, controlling ovarian follicle atresia and eventually leading to the selection of a single follicle for ovulation. We used Drosophila follicles as a model to study the effect of starvation on follicle maturation. Upon starvation, Drosophila vitellogenic follicles adopt an ‘atresia-like’ behavior, in which some slow down their development whereas others enter degeneration. The mitotic-to-endocycle (M/E) transition is a critical step during Drosophila oogenesis, allowing the entry of egg chambers into vitellogenesis. Here, we describe a specific and transient phase during M/E switching that is paused upon starvation. The Insulin pathway induces the pausing of the M/E switch, blocking the entry of egg chambers into vitellogenesis. Pausing of the M/E switch involves a previously unknown crosstalk between FoxO, Cut and Notch that ensures full reversion of the pausing during

INTRODUCTION

Nutrient sensing is essential to coordinate growth and development during organogenesis. The conserved Insulin/Insulin-like growth factor (IIS) and Target of rapamycin (TOR) signaling pathways play a central role in coupling growth with nutrition in Drosophila (Edgar, 2006; Andersen et al., 2013). The TOR pathway controls cell-autonomous growth downstream of amino acids (Wang and Proud, 2009), whereas the IIS pathway acts as a systemic regulator. Under the conditions of a protein-rich diet, Drosophila insulin-like peptides (Dilps) secreted from the brain directly activate the insulin receptor homolog (InR) in peripheral tissues to control metabolism, stress response, lifespan and reproduction (Brogiole et al., 2001; Ikeya et al., 2002). Signaling downstream of InR involves PI3K and AKT, leading to the phosphorylation and subsequent cytoplasmic retention of the Forkhead transcription factor FoxO (Puig et al., 2003). On a protein-poor diet Dilp secretion is blocked (Géminard et al., 2009; Grönke et al., 2010), which leads to reduced InR signaling and subsequent translocation of FoxO into the nucleus of target tissues, where it acts as a growth inhibitor.

During prolonged nutritional stress, the IIS and TOR pathways interact to adjust development and growth rates according to nutrient availability, allowing proper organ development (Colombani et al., 2003). However, the effects of transient diet change on organ development remain poorly understood. To study this question, we used oogenesis as a model to investigate how the high-energy-consuming egg chambers cope with nutrient variations, to which animals are submitted in the wild.

Egg chambers are composed of a cyst of 16 germine cells (1 oocyte and 15 nurse cells) surrounded by a single layer of somatic follicle cells (Fig. 1A). These two cell lineages originate, respectively, from germline and follicle stem cells, which are both present in the germarium. When flies are grown on a protein-rich medium, egg chambers are produced unceasingly, leading to the formation of regular strings of eggs of all developing stages (1 to 14) assembled into ovarioles. Two main phases of egg chamber development are distinguishable based on the follicle cell nuclear cycle: (1) a mitotic (M) phase from stages 1 to 6; and (2) an endocycle (E) phase (genomic DNA replication without cell division) from stages 7 to 10. During the mitotic phase, follicle cells are immature and express the homeobox transcription factor Cut (Fig. 1A,B,E) (Sun and Deng, 2005). Then, between stages 6 and 7, follicle cells switch their cell cycle program, exiting the mitotic cycle and entering the endocycle (Deng et al., 2001; Lopez-Schier and Johnston, 2001; Tamori and Deng, 2013). This transition is known as the mitotic-to-endocycle (M/E) switch. This switch is under the control of the evolutionarily conserved Notch (N) signaling pathway (Deng et al., 2001; Lopez-Schier and Johnston, 2001; Schaeffer et al., 2004; Shcherbata et al., 2004). N activation induces expression of the zinc-finger transcription factor Hindsight (Hnt, Pebbled – FlyBase), which in turn inhibits cut expression (Fig. 1A-E) (Sun and Deng, 2007). Cut downregulation is necessary and sufficient to promote entry into the endocycle, allowing follicle cell differentiation and maturation (Sun and Deng, 2005). At stage 8, N activity eventually returns to basal levels (Fig. 1B,C) (Sun et al., 2008).

