Supporting Information

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SI Methods

Histological Sections. The ovaries were those described in ref. 1. Sections were scanned visually to identify large follicles and were photographed using a Leica DM6000 microscope.

GC Monolayer. Ovaries were harvested from *Fshb*$^{+/-}$ and *Fshb*$^{-/-}$ females at P21, and granulosa were isolated (see *Methods* in the main text). Cells then were seeded onto glass chamber-culture slides (Becton Dickinson) and cultured in MEM (Gibco) supplemented with 5% (vol/vol) FBS (Life Technologies) at 37 °C in an atmosphere of 5% CO_2 in air. Bright-field images of the monolayers were taken with a Zeiss LSM 510 confocal microscope.

Quantitative PCR Analysis. Ovaries were harvested from *Fshb*$^{+/-}$, *Fshb*$^{-/-}$, eCG-injected *Fshb*$^{-/-}$, and eCG-injected *Fshb*$^{+/-}$ females at P16, P18, or P21/23, depending on experiment. Follicles, COCs, or GCs, depending on experiment, were collected and treated accordingly. RNA extraction followed by cDNA synthesis and quantitative PCR then were performed (see *Methods* in the main text). Primer sequences are given in Table S1.

1. Demeestere I, et al. (2012) Follicle-stimulating hormone accelerates mouse oocyte development in vivo. *Biol Reprod* 87(1):3, 1-11.

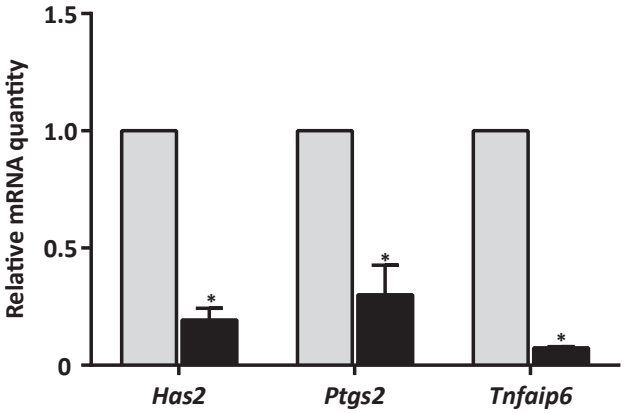

Fig. S1. Quantities of *Has2*, *Ptgs2*, and *Tnfaip6* are higher in the COCs of *Fshb*$^{+/-}$ females (gray bars) than in the COCs of *Fshb*$^{-/-}$ females (black bars) at P21/23. Data were analyzed using a single-sample *t* test. *$P < 0.05$.

