

1 **Erosion of somatic tissue identity with loss of the X-linked**
2 **intellectual disability factor KDM5C**

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5 **Abstract**

6 Mutations in numerous chromatin-modifying enzymes cause neurodevelopmental disorders (NDDs) with
7 unknown mechanisms. Loss of repressive chromatin regulators can lead to the aberrant transcription of
8 tissue-specific genes outside of their intended context, however the mechanisms and consequences of
9 their dysregulation are largely unknown. Here, we examine the role of lysine demethylase 5c (KDM5C),
10 an eraser of histone 3 lysine 4 di and tri-methylation (H3K4me2/3) mutated in Claes-Jensen X-linked
11 intellectual disability, in tissue identity. We found male *Kdm5c* knockout (-KO) mice, which recapitulate
12 key human neurological phenotypes, aberrantly expresses many liver, muscle, ovary, and testis genes
13 within the amygdala and hippocampus. Gonad-enriched genes misexpressed in the *Kdm5c*-KO brain are
14 unique to germ cells, indicating an erosion of the soma-germline boundary. Germline genes are typically
15 decommissioned in somatic lineages in the post-implantation epiblast, yet *Kdm5c*-KO epiblast-like cells
16 (EpiLCs) aberrantly expressed key regulators of germline identity and meiosis, including *Dazl* and *Stra8*.
17 Germline gene suppression is sexually dimorphic, as female EpiLCs required a higher dose of KDM5C
18 to maintain germline gene suppression. Using a comprehensive list of mouse germline-enriched genes,
19 we found KDM5C is selectively recruited to a subset of germline gene promoters that contain CpG islands
20 (CGIs) to facilitate DNA CpG methylation (CpGme) during ESC to EpiLC differentiation. However, late stage
21 spermatogenesis genes devoid of promoter CGIs can also become activated in *Kdm5c*-KO cells via ectopic
22 activation by RFX transcription factors. Thus, distinct mechanisms govern the misexpression of germline
23 gene classes, including activation by ectopic germline programs that mirror germ cell development within
24 somatic tissues.

25 **Introduction**

26 A single genome holds the instructions to generate the myriad of cell types found within an organism.
27 This is, in part, accomplished by chromatin regulators that can either promote or impede lineage-specific

28 gene expression through DNA and histone modifications^{1–5}. Human genetic studies revealed mutations in
29 chromatin regulators are a major cause of neurodevelopmental disorders (NDDs)⁶ and many studies have
30 identified their importance for regulating brain-specific transcriptional programs. Loss of some chromatin
31 regulators can also result in the ectopic expression of tissue-specific genes outside of their target environment,
32 such as the misexpression of liver-specific genes within adult neurons⁷. However, the mechanisms underlying
33 ectopic gene expression and its impact upon neurodevelopment are poorly understood.

34 To elucidate the role of tissue identity in chromatin-linked NDDs, it is essential to first characterize the
35 nature of the dysregulated genes and the molecular mechanisms governing their de-repression. Here we
36 focus on lysine demethylase 5C (KDM5C, also known as SMCX or JARID1C), which erases histone 3 lysine
37 4 di- and trimethylation (H3K4me2/3), a permissive chromatin modification enriched at gene promoters⁸.
38 Pathogenic mutations in *KDM5C* cause Intellectual Developmental Disorder, X-linked, Syndromic, Claes-
39 Jensen Type (MRXSCJ, OMIM: 300534). MRXSCJ is more common and severe in males and its neurological
40 phenotypes include intellectual disability, seizures, aberrant aggression, and autistic behaviors^{9–11}. Male
41 *Kdm5c* knockout (-KO) mice recapitulate key MRXSCJ phenotypes, including hyperaggression, increased
42 seizure propensity, and learning impairments^{12,13}. RNA sequencing (RNA-seq) of the *Kdm5c*-KO hippocam-
43 pus revealed ectopic expression of some germline genes within the brain¹³. However, it is unclear if other
44 tissue-specific genes are aberrantly transcribed with KDM5C loss, at what point in development germline
45 gene misexpression begins, and what mechanisms underlie their dysregulation.

46 Distinguishing between germ cells and somatic cells is a key feature of multicellularity¹⁴ that occurs
47 during early embryogenesis in many metazoans¹⁵. In mammals, chromatin regulators are crucial for
48 decommissioning germline genes during the transition from naïve to primed pluripotency. Initially, germline
49 gene promoters gain repressive histone H2A lysine 119 monoubiquitination (H2AK119ub1)¹⁶ and histone 3
50 lysine 9 trimethylation (H3K9me3)^{16,17} in embryonic stem cells (ESCs) and are then decorated with DNA
51 CpG methylation (CpGme) in the post-implantation embryo^{17–20}. The contribution of KDM5C to this process
52 remains unclear. Furthermore, studies on germline gene repression have primarily been conducted in
53 males and focused on marker genes important for germ cell development rather than germline genes as a
54 whole, given the lack of a curated germline-enriched gene list. Therefore, it is unknown if the mechanism
55 of repression differs between sexes or for certain classes of germline genes, e.g. meiotic genes versus
56 spermatid differentiation genes.

57 To illuminate KDM5C's role in tissue identity, here we characterized the aberrant expression of tissue-
58 enriched genes within the *Kdm5c*-KO brain and epiblast-like stem cells (EpiLCs), an *in vitro* model of the
59 post-implantation embryo. We curated a list of mouse germline-enriched genes, which enabled genome-wide
60 analysis of germline gene silencing mechanisms for the first time. Based on the data presented below, we
61 propose KDM5C plays a fundamental, sexually dimorphic role in the development of tissue identity during
62 early embryogenesis, including the establishment of the soma-germline boundary.

63 **Results**

64 **Tissue-enriched genes are aberrantly expressed in the *Kdm5c*-KO brain**

65 Previous RNA sequencing (RNA-seq) of the adult male *Kdm5c*-KO hippocampus revealed ectopic
66 expression of some germline genes unique to the testis¹³. It is currently unknown if the testis is the only
67 tissue type misexpressed in the *Kdm5c*-KO brain. We thus systematically tested whether other tissue-specific
68 genes are misexpressed in the male brain with constitutive knockout of *Kdm5c* (*Kdm5c*^{-Y})²¹ by using a
69 published list of mouse tissue-enriched genes²².

70 We found a large proportion of significantly upregulated genes (DESeq2²³, log2 fold change > 0.5, q <
71 0.1) within the male *Kdm5c*-KO (5CKO) amygdala and hippocampus are typically enriched within non-brain
72 tissues (Amygdala: 35%, Hippocampus: 24%) (Figure 1A-B). For both the amygdala and hippocampus,
73 the majority of tissue-enriched differentially expressed genes (DEGs) were testis genes (Figure 1A-B).
74 Even though the testis has the largest total number of tissue-biased genes (2,496 genes) compared to any
75 other tissue, testis-biased DEGs were significantly enriched for both brain regions (Amygdala p = 1.83e-05,
76 Odds Ratio = 5.13; Hippocampus p = 4.26e-11, Odds Ratio = 4.45, Fisher's Exact Test). An example of a
77 testis-enriched gene misexpressed in the *Kdm5c*-KO brain is *FK506 binding protein 6* (*Fkbp6*), a known
78 regulator of PIWI-interacting RNAs (piRNAs) and meiosis^{24,25} (Figure 1C).

79 Interestingly, we also observed significant enrichment of ovary-biased DEGs in both the amygdala and
80 hippocampus (Amygdala p = 0.00574, Odds Ratio = 18.7; Hippocampus p = 0.048, Odds Ratio = 5.88,
81 Fisher's Exact) (Figure 1A-B). Ovary-enriched DEGs included *Zygotic arrest 1* (*Zar1*), which sequesters
82 mRNAs in oocytes for meiotic maturation²⁶ (Figure 1D). Given that the *Kdm5c*-KO mice we analyzed are
83 male, these data demonstrate that the ectopic expression of gonad-enriched genes is independent of
84 organismal sex.

85 Although not consistent across brain regions, we also found significant enrichment of DEGs biased
86 towards two non-gonadal tissues - the liver (Amygdala p = 0.04, Odds Ratio = 6.58, Fisher's Exact Test) and
87 muscles (Hippocampus p = 0.01, Odds Ratio = 6.95, Fisher's Exact Test) (Figure 1A-B). *Apolipoprotein C-I*
88 (*Apoc1*) a lipoprotein metabolism and transport gene, is among the liver-biased DEG derepressed in both
89 the hippocampus and amygdala²⁷ and its brain overexpression has been implicated in Alzheimer's disease²⁸
90 (Figure 1E).

91 For all *Kdm5c*-KO tissue-enriched DEGs, aberrantly expressed mRNAs are polyadenylated and spliced
92 into mature transcripts (Figure 1C-E). Of note, we observed little to no dysregulation of brain-enriched genes
93 (Amygdala p = 1, Odds Ratio = 1.22; Hippocampus p = 0.74, Odds Ratio = 1.22, Fisher's Exact), despite the
94 fact these are brain samples and the brain has the second highest total number of tissue-enriched genes
95 (708 genes). Altogether, these results suggest the aberrant expression of tissue-enriched genes within the
96 brain is a major effect of KDM5C loss.

97 **Germline genes are misexpressed in the *Kdm5c*-KO brain**

98 *Kdm5c*-KO brain expresses testicular germline genes¹³, however the testis also contains somatic cells that
99 support hormone production and germline functions. To determine if *Kdm5c*-KO results in ectopic expression
100 of somatic testicular genes, we first evaluated the known functions of testicular DEGs through gene ontology.
101 We found *Kdm5c*-KO testis-enriched DEGs had high enrichment of germline-relevant ontologies, including
102 spermatid development (GO: 0007286, p.adjust = 6.2e-12) and sperm axoneme assembly (GO: 0007288,
103 p.adjust = 2.45e-14) (Figure 2A).

