Supplementary Table 1: Follicle size, time of surgery in relation to hCG treatment, preoperative serum hormone concentrations, menstrual cycle day at the time of surgery, menstrual cycle length, and age of the study population. All data are given as means ± SEM.

	Preovulatory phase	Early ovulatory phase	Late ovulatory phase
Follicle size (mm)	15.9 ± 0.7 range 14.0 – 17.0	17.1 ± 0.8 range 15.0 – 19.0	17.2 ± 0.8 range 15.0 – 20.0
Hours after rhCG		14.0 ± 0.9 range 12.0 – 18.0	21.9 ± 0.8 range 19.0 – 24.0
Progesterone (nmol/L)	0.4 ± 0.04 range 0.3 – 0.5	1.2 ± 0.22 range 0.5 – 1.9	2.1 ± 0.3 range 1.5 – 3.0
Estradiol (nmol/L)	0.5 ± 0.1 range 0.2 – 1.0	0.6 ± 0.1 range 0.4 – 0.9	0.7 ± 0.1 range 0.6 – 0.9
Cycle day of surgery	14.0 ± 0.3 range 13 – 15	12.6 ± 0.5 range 11 – 14	13 ± 0.6 range 11 – 15
Cycle length (days)	29.0 ± 0.6 range 28-35	27.2 ± 0.5 range 26 – 28	29.4 ± 0.9 range 28 – 32
Age (years)	35.4 ± 1.2 range 31 – 38	33.8 ± 1.4 range 30 – 38	37.4 ± 1.4 range 36 – 38

All the patients recruited had a planned laparoscopic sterilization as a means of contraception and participated in the study voluntarily.

Supplementary Table 2: Antibodies used for immunohistochemical, Western blot, and ChIP analyses.

Target protein	Immunogen	Entrez-Gene ID	Host	Clonality	Isotype	Name of Antibody	Manufacturer, Catalog #
FOS	Synthetic peptide corresponding to the sequence of human c-FOS	2353	Rabbit	Mono-clonal	IgG	c-Fos (9F6) Rabbit mAb	Cell Signaling, #2250
JUN	GST-c-JUN protein derived from the N-terminal sequence of human c-JUN	3725	Rabbit	Mono-clonal	IgG	C-Jun (60A8) Rabbit mAb	Cell Signaling, #9165
JUNB	Synthetic peptide corresponding to residues surrounding Pro169 of human JUNB	3726	Rabbit	Mono-clonal	IgG	JunB (C37F9) Rabbit mAb	Cell Signaling, #3753
JUND	Synthetic peptide corresponding to residues surrounding Pro250 of human JUND	3727	Rabbit	Mono-clonal	IgG	JunD (D17G2) Rabbit mAb	Cell Signaling, #5000
PGR	Synthetic peptide corresponding to residues surrounding Tyr541 of human PR	5241	Rabbit	Mono-clonal	IgG	PR A/B (DbQ2J) XP® Rabbit mAb	Cell Signaling, #8757
RNA polymerase II	Synthetic peptide YSPTSpPS corresponding to human RNA pol II	5430	Mouse	Mono-clonal	IgG	RNA pol II mAb	Active Motif #39097
Rabbit Control IgG for IHC	No immunogen	-	Rabbit	Mono-clonal	IgG	Rabbit (DA1E) mAb IgG XP® Isotype Control	Cell signaling, #3900
Rabbit Control IgG for ChIP	No immunogen	-	Rabbit	Poly-clonal	IgG	Normal Rabbit IgG	Cell Signaling, #2729

Secondary antibodies	Conjugants	Host	Isotype	Application	Manufacturer, Catalog #
Goat anti-rabbit antibody	HRP-labeled polymer	Goat	IgG	Immunohisto chemistry	Dako, K4065
Goat anti-rabbit antibody	HRP	Goat	IgG	Western blotting	Santa Cruz Biotechnology, #sc-2030

Supplementary Table 3: Primer sequences (Forward and Reverse) used for real-time PCR analyses and ChIP assays