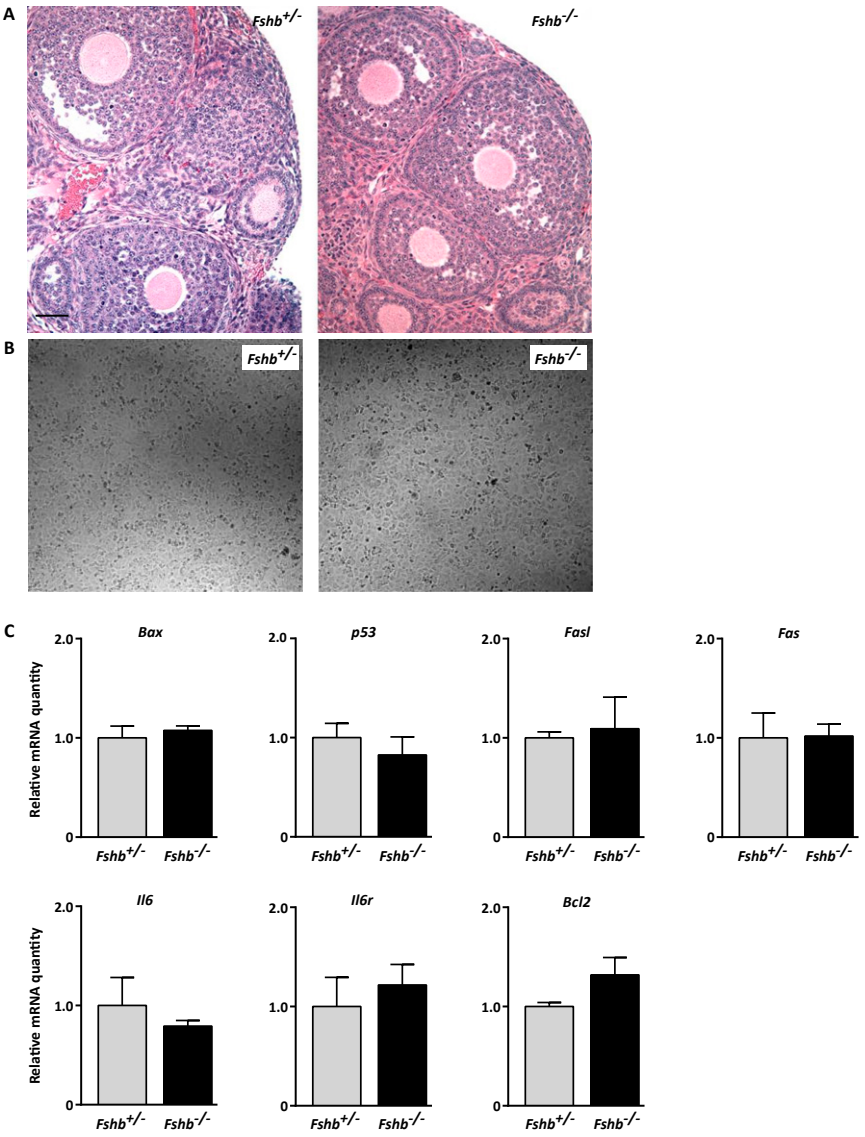

Fig. S2. (*A*) Histological sections of ovaries of *Fshb*$^{+/-}$ and *Fshb*$^{-/-}$ females at P24. Ovarian follicles of the *Fshb*$^{-/-}$ females do not contain an increased number of pycnotic or otherwise abnormal nuclei. (*B*) GCs of *Fshb*$^{+/-}$ and *Fshb*$^{-/-}$ females form morphologically indistinguishable monolayers in vitro. Shown are bright-field images of monolayers formed by GCs of *Fshb*$^{+/-}$ and *Fshb*$^{-/-}$ females collected at P21 and cultured for 3 d. (*C*) Quantities of mRNAs encoding proapoptotic and antiapoptotic factors are similar in follicles of *Fshb*$^{+/-}$ and *Fshb*$^{-/-}$ females. Quantitative PCR analysis of the proapoptotic factors *Bax*, *p53*, *Fasl*, and *Fas* and the antiapoptotic factors *Il6*, *Il6r*, and *Bcl2* in follicles of *Fshb*$^{+/-}$ females (gray bars) and *Fshb*$^{-/-}$ females (black bars) at P18. Data were analyzed using a two-sample *t* test. *P* values <0.05 were considered statistically significant.

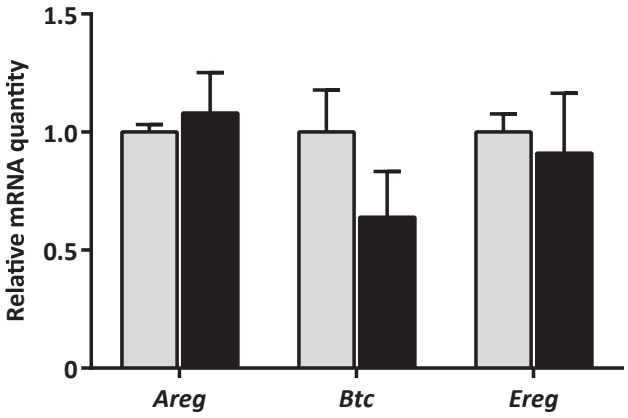

Fig. S3. Quantities of *Areg*, *Ereg*, and *Btc* are not significantly different in the GCs of *Fshb*$^{+/-}$ females (gray bars) and *Fshb*$^{-/-}$ females (black bars) at P21/23. Data were analyzed using a two-sample *t* test. *P* values <0.05 were considered statistically significant.

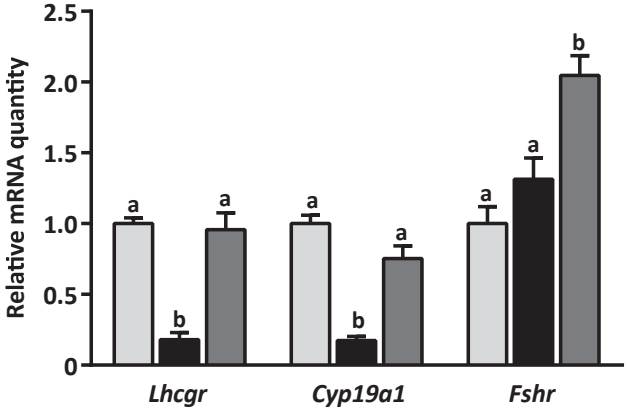

Fig. S4. Quantities of *Lhcgr*, *Cyp19a1*, and *Fshr* in follicles of P18 *Fshb*$^{+/-}$ females (light gray bars), *Fshb*$^{-/-}$ females (black bars), or eCG-injected *Fshb*$^{-/-}$ females (dark gray bars). Data were analyzed using one-way ANOVA and Tukey HSD. Different letters above bars indicate $P < 0.05$.

