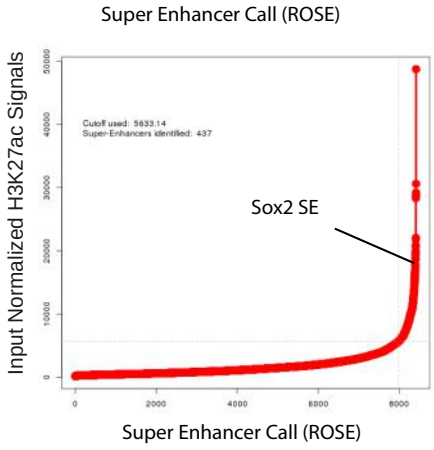
Figure S1

A



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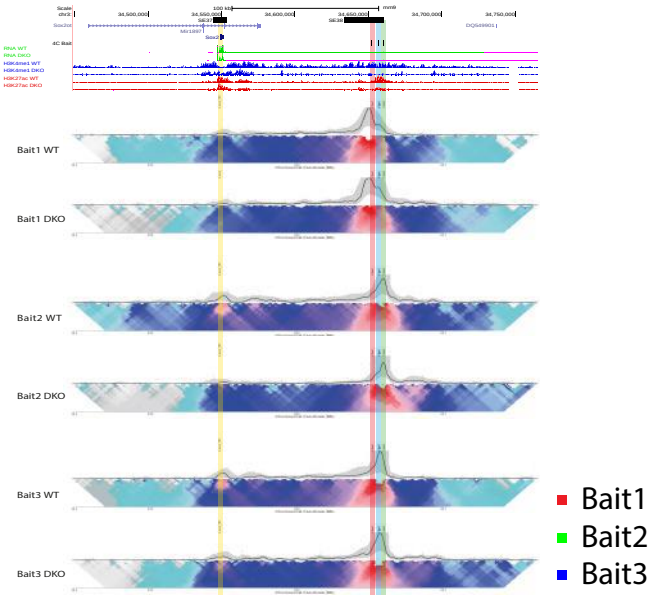

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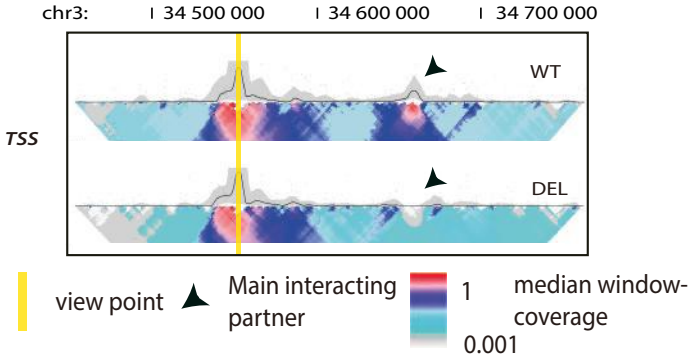

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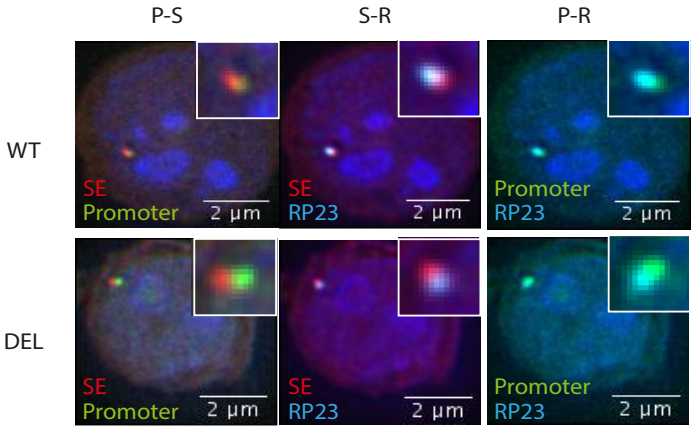