104 We then evaluated testicular DEG expression in wild-type testes versus testes with germ cell depletion²⁹,
105 which was accomplished by heterozygous *W* and *Wv* mutations in the enzymatic domain of *c-Kit* (*Kit*^{W/Wv})³⁰.
106 Almost all *Kdm5c*-KO testis-enriched DEGs lost expression with germ cell depletion (Figure 2B). We then
107 assessed testis-enriched DEG expression in a published single cell RNA-seq dataset that identified cell
108 type-specific markers within the testis³¹. Some *Kdm5c*-KO testis-enriched DEGs were classified as specific
109 markers for different germ cell developmental stages (e.g. spermatogonia, spermatocytes, round spermatids,
110 and elongating spermatids), yet none marked somatic cells (Figure 2C). Together, these data demonstrate
111 that the *Kdm5c*-KO brain aberrantly expresses germline genes, but not somatic testicular genes, reflecting
112 an erosion of the soma-germline boundary.

113 As of yet, research on germline gene silencing mechanisms has focused on a handful of key genes
114 rather than assessing germline gene suppression genome-wide due to the lack of a comprehensive gene list.
115 We therefore generated a list of mouse germline-enriched genes using RNA-seq datasets of *Kit*^{W/Wv} mice
116 that included males and females at embryonic day 12, 14, and 16³² and adult male testes²⁹. We defined
117 genes as germline-enriched if their expression met the following criteria: 1) their expression is greater than
118 1 FPKM in wild-type gonads 2) their expression in any non-gonadal tissue of adult wild type mice²² does
119 not exceed 20% of their maximum expression in the wild-type germline, and 3) their expression in the germ
120 cell-depleted gonads, for any sex or time point, does not exceed 20% of their maximum expression in the
121 wild-type germline. These criteria yielded 1,288 germline-enriched genes (Figure 2D), which was hereafter
122 used as a resource to globally characterize germline gene misexpression with *Kdm5c* loss (Supplementary
123 table 1).

124 ***Kdm5c*-KO epiblast-like cells aberrantly express key regulators of germline identity**

125 Germ cells are typically distinguished from somatic cells soon after the embryo implants into the uterine
126 wall^{33,34}, when germline genes are silenced in epiblast stem cells that will form the somatic tissues³⁵. This
127 developmental time point can be modeled *in vitro* through differentiation of naïve embryonic stem cells
128 (nESCs) into epiblast-like stem cells (EpiLCs) (Figure 3A)^{36,37}. While some germline-enriched genes are
129 also expressed in nESCs and in the 2-cell stage^{38–40}, they are silenced as they differentiate into EpiLCs^{17,18}.
130 Therefore, we tested if KDM5C was necessary for the initial silencing of germline genes in somatic lineages

131 by evaluating the impact of *Kdm5c* loss in male EpiLCs.
132 *Kdm5c*-KO cell morpholgy during ESC to EpiLC differentiation appeared normal (Figure 3B) and EpiLCs
133 properly expressed markers of primed pluripotency, such as *Dnmt3b*, *Fgf5*, *Pou3f1*, and *Otx2* (Figure 3C). We
134 then identified tissue-enriched DEGs in a RNA-seq dataset of wild-type and *Kdm5c*-KO EpiLCs⁴¹ (DESeq2,
135 log2 fold change > 0.5, q < 0.1). Similar to the *Kdm5c*-KO brain, we observed general dysregulation of
136 tissue-enriched genes, with the largest number of genes belonging to the brain and testis, although they
137 were not significantly enriched (Figure 3D). Using our list of mouse germline-enriched genes assembled
138 above, we found 68 germline genes were misexpressed in male *Kdm5c*-KO EpiLCs.

139 We then compared EpiLC germline DEGs to those expressed in the *Kdm5c*-KO brain to determine if
140 germline genes are constitutively dysregulated or change over the course of development. The majority of
141 germline DEGs were unique to either EpiLCs or the brain, with only *D1Pas1* and *Cyct* shared across all
142 tissue/cell types (Figure 3E-F). EpiLCs had particularly high enrichment of meiosis-related gene ontologies
143 (Figure 3G), such as meiotic cell cycle process (GO:1903046, p.adjust = 2.2e-07) and meiotic nuclear
144 division (GO:0140013, p.adjust = 1.37e-07). While there was modest enrichment of meiotic gene ontologies
145 in both brain regions, the *Kdm5c*-KO hippocampus primarily expressed late-stage spermatogenesis genes
146 involved in sperm axoneme assembly (GO:0007288, p.adjust = 0.00621) and sperm motility (GO:0097722,
147 p.adjust = 0.00612).

148 Notably, DEGs unique to *Kdm5c*-KO EpiLCs included key drivers of germline identity, such as *Stimulated*
149 *by retinoic acid 8* (*Stra8*: log2 fold change = 3.73, q = 2.17e-39) and *Deleted in azoospermia like* (*Dazl*):
150 log2 fold change = 3.36, q = 3.19e-12) (Figure 3H). These genes are typically expressed when primordial
151 germ cells (PGCs) are committed to the germline fate and later in life to trigger meiotic gene expression
152 programs⁴²⁻⁴⁴. Of note, some germline genes, including *Dazl*, are also expressed in the two-cell embryo^{39,45}.
153 However, we did not see derepression of two-cell stage-specific genes, like *Duxf3* (*Dux*) (log2 fold change
154 = -0.282, q = 0.337) and *Zscan4d* (log2 fold change = 0.25, q = 0.381) (Figure 3H), indicating *Kdm5c*-KO
155 EpiLCs do not revert back to a 2-cell state. Altogether, *Kdm5c*-KO EpiLCs express key drivers of germline
156 identity and meiosis while the brain primarily expresses spermiogenesis genes, indicating germline gene
157 misexpression mirrors germline development during the progression of somatic development.

158 **Female epiblast-like cells have increased sensitivity to germline gene misexpression
159 with *Kdm5c* loss**

160 It is currently unknown if the misexpression of germline genes is influenced by sex, as previous studies
161 on germline gene repressors have focused on male cells^{16,17,19,46,47}. Sex is particularly pertinent in the case
162 of KDM5C because it partially escapes X chromosome inactivation (XCI), resulting in a higher dosage in
163 females⁴⁸⁻⁵¹. We therefore explored the impact of chromosomal sex upon germline gene suppression by
164 comparing their dysregulation in male *Kdm5c* hemizygous knockout (XY *Kdm5c*-KO, XY 5CKO), female

165 homozygous knockout (XX *Kdm5c*-KO, XX 5CKO), and female heterozygous knockout (XX *Kdm5c*-HET, XX
166 5CHET) EpiLCs⁴¹.

167 Homozygous and heterozygous *Kdm5c* knockout females expressed over double the number of germline-
168 enriched genes than hemizygous males (Figure 4A). While the majority of germline DEGs in *Kdm5c*-KO
169 males were also dysregulated in females (74%), many were sex-specific, such as *Tktl2* and *Esx1* (Figure
170 4B). We then compared the known functions of germline genes dysregulated only in females (XX only -
171 dysregulated in XX *Kdm5c*-KO, XX *Kdm5c*-HET, or both), only in males (XY only), or in all samples (shared)
172 (Figure 4C). Female-specific germline DEGs were enriched for meiotic (GO:0051321 meiotic cell cycle) and
173 flagellar (GO:0003341 cilium movement) functions, while male-specific DEGs had roles in mitochondrial
174 and cell signaling (GO:0070585 protein localization to mitochondrion). Germline transcripts expressed in
175 both sexes were enriched for meiotic (GO:0140013 meiotic nuclear division) and egg-specific functions
176 (GO:0007292 female gamete generation).

177 The majority of germline genes expressed in both sexes were more highly dysregulated in females
178 compared to males (Figure 4D-F). This increased degree of dysregulation in females, along with the
179 increased total number of germline genes, indicates females are more sensitive to losing KDM5C-mediated
180 germline gene suppression. Female sensitivity could be due to impaired XCI in *Kdm5c* mutants⁴¹, as many
181 spermatogenesis genes lie on the X chromosome^{52,53}. However, female germline DEGs were not biased
182 towards the X chromosome and had a similar overall proportion of X chromosome DEGs compared to
183 males (XY *Kdm5c*-KO - 10.29%, XX *Kdm5c*-HET - 7.43%, XX *Kdm5c*-KO - 10.59%) (Figure 4G). The
184 majority of germline DEGs instead lie on autosomes for both male and female *Kdm5c* mutants (Figure 4G).
185 Thus, while female EpiLCs are more prone to germline gene misexpression with KDM5C loss, it is likely
186 independent of XCI defects.

187 **Germline gene misexpression in *Kdm5c* mutants is independent of germ cell sex**

188 Although many germline genes have shared functions in the male and female germline, some have
189 unique or sex-biased expression. Therefore, we wondered if *Kdm5c* mutant males would primarily express
190 sperm genes while mutant females primarily expressed egg genes. To comprehensively assess whether
191 germline gene sex corresponds with *Kdm5c* mutant sex, we first filtered our list of germline-enriched genes
192 for egg and sperm-biased genes (Figure 4H). We defined germ cell sex-biased genes as those whose
193 expression in the opposite sex, at any time point, is no greater than 20% of the gene's maximum expression
194 in a given sex. This yielded 67 egg-biased, 1,024 sperm-biased, and 197 unbiased germline-enriched genes.
195 We found egg, sperm, and unbiased germline genes were dysregulated in all *Kdm5c* mutants at similar
196 proportions (Figure 4I-J). Furthermore, germline genes dysregulated exclusively in either male or female
197 mutants were also not biased towards their corresponding germ cell sex (Figure 4I). Altogether, these results
198 demonstrate sex differences in germline gene dysregulation is not due to sex-specific activation of sperm or
199 egg transcriptional programs.

200 **KDM5C binds to a subset of germline gene promoters during early embryogenesis**

201 KDM5C binds to the promoters of several germline genes in embryonic stem cells (ESCs) but its binding
202 is absent in neurons¹³. However, the lack of a comprehensive list of germline-enriched genes prohibited
203 genome-wide characterization of KDM5C binding at germline gene promoters. Thus, it is unclear if KDM5C
204 is enriched at germline gene promoters, what types of germline genes KDM5C regulates, and if its binding is
205 maintained at any germline genes in neurons.

206 To address these questions, we analyzed KDM5C chromatin immunoprecipitation followed by DNA
207 sequencing (ChIP-seq) datasets in EpiLCs⁴¹ and primary forebrain neuron cultures (PNCs)¹². EpiLCs had a
208 higher total number of high-confidence KDM5C peaks than PNCs (EpiLCs: 5,808, PNCs: 1,276, MACS2 q <
209 0.1 and fold enrichment > 1). KDM5C was primarily localized to gene promoters in both cell types (EpiLCs:
210 4,190, PNCs: 745 ± 500bp from the TSS), although PNCs showed increased localization to non-promoter
211 regions (Figure 5A).

