

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

3

4 **Abstract**

5 **Introduction**

6 A single genome holds the instructions to generate the myriad of cell types found within the adult organism. This is, in
7 part, accomplished by chromatin regulators that can either promote or impede lineage-specific gene expression through DNA
8 and histone modifications^{1,2}. Although many chromatin regulators were initially identified for their roles in shaping cellular and
9 tissue identity^{3,4}, recent advancements in next generation sequencing unexpectedly revealed many neurodevelopmental
10 disorders (NDDs) are caused by mutations in chromatin regulators⁵. Several studies have suggested this connection
11 between chromatin regulators and neurodevelopment is due to their regulation of brain-specific genes, such as orchestrating
12 transcriptional programs for synaptic maturation⁶ and transitioning between neuronal and glial fates during neural precursor
13 differentiation⁷. However, loss of some chromatin regulators can also result in the ectopic transcription of tissue-specific
14 genes outside of their target environment^{3,4,8}, such as the misexpression of liver-specific genes within adult neurons⁹. Very
15 few studies have investigated the misexpression of tissue-specific genes in chromatin-linked NDDs^{9,10} and it is currently
16 unknown if this partial loss of brain identity contributes to neurodevelopmental impairments.

17 To elucidate the role of tissue identity in chromatin-linked neurodevelopmental disorders, it is essential to first characterize
18 the types of genes dysregulated and the molecular mechanisms governing their de-repression. In this study, we characterized
19 the aberrant expression of tissue-enriched genes with loss of lysine demethylase 5C (KDM5C). KDM5C, , also known
20 as SMCX or JARID1C, is a chromatin regulator that can repress gene expression through erasure of histone 3 lysine 4
21 di- and trimethylation (H3K4me2/3)¹¹, marks enriched at active gene promoters. Pathogenic mutations in *KDM5C* cause
22 Intellectual Developmental Disorder, X-linked, Syndromic, Claes-Jensen Type (MRXSCJ, OMIM: 300534), whose predominant
23 features include intellectual disability, seizures, aberrant aggression, and autistic behaviors^{12–14}. *Kdm5c* knockout (-KO)
24 mice recapitulate key MRXSCJ patient phenotypes, including hyperaggression, increased seizure propensity, and learning
25 impairments^{10,15}. Unexpectedly, RNA sequencing (RNA-seq) of the *Kdm5c*-KO hippocampus revealed ectopic expression of
26 testis genes within the brain¹⁰. It is currently unknown if this dysregulation of brain tissue identity further impairs *Kdm5c*-KO
27 neurodevelopment and if ectopic gene expression within the *Kdm5c*-KO brain is unique to testis genes.

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

29 Distinguishing between the germline (cells that pass on their genetic material, e.g. sperm and eggs) and the soma (cells
30 that perform all other bodily functions) is a key feature of multicellularity and occurs during early embryogenesis. In mammals,
31 chromatin regulators play a key role in decommissioning germline genes in somatic cells during the transition from naive to
32 primed pluripotency by placing repressive histone H2A lysine 119 monoubiquitination (H2AK119ub1)¹⁶, histone 3 lysine 9

33 trimethylation (H3K9me3)^{16,17}, and DNA CpG methylation¹⁷⁻¹⁹ at germline gene promoters. Systematically characterizing
34 KDM5C's role in germline gene repression during early embryogenesis will unveil key mechanisms underlying the demarcation
35 between soma and germline identity and while also providing molecular footholds to test the impact of ectopic germline genes
36 on neurodevelopment.

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

49 Results

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

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

52 Previous RNA sequencing (RNA-seq) in the adult hippocampus revealed ectopic expression of some testis genes within
53 the *Kdm5c* knockout (-KO) brain¹⁰. Since tissue-enriched genes have not been systematically characterized in the *Kdm5c*-KO
54 brain, it is currently unclear if this erosion of brain tissue identity is a major consequence of *Kdm5c* loss and if it is unique to
55 testis-enriched genes. Therefore, we first globally assessed the expression of genes enriched in 17 mouse tissues²⁰ in our
56 published mRNA-seq datasets of the adult amygdala and hippocampus in mice with constitutive knockout of *Kdm5c*²¹.

57 We found a large proportion of genes that are significantly upregulated within the *Kdm5c*-KO brain (DESeq2²², log2 fold
58 change > 0.5, q < 0.1) are typically enriched in non-brain tissues (Amygdala: 35%, Hippocampus: 24%) (Figure 1A-B). The
59 majority of tissue-enriched differentially expressed genes (tissue-enriched DEGs) were testis genes (Figure 1A-C). Even
60 though the testis has the largest total number of tissue-biased genes compared to any other tissue (2,496 genes), testis-biased
61 DEGs were significantly enriched for both brain regions (Amygdala p = 1.83e-05, Odds Ratio = 5.13; Hippocampus p =
62 4.26e-11, Odds Ratio = 4.45, Fisher's Exact Test). One example of a testis-enriched DEG is *FK506 binding protein 6* (*Fkbp6*),
63 a known regulator of piRNA expression and meiosis in germ cells^{23,24} (Figure 1C).

64 In addition to the high enrichment of testis genes, we also identified aberrant expression of other tissue-enriched genes
65 within the *Kdm5c*-KO brain. Although the *Kdm5c*-KO mice were male, we observed significant enrichment of ovary-biased
66 DEGs in both the amygdala and hippocampus (Amygdala p = 0.00574, Odds Ratio = 18.7; Hippocampus p = 0.048, Odds
67 Ratio = 5.88, Fisher's Exact) (Figure 1D). Ovary-enriched DEGs included *Zygotic arrest 1* (*Zar1*), which was recently shown
68 to sequester mRNAs in oocytes for meiotic maturation and early zygote development²⁵ (Figure 1D). Although not consistent
69 across brain regions, we also found significant enrichment of DEGS biased towards two non-gonadal tissues - the liver

70 (Amygdala p = 0.0398, Odds Ratio = 6.58, Fisher's Exact Test) and the muscle (Hippocampus p = 0.0104, Odds Ratio = 6.95, 71 Fisher's Exact Test). An example of a liver-biased DEG dysregulated in both the hippocampus and amygdala is *Apolipoprotein* 72 *C-I* (*Apoc1*), which is involved in lipoprotein metabolism (Figure 1E). Testis, ovary, and liver-enriched DEGs showed little to no 73 expression in the developing and adult wild-type brain, yet our mRNA-seq data indicate they are polyadenylated and spliced 74 into mature transcripts (Figure 1C-E). Of note, we did not observe enrichment of brain-enriched genes (Amygdala p = 1; 75 Hippocampus p = 0.74, Fisher's Exact), despite the fact these are brain samples and the brain has the second highest total 76 number of tissue-enriched genes (708 genes). Together, these results suggest misexpression of tissue-enriched genes within 77 the brain is a major effect of KDM5C loss.

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

79 • Intriguingly, some of the ectopic testis transcripts identified within the *Kdm5c*-KO hippocampus have known functions 80 unique to germ cells¹⁰, suggesting KDM5C may play a role in demarcating somatic versus germline identity.

81 The testis contains both germ cells (meiotic cells, e.g. spermatogonia) and somatic cells (non-meiotic, e.g. Leydig cells) 82 that support hormone production and germline functions. Intriguingly, many *Kdm5c*-KO testis and ovary enriched-DEGs have 83 germline-specific functions, suggesting *Kdm5c*-KO cells fail to distinguish between the soma and germline. To test if this holds 84 true for all *Kdm5c*-KO testis-biased DEGs, we first assessed their known functions through gene ontology analysis. We 85 found *Kdm5c*-KO testis-enriched DEGs high enrichment of germline-relevant ontologies, including spermatid development 86 (GO: 0007286, p.adjust = 6.2e-12) and sperm axoneme assembly (GO: 0007288, p.adjust = 2.45e-14) (Figure 2A).

87 To further validate if these testis DEGs are truly germline genes, we then evaluated their expression in somatic versus germ 88 cells within the testis. We first compared their expression in the testis with germ cell depletion²⁶, which was accomplished by 89 heterozygous *W* and *Wv* mutations in the enzymatic domain of *c-Kit* (*Kit*^{W/Wv}) that prevent the maturation of germ cells²⁷. 90 Almost all *Kdm5c*-KO testis-enriched DEGs lost expression with germ cell depletion (Figure 2B). The only testis-enriched 91 DEG that did not show considerable downregulation with germline depletion was *FK506 binding protein 6* (*Fkbp6*), the 92 aforementioned testis gene that regulates piRNA expression and meiosis in germ cells^{23,24}. We then assessed testis- 93 enriched DEG expression in a published single cell RNA-seq dataset that identified cell type-specific markers within the 94 testis²⁸. We found that while some testis-enriched DEGs were classified as specific markers for different germ cell types 95 (e.g. spermatogonia, spermatocytes, round spermatids, and elongating spermatids) none marked somatic cells (Figure 2C). 96 Together, these data suggest the somatic *Kdm5c*-KO brain aberrantly expresses germline genes.

