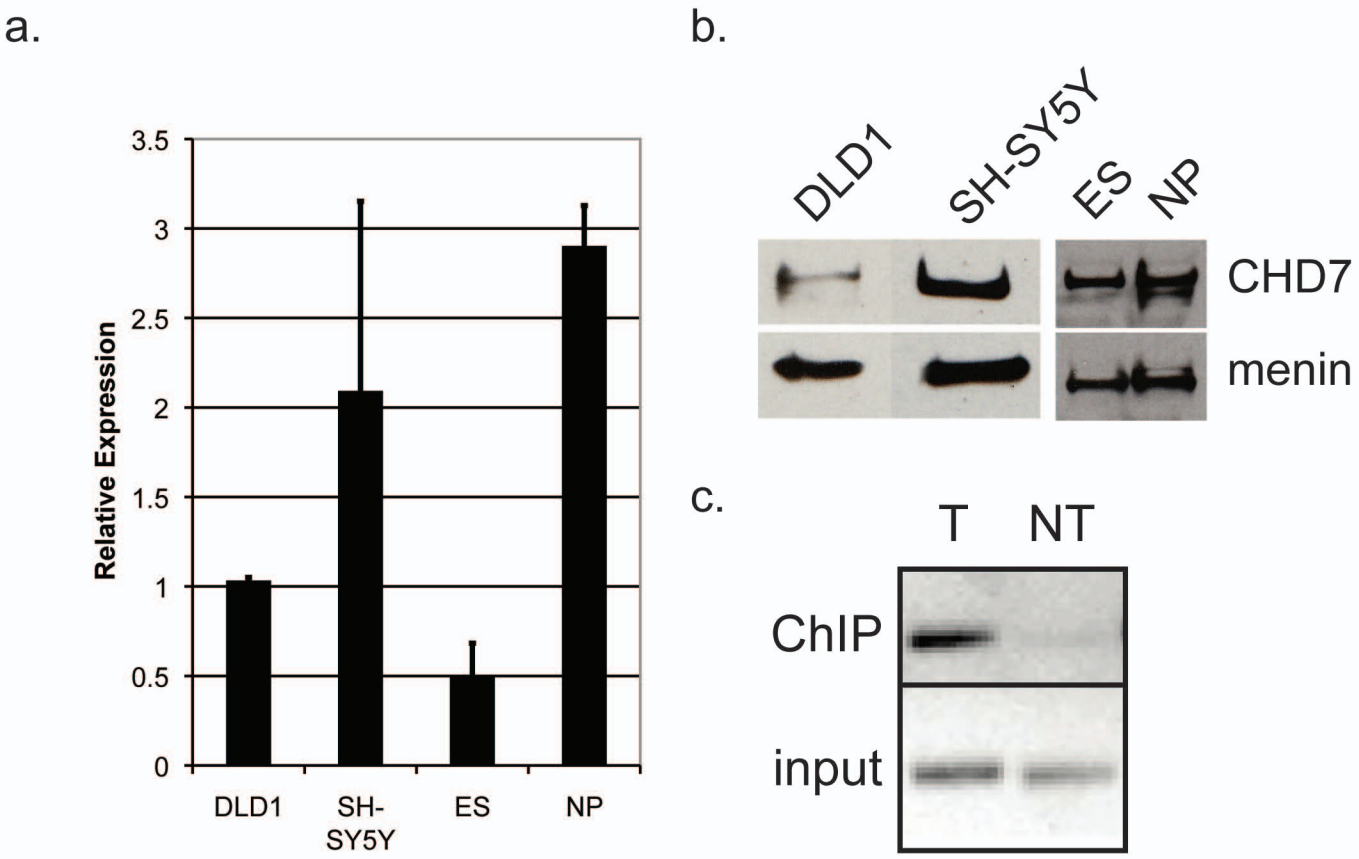
Supplementary Figure 1

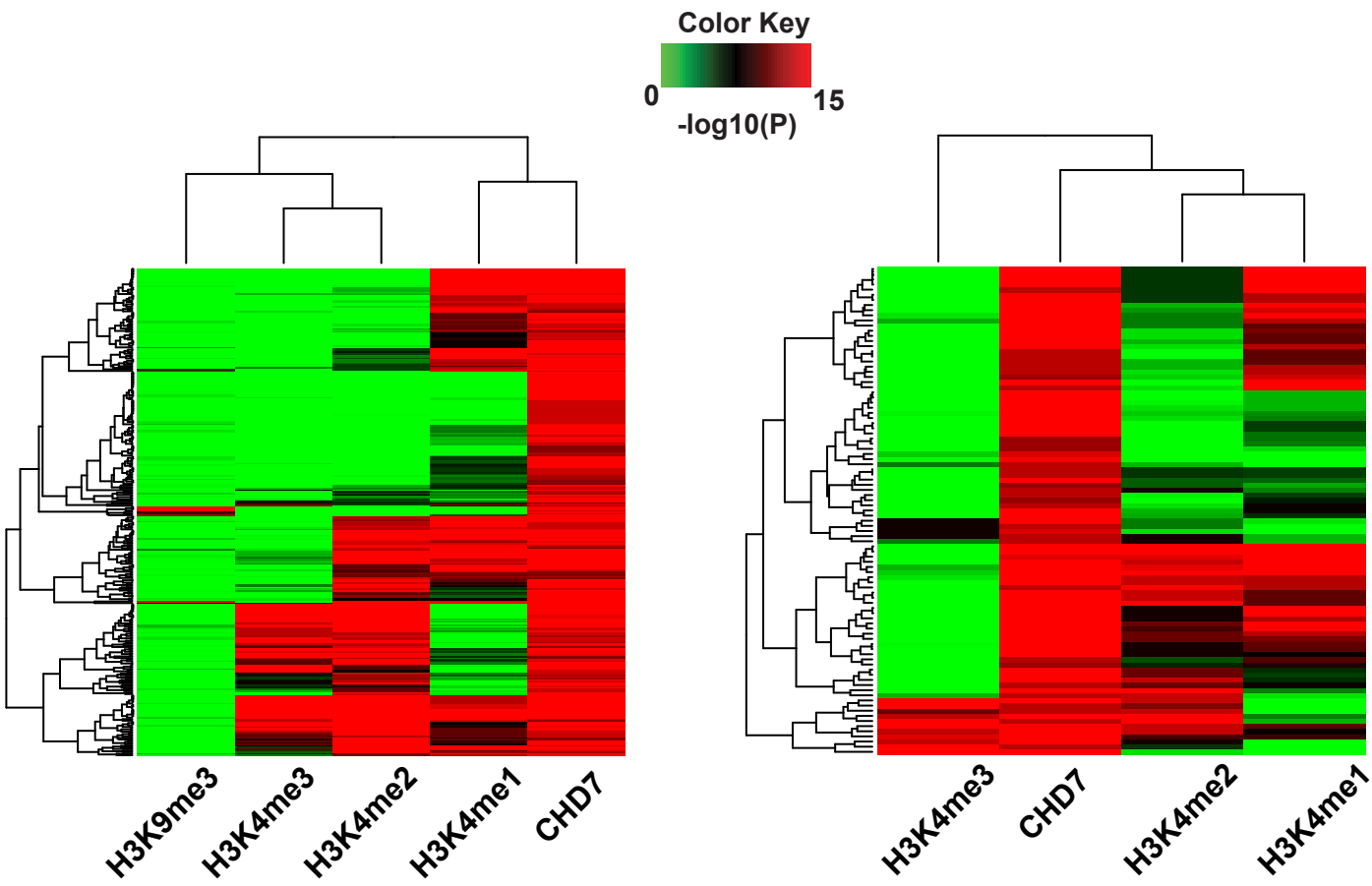
Schnetz _FigS1



Supplementary Figure 1. (a) Real-time RT-PCR of CHD7 in each of the 4 cell types used in this study. Expression levels are relative to GAPDH. (b) Western blot analyses of CHD7 in each of the four indicated cell types. Menin is a nuclear protein shown as a loading control. (c) Standard CHD7 ChIP-PCR analysis of a CHD7 site (T) compared to a non-target (NT) region in DLD1 cells.