Genes	Accession No.	Forward primers	Reverse primers
For Real-time PCR			
FOS	NM_005252.3	AGGAGAATCCGAAGGGAAAG	CTTCTCCTCCAGCAGGTTGG
JUN	NM_002228.3	TGACTGCAAAGATGGAAACG	GGGTCATGCTCTGTTTCAGG
JUNB	NM_002229.2	TTAACAGGGAGGGGAAGAGG	CACAGTACGGTGCAGAGAGG
JUND	NM_005354.5	AGGCCCTGGAGGATTTACAC	CTCAGGTTCGCGTAGACAGG
PTGES	NM_004878.4	GCTGATCACACCCACAGTTG	CCAGGAAAAGGAAGGGGTAG
SLCO2A1	NM_005630.2	TCAACATGAGCTCTGCAACC	ATCAACAAGAACTGCACCCC
ABCC4	NM_005845.4	GGCTTGTGCTCTGAAAAAGG	CTGAGAGGATCGTCCAGGAG
RNA18S5	NR_046235.1	GTAACCCGTTGAACCCCATT	CCATCCAATCGGTAGTAGGG
For ChIP assay			
FOS		CACCCCCTTCAAATGTCTTC	GCCCTAATTCAGTGCAAAGC
PTGES		GGCTAAAGGGATCAGCAGTG	TCTGCACGTGGTGATTATCG
SLCO2A1 (1)		ACCTCCTTCCCTCCCTCTC	CCTCTTTTCCTCGGGTGTC
SLCO2A1 (2)		CATTCCAGCACTGAGAAGGAG	GTCTCTGGACCTGAGCCAAG
ABCC4 (1)		CGACAGCATTCATCCATCTC	AGGCTCTTCAACCTGTGAGC
ABCC4 (2)		CCTCCATGACAATCATTTGG	CTGTCGTCAAGCCCTAAAGC

Supplementary Table 4. Relative abundance of FOS, JUN, JUNB, and JUND staining in granulosa and theca cells of human periovulatory follicles

		Pre	EO	Late
FOS	**GC**	-	+	+++
	Th	-	+	+++
JUN	**GC**	-	+	+
	Th	-	+	+
JUNB	**GC**	-	+++	+++
	Th	-	+++	+++
JUND	**GC**	-	+++	+++
	Th	-	+++	+++
IgG Control	**GC**	N/A	N/A	-
	Th	N/A	N/A	-

Staining intensity: −, no staining detected; +, weak; ++, moderate; + + +, Strong. N/A, Not Available. GC, granulosa cells; Th, theca cells.

A. Sequence of human *FOS* gene

−1517 AGCAGGATCTCCTGGCTCCCGGGCGCGGCGGCTGGAGGCAGGTCTGCGGTCCGGCTCCCCGCGCGCGCCCCGAACTATCCGCCCGCCGGCCTCATCCTGCCT

−1417 CGCCCCTCTCCAGGTGCCCACCGCGGGCCCCGACCCCCGGGCCCGAAGAGTGGAGAAGGGAAGACCGGGGCTGTGCGGGGACATGCGTCTTCGCGCCCTG

−1317 GAGGTGGCCAGCGCGCTGGGGCTGAGCCCCGGCAGCGTGACCCCGGCTGTCCTACGCAGCAGGGCAGGAGATTGGGGGGCGTGGCACACTCTGGAGCACC

−1217 TTGCCTCCCCAAAGCCᴄCGTGTTᴄCAGGACGTGGAGCCGCTCCTGGGGTCCCAGCAGTCGAGGTATTCCGCCCAGGCGCAGCTGGACACTGTCCTTCCAG
PRA & PRB[-1196]

−1117 CCCCCGTCCTCCACCCTCCAAGTCCGCGCTGGAAAAATCACCCGCTGCGGGCTCCCGTAAGCACAGCTTCCTGGCGGGACCGAACCAGCCCTCAGCGCAGA

−1017 TTTGAGTTCCCCGCAGGAAGCACACCCCGCCTTGTCATCCCGAACTGACCACCCTGCCCACATAACCACACCTCGCACTCCCTACCCCTGGGGCCCAGCT

−917 CAGAACCGGGCAGAᴄ**CACCCCCTTCAAATGTCTTC**GCACGTAGGTTTTGCAᴄCAGTGTTᴄTATCTGCTGGTGTCTCAGGGATTTGACAGTTTCCTTAATATTC
primer - F   **PRA & PRB**[-861]