97 We then wanted to more deeply characterize germline gene misexpression with *Kdm5c* loss, but lacked a comprehensive 98 list of mouse germline-enriched genes. To facilitate downstream analyses, we generated a curated list of germline-enriched 99 genes using currently available RNA-seq datasets in *Kit*^{W/Wv} mice. Wild-type and *Kit*^{W/Wv} datasets included males and females 100 at embryonic day 12, 14, and 16²⁹, as well as adult male testes²⁶. We defined genes as germline-enriched if their expression 101 met the following criteria: 1) their expression is greater than 1 FPKM in wild-type gonads 2) their expression in any adult 102 wild-type, non-gonadal tissue²⁰ does not exceed 20% of their maximum expression in the wild-type germline, and 3) their 103 expression in the germ cell-depleted germline, for any sex or time point, does not exceed 20% of their maximum expression 104 in the wild-type germline. These criteria yielded 1,288 germline-enriched genes (Figure 2D), which was hereafter used as a 105 resource for assessing germline gene misexpression with *Kdm5c* loss (Supplementary table 1).

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

107 Misexpression of germline genes in the adult brain suggests *Kdm5c*-KO cells fail to demarcate between germline and
108 somatic identity. Germ cells are typically distinguished from somatic cells soon after the embryo implants into the uterine
109 wall^{30,31} when a subset of epiblast stem cells become the primordial germ cells (PGCs) while the remainder differentiate into
110 the ectoderm, mesoderm, and endoderm to form the somatic tissues³². This developmental time point can be modeled *in*
111 *vitro* through differentiation of embryonic stem cells (ESCs) into post-implantation epiblast-like stem cells (EpiLCs) (Figure 3A,
112 top). Previous studies have demonstrated that while some germline-enriched genes are also expressed in embryonic stem
113 cells (ESCs) and in the 2-cell stage^{33–35}, they are silenced as they differentiate into EpiLCs¹⁷. Therefore, we assessed if
114 KDM5C was necessary for embryonic silencing of germline genes by evaluating the impact of *Kdm5c* loss in EpiLCs.

115 We first identified *Kdm5c*-KO EpiLC DEGs in of our previously published RNA-seq dataset³⁶ (DESeq2, log2 fold change
116 > 0.5, q < 0.1) and assessed tissue-enriched gene expression. Similar to the *Kdm5c*-KO brain, we observed general
117 dysregulation of tissue-enriched genes, with the largest number of genes belonging to the brain and testis, although they were
118 not significantly enriched (Figure 3B). Using the curated list of germline genes generated above, we found *Kdm5c*-KO EpiLCs
119 aberrantly expressed 54 germline-enriched genes, including the previously characterized hippocampal DEG¹⁰ *Cytochrome*
120 *C, testis-specific (Cyct)* (Figure 3C). Although we observed aberrant expression of many tissue-enriched genes, we did not
121 observe any significant difference in primed pluripotency genes (Figure 3D) or gross changes in *Kdm5c*-KO cell morpholgy
122 during differentiation (Figure 3E), indicating KDM5C loss does not impair EpiLC formation.

123 We then compared EpiLC germline DEGs to those expressed in the *Kdm5c*-KO brain to determine if all germline DEGs,
124 like *Cyct*, are constitutively dysregulated or if they can change over the course of development. We found this was primarily
125 not the case, as the majority of germline DEGs expressed in EpiLCs and the brain were unique, with only *Cyct* shared across
126 all sequencing datasets (Figure 3F). We then compared the known functions of EpiLC and brain germline DEGs and found
127 particularly high enrichment of meiosis-related gene ontologies in EpiLCs (Figure 3G), such as meiotic cell cycle process (GO:
128 1903046, p.adjust = 1.59e-08) and meiotic nuclear division (GO: 0140013, p.adjust = 9.76e-09). While there was modest
129 enrichment of meiotic gene ontologies in both brain regions, the *Kdm5c*-KO hippocampus primarily expressed late-stage
130 spermatogenesis genes, such those involved in the sperm axoneme structure.

131 Interestingly, DEGs unique to *Kdm5c*-KO EpiLCs included key drivers of germline identity, such as *Stimulated by retinoic*
132 *acid 8 (Stra8)* and *Deleted in azoospermia like (Dazl)* (Figure 3H). These genes are typically expressed during embryonic
133 germ cell development to commit PGCs to the germline fate, but are also expressed later in life to trigger meiotic gene
134 expression programs^{37–39}. Of note, some germline genes, including *Dazl*, are also expressed in the two-cell embryo^{34,40}.
135 However, we did not see misexpression of two-cell embryo-specific genes, like *Duxf3 (Dux)* (q = 0.337) and *Zscan4d* (q =
136 0.381), indicating *Kdm5c*-KO in EpiLCs do not revert back to a 2-cell state (Figure 3H).

137 We were particularly interested in the aberrant transcription of *Dazl*, since it is essential for germ cell development and
138 promotes the translation of germline mRNAs⁴¹. A significant portion of germline transcripts misexpressed in *Kdm5c*-KO
139 EpiLCs are known binding targets of DAZL, including *Stra8*⁴² (p = 1.698e-07, Fisher's Exact Test). This suggests expression
140 of DAZL protein could promote the translation of other aberrant germline transcripts, influencing their ability to impact
141 *Kdm5c*-KO cellular function. We thus tested DAZL protein expression in *Kdm5c*-KO EpiLCs through immunocytochemistry
142 (Figure 3I). We observed about 25% of *Kdm5c*-KO EpiLCs expressed DAZL protein and it was localized to the cytoplasm (p =
143 0.0015, Welch's t-test), consistent with the pattern of DAZL expression in spermatogonia⁴². Altogether these results suggest
144 tissue-specific genes are misexpressed during *Kdm5c*-KO embryogenesis, including key drivers of germline identity that can
145 be translated into protein.

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

147 • KDM5C may also be involved in this early decommissioning of germline genes, as re-expression of KDM5C in knockout
148 neurons fails to suppress their dysregulation¹⁰.

149 Previous work suggests KDM5C represses germline genes during early development, as re-expression of KDM5C in
150 knockout neuronal cultures fails to suppress hippocampal germline DEGs and KDM5C is not bound to their promoters in
151 neurons¹⁰. There is some evidence KDM5C binds to select germline gene promoters in ESCs¹⁰, including *Dazl*^{40,43}. As
152 KDM5C's binding at germline gene promoters has not been systematically characterized, it is currently unclear if KDM5C is
153 enriched at germline gene promoters, what types of germline genes KDM5C regulates, and if its binding is maintained at any
154 germline genes in neurons.

155 To further characterize the mechanism behind *Kdm5c*-KO germline gene misexpression, we analyzed KDM5C chromatin
156 immunoprecipitation followed by DNA sequencing (ChIP-seq) datasets in EpiLCs³⁶ and primary neuron cultures (PNCs) from
157 the cortex and hippocampus¹⁵. EpiLCs had a higher total number of KDM5C peaks than PNCs (EpiLCs: 5,808, PNCs: 1,276,
158 MACS2 q < 0.1 and fold enrichment > 1, removal of *Kdm5c*-KO false positive peaks) and KDM5C was primarily localized to
159 gene promoters in both cell types (EpiLCs: 4,190, PNCs: 745 +/- 500bp from the TSS), although PNCs showed increased
160 localization to non-promoter regions (Figure 4A).

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

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

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

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

184 Although KDM5C is generally thought to suppress transcription through erasure of histone 3 lysine 4 di- and trimethylation
185 (H3K4me2/3)¹¹, recent studies in ESCs have suggested KDM5C's repression *Dazl* is independent of its catalytic activity⁴⁰.
186 Somatic repression of germline genes is typically established during the transition between naive and primed pluripotency,
187 which modeled *in vitro* as ESCs to EpiLC differentiation. In ESCs, chromatin regulators place repressive histone modifications
188 at germline gene promoters, including histone 2A 119 monoubiquitination (H2AK119ub1) and histone 3 lysine 9 trimethylation
189 (H3K9me3)^{16,17,44}. Germline genes are then silenced long-term in EpiLCs by *de novo* placement of DNA CpG methylation
190 (DNAme)¹⁷. Although KDM5C's catalytic activity is not required to suppress *Dazl* in ESCs, KDM5C may promote long-term
191 germline gene silencing via H3K4me3 removal since H3K4me3 can impede DNAme placement^{45,46} and DNAme is lost at
192 select germline gene promoters in the hippocampus¹⁰. Because KDM5C's role in germline gene repression has only been
193 characterized in ESCs and in the mature brain, it is currently unclear to what extent KDM5C is involved during transition
194 between ESCs and EpiLCs and if its catalytic activity is required for long-term silencing.

