

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

3

4    **Abstract**

5       It is currently unclear why mutations in numerous chromatin-modifying enzymes cause neurodevelopmen-  
6       tal disorders (NDDs). While some chromatin regulators are important for neuron-specific gene expression,  
7       loss of repressive chromatin regulators can also lead to the aberrant transcription of tissue-specific genes  
8       outside of their intended context. Because very few studies have characterized the these aberrant, tissue-  
9       specific transcripts, the mechanisms behind their dysregulation and their functional consequences are  
10      largely unknown. Here, we explored this crisis in cellular identity in NDDs by investigating the ectopic  
11      expression of germline (e.g. sperm and egg) genes in mice lacking lysine demethylase 5c (KDM5C, also  
12      known as JARID1C or SMCX), an eraser of histone 3 lysine 4 di and tri-methylation (H3K4me2/3). We found  
13      male *Kdm5c* knockout (-KO) mice, which recapitulate key behavioral phenotypes of Claes-Jensen X-linked  
14      intellectual disability (MRXSCJ, OMIM: 300534), aberrantly expresses many liver, muscle, ovary, and testis  
15      genes within the amygdala and hippocampus. Many genes expressed in the *Kdm5c*-KO brain were typically  
16      unique to germ cells, indicating an erosion of the soma-germline boundary. Using germ cell-depleted RNA  
17      sequencing datasets, we curated a a list of germline-enriched genes for unbiased characterization of KDM5C  
18      in germline gene repression. Germline genes are typically decommissioned in somatic lineages in the  
19      post-implantation epiblast, yet *Kdm5c*-KO epiblast-like cells (EpiLCs) aberrantly expressed key regulators of  
20      germline identity and meiosis, including *Dazl* and *Stra8*. We found that while KDM5C promotes the initial  
21      placement of DNA methylation at a subset of germline gene promoters in EpiLCs, germline genes can also  
22      become activated independent of direct KDM5C regulation. Intriguingly, many of the germline transcripts  
23      expressed in the *Kdm5c*-KO brain were late-stage spermatogenesis genes that are not directly bound  
24      by KDM5C. This suggests germline developmental programs can progress ectopically in the background  
25      of typical *Kdm5c*-KO development. Ultimately, this work provides novel insight into the demarcation of  
26      somatic and germline lineages in mammals while also characterizing the cellular identity crisis within a  
27      chromatin-linked neurodevelopmental disorder.

## 28 Introduction

29 A single genome holds the instructions to generate the myriad of cell types found within the adult organism.  
30 This is, in part, accomplished by chromatin regulators that can either promote or impede lineage-specific  
31 gene expression through DNA and histone modifications<sup>1,2</sup>. Although many chromatin regulators were initially  
32 identified for their roles in shaping cellular and tissue identity<sup>3,4</sup>, recent advancements in next generation  
33 sequencing unexpectedly revealed many neurodevelopmental disorders (NDDs) are caused by mutations in  
34 chromatin regulators<sup>5</sup>. Several studies have suggested this connection between chromatin regulators and  
35 neurodevelopment is due to their regulation of brain-specific genes, such as orchestrating transcriptional  
36 programs for synaptic maturation<sup>6</sup> and transitioning between neuronal and glial fates during neural precursor  
37 differentiation<sup>7</sup>. However, loss of some chromatin regulators can also result in the ectopic transcription of  
38 tissue-specific genes outside of their target environment<sup>3,4,8</sup>, such as the misexpression of liver-specific  
39 genes within adult neurons<sup>9</sup>. Very few studies have investigated the misexpression of tissue-specific genes  
40 in chromatin-linked NDDs<sup>9,10</sup> and it is currently unknown if this partial loss of brain identity contributes to  
41 neurodevelopmental impairments.

42 To elucidate the role of tissue identity in chromatin-linked neurodevelopmental disorders, it is essential  
43 to first characterize the types of genes dysregulated and the molecular mechanisms governing their de-  
44 repression. In this study, we characterized the aberrant expression of tissue-enriched genes with loss of  
45 lysine demethylase 5C (KDM5C). KDM5C, , also known as SMCX or JARID1C, is a chromatin regulator that  
46 can repress gene expression through erasure of histone 3 lysine 4 di- and trimethylation (H3K4me2/3)<sup>11</sup>,  
47 marks enriched at active gene promoters. Pathogenic mutations in *KDM5C* cause Intellectual Developmental  
48 Disorder, X-linked, Syndromic, Claes-Jensen Type (MRXSCJ, OMIM: 300534), whose predominant features  
49 include intellectual disability, seizures, aberrant aggression, and autistic behaviors<sup>12–14</sup>. *Kdm5c* knockout  
50 (-KO) mice recapitulate key MRXSCJ patient phenotypes, including hyperaggression, increased seizure  
51 propensity, and learning impairments<sup>10,15</sup>. Unexpectedly, RNA sequencing (RNA-seq) of the *Kdm5c*-KO  
52 hippocampus revealed ectopic expression of testis genes within the brain<sup>10</sup>. It is currently unknown if this  
53 dysregulation of brain tissue identity further impairs *Kdm5c*-KO neurodevelopment and if ectopic gene  
54 expression within the *Kdm5c*-KO brain is unique to testis genes.

- 55 • one key process chrom reg are involved in are is distinguishing bw germ + soma cell identity

56 Distinguishing between the germline (cells that pass on their genetic material, e.g. sperm and eggs) and  
57 the soma (cells that perform all other bodily functions) is a key feature of multicellularity and occurs during  
58 early embryogenesis. In mammals, chromatin regulators play a key role in decommissioning germline genes  
59 in somatic cells during the transition from naïve to primed pluripotency by placing repressive histone H2A  
60 lysine 119 monoubiquitination (H2AK119ub1)<sup>16</sup>, histone 3 lysine 9 trimethylation (H3K9me3)<sup>16,17</sup>, and DNA  
61 CpG methylation<sup>17–19</sup> at germline gene promoters. Systematically characterizing KDM5C's role in germline  
62 gene repression during early embryogenesis will unveil key mechanisms underlying the demarcation between

63 soma and germline identity and while also providing molecular footholds to test the impact of ectopic germline  
64 genes on neurodevelopment.

65 To illuminate KDM5C's role in tissue identity, here we characterized the aberrant transcription of tissue-  
66 enriched genes within the *Kdm5c*-KO brain and epiblast-like stem cells (EpiLCs), an *in vitro* model of  
67 the post-implantation embryo. We observed general dysregulation of tissue-enriched genes in both the  
68 *Kdm5c*-KO brain and EpiLCs, including misexpression of genes typically highly enriched within the testis,  
69 liver, muscle, and ovary. Both the *Kdm5c*-KO amygdala and hippocampus had significant enrichment of testis  
70 genes that are typically uniquely expressed in germ cells. While the *Kdm5c*-KO brain primarily expressed  
71 germline genes important for late spermatogenesis, *Kdm5c*-KO EpiLCs aberrantly expressed key drivers  
72 of germline identity and meiosis, including *Dazl* and *Stra8*. KDM5C was highly enriched at germline gene  
73 promoters in EpiLCs but only bound to a subset of germline genes expressed in *Kdm5c*-KO cells, indicating  
74 germline-enriched mRNAs can be aberrantly transcribed through indirect mechanisms. Finally, we found  
75 KDM5C promotes the long-term silencing of germline genes in somatic cells by aiding the placement of  
76 DNA methylation in EpiLCs through H3K4me2/3 removal. Thus, we propose KDM5C plays a fundamental  
77 role in the development of tissue identity during early embryogenesis, including the establishment of the  
78 soma-germline boundary.

## 79 Results

### 80 **Tissue-enriched genes, including testis genes, are aberrantly expressed in the** 81 ***Kdm5c*-KO brain**

- 82 • note: should I compare amygdala and hippocampus? scandaglia only looked at hippocampus

83 Previous RNA sequencing (RNA-seq) in the adult hippocampus revealed ectopic expression of some testis  
84 genes within the *Kdm5c* knockout (-KO) brain<sup>10</sup>. Since tissue-enriched genes have not been systematically  
85 characterized in the *Kdm5c*-KO brain, it is currently unclear if this erosion of brain tissue identity is a major  
86 consequence of *Kdm5c* loss and if it is unique to testis-enriched genes. Therefore, we first globally assessed  
87 the expression of genes enriched in 17 mouse tissues<sup>20</sup> in our published mRNA-seq datasets of the adult  
88 amygdala and hippocampus in mice with constitutive knockout of *Kdm5c*<sup>21</sup>.

89 We found a large proportion of genes that are significantly upregulated within the *Kdm5c*-KO brain  
90 (DESeq2<sup>22</sup>, log2 fold change > 0.5, q < 0.1) are typically enriched in non-brain tissues (Amygdala: 35%,  
91 Hippocampus: 24%) (Figure 1A-B). The majority of tissue-enriched differentially expressed genes (tissue-  
92 enriched DEGs) were testis genes (Figure 1A-C). Even though the testis has the largest total number of  
93 tissue-biased genes compared to any other tissue (2,496 genes), testis-biased DEGs were significantly  
94 enriched for both brain regions (Amygdala p = 1.83e-05, Odds Ratio = 5.13; Hippocampus p = 4.26e-11,  
95 Odds Ratio = 4.45, Fisher's Exact Test). One example of a testis-enriched DEG is *FK506 binding protein 6*

96 (*Fkbp6*), a known regulator of piRNA expression and meiosis in germ cells<sup>23,24</sup> (Figure 1C).

