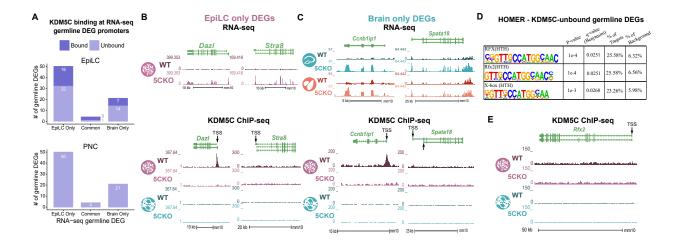
- ¹ Supplement Erosion of somatic tissue identity with loss of the
- 2 X-linked intellectual disability factor KDM5C

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Supplementary Figure 1: KDM5C binds to a subset of germline RNA-seq differentially expressed genes. A. Bar graph of the number of germline-enriched DEGs with promoter KDM5C ChIP-seq peaks in wild-type EpiLCs (Top) and PNCs (Bottom). RNA-seq DEGs were classified as shared betwen EpiLCs and the brain (Common), unique to EpiLCs (EpiLC Only), or unique to one or multiple brain regions (Brain Only). B. Average bigwigs of two example RNA-seq DEGs dysregulated in EpiLCs but not the brain, Dazl and Stra8. Top is the RNA-seq tracks for wild-type (WT) and Kdm5c-KO (5CKO) EpiLCs, bottom is the KDM5C ChIP-seq tracks, with the annotated transcription start site (TSS) for each gene. C. Same as B but for two example DEGs only dysregualted in the brain and not expressed in EpiLCs, Ccnb1ip1 and Spata18. D. HOMER motif analysis of all KDM5C-unbound germline DEGs shows significant enrichment of multiple RFX members and their X-box motif. E. KDM5C ChIP-seq shows no KDM5C accumulation at the Rfx2 promoter in EpiLCs or PNCs.