

Fig. S1. Analysis of scRNA-seq dataset of E11.5 to E14.5 female germ cells. (A) Uniform Manifold Approximation and Projection (UMAP) of oocytes colored by embryonic time point. (B) UMAP of oocytes colored by pseudotime analysis. (C) Expression of *Pou5f1*, *Stra8*, *Taf4b*, and *Taf4a* plotted in terms of pseudotime and colored based on embryonic time point. (D) Table of top 10 genes (in addition to *Taf4b*) that are expressed significantly higher in *Taf4b*-expressing oocytes. Colors indicate association with gene ontology (GO) term synaptonemal complex assembly (yellow) and meiosis I/meiotic cell cycle (red).

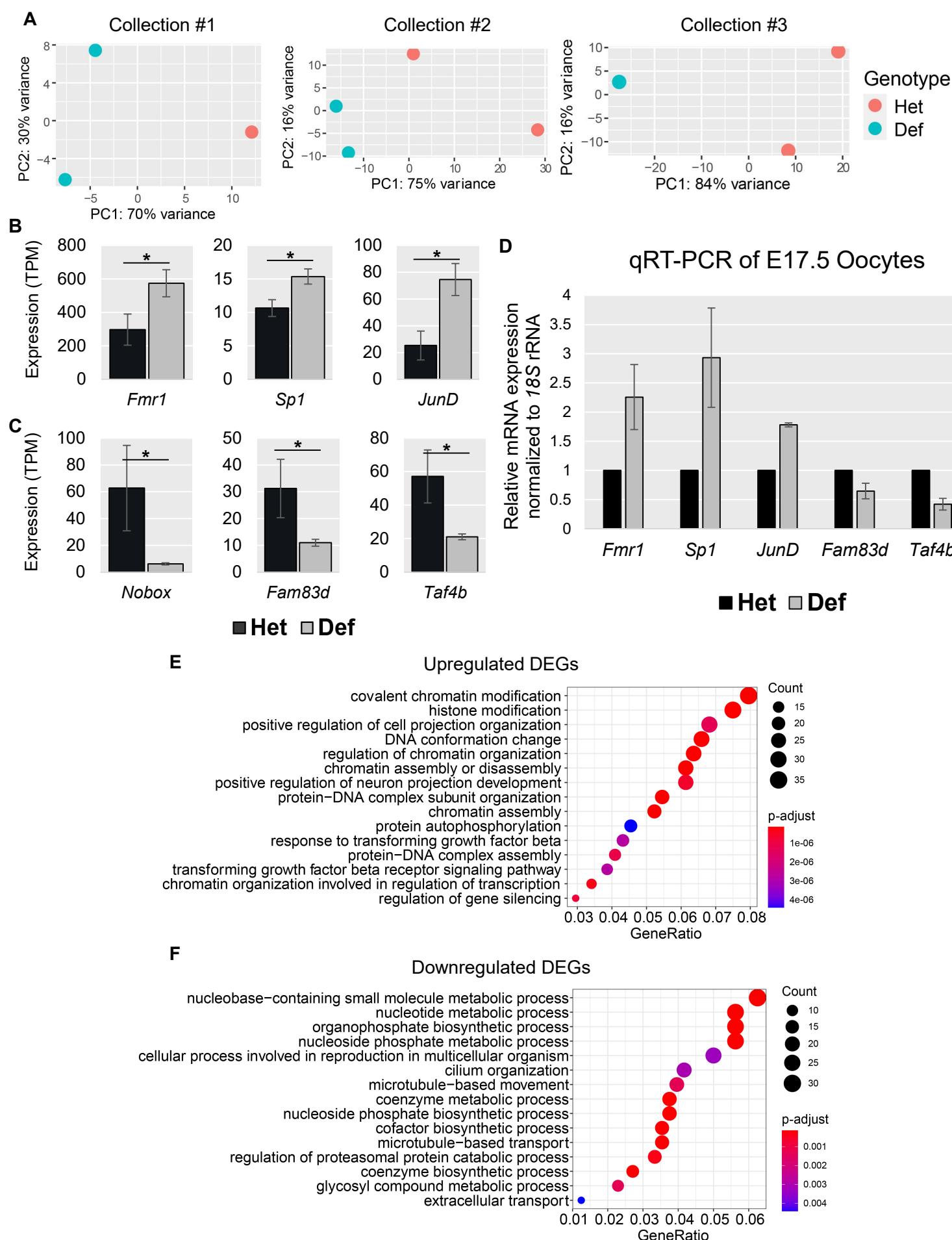


Fig. S2. E16.5 RNA-seq details. (A) PCA plots of different E16.5 RNA-seq collections colored by genotype. (B) Expression levels of upregulated DEGs in TPMs. (C) Expression levels of downregulated DEGs. (D) qRT-PCR results of E17.5 Oct4-EGFP⁺ oocytes for *Fmr1*, *Sp1*, *JunD*, *Fam83d*, and *Taf4b* from *Taf4b*-heterozygous (n=1) and *Taf4b*-deficient (n=2) samples. (E) Biological process GO analysis dotplot of DEGs that were increased in *Taf4b*-deficient oocytes (“Upregulated”). (F) Biological process GO analysis dotplot of DEGs that were decreased in *Taf4b*-deficient oocytes (“Downregulated”).