97 In addition to the high enrichment of testis genes, we also identified aberrant expression of other  
98 tissue-enriched genes within the *Kdm5c*-KO brain. Although the *Kdm5c*-KO mice were male, we observed  
99 significant enrichment of ovary-biased DEGs in both the amygdala and hippocampus (Amygdala p = 0.00574,  
100 Odds Ratio = 18.7; Hippocampus p = 0.048, Odds Ratio = 5.88, Fisher's Exact) (Figure 1D). Ovary-enriched  
101 DEGs included *Zygotic arrest 1* (*Zar1*), which was recently shown to sequester mRNAs in oocytes for meiotic  
102 maturation and early zygote development<sup>25</sup> (Figure 1D). Although not consistent across brain regions, we  
103 also found significant enrichment of DEGS biased towards two non-gonadal tissues - the liver (Amygdala p =  
104 0.0398, Odds Ratio = 6.58, Fisher's Exact Test) and the muscle (Hippocampus p = 0.0104, Odds Ratio =  
105 6.95, Fisher's Exact Test). An example of a liver-biased DEG dysregulated in both the hippocampus and  
106 amygdala is *Apolipoprotein C-I* (*Apoc1*), which is involved in lipoprotein metabolism (Figure 1E). Testis,  
107 ovary, and liver-enriched DEGs showed little to no expression in the developing and adult wild-type brain,  
108 yet our mRNA-seq data indicate they are polyadenylated and spliced into mature transcripts (Figure 1C-E).  
109 Of note, we did not observe enrichment of brain-enriched genes (Amygdala p = 1; Hippocampus p = 0.74,  
110 Fisher's Exact), despite the fact these are brain samples and the brain has the second highest total number  
111 of tissue-enriched genes (708 genes). Together, these results suggest misexpression of tissue-enriched  
112 genes within the brain is a major effect of KDM5C loss.

### 113 Germline genes are misexpressed in the *Kdm5c*-KO brain

- 114 • Intriguingly, some of the ectopic testis transcripts identified within the *Kdm5c*-KO hippocampus have  
115 known functions unique to germ cells<sup>10</sup>, suggesting KDM5C may play a role in demarcating somatic  
116 versus germline identity.

117 The testis contains both germ cells (meiotic cells, e.g. spermatogonia) and somatic cells (non-meiotic,  
118 e.g. Leydig cells) that support hormone production and germline functions. Intriguingly, many *Kdm5c*-  
119 KO testis and ovary enriched-DEGs have germline-specific functions, suggesting *Kdm5c*-KO cells fail to  
120 distinguish between the soma and germline. To test if this holds true for all *Kdm5c*-KO testis-biased DEGs, we  
121 first assessed their known functions through gene ontology analysis. We found *Kdm5c*-KO testis-enriched  
122 DEGs high enrichment of germline-relevant ontologies, including spermatid development (GO: 0007286,  
123 p.adjust = 6.2e-12) and sperm axoneme assembly (GO: 0007288, p.adjust = 2.45e-14) (Figure 2A).

124 To further validate if these testis DEGs are truly germline genes, we then evaluated their expression in  
125 somatic versus germ cells within the testis. We first compared their expression in the testis with germ cell  
126 depletion<sup>26</sup>, which was accomplished by heterozygous *W* and *Wv* mutations in the enzymatic domain of  
127 *c-Kit* (*Kit*<sup>W/Wv</sup>) that prevent the maturation of germ cells<sup>27</sup>. Almost all *Kdm5c*-KO testis-enriched DEGs lost  
128 expression with germ cell depletion (Figure 2B). The only testis-enriched DEG that did not show considerable  
129 downregulation with germline depletion was *FK506 binding protein 6* (*Fkbp6*), the aforementioned testis

130 gene that regulates piRNA expression and meiosis in germ cells<sup>23,24</sup>. We then assessed testis-enriched  
131 DEG expression in a published single cell RNA-seq dataset that identified cell type-specific markers within  
132 the testis<sup>28</sup>. We found that while some testis-enriched DEGs were classified as specific markers for different  
133 germ cell types (e.g. spermatogonia, spermatocytes, round spermatids, and elongating spermatids) none  
134 marked somatic cells (Figure 2C). Together, these data suggest the somatic *Kdm5c*-KO brain aberrantly  
135 expresses germline genes.

136 We then wanted to more deeply characterize germline gene misexpression with *Kdm5c* loss, but lacked  
137 a comprehensive list of mouse germline-enriched genes. To facilitate downstream analyses, we generated a  
138 curated list of germline-enriched genes using currently available RNA-seq datasets in *Kit*<sup>W/Wv</sup> mice. Wild-type  
139 and *Kit*<sup>W/Wv</sup> datasets included males and females at embryonic day 12, 14, and 16<sup>29</sup>, as well as adult  
140 male testes<sup>26</sup>. We defined genes as germline-enriched if their expression met the following criteria: 1)  
141 their expression is greater than 1 FPKM in wild-type gonads 2) their expression in any adult wild-type,  
142 non-gonadal tissue<sup>20</sup> does not exceed 20% of their maximum expression in the wild-type germline, and  
143 3) their expression in the germ cell-depleted germline, for any sex or time point, does not exceed 20% of  
144 their maximum expression in the wild-type germline. These criteria yielded 1,288 germline-enriched genes  
145 (Figure 2D), which was hereafter used as a resource for assessing germline gene misexpression with *Kdm5c*  
146 loss (Supplementary table 1).

147 ***Kdm5c*-KO epiblast-like cells aberrantly express master regulators of germline  
148 identity**

149 Misexpression of germline genes in the adult brain suggests *Kdm5c*-KO cells fail to demarcate between  
150 germline and somatic identity. Germ cells are typically distinguished from somatic cells soon after the embryo  
151 implants into the uterine wall<sup>30,31</sup> when a subset of epiblast stem cells become the primordial germ cells  
152 (PGCs) while the remainder differentiate into the ectoderm, mesoderm, and endoderm to form the somatic  
153 tissues<sup>32</sup>. This developmental time point can be modeled *in vitro* through differentiation of embryonic stem  
154 cells (ESCs) into post-implantation epiblast-like stem cells (EpiLCs) (Figure 3A, top). Previous studies have  
155 demonstrated that while some germline-enriched genes are also expressed in embryonic stem cells (ESCs)  
156 and in the 2-cell stage<sup>33–35</sup>, they are silenced as they differentiate into EpiLCs<sup>17</sup>. Therefore, we assessed if  
157 KDM5C was necessary for embryonic silencing of germline genes by evaluating the impact of *Kdm5c* loss in  
158 EpiLCs.

159 We first identified *Kdm5c*-KO EpiLC DEGs in of our previously published RNA-seq dataset<sup>36</sup> (DESeq2,  
160 log2 fold change > 0.5, q < 0.1) and assessed tissue-enriched gene expression. Similar to the *Kdm5c*-KO  
161 brain, we observed general dysregulation of tissue-enriched genes, with the largest number of genes  
162 belonging to the brain and testis, although they were not significantly enriched (Figure 3B). Using the curated  
163 list of germline genes generated above, we found *Kdm5c*-KO EpiLCs aberrantly expressed 54 germline-

164 enriched genes, including the previously characterized hippocampal DEG<sup>10</sup> *Cytochrome C, testis-specific*  
165 (*Cyct*) (Figure 3C). Although we observed aberrant expression of many tissue-enriched genes, we did not  
166 observe any significant difference in primed pluripotency genes (Figure 3D) or gross changes in *Kdm5c*-KO  
167 cell morphology during differentiation (Figure 3E), indicating KDM5C loss does not impair EpiLC formation.

168 We then compared EpiLC germline DEGs to those expressed in the *Kdm5c*-KO brain to determine  
169 if all germline DEGs, like *Cyct*, are constitutively dysregulated or if they can change over the course of  
170 development. We found this was primarily not the case, as the majority of germline DEGs expressed  
171 in EpiLCs and the brain were unique, with only *Cyct* shared across all sequencing datasets (Figure 3F).  
172 We then compared the known functions of EpiLC and brain germline DEGs and found particularly high  
173 enrichment of meiosis-related gene ontologies in EpiLCs (Figure 3G), such as meiotic cell cycle process (GO:  
174 1903046, p.adjust = 1.59e-08) and meiotic nuclear division (GO: 0140013, p.adjust = 9.76e-09). While there  
175 was modest enrichment of meiotic gene ontologies in both brain regions, the *Kdm5c*-KO hippocampus  
176 primarily expressed late-stage spermatogenesis genes, such those involved in the sperm axoneme structure.

177 Interestingly, DEGs unique to *Kdm5c*-KO EpiLCs included key drivers of germline identity, such as  
178 *Stimulated by retinoic acid 8 (Stra8)* and *Deleted in azoospermia like (Dazl)* (Figure 3H). These genes are  
179 typically expressed during embryonic germ cell development to commit PGCs to the germline fate, but are  
180 also expressed later in life to trigger meiotic gene expression programs<sup>37-39</sup>. Of note, some germline genes,  
181 including *Dazl*, are also expressed in the two-cell embryo<sup>34,40</sup>. However, we did not see misexpression of  
182 two-cell embryo-specific genes, like *Duxf3 (Dux)* (q = 0.337) and *Zscan4d* (q = 0.381), indicating *Kdm5c*-KO  
183 in EpiLCs do not revert back to a 2-cell state (Figure 3H).

184 We were particularly interested in the aberrant transcription of *Dazl*, since it is essential for germ cell  
185 development and promotes the translation of germline mRNAs<sup>41</sup>. A significant portion of germline transcripts  
186 misexpressed in *Kdm5c*-KO EpiLCs are known binding targets of DAZL, including *Stra8*<sup>42</sup> (p = 1.698e-07,  
187 Fisher's Exact Test). This suggests expression of DAZL protein could promote the translation of other  
188 aberrant germline transcripts, influencing their ability to impact *Kdm5c*-KO cellular function. We thus tested  
189 DAZL protein expression in *Kdm5c*-KO EpiLCs through immunocytochemistry (Figure 3I). We observed  
190 about 25% of *Kdm5c*-KO EpiLCs expressed DAZL protein and it was localized to the cytoplasm (p = 0.0015,  
191 Welch's t-test), consistent with the pattern of DAZL expression in spermatogonia<sup>42</sup>. Altogether these results  
192 suggest tissue-specific genes are misexpressed during *Kdm5c*-KO embryogenesis, including key drivers of  
193 germline identity that can be translated into protein.