212 The majority of promoters bound by KDM5C in PNCs were also bound in EpiLCs (513 shared promoters),
213 however a large portion of gene promoters were bound by KDM5C only in EpiLCs (3,677 EpiLC only
214 promoters) (Figure 5B). Genes bound by KDM5C in both PNCs and EpiLCs were enriched for functions
215 involving nucleic acid turnover, such as deoxyribonucleotide metabolic process (GO:0009262, p.adjust =
216 8.28e-05) (Figure 5C). Germline-specific ontologies were enriched only in EpiLC-specific KDM5C-bound
217 promoters, such as meiotic nuclear division (GO: 0007127 p.adjust = 6.77e-16) (Figure 5C). There were no
218 ontologies significantly enriched for PNC-specific KDM5C target genes. Using our mouse germline gene list,
219 we observed evident KDM5C signal around the TSS of many germline genes in EpiLCs, but not in PNCs
220 (Figure 5D). Based on our ChIP-seq peak cut-off criteria, KDM5C was highly enriched at 211 germline gene
221 promoters in EpiLCs (16.4% of all germline genes) (Figure 5E). Of note, KDM5C was only bound to about
222 one third of *Kdm5c*-KO RNA-seq DEG promoters (EpiLC only DEGs: 34.92063%, Brain only DEGs: 30%)
223 (Supplementary figure 1A-C). However, KDM5C did bind the promoter of 4 out of the 5 genes dysregulated
224 in both the brain and EpiLCs. Representative examples of KDM5C-bound and unbound germline DEGs
225 are *Dazl* and *Stra8*, respectively (Figure 5F). Together, these results demonstrate KDM5C is recruited to a
226 subset of germline genes in EpiLCs, including meiotic genes, but does not directly regulate germline genes
227 in neurons. Furthermore, the majority of germline mRNAs expressed in *Kdm5c*-KO cells are dysregulated
228 independent of direct KDM5C binding to their promoters.

229 Many germline-specific genes are suppressed by the polycomb repressive complex 1.6 (PRC1.6), which
230 contains transcription factor heterodimers E2F6/DP1 and MGA/MAX that respectively bind E2F and E-box
231 motifs⁵⁶. PRC1.6 members may recruit KDM5C to germline gene promoters, given their association with
232 KDM5C in HeLa cells and ESCs^{45,57}. We thus used HOMER⁵⁸ to identify transcription factor motifs enriched
233 at KDM5C-bound or unbound germline gene promoters (TSS ± 500 bp, q-value < 0.1). MAX and E2F6 binding
234 sites were significantly enriched at germline genes bound by KDM5C in EpiLCs (MAX q-value: 0.0068, E2F6
235 q-value: 0.0673, E2F q-value: 0.0917), but not at germline genes unbound by KDM5C (Figure 5G). One third

236 of KDM5C-bound promoters contained the consensus sequence for either E2F6 (E2F, 5'-TCCCGC-3'), MGA
237 (E-box, 5'-CACGTG-3'), or both, but only 17% of KDM5C-unbound genes contained these motifs (Figure
238 5H). KDM5C-unbound germline genes were instead enriched for multiple RFX transcription factor binding
239 sites (RFX q-value < 0.0001, RFX2 q-value < 0.0001, RFX5 q-value < 0.0001) (Figure 5I, Supplementary
240 figure 1D). RFX transcription factors bind X-box motifs⁵⁹ to promote ciliogenesis^{60,61} and among them is
241 RFX2, a central regulator of post-meiotic spermatogenesis^{62,63}. Interestingly, RFX2 mRNA is derepressed
242 in *Kdm5c*-KO EpiLCs (Figure 5J), however it is also not a direct target of KDM5C (Supplementary figure
243 1E). Thus, RFX2 is a candidate transcription factor for driving the ectopic expression of KDM5C-unbound
244 germline genes in *Kdm5c*-KO cells.

245 **KDM5C is recruited to CpG islands at germline promoters to facilitate *de novo* DNA
246 methylation**

247 Previous work found two germline gene promoters have a marked reduction in DNA CpG methylation
248 (CpGme) in the *Kdm5c*-KO adult hippocampus¹³. Since histone 3 lysine 4 di- and trimethylation (H3K4me2/3)
249 impede *de novo* CpGme^{64,65}, KDM5C's removal of H3K4me2/3 may be required to suppress germline genes.
250 However, KDM5C's catalytic activity was recently shown to be dispensable for suppressing *Dazl* in ESCs⁴⁵.
251 To reconcile these observations, we hypothesized KDM5C erases H3K4me3 to promote the initial placement
252 of CpGme at germline gene promoters in EpiLCs.

253 To test this hypothesis, we first characterized KDM5C's expression as naïve ESCs differentiate into
254 EpiLCs (Figure 6A). While *Kdm5c* mRNA steadily decreased from 0 to 48 hours of differentiation (Figure
255 6B), KDM5C protein initially increased from 0 to 24 hours but then decreased to near knockout levels by 48
256 hours (Figure 6C). We then characterized KDM5C's substrates (H3K4me2/3) at germline gene promoters
257 with *Kdm5c* loss using published ChIP-seq datasets^{21,41}. *Kdm5c*-KO samples showed a marked increase in
258 H3K4me2 in EpiLCs (Figure 6D) and H3K4me3 in the amygdala (Figure 6E) around the TSS of germline
259 genes. Together, these data suggest KDM5C acts during the transition between ESCs and EpiLCs to remove
260 H3K4me2/3 at germline gene promoters.

261 Germline genes accumulate CpG methylation (CpGme) at CpG islands (CGIs) during the transition
262 from naïve to primed pluripotency^{18,20,66}. We first examined how many of our germline-enriched genes had
263 promoter CGIs (TSS ± 500 bp) using the UCSC genome browser⁶⁷. Notably, out of 1,288 germline-enriched
264 genes, only 356 (27.64%) had promoter CGIs (Figure 6F). CGI-containing germline genes had substantial
265 enrichment of meiotic gene ontologies compared to CGI-free genes, including meiotic nuclear division
266 (GO:0140013, p.adjust = 2.17e-12) and meiosis I (GO:0007127, p.adjust = 3.91e-10) (Figure 6G). Germline
267 genes with promoter CGIs were more highly expressed than CGI-free genes across spermatogenesis stages,
268 with highest expression in meiotic spermatocytes (Figure 6H). Contrastingly, CGI-free genes only displaying
269 substantial expression in post-meiotic round spermatids. Although only a minor portion of germline gene

270 promoters contained CGIs, CGIs strongly determined KDM5C's recruitment to germline genes, with 79.15%
271 ($p = 2.37e-67$, Odds Ratio = 17.8, Fisher's exact test) of KDM5C-bound germline gene promoters harboring
272 CGIs (Figure 6G).

273 To assess how KDM5C loss impacts initial CpGme placement at germline gene promoters, we performed
274 whole genome bisulfite sequencing (WGBS) in male wild-type and *Kdm5c*-KO ESCs and 96-hour extend
275 EpiLCs (exEpiLCs), when germline genes reach peak methylation level¹⁷ (Figure 6I). We first identified
276 which germline gene promoters significantly gained CpGme in wild-type cells during nESC to exEpiLCs
277 differentiation (methylKit⁶⁸, $q < 0.01$, $|methylation\ difference| \geq 25\%$, TSS ± 500 bp). In wild-type cells,
278 the majority of germline genes gained substantial CpGme at their promoter during differentiation (60.08%),
279 regardless if their promoter contained a CGI (Figure 6J).

280 We then identified promoters differentially methylated in wild-type versus *Kdm5c*-KO exEpiLCs (methylKit,
281 $q < 0.01$, $|methylation\ difference| > 25\%$, TSS ± 500 bp). Of the 48,882 promoters assessed, 274 promoters
282 were significantly hypomethylated and 377 promoters were significantly hypermethylated with KDM5C
283 loss (Supplementary figure 2A). Hypomethylated promoters were significantly enriched for germline gene
284 ontologies, such as meiotic nuclear division (GO:0140013, p.adjust = 0.012)(Supplementary figure 2B), with
285 10.22% of hypomethylated promoters belonging to germline genes. Approximately half of germline promoters
286 hypomethylated in *Kdm5c*-KO exEpiLCs are direct targets of KDM5C in EpiLCs (13 out of 28 hypomethylated
287 promoters). Promoters that showed the most robust loss of CpGme (lowest q-values) harbored CGIs (Figure
288 6K). CGI promoters, but not CGI-free promoters, had a significant reduction in CpGme with KDM5C loss
289 as a whole (Figure 6L) (Non-CGI promoters $p = 0.0846$, CGI promoters $p = 0.0081$, Mann-Whitney U test).
290 Significantly hypomethylated promoters included germline genes consistently dysregulated across multiple
291 *Kdm5c*-KO RNA-seq datasets¹³, such as *Naa11* and *D1PAs1* (methylation difference = -60.03%, q-value
292 = 3.26e-153) (Figure 6M). Surprisingly, we found only a modest reduction in CpGme at *Dazl*'s promoter
293 (methylation difference = -6.525%, q-value = 0.0159) (Figure 6N). Altogether, these results demonstrate
294 KDM5C is recruited to germline gene CGIs to promote CpGme at germline gene promoters. This suggests
295 KDM5C's catalytic activity is required for germline gene repression in EpiLCs, however some loci can
296 compensate for KDM5C loss through other silencing mechanisms, even when retaining H3K4me around
297 the TSS.

