Supplementary Figures:

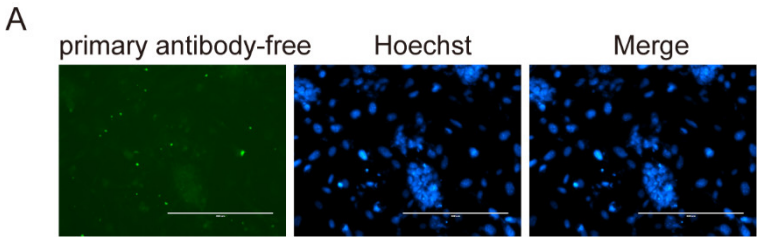


Figure S1. Immunofluorescence staining of no primary antibody (anti-Rabbit second antibody) control in the CON-piPSCs.

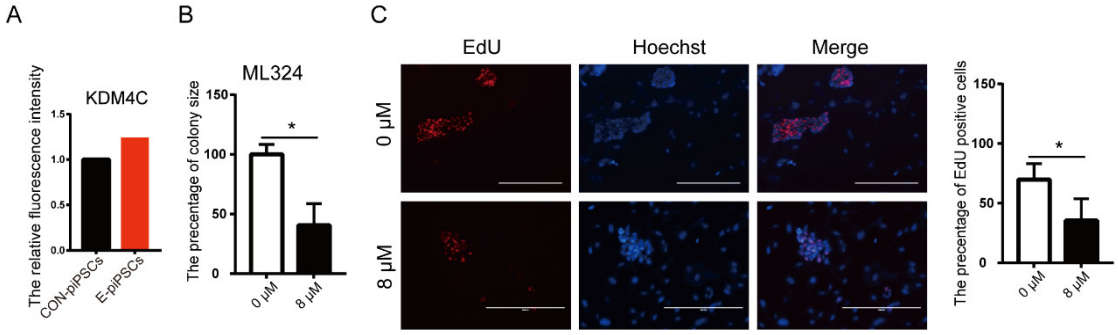


Figure S2. EdU staining analysis of CON-piPSCs after 8 μM supplement. (**A**) the quantification analysis of immunofluorescence staining of KDM4C in CON- and E-piPSCs. (**B**) The quantification analysis of colony size with adding 8 μM ML324 in CON-piPSCs; * represents $p < 0.05$. (**C**) EdU staining result and qualities analysis of the CON-piPSCs with adding 8 μM ML324; The scale bar represents 200 μm.