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

195 • KDM5C may also be involved in this early decommissioning of germline genes, as re-expression of  
196 KDM5C in knockout neurons fails to suppress their dysregulation<sup>10</sup>.

197 Previous work suggests KDM5C represses germline genes during early development, as re-expression

198 of KDM5C in knockout neuronal cultures fails to suppress hippocampal germline DEGs and KDM5C is not  
199 bound to their promoters in neurons<sup>10</sup>. There is some evidence KDM5C binds to select germline gene  
200 promoters in ESCs<sup>10</sup>, including *Dazl*<sup>40,43</sup>. As KDM5C's binding at germline gene promoters has not been  
201 systematically characterized, it is currently unclear if KDM5C is enriched at germline gene promoters, what  
202 types of germline genes KDM5C regulates, and if its binding is maintained at any germline genes in neurons.

203 To further characterize the mechanism behind *Kdm5c*-KO germline gene misexpression, we analyzed  
204 KDM5C chromatin immunoprecipitation followed by DNA sequencing (ChIP-seq) datasets in EpiLCs<sup>36</sup> and  
205 primary neuron cultures (PNCs) from the cortex and hippocampus<sup>15</sup>. EpiLCs had a higher total number of  
206 KDM5C peaks than PNCs (EpiLCs: 5,808, PNCs: 1,276, MACS2 q < 0.1 and fold enrichment > 1, removal  
207 of *Kdm5c*-KO false positive peaks) and KDM5C was primarily localized to gene promoters in both cell types  
208 (EpiLCs: 4,190, PNCs: 745 +/- 500bp from the TSS), although PNCs showed increased localization to  
209 non-promoter regions (Figure 4A).

210 The majority of promoters bound by KDM5C in PNCs were also bound in EpiLCs (513 shared promoters),  
211 however a large portion of gene promoters were only bound by KDM5C in EpiLCs (3677 EpiLC only  
212 promoters) (Figure 4B). We then performed gene ontology analysis to compare the known functions of genes  
213 with KDM5C bound to their promoter in EpiLCs and PNCs. While there were no ontologies significantly  
214 enriched for genes only bound by KDM5C in PNCs, gene ontologies for genes shared between PNCs and  
215 EpiLCs were enriched for functions involving nucleic acid turnover, such as deoxyribonucleotide metabolic  
216 process (GO:0009262, p.adjust = 8.28e-05) (Figure 4C). Germline-specific ontologies were only enriched  
217 in promoters unique to EpiLCs, such as meiotic nuclear division (GO: 0007127 p.adjust = 6.77e-16) and  
218 meiotic cell cycle process (GO:1903046, p.adjust = 5.05e-16) (Figure 3C). We then evaluated KDM5C  
219 binding around the transcription start site (TSS) of all germline-enriched genes. While KDM5C was bound  
220 to a subset of germline gene promoters in EpiLCs, it was not bound to any in PNCs (Figure 4D). Together,  
221 this suggests KDM5C is significantly enriched at a subset of germline gene promoters in EpiLCs, including  
222 meiotic genes, but does not regulate germline genes in neurons.

223 We then compared KDM5C binding at RNA-seq DEG promoters to determine if the germline mRNAs  
224 expressed in the *Kdm5c*-KO brain and EpiLCs are direct targets of KDM5C (Figure 4E). About one third  
225 of EpiLC-specific and brain-specific (hippocampus, amygdala, or both) germline DEGs were bound by  
226 KDM5C in EpiLCs (EpiLC only: 36%, Brain only: 33.3%). Some notable differences in KDM5C binding  
227 for EpiLC-specific DEGs included *Dazl* and *Stra8*, two key drivers of germline identity discussed above.  
228 Although both mRNAs are expressed in *Kdm5c*-KO EpiLCs, KDM5C is only bound to *Dazl*'s promoter and  
229 not *Stra8*'s in EpiLCs (Figure 4F). In contrast to the unique DEGs, 3 out of the 4 genes dysregulated in both  
230 the brain and EpiLCs are bound by KDM5C around the TSS (Figure 4G). Again, we did not observe any  
231 KDM5C binding at germline gene promoters in PNCs, even for brain-specific DEGs (Figure 4H). Altogether,  
232 this suggests the majority of germline mRNAs expressed in *Kdm5c*-KO cells are dysregulated independent  
233 of direct KDM5C recruitment to their promoters during embryogenesis.

234      **notes:** - do Direct vs indirect DEGs motif analysis

235 **KDM5C erases H3K4me3 to promote long-term repression of germline genes via**  
236 **DNA methylation**

237      Although KDM5C is generally thought to suppress transcription through erasure of histone 3 lysine 4 di-  
238 and trimethylation (H3K4me2/3)<sup>11</sup>, recent studies in ESCs have suggested KDM5C's repression *Dazl* is  
239 independent of its catalytic activity<sup>40</sup>. Somatic repression of germline genes is typically established during the  
240 transition between naïve and primed pluripotency, which modeled *in vitro* as ESCs to EpiLC differentiation.  
241 In ESCs, chromatin regulators place repressive histone modifications at germline gene promoters, including  
242 histone 2A 119 monoubiquitination (H2AK119ub1) and histone 3 lysine 9 trimethylation (H3K9me3)<sup>16,17,44</sup>.  
243 Germline genes are then silenced long-term in EpiLCs by *de novo* placement of DNA CpG methylation  
244 (DNAme)<sup>17</sup>. Although KDM5C's catalytic activity is not required to suppress *Dazl* in ESCs, KDM5C may  
245 promote long-term germline gene silencing via H3K4me3 removal since H3K4me3 can impede DNAme  
246 placement<sup>45,46</sup> and DNAme is lost at select germline gene promoters in the hippocampus<sup>10</sup>. Because  
247 KDM5C's role in germline gene repression has only been characterized in ESCs and in the mature brain, it is  
248 currently unclear to what extent KDM5C is involved during transition between ESCs and EpiLCs and if its  
249 catalytic activity is required for long-term silencing.

250      To elucidate KDM5C's role in germline gene silencing, we first characterized KDM5C's substrates, histone  
251 3 lysine 4 di- and trimethylation (H3K4me2/3) in our previously published ChIP-seq datasets in wild type and  
252 *Kdm5c*-KO amygdala<sup>21</sup> and EpiLCs<sup>36</sup>. In congruence with previous work in the *Kdm5c*-KO hippocampus<sup>10</sup>,  
253 we observed aberrant accumulation of H3K4me3 around the transcription start site (TSS) of germline genes  
254 in the *Kdm5c*-KO amygdala (Figure 5A). We additionally found a marked increase in H3K4me2 around the  
255 TSS of germline genes in *Kdm5c*-KO EpiLCs (Figure 5B).

256      We then evaluated KDM5C's embryonic role in germline gene silencing during ESC to EpiLC differentiation.  
257 We first characterized KDM5C's mRNA and protein expression at 0, 24, and 48 hours of differentiation  
258 (Figure 5C). While *Kdm5c* mRNA steadily decreased from 0 to 48 hours of differentiation (Figure 5D), KDM5C  
259 protein initially increased from 0 to 24 hours but then decreased to near knockout levels by 48 hours (Figure  
260 5E). We then performed whole genome bisulfite sequencing in wild-type and *Kdm5c*-KO ESCs and 96 hour  
261 extended EpiLCs (exEpiLCs) to determine KDM5C's role in the initial placement of DNA methylation at  
262 germline gene promoters. While wild-type cells accumulated high levels of DNA methylation at germline  
263 gene promoters over the course of ESCs to exEpiLC differentiation, DNA methylation was markedly reduced  
264 in *Kdm5c*-KO exEpiLCs (Figure 5F).

- 265      • Catalytic activity  
266      • Altogether, this suggests KDM5C is dynamically regulated during ESC to EpiLC differentiation and  
267 promotes germline gene silencing via removal of H3K4me2/3 during early embryogenesis.

- 268 • **note:** should I test if increase in H3K4me2 and H3K4me3 was highest in *Kdm5c*-KO cells at genes  
269 bound by KDM5C at their promoter in EpiLCs? Don't think it's that impactful

270 **Discussion**

271 In the above study, we demonstrate KDM5C's pivotal role in the development of tissue identity, resulting in  
272 substantial misexpression of tissue-enriched genes within the adult *Kdm5c*-KO hippocampus and amygdala.  
273 We defined tissue-enriched genes based on the criteria used in a previously published dataset of 17 C57/Bl6J  
274 mouse tissues<sup>20</sup>, which defined genes as tissue-enriched if they had more than 4-fold higher expression  
275 when compared to any other tissue. In addition to testis genes identified previously<sup>10</sup>, we found significant  
276 enrichment of muscle, liver, and even ovary-biased genes aberrantly expressed within the male *Kdm5c*-KO  
277 brain. It is currently unclear what the impact of these tissue-enriched genes are upon *Kdm5c*-KO brain  
278 function and if they ultimately contribute to MRXSCJ-related phenotypes. While the majority of tissue-  
279 enriched DEGs were testis and ovary genes with no known brain functions, select liver and muscle-biased  
280 DEGs do have known roles in the wild-type brain. For example, *Apolipoprotein C-I (Apoc1)* is a lipid transport  
281 gene highly enriched within the liver, but is also lowly expressed in the wild-type brain. Intriguingly, *Apoc1*  
282 overexpression in the mouse brain can impair learning and memory<sup>47</sup> and is implicated in Alzheimer's  
283 disease in humans<sup>48</sup>. Our results suggest KDM5C fine-tunes the expression of tissue-enriched genes like  
284 *Apoc1* to match the level required for proper brain function. However, further studies are required to determine  
285 if these genes contribute to *Kdm5c*-KO neuronal impairments and MRXSCJ pathology.

