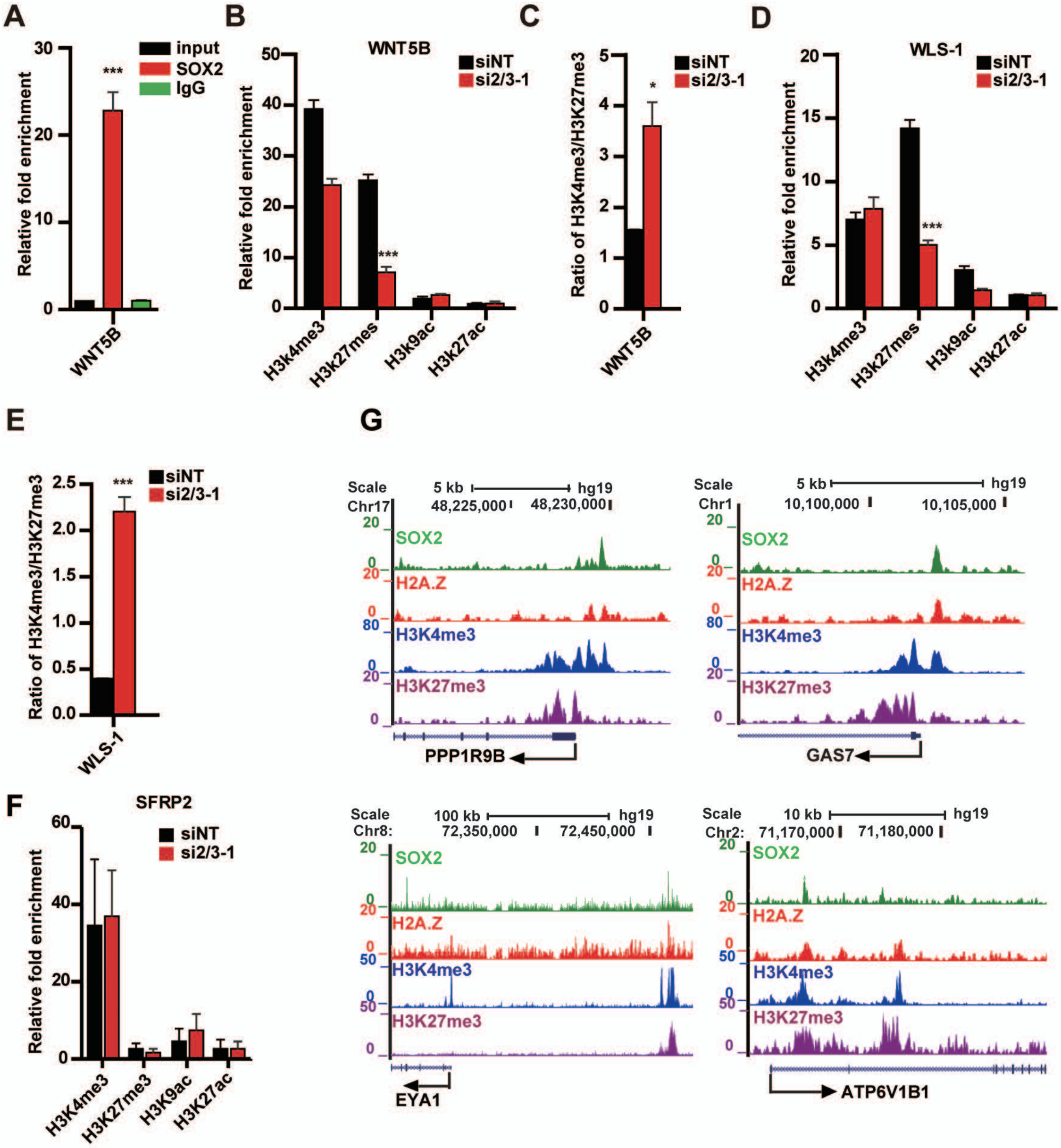
A
Relative fold enrichment
30
20
10
0
input
SOX2
IgG
***
WNT5B
B
WNT5B
siNT
si2/3-1
Relative fold enrichment
50
40
30
20
10
0
***
H3k4me3
H3k27mes
H3k9ac
H3k27ac
C
Ratio of H3K4me3/H3K27me3
5
4
3
2
1
0
siNT
si2/3-1
*
WNT5B
D
WLS-1
siNT
si2/3-1
Relative fold enrichment
20
15
10
5
0
***
H3k4me3
H3k27mes
H3k9ac
H3k27ac
E
Ratio of H3K4me3/H3K27me3
2.5
2.0
1.5
1.0
0.5
0.0
siNT
si2/3-1
***
WLS-1
F
SFRP2
Relative fold enrichment
60
40
20
0
siNT
si2/3-1
H3K4me3
H3K27me3
H3K9ac
H3K27ac
G
Scale
5 kb
hg19
Chr17
48,225,000
48,230,000
20
0
SOX2
20
0
H2A.Z
80
0
H3K4me3
20
0
H3K27me3
PPP1R9B
Scale
5 kb
hg19
Chr1
10,100,000
10,105,000
20
0
SOX2
20
0
H2A.Z
80
0
H3K4me3
20
0
H3K27me3
GAS7
Scale
100 kb
hg19
Chr8:
72,350,000
72,450,000
20
0
SOX2
20
0
H2A.Z
50
0
H3K4me3
50
0
H3K27me3
EYA1
Scale
10 kb
hg19
Chr2:
71,170,000
71,180,000
20
0
SOX2
20
0
H2A.Z
50
0
H3K4me3
50
0
H3K27me3
ATP6V1B1

Figure S5. SOX2 and H2A.Z co-localize to development genes for the establishment of H3K27me3 modification. Related to Figure 7.

(A) ChIP-qPCR validation of SOX2 enrichments on *WNT5B* in H9 hESCs.

(B) ChIP-qPCR results of histone modification enrichments at SOX2 binding site of *WNT5B* promoter, showing decreased H3K27me3 and unaffected acetylation modification after *SOX2/3* knock down in H9 hESCs.

(C) The ratio of H3K4me3/H3K27me3 at the promoter of *WNT5B* increased after *SOX2/3* knock down in H9 hESCs.

(D) ChIP-qPCR results of histone modification enrichments at SOX2 binding site of the *WLS-1*, showing decreased H3K27me3 and unaffected acetylation modification after *SOX2/3* knock down in H9 hESCs.

(E) The ratio of H3K4me3/H3K27me3 at the *WLS-1* increased after *SOX2/3* knock down in H9 hESCs.

(F) ChIP-qPCR analysis showing the SOX2 binding site at *SFRP2* were mainly methylation modified and unaffected by *SOX2/3* KD.

(G) Integrative Genomics Viewer screenshots for co-localization of SOX2, H2A.Z, H3K4me3 and H3K27me3 on representative developmental genes.