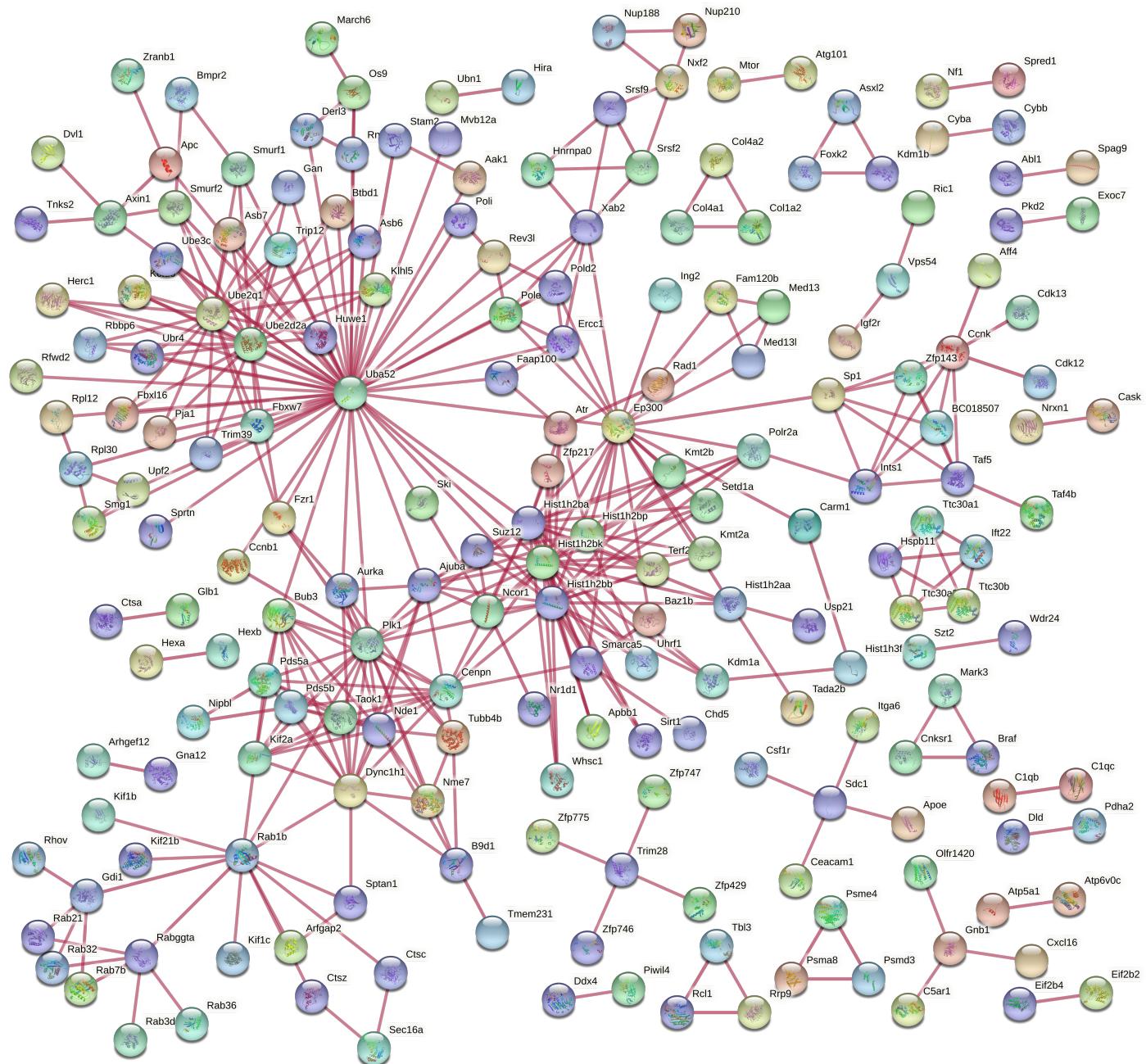


Fig. S3. Protein-protein interactions (PPIs) of E16.5 DEGs. Plot generated by STRING of DEGs from E16.5 RNA-seq that had at least one PPI (physical network, highest confidence) (Szklarczyk et al. 2019). There was a significant enrichment of PPIs ($p < 0.01$).