286 A substantial portion of genes upregulated in *Kdm5c*-KO brain are testis genes that have no known  
287 function within the brain. Through the use of publically available RNA-seq datasets, we demonstrated these  
288 testis-enriched DEGs are typically unique to germ cells. Misexpression of germline genes in the brain sug-  
289 gests *Kdm5c*-KOs fail to demarcate between somatic and germline lineages, a key feature of multicellularity  
290 and sexual reproduction. Previous studies have demonstrated germline genes are decommissioned in  
291 somatic cells by multiple chromatin-modifying enzymes, but have primarily focused on the repression of  
292 key marker genes. To globally characterize KDM5C's role in germline gene repression, we curated a list  
293 of mouse germline-enriched genes using publically available germ cell-depleted RNA-seq datasets. This  
294 resource enabled us to identify 1) the extent of germline gene dysregulation in *Kdm5c*-KO cells, 2) the types  
295 of germline genes misexpressed at different developmental time points, and 3) which types of germline  
296 genes are directly or indirectly regulated by KDM5C.

297 Dysregulation of *Kdm5c*-KO tissue identity begins during early embryogenesis, as germline and other  
298 tissue-enriched genes are aberrantly expressed in epiblast-like cells (EpiLCs). *In vivo*, germline genes  
299 are typically decommissioned in epiblast stem cells and remain silenced as the epiblast differentiates  
300 into the body's somatic tissues<sup>32</sup>. However, a small subset of epiblast stem cells will receive signals to  
301 reactivate germline gene expression to become the primordial germ cells (PGCs) that will ultimately form

302 the mature germline<sup>30,31</sup>. This process can be mimicked *in vitro* by differentiating EpiLCs into primordial  
303 germ cell-like cells (PGCLCs)<sup>49</sup>. Thus, misexpression of germline genes in *Kdm5c*-KO EpiLCs might  
304 suggest they are progressing beyond EpiLC differentiation and becoming PGCLCs. Yet, *Kdm5c*-KO EpiLCs  
305 had proper expression of EpiLC marker genes for primed pluripotency and we observed no difference in  
306 cellular morphology during ESC to EpiLC differentiation. Furthermore, we saw no significant change in *Otx2*  
307 expression, an epiblast stem cell marker that is known to repress epiblast and EpiLC differentiation into PGC  
308 and PGCLCs<sup>50</sup>. This, in conjunction with *Kdm5c*-KO mice being viable, suggests germline gene expression  
309 is occurring ectopically in conjunction with typical developmental programs, rather than a complete shift to  
310 germline identity.

311 • change first sentence: Other chromatin regulators involved in germline gene repression act in ESCs  
312 and EpiLCs. We observed this is true for KDM5C

313 We then globally characterized KDM5C binding at germline-enriched gene promoters through analysis  
314 of KDM5C ChIP-seq in EpiLCs and primary hippocampus and cortex neuron cultures (PNCs). While we  
315 observed high enrichment of KDM5C peaks at germline genes in EpiLCs, KDM5C was not bound to germline  
316 gene promoters in PNCs. This suggests dysregulation of germline genes in the mature *Kdm5c*-KO brain is  
317 due to loss of repression during embryogenesis, which is consistent with previous work that found introducing  
318 human KDM5C into *Kdm5c*-KO PNCs does not repress germline transcripts<sup>10</sup>. Although KDM5C is enriched  
319 at germline gene promoters in EpiLCs, KDM5C was only bound to about a third of EpiLC germline-enriched  
320 DEGs. One notable DEG not bound by KDM5C is *Stra8*, a transcription factor activated by retinoic acid  
321 signaling in germ cells that promotes meiotic initiation<sup>51,52</sup>. Retinoic acid can only activate *Stra8* expression  
322 when DAZL is present, which is a direct target of KDM5C and is aberrantly transcribed and translated in  
323 *Kdm5c*-KO EpiLCs. This indicates germline genes can be aberrantly expressed in *Kdm5c*-KO cells indirectly  
324 of KDM5C regulation through activation by other ectopic germline programs. Consistent with this idea, many  
325 *Kdm5c*-KO EpiLC germline DEGs are important for early germ cell development and meiosis while those  
326 expressed in the mature *Kdm5c*-KO brain are involved in late sperm development. Altogether, this indicates  
327 ectopic germline programs are, to some extent, progressing through germ cell developmental stages over  
328 the course of *Kdm5c*-KO development.

329 • Talk about different motifs if we do see differences there and if it explains direct vs indirect dysregulation  
330 – Could also mention PRC1.6/KDM5C binds pcgf6 in ESCs  
331 • Maybe talk about other regulators/if anything is known about them long term? Or save for 2nd paper.  
332 – another germline repressor: <https://pubmed.ncbi.nlm.nih.gov/35345626/>  
333 • Might be good to look at for retinoic acid paper (WT germ expression): <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0005654>

335 It is important to note that while we focused on KDM5C's regulation of germline genes, some germline-  
336 enriched genes are also expressed in naïve ESCs and at the 2-cell stage due to their roles in pluripotency  
337 and self-renewal. For example, although primarily known for committing PGCs to the germline fate and  
338 regulating the translation of germline-specific RNAs, *Dazl* is also expressed in naïve ESCs *in vitro*<sup>33</sup>, the  
339 inner cell mass *in vivo*<sup>33</sup>, and at the 2-cell stage<sup>53</sup>, but is silenced when cells transition from naïve to primed  
340 pluripotency during ESC to EpiLC differentiation<sup>17</sup>. Very recently, two screens of *Dazl*-repressors in ESCs  
341 identified KDM5C as a direct regulator of *Dazl* expression<sup>40,43</sup>. Interestingly, one screen found *Kdm5c*-KO  
342 ESCs also aberrantly expressed 2-cell-specific genes, indicating KDM5C negatively regulates totipotency in  
343 ESCs<sup>40</sup>. We found that while KDM5C also represses *Dazl* expression in EpiLCs, *Kdm5c*-KO EpiLCs do not  
344 express 2-cell specific genes like *Dux* and *Zscan4c*. Out of the four 2-cell regulators characterized in ESCs,  
345 KDM5C was the only factor whose repression of *Dazl* was independent of *Dux* expression<sup>40</sup>. Together, this  
346 suggests the 2-cell-like state in *Kdm5c*-KO ESCs is an indirect consequence of KDM5C's primary role in  
347 germline gene repression, including germline genes that are also involved in pluripotency and self-renewal.

348 It is hypothesized distinct repressive chromatin marks are placed at germline gene promoters as the  
349 embryo transitions from naïve to primed pluripotency. Initially, germline genes are repressed by placement of  
350 histone 2A lysine 119 monoubiquitination (H2AK119ub1) and histone 3 lysine 9 trimethylation (H3K9me3)  
351 in ESCs and then gain *de novo* DNA CpG methylation (CpGme) in EpiLCs<sup>17–19,44,54,55</sup>. KDM5C may be  
352 instead required to remove an active mark, histone 3 lysine 4 trimethylation (H3K4me3), since H3K4me3  
353 can impede *de novo* CpGme placement<sup>45,46</sup>. This is supported by previous work in the *Kdm5c*-KO adult  
354 hippocampus, which found an increase in H3K4me3 around the transcription start site (TSS) of germline  
355 DEGs and loss of CpGme at at least two germline promoters<sup>10</sup>. However, KDM5C's role in embryonic  
356 germline gene silencing is still unclear, as KDM5C's catalytic activity was recently found to be dispensable  
357 for silencing DAZL in ESCs<sup>40</sup>. In this study, we observed a global increase in H3K4me3 around the TSS of  
358 germline-enriched gene in the *Kdm5c*-KO amygdala and an increase in H3K4me2 in *Kdm5c*-KO EpiLCs. We  
359 found KDM5C's expression is dynamically regulated during ESC to EpiLC differentiation and loss of KDM5C  
360 leads to impaired placement of CpGme in extended EpiLCs. Altogether, this suggests KDM5C is necessary  
361 during the transition from naïve to primed pluripotency to promote the initial placement of CpGme at CpG  
362 islands for the long-term silencing of germline genes.

363 In summary, we demonstrate loss of the X-linked intellectual disability gene KDM5C leads to widespread  
364 dysregulation of brain tissue identity, including misexpression of germline genes in the somatic brain. In  
365 EpiLCs, KDM5C directly represses key drivers of germline identity like *Dazl*, by promoting initial CpG methy-  
366 lation placement in the post-implantation embryo. However, germline genes can also become ectopically  
367 expressed in *Kdm5c*-KO cells independent of direct KDM5C regulation, including the meiotic transcription  
368 factor *Stra8*. These ectopic germline developmental programs can, to some extent, mimic typical germ  
369 cell development, resulting in aberrant transcription early developmental and meiotic genes in *Kdm5c*-KO  
370 EpiLCs and late-stage spermatogenesis genes in the *Kdm5c*-KO brain. Altogether, these results define

371 KDM5C's role in the demarcation between soma and germline identity and offers novel insight into how this  
372 dysregulation of tissue identity changes over the course of development. Additionally, this study provides  
373 the mechanistic foundation required to ultimately investigate the impact of aberrant germline identity upon  
374 neurodevelopment.

375 • include cancer in there somewhere (Somatic misexpression of germline genes has been implicated in  
376 many cancers.)

## 377 Materials and Methods

### 378 Classifying tissue-enriched and germline-enriched genes

379 Tissue-enriched differentially expressed genes were determined by their classification in a previously  
380 published list of genes enriched in 17 male and female mouse tissues<sup>20</sup>. This study defined expression as  
381 greater than 1 Fragments Per Kilobase of transcript per Million mapped read (FPKM) and tissue enrichment  
382 as at least 4-fold higher expression than any other tissue.

383 We curated a list of germline-enriched genes using an RNA-seq dataset from wild-type and germline-  
384 depleted (Kit<sup>W/Wv</sup>) male and female mouse embryos from embryonic day 12, 14, and 16<sup>29</sup>, as well as adult  
385 male testes<sup>26</sup>. Germline-enriched genes met the following criteria: 1) their expression is greater than 1  
386 FPKM in wild-type germline 2) their expression in any wild-type somatic tissues<sup>20</sup> does not exceed 20%  
387 of maximum expression in wild-type germline, and 3) their expression in the germ cell-depleted (Kit<sup>W/Wv</sup>)  
388 germline, for any sex or time point, does not exceed 20% of maximum expression in wild-type germline.