The mitotic and endocycle phases roughly correspond to the early and vitellogenic phases of egg chamber development, respectively. These two phases have previously been shown to behave differentially upon starvation (Drummond-Barbosa and Spradling, 2001). During the early mitotic phase, starvation causes microtubule reorganization (Shimada et al., 2011) and germline and follicle cell division rates and growth slow down, leading to a developmental delay (LaFever and Drummond-Barbosa, 2005) as well as triggering the loss of germline stem cells in the germarium (Hsu et al., 2008; Hsu and Drummond-Barbosa, 2009, 2011; Yang et al., 2013). Mutations in InR reduce follicle cell proliferation, whereas some Tor mutations extend the mitotic phase (LaFever et al., 2010). By contrast, starvation during the endocycle phase triggers egg chamber degeneration (Drummond-Barbosa and Spradling, 2001; Pritchett and McCall,
2012) in addition to a delayed growth rate (Drummond-Barbosa and Spradling, 2001; Ikeya et al., 2002; Tu et al., 2002; Richard et al., 2005; Schiesari et al., 2011). These observations reflect a sharp change in the survival/developmental response to nutrient shortage occurring at the M/E switch. Yet, the effects of starvation and the role of IIS during this important transition remain unknown.

In this study, we characterized the egg chamber response to nutrient variations specifically during the M/E transition. We show that nutrient deprivation stalls stage 6 egg chambers in a previously uncharacterized state that we term the ‘paused M/E switch’ (paused MES). We show that paused MES is reversible, with oogenesis resuming remarkably quickly following refeeding of starved flies. Paused MES is induced by a reduction of InR signaling. FoxO is dispensable for the normal M/E switch; however, it is essential for paused MES induction. In these conditions, FoxO activates Cut expression cell-autonomously in follicle cells, which maintains N in a paused MES-specific regulatory loop. Altogether, these results reveal that upon starvation the M/E switch is paused, preserving the coupling between growth and development. This FoxO-dependent process enables prompt and efficient adaptation to nutrient supplies, thereby contributing to maintaining the balance between reproduction and nutrient availability.

RESULTS

Starvation induces a paused MES state

The M/E switch is a rapid transition that takes place in egg chambers at the end of stage 6, lasting ~3 h under normal conditions (Lin and Spradling, 1993). It has been characterized by N activation at the end of stage 6, followed by the loss of Cut at stage 7 (Sun and Deng, 2005). We performed a detailed analysis of the switch using (1) egg morphology, (2) the expression of Cut, which stains mitotic egg chambers, and (3) N signaling pathway reporters (NRE, Notch reporter element) that mark endocycling egg chambers (NRE>GFP or NRE-lacZ) (Fig. 1C,E) (Furriols and Bray, 2001; Zeng et al., 2010). Results show that the switch proceeds through an intermediate step between stages 6 and 7, during which follicle cells co-express N activity reporters (NRE-lacZ), Hnt and Cut (Fig. 1; supplementary material Fig. S1A). Statistical analysis shows that this intermediate stage lasts for ~2 h (supplementary material Table S1). Therefore, there is a specific and transient phase during which markers of the mitotic and endocycle phases show overlapping expression. Hereafter, we refer to this intermediate stage as the M/E switch (MES) stage. The Hnt and Cut markers suggest that MES stage egg chambers are in between cell cycle programs. We assessed the cell cycle state of MES cells and found that they exhibit neither mitotic (CycB, String-lacZ, phosphorylated Histone H3) nor endocyte (Fizzy related-lacZ, EdU incorporation) markers; hence, they are blocked exactly at the transition between the mitotic and endocycle phases (supplementary material Fig. S1).

To analyze MES behavior during starvation, we first verified that MES stage egg chambers showed the same overlapping Cut and NRE expressions (Fig. 2A,B) and intermediate cell cycle state (supplementary material Fig. S2). Next, we took advantage of the GAL80ts system to pulse label newly generated MES stage egg chambers with GFP (McGuire et al., 2003). Briefly, fed or starved NRE>GFP flies were raised for 24 h at 29°C (a temperature permissive for GFP expression) in order to label egg chambers from MES stage onwards. Then, the egg chambers were shifted to a restrictive temperature (20°C) for 24 h to stop de novo GFP expression (Fig. 2F; see Materials and Methods). The MES stage was determined by the expression of NRE>GFP and Cut (Fig. 2C,D).