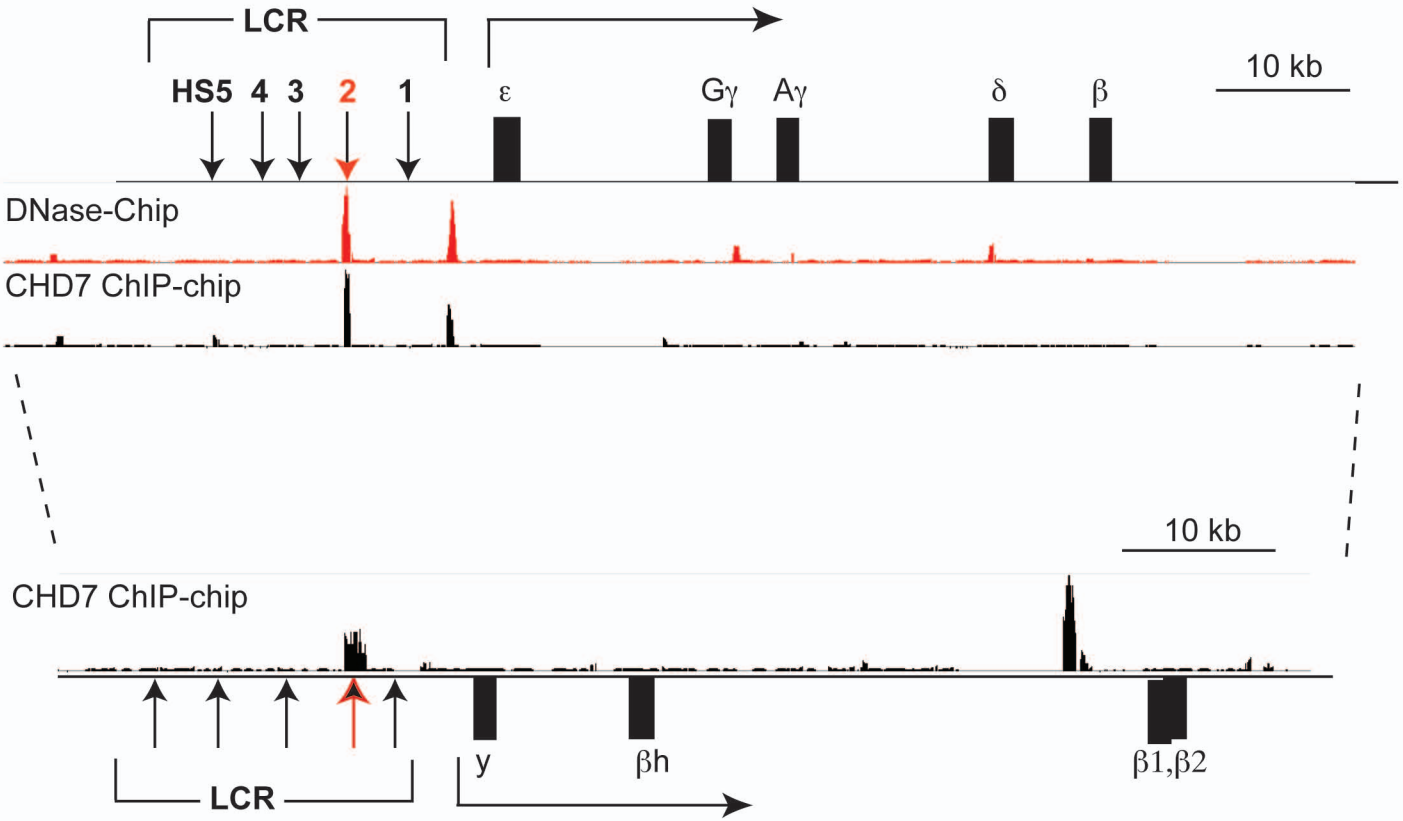
Supplementary Figure 2

Schnetz _FigS2



Supplementary Figure 2. Comparison of CHD7 and H3K4 methylation patterns in ES (left) and NP (right) cells.

Supplementary Figure 3



Supplementary Figure 3. CHD7 occupancy across the human and mouse beta-globin clusters. (top) DNase-ChIP and CHD7 ChIP-chip profiles from human (DLD1) cells. ACME processed data is plotted (see methods). Globin genes are represented as dark rectangles, and the relative positions of the five HS sites in the locus control region (LCR) are indicated by the arrows. (bottom) CHD7 ChIP-chip results from the orthologous region in mouse. Note the presence of CHD7 binding sites at the HS2 enhancer in both human and mouse (red arrow). Both CHD7 sites were also marked with significant levels of H3K4me1 (not shown).