### 389 Cell culture

390 We utilized our previously established cultures of male wild-type and *Kdm5c* knockout (-KO) embryonic  
391 stem cells<sup>36</sup>. Sex was confirmed by genotyping *Uba1* on the X and Y chromosomes with the following  
392 primers: 5'-TGGATGGTGTGCCAATG-3', 5'-CACCTGCACGTTGCCCT-3'. Deletion of *Kdm5c* was  
393 confirmed through the primers 5'-ATGCCCATATTAAGAGTCCTG-3', 5'-TCTGCCCTGATGGACTGTT-3',  
394 and 5'-GGTTCTCAACACTCACATAGTG-3'.

395 Embryonic stem cells (ESCs) were initially cultured in primed ESC (pESC) media consisting of Knock-  
396 Out DMEM (Gibco#10829-018), fetal bovine serum (Gibco#A5209501), KnockOut serum replacement  
397 (Invitrogen#10828-028), Glutamax (Gibco#35050-061), Anti-Anti (Gibco#15240-062), MEM Non-essential  
398 amino acids (Gibco#11140-050), and beta-mercaptoethanol (Sigma#M7522). They were then transitioned  
399 into ground-state "naive" ESCs (nESCs) by culturing for four passages in N2B27 media containing DMEM/F12  
400 (Gibco#11330-032), Neurobasal media (Gibco#21103-049), Gluamax, Anti-Anti, N2 supplement (Invitro-  
401 gen#17502048), and B27 supplement without vitamin A (Invitrogen#12587-010), and beta-mercaptoethanol.

402 Both pESC and nESC media were supplemented with the GSK3 inhibitor CHIR99021 (Sigma #SML1046-  
403 5MG), the MEK inhibitor PD0325901 (Sigma #PZ0162-5MG), and leukemia inhibitory factor (LIF, Milli-  
404 pore#ESG1107).

405 nESCs were differentiated into epiblast-like cells (EpiLCs, 48 hours) and extendend EpiLCs (exEpiLCs,  
406 96 hours) by culturing in N2B27 media containing DMEM/F12, Neurobasal media, Gluamax, Anti-Anti,  
407 N2 supplement, B27 supplement (Invitrogen#17504044), beta-mercaptoethanol, fibroblast growth factor 2  
408 (FGF2, R&D Biotechne 233-FB), and activin A (R&D Biotechne 338AC050CF).

## 409 **Immunocytochemistry (ICC)**

410 ICC of DAZL in EpiLCs was performed by washing cells thrice with phosphobuffered saline (PBS), fixing  
411 cells in 4% paraformaldehyde, washing thrice in PBS, blocking in PBS containing 0.3% Triton X-100, and 5%  
412 fetal bovine serum for 1 hour, washing thrice with PBS, and incubating in primary antibody (Rabbit anti DAZL,  
413 abcam ab34139, 1:200) in the blocking solution overnight at 4C. The next day cells were rinsed thrice with  
414 PBS, incubated in secondary antibody (Alexafluor 488 Invitrogen #710369, 1:1000) in blocking buffer, rinsed  
415 thrice in PBS, and then imaged. Images were taken blinded for genotype, chosen based on similar levels of  
416 DAPI signal, and then quantified via ImageJ.

## 417 **RNA sequencing**

### 418 **Published datasets**

419 All published datasets are available at the Gene Expression Omnibus (GEO) <https://www.ncbi.nlm.nih.gov/geo/>. Previously published RNA sequencing datasets analyzed in this study included the male wild-type  
420 and *Kdm5c*-KO adult amygdala and hippocampus<sup>21</sup> (available at GEO: GSE127722) and male wild-type and  
421 *Kdm5c*-KO EpiLCs<sup>36</sup> (available at GSE: GSE96797).

### 423 **Alignment and analysis**

424 After ensuring read quality via FastQC (v0.11.8), reads were then mapped to the mm10 *Mus musculus*  
425 genome (Gencode) using STAR (v2.5.3a), during which we removed duplicates and kept only uniquely  
426 mapped reads. Count files were generated by FeatureCounts (Subread v1.5.0), and BAM files were  
427 converted to bigwigs using deeptools (v3.1.3) and visualized by the UCSC genome browser. RStudio (v3.6.0)  
428 was then used to analyze counts files by DESeq2 (v1.26.0)<sup>22</sup> to identify differentially expressed genes  
429 (DEGs) with a q-value (p-adjusted via FDR/Benjamini–Hochberg correction) less than 0.1 and a log2 fold  
430 change greater than 0.5. For all DESeq2 analyses, log2 fold changes were calculated with IfcShrink using  
431 the ashR package<sup>56</sup>. MA-plots were generated by ggpubr (v0.4.0), and Eulerr diagrams were generated by  
432 eulerr (v6.1.1). Boxplots and scatterplots were generated by ggpubr (v0.6.0) and ggplot2 (v3.3.2). Heatmaps

433 of gene expression were generated using the base R functions scale and hclust and visualized using the R  
434 package ComplexHeatmap (v2.12.1). The Upset plot was generated via the package UpSetR (v1.4.0)<sup>57</sup>.  
435 Gene ontology (GO) analyses were performed by the R package enrichPlot (v1.16.2) using the biological  
436 processes setting.

#### 437 **Chromatin immunoprecipitation followed by DNA sequencing (ChIP-seq)**

438 We analyzed our previously published KDM5C ChIP-seq experiments in primary neuron cultures from  
439 the cortex and hippocampus<sup>15</sup> (available at GEO: GSE61036) and EpiLCs<sup>36</sup> (available at GEO: GSE96797).  
440 ChIP-seq of histone 3 lysine 4 dimethylation in male EpiLCs<sup>36</sup> is also available at GEO: GSE96797. ChIP-seq  
441 of histone 3 lysine 4 trimethylation in the male amygdala<sup>21</sup> are available at GEO: GSE127817.

442 ChIP-seq reads were aligned to mm10 using Bowtie1 (v1.1.2) allowing up to two mismatches. Only  
443 uniquely mapped reads were used for analysis. Peaks were called using MACS2 software (v2.1.0.20140616)  
444 using input BAM files for normalization, with filters for a q-value < 0.1 and a fold enrichment > 1. Common  
445 peak sets were obtained in R via DiffBind (v3.6.5), and count tables for the common peaks were generated  
446 with the Bedtools multicov command. We removed “black-listed” genomic regions that often give aberrant  
447 signals. Peak proximity to genome annotations was determined by ChIPSeeker (v1.32.1). Enriched motifs  
448 were identified using HOMER<sup>58</sup>. Gene ontology (GO) analyses were performed by the R package enrichPlot  
449 (v1.16.2) using the biological processes setting. Average binding across the genome was visualized using  
450 deeptools (v3.1.3). Bigwigs were visualized using the UCSC genome browser.