These experiments show that upon starvation MES egg chambers are paused, with the percentage of MES egg chambers increasing with time (supplementary material Fig. S2E). Indeed, there were no GFP-labeled MES stage egg chambers from control fed flies (Fig. 2C-C′,E), with GFP being expressed in later, stage 8 egg chambers indicating that oogenesis proceeded normally. By contrast, most starved MES stage egg chambers were still labeled with GFP (Fig. 2D-D′,E), indicating retention at the MES stage. We conclude that upon starvation MES stage egg chambers are maintained in the paused MES state.

MES pausing is a reversible process upon refeeding

Next, we analyzed the effect of refeeding on starvation-induced paused MES egg chambers. Flies were starved on poor medium to induce paused MES and then refed during different periods to test the ability of the paused egg chambers to proceed through the M/E switch once food was available again (Fig. 3A; see Materials and Methods). Egg chambers were marked using GFP flip-out clones

![Fig. 1. Marker and gene expression profiles during the M/E switch.](image-url)
before starvation, in order to make sure that they experienced the full protocol (Fig. 3A; supplementary material Fig. S3A). To characterize the ability of paused MES to enter the endocycle, we measured the ratio of paused MES versus newly born non-degenerating stage 7-8 egg chambers. After 15 h of starvation (t0 in Fig. 3), the proportion of MES stage relative to live stage 7-8 egg chambers increased compared with control fed flies (Fig. 3B,C), reflecting both the pausing of MES stage and degeneration of stage 7-8 egg chambers. Strikingly, after only 1 h of refeeding, we already observed Cut downregulation in a significant proportion of GFP-positive stage 7-8 egg chambers, indicating that they had entered the endocycle (Fig. 3B,C). Increasing the refeeding period to 9 h allowed most MES egg chambers to develop into stage 8 egg chambers (Fig. 3B,E). After 24 h of rich food uptake, the ratio of MES/stage 7-8 was back to that of control fed flies (Fig. 3B).

Thus, upon nutrient supply, starvation-induced paused MES egg chambers are able to quickly revert to normal oogenesis by entering the endocycle. These data suggest that the M/E switch might serve as a nutritional checkpoint during oogenesis, responding rapidly to starvation and refeeding to allow processing through vitellogenesis.

**IIS acts cell-autonomously in follicle cells to induce paused MES**

The IIS pathway is known to mediate the response to starvation during development. In order to analyze the role of InR signaling in follicle cells during the M/E switch, we generated clones of follicle cells mutant for different components of the IIS pathway: InR, the catalytic subunit of PI3K (dp110; Pi3K92E – FlyBase) and akt (Akt1 – FlyBase) (Fig. 4A-C). All these conditions showed the same phenotype. Mutant follicle cells in otherwise wild-type endocycle egg chambers still expressed the mitotic stage marker Cut (Fig. 4A‴; data not shown), indicating that the mutant cells had not yet entered the endocycle (supplementary material Fig. S4). Consistently, mutant cells had smaller nuclei than their wild-type neighbors (Fig. 4A″-C″) and quantitative analysis of their DNA content indicated that they are diploid (supplementary material Fig. S4E). In addition, IIS pathway mutant cells showed N activation, as evidenced by the expression of Notch intracellular domain (Nicd), Hnt and NRE-lacZ (Fig. 4B‴,C‴,A⁷-C⁷; data not shown). Altogether, these results indicate that the reduction in N activity characteristic of stage 9 follicles had not occurred. Thus, IIS mutant follicle cells have all the features of paused MES cells.

In order to test whether activation of IIS is sufficient to force paused cells to proceed through the M/E switch, we generated IIS gain-of-function clones in starved egg chambers. In such conditions the expression of both Cut and NRE-lacZ was abolished, showing that ectopic IIS activity is sufficient to prompt follicle cells into progressing through the M/E switch regardless of the shortage of food supply (Fig. 4D-D⁷).