195 To elucidate KDM5C's role in germline gene silencing, we first characterized KDM5C's substrates, histone 3 lysine 4
196 di- and trimethylation (H3K4me2/3) in our previously published ChIP-seq datasets in wild type and *Kdm5c*-KO amygdala²¹
197 and EpiLCs³⁶. In congruence with previous work in the *Kdm5c*-KO hippocampus¹⁰, we observed aberrant accumulation of
198 H3K4me3 around the transcription start site (TSS) of germline genes in the *Kdm5c*-KO amygdala (Figure 5A). We additionally
199 found a marked increase in H3K4me2 around the TSS of germline genes in *Kdm5c*-KO EpiLCs (Figure 5B).

200 We then evaluated KDM5C's embryonic role in germline gene silencing during ESC to EpiLC differentiation. We first
201 characterized KDM5C's mRNA and protein expression at 0, 24, and 48 hours of differentiation (Figure 5C). While *Kdm5c*
202 mRNA steadily decreased from 0 to 48 hours of differentiation (Figure 5D), KDM5C protein initially increased from 0 to
203 24 hours but then decreased to near knockout levels by 48 hours (Figure 5E). We then performed whole genome bisulfite
204 sequencing in wild-type and *Kdm5c*-KO ESCs and 96 hour extended EpiLCs (exEpiLCs) to determine KDM5C's role in the
205 initial placement of DNA methylation at germline gene promoters. While wild-type cells accumulated high levels of DNA
206 methylation at germline gene promoters over the course of ESCs to exEpiLC differentiation, DNA methylation was markedly
207 reduced in *Kdm5c*-KO exEpiLCs (Figure 5F).

- 208
 - Catalytic activity
 - Altogether, this suggests KDM5C is dynamically regulated during ESC to EpiLC differentiation and promotes germline
210 gene silencing via removal of H3K4me2/3 during early embryogenesis.
 - **note:** should I test if increase in H3K4me2 and H3K4me3 was highest in *Kdm5c*-KO cells at genes bound by KDM5C
212 at their promoter in EpiLCs? Don't think it's that impactful

213 **Experimental Procedures**

214 **Discussion**

215 In the above study, we demonstrate KDM5C's pivotal role in the development of tissue identity, resulting in substantial
216 misexpression of tissue-enriched genes within the adult *Kdm5c*-KO hippocampus and amygdala. We defined tissue-enriched
217 genes based on the criteria used in a previously published dataset of 17 C57/Bl6J mouse tissues²⁰, which defined genes as

218 tissue-enriched if they had more than 4-fold higher expression when compared to any other tissue. In addition to testis genes
219 identified previously¹⁰, we found significant enrichment of muscle, liver, and even ovary-biased genes aberrantly expressed
220 within the male *Kdm5c*-KO brain. It is currently unclear what the impact of these tissue-enriched genes are upon *Kdm5c*-KO
221 brain function and if they ultimately contribute to MRXSCJ-related phenotypes. While the majority of tissue-enriched DEGs
222 were testis and ovary genes with no known brain functions, select liver and muscle-biased DEGs do have known roles in
223 the wild-type brain. For example, *Apolipoprotein C-I* (*Apoc1*) is a lipid transport gene highly enriched within the liver[XXX],
224 but is lowly expressed in the wild-type brain. Intriguingly, *Apoc1* overexpression in the mouse brain can impair learning and
225 memory⁴⁷ and is implicated in Alzheimer's disease in humans⁴⁸. Our results suggest KDM5C fine-tunes the expression of
226 tissue-enriched genes like *Apoc1* to match the level required for proper brain function. However, futher studies are required to
227 determine if these genes contribute to *Kdm5c*-KO neuronal impairments and MRXSCJ pathology.

- 228 • testis genes are germline genes, germline gene list
- 229 – While a select few tissue-enriched DEGs had known roles in the brain, the majority were testis genes with no
230 known function outside the germline.
- 231 – distinguishing between germline and soma a key feature of multicellularity, chromatin regulators are important for
232 this process
- 233 – Studies on chromatin regulators in germline gene repression has focused on specific genes
- 234 – Curated a list of germline-enriched genes to robustly assess the types of genes dysregulated and KDM5C's role
- 235 • KDM5C represses germline genes during early embryogenesis
- 236 – Found this dysregulation in tissue identity begins during *Kdm5c*-KO early embryogenesis
- 237 – EpiLC express early regualtors, Brain late sperm - program seems to be continuing across development
- 238 – Importantly, even though germline genes are misexpressed, markers of EpiLC differentiation and EpiLC morphology
239 is unimpaired.
- 240 * Epiblast can become primordial germ cells
- 241 * Otx2 is expressed in EpiLCs and is known to repress PGC identity. It's properly expressed in *Kdm5c*-KO
242 EpiLCs, further supporting they aren't just becoming PGCs <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6485399/>
- 243 * Germline Program happening in the background of typical development.
- 244 • One of the genes misexpressed in *Kdm5c*-KO EpiLCs is *Dazl*, *Deleted in azoospermia like* (*Dazl*), a key regulator of
245 germline development that promotes the translation of germline-specific transcripts[XXX].
- 246 – 2 other studies of *dazl* regulators in ESCs also found KDM5C represses *dazl*.
- 247 – While crucial for germ cell development, *Dazl* is also expressed in ESCs and at the 2-cell stage.
- 248 – Some genes important for germ cell, ESC, and 2-cell development given they are important for self-renewal.
- 249
- 250 – We did not observe dysregulation of 2-cell-specific regulators like *Dux*.
- 251 – We found *Dazl* was expressed in *Kdm5c*-KO EpiLCs, when *Dazl* it typically decommissioned. This indicates
252 KDM5C loss results in long-term ectopic expression.
- 253 – We additionally found DAZL protein is ectopically expressed and localized to the cytoplasm. Given that a significant
254 number of KDM5C-KO germline DEGs are DAZL targets, it may promote the ectopic germline program.

256 – Very recently two other studies identified KDM5C represses *Dazl* in ESCs.
257 – * KDM5C was very recently shown to repress *Deleted in azoospermia like (Dazl)*, a key regulator of germline
258 development, in mouse embryonic stem cells (ESCs)^{40,43}. However, KDM5C binding and *Kdm5c*-KO germline
259 gene misexpression has yet to be globally characterized during early embryogenesis. Given that *Dazl* and
260 other germline-enriched genes can also be expressed in ESCs and at the 2-cell stage, it is unclear if KDM5C
261 has a direct role in the long-term germline gene silencing that occurs in the post-implantation epiblast.

262 • We globally characterized KDM5C's repression of germline genes during early embryogenesis and in mature neurons.

263 – In line with previous work, we found KDM5C did not regulate germline genes in neurons.
264 – KDM5C-bound genes in EpiLCs were enriched for germline ontologies, suggesting a major role of KDM5c during
265 embryogenesis
266 – While KDM5C directly binds some germline genes, including *Dazl*, many of the genes dysregulated in *Kdm5c*-KO
267 were not direct targets.
268 * *Stra8* notable exception
269 * Brain genes, including late-stage spermatogenesis genes
270 * Suggests germline genes can be dysregulated direct and indirect of KDM5C regulation
271 * Further supports germline programs can be ectopically activated
272 * Talk about different motifs if we do see differences there and if it explains direct vs indirect dysregulation
273 · Could also mention PRC1.6/KDM5C binds *pcgf6* in ESCs

274 • We demonstrated KDM5C is important for the transition between histone-mediated to DNAme-mediated silencing of
275 germline genes during the transition from naive to primed pluripotency.

276 – Loss of DNAme can last throughout life at at least two germline gene promoters (hippocampus barco)
277 – KDM5C could be important for DNAme is that KDM5C erases H3K4me3 which can impede CpGme.
278 * In support of this, KDM5C is highly enriched at the CpG islands near germline TSS that are methylated in
279 EpiLCs
280 – However, Recently KDM5C's catalytic activity was found to be unnecessary for *dazl* suppression in ESCs.
281
282 – Since DNAme is not placed until EpiLC stage, KDM5C's catalytic activity may be required for long-term silencing
283 of germline genes.

284 • In summary, we demonstrate loss of the X-linked intellectual disability gene KDM5C leads to widespread dysregulation
285 of brain tissue identity, including misexpression of germline genes in the somatic brain.

286 – In EpiLCs, KDM5C directly represses key drivers of germline identity like *Dazl*, likely through PRC1.6 recruitment
287 and promoting CpG methylation. However, *Kdm5c*-KO also ectopically expresses germline genes activated
288 indirectly, including *Stra8*.

289
290 – The germline developmental program to some extent continues ectopically during *Kdm5c*-KO development,
291 resulting in aberrant transcription of late stage spermatogenesis genes later in life.
292 – These results define KDM5C's role in the demarcation between soma and germline identity and offer a window
293 into potential targets to assess the deleterious effects these ectopic genes on neurodevelopment.