−817 CCACACATGGCCGAGAAAAATAAATAAATAAATGCGCTGTCTTCTTTAAAAAAAATAAATAAATAAAGTACCCAGTATCGTAAAGTAGGTTATCGTATTCT

−717 CTTATTTTGGATCCTCCACTTTCTGCTTCCAAACGCAGGᴀACAGTGᴄTAGTATTGCTCGAGCCCGAGGGCTGGAGGTTAGGGGATGAAGGTCTGCTTCCA
PRA & PRB[-672]

−617 ᴄ**GCTTTGCACTGAATTAGGGC**TAGAATTGGGGATGGGGGTAGGGGCGCATTCCTTCGGGAGCCGAGGCTTAAGTCCTCGGGGTCCTGTACTCGATGCCGT
primer - R

−517 TTCTCCTATCTCTGAGCCTCAGAACTGTCTTCAGTTTCCGTACAAGGGTAAAAAGGCGCTCTCTGCCCCATCCCCCCCGACCTCGGᴄAACAAGGᴄGTCCGC
PRA & PRB[-424]

−417 ATTGAACCAGGTGᴄGAATGTTᴄCTCTCTCATTCTGCGCCGTTCCCGCCTCCCCTCCCCCAGCCGCGGGCCCCGCTCCCCCGCACTGCACCCTᴄGGTGTTᴄ
PRA & PRB[-397]   **PRA & PRB**[-318]

−317 GGCTGCAGCCCGCGAGCAGTTCCCGTCAATCCCTCCCCCCTTACACACAGGATGTCCATATTAGGACATCTGCGTCAGCAGGTTTCCACGGCCTTTCCCTGT

−217 AGCCCTGGGGGGAGCCATCCCCGAAACCCCTCATCTTGGGGGGCCCACGAGACCTCTGAGACAGGAACTGCGAAATGCTCACGAGATTAGGACACGCGCC

−117 AAGGCGGGGGCAGGGAGCTGCGAGCGCTGGGGACGCAGCCGGGCGGCCGCAGAAGCGCCCAGGCCCGCGCGCCACCCCTCTGGCGCCACCGTGGTTGAGC

−17 CCGTGACGTTTACACTCᴀTTCATAAAAᴄGCTTGTTᴄATAAAAGCAGTGGCTGCGGCGCCTCGTACTCCAACCGCATCTGCAGCGAGCATCTGAGAAGCCAA
→TSS   **PRA & PRB**[+12]

