

Figure S1: Somatic cell manipulation of β -catenin in the developing gonad
E14.5 (A) Control ovary (No Cre; *Ctnnb1*^{F/F}) and (B) mutant ovary (*Sf1Cre; Ctnnb1*^{F/F}) β -catenin green, DAPI blue. The remaining β -catenin in the mutant ovary resides in the germ cell membrane. E14.5 (C) Control testis (No Cre; *Ctnnb1*^{Δex3/+}) and (D) mutant testis (*Sf1Cre; Ctnnb1*^{Δex3/+}) β -catenin green, DAPI blue. β -catenin is highly stabilized in the mutant testis.

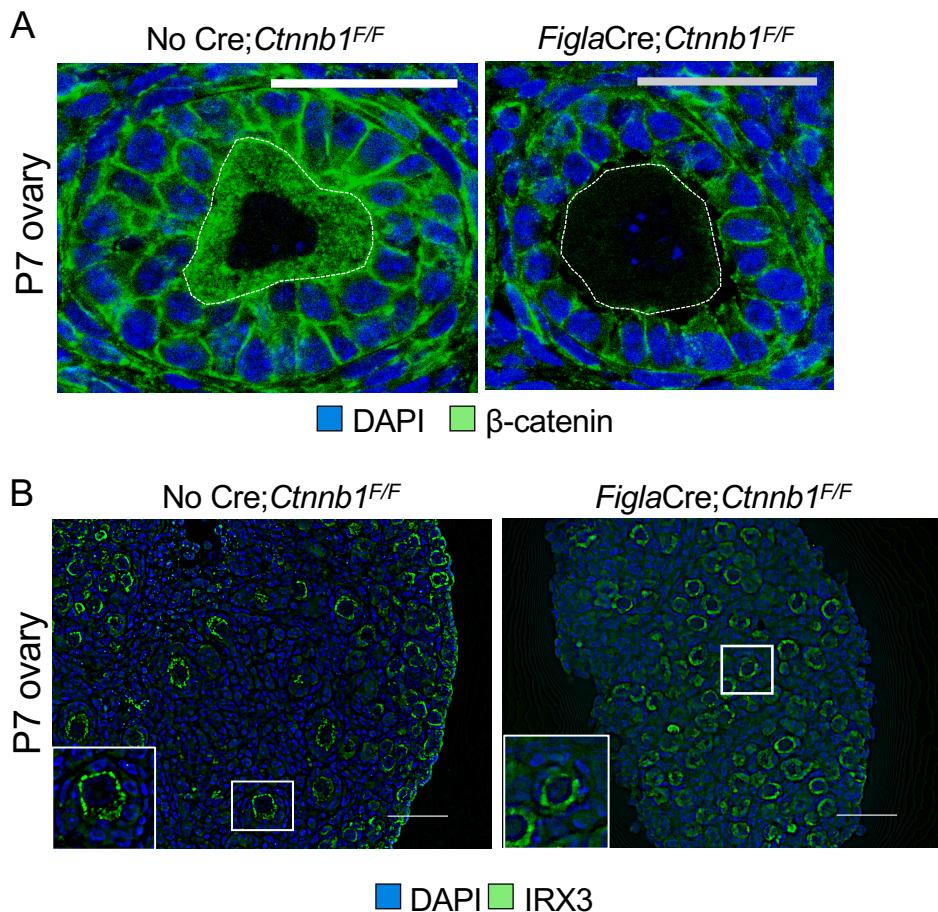


Figure S2: *FiglaCre* targeted loss of β -catenin does not affect IRX3 expression in oocytes

(A) Immunofluorescence image of a primary/transiting follicle in a P7 ovary showing that β -catenin is knocked out specifically in the oocyte. No Cre; *Ctnnb1*^{F/F} (control, left panel). *FiglaCre; Ctnnb1*^{F/F} (mutant, right panel). DAPI (blue) and β -catenin (green), White dotted lines outline the membrane of the germ cell. (B) IHC images of P7 ovaries for DAPI (blue) and IRX3 (green). No difference was observed in IRX3 staining between the oocytes of the control and mutant ovaries, including growing follicles (inset). Timing starting at secondary follicles is consistent with the onset of transcriptional activity of β -catenin in postnatal ovaries as reported by Usongo *et al.* 2012. Scale bars set to 50 μ m.