294 **Discussion notes**

- 295 • Our results indicate KDM5C is a pivotal repressor of germline programs in somatic cells.
- 296 • Studies on other chromatin regulators have focused on key marker genes to identify germline gene misexpression,
- 297 such as *Dazl*.
- 298 • Using a germline-depleted mouse model, we curated a list of mouse germline-enriched genes to globally assess
- 299 germline gene dysregulation.
- 300 • Many of the genes dysregulated in the mature *Kdm5c*-KO brain were important for late stages of spermatogenesis,
- 301 such as those important for sperm flagellar structure. Contrastingly, *Kdm5c*-KO EpiLCs aberrantly expressed key drivers
- 302 of germ cell identity, including *Dazl* and *Stra8*.
- 303 • While a significant portion of KDM5C-bound promoters are germline genes, many germline genes expressed during
- 304 *Kdm5c*-KO embryogenesis are not directly bound by *kdm5c*.
- 305 • One notable example is *Stra8*, a transcription factor important for germ cell specific transcription and meiotic initiation
- 306 •

307 While Directly binds to a subset of germline genes during early embryogenesis - KDM5C binds to a subset of germline
308 genes during early embryogenesis

- 309 • The including the demarcation between soma and germline fates.
- 310 the *Kdm5c*-KO brain also Previous work identified testis-enriched genes in *Kdm5c* genes
- 311 –
- 312 – However unlike the gonadal-biased DEGs,
- 313 • The demarcation of the germline versus soma is a key feature of multicellularity and sexually dimorphic reproduction
- 314 • Anything known about tissue-biased gene expression in other H3K4me regulators?
- 315 • Our data suggests the germline developmental program is occurring ectopically as *Kdm5c*-KOs progresses through
- 316 somatic tissue development
- 317 • tissue-biased gene expression:
- 318 • Altogether, these data indicate that while some germline genes are misexpressed due to direct loss of KDM5C binding
- 319 during emryogenesis, secondary downstream mechanisms can also promote their aberrant transcription.
- 320 – This shift from meiotic genes to later spermatogenesis genes in the hippocampus suggests the germline devel-
- 321 opmental program could occur ectopically as *Kdm5c*-KO cells progresses through somatic tissue development.
note: this is strengthened by the ChIP-seq data since KDM5C is not directly bound to many brain/flagellar
DEGs.This point might be stronger in the ChIPseq figure
- 324 • KDM5C is dynamically regulated during the window of embryonic germline gene silencing, our EpiLC ChIP-seq is likely
- 325 catching the tail end of KDM5C's main involvement.

- 326 • Papers to read/reference:
- 327 – Reconstitution of the Mouse Germ Cell Specification Pathway in Culture by Pluripotent Stem Cells: [https://www.cell.com/fulltext/S0092-8674\(11\)00771-9](https://www.cell.com/fulltext/S0092-8674(11)00771-9)
- 328 – 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/>
- 330

331 References

- 332 1. Strahl, B.D., and Allis, C.D. (2000). The language of covalent histone modifications. *Nature* **403**, 41–45. <https://doi.org/10.1038/47412>.
- 333 2. Jenuwein, T., and Allis, C.D. (2001). Translating the Histone Code. *Science* **293**, 1074–1080. <https://doi.org/10.1126/science.1063127>.
- 334 3. Lewis, E.B. (1978). A gene complex controlling segmentation in *Drosophila*. *Nature* **276**, 565–570. <https://doi.org/10.1038/276565a0>.
- 335 4. Kennison, J.A., and Tamkun, J.W. (1988). Dosage-dependent modifiers of polycomb and antennapedia mutations in *Drosophila*. *Proc. Natl. Acad. Sci. U.S.A.* **85**, 8136–8140. <https://doi.org/10.1073/pnas.85.21.8136>.
- 336 5. Gabriele, M., Lopez Tobon, A., D'Agostino, G., and Testa, G. (2018). The chromatin basis of neurodevelopmental disorders: Rethinking dysfunction along the molecular and temporal axes. *Prog Neuropsychopharmacol Biol Psychiatry* **84**, 306–327. <https://doi.org/10.1016/j.pnpbp.2017.12.013>.
- 337 6. Zhou, Z., Hong, E.J., Cohen, S., Zhao, W.-N., Ho, H.-Y.H., Schmidt, L., Chen, W.G., Lin, Y., Savner, E., Griffith, E.C., et al. (2006). Brain-specific phosphorylation of MeCP2 regulates activity-dependent Bdnf transcription, dendritic growth, and spine maturation. *Neuron* **52**, 255–269. <https://doi.org/10.1016/j.neuron.2006.09.037>.
- 338 7. Hirabayashi, Y., Suzuki, N., Tsuboi, M., Endo, T.A., Toyoda, T., Shinga, J., Koseki, H., Vidal, M., and Gotoh, Y. (2009). Polycomb Limits the Neurogenic Competence of Neural Precursor Cells to Promote Astrocytic Fate Transition. *Neuron* **63**, 600–613. <https://doi.org/10.1016/j.neuron.2009.08.021>.
- 339 8. Kassis, J.A., Kennison, J.A., and Tamkun, J.W. (2017). Polycomb and Trithorax Group Genes in *Drosophila*. *Genetics* **206**, 1699–1725. <https://doi.org/10.1534/genetics.115.185116>.
- 340 9. Schaefer, A., Sampath, S.C., Intrator, A., Min, A., Gertler, T.S., Surmeier, D.J., Tarakhovsky, A., and Greengard, P. (2009). Control of cognition and adaptive behavior by the GLP/G9a epigenetic suppressor complex. *Neuron* **64**, 678–691. <https://doi.org/10.1016/j.neuron.2009.11.019>.
- 341 10. Scandaglia, M., Lopez-Atalaya, J.P., Medrano-Fernandez, A., Lopez-Cascales, M.T., Del Blanco, B., Lipinski, M., Benito, E., Olivares, R., Iwase, S., Shi, Y., et al. (2017). Loss of Kdm5c Causes Spurious Transcription and Prevents the Fine-Tuning of Activity-Regulated Enhancers in Neurons. *Cell Rep* **21**, 47–59. <https://doi.org/10.1016/j.celrep.2017.09.014>.
- 342 11. Iwase, S., Lan, F., Bayliss, P., De La Torre-Ubieta, L., Huarte, M., Qi, H.H., Whetstone, J.R., Bonni, A., Roberts, T.M., and Shi, Y. (2007). The X-Linked Mental Retardation Gene SMCX/JARID1C Defines a Family of Histone H3 Lysine 4 Demethylases. *Cell* **128**, 1077–1088. <https://doi.org/10.1016/j.cell.2007.02.017>.
- 343 12. Claes, S., Devriendt, K., Van Goethem, G., Roelen, L., Meireleire, J., Raeymaekers, P., Cassiman, J.J., and Fryns, J.P. (2000). Novel syndromic form of X-linked complicated spastic paraparesis. *Am J Med Genet* **94**, 1–4.
- 344
- 345
- 346
- 347
- 348
- 349
- 350
- 351
- 352
- 353
- 354
- 355

