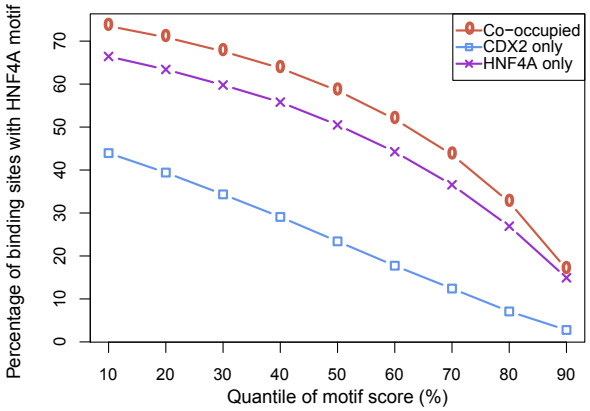
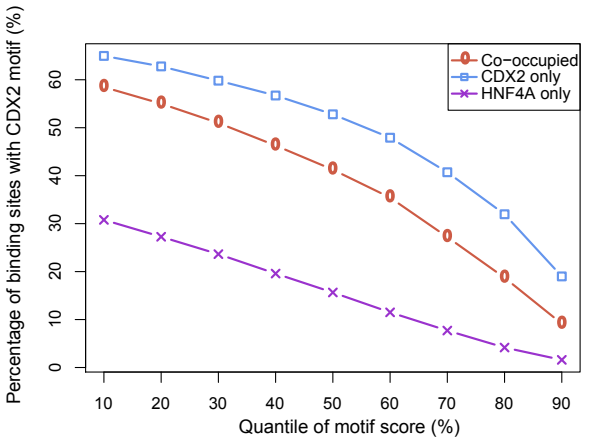
Verzi/Shin_Supplemental Figure 1