+84 GACTGAGCCGGCGGCCGCGGCGCAGCGAACGAGCAGTGACCGTGCTCCTACCCAGCTCTGCTCCACAGCGCCCACCTGTCTCCGCCCCTCGGCCCCTCGC

+184 CCGGCTTTGCCTAACCGCCACG**ATG**ATGTTCTCGGGCTTCAACGCAGACTACGAGGCGTCATCCTCCCGCTGCAGCAGCGCGTCCCCGGCCGGGGATAGC

B. Sequence of human *PTGES* gene

```
-1385  TGATGACCCCGAAGGCTCAGCGCCCTGATGGAGGCAGATGGGGCCTTTTAACCCCTGCTGGGGAGCGGCTGCCTGGGGAGGGGGCAACTCACCTGCGGTGG
            c-Fos⁻¹¹¹²

-1285  GGGGTGAAAGAGCGGGTTTTTAAGGGGACCATCCAAGCCAAGAAAGCAAGGAGCAAAGAGAAGAGCTCAGCAGCTCTCCCCAGACCCCTCCACCTTGAGCTT

-1185  GGGAAGTGGAGGGCGGTGGGGAAAGTTGGGGAGGAAAAGTGTGAGGGTTGATGGTGTGGAGGGGAGATGTACGGAGGGGCGTGGGGGTAGGGGGAGGGAG

-1085  TGGGGATGGGGGAGGGATGGGGTATGAAAGGGAGGCGTGGGGGGTGTGGAGAAGGGGTGGATATGGAAGGGAGGGGTAGGGGTGGGGTGGGTGTTGGGGA

 -985  TGAGTGTGGGGGGAGGGGTGGGTATGGAAAGGAGGGGCAGGGGTCGGGGTGGTTGTGGGGGAAGATTGGGACATGGAAGGGAGGGGTGGGGTGGGGTGGGT

 -885  GTTGGGGATGTGTGTGGGGGAGGATTGGGGTATGGAAGGAAGACAGGGTGGGGTGGGGTGGGTGAGGGTGTTGTGGGAGTGGTGCGTATGGAAGGGAGGC

 -785  TTGGGTTGGGCTGGGTTGGGGGTGGGTGTCGGGGAGTGGTGGGTATGGAAGGGAGGTGGGGGTGGGAGACAGATGGGCATAGAAATGAGGTGTAAGTGTG

                      primer - F
 -685  GGAGGGGCTAAAGGGATCAGCAGTGTGGGGTCACGAGCCTCTGGCCCTTATCAGGGAGTCTGGGGCTGTGGGTCACGCGGGATGGGCTTGGCATGGCTG
                                  c-Fos⁻⁶⁵⁹                                    c-Fos⁻⁶¹⁰

 -585  GCTTTGTTTCCTAAGAGGACCTCTGGCTCTGCCGTGGGAGGGCAGGGGGTGTGGACAGCCAGGCAGTGGACACAGTGGGCAGTGGCATGGCTCTTGCTTC

 -485  CCCAGTGGCTTGGACAGTCCCCTGGCTACTCGCCCAGGAGCTGGAGGACCCAGGTGCGGGGGAGAGAAGAGAGGGGCAGTACCCAGGATGGGGGGCGCAT

                                                          primer - R
 -385  GGCGTGGTTCTCATGCCCACCACCTACCCTGACCCTCGGAGGTGGGCAGGAGGCAGCGATAATCACCACGTGCAGAGGTCCTGCCAGGTGCCCAGCCTC
                                  c-Fos⁻³⁵⁰

 -285  ATCATTCCCTAGAAGGCAGGCACCACCACATGCTCCCACACTGTAGATAAGGAAACAGCTTTGAAACAGATTTGAAAGTGTTTGAGGATTTGCCTGGAAG

 -185  GAGGGCTCCAGAGCCAGGGACTGGGTCGGGACACCCGGAGACTCTCTGCTTCTTGGAGCTCCGGCAACTGCTTGTCTTTCTCTTCACAGGAGAAGGGGG

  -85  CCCTGCTGCCGCTGCCGTGGGGCGGGGCGTGGGCGGTGCTGGCTGCAGGAAGGCTCTCCCCTCCCACTTTGTGCTTTCCCTGCAGGCTGCTCCTCTGTCG
                                                                                            └→TSS

  +15  AGCTGATCACACCCACAGTTGAGCTGCGCTGGCCAGAGATGCCTGCCCACAGCCTGGTGATGAGCAGCCCGGCCCTCCCGGCCTTCCTG
```

C. Sequence of human *SLCO2A1* gene

−1434 GGCTGAATTCAGGGTCCAGCTCCACCACTTGCTAGCTGTGTGGCTTTCAGACAGCTTTCTTAGCCGACTGCTCTAGCATCCTTGTTTGTGGAGTCCAGAC

−1334 TCCATCAGTACCTATACCTGTAGGGCTAACGTTGGGGCTTCATGAAATCATGCATGTGGGTGCTCAGCAGAGGGCCTGGTATGCCCAGCACACACCAAGT

−1234 GCTCCATGCTGGTACCTGTCCTTGTGTGCCATGTTCTCCCAGTGGACAGATGGGACCTGGAATTCATGCCTCCTCTGGGGCTGGGGCTGGGGCTGCTACA

−1134 GTGCTGTGGAAAG[CCTGTCAG]GATGTACCTCGCTCTGTGGCTGAGTGAAGAGGCCAGAGGCTGCCCACTGTTCAACATCTTTGGAATGCTGCCGTGTCCA
         c-Fos-1112

−1034 GGGAACTTGGGTCGCAGGTGGATAGAAGCCCCCAAGCCCAGGCCAGGCCAGACCAGGCCCAGAAAGGTATCAGGTCTTGGGTAGAATAAGAAGCCTATGT

−934 GGTCTATCTATCCTGTGGCCTTTGTCTTAGCCAAAGCCTCCTGGATA[TTGACGGC]ATCTTTTCCTGGGTTTGGGGTGGGCTTGGAGAGGTTCCCTCTGCA
                                                      c-Fos-878