#### 451 **Whole genome bisulfite sequencing (WGBS)**

#### 452 **Data availability**

#### 453 **Acknowledgements**

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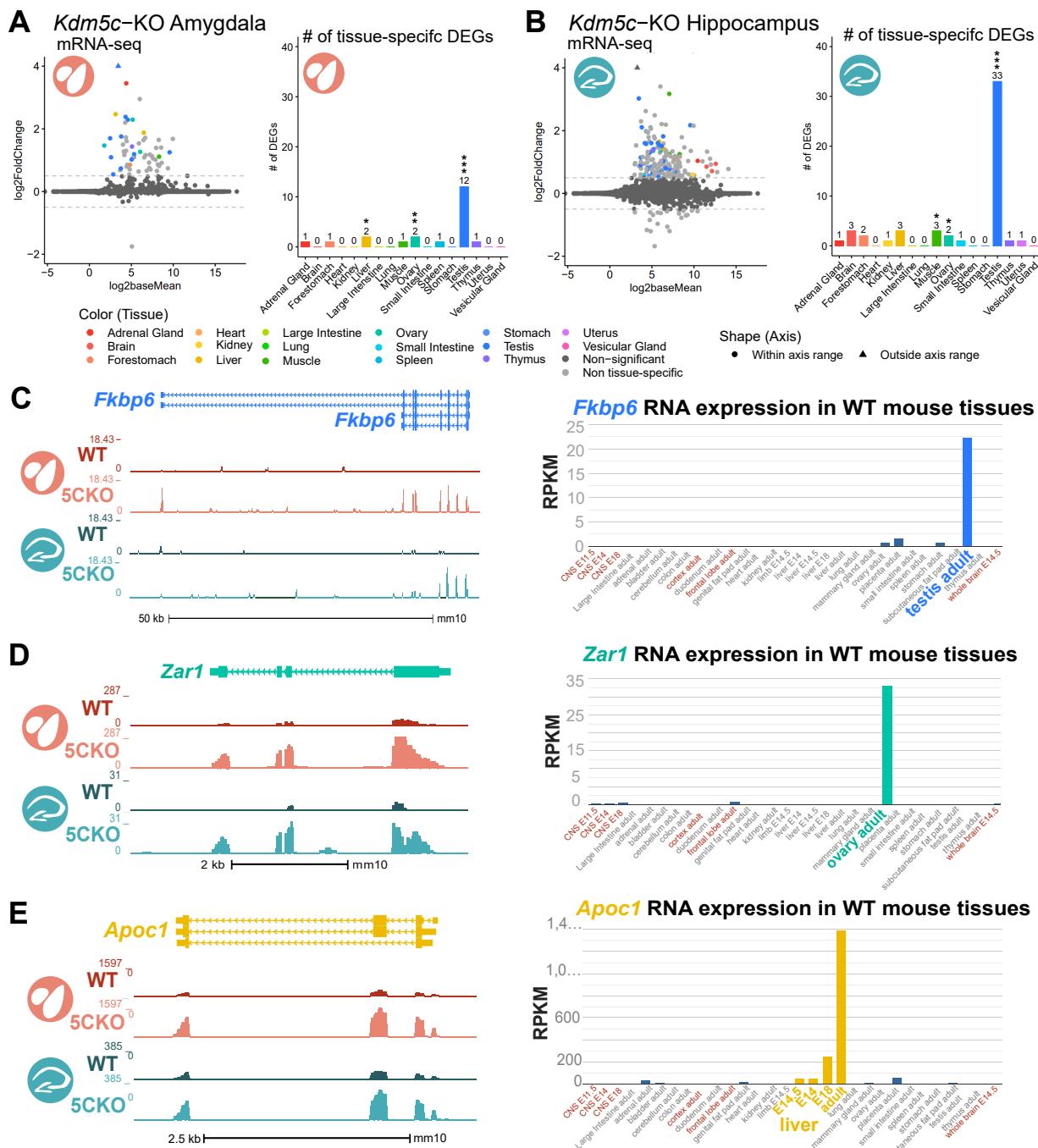
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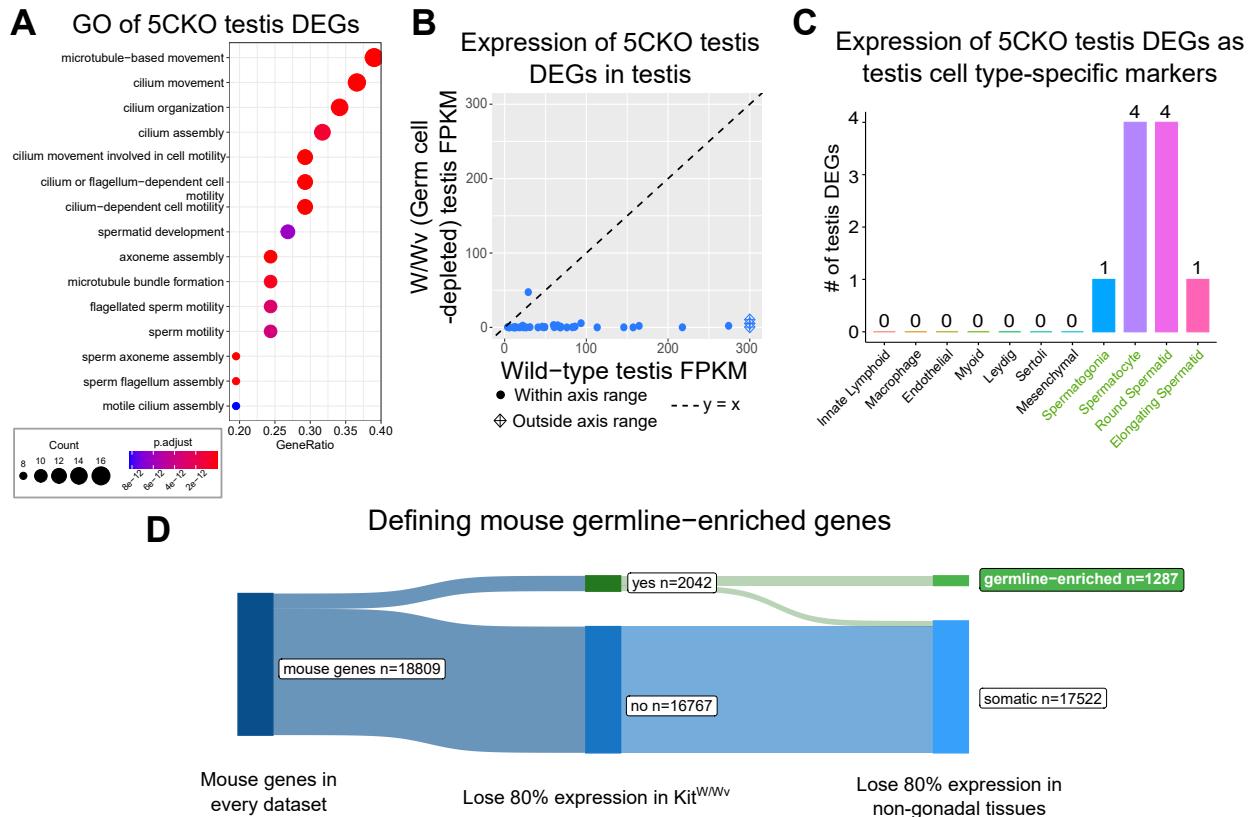
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571 **Figures and Tables**

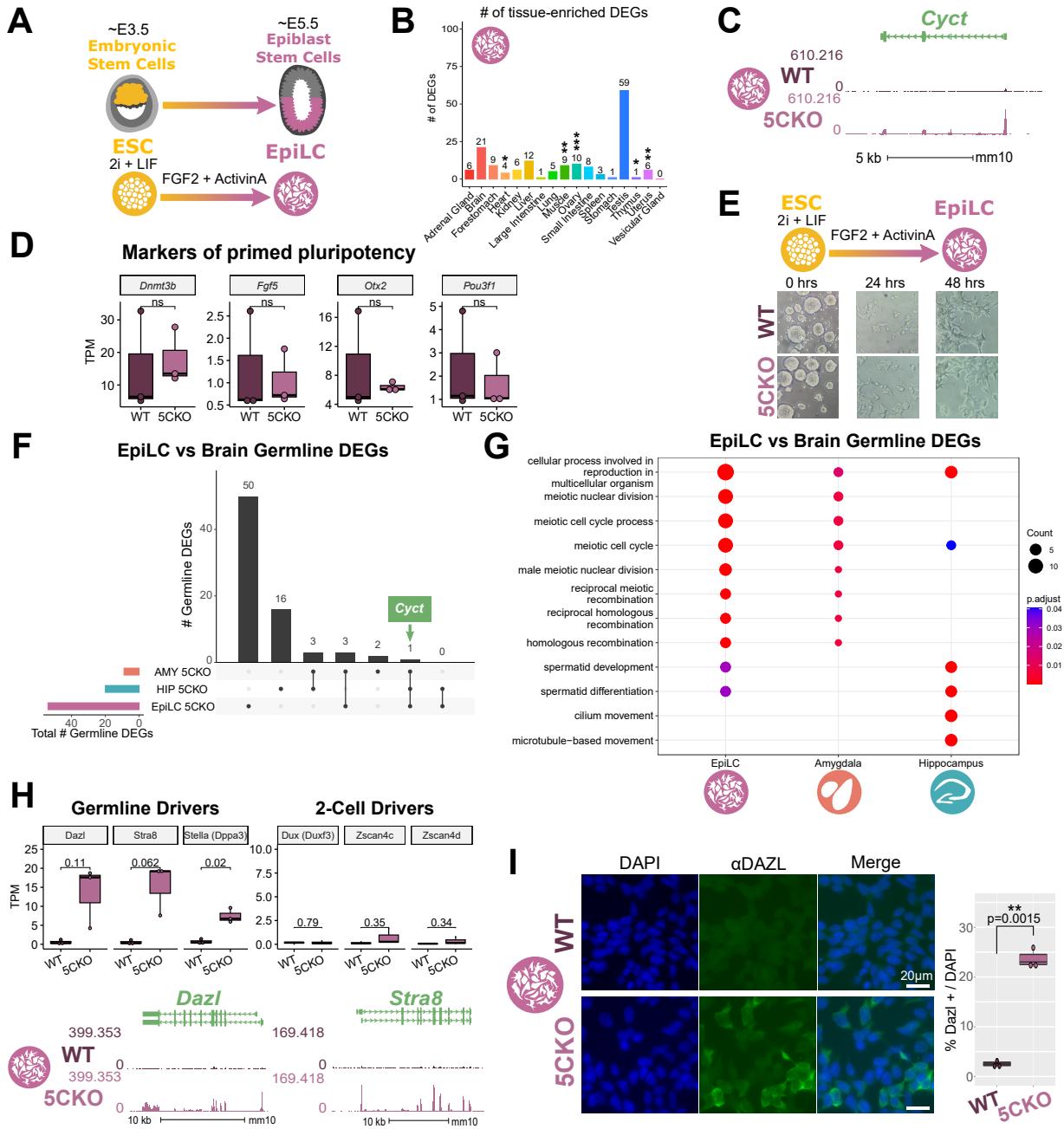
- 572     • Supplementary table 1: list of all germline genes.
- 573       – Columns to include:
- 574           \* KDM5C bound vs not
- 575           \* DEG in EpiLC, brain, both, neither (separate columns?)