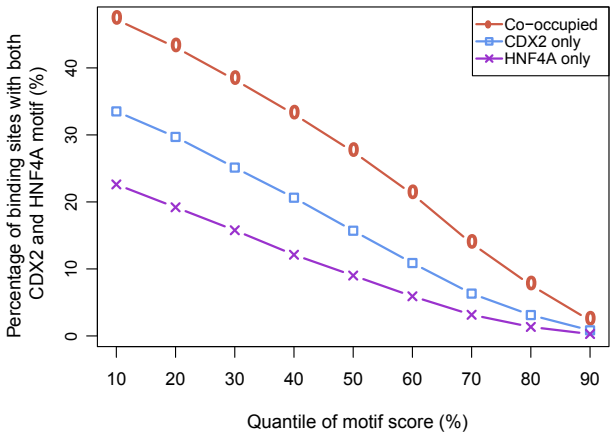
A



B

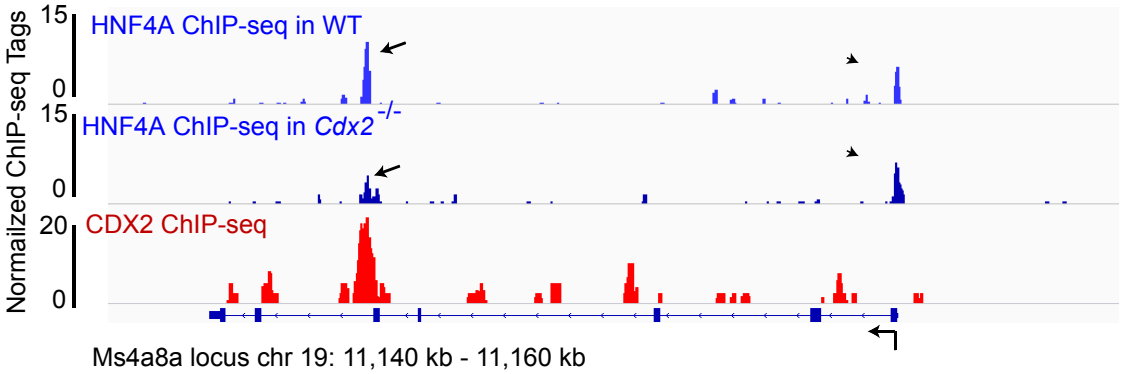


C

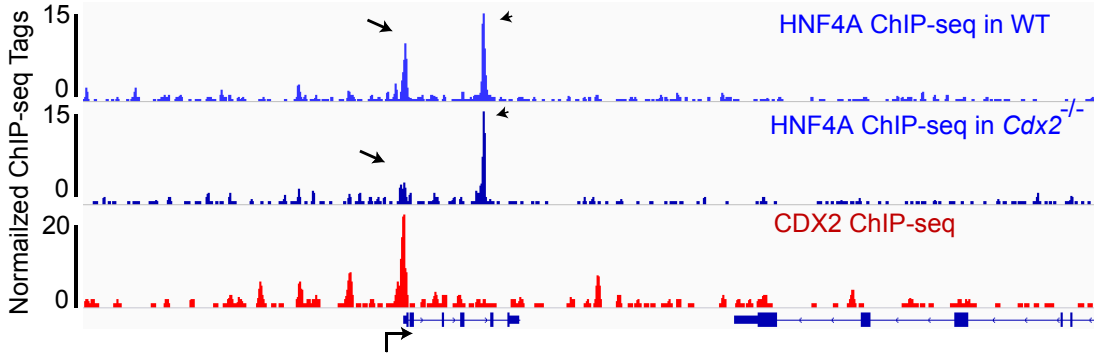


Verzi/Shin Supplemental Figure 2

A

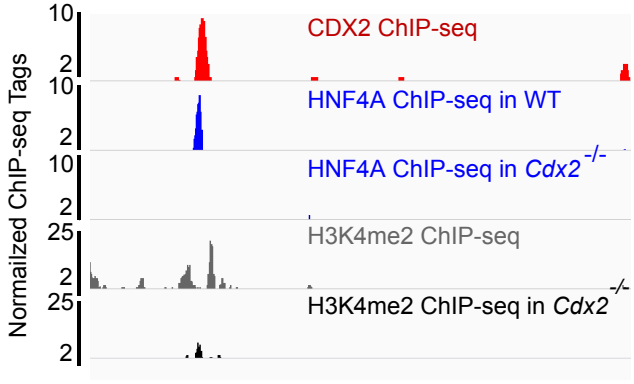


Ms4a8a locus chr 19: 11,140 kb - 11,160 kb

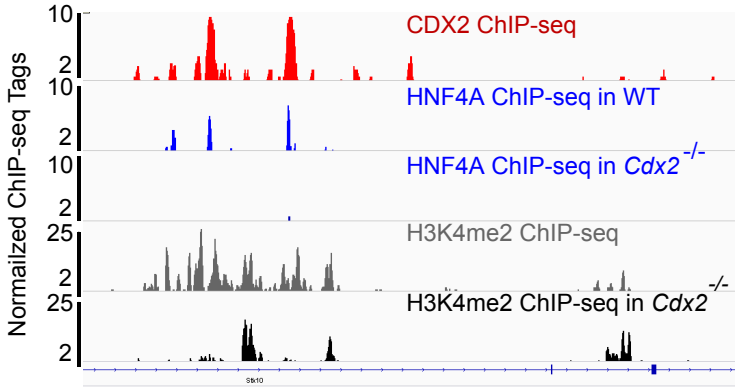


Aqp8 and Zkscan2 loci, chr 7: 130,590 kb - 130,640 kb

B



Intergenic region chr 4: 115,686kb - 115,706kb



Stk10 intron chr 11: 32,460kb - 32,480kb

Supplemental Figure 1. To assess the degree to which preferred TF motifs occur in regions identified by ChIP-seq, we plotted the frequency of HNF4A motifs (A), CDX2 motifs (B), or both motifs (C) in regions that bind CDX2 only, HNF4 only, or both TFs. The fraction of sites bearing canonical TF motifs (y-axis) declined with increasing stringency of motif-score requirements (x-axis), as defined by quantiles of all significant scores found in the union of all binding sites identified in ChIP-seq for CDX2 and HNF4A. Mathematically, a motif score indicates the log fold-difference between the probabilities of background motif enrichment and real TF motif (e.g., CDX2 or HNF4A) enrichment in a given genomic region (e.g., CDX2 or HNF4A binding site). Motif score ranges (x-axis) are 124 (10%) to 7491 (90%) for CDX2 and 127 (10%) to 11802 (90%) for HNF4A. The analysis shows that HNF4A binding sites harbor more HNF4A-binding than CDX2-binding motifs, that CDX2-occupied sites harbor more CDX2 motifs, and that many co-occupied regions carry both CDX2 and HNF4A motifs.

Supplemental Figure 2. (A) In the absence of CDX2, HNF4A binding is especially compromised at sites of CDX2 co-occupancy. ChIP-seq data from a representative region that contains both a co-occupied site and a site bound only by HNF4A (as in Figure 5D-E). HNF4A occupancy is affected less or not at all at sites without CDX2 binding (arrowheads) and severely compromised at sites where both TFs normally co-occupy DNA (arrows). **(B)** In the absence of CDX2, the H3K4me2 nucleosome signal is selectively affected at sites normally bound by CDX2. ChIP-seq data from representative regions illustrate the requirement for CDX2 in regions where it occupies DNA. H3K4me2 signal is selectively lost in such regions and preserved elsewhere (as in Figure 6D), suggesting a direct and local requirement for CDX2 in enhancer chromatin structure.