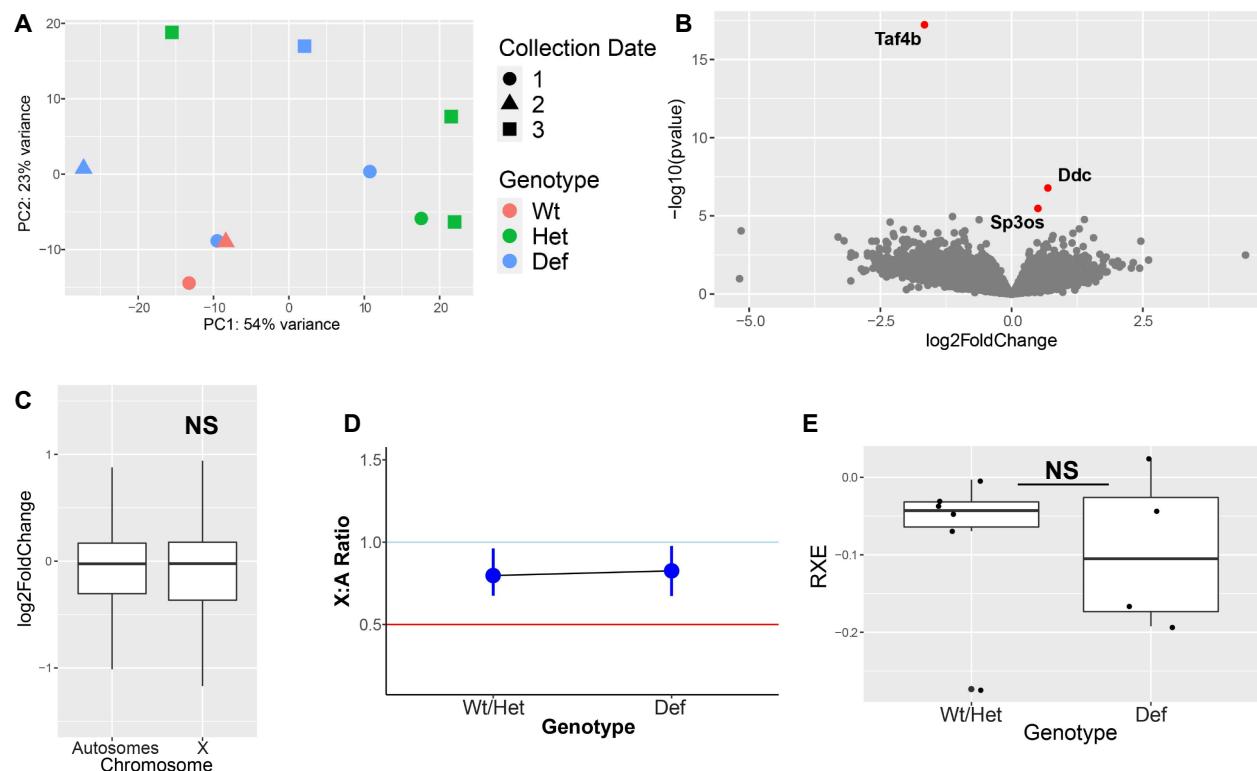


Fig. S4. E14.5 oocyte RNA-seq experiment. (A) PCA of E14.5 RNA-seq with genotype and collection date plotted. (B) Volcano plot of E14.5 RNA-seq with DEGs labeled (red). (C) Boxplots of \log_2 fold change values from DESeq2 of all genes comparing autosomal versus X chromosome \log_2 fold change (outliers removed), NS = not significant. (D) X:A ratio plot calculated through pairwiseCI after filtering for average TPM > 1 comparing Wt/Het X:A ratio to *Taf4b*-deficient X:A Ratio. (E) Boxplots of relative X expression (RXE) calculations after filtering for average TPM > 1 and adding pseudocounts for log-transformation for each *Taf4b*-Wt, -heterozygous, and -deficient sample. Wt/Het samples compared to Defs, NS = not significant.