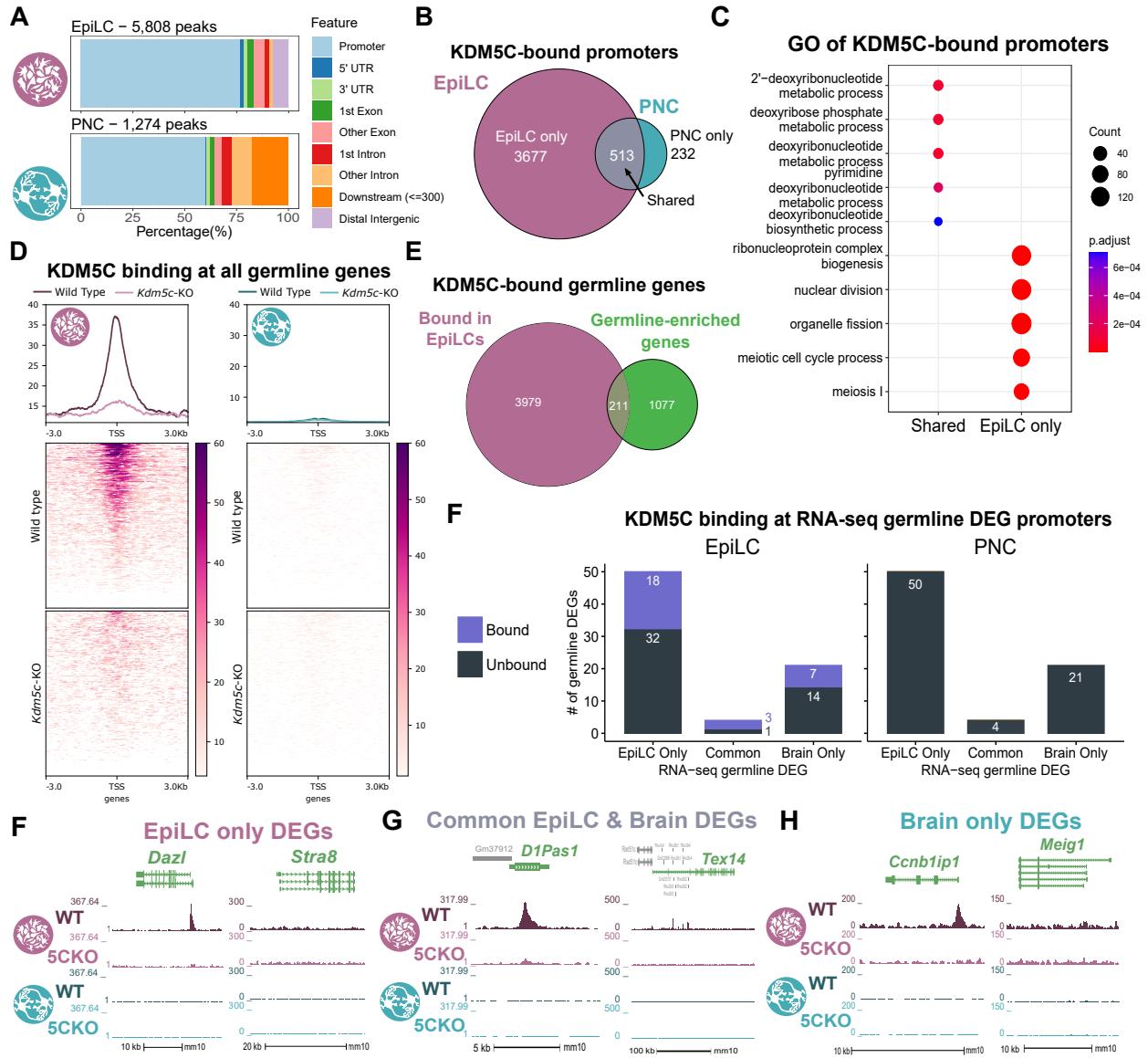
**Figure 1: Tissue-enriched genes are misexpressed in the *Kdm5c*-KO brain.** **A-B.** Expression of tissue-enriched genes (Li et al 2017) in the male *Kdm5c*-KO amygdala (A) and hippocampus (B). Left - MA plot of mRNA-sequencing. Right - Number of tissue-enriched differentially expressed genes (DEGs). \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , Fisher's exact test. **C.** Left - Average bigwigs 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). Right - Expression of *Cyct* in wild-type tissues from NCBI Gene, with testis highlighted in blue and brain tissues highlighted in red. **D.** Left - Average bigwigs 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 - Average bigwigs 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 germline-depleted mice and in adult mouse non-gonadal tissues (Li et al 2017).

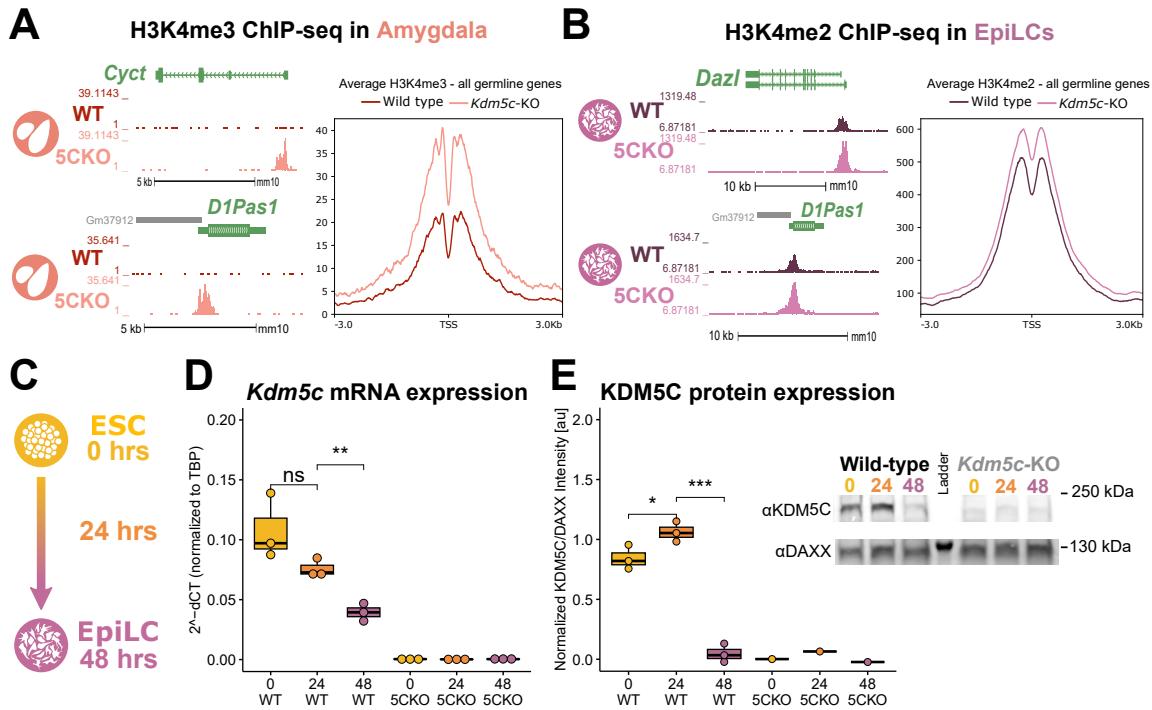


**Figure 3: Kdm5c-KO epiblast-like cells express key drivers of germline identity** **A.** Top - Diagram of *in vivo* differentiation of embryonic stem cells (ESCs) of the inner cell mass into epiblast stem cells. Bottom - *in vitro* differentiation of ESCs into epiblast-like cells (EpiLCs). **B.** Number of tissue-enriched differentially expressed genes (DEGs) in *Kdm5c*-KO EpiLCs. \*  $p<0.05$ , \*\*  $p<0.01$ , \*\*\*  $p<0.001$ , Fisher's exact test. **C.** Average bigwigs of an example germline gene, *Cyct*, that is dysregulated *Kdm5c*-KO EpiLCs. **D.** 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). **E.** Representative images of wild-type (WT) and *Kdm5c*-KO cells during ESC to EpiLC differentiation. Brightfield images taken at 20X. **F.** Upset plot displaying the overlap of germline DEGs expressed in *Kdm5c*-KO EpiLCs, amygdala (AMY), and hippocampus (HIP) RNA-seq datasets. **G.** enrichPlot comparing enriched biological process gene ontologies 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 - Average bigwigs of *Dazl* and *Stra8* expression in wild-type and *Kdm5c*-KO EpiLCs. **I.** Immunocytochemistry of DAZL in male wild-type (WT) and *Kdm5c*-KO (5CKO) EpiLCs. Percentage of DAZL-positive cells normalized to number of DAPI-positive cells, p-value for Welch's t-test.



**Figure 4: 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 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.** KDM5C binding at the promoters of RNA-seq germline DEGs. Genes were classified as either only dysregulated in EpiLCs (EpiLC only), genes dysregulated in the hippocampus or amygdala but not EpiLCs (brain only), or genes dysregulated in both EpiLCs and the brain (common). (Legend continued on next page.)

**Figure 4: KDM5C binds to a subset of germline gene promoters during early embryogenesis.** (Legend continued.) **F.** Example KDM5C ChIP-seq bigwigs of DEGs unique to EpiLCs. Although both are expressed in *Kdm5c*-KO EpiLCs, KDM5C is only bound to the *Dazl* promoter and not the *Stra8* promoter in EpiLCs. **G.** Example KDM5C ChIP-seq bigwigs of RNA-seq DEGs common between the brain and EpiLCs. KDM5C is bound to the *D1Pas1* promoter but not the *XXX* promoter in EpiLCs. **H.** Example KDM5C ChIP-seq bigwigs of RNA-seq DEGs unique to the brain. KDM5C is bound to the *XXX* promoter but not the *Meig1* promoter



**F**

**G**

**Figure 5: KDM5C's catalytic activity promotes long-term silencing of germline genes via DNA methylation.** **A.** Left - Bigwigs of representative histone 3 lysine 4 trimethylation (H3K4me3) ChIP-seq peaks at two germline genes in the wild-type (WT) and *Kdm5c*-KO (5CKO) adult amygdala. Right - Average H3K4me3 at the transcripton start site (TSS) of all germline-enriched genes in wild-type (dark red) and *Kdm5c*-KO (light red) amygdala. **B.** Left - Bigwigs of representative histone 3 lysine 4 dimethylation (H3K4me2) ChIP-seq peaks at representative germline genes in wild-type and *Kdm5c*-KO EpiLCs. Right - Average H3K4me2 at the TSS of all germline-enriched genes in wild-type (dark purple) and *Kdm5c*-KO (light purple) EpiLCs. **C.** Diagram of embryonic stem cell (ESC) to epiblast-like cell (EpiLC) differentiation protocol and collection time points for RNA and protein. **D.** Real time quantitative PCR (RT-qPCR) of *Kdm5c* RNA expression, calculated in comparision to TBP expression ( $2^{-\Delta\Delta CT}$ ). \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , Welch's t-test. **E.** 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 **F.** XXX **G.** XXX

576 **Notes**

577 **Discussion notes**

- 578 • We additionally found *Kdm5c*-KO EpiLCs ectopically express DAZL protein that is localized to the  
579 cytoplasm, similar to its morphology in spermatogonia<sup>42</sup>. **note: maybe just put in results.** Could  
580 move around depending upon if I get pheno working.
- 581 • end with something like: this indicates kdm5c not only modulates pluripotency and self-renewal in  
582 ESCs, but also has a role in long-term silencing of germline genes
  - 583 – then transition into the long term silencing mechanism paragraph
- 584 • KDM5C is dynamically regulated during the window of embryonic germline gene silencing, our EpiLC  
585 ChIP-seq is likely catching the tail end of KDM5C's main involvement.
- 586 • Our results indicate KDM5C is a pivotal repressor of germline programs in somatic cells.
- 587 • Studies on other chromatin regulators have focused on key marker genes to identify germline gene  
588 misexpression, such as *Dazl*.
- 589 • Using a germline-depleted mouse model, we curated a list of mouse germline-enriched genes to  
590 globally assess germline gene dysregulation.
- 591 • Many of the genes dysregulated in the mature *Kdm5c*-KO brain were important for late stages of  
592 spermatogenesis, such as those important for sperm flagellar structure. Contrastingly, *Kdm5c*-KO  
593 EpiLCs aberrantly expressed key drivers of germ cell identity, including *Dazl* and *Stra8*.
- 594 • While a significant portion of KDM5C-bound promoters are germline genes, many germline genes  
595 expressed during *Kdm5c*-KO embryogenesis are not directly bound by kdm5c.
- 596 • One notable example is *Stra8*, a transcription factor important for germ cell specific transcription and  
597 meiotic initiation
- 598 • The including the demarcation between soma and germline fates.  
599 the *Kdm5c*-KO brain also Previous work identified testis-enriched genes in *Kdm5c* genes
- 600 –  
601 – However unlike the gonadal-biased DEGs,
- 602 • The demarcation of the germline versus soma is a key feature of multicellularity and sexually dimorphic  
603 reproduction
- 604 • Anything known about tissue-biased gene expression in other H3K4me regulators?