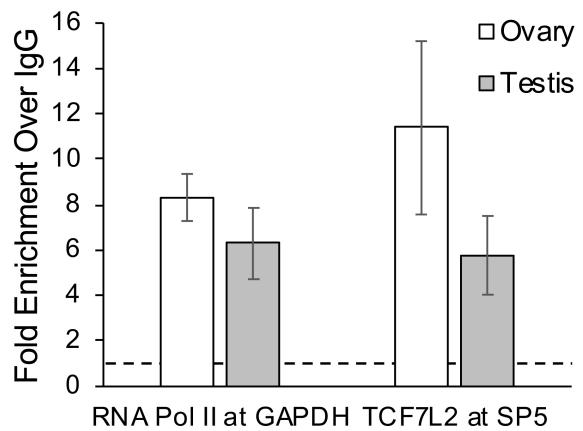


Figure S3: Chromatin Immunoprecipitation controls
RNA Pol II is enriched at the GAPDH promoter and
TCF7L2 is enriched at the SP5 promoter in both
ovaries and testes

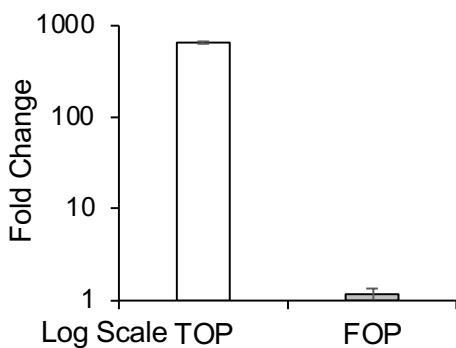


Figure S4: Validation of β -catenin specific responsiveness for CMV-S37A expression vector
TOPflash and FOPflash constructs were co-transfected with 50ng/well CMV-EGFP or CMV-S37A and normalized to pGL3Basic. Only TOPflash co-transfected with CMV-S37A showed a specific and robust increase in luciferase expression.