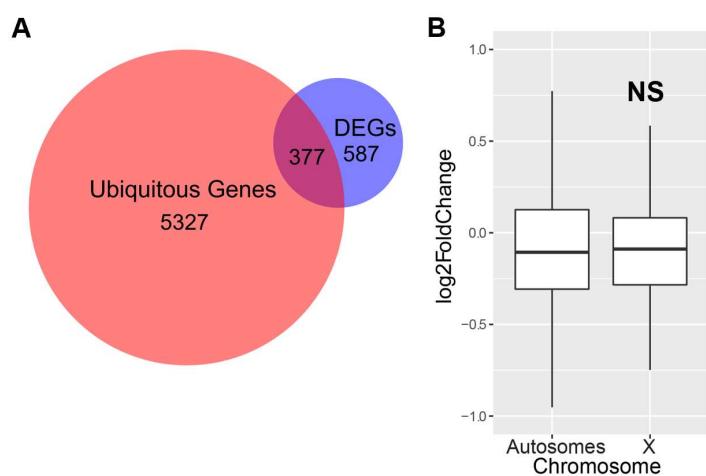
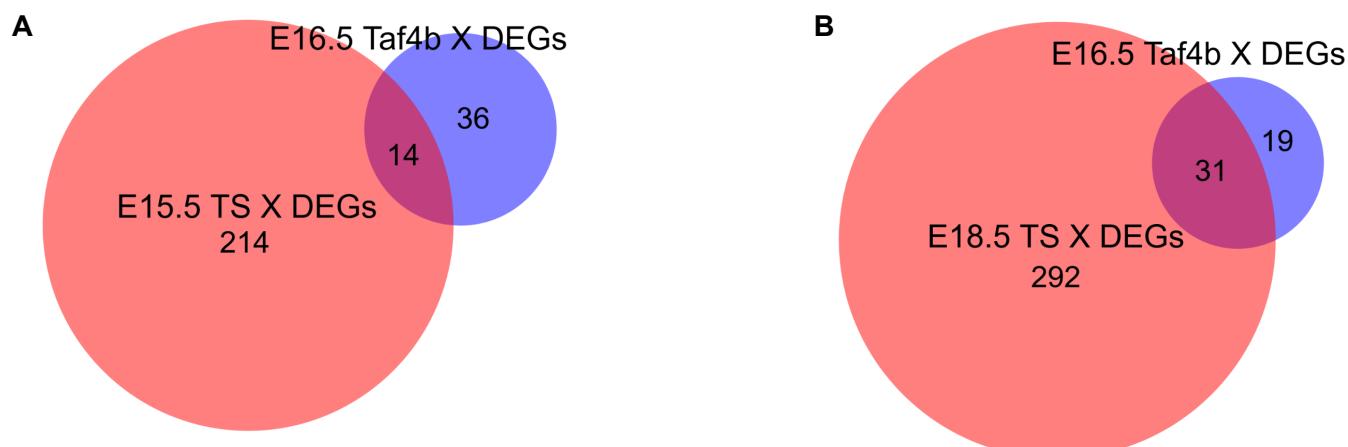


Fig. S5. Ubiquitous gene expression in E16.5 oocytes. (A) Venn diagram of E16.5 DEGs and “Ubiquitous Genes” as identified in Sangrithi et al. 2017. Significant overlap in Venn diagram ($p < 0.0001$, hypergeometric test). (B) Boxplots of \log_2 fold change values from DESeq2 of all ubiquitous genes comparing autosomal \log_2 fold change versus X chromosome \log_2 fold change, NS = not significant (outliers removed).



C

Gene Name	Ensembl Gene ID
4930550L24Rik (Magea13)	ENSMUSG00000046180
Atg4a	ENSMUSG00000079418
Ccdc160	ENSMUSG00000073207
Clcn5	ENSMUSG00000004317
Fmr1	ENSMUSG00000000838
Gdi1	ENSMUSG00000015291
Huwe1	ENSMUSG00000025261
Magea10	ENSMUSG00000043453
Mageb4	ENSMUSG00000035427
Nsdhl	ENSMUSG00000031349
Nxf2	ENSMUSG00000009941
Rps4x	ENSMUSG00000031320
Shroom4	ENSMUSG00000068270
Slc35a2	ENSMUSG00000031156

D

Gene Name	Ensembl Gene ID
1700080O16Rik (Magea14)	ENSMUSG00000031118
Atg4a	ENSMUSG00000079418
AV320801	ENSMUSG00000054994
Bcorl1	ENSMUSG00000036959
Ccdc160	ENSMUSG00000073207
Clcn5	ENSMUSG00000004317
Cybb	ENSMUSG00000015340
Fgf13	ENSMUSG00000031137
Fmr1	ENSMUSG00000000838
Gab3	ENSMUSG00000032750
Gdi1	ENSMUSG00000015291
Gla	ENSMUSG00000031266
Gm15023	ENSMUSG00000079432
Gm364 (Tm9sf5)	ENSMUSG00000079584
Gm5128	ENSMUSG00000094004
Gm7173 (Cfap47)	ENSMUSG00000073077
Huwe1	ENSMUSG00000025261
Mageb18	ENSMUSG00000035427
Mageb4	ENSMUSG00000035427
Mbnl3	ENSMUSG00000036109
Nkrf	ENSMUSG00000044149
Nsdhl	ENSMUSG00000031349
Nup62cl	ENSMUSG00000072944
Nxf2	ENSMUSG00000009941
Pja1	ENSMUSG00000034403
Rhox2d	ENSMUSG00000095698
Rps4x	ENSMUSG00000031320
Shroom4	ENSMUSG00000068270
Slc35a2	ENSMUSG00000031156
Tktl1	ENSMUSG00000031397
Tsga8	ENSMUSG00000035522