- 356 13. Jensen, L.R., Amende, M., Gurok, U., Moser, B., Gimmel, V., Tzschach, A., Janecke, A.R., Tariverdian, G., Chelly, J.,
Fryns, J.P., et al. (2005). Mutations in the JARID1C gene, which is involved in transcriptional regulation and chromatin
357 remodeling, cause X-linked mental retardation. *Am J Hum Genet* **76**, 227–236. <https://doi.org/10.1086/427563>.
- 358 14. Carmignac, V., Nambot, S., Lehalle, D., Callier, P., Moortgat, S., Benoit, V., Ghoumid, J., Delobel, B., Smol, T., Thuillier,
359 C., et al. (2020). Further delineation of the female phenotype with KDM5C disease causing variants: 19 new individuals
and review of the literature. *Clin Genet* **98**, 43–55. <https://doi.org/10.1111/cge.13755>.
- 360 15. Iwase, S., Brookes, E., Agarwal, S., Badeaux, A.I., Ito, H., Vallianatos, C.N., Tomassy, G.S., Kasza, T., Lin, G.,
Thompson, A., et al. (2016). A Mouse Model of X-linked Intellectual Disability Associated with Impaired Removal of
361 Histone Methylation. *Cell Reports* **14**, 1000–1009. <https://doi.org/10.1016/j.celrep.2015.12.091>.
- 362 16. Endoh, M., Endo, T.A., Shinga, J., Hayashi, K., Farcas, A., Ma, K.W., Ito, S., Sharif, J., Endoh, T., Onaga, N., et
363 al. (2017). PCGF6-PRC1 suppresses premature differentiation of mouse embryonic stem cells by regulating germ
cell-related genes. *eLife* **6**. <https://doi.org/10.7554/eLife.21064>.
- 364 17. Mochizuki, K., Sharif, J., Shirane, K., Uranishi, K., Bogutz, A.B., Janssen, S.M., Suzuki, A., Okuda, A., Koseki, H.,
365 and Lorincz, M.C. (2021). Repression of germline genes by PRC1.6 and SETDB1 in the early embryo precedes DNA
methylation-mediated silencing. *Nat Commun* **12**, 7020. <https://doi.org/10.1038/s41467-021-27345-x>.
- 366 18. Velasco, G., Hubé, F., Rollin, J., Neuillet, D., Philippe, C., Bouzinba-Segard, H., Galvani, A., Viegas-Péquignot, E., and
367 Francastel, C. (2010). Dnmt3b recruitment through E2F6 transcriptional repressor mediates germ-line gene silencing
in murine somatic tissues. *Proc Natl Acad Sci U S A* **107**, 9281–9286. <https://doi.org/10.1073/pnas.1000473107>.
- 368 19. Hackett, J.A., Reddington, J.P., Nestor, C.E., Dunican, D.S., Branco, M.R., Reichmann, J., Reik, W., Surani, M.A.,
Adams, I.R., and Meehan, R.R. (2012). Promoter DNA methylation couples genome-defence mechanisms to epigenetic
369 reprogramming in the mouse germline. *Development* **139**, 3623–3632. <https://doi.org/10.1242/dev.081661>.
- 370 20. Li, B., Qing, T., Zhu, J., Wen, Z., Yu, Y., Fukumura, R., Zheng, Y., Gondo, Y., and Shi, L. (2017). A Comprehensive
371 Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. *Sci Rep* **7**, 4200. <https://doi.org/10.1038/s41598-017-04520-z>.
- 372 21. Vallianatos, C.N., Raines, B., Porter, R.S., Bonefas, K.M., Wu, M.C., Garay, P.M., Collette, K.M., Seo, Y.A., Dou, Y.,
Keegan, C.E., et al. (2020). Mutually suppressive roles of KMT2A and KDM5C in behaviour, neuronal structure, and
373 histone H3K4 methylation. *Commun Biol* **3**, 278. <https://doi.org/10.1038/s42003-020-1001-6>.
- 374 22. Love, M.I., Huber, W., and Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data
375 with DESeq2. *Genome Biol* **15**, 550. <https://doi.org/10.1186/s13059-014-0550-8>.
- 376 23. Crackower, M.A., Kolas, N.K., Noguchi, J., Sarao, R., Kikuchi, K., Kaneko, H., Kobayashi, E., Kawai, Y., Kozieradzki, I.,
Landers, R., et al. (2003). Essential Role of Fkbp6 in Male Fertility and Homologous Chromosome Pairing in Meiosis.
377 *Science* **300**, 1291–1295. <https://doi.org/10.1126/science.1083022>.
- 378 24. Xiòl, J., Cora, E., Koglgruber, R., Chuma, S., Subramanian, S., Hosokawa, M., Reuter, M., Yang, Z., Berninger, P.,
Palencia, A., et al. (2012). A Role for Fkbp6 and the Chaperone Machinery in piRNA Amplification and Transposon
379 Silencing. *Molecular Cell* **47**, 970–979. <https://doi.org/10.1016/j.molcel.2012.07.019>.
- 380 25. Cheng, S., Altmeppen, G., So, C., Welp, L.M., Penir, S., Ruhwedel, T., Menelaou, K., Harasimov, K., Stützer, A.,
Blayney, M., et al. (2022). Mammalian oocytes store mRNAs in a mitochondria-associated membraneless compartment.
381 *Science* **378**, eabq4835. <https://doi.org/10.1126/science.abq4835>.

- 382 26. Mueller, J.L., Skaletsky, H., Brown, L.G., Zaghlul, S., Rock, S., Graves, T., Auger, K., Warren, W.C., Wilson, R.K., and
383 Page, D.C. (2013). Independent specialization of the human and mouse X chromosomes for the male germ line. *Nat Genet* **45**, 1083–1087. <https://doi.org/10.1038/ng.2705>.
- 384 27. Handel, M.A., and Eppig, J.J. (1979). Sertoli Cell Differentiation in the Testes of Mice Genetically Deficient in Germ
385 Cells. *Biology of Reproduction* **20**, 1031–1038. <https://doi.org/10.1095/biolreprod20.5.1031>.
- 386 28. Green, C.D., Ma, Q., Manske, G.L., Shami, A.N., Zheng, X., Marini, S., Moritz, L., Sultan, C., Gurczynski, S.J., Moore,
387 B.B., et al. (2018). A Comprehensive Roadmap of Murine Spermatogenesis Defined by Single-Cell RNA-Seq. *Dev Cell* **46**, 651–667.e10. <https://doi.org/10.1016/j.devcel.2018.07.025>.
- 388 29. Soh, Y.Q., Junker, J.P., Gill, M.E., Mueller, J.L., van Oudenaarden, A., and Page, D.C. (2015). A Gene Regulatory
389 Program for Meiotic Prophase in the Fetal Ovary. *PLoS Genet* **11**, e1005531. <https://doi.org/10.1371/journal.pgen.1005531>.
- 390 30. Magnúsdóttir, E., and Surani, M.A. (2014). How to make a primordial germ cell. *Development* **141**, 245–252.
391 <https://doi.org/10.1242/dev.098269>.
- 392 31. Günesdogan, U., Magnúsdóttir, E., and Surani, M.A. (2014). Primordial germ cell specification: A context-dependent
393 cellular differentiation event [corrected]. *Philos Trans R Soc Lond B Biol Sci* **369**. <https://doi.org/10.1098/rstb.2013.0543>.
- 394 32. Bardot, E.S., and Hadjantonakis, A.-K. (2020). Mouse gastrulation: Coordination of tissue patterning, specification and
395 diversification of cell fate. *Mechanisms of Development* **163**, 103617. <https://doi.org/10.1016/j.mod.2020.103617>.
- 396 33. Welling, M., Chen, H., Muñoz, J., Musheev, M.U., Kester, L., Junker, J.P., Mischerikow, N., Arbab, M., Kuijk, E.,
397 Silberstein, L., et al. (2015). DAZL regulates Tet1 translation in murine embryonic stem cells. *EMBO Reports* **16**,
791–802. <https://doi.org/10.15252/embr.201540538>.
- 398 34. Macfarlan, T.S., Gifford, W.D., Driscoll, S., Lettieri, K., Rowe, H.M., Bonanomi, D., Firth, A., Singer, O., Trono, D., and
399 Pfaff, S.L. (2012). Embryonic stem cell potency fluctuates with endogenous retrovirus activity. *Nature* **487**, 57–63.
<https://doi.org/10.1038/nature11244>.
- 400 35. Suzuki, A., Hirasaki, M., Hishida, T., Wu, J., Okamura, D., Ueda, A., Nishimoto, M., Nakachi, Y., Mizuno, Y., Okazaki,
401 Y., et al. (2016). Loss of MAX results in meiotic entry in mouse embryonic and germline stem cells. *Nat Commun* **7**,
11056. <https://doi.org/10.1038/ncomms11056>.
- 402 36. Samanta, M.K., Gayen, S., Harris, C., Maclary, E., Murata-Nakamura, Y., Malcore, R.M., Porter, R.S., Garay, P.M.,
403 Vallianatos, C.N., Samollow, P.B., et al. (2022). Activation of Xist by an evolutionarily conserved function of KDM5C
demethylase. *Nat Commun* **13**, 2602. <https://doi.org/10.1038/s41467-022-30352-1>.
- 404 37. Koubova, J., Menke, D.B., Zhou, Q., Capel, B., Griswold, M.D., and Page, D.C. (2006). Retinoic acid regulates
405 sex-specific timing of meiotic initiation in mice. *Proc. Natl. Acad. Sci. U.S.A.* **103**, 2474–2479. <https://doi.org/10.1073/pnas.0510813103>.
- 406 38. Lin, Y., Gill, M.E., Koubova, J., and Page, D.C. (2008). Germ Cell-Intrinsic and -Extrinsic Factors Govern Meiotic
407 Initiation in Mouse Embryos. *Science* **322**, 1685–1687. <https://doi.org/10.1126/science.1166340>.
- 408 39. Endo, T., Mikedis, M.M., Nicholls, P.K., Page, D.C., and De Rooij, D.G. (2019). Retinoic Acid and Germ Cell
409 Development in the Ovary and Testis. *Biomolecules* **9**, 775. <https://doi.org/10.3390/biom9120775>.