Altogether, these results show that the IIS pathway acts cell-autonomously in follicle cells to induce the paused MES state in response to starvation.
FoxO is essential to trigger paused MES upon starvation

It has been shown that reduction of the IIS pathway upon starvation leads to the translocation of the transcription factor FoxO to the nucleus, where it acts as a negative regulator of growth (Jünger et al., 2003; Puig et al., 2003). We were able to confirm that in fed flies, InR mutant follicle cells show high levels of nuclear FoxO, indicating that FoxO is activated cell-autonomously in response to loss of IIS function (Fig. 5A). To test the role of FoxO in triggering the MES, we analyzed follicle cells mutant for foxo. In fed conditions, the levels of Cut and NRE-lacZ in foxo mutant cells were comparable to wild-type levels in both mitotic cycle and endocycle egg chambers (Fig. 5B-C). These results indicate that, in the absence of nutritional stress, FoxO has no effect on the M/E switch, neither promoting nor delaying it.

To test whether FoxO is involved in generating starvation-induced paused MES, foxoΔ94 homozygous mutant flies were grown on poor medium and the MES/stage 7-10 ratio was measured (see Materials and Methods). In control heterozygous flies the ratio was doubled in poor diet conditions, reflecting the pausing of MES stages and leading to its increase compared with fed conditions (Fig. 5D). By contrast, in foxoΔ94 homozygous mutant flies, starvation no longer triggered MES pausing (Fig. 5D), indicating that FoxO is indeed required to induce paused MES in response to the lack of nutrients.

To verify that FoxO induces paused MES as a result of IIS downregulation, we generated clones of follicle cells that were mutant for InR or that overexpressed a dominant-negative form of PI3K. In either case, the loss of IIS function mimicked the starvation-induced paused MES state as shown by Cut misexpression (Fig. 5A-A‴). However, this phenotype was fully suppressed in the absence of FoxO (compare Fig. 5E-E‴ with 5F-F‴), indicating that upon starvation IIS acts through FoxO to induce paused MES.

Finally, to assess whether FoxO is sufficient to induce paused MES, we generated clones overexpressing an active form of human FOXO3 [hFOXO3a-TM; mimicking FoxO gain-of-function (Jünger et al., 2003)] in the absence of any nutritional stress. Interestingly, activated human FOXO3 was able to induce the concomitant expression of Cut and NRE-lacZ (Fig. 5G-G‴), indicating that FoxO is sufficient to trigger paused MES.

Altogether, these results indicate that, in the absence of nutritional stress, FoxO is dispensable for the formation of the MES. However, during starvation periods, FoxO plays a crucial role specifically at the M/E switch downstream of IIS, leading to the induction of paused MES egg chambers.

Cut activates Notch in a specific regulatory loop during paused MES

Paused MES egg chambers are characterized by a puzzling concomitant activation of Cut and N. Indeed, in normal egg...
chambers from MES stage onwards, a peak of N activity downregulates cut through Hnt and this is followed by a strong reduction of N activity (Fig. 1) (Sun and Deng, 2007; Sun et al., 2008). The paused MES-specific expression pattern therefore raises two questions: what maintains N activation and how is Cut expression preserved in the presence of N? We first tested whether Cut could be the regulator of N during paused MES. We inhibited Cut expression in follicle cells while overexpressing the active form of human FOXO3 to mimic paused MES (>hFOXO3a-TM; cutRNAi). Interestingly, loss of Cut activity led to the absence of both NRE-lacZ upregulation and N overexpression (Fig. 6A″,A‴, compare with Fig. 5G‴; supplementary material Fig. S5). These results suggest that Cut itself maintains N activity during the paused MES stage. To test whether Cut is sufficient to maintain N, Cut was misexpressed in post-switch egg chambers. Ectopic Cut expression led to NRE-lacZ, N and Hnt upregulation (Fig. 6B–C‴), indicating that Cut activates the N signaling pathway cell-autonomously. Furthermore, we found that N is essential for Cut-induced activation of N target genes. Indeed, upon N silencing Hnt is no longer activated by Cut (Fig. 6D–D‴), indicating that N is epistatic to Cut on hnt regulation and that Cut does not regulate hnt directly. We next analyzed the role of N in the paused MES regulatory pathway and in particular we tested whether N is also a negative regulator of cut in paused MES egg chambers. We made use of the IIS mutant paused MES egg chambers to overexpress the activated form of N (A″(N)*) . N gain-of-function led to the absence of Cut upregulation (Fig. 6E–E‴), compare with Fig. 4A and Fig. 5A; data analysis (Fig. 4. IIS acts cell-autonomously in follicle cells to induce paused MES. (A–C‴) IIS loss-of-function clones generated in stage 9 egg chambers. Mutant follicle cell clones are outlined and marked by the absence of GFP (A–C). (A″–C‴) Apical view of a dp110(1)C1 (P[3K]) mosaic egg chamber. Mutant clones express Cut (A‴). (B‴–B‴) Transverse section of an akt(1) mosaic egg chamber. Mutant clones show stronger N staining compared with wild-type cells (B‴). (C‴–C‴) Apical view of an inr17 mosaic egg chamber. Mutant clones show similar Hnt expression to wild-type cells (C‴). (D‴–D‴) Transverse section of a flip-out clone (marked by the presence of GFP, outlined) expressing UAS-dInrdel (activated form). Cut (D‴) and NRE-lacZ (D‴) expression is lost. The boxed regions in the merge are magnified in the single-channel images to the right. Scale bars: 50 µm.