Fig. S6. Shared X chromosome DEGs between TS dataset and *Taf4b*-deficiency. (A) Venn diagram of all E16.5 *Taf4b* X chromosome DEGs compared with E15.5 TS X chromosome DEGs (protein-coding, p-adj < 0.05, avg TPM > 1). No significant overlap in Venn diagram (hypergeometric test). (B) Venn diagram of all E16.5 *Taf4b* X chromosome DEGs compared with E18.5 TS X chromosome DEGs (protein-coding, p-adj < 0.05, avg TPM > 1). Significant overlap in Venn diagram ($p < 0.0001$, hypergeometric test). (C) List of the 14 DEGs shared in (A). (D) List of the 31 DEGs shared in (B).

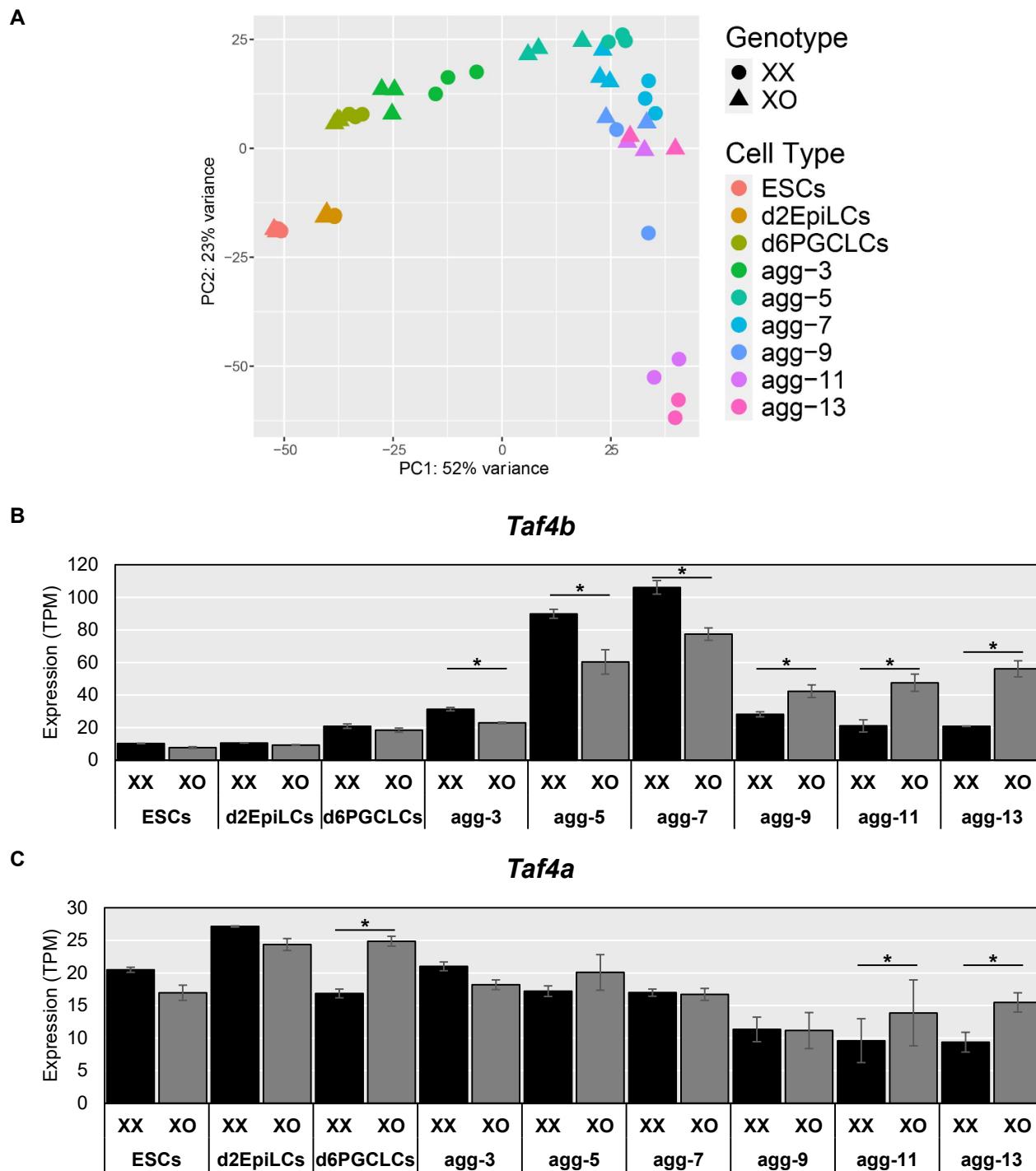


Fig. S7. Effects of XO on *Taf4b* in *in vitro* germ cell differentiation culture system.