- 410 40. Gupta, N., Yakhou, L., Albert, J.R., Azogui, A., Ferry, L., Kirsh, O., Miura, F., Battault, S., Yamaguchi, K., Laisné, M., et al. (2023). A genome-wide screen reveals new regulators of the 2-cell-like cell state. *Nat Struct Mol Biol.*
411 <https://doi.org/10.1038/s41594-023-01038-z>.
- 412 41. Li, H., Liang, Z., Yang, J., Wang, D., Wang, H., Zhu, M., Geng, B., and Xu, E.Y. (2019). DAZL is a master translational
413 regulator of murine spermatogenesis. *Natl Sci Rev* *6*, 455–468. <https://doi.org/10.1093/nsr/nwy163>.
- 414 42. Mikedis, M.M., Fan, Y., Nicholls, P.K., Endo, T., Jackson, E.K., Cobb, S.A., De Rooij, D.G., and Page, D.C. (2020).
415 DAZL mediates a broad translational program regulating expansion and differentiation of spermatogonial progenitors.
eLife *9*, e56523. <https://doi.org/10.7554/eLife.56523>.
- 416 43. Al Adhami, H., Vallet, J., Schaal, C., Schumacher, P., Bardet, A.F., Dumas, M., Chicher, J., Hammann, P., Daujat,
417 S., and Weber, M. (2023). Systematic identification of factors involved in the silencing of germline genes in mouse
embryonic stem cells. *Nucleic Acids Research* *51*, 3130–3149. <https://doi.org/10.1093/nar/gkad071>.
- 418 44. Liu, M., Zhu, Y., Xing, F., Liu, S., Xia, Y., Jiang, Q., and Qin, J. (2020). The polycomb group protein PCGF6
419 mediates germline gene silencing by recruiting histone-modifying proteins to target gene promoters. *J Biol Chem* *295*,
9712–9724. <https://doi.org/10.1074/jbc.RA119.012121>.
- 420 45. Otani, J., Nankumo, T., Arita, K., Inamoto, S., Ariyoshi, M., and Shirakawa, M. (2009). Structural basis for recognition
421 of H3K4 methylation status by the DNA methyltransferase 3A ATRX–DNMT3–DNMT3L domain. *EMBO Reports* *10*,
1235–1241. <https://doi.org/10.1038/embor.2009.218>.
- 422 46. Guo, X., Wang, L., Li, J., Ding, Z., Xiao, J., Yin, X., He, S., Shi, P., Dong, L., Li, G., et al. (2015). Structural insight into
423 autoinhibition and histone H3-induced activation of DNMT3A. *Nature* *517*, 640–644. <https://doi.org/10.1038/nature13899>.
- 424 47. Abildayeva, K., Berbée, J.F.P., Blokland, A., Jansen, P.J., Hoek, F.J., Meijer, O., Lütjohann, D., Gautier, T., Pillot, T., De
425 Vente, J., et al. (2008). Human apolipoprotein C-I expression in mice impairs learning and memory functions. *Journal of Lipid Research* *49*, 856–869. <https://doi.org/10.1194/jlr.M700518-JLR200>.
- 426 48. Leduc, V., Jasmin-Bélanger, S., and Poirier, J. (2010). APOE and cholesterol homeostasis in Alzheimer's disease.
427 *Trends in Molecular Medicine* *16*, 469–477. <https://doi.org/10.1016/j.molmed.2010.07.008>.

428 **Figures and Tables**

- 429 • Supplementary table 1: list of all germline genes.
- 430 – Columns to include:
- 431 * KDM5C bound vs not
- 432 * DEG in EpiLC, brain, both, neither (separate columns?)

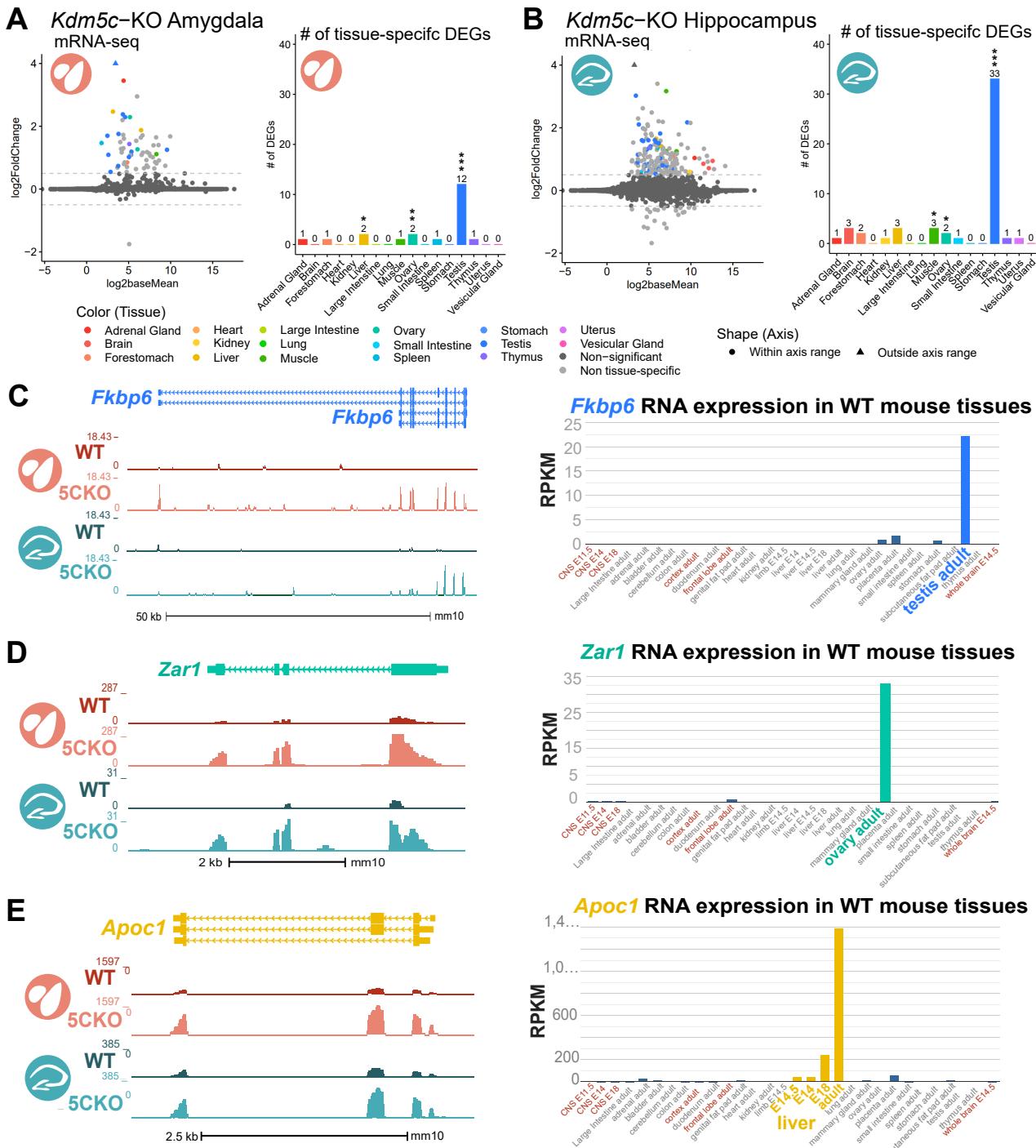


Figure 1: Tissue-enriched genes are misexpressed in the *Kdm5c*-KO brain. **A-B.** Expression of tissue-enriched genes (Li et al 2017) in the male *Kdm5c*-KO amygdala (A) and hippocampus (B). Left - MA plot of mRNA-seq. Right - Number of tissue-enriched differentially expressed genes (DEGs). * $p<0.05$, ** $p<0.01$, *** $p<0.001$, 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.

