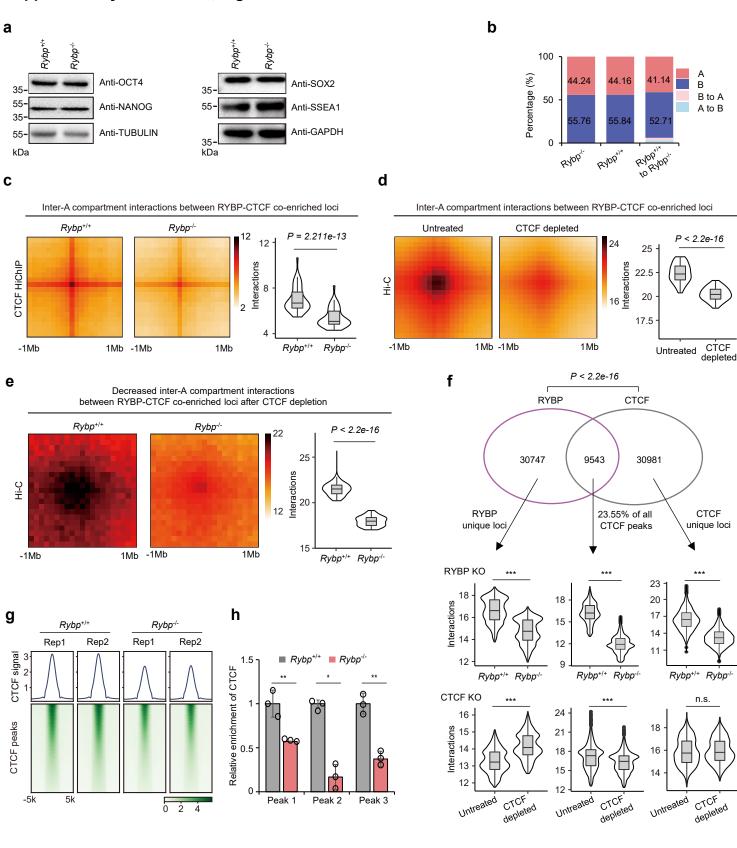
Supplementary information, Fig.S6



Supplementary information, Fig. S6 RYBP depletion attenuates CTCF-connected inter-A compartment interactions. a Western blot showing the expression level of OCT4, NANOG, SOX2 and SSEA1 after inducing RYBP depletion for 2 days. b Hi-C data showing the percentages of compartment switching between Rybp^{-/-} and Rybp^{+/+} mESCs. **c** APA plots (left) and quantitation (right) showing the genome-wide aggregate strength between RYBP-CTCF co-enriched loci from different A compartments after RYBP depletion (CTCF HiChIP data), Wilcoxon rank-sum test. d APA plots (left) and quantitation (right) showing the genome-wide aggregate strength between RYBP-CTCF co-enriched loci from different A compartments after CTCF depletion (Hi-C data), Wilcoxon rank-sum test. e APA plots (left) and quantitation (right) showing the genome-wide aggregate strength of inter-A compartment interactions between RYBP-CTCF co-enriched loci after RYBP depletion (Hi-C data), the most strongly decreased (top 10%) inter-A compartment interactions between RYBP-CTCF co-enriched loci after CTCF depletion were used for the analysis, Wilcoxon rank-sum test. f Top: the overlap between RYBP (GSM4052120) and CTCF (GSE29218) peaks, permutation test. Middle and bottom: Hi-C data showing the interaction alteration between RYBP unique loci, between RYBP-CTCF co-binding loci or between CTCF unique loci after RYBP (middle) or CTCF (bottom) depletion, Wilcoxon rank-sum test; all p values were P < 2.2e-16 except the last one (bottom right) with the P = 0.998. **g** ChIP-seq showing the CTCF signal at CTCF center of Rybp^{+/+} ESCs. h ChIP-qPCR showing the reduced enrichment of CTCF at these CTCF deposited loci after RYBP depletion. Welch's t-test; P values are (from left to right): P = 0.0028; P = 0.025; P = 0.0066, n = 3.