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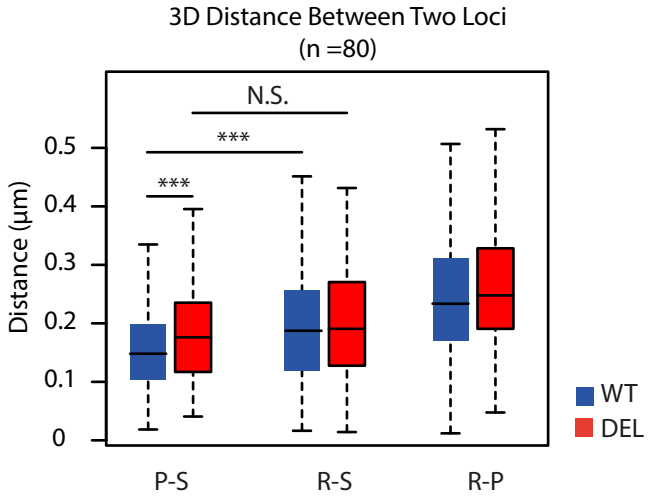

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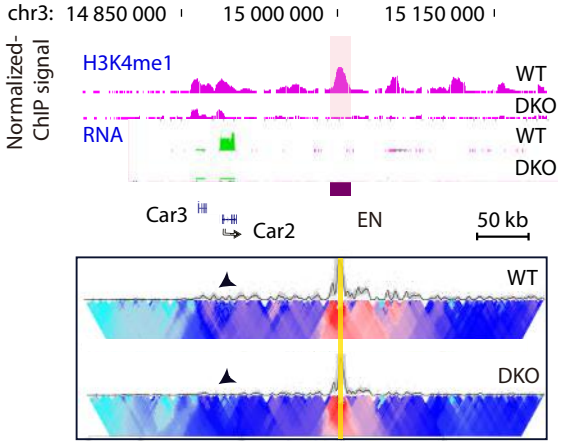

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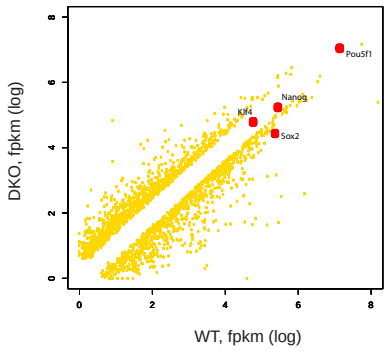

Figure S1. Mll3/4 Deficient mESCs Reveal Lost Interaction between *Sox2* Gene Body and SE, Related to Figure 1

(A) Super-enhancer call using H3K27ac ChIP-seq data in WT cells. x-axis shows the rank of enhancers, and larger number represents higher rank of peaks with H3K27ac signals. y-axis is the input normalized H3K27ac ChIP-seq coverage within the peak.

(B) Similar to Fig. 1b, the 4C-seq data from different viewpoints shows that the interaction between *Sox2* gene body and SE is lost upon Mll3/4 depletion in mESCs.

(C) A 2D-heat map of 4C-seq analysis shows a significant reduction in contact frequency between *Sox2* TSS and *Sox2*-SE in DEL cells compared to F123 WT cells.

(D) Microscopy images of 3D FISH show that physical distance between *SOX2* SE and promoter becomes larger in DEL cells than F123 WT. Red dots, probes hybrid to SE locus, Green dots, probes detecting promoter locus; Cyan dots, probes detecting a region (RP23 locus) that is located 170 kb downstream from SE.

(E) Summary of FISH data from 80 different cells for both cell types respectively. Note that distance between promoter and SE was significantly larger in DKO than WT. In WT cells, SE is significantly closer to promoter than to RP23 while the difference was not observed in DEL cells, indicating the loss of interaction between SE and Promoter in DEL cells. S-R, distance between RP23 and SE; P-R, distance between RP23 and Promoter; P-S, distance between Promoter and SE. Asterisks indicate statistical significance tested with student t-test (*** $p<0.005$).

(F) 4C-seq analysis showing that the enhancer interacts with *Car2* gene in WT cells but not in DKO cells (lower). The H3K4me1 ChIP-seq tracks are shown as a reference (upper). Note that H3K4me1 signals at both *Car2* enhancer and *Car2* gene body are decreased in DKO cells. EN indicates the location of the enhancer.

(G) RNA-seq data showing that except Sox2, transcription level of other pluoripoteny factors (labeled with red dot) is not changed. FPKM is computed using cufflink with three biological replicates.