- 605 • Our data suggests the germline developmental program is occurring ectopically as *Kdm5c*-KOs pro-  
606 gresses through somatic tissue development
- 607 • tissue-biased gene expression:
- 608 • Altogether, these data indicate that while some germline genes are misexpressed due to direct loss of  
609 KDM5C binding during embryogenesis, secondary downstream mechanisms can also promote their  
610 aberrant transcription.
- 611 • Papers to read/reference:
- 612 – Reconstitution of the Mouse Germ Cell Specification Pathway in Culture by Pluripotent Stem Cells:  
613 [https://www.cell.com/fulltext/S0092-8674\(11\)00771-9](https://www.cell.com/fulltext/S0092-8674(11)00771-9)
- 614 – two cell gene list used by Suzuki et al Max paper is based on 2 cell sequencing: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3395470/>

616 **Figure outline:**

617 **Figure 1: Misexpression of tissue-specific genes in the *Kdm5c*-KO brain** \* MA-plot and bar graphs of  
618 tissue-enriched genes \* Example testis-specific genes (NCBI and bigwigs) \* An example ovary tissue-specific  
619 gene \* An example muscle/liver tissue-specific gene (NCBI and bigwigs)

620 **Figure 2: The male *Kdm5c*-KO brain expresses male and female germline-enriched genes** \* Gene  
621 ontology of testis DEGs in the amygdala and hippocampus - ontologies are germline ontologies \* Expression  
622 of testis DEGs in germline-depleted testis (this is adult testis data) \* scRNASeq of testis - # of testis DEGs that  
623 are germline-specific markers \* Although far fewer, 5CKO brain also expresses ovary-enriched genes(NCBI  
624 and bigwigs of Zar1) \* These ovary enriched genes are also germline specific (NCBI/Li tissues are in adult  
625 ovary, so it would be best to show they're oocyte-specific in adult ovary. But I don't think there's a published  
626 adult female W/Wv dataset. Could try looking at scRNASeq or just do TPM in embryonic W/Wv data since  
627 oocytes are developed at this point? Or both?) \* Defining what is/isn't a germline gene, and which are  
628 male/female biased using embryonic W/Wv data

629 **Figure 3: *Kdm5c*-KO epiblast-like cells express key drivers regulators of germline identity** \* A) ESC  
630 to EpiLC differentiation Left - Morphology is unchanged, \* B) 5CKO EpiLCs express EpiLC differentiation  
631 genes similar to WT lvs \* C) Male EpiLCs express germline genes (example Cyct again) \* Overlap between  
632 brain and EpiLC germline genes - show they're mostly unique \* GO of Brain and EpiLC germline genes  
633 (meiotic enriched) \* Bigwigs or TPM of master regulators \* Show that while some are also 2-cell genes  
634 (Dazl), 2-cell specific genes aren't dysregulated (Zscan4). Important point because published KDM5C dazl  
635 paper is saying KDM5C is a 2-cell regulator, but as far as I can tell only genes shared between germline and  
636 2-cell are dysregulated.

637 Staining of Dazl (+ Stra8 if I can get it to work)

638       **Figure 4: Loss of KDM5C's catalytic activity impairs DNAme placement and long-term silencing of**  
639       **germline genes** \* Increase in H3K4me3 in Kdm5c-KO amygdala at germline genes \* Increase in H3K4me2  
640       in EpiLCs at germline genes \* Kdm5c binding in EpiLCs vs PNCs to show that germline repression is  
641       happening in early embryo \* Previous studies only looked at ESCs, unknown if catalytic activity is required  
642       for long-term repression, especially since DNA methylation is placed later). KDM5C RNA and protein ESC →  
643       EpiLC (increasing then decreasing) \* RNA expression of germline genes with catalytic dead rescue (Ilakkiya)  
644       \* DNA methylation in WT and 5CKO EpiLCs (Ilakkiya)

645       **Figure 5: Ectopic, germline-like phenotypes in Kdm5c-KO ESCs/EpiLCs** \* Sycp3 staining \* DDX4  
646       staining and repression of retrotransposons \* Cilia??

647       Gaps in knowledge addressed: \* Are other tissue-enriched genes dysregulated, or only testis, germline  
648       genes? \* Curating a robust list of male and female germline genes \* Should talk about 2-cell genes  
649       vs germline genes - way to systematically categorize? \* Mechanism behind long-term germline gene  
650       misexpression \* Recent evidence suggests loss of KDM5C in ESCs express some germline genes \* Unclear  
651       if catalytic activity is required for long-term silencing \* Unclear if their dysregulation lasts throughout life or  
652       the same between brain or not \* When in development does it begin? - Recent evidence suggests some  
653       germline genes expressed in 5CKO ESCs but unclear if their dysregulation lasts throughout differentiation  
654       and if the identity of germline genes are different compared to the brain \* Are there functional consequences  
655       to germline gene misexpression?

656       Introduction: \* Chromatin regulators are important for cellular identity \* H3K4me1-3 linked to active  
657       gene promoters and enhancers \* Surprisingly, mutations in Chromatin regulators lead to many NDDs  
658       (including many H3K4 regulators) \* Recent studies have shown some chromatin regulators are important  
659       for regulating neuron-specific gene expression/chromatin stat\_compare\_means \* However, loss of some  
660       chromatin regulators can also lead to ectopic expression of tissue-enriched genes \* Very few studies have  
661       looked at these genes and it's unclear if these genes contribute to NDD impairments. \* Necessary to  
662       first characterize the mechanism behind their derepression to identify molecular footholds into testing their  
663       contribution to neuronal impairments and potential for therapeutic intervention

- 664       • Loss of KDM5C can result in the misexpression of genes typically only found in the testis
- 665           – Misexpression of tissue-enriched genes hasn't been systematically characterized - Unclear if  
666           these genes are exceptions or if other tissue-specific genes are dysregulated
- 667           – Interestingly, these genes (Cyct, D1pas1) typically function in the germline
- 668           – Germ cells (meiotic cells) are typically distinguished from somatic cells very early on in embryogenesis  
669           and is a key feature of multicellularity
- 670           – Chromatin regulators are very important for decommissioning germline genes and act successively  
671           the embryo implants into the uterine wall
- 672           \* Most studies have focused on ESCs, which have a similar transcriptome to germ cells / 2-cells

- 673           \* recently, KDM5C was shown to repress DAZL in ESCs, independent of its catalytic activity  
674           \* However, DNA methylation is lost in the mature 5CKO brain, DNA methylation is placed later  
675           and it's Unclear if it's required for long-term repression (maybe too specific, just trying to go  
676           into the fact that the mechanism is partially understood but unclear)  
677           – Systematic characterization of ectopic germline genes hasn't been done  
678           \* unknown if other germline-enriched genes are dysregulated, including oocyte-specific genes  
679           \* Crucially, it's unknown if misexpression of the germline program leads to functional conse-  
680           quences in 5CKO cells.

681           **Germline gene repression background:**

682           Interestingly, some of the ectopic testis transcripts identified in the *Kdm5c*-KO brain are typically ex-  
683           pressed in germ cells<sup>10</sup>. Unlike somatic cells, germ cells (e.g. sperm and eggs) undergo meiosis and pass  
684           on their genetic material to the next generation. The germline and the soma are typically distinguished during  
685           early embryogenesis, when germline genes are silenced in epiblast stem cells soon after implantation and  
686           only reactivated in a subset to form the germline. Chromatin regulators play a key role in decommissioning  
687           germline genes as the embryo transitions from naïve to primed pluripotency by placing repressive histone  
688           H2A lysine 119 monoubiquitination (H2AK119ub1)<sup>16</sup>, histone 3 lysine 9 trimethylation (H3K9me3)<sup>16,17</sup>, and  
689           DNA CpG methylation<sup>17–19</sup> at germline gene promoters. KDM5C may also be involved in this early decom-  
690           missioning of germline genes, as re-expression of KDM5C in neurons fails to suppress their dysregulation<sup>10</sup>.  
691           In support of this, KDM5C was very recently shown to repress *Deleted in azoospermia like* (*Dazl*), a key  
692           regulator of germline development, in mouse embryonic stem cells (ESCs)<sup>40,43</sup>. In support of this, two  
693           independent screens in mouse embryonic stem cells (ESCs) recently identified KDM5C as a repressor of  
694           *Deleted in azoospermia like* (*Dazl*), a key regulator of germline development. However, KDM5C's role in  
695           embryonic germline gene repression is currently unclear, given that *Dazl* is also expressed in ESCs and in  
696           the 2-cell stage and germline gene misexpression has yet to be globally characterized during *Kdm5c*-KO  
697           embryogenesis.