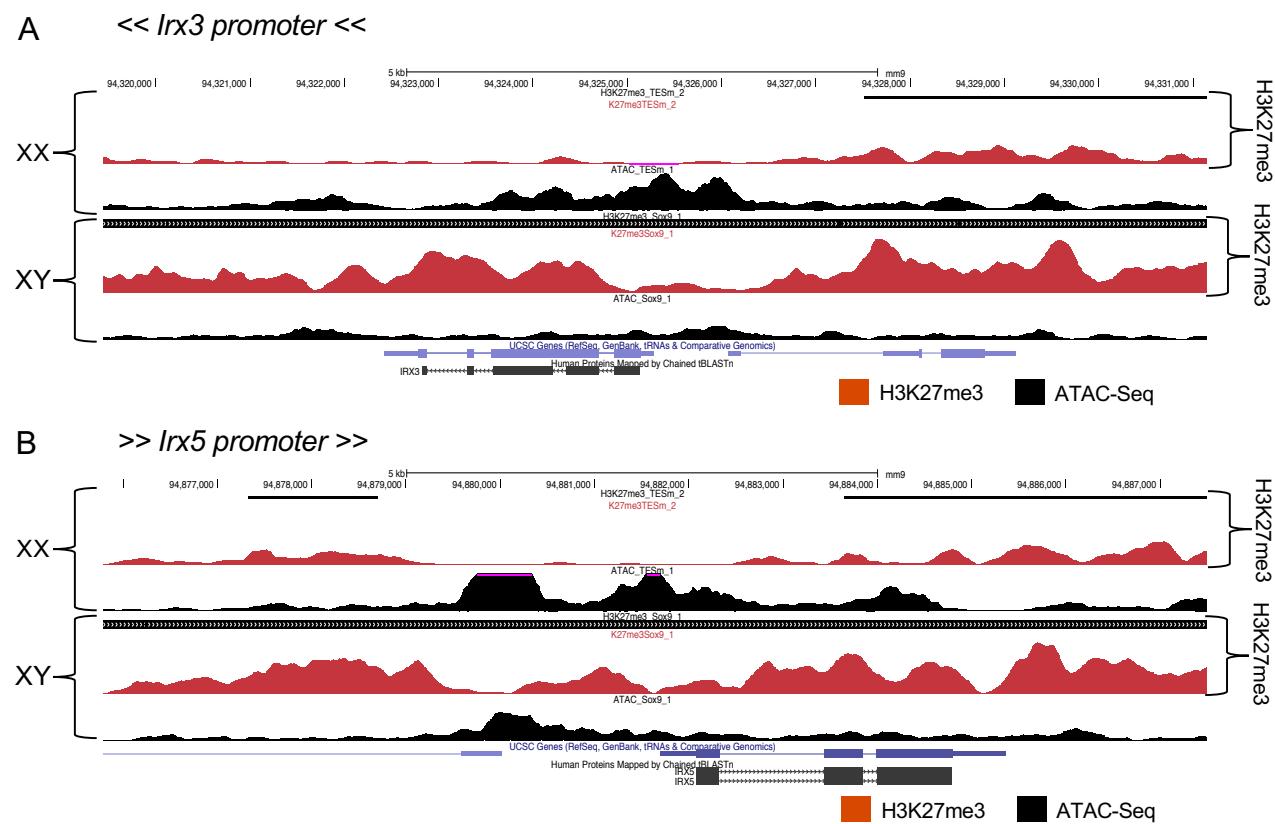


Figure S5: Epigenetic marks on *Irx3* and *Irx5* promoters

H3K27me3 (red peaks and back solid lines) and open chromatin sites (ATAC-Seq, black peaks) are shown for *Irx3* (**C**) and *Irx5* (**D**) promoters in male and female somatic cell populations. Arrows in label match the direction for coding sequences of each gene. ATAC-Seq peaks are enriched while there is a paucity of H3K27me3 peaks in XX samples. Black bars represent regions of significant enrichment when compared to flanking regions as determined by HOMER, thicker lines represent increased enrichment. Black bars are absent in both proximal promoter regions in XX samples.

Site Label	Forward Primer	Reverse Primer	Total insert length	
+205kb	5'- GCGCGGTACCTCACCTGGTAACTTGT GCTGT-3'	5'- GCGCCTCGAGCCAAGGCTCCGGT ATCAGC-3'	108bp	
+86kb	5'- GCGCGGTACCTCCCTTCCTATTGTT CAGAAG-3'	5'- GCGCCTCGAGTTCCCTCGGCTGAC AGAG-3'	59bp	
-305AB kb	5'- GCGCGGTACCGGTTCAAAAAGCCCAA GTG-3'	5'- GCGCCTCGAGTTATTCTCTCTTTC TCTCTCTCCA-3'	250bp	
-580kb	5'- GCGCGGTACCCGCCATGATAGGAGT CAAC-3'	5'- GCGCCTCGAGGGCAGCCCTTGTA AATGTT-3'	89bp	
Mutation Site	+205kb	+86kb	-305kb (AB)	-580kb
Wild Type Sequence	GTTCAAAGGC	GTTCAAAGCG	(A) GTTCAAAGTC (B) TTTCAAAGGG	CATCAAAGAC
Mutated Sequence	GTCCAAGGC	GTC CAAAGCG	(A) GT CCAAGTC (B) TT CCAAGGG	CAC CAAAGAC

Table S1: Individual potential enhancer sites containing TCF/LEF motif were cloned into the pGL3 Basic backbone using KpnI and Xhol. Primer sequences listed above and the insert size. DNA was generated by PCR with mouse genomic DNA. Wild type and mutated TCF/LEF binding motif for each enhancer site. The mutated base pair is in bold.

Supplementary Table S2: Real-time qPCR primer sequences

Gene	Forward Primer	Reverse Primer
<i>36B4</i>	5' – CGACCTGGAAGTCCAATAC – 3'	5' – ATCTGCTGCATCTGCTTG – 3'
<i>Gapdh</i>	5' – TTCACCACCATGGAGAAGGC – 3'	5' – GGCATGGACTGTGGTCATGA – 3'
<i>Rps29</i>	5' - TGAAGGCAAGATGGGTCACT - 3'	3' - GCACATGTTCAGCCCCGTATT - 5'
<i>Axin2</i>	5' – CCAGGCTGGAGAAACTGAAACT - 3'	5' – CCTGCTCAGACCCCTCCTT - 3'
<i>Fst</i>	5' - AAAACCTACCGAACGAATG - 3'	5' - TTCAGAAGAGGAGGGCTCTG - 3'
<i>Bmp2</i>	5' – CGGACTGCGGTCTCCTAA – 3'	5' – GGGGAAGCAGCAACACTAGA – 3'
<i>Irx3</i>	5' - CGCCTCAAGAAGGAGAACAGA - 3'	5' - CGCTCGCTCCCATAAGCAT - 3'
<i>Irx5</i>	5' - GGCTACAACCTCGCACCTCCA - 3'	5' - CCAAGGAACCTGCCATACCG - 3'