−834 CGGGACTACAGAAGTGAGGGAGCTGGAAAAATGCCTCCAGAGCTGGATTCCTCACTGCAGCTGCTTTTGGAAGAACCTTCTTATCCTTCCCTTGAGAAGC

                                                                                         primer - F
−734 CTCACTGTCTCTTCTCGGCGCTTGGAATCCTGTTAGTAGAAAATCTTGGGGAAAAAATAAACCCACTATT**CATTCCAGCACTGAGAAC**[GAG]GTCAGTGGG
                                                                                          c-Fos-639

−634 GTGCGTCCTGTTTGTCCACACCCCCCCCACCCCCTCTACCCCTCCCCCCAGCACCCCAGGCCAGACCCAGCCATG[CTGACAC]T[TGACAGC]CCCTGCAGTT
         primer - R   **c-Fos**-545
−534 TAC**CTTGGCTCAGGTCCAGAGAC**TTCGGGCCCAGCCCCCACCTTTTCACCTTGTTACCCAGCCCCCTCTCCAGCGCAAAGAGCAGTTTAAATATAAATCA

−434 GTCCTCAACACAAACAGAGCTGCAGCGAGTCTCAGAGCCATCACCGGAACTGAGGGCCCAGGTTTTCTGCGAGTGCAAACAAGCAGAGACTGGCTCCGTA

−334 AATCTCCCCAAGAACGTCGGGAGGGGTGCTGGGGCTCCCCTCCACCCCCGGCTCACGTTGGCCCCTCCAGCGCCCGCCTCGGGCACCCTCATATCCCAGC

−234 CTTCCTGCCCCCCAGCCCTGCCAACCTCTTTCTCCATCCCCTCCACTCACCCACCTTCGCTTCGCCCACCCTCTCTTCGCCAGTCCCCAGGAACCTCCAC

−134 CCCCTTGCAACCTCCTGCCCCCGCACAGCCCTCACCTCCCCTCCCGGGCCCGCCACCTCCTTCCCTCCCTCTCCGCCTCCCGGCAGGCGGGATCTTCTC

      c-Fos-23
−34 GGG[GCAGTCAA]GCCTCGCGGGTCGCTG[CGGCGTCAC]ACCTGTCTGAGGGGGCGGCGGCGGCGGCGGCGGCGGCGGGGCGGGGGCTCGTAGCGCC[TTGACACC]
                                 c-Fos+2 →TSS   **c-Fos**+65