Fig. 5. Foxo is essential to trigger paused MES egg chambers. (A–A‴) Endocycle (stage 8) in >hFOXO3a-TM; foxoΔ94/TM6B mosaic egg chamber showing Cut expression (A‴) and strong FoxO nuclear staining (A‴) in mutant follicle cells. Mutant clones are marked by the absence of GFP (arrows). (B–C‴) Mitotic (stage 5) (B) and endocycle (stage 8) (C) foxoΔ94 mosaic egg chambers showing similar stainings for Cut (B‴–C‴) and NRE-lacZ (B‴–C‴) in wild-type and mutant follicle cells (marked by the absence of GFP, outlined). (D) The ratio of MES/stage 7-10 egg chambers from fed or starved foxoΔ94 and control foxoΔ94/TM6B flies. Data are the mean of duplicate experiments with s.d. (n=200 in each experiment). **P<0.01 (t-test). (E–E‴) Endocycle (stage 8) egg chamber with UAS-p60(P[3K])–expressing clones (marked by the presence of GFP, outlined), in which the expression of Cut is induced (E‴). (F–F‴) Endocycle (stage 8) egg chamber with UAS-p60(P[3K])–foxoΔ94 follicle cell clones (marked by the presence of GFP, outlined). Loss of foxo activity suppresses the expression of Cut (F‴). (G–G‴) Endocycle (stage 8) egg chamber containing UAS-hFOXO3a-TM follicle cell clones (marked by the presence of GFP, arrows). Ectopic activation of FoxO leads to Cut expression (G‴) and upregulation of NRE-lacZ (G‴). Loss-of-function (A–C), MARCM (E,F) or flip-out clones (G) are marked by the absence (green, A–C) or presence (E–G) of GFP, respectively. Egg chambers are marked with the clonal marker GFP (A″-C″, E–G″), DAPI staining (A‴–C‴, E‴–G‴), Cut (A‴–C‴, E‴–G‴), FoxO (A‴–C‴) and NRE-lacZ (B‴–C‴, G‴). The boxed regions in the merge are magnified in the single-channel images to the right. Scale bars: 50 µm.
through the downregulation of FoxO and Cut, thus allowing oogenesis to resume. Upon refeeding, cells respond quickly (within 1 h; Fig. 3) activation through FoxO, thereby linking nutrient levels to the state of established through a specific regulatory loop (Fig. 7). The onset of Paused MES maintenance relies on a particular regulatory pathway protecting developing eggs from starvation-induced degeneration. Nutritional checkpoint that is capable of restraining egg chamber progression into the energy-consuming vitellogenic stages, hence unnecessary energy expenditure when nutrients become limited. Altogether, the developmental delay that occurs during the mitotic phase combined with the paused MES state provides an reactive and reversible mechanism to help control the flow of egg chambers towards vitellogenesis, as well as supplying a reservoir of preserved egg chambers that are ready to quickly resume oogenesis when nutritional conditions are favorable.

Depending on their stage of maturation, egg chambers behave differentially upon starvation. During early mitotic phase, prolonged nutrient deprivation and reduction of IIS activity slows egg chamber growth, which leads to a delay in egg maturation. Starvation during the later, vitellogenic stages induces progressive cell degeneration, a process that can be compared to vertebrate atresia (Hsueh et al., 1994).