(A) PCA plot of cultured cells from Hamada et al., 2020, labeled based on cell type and genotype. (B) Expression levels of *Taf4b* in XX versus XO cultured cells (* = p < 0.05, protein-coding, avg TPM >1). (C) Expression levels of *Taf4a* in XX versus XO cultured cells. Error bars indicate \pm standard error of the mean (SEM).

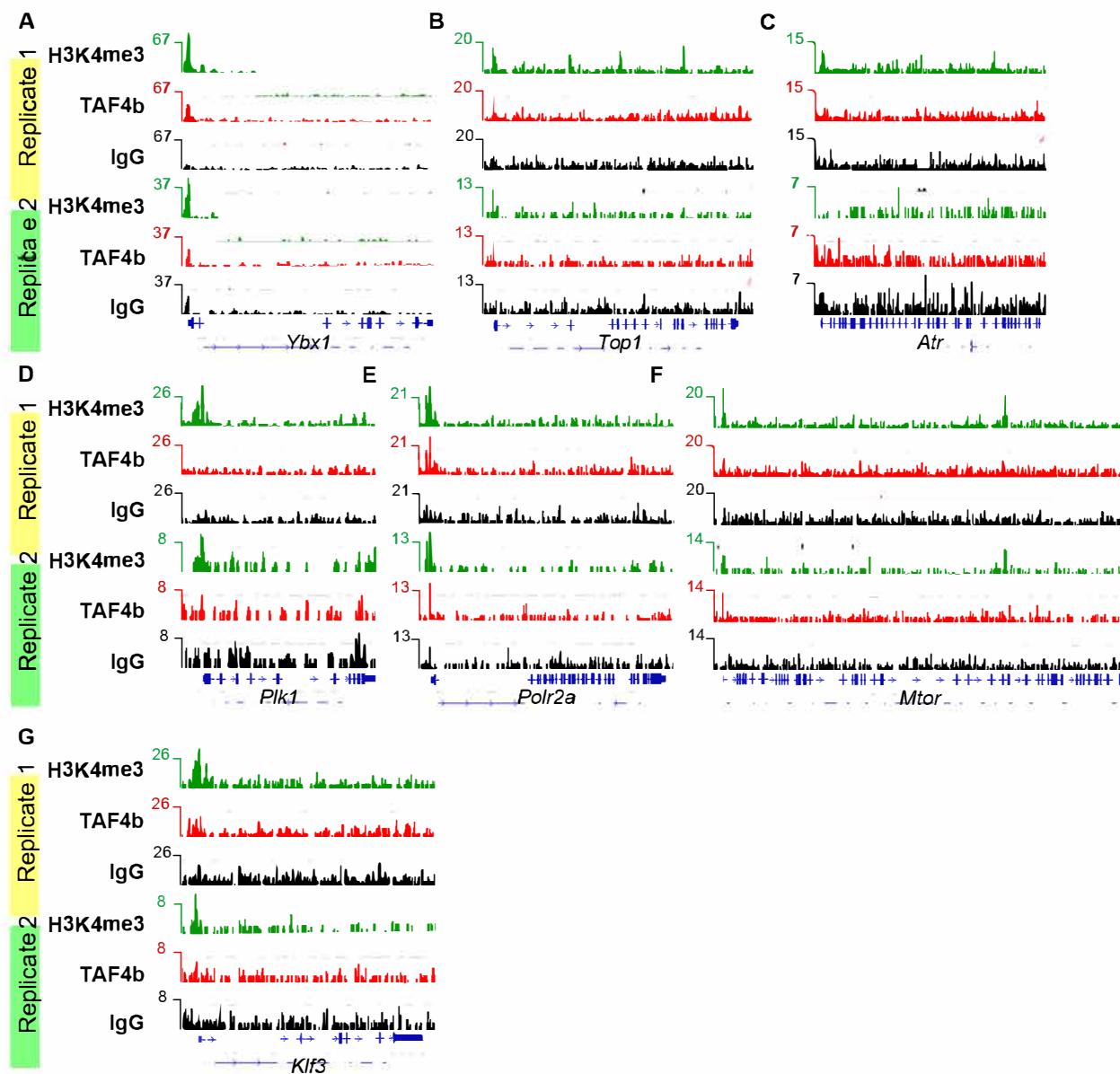


Fig. S8. Selected gene tracks. Genes tracks of *Ybx1* (A) and *Top1* (B), which were TAF4b CUT&RUN “promoter-TSS” peaks shared between the replicates but not DEGs. Gene tracks of *Atr* (C) and *Plk1* (D), which were DEGs but had no TAF4b peaks called. (E) Gene track for *Polr2a*, a DEG that had a TAF4b peak called in only Replicate 1. (F) Gene track for *Mtor*, a DEG that had a TAF4b peak called in only Replicate 2. (G) Gene track for *Klf3*, a non-DEG that had no TAF4b peaks called but did have H3K4me3 peaks called for replicates.