+66 CGAGGAAAAGAGGGAGGAGGGAGAGCGCGTTTCATCATCGGCGGCGGCCACTTATAAAAACTTCTAGGCGCGCACTCGCTGGCTCAGTCTCCGCTCCGCG

+166 AATCTCCTCCGGCCACTGCCGCCGCGGTCGCCTCTCACCCGCCCGGCCGCTCCAGCCCGAGGCGCCCCGACCCCGCGCCACTCCGCGCCCGGCCAGCCGC

+266 CCGCAGCCC**ATG**GGGCTCCTGCCCAAGCTCGGCGCGTCCCAGGGCAGCGACACCTCTACTAGCCGAGCCGGCCGCTGTGCCCGCTCGGTCTTCGGCAACAT

+366 TAAG

D. Sequence of human *ABCC4* gene

```
-1534  CAACCAGCATATTCTGGGCACTTCTCATGCACACTGGCCATCCACCAGGGAGACAGGCCATGCTTAGACATAGGCTTATTGCAAATCATGTTTTATCCTT

-1434  TCTTGGCTCTAAGACTGGACAAGTTCTGCCTTTCAGCTTCACCTTCCTCATCTATAAAGTAAGGATAACCTTGAATGGGGCACTGATAGAATTAAAAGTG

-1334  AGATAATTGGTCGGGCGTGGTGGTACATGCCTGTAATCCTAGCACTTTGGGAGGCCACGGTGGGAGGATCACTTGAGCCTAGGAGTTTGAGACCAGCCTG

-1234  GGCAACAAAGTGAGAAATTATCAAGGAACAATAAAATGATCTTATTACAAAGAAAACCAAATTCTCAAACATGCATGAAATATGAAGAAAATAAACCTCC
```
2nd primer - F
```
-1134  ATGACAATCATTGGCTTCAAAAATTATCAGTATTTGAACTTGGAGCCTTTGATTTTGATTTTTGCATCTCTACAAAAATTACAAAATATGAGCCGGGTG
```
c-Fos-1127
```
-1034  TGGTGGCGGGTGCCTGTAGTCCTAGCTACTTAAACTGAGTTGGGAGGATTGCTTGAGCCCTGGGAGGTCGAGGGTGCAATGAGCCATAATGTGACACTG
```
c-Fos-936
```
 -934  TGTGTGAGACTGCCACACACACACACACACACACACACTAGTGAGGCTACGCACTCAGAAATGCACATGAACATCACTGGTATTCTGGAACCCACGTGTC
```
2nd primer - R
```
 -834  GTTTGCCACTGTTATCTGTTAGGCTTTAGGGCTTGACGACAGAAATCATCAGGCAGTCTCTCTTTCCTCTTATATTCCTTTCCCAATCTAAGGGGGCAGC
```
c-Fos-799   **1st primer - F**
```
 -734  AAAAAGCTCAGAGGTCCACCGTAGCATGCAACATGTGAGATGCCTAAAGCCCGCCCCCATGGACGACAGCATTCATCCATCTCCCGGAATTCATCTGGGTC
```
c-Fos-632
```
 -634  ATACTCTCGAGTTACCCGGCTTTCTTGAGGTCTTGCAGCTCTACAAGGATAATCTGTGGCTAAACTTTGCTGTCGTCCAAGGTCAAATGTTTGGCTCACA
```
1st primer - R   **c-Fos-548**
```
 -534  GGTTGAAGAGCCTCCCATGGCACCGTCGTTTGGTCCTGAGAAGGGAAAGGCGCCCAGGGGCGGGCTGCTAGAGCACGAGGCAGCTGTCTCCCAGTCTTC

 -434  CCAAACCCGTAGCCGAGGGGGCGTTTCTGCGGCGCAGGGGCGGGCACAGCCGACGCCTCCCTGCTCCACCTTCTGTGTCGGCGCCTAGACTCGGATAGTG

 -334  AATTTCGGAAAGTTTCACTCGGGTTCGTGCACGTGGGCACCTCCGGACCCGGCCTCCTTGCCGCGCGCTCTGCTACCCTCTCCATCCAGCGGCGCAGGCG

 -234  GCCCTCGCCTCACCCCTGGGCGTAGCTCTGGGCTCCCTTTGGCGTCGCCAGCTTCGCCTCCTCCCGCCGCGGTCTCCTCCCGCCGCGGTCACCGTCGGTCC
```
c-Fos-145
```
 -134  CGGCCGCGCTCGCACGCGGTGCGCAGCTCCCGGGCTCCAGGCGGCGGCGCGTAGCGGGCGCGCCCCGAGGCGGCGGGCCTGAGAGGCGGGGACGGGGCGTG

  -34  CCGCCGGCGCGCCCGGCTCCCGGAAGCGGGCTGCTTCACAGGCTCCAGCCGAGCGGACAGGCGTGGCGGCCGGAGCCCCAGCATCCCTGCTTGAGGTCCAGGA
```
→TSS
```
  +66  GCGGAGCCCGCGGCCACCGCCGCCTGATCAGCGCGGACCCCGGCCCGCGCCCGCCCCGCCCGGCAAGATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACC
```

Supplementary Fig. 1: Transcription factor binding motifs in nucleotide sequences of promoter regions for human FOS, *PTGES*, *SLCO2A1*, and *ABCC4*.