298 Discussion

299 In the above study, we demonstrate KDM5C's pivotal role in the development of tissue identity. We
300 first characterized tissue-enriched genes expressed within the *Kdm5c*-KO brain and identified substantial
301 derepression of testis, liver, muscle, and ovary-enriched genes. Testis genes significantly enriched within
302 the *Kdm5c*-KO amygdala and hippocampus are specific to the germline and not expressed within somatic
303 cells. *Kdm5c*-KO epiblast-like cells (EpiLCs) aberrantly express key drivers of germline identity and meiosis,

304 including *Dazl* and *Stra8*, while the adult brain primarily expresses genes important for late spermatogenesis.
305 We demonstrated that although *Kdm5c* mutant sex did not influence whether sperm or egg-specific genes
306 were misexpressed, female EpiLCs are more sensitive to germline gene de-repression. Germline genes
307 can become aberrantly expressed in *Kdm5c*-KO cells via an indirect mechanism, such as activation via
308 ectopic RFX transcription factors. Finally, we found KDM5C is dynamically regulated during ESC to EpiLC
309 differentiation to promote long-term germline gene silencing through DNA methylation at CpG islands.
310 Therefore, we propose KDM5C plays a fundamental role in the development of tissue identity during early
311 embryogenesis, including the establishment of the soma-germline boundary. By systematically characterizing
312 KDM5C's role in germline gene repression, we unveiled derepressive mechanisms governing distinct classes
313 of germline gene in somatic lineages. Furthermore, these data provide molecular footholds which can be
314 exploited to test the overarching contribution of ectopic germline gene expression upon neurodevelopment.

315 Although eggs and sperm employ the same transcriptional programs for shared functions, e.g. PGC
316 formation, meiosis, and genome defense, some germline genes are sex specific. We found *Kdm5c* mutant
317 males and females expressed both sperm and egg-biased genes, indicating the mechanism of derepression
318 is independent of a given germline gene's sex. However, organismal sex did greatly influence the degree of
319 germline gene dysregulation, as female *Kdm5c*-KO EpiLCs had over double the number of germline-enriched
320 DEGs compared to males. The lack of X-linked gene enrichment in females suggests that this greater
321 sensitivity to germline gene misexpress is not due to XCI defects previously reported in *Kdm5c*-KO females⁴¹.
322 Intriguingly, females with heterozygous loss of *Kdm5c* also had over double the number of germline DEGs
323 than hemizygous knockout males, even though their level of KDM5C should be roughly equivalent to that
324 of wild-type males. Increased female sensitivity to germline gene de-repression may be related to females
325 having a higher dose of KDM5C than males, due to its escape from XCI^{48–51}. KDM5C's Y-chromosome
326 homolog, KDM5D, exhibits weaker demethylase activity than KDM5C⁸ and it is currently unknown to regulate
327 germline gene expression. Altogether, these results suggests germline gene silencing mechanisms differ
328 between males and females, which warrants further study to identify the biological implications and underlying
329 mechanisms.

330 We found KDM5C is largely dispensable for promoting normal gene expression during development, yet is
331 critical for suppressing ectopic developmental programs. It is important to note that while we highlighted
332 KDM5C's regulation of germline genes, some germline-enriched genes are also expressed at the 2-cell
333 stage and in naïve ESCs for their role in pluripotency and self-renewal^{40,45,69,70}. Although expressed in
334 naïve ESCs, “self-renewal” germline genes like *Dazl* are silenced during ESC differentiation into epiblast
335 stem cells/EpiLCs^{17,18}. We found that while *Kdm5c*-KO EpiLCs also express *Dazl*, they did not express
336 2-cell-specific genes. These data suggest the 2-cell-like state reported in *Kdm5c*-KO ESCs⁴⁵ likely reflects
337 KDM5C's primary role in germline gene repression. Germline gene misexpression in *Kdm5c*-KO EpiLCs may
338 indicate they are differentiating into primordial germ cell-like cells (PGCLCs), rather than de-differentiating
339 into 2-cell-like cells^{33,34,36}. Yet, *Kdm5c*-KO EpiLCs had normal cellular morphology and properly expressed

340 markers for primed pluripotency, including *Otx2* which blocks EpiLC differentiation into PGCs/PGCLCs⁷¹.
341 In addition to unimpaired EpiLC differentiation, *Kdm5c*-KO gross brain morphology is overall normal¹² and
342 hardly any brain-specific genes were significantly dysregulated. Thus, ectopic germline gene expression
343 occurs along with proper somatic development in *Kdm5c*-KO animals.

344 Our work provides novel insight into the cross-talk between H3K4me and CpGme. In EpiLCs, loss of
345 KDM5C binding at a subset of germline gene promoters, e.g. *D1Pas1* and *Naa11*, strongly impaired CGI
346 methylation, and resulted in their long-lasting de-repression into adulthood. Removal of H3K4me2/3 at CGIs
347 is a plausible mechanism for KDM5C-mediated germline gene suppression^{13,72}, given H3K4me2/3 primarily
348 do not colocalize with CpGme⁷³ and can oppose DNMT3 activity^{64,65}. However, emerging work indicates
349 many histone-modifying enzymes have non-catalytic functions that influence gene expression, sometimes
350 even more potently than their catalytic roles^{74,75}. Indeed, KDM5C's catalytic activity was recently found to be
351 dispensible for repressing *Dazl* in ESCs⁴⁵. In our study, *Dazl*'s promoter still gained CpGme in *Kdm5c*-KO
352 exEpiLCs, even with elevated H3K4me2. *Dazl* and a few other germline gene CGIs use multiple repressive
353 mechanisms to facilitate CpGme^{16,17,46,47}. Together, this suggests alternative silencing mechanisms are
354 sufficient to recruit DNMT3s to some germline CGIs, while others may require KDM5C-mediated H3K4me
355 removal to overcome promoter CGI escape from CpGme^{73,76}. Furthermore, these results indicate the
356 requirement for catalytic activity can change depending upon the locus and developmental stage, even for
357 the same class of genes.

358 By generating a comprehensive list of mouse germline-enriched genes, we were able to reveal distinct
359 derepressive mechanisms governing early versus late-stage germline developmental programs. Previous
360 work on germline gene silencing has focused on genes with promoter CGIs^{18,73}, and indeed the major-
361 ity of KDM5C targets in EpiLCs were germ cell identity genes harboring CGIs. However, over 70% of
362 germline-enriched gene promoters lacked CGIs, including the many KDM5C-unbound germline genes
363 that were de-repressed in *Kdm5c*-KO cells. CGI-free, KDM5C-unbound germline genes were primarily
364 late-stage spermatogenesis genes and significantly enriched for RFX2 binding sites, a central regulator
365 of spermiogenesis^{62,63}. These data suggest that once activated during early embryogenesis, drivers of
366 germline identity like *Rfx2*, *Stra8*, and *Dazl* turn on downstream germline programs, ultimately culminating in
367 the expression of spermiogenesis genes in the adult *Kdm5c*-KO brain. Therefore, we propose KDM5C is
368 recruited via promoter CGIs to genes that shape germ cell formation and acts as break against runaway
369 activation of germline-specific programs.

370 The above work provides the mechanistic foundation for KDM5C-mediated repression of tissue and
371 germline-specific genes. However, the contribution of these ectopic, tissue-specific genes towards *Kdm5c*-
372 KO neurological impairments is still unknown. In addition to germline genes, we also identified significant
373 enrichment of muscle, liver, and even ovary-biased transcripts within the male *Kdm5c*-KO brain. Intriguingly,
374 select liver and muscle-biased DEGs do have known roles within the brain, such as the liver-enriched lipid
375 metabolism gene *Apolipoprotein C-I (Apoc1)*²⁷. *APOC1* dysregulation is implicated in Alzheimer's disease in

376 humans²⁸ and overexpression of *Apoc1* in the mouse brain can impair learning and memory⁷⁷. KDM5C may
377 therefore be crucial for neurodevelopment by fine-tuning the expression of tissue-enriched, dosage-sensitive
378 genes like *Apoc1*. Given germline genes have no known functions within the brain, their impact upon
379 neurodevelopment is currently unknown. Ectopic testicular germline transcripts have been observed in a
380 variety of cancers^{78,79}, including brain tumors in *Drosophila* and mammals and shown to promote cancer
381 progression^{80–82}. Intriguingly, mouse and human models for other chromatin-linked neurodevelopmental
382 disorders also display impaired soma-germline demarcation^{7,83–86}, such as DNA methyltransferase 3b
383 (DNMT3B), H3K9me1/2 methyltransferases G9A/GLP, methyl-CpG -binding protein 2 (MECP2)⁸³. Thus,
384 KDM5C is among a growing cohort of chromatin-linked neurodevelopmental disorders with similar erosion of
385 the germline versus soma boundary. Further research is required to determine the impact of these germline
386 genes and the extent to which this phenomenon occurs in humans.

387 Materials and Methods

388 Classifying tissue-enriched and germline-enriched genes

389 Tissue-enriched differentially expressed genes (DEGs) were determined by their classification in a previ-
390 ously published dataset from 17 male and female mouse tissues²². This study defined tissue expression as
391 greater than 1 Fragments Per Kilobase of transcript per Million mapped read (FPKM) and tissue enrichment
392 as at least 4-fold higher expression than any other tissue.

393 We curated a list of germline-enriched genes using an RNA-seq dataset from wild-type and germline-
394 depleted (Kit^{W/Wv}) male and female mouse embryos from embryonic day 12, 14, and 16³², as well as adult
395 male testes²⁹. Germline-enriched genes met the following criteria: 1) their expression is greater than 1
396 FPKM in wild-type germline 2) their expression in any wild-type somatic tissues²² does not exceed 20%
397 of maximum expression in wild-type germline, and 3) their expression in the germ cell-depleted (Kit^{W/Wv})
398 germline, for any sex or time point, does not exceed 20% of maximum expression in wild-type germline. We
399 defined sperm and egg-biased genes as those whose expression in the opposite sex, at any time point, is no
400 greater than 20% of the gene's maximum expression in a given sex. Genes that did not meet this threshold
401 for either sex were classified as 'unbiased'.

402 Cell culture

403 We utilized our previously established cultures of male wild-type and *Kdm5c* knockout (-KO) embryonic
404 stem cells⁴¹. Sex was confirmed by genotyping *Uba1/Uba1y* on the X and Y chromosomes with the following
405 primers: 5'-TGGATGGTGTGCCAATG-3', 5'-CACCTGCACGTTGCCCTT-3'. Deletion of *Kdm5c* was
406 confirmed through the primers 5'-ATGCCCATATTAAGAGTCCTG-3', 5'-TCTGCCTTGATGGGACTGTT-3',
407 and 5'-GGTTCTCAACACTCACATAGTG-3'.