Our results add a new step to the control of oogenesis upon nutrient challenge, participating in developmental delay. Indeed, pausing egg chamber development at the transition between the mitotic and endocycle phases is an ideal strategy to rapidly control the flow of egg chambers and prevent counterproductive and unnecessary energy expenditure when nutrients become limited. Altogether, the developmental delay that occurs during the mitotic phase combined with the paused MES state provide an efficient response to nutrient deprivation, preventing energy loss and protecting egg chambers from degeneration, as well as ensuring rapid oogenesis restart upon refeeding.

Induction of the paused MES state upon starvation relies on the maintenance of a specific regulatory loop involving the concomitant activity of Cut and N (Fig. 7), thus mimicking the normal M/E transition. The equilibrium between Cut and N activity depends on the balance between active nuclear FoxO and repressive N. Reduction of nuclear FoxO upon refeeding leads to disruption of the Cut/N equilibrium and subsequent progression through the M/E switch. A key aspect of the paused MES molecular pathway is the finding that Cut itself can maintain N at high levels. Therefore, Cut translates IIS activity into the N pathway, thus linking nutrient sensing and vitellogenesis. This association is likely to participate in setting a good balance between homeostasis/survival and reproduction, in register with nutrient availability.

The coupling of IIS with N signaling through Cut might represent a widespread means to link growth and other developmental/
Fig. 7. The M/E switch pathway in normal and starvation conditions. The genetic pathway leading to the formation of paused MES egg chambers during starvation and its reversal to normal development upon refeeding. Paused MES maintenance involves the activation of N by Cut, their concomitant activity being established through a specific regulatory loop. The onset of paused MES is dependent on the loss of IIS signaling inducing Cut activation through FoxO. Upon refeeding, cells respond quickly by downregulating FoxO and Cut, thus allowing oogenesis to resume.

**MATERIALS AND METHODS**

*Drosophila* strains and culture

Flies were grown on protein-rich medium (10 g/l agar, 17 g/l yeast extract, 82.5 g/l polenta, 60 g/l sugar with wet yeast paste). For starvation experiments, 2-day-old flies were switched from protein-rich medium to a 0.1× protein-poor medium (as above but with 1.7 g/l yeast extract and 82.5 g/l polenta, 60 g/l sugar with wet yeast paste). For starvation experiments, 2-day-old flies were switched from protein-rich medium to a 0.1× protein-poor medium (as above but with 1.7 g/l yeast extract and 82.5 g/l polenta, 60 g/l sugar with wet yeast paste). For starvation experiments, 2-day-old flies were switched from protein-rich medium to a 0.1× protein-poor medium (as above but with 1.7 g/l yeast extract and 82.5 g/l polenta, 60 g/l sugar with wet yeast paste). For starvation experiments, 2-day-old flies were switched from protein-rich medium to a 0.1× protein-poor medium (as above but with 1.7 g/l yeast extract and 82.5 g/l polenta, 60 g/l sugar with wet yeast paste).

The following *Drosophila* stocks were used: *Ghe-Su(H)-lacZ (NRE-lacZ)* (Furriols and Bray, 2001), *Ghe-Su(H)-Gal4 (NRE-Gal4)* (Zeng et al., 2010), FRT82B dahl1 (Rintelen et al., 2001), FRT82B inv12 (Brogiolo et al., 2001), *UAS-dinrRNAi RII2* (a gift from B. Edgar, ZMBH, Heidelberg), *UAS-dinrdel* (Brogiolo et al., 2001), *UAS-cut5* (Krupp et al., 2005), *foxo*Δ94 and FRT82B foxoΔ494 (Slack et al., 2011), FRT82B invΔ11 (Song et al., 2003) and *string-lacZ (p[w+ stgB R6.4])* (a gift from B. Edgar, ZMBH, Heidelberg). *Tub-gal80ts*, *UAS-rpr*, *UAS-dinrRNAi*, *UAS-cutRNAi*, TRIP29625, *UAS-NRE-Gal4*, *NRE-lacZ*, *p[w+ stgB R6.4]*, *fizzy related-lacZ* and FRT82B strains were from the Bloomington Stock Center.