Promoter sequences of human *FOS* (A), *PTGES* (B), *SLCO2A1* (C), and *ABCC4* (D) were analyzed using a genomic library. Nucleotide sequences are numbered from TSS at +1. The sequences of the oligonucleotide primers are colored in red. Putative PRA, PRB, or c-FOS transcription factor binding sites (highlighted in black boxes) are predicted by TFSEARCH.
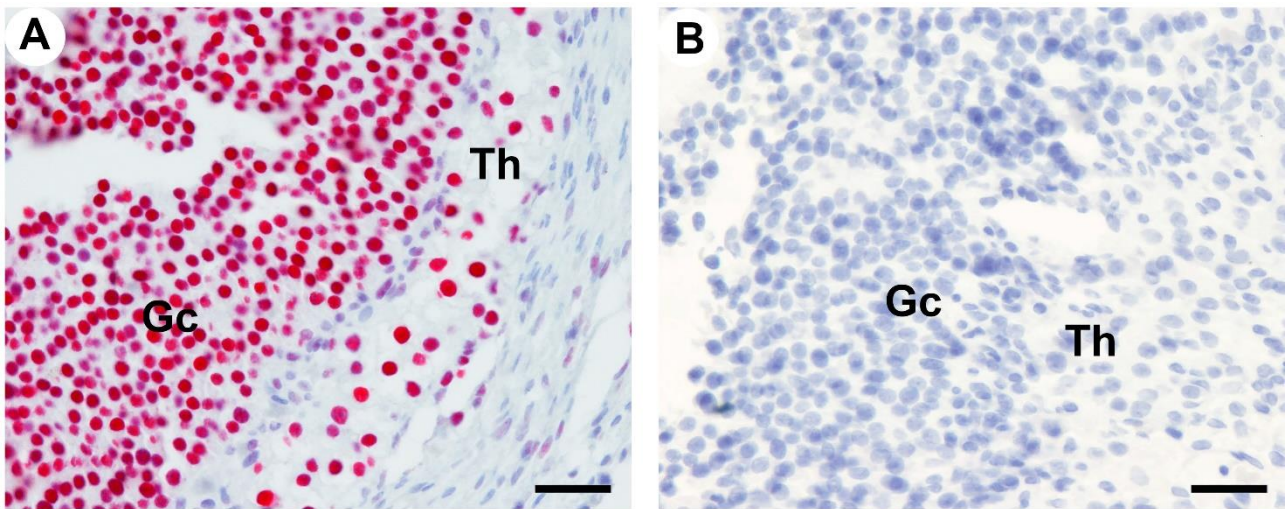
Supplemental Fig. 2: Immunohistochemical analyses of human periovulatory follicles with the antibody for JUND and rabbit IgG as a negative control.

Paraffin-embedded sections of dominant follicles collected during the late ovulatory period were subjected to immunohistochemical analyses by incubating with the antibody for JUND (A) and concentration matching normal rabbit IgG (B) as a negative control. The red/pink staining represents immunopositive staining for JUND. The section was lightly stained with hematoxylin (blue) for nuclear staining. Gc, granulosa cells; Tc, theca cells. Scale bar, 100 μM for all the images.
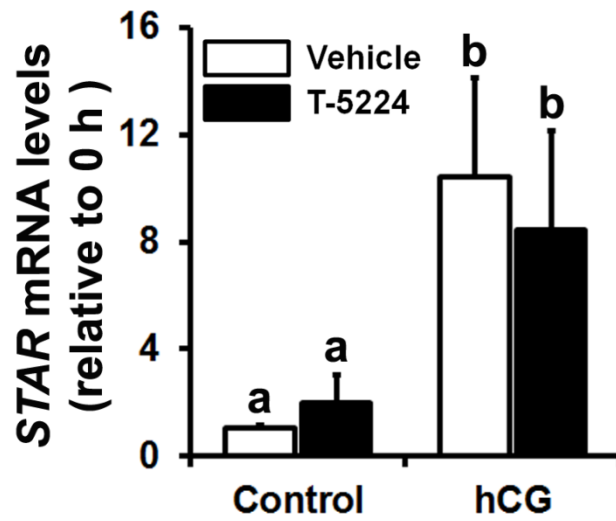
Supplemental Fig. 3: Effect of FOS inhibitor on the expression of mRNA for *STAR* in hGLC.

Primary hGLC were treated with or without T-5224 (FOS inhibitor, 20 µM) in the absence or presence of hCG (1 IU/ml). The levels of mRNA for *STAR* at 12 h were measured by qPCR. The levels of transcripts were normalized to those of *RNA18S5* mRNA in each sample (n = 3 independent experiments). Bars with no common superscripts in each time point are significantly different ($p < 0.05$).