408 Embryonic stem cells (ESCs) and epiblast-like cells were cultured using previously established
409 methods³⁷. Briefly, ESCs were initially cultured in primed ESC (pESC) media consisting of KnockOut
410 DMEM (Gibco#10829–018), fetal bovine serum (Gibco#A5209501), KnockOut serum replacement
411 (Invitrogen#10828–028), Glutamax (Gibco#35050-061), Anti-Anti (Gibco#15240-062), MEM Non-essential
412 amino acids (Gibco#11140-050), and beta-mercaptoethanol (Sigma#M7522). They were then transitioned
413 into ground-state, “naïve” ESCs (nESCs) by culturing for four passages in N2B27 media containing
414 DMEM/F12 (Gibco#11330–032), Neurobasal media (Gibco#21103–049), Gluamax (Gibco#35050-061),
415 Anti-Anti (Gibco#15240-062), N2 supplement (Invitrogen#17502048), and B27 supplement without vitamin
416 A (Invitrogen#12587-010), and beta-mercaptoethanol. Both pESC and nESC media were supplemented
417 with 3 μ M GSK3 inhibitor CHIR99021 (Sigma #SML1046-5MG), 1 μ M MEK inhibitor PD0325901 (Sigma
418 #PZ0162-5MG), and 1,000 units/mL leukemia inhibitory factor (LIF, Millipore#ESG1107).

419 nESCs were differentiated into epiblast-like cells (EpiLCs, 48 hours) and extendend EpiLCs (exEpiLCs,
420 96 hours) by culturing in N2B27 media containing DMEM/F12, Neurobasal media, Gluamax, Anti-Anti,
421 N2 supplement, B27 supplement (Invitrogen#17504044), beta-mercaptoethanol, fibroblast growth factor 2
422 (FGF2, R&D Biotechne 233-FB), and activin A (R&D Biotechne 338AC050CF), as previously described³⁷.

423 Real time quantitative PCR (RT-qPCR)

424 nESCs were differentiated into EpiLCs as described above. Cells were lysed with Tri-reagent BD (Sigma
425 #T3809) at 0, 24, and 48 hours of differentiation. RNA was phase separated with 0.1 uL/uL 1-bromo-3-
426 chloropropane (Sigma #B9673) and then precipitated with isopropanol (Sigma #I9516). For each sample,
427 2 ug of RNA was reverse transcribed using the ProtoScript II Reverse transcriptase kit from New England
428 Biolabs (NEB #M0368S) and primed with oligo dT. Expression of *Kdm5c* was detected using the primers
429 5'-CCCATGGAGGCCAGAGAATAAG-3' 5'-CTCAGCGATAAGAGAATTGCTAC-3' and normalized to TBP
430 with the Power SYBR™ Green PCR Master Mix (ThermoFisher #4367659).

431 Western Blot

432 Total protein was extracted during nESC to EpiLC differentiation at 0, 24, and 48 hours by sonicating cells
433 at 20% amplitude for 15 seconds in 2X SDS sample buffer, then boiling at 100 °C for 10 minutes. Proteins
434 were separated on a 7.5% SDS page gel, transferred overnight onto a fluorescent membrane, blotted for
435 rabbit anti-KDM5C (in house, 1:500) and mouse anti-DAXX (Santa Cruz #(H-7): sc-8043, 1:500) imaged
436 using the LiCor Odyssey CLx system. Band intensity was quantified using ImageJ.

437 RNA sequencing (RNA-seq) data analysis

438 After ensuring read quality via FastQC (v0.11.8), reads were then mapped to the mm10 *Mus musculus*
439 genome (Gencode) using STAR (v2.5.3a), during which we removed duplicates and kept only uniquely

440 mapped reads. Count files were generated by FeatureCounts (Subread v1.5.0), and BAM files were
441 converted to bigwigs using deeptools (v3.1.3) and visualized by the UCSC genome browser. RStudio (v3.6.0)
442 was then used to analyze counts files by DESeq2 (v1.26.0)²³ to identify differentially expressed genes
443 (DEGs) with a q-value (p-adjusted via FDR/Benjamini–Hochberg correction) less than 0.1 and a log2 fold
444 change greater than 0.5. For all DESeq2 analyses, log2 fold changes were calculated with IfcShrink using
445 the ashr package⁸⁷. MA-plots were generated by ggpahr (v0.6.0), and Eulerr diagrams were generated by
446 eulerr (v6.1.1). Boxplots and scatterplots were generated by ggpahr (v0.6.0) and ggplot2 (v3.3.2). The Upset
447 plot was generated via the package UpSetR (v1.4.0)⁸⁸. Gene ontology (GO) analyses were performed by
448 the R package enrichPlot (v1.16.2) using the biological processes setting and compareCluster.

449 **Chromatin immunoprecipitation followed by DNA sequencing (ChIP-seq) data analysis**

450 ChIP-seq reads were aligned to mm10 using Bowtie1 (v1.1.2) allowing up to two mismatches. Only
451 uniquely mapped reads were used for analysis. Peaks were called using MACS2 software (v2.2.9.1) using
452 input BAM files for normalization, with filters for a q-value < 0.1 and a fold enrichment > 1. We removed
453 “black-listed” genomic regions that often give aberrant signals. Common peak sets were obtained in R via
454 DiffBind[estrogen@ross-innesDifferentialOestrogenReceptor2012] (v3.6.5). In the case of KDM5C ChIP-seq,
455 *Kdm5c*-KO peaks were then subtracted from wild-type samples using bedtools (v2.25.0). Peak proximity
456 to genome annotations was determined by ChIPSeeker⁸⁹ (v1.32.1). Gene ontology (GO) analyses were
457 performed by the R package enrichPlot (v1.16.2) using the biological processes setting and compareCluster.
458 Enriched motifs were identified using HOMER⁵⁸. Average binding across the genome was visualized using
459 deeptools (v3.1.3). Bigwigs were visualized using the UCSC genome browser.

460 **CpG island (CGI) analysis**

461 Locations of CpG islands were determined through the mm10 UCSC genome browser CpG island track⁶⁷,
462 which classified CGIs as regions that have greater than 50% GC content, are larger than 200 base pairs,
463 and have a ratio of CG dinucleotides observed over the expected amount greater than 0.6. CGI genomic
464 coordinates were then annotated using ChIPseeker⁸⁹ (v1.32.1) and filtered for ones that lie within promoters
465 of our germline-enriched genes (TSS ± 500).

466 **Whole genome bisulfite sequencing (WGBS)**

467 Genomic DNA (gDNA) from naïve ESCs and extended EpiLCs was extracted using the Wizard Genomic
468 DNA Purification Kit (Promega A1120), following the instructions for Tissue Culture Cells. gDNA from
469 two wild-types and two *Kdm5c*-KOs of each cell type was sent to Novogene for WGBS using the Illumina
470 NovaSeq X Plus platform and sequenced for 150bp paired-end reads (PE150). All samples had greater
471 than 99% bisulfite conversion rates. Reads were adapter and quality trimmed with Trim Galore (v0.6.10)

472 and aligned to the mm10 genome using Bismark⁹⁰ (v0.22.1). Analysis of differential methylation at germline
473 gene promoters was performed using methylKit⁶⁸ (v1.28.0) with a minimum coverage of 3 paired reads, a
474 percentage cut-off of 25%, and q-value of 0.01. methylKit was also used to calculate average percentage
475 methylation at germline gene promoters. Methylation bedgraph tracks were generated via Bismark and
476 visualized using the UCSC genome browser.

477 **Data availability**

478 **Published datasets**

479 All published datasets are available at the Gene Expression Omnibus (GEO) <https://www.ncbi.nlm.nih.gov/geo>. Published RNA-seq datasets analyzed in this study included the male wild-type and *Kdm5c*-KO
480 adult amygdala and hippocampus²¹ (available at GEO: GSE127722) and male wild-type and *Kdm5c*-KO
481 EpiLCs⁴¹ (available at GEO: GSE96797).

482 Previously published ChIP-seq experiments included KDM5C in wild-type and *Kdm5c*-KO EpiLCs⁴¹ (avail-
483 able at GEO: GSE96797) and mouse primary neuron cultures (PNCs) from the cortex and hippocampus¹²
484 (available at GEO: GSE61036). ChIP-seq of histone 3 lysine 4 dimethylation in male wild-type and *Kdm5c*-KO
485 EpiLCs⁴¹ is also available at GEO: GSE96797. ChIP-seq of histone 3 lysine 4 trimethylation in wild-type and
486 *Kdm5c*-KO male amygdala²¹ are available at GEO: GSE127817.

488 **Data analysis**

489 Scripts used to generate the results, tables, and figures of this study are available via the GitHub
490 repository: XXX

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503 **Author contributions**

504 K.M.B. and S.I. conceived the study and designed the experiments. I.V. generated the ESC and exEpiLC
505 WGBS data. K.M.B performed the data analysis and all other experiments. K.M.B and S.I. wrote and edited
506 the manuscript.

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688 **Figures and Tables**

- 689 • Supplementary table 1: list of all germline genes.
- 690 – Columns to include:
- 691 * KDM5C bound vs not
- 692 * Log2fc in EpiLC, brain (separate columns?)
- 693 – CGI vs non