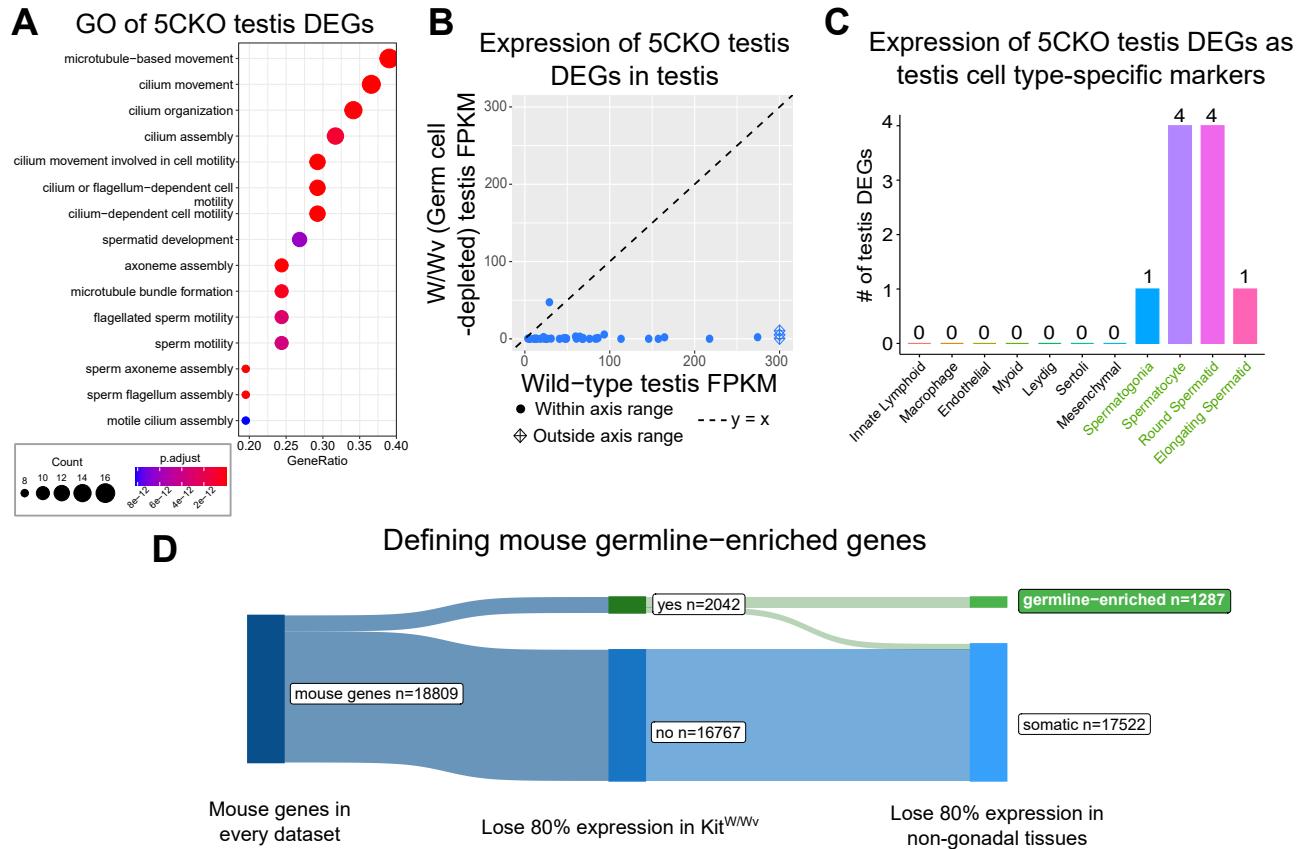


Figure 2: Aberrant transcription of germline genes in the *Kdm5c*-KO in the brain. **A.** enrichPlot gene ontology (GO) of *Kdm5c*-KO amygdala and hippocampus testis-enriched DEGs **B.** Expression of testis DEGs in wild-type (WT) testis versus germ cell-depleted (W/Wv) testis (Mueller et al 2013). Expression 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).

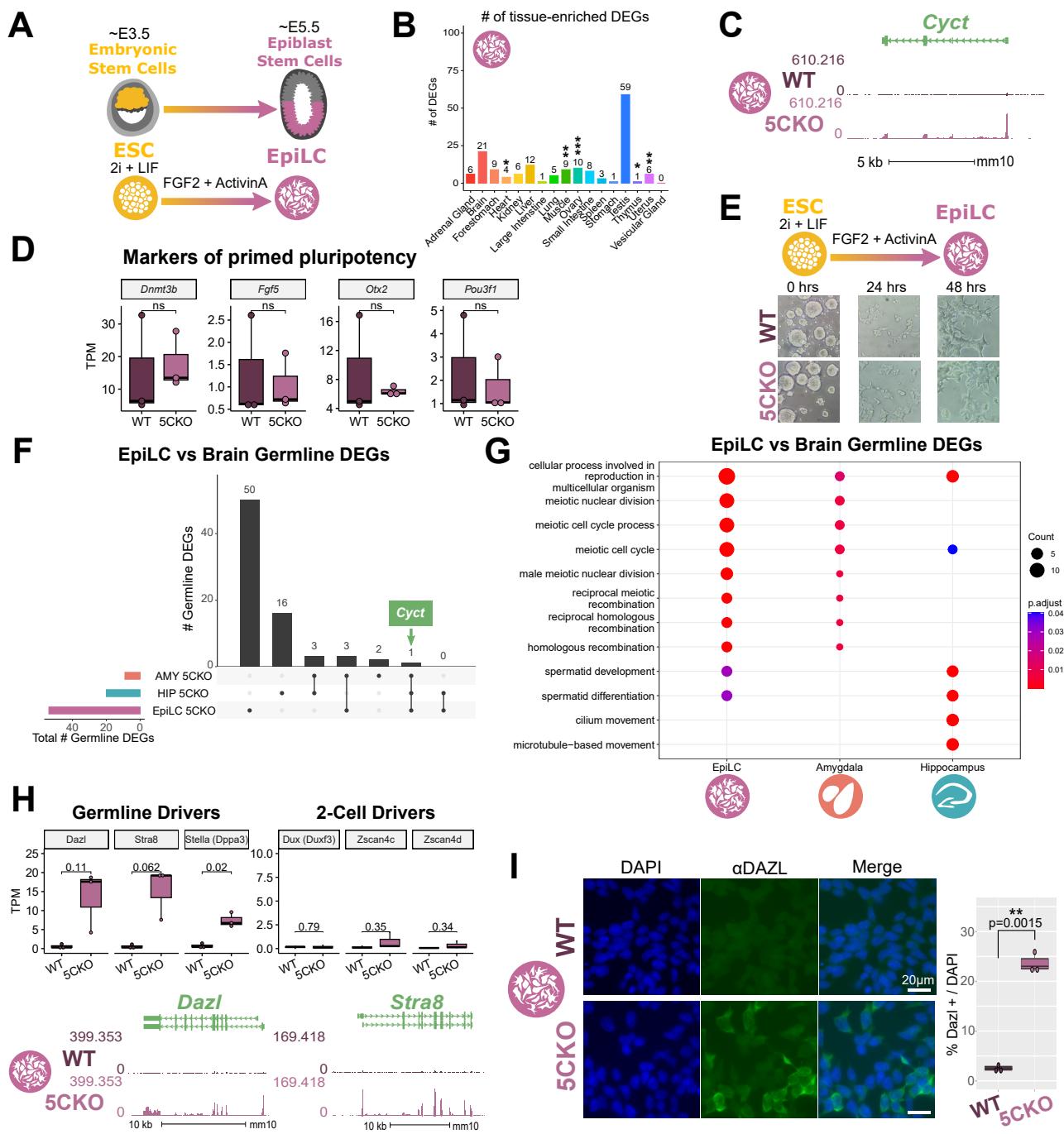


Figure 3: *Kdm5c*-KO epiblast-like cells express key drivers of germline identity

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.