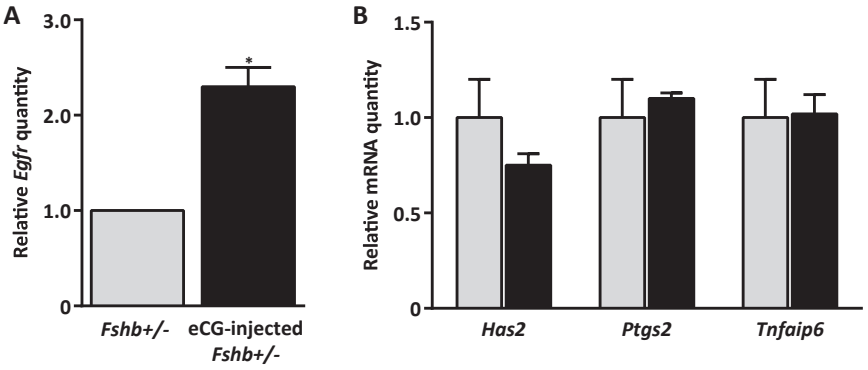

Fig. S5. (*A*) Quantity of *Egfr* in follicles of *Fshb*$^{+/-}$ and eCG-injected *Fshb*$^{+/-}$ P18 females. Data were analyzed using a single-sample *t* test. *$P < 0.05$. (*B*) Quantity of *Has2*, *Ptgs2*, and *Tnfaip6* after EGF stimulation of follicles of *Fshb*$^{+/-}$ females (gray bars) and eCG-injected *Fshb*$^{+/-}$ females (black bars) P18. Data were analyzed using a two-sample *t* test. A *P* value <0.05 was considered statistically significant.

Table S1. Primer sequences used for quantitative PCR analysis

Gene/transcript	Primer sequence
Actb	F: 5′-GGCTGTATTCCCCTCCATCG-3′
	R: 5′-CCAGTTGGTAACAATGCCATGT-3′
Areg	F: 5′- CCTTCTGGCAGTGAACTCTCCAC-3′
	R: 5′-GGTCCTTGTCATCCTCGCTGTGA-3′
Bax	F: 5′-CGAGCTGATCAGAACCATCA-3′
	R: 5′-GAAAAATGCCTTTCCCCTTC-3′
Bcl2	F: 5′-TAAGCTGTCACAGAGGGGCT-3′
	R: 5′-TGAAGAGTTCCTCCACCACC-3′
Bmp15	F: 5′-GAGCGAAAATGGTGAGGCTG-3′
	R: 5′-GGCGAAGAACACTCCGTCC-3′
Btc	F: 5′-CGGGTAGCAGTGTCAGCTC-3′
	R: 5′-CGATGTTTCCGAAGAGGATG-3′
Cyp19a1	F: 5′-ACACGTCTGGTCTCCTGCTAGAGT-3′
	R: 5′-GATCCACCGTAAGCAACTGGGTTT-3′
Egfr	F: 5′-GTGGAGGGACATCGTCCAAA-3′
	R: 5′-ATTGGGACAGCTTGGATCACAT-3′
Ereg	F: 5′-AACTCAGGAACAATTTACGTCTCTG-3′
	R: 5′-GCTTTGGTTCTCAGTATAGAGAGAGA-3′
Fas	F: 5′-GAGAATTGCTGAAGACATGACAATCC-3′
	R: 5′-GTAGTTTTCACTCCAGACATTGTCC-3′
Fasl	F: 5′-TTAGCTTCTCTGGAGCAGTCAGCGTC-3′
	R: 5′-CCTTCTTCTTTAGAGGGGTCAGTGGC-3′
Fshr	F: 5′-CAGGTCAACATACCGCTTGA-3′
	R: 5′-GATCCCCAGGCTGAGTCATA-3′
Gdf9	F: 5′-GCTCTATAAGACGTATGCTACC-3′
	R: 5′-CAGAGTGTATAGCAAGACCGAT-3′
Has2	F: 5′-AAGACCCTATGGTTGGAGGTGTT-3′
	R: 5′-CATTCCCAGAGGACCGCTTAT-3′
Il6	F: 5′-AGAGGATACCACTCCCAACAGA-3′
	R: 5′-ATCTCTCTGAAGGACTCTGGCT-3′
Il6r	F: 5′-CACTCCTTGGATAGCAGAGCC-3′
	R: 5′-GACACAGAGAAGCAACCCAAAC-3′
Lhcgr	F: 5′-CGGACCCTCCCAGATGTTTCG-3′
	R: 3′-GTGGCGATGAGCGTCTGAAGT-3′
Ptgs2	F: 5′-CCTTCCTCCCGTAGCAGATG-3′
	R: 5′-ATGAACTCTCTCCGTAGAAGAACCTT-3′
p53	F: 5′-GGAGTATTTGGACGACCG-3′
	R: 5′-TCAGTCTGAGTCAGGCCC-3′
Tnfaip6	F: 5′-GATGGTCGTCCTCCTTTGCTT-3′
	R: 5′-TATCTGCCAGCCCGAGCTT-3′