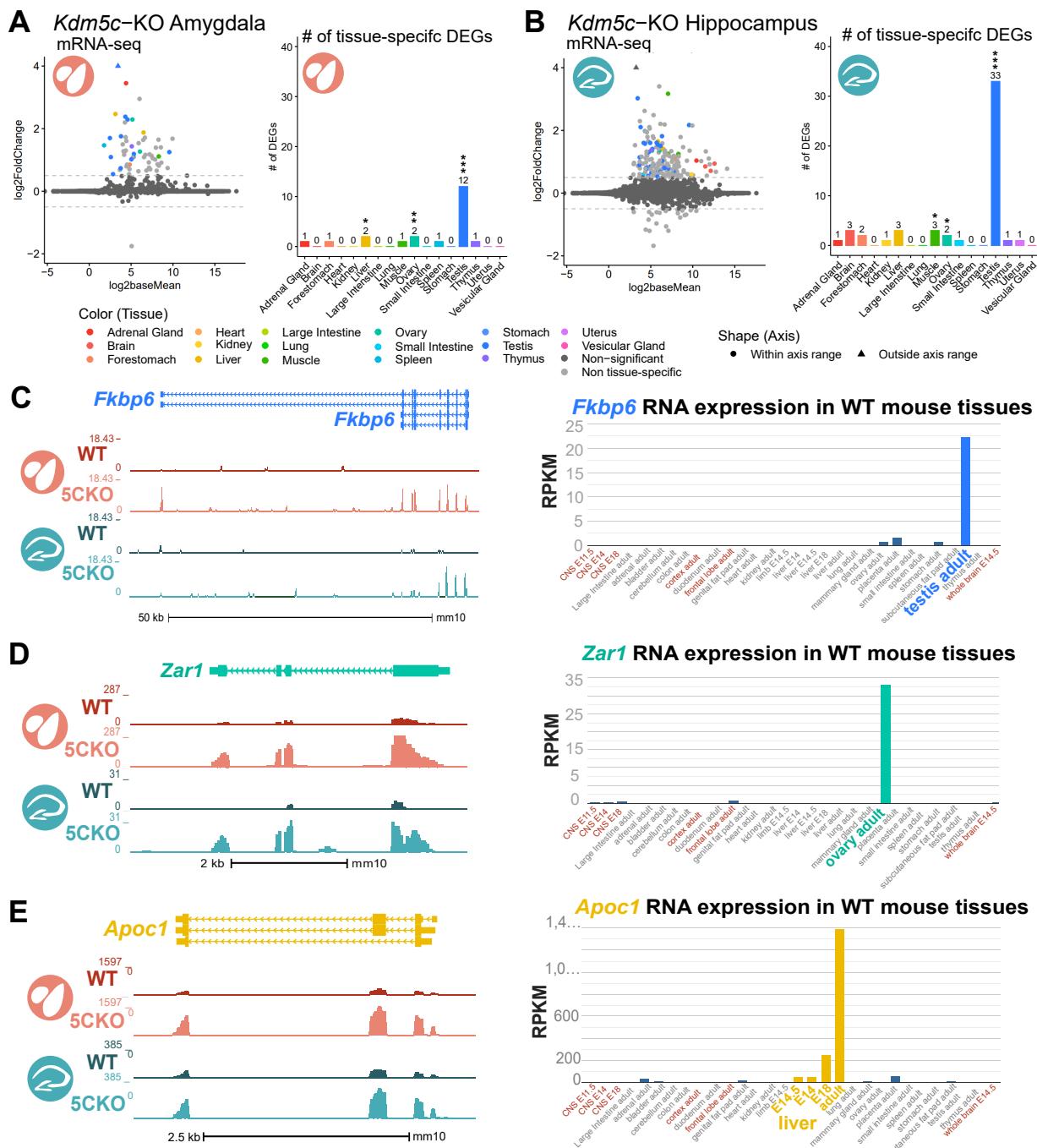


Figure 1: Tissue-enriched genes are misexpressed in the *Kdm5c*-KO brain. **A-B.** Expression of tissue-enriched genes (Li et al 2017) in the male *Kdm5c*-KO amygdala (A) and hippocampus (B). Left - MA plot of mRNA-sequencing. Right - Number of tissue-enriched differentially expressed genes (DEGs). * p<0.05, ** p<0.01, *** p<0.001, Fisher's exact test. **C.** Left - UCSC browser view of an example aberrantly expressed testis-enriched DEG, *FK506 binding protein 6* (*Fkbp6*) in the wild-type (WT) and *Kdm5c*-KO (5CKO) amygdala (red) and hippocampus (teal) (Average, n = 4). Right - Expression of *Cyct* in wild-type tissues from NCBI Gene, with testis highlighted in blue and brain tissues highlighted in red. **D.** Left - UCSC browser view of an example ovary-enriched DEG, *Zygotic arrest 1* (*Zar1*). Right - Expression of *Zar1* in wild-type tissues from NCBI Gene, with ovary highlighted in teal and brain tissues highlighted in red. **E.** Left - UCSC browser view of an example liver-enriched DEG, *Apolipoprotein C-I* (*Apoc1*). Right - Expression of *Apoc1* in wild-type tissues from NCBI Gene, with liver highlighted in orange and brain tissues highlighted in red.

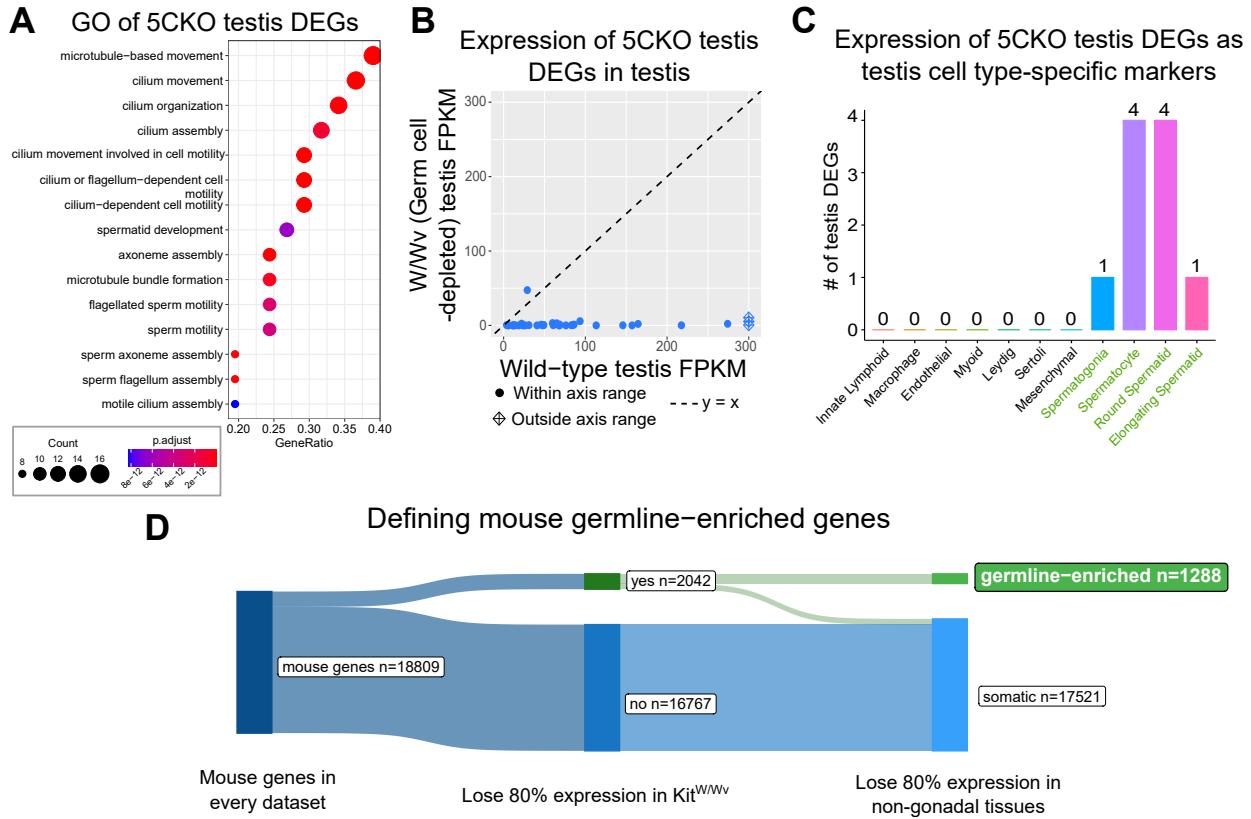


Figure 2: Aberrant transcription of germline genes in the *Kdm5c*-KO in the brain. **A.** enrichPlot gene ontology (GO) of *Kdm5c*-KO amygdala and hippocampus testis-enriched DEGs **B.** Expression of testis DEGs in wild-type (WT) testis versus germ cell-depleted (W/Wv) testis (Mueller et al 2013). Expression is in Fragments Per Kilobase of transcript per Million mapped reads (FPKM). **C.** Number of testis DEGs that were classified as cell-type specific markers in a single cell RNA-seq dataset of the testis (Green et al 2018). Germline cell types are highlighted in green, somatic cell types in black. **D.** Sankey diagram of mouse genes filtered for germline enrichment based on their expression in wild-type and W/Wv mice and in adult mouse non-gonadal tissues (Li et al 2017).