**Generation of mosaic clones**

Miotic clones were generated using the FLP/FRT technique (Xu and Rubin, 1993). Flies with mutant alleles recombined on FRT82B chromosomes were crossed to hsFLP::FRT82B UbiGFP flies. UASp60; FRT82B foxoΔ494 and UASp60; FRT82B flies were crossed to yw, tubgal4-UAS GFP, FRT82B, tub gal80 flies (a gift from A. Ephrussi, EMBL, Heidelberg) to generate MARCM clones (Lee and Luo, 1999). Females with the required genotypes were heat shocked for 1 h at 37°C, twice a day for 3 days, and dissected 2 days later. Mosaic mutant clones were marked by the absence of GFP (FLP/FRT) or by GFP expression (MARM). Gain-of-function clones were generated using the flip-out technique by crossing flies to hsFLP::act<CD2<gal4, UAS-GFP (a gift from D. J. Montell, MCB/UCSB, University of California, Santa Barbara). The progeny were heat shocked for 1 h at 37°C and dissected 1 or 2 days later or as indicated in the text.

**TARGET technique and refeeding experiment**

For the TARGET (McGuire et al., 2003) experiment, fed or starved *Ghe-Su(H)-Gal4, UAS GFP; tubgal80td* flies were raised for 24 h at 29°C to allow GFP expression, then switched to 20°C for 24 h. For the refeeding experiment, hsFLP::act<CD2<gal4, UAS-GFP flies were crossed to *Ghe-Su(H)-lacZ*. The progeny were fed for 2 days and heat shocked for 1 h at 37°C to induce GFP-expressing clones. Flies were then starved for 15 h and reared during different periods of time as indicated.

**Scoring of MES stage egg chambers**

The experiments described in Figs 3 and 5 were performed on separate occasions. Stage 7-10 egg chambers were scored in starved *foxo* homozygotes (Fig. 5D) because frequent morphological defects at vitellogenic stages made staging difficult. Although the ratios cannot be compared directly (due to a change in the denominator), the relative increase in MES is similar, with a doubling of MES (1 to 2 in Fig. 3 and 0.2 to 0.4 in Fig. 5). Furthermore, the percentage of MES versus stage 7-10 egg chambers was similar in the two conditions (9% in starvation conditions compared with 13% in homozygous *foxo* flies; data not shown).

**Ploidy measurement**

Flies were dissected, ovaries fixed and mounted in VECTASHIELD with DAPI (Vector Laboratories). Series of z-sections at 0.45 μm increments were acquired with a Zeiss LSM710 with 40× objective (zoom 7). Images were processed and analyzed using ImageJ (NIH). DAPI integrated density (intensity×area/cell) was scored for each nucleus. Nuclei from stage 5 and 6 egg chambers were used as diploid control cells and compared with *intr15* mutant clones from stage 7-9 egg chambers. Results were analyzed using Student’s t-test for non-parametric distributions (n≥50 for both control and mutant cells).

**EdU labeling**

Ovaries from fed or starved flies were quickly dissected in fresh PBS/EdU followed by a 1 h incubation in the same buffer before fixation. Staining was according to the manufacturer’s protocol (Click-iT EdU Alexa Fluor Imaging Kit, Invitrogen).

**Immunohistochemistry and microscopy**

Antibody staining was carried out according to standard protocols. The following antibodies were used: mouse anti-Cut (1:100; 2B10, DSHB), rabbit anti-Cut (1:500; a gift from Y. N. Jan, UCSF, San Francisco), mouse anti-Hnt (1:100; 1G9, DSHB), mouse anti-Notch intracellular domain.
(1:15; C17.9C6, DSHB), rabbit anti-FoxO (1:500; a gift from P. Léopold, W. M. Deng, A. Ephrussi, S. X. Hou, Y. N. Jan, P. Léopold, D. J. Montell, L. Partridge, L. Pick, H. Stocker, G. Struhl and R. Ueda for sharing reagents and fly lines; the TRIP at Harvard Medical School [NHN/IGRNS R01-GM084947] for transgenic RNAi fly stocks; the Bloomington Stock Center and Developmental Studies Hybridoma Bank (DSHB) for reagents; the iBV PRISM imaging facility for advice and support; the anonymous reviewers for their suggestions; and members of the laboratory and P. Léopold for discussion and comments.

Competing interests
The authors declare no competing financial interests.

Author contributions
P.J. and S.N. designed the experiments; P.J. and C.G. performed the experiments; and P.J. and S.N. wrote the manuscript.

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Supplementary material
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