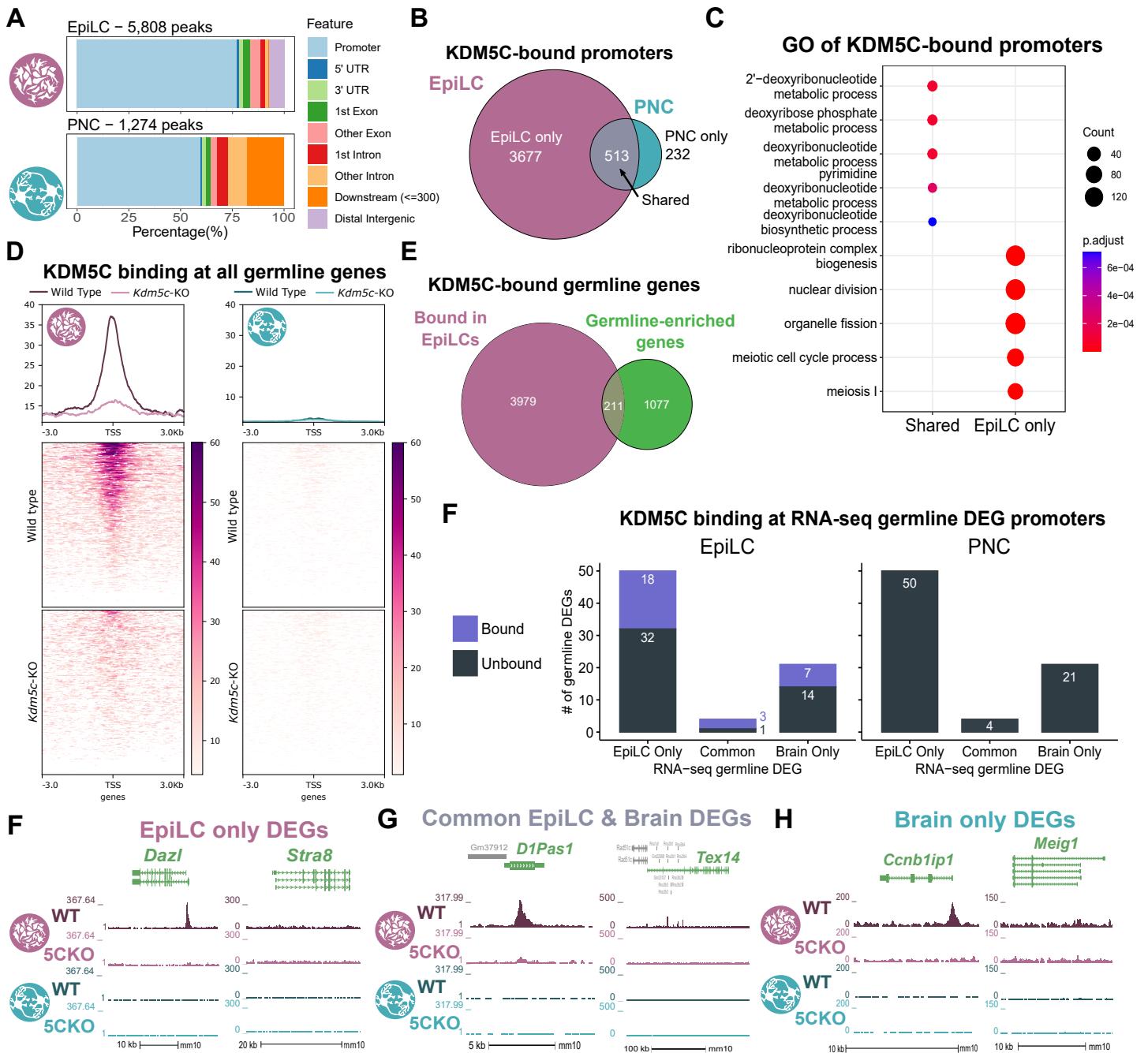


Figure 4: KDM5C binds to a subset of germline gene promoters during early embryogenesis **A.** ChIPseeker localization of KDM5C peaks at different genomic regions in EpiLCs (top) and hippocampal and cortex primary neuron cultures (PNCs, bottom). **B.** Overlap of genes with KDM5C bound to their promoters 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

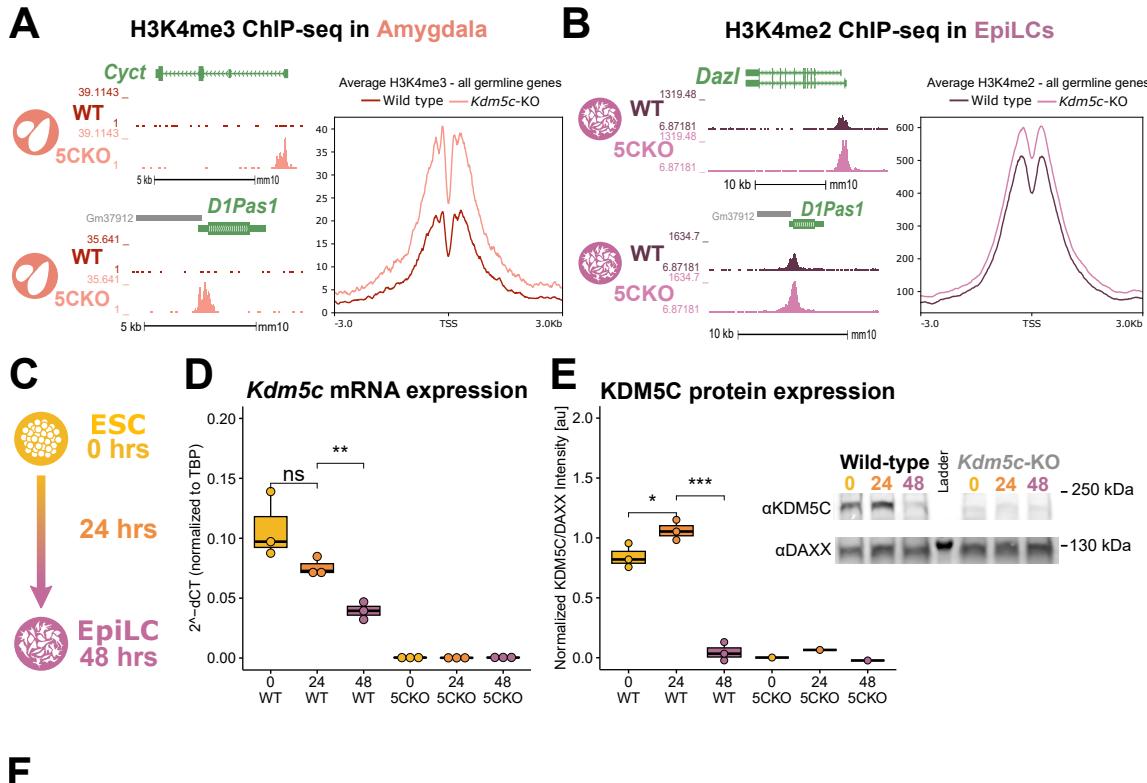


Figure 5: KDM5C's catalytic activity promotes long-term silencing of germline genes via DNA methylation. **A.** Left - Bigwigs of representative histone 3 lysine 4 trimethylation (H3K4me3) ChIP-seq peaks at two germline genes in the wild-type (WT) and *Kdm5c*-KO (5CKO) adult amygdala. Right - Average H3K4me3 at the transcription 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 comparison 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

433 **Notes**

434 **Figure outline:**

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

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

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

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

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

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

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

470 Introduction: * Chromatin regulators are important for cellular identity * H3K4me1-3 linked to active gene promoters and
471 enhancers * Surprisingly, mutations in Chromatin regulators lead to many NDDs (including many H3K4 regulators) * Recent

472 studies have shown some chromatin regulators are important for regulating neuron-specific gene expression/chromatin
473 stat_compare_means * However, loss of some chromatin regulators can also lead to ectopic expression of tissue-enriched
474 genes * Very few studies have looked at these genes and it's unclear if these genes contribute to NDD impairments. *
475 Necessary to first characterize the mechanism behind their derepression to identify molecular footholds into testing their
476 contribution to neuronal impairments and potential for therapeutic intervention

- 477 • Loss of KDM5C can result in the misexpression of genes typically only found in the testis
- 478 – Misexpression of tissue-enriched genes hasn't been systematically characterized - Unclear if these genes are
479 exceptions or if other tissue-specific genes are dysregulated
- 480 – Interestingly, these genes (Cyct, D1pas1) typically function in the germline
- 481 – Germ cells (meiotic cells) are typically distinguished from somatic cells very early on in embryogenesis and is a
482 key feature of multicellularity
- 483 – Chromatin regulators are very important for decommissioning germline genes and act successively the embryo
484 implants into the uterine wall
- 485 * Most studies have focused on ESCs, which have a similar transcriptome to germ cells / 2-cells
- 486 * recently, KDM5C was shown to repress DAZL in ESCs, independent of its catalytic activity
- 487 * However, DNA methylation is lost in the mature 5CKO brain, DNA methylation is placed later and it's unclear if
488 it's required for long-term repression (maybe too specific, just trying to go into the fact that the mechanism is
489 partially understood but unclear)
- 490 – Systematic characterization of ectopic germline genes hasn't been done
- 491 * unknown if other germline-enriched genes are dysregulated, including oocyte-specific genes
- 492 * Crucially, it's unknown if misexpression of the germline program leads to functional consequences in 5CKO
493 cells.

494 **Germline gene repression background:**

495 Interestingly, some of the ectopic testis transcripts identified in the *Kdm5c*-KO brain are typically expressed in germ cells¹⁰.
496 Unlike somatic cells, germ cells (e.g. sperm and eggs) undergo meiosis and pass on their genetic material to the next genera-
497 tion. The germline and the soma are typically distinguished during early embryogenesis, when germline genes are silenced
498 in epiblast stem cells soon after implantation and only reactivated in a subset to form the germline. Chromatin regulators
499 play a key role in decommissioning germline genes as the embryo transitions from naive to primed pluripotency by placing
500 repressive histone H2A lysine 119 monoubiquitination (H2AK119ub1)¹⁶, histone 3 lysine 9 trimethylation (H3K9me3)^{16,17},
501 and DNA CpG methylation¹⁷⁻¹⁹ at germline gene promoters. KDM5C may also be involved in this early decommissioning of
502 germline genes, as re-expression of KDM5C in neurons fails to suppress their dysregulation¹⁰. In support of this, KDM5C
503 was very recently shown to repress *Deleted in azoospermia like* (*Dazl*), a key regulator of germline development, in mouse
504 embryonic stem cells (ESCs)^{40,43}. In support of this, two independent screens in mouse embryonic stem cells (ESCs) recently
505 identified KDM5C as a repressor of *Deleted in azoospermia like* (*Dazl*), a key regulator of germline development. However,
506 KDM5C's role in embryonic germline gene repression is currently unclear, given that *Dazl* is also expressed in ESCs and in
507 the 2-cell stage and germline gene misexpression has yet to be globally characterized during *Kdm5c*-KO embryogenesis.