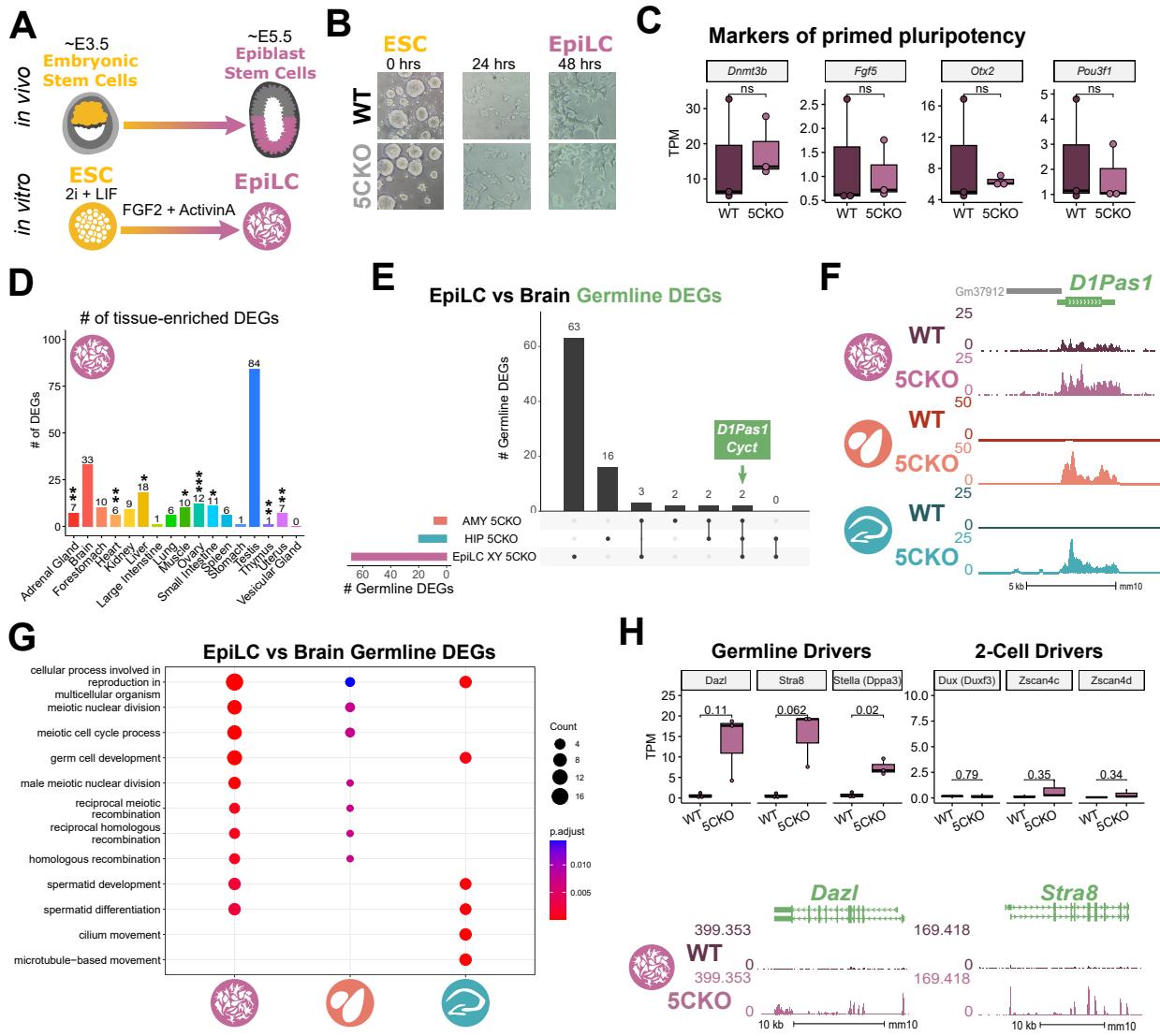


Figure 3: Kdm5c-KO epiblast-like cells express key drivers of germline identity **A.** Top - Diagram of *in vivo* differentiation of embryonic stem cells (ESCs) of the inner cell mass into epiblast stem cells. Bottom - *in vitro* differentiation of ESCs into epiblast-like cells (EpiLCs). **B.** Representative images of male wild-type (WT) and *Kdm5c*-KO (5CKO) cells during ESC to EpiLC differentiation. Brightfield images taken at 20X. **C.** No significant difference in primed pluripotency marker expression in wild-type versus *Kdm5c*-KO EpiLCs. Welch's t-test, expression in transcripts per million (TPM). **D.** Number of tissue-enriched differentially expressed genes (DEGs) in *Kdm5c*-KO EpiLCs. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Fisher's exact test. **E.** Upset plot displaying the overlap of germline DEGs expressed in *Kdm5c*-KO EpiLCs, amygdala (AMY), and hippocampus (HIP) RNA-seq datasets. **F.** UCSC browser view of an example germline gene, *D1Pas1*, that is dysregulated *Kdm5c*-KO EpiLCs (top, purple. Average, $n = 3$), amygdala (middle, red. Average, $n = 4$), and hippocampus (bottom, blue. Average, $n = 4$). **G.** enrichPlot gene ontology analysis comparing enriched biological processes for *Kdm5c*-KO EpiLC, amygdala, and hippocampus germline DEGs. **H.** Top left - Example germline identity DEGs unique to EpiLCs. Top right - Example 2-cell genes that are not dysregulated in *Kdm5c*-KO EpiLCs. p-values for Welch's t-test. Bottom - UCSC browser view of *Dazl* and *Stra8* expression in wild-type and *Kdm5c*-KO EpiLCs (Average, $n = 3$).

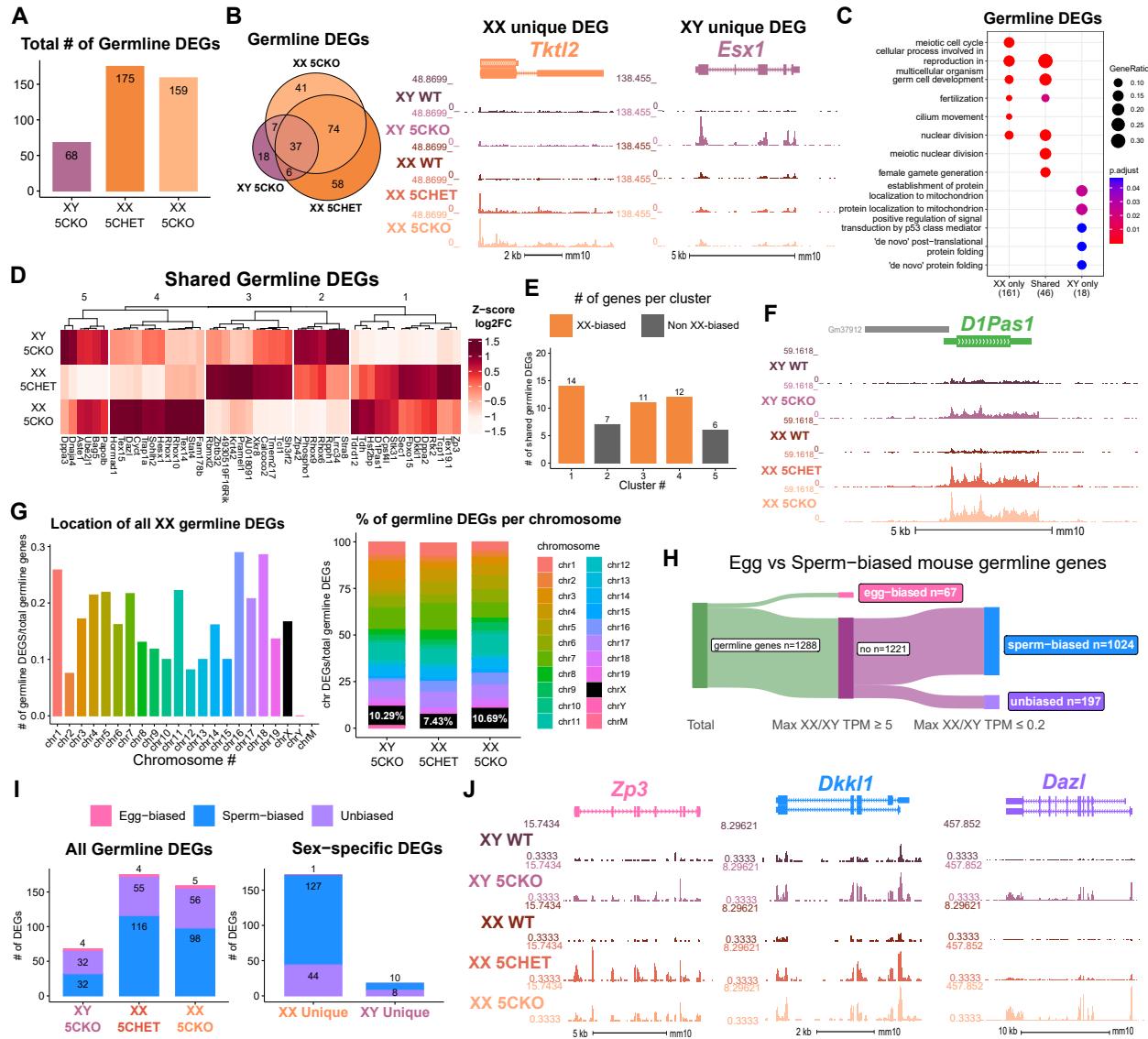


Figure 4: Chromosomal sex influences *Kdm5c*-KO germline gene misexpression. **A.** Total number of germline-enriched RNA-seq DEGs for male hemizygous *Kdm5c* knockout EpilCs (XY 5CKO, purple), female heterozygous *Kdm5c* knockout (XX 5CHET, orange), female homozygous *Kdm5c* knockout (XX 5CKO, light orange) EpilCs. **B.** Left - Eulerr overlap of *Kdm5c* mutant male and female EpilC germline DEGs. Right - Example of germline DEGs unique to females or males, *Tktl2* and *Esx1*. **C.** enrichPlot gene ontology analysis comparing enriched biological processes for germline DEGs shared between *Kdm5c* mutant males and females, or unique to one sex (XX only or XY only). **D.** Heatmap of germline DEGs shared between male and female mutants. Color is the average log 2 fold change from sex-matched wild-type. **E.** Number of genes within each cluster from D. Clusters with higher expression in females compared to males (XX-biased) highlighted in orange. **F.** UCSC browser view of a male and female shared germline DEG *D1Pas1* that is more highly expressed in female mutants (Average, n = 3). **G.** Left - Number of all female germline DEGs located on each chromosome over the total number of germline-enriched genes on that chromosome. Right - Percentage of germline DEGs that lie on each chromosome for each *Kdm5c* mutant. X chromosome highlighted in black. **H.** Sankey diagram classifying egg-biased (pink) and sperm-biased (blue) and unbiased (purple) mouse germline-enriched genes. **I.** Number of egg, sperm, or unbiased germline DEGs for male and female *Kdm5c* mutants. **J.** Example bigwigs of egg-biased (*Zp3*), sperm-biased (*Dkk1*), and unbiased (*Dazl*) germline genes dysregulated in both male and female *Kdm5c* mutants.