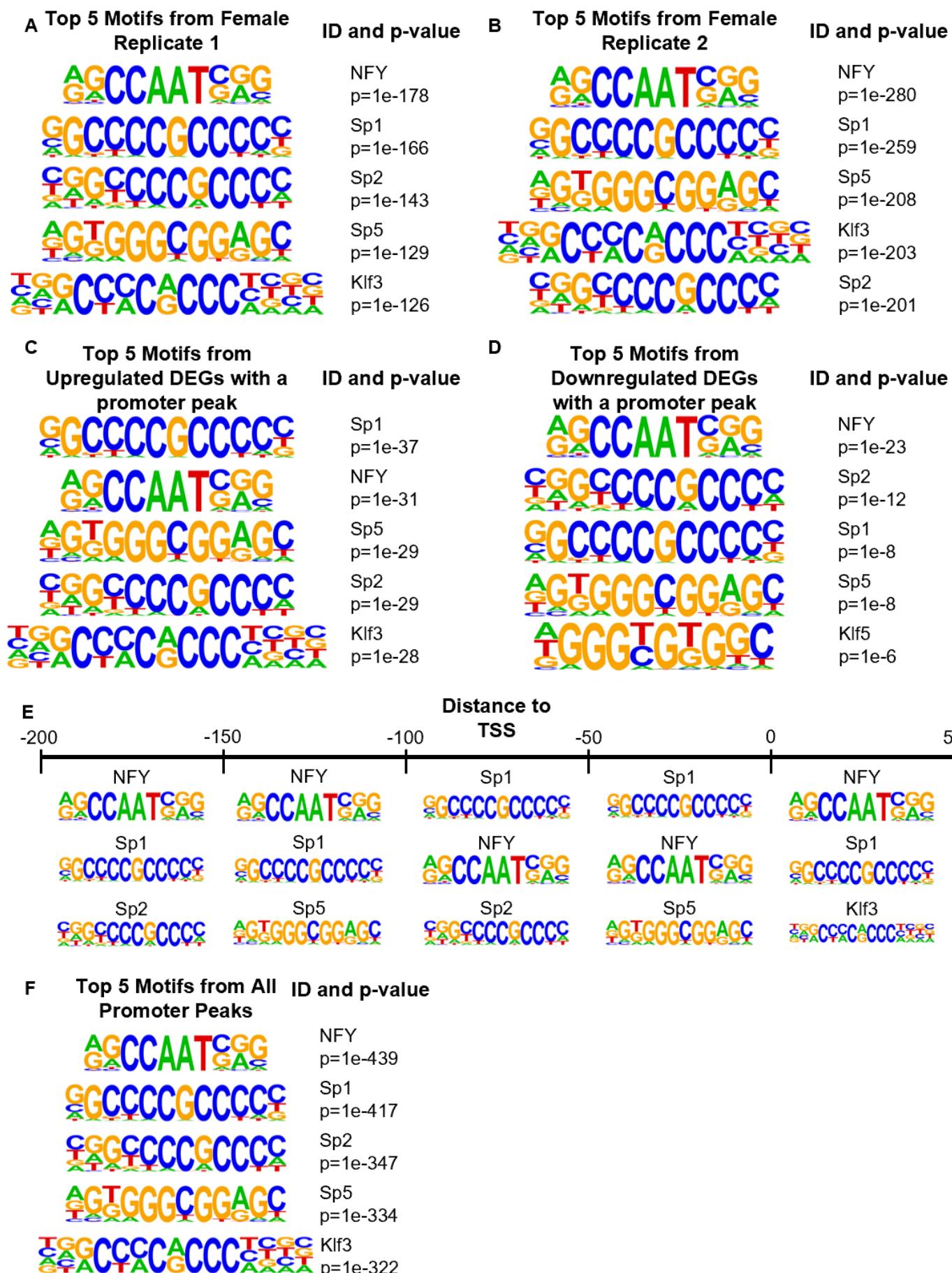


Fig. S9. Strong motif consistency when examining subsets of E16.5 oocyte CUT&RUN data. (A) Top five TAF4b motifs from “promoter-TSS” peaks in female Replicate 1. (B) Top five TAF4b motifs from “promoter-TSS” peaks in female Replicate 2. (C) Top five TAF4b motifs from Upregulated DEGs that had at least one TAF4b “promoter-TSS” peak. (D) Top five TAF4b motifs from Downregulated DEGs that had at least one TAF4b “promoter-TSS” peak. (E) Diagram of the top three TAF4b “promoter-TSS” motifs in 50 bp windows relative to the TSS. (F) Top five motifs enriched at all TAF4b “promoter-TSS” peaks, the promoter ID, and the associated p-value.

