Figure S5

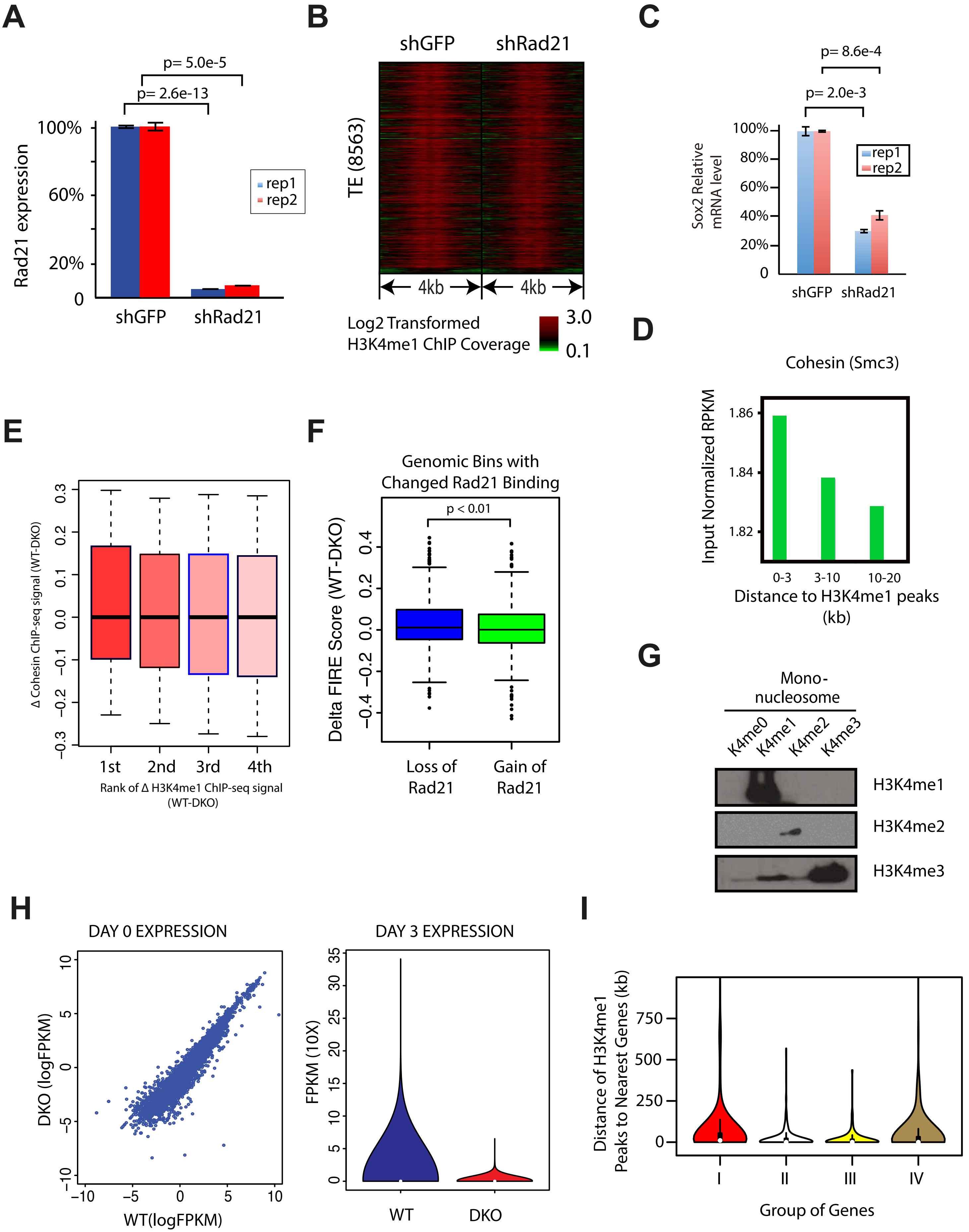
A
p= 5.0e-5
p= 2.6e-13
Rad21 expression
100%
60%
20%
0
rep1
rep2
shGFP
shRad21
B
shGFP
shRad21
TE (8563)
4kb
4kb
Log2 Transformed
H3K4me1 ChIP Coverage
3.0
0.1
C
p= 8.6e-4
p= 2.0e-3
Sox2 Relative
mRNA level
100%
80%
60%
40%
20%
0
rep1
rep2
shGFP
shRad21
D
Cohesin (Smc3)
Input Normalized RPKM
1.86
1.84
1.82
0-3
3-10
10-20
Distance to H3K4me1 peaks
(kb)
E
Δ Cohesin ChIP-seq signal (WT-DKO)
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
1st
2nd
3rd
4th
Rank of Δ H3K4me1 ChIP-seq signal
(WT-DKO)
F
Genomic Bins with
Changed Rad21 Binding
p < 0.01
Delta FIRE Score (WT-DKO)
0.4
0.2
0.0
−0.2
−0.4
Loss of
Rad21
Gain of
Rad21
G
Mono-
nucleosome
K4me0
K4me1
K4me2
K4me3
H3K4me1
H3K4me2
H3K4me3
H
DAY 0 EXPRESSION
DKO (logFPKM)
WT(logFPKM)
10
5
0
−5
−10
DAY 3 EXPRESSION
FPKM (10X)
35
30
25
20
15
10
5
0
WT
DKO
I
Distance of H3K4me1
Peaks to Nearest Genes (kb)
750
500
250
0
I
II
III
IV
Group of Genes

Figure S5. H3K4me1 Assisted Cohesin Binding to Chromatin, Related to Figure 3, 4

(A) qPCR assay confirming that Rad21 knock-down drops the mRNA level of Rad21 to less than 10% in WT cells. Error bars show standard error of three qPCR replicates and p value is computed with student t test.

(B) Heatmap showing H3K4me1 signals at typical enhancers upon depletion of Cohesin. Each row show 4-kb bin centered around enhancer.

(C) qPCR assay confirming that Rad21 knock-down drops the mRNA level of Sox2 to less than 50% in WT cells. Error bars show standard error of three qPCR replicates and p value is computed with student t test.

(D) Barplot showing that Cohesin/Smc3 is associated with Mll3/4 dependent H3K4me1 peaks. Cohesin is more enriched in the regions that are closer to Mll3/4 dependent H3K4me1 peaks than the distal regions.

(E) Similar to **Figure S4G,** Boxplot showing the correlation between the change of H3K4me1 and change of Rad21 binding throughout the genome. The change of H3K4me1 is classified into 4 different quantiles according to the change of the input normalized RPKM value.

(F) Change of FIRE score (WT-DKO) at genomic bins where binding of Rad21 is altered. Note that FIRE scores decrease as Rad21 signals decrease.

(G) Gel image showing the quality of mononucleosome assembly. Western blot shows that the assembled nucleosomes are modified specifically at lysine 4 of histone H3 (right).

(H) Left: scatter plot showing association of gene expression between WT and DKO cells at Day 0 of Group III genes highlighted in Figure 4C. Right: Violin plot showing the Expression level of Group III genes in WT and DKO cells at Day 3.

(I) Violin plot showing the distribution of distance between H3K4me1 peaks that are highlighted in **Figure 6A** and different groups of genes in **Figure 5C**. Group III genes show the shortest distance indicating the association of the highlighted H3K4me1 peaks with Group III genes.