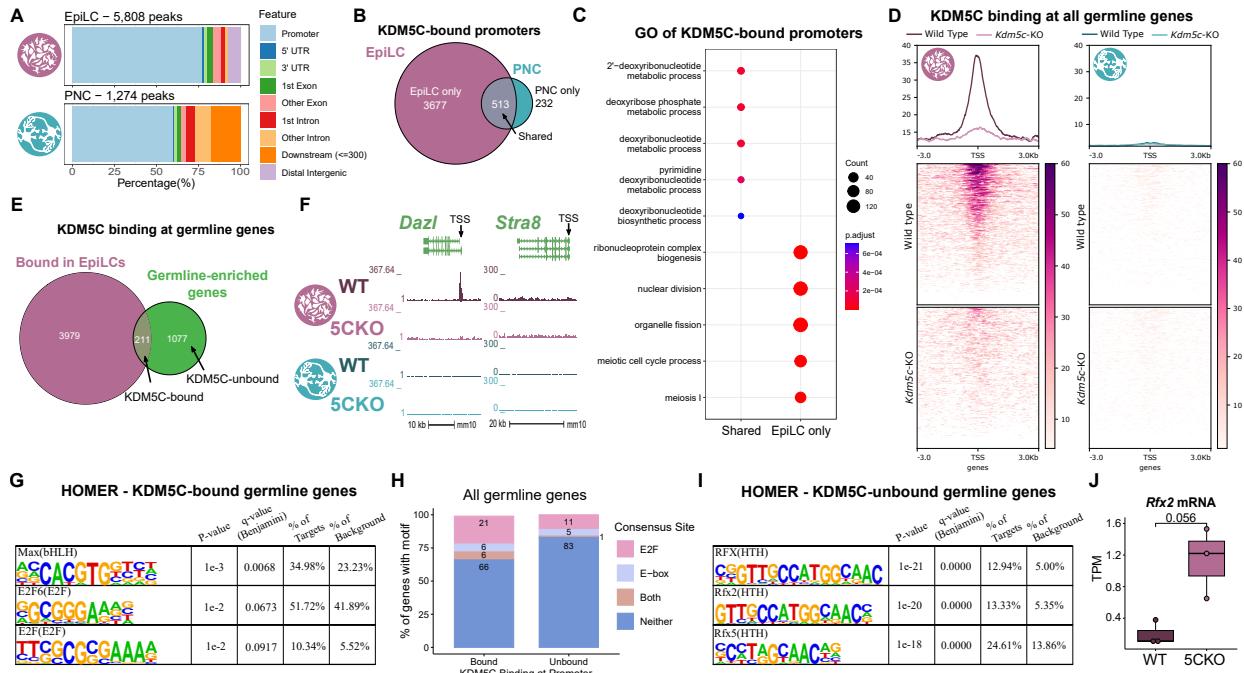


Figure 5: KDM5C binds to a subset of germline gene promoters during early embryogenesis. **A.** ChIPseeker localization of KDM5C peaks at different genomic regions in EpiLCs (top) and hippocampal and cortex primary neuron cultures (PNCs, bottom). **B.** Overlap of genes with KDM5C bound to their promoters ($TSS \pm 500$) in EpiLCs (purple) and PNCs (blue). **C.** Gene ontology (GO) comparison of genes with KDM5C bound to their promoter in EpiLCs and PNCs. Genes were classified as either bound in EpiLCs only (EpiLC only), unique to PNCs (PNC only, no significant ontologies) or bound in both PNCs and EpiLCs (Shared). **D.** Average KDM5C binding around the transcription start site (TSS) of all germline-enriched genes in EpiLCs (left) and PNCs (right). **E.** Eulerr overlap of germline-enriched genes (green) with significant KDM5C binding at their promoter in EpiLCs (purple). **F.** Example KDM5C ChIP-seq signal around the *Dazl* TSS but not *Stra8* in EpiLCs. **G.** HOMER motif analysis of all KDM5C-bound germline gene promoters, highlighting significant enrichment of MAX, E2F6, and E2F motifs. **H.** Number of all gene promoters bound or unbound by KDM5C with instances of the E2F or E-box consensus sequence. **I.** HOMER motif analysis of all KDM5C-unbound germline gene promoters, highlighting significant enrichment of RFX family transcription factor motifs. **J.** Expression of RNA-seq DEG *Rfx2* in wild-type and *Kdm5c*-KO EpiLCs. P-value of Welch's t-test, expression in transcripts per million (TPM).

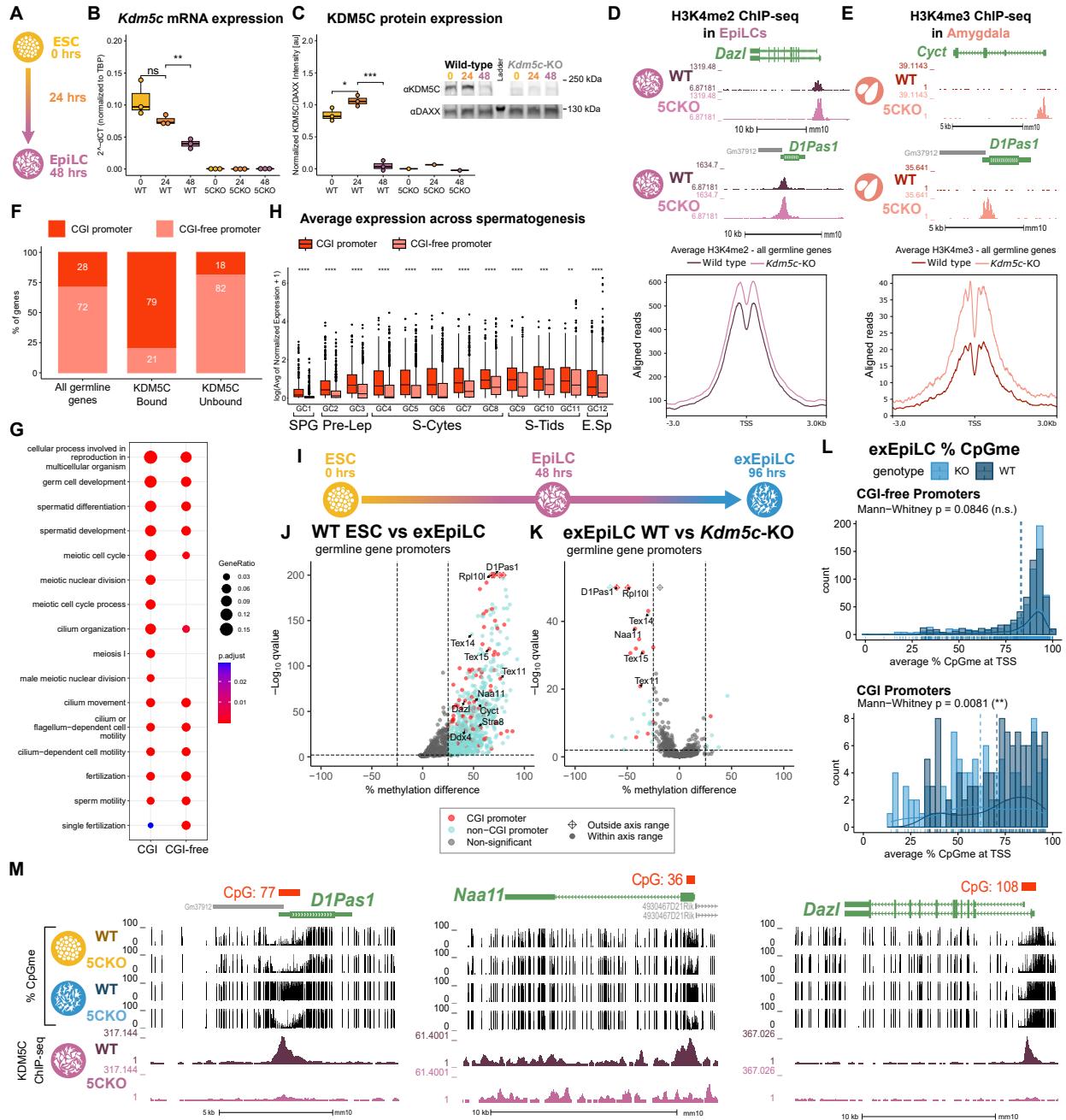


Figure 6: KDM5C promotes long-term silencing of germline genes via DNA methylation at CpG islands. **A.** Diagram of embryonic stem cell (ESC) to epiblast-like cell (EpiLC) differentiation and collection time points. **B.** Real time quantitative PCR (RT-qPCR) of *Kdm5c* mRNA expression in wild-type (WT) and *Kdm5c*-KO (5CKO) ESCs at 0, 24, and 48 hours of differentiation into EpiLCs. Expression calculated in comparison to TBP mRNA expression ($2^{-\Delta\Delta CT}$). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Welch's t-test. **C.** KDM5C protein expression normalized to DAXX. Quantified intensity using ImageJ (artificial units - au). Right - representative lanes of Western blot for KDM5C and DAXX. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Welch's t-test. **D.** Top - Representative UCSC browser view of histone 3 lysine 4 dimethylation (H3K4me2) ChIP-seq signal at two germline genes in wild-type and *Kdm5c*-KO EpiLCs. Bottom - Average H3K4me2 signal at the TSS of all germline-enriched genes in wild-type (dark purple) and *Kdm5c*-KO (light purple) EpiLCs. **E.** Top - Representative UCSC browser view of histone 3 lysine 4 trimethylation (H3K4me3) ChIP-seq signal at two germline genes in the wild-type (WT) and *Kdm5c*-KO (5CKO) adult amygdala. Bottom - Average H3K4me3 signal at the transcription start site (TSS) of all germline-enriched genes in wild-type (dark red) and *Kdm5c*-KO (light red) amygdala. **F.** Percentage of germline genes that harbor CpG islands (CGIs) in their promoters (CGI promoter, red), based on UCSC annotation. Left - percentage of all germline-enriched genes, middle - KDM5C-bound germline genes, and right - KDM5C-unbound germline genes. (Legend continued on next page.)

Figure 6: KDM5C promotes long-term silencing of germline genes via DNA methylation at CpG islands. (Legend continued.) **G.** enrichPlot gene ontology analysis of germline genes with (CGI-promoter) or without (CGI-free) CGIs in their promoter. **H.** Expression of germline genes with (CGI-promoter, red) or without (CGI-free, salmon) CGIs in their promoter across stages of spermatogenesis from Green et al 2018. SPG - spermatogonia, Pre-Lep - preleptotene spermatocytes, S-Cytes - meiotic spermatocytes, S-Tids - post-meiotic haploid round spermatids, E.Sp - elongating spermatids. Wilcoxon test, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$. **I.** Diagram of ESC to extended EpiLC (exEpiLC) differentiation. **J.** Volcano plot of whole genome bisulfite sequencing (WGBS) comparing CpG methylation (CpGme) at germline gene promoters ($TSS \pm 500$) in wild-type (WT) ESCs versus exEpiLCs. Significantly differentially methylated promoters ($q < 0.01$, $|methylated difference| > 25\%$) with CGIs in red, CGI-free promoters in light blue **K.** Volcano plot of WGBS of wild-type (WT) versus *Kdm5c*-KO exEpiLCs for germline gene promoters. Promoters with CGIs in red, CGI-free promoters in light blue. **L.** Histogram of average percent CpGme at the promoter of germline genes with or without CGIs. Wild-type in navy and *Kdm5c*-KO (KO) in light blue. Dashed lines are average methylation for each genotype, p-values for Mann-Whitney U test. **M.** UCSC browser view of germline genes, showing UCSC annotated CGI with number of CpGs, representative CpGme in wild-type (WT) and *Kdm5c*-KO (5CKO) ESCs and exEpiLCs, and KDM5C ChIP-seq signal in EpiLCs.