Table S1. Output for scRNA-seq analysis.

[click here to download Table S1](#)

Table S2. Cell numbers for RNA-seq samples.

Age	Genotype	Sample #	Cell #
E14.5	Wildtype	1	7,942
		2	18,256
	Heterozygous	1	12,553
		2	12,897
		3	2,822
		4	19,308
	Deficient	1	9,112
		2	5,233
		3	9,893
		4	7,035
E16.5	Heterozygous	1	7,199
		2	2,512
		3	3,399
		4	9,369
		5	14,402
	Deficient	1	2,181
		2	3,547
		3	19,089
		4	5,688
		5	9,076

Table S3. Output of E16.5 oocyte RNA-seq.

[Click here to download Table S3](#)

Table S4. Output of E14.5 oocyte RNA-seq.

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Table S5. Chromosome distribution of Downregulated DEGs.

Chromosome	Total Genes	Observed	Expected	Chi ²	p-value
1	1439	32	32.41	0.006	0.9406
2	1630	35	36.71	0.086	0.7694
3	1178	21	26.53	1.217	0.2699
4	1290	28	29.05	0.04	0.8409
5	1499	20	33.76	6.014	0.0142
6	1145	17	25.79	3.158	0.0755
7	1750	33	39.42	1.135	0.2867
8	1116	25	25.14	0.001	0.9771
9	1281	34	28.85	0.975	0.3233
10	1039	27	23.40	0.581	0.4459
11	1592	38	35.86	0.138	0.7107
12	901	21	20.29	0.026	0.8722
13	940	26	21.17	1.156	0.2823
14	764	16	17.21	0.088	0.7666
15	825	23	18.58	1.092	0.296
16	655	11	14.75	0.982	0.3216
17	1056	21	23.78	0.341	0.5591
18	571	15	12.86	0.365	0.5455
19	673	17	15.16	0.23	0.6313
X	900	41	20.27	22.094	<0.0001

Table S6. Chromosome distribution of Upregulated DEGs.

Chromosome	Total Genes	Observed	Expected	Chi ²	p-value
1	1439	24	29.95	1.264	0.2609
2	1630	40	33.93	1.172	0.279
3	1178	14	24.52	4.766	0.029
4	1290	30	26.85	0.392	0.5311
5	1499	38	31.20	1.589	0.2074
6	1145	18	23.83	1.504	0.2201
7	1750	40	36.43	0.381	0.5372
8	1116	21	23.23	0.225	0.6351
9	1281	28	26.66	0.071	0.7898
10	1039	18	21.63	0.638	0.4245
11	1592	48	33.14	7.181	0.0074
12	901	24	18.75	1.529	0.2162
13	940	31	19.57	6.977	0.0083
14	764	10	15.90	2.269	0.132
15	825	14	17.17	0.609	0.4353
16	655	9	13.63	1.623	0.2027
17	1056	19	21.98	0.424	0.5148
18	571	12	11.89	0.001	0.9731
19	673	16	14.01	0.292	0.5889
X	900	9	18.73	5.268	0.0217

Table S7. Ubiquitous gene exploration.

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Table S8. Mouse Turner Syndrome dataset.

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Table S9. *In vitro* differentiation mouse TS dataset.

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Table S10. TAF4b and H3K4me3 CUT&RUN in E16.5 oocytes.

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Table S11. Quantitative real-time PCR primers

Gene	Primer Sequence
<i>Fmr1</i>	Forward - CAATGGCGCTTCTACAAGGC
	Reverse - TCTGGTTGCCAGTTGTTCA
<i>Sp1</i>	Forward – GCCACCATGAGCGACCAAG
	Reverse – GAGTCTGAGAAAAGGCGGCA
<i>Fam83d</i>	Forward - CGTGTGAGGCTCATTTCC
	Reverse - CCACAGCAATCACCTCTCGG
<i>JunD</i>	Forward - CCCCGGACTCTTCGAGACT
	Reverse - CCTTAGAGCCCCCTACTCGGA
<i>Taf4b</i>	Forward - GATGTTACTAAAGGCAGCCAAGAGT
	Reverse – CTGCTCTGGATCTTCTTATTGGAG
<i>18S rRNA</i>	Forward – GTAACCCGTTGAACCCCATT
	Reverse – CCATCCAATCGGTAGTAGCG