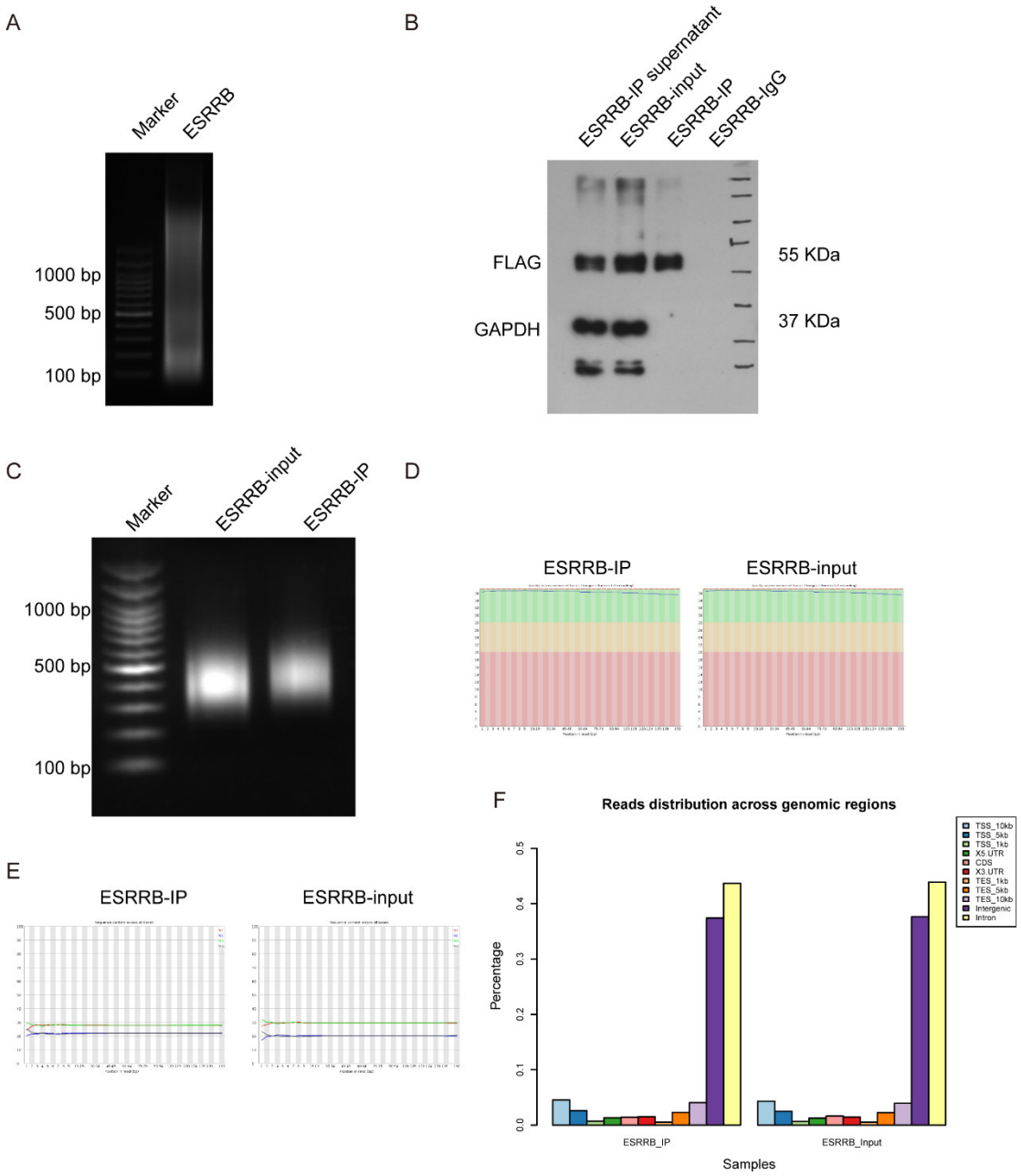


Figure S3. ChIP-seq quality inspection of E-piPSCs. (**A**) DNA ultrasonic results of E-piPSCs; the DNA fragments are distributed at 100–1000bp. (**B**) IP result of GAPDH and FLAG antibodies; the FLAG represents the expression of ESRRB. (**C**) the DNA database creation report. (**D**) Base mass distribution of ESRRB-FLAG ChIP-seq results. (**E**) Base balance of ESRRB-FLAG ChIP-seq results. (**F**) Histogram of the distribution of reads in different regions of the reference genome.

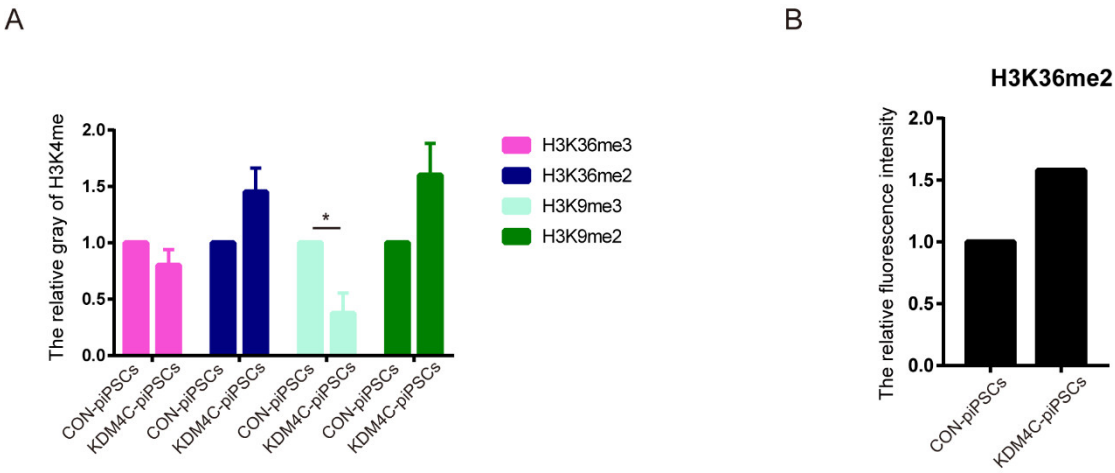


Figure S4. Quantification analysis of histone methylation in the CON- and KDM4C-piPSCs. (**A**) Quantification analysis of H3K36me3/2 and H3K9me3/2 of western blot in the CON- and KDM4C-piPSCs; (**B**) Quantification analysis of H3K36me2 immunofluorescence staining in the CON- and KDM4C-piPSCs.