A

hESCs

SOX2 — Relative fold enrichment (0–60):
NC, AFP, GLI2, FOXO1, NANOG, POU5F1, FOXA2, CDX2, GATA4, SOX2

Pol II — Relative fold enrichment (0–500):
NC, NBPF11, KIF2C, SOX2, PILRB, HIST2H3A, FAM138F, PACSIN2, HIST2H3C

hNPCs

SOX2 — Relative fold enrichment (0–200):
NC, POU3F2, ASPM, EPHB1, PAFAH1B1, RACGAP1, NCOR2, TACC2, MAP2, ZEB2, NOTCH1, SOX2, FZD9, MAP1B, PLAGL1

Pol II — Relative fold enrichment (0–20):
NC, HIST2H3C, HIST2H3A, POU3F2, MAP1B, NOTCH2, AL137798.1

B

hESCs / hNPCs

Active promoter genes: 284 | 1476 | 4458

Poised enhancer genes: 2024 | 1236 | 857

C

chrX: 70,337,000–70,344,000

- 20 hESCs SOX2
- 60 hESCs H3K4me3
- 20 hESCs H3K27me3
- 20 hNPCs SOX2
- 170 hNPCs H3K4me3
- 20 hNPCs H3K27me3

MED12

chr6:114,284,000–114,292,500

- 20 hESCs SOX2
- 120 hESCs H3K4me3
- 30 hESCs H3K27me3
- 40 hNPCs SOX2
- 240 hNPCs H3K4me3
- 30 hNPCs H3K27me3

HDAC2

chr8: 48,872,000–48,877,000

- 15 hESCs SOX2
- 80 hESCs H3K4me3
- 20 hESCs H3K27me3
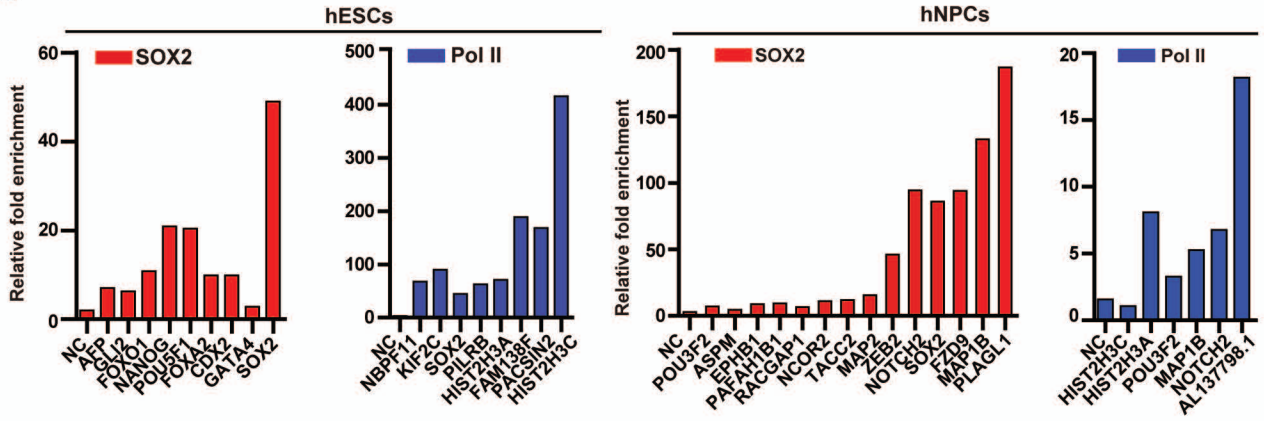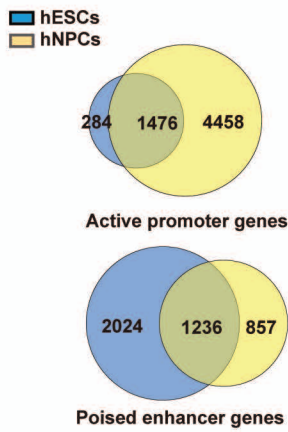- 25 hNPCs SOX2
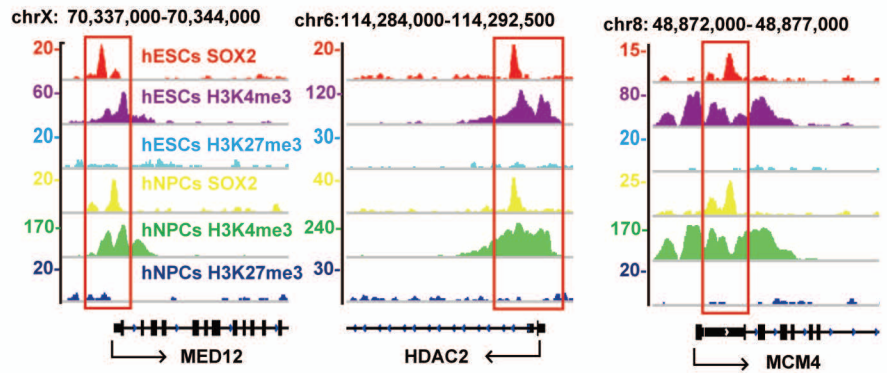- 170 hNPCs H3K4me3
- 20 hNPCs H3K27me3

MCM4

Figure S1. SOX2 binds to genes involved in diverse aspects of hESCs and hNPCs maintenance. Related to Figure 1.

(A) ChIP-qPCR verification of SOX2 enrichments at randomly selected peaks from the SOX2 and Pol II ChIP-seq result of in hESCs and hNPCs, respectively. Selected peaks include peaks with both high and low enrichment scores by MACS results.

(B) Venn diagrams showing the overlap status of active promoter bound genes and poised enhancer bound genes in hESCs and hNPCs.

(C) Integrative Genomics Viewer screenshots for common SOX2 peaks at the promoter regions of *HDAC2*, *MCM4* and *MED12* in both hESCs and hNPCs.