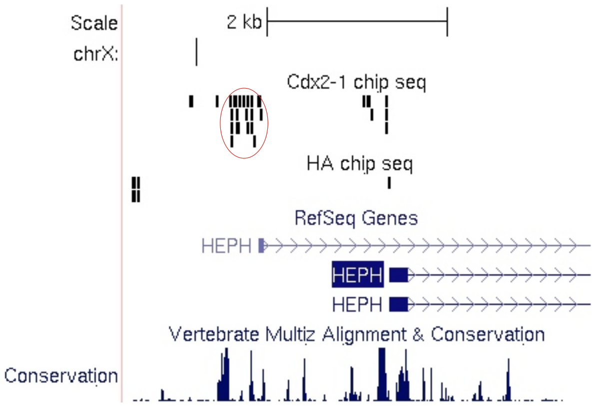
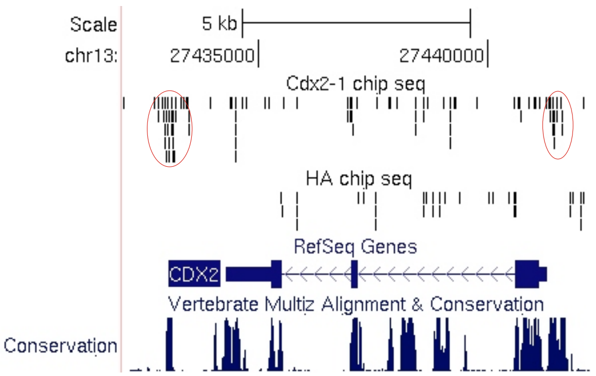
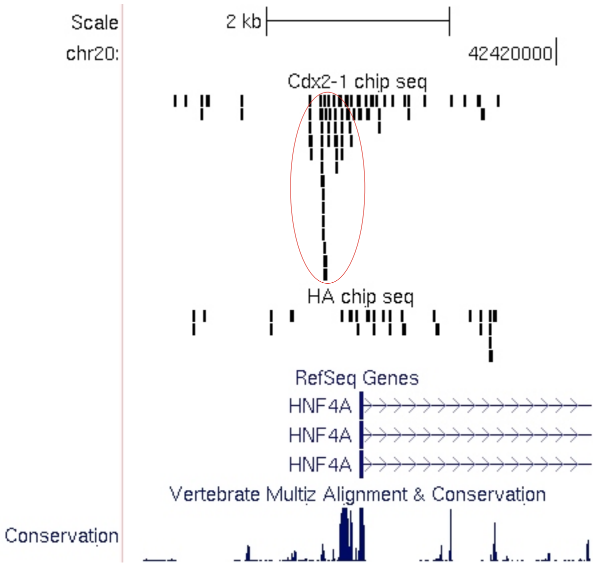
Supplementary data S2

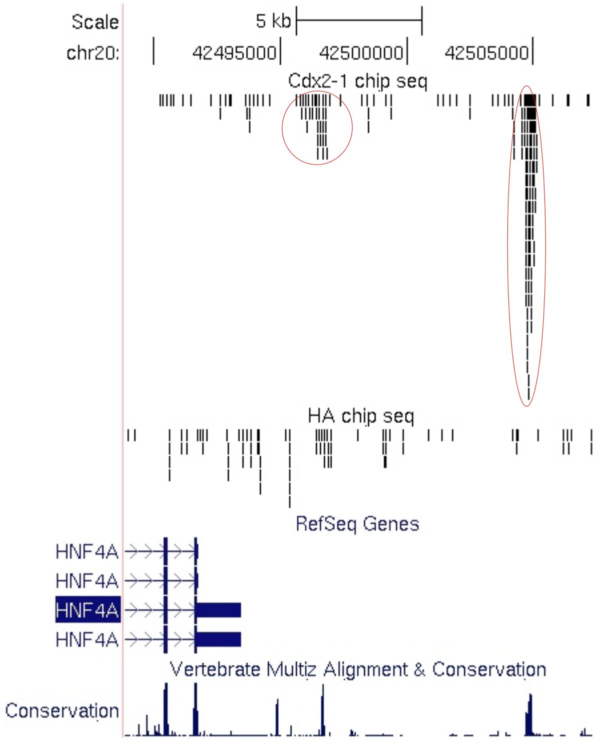
Screenshots of the region with a CDX2 ChIP-seq peak for each of the genes chosen for further *in vitro* analysis in this study. The CDX2 ChIP-seq results are aligned to the human genome and visualized with the UCSC genome browser: http://genome.ucsc.edu/cgi-bin/hgTracks. At the top is indicated the scale and the position on the chromosome. Underneath are the taqs from the CDX2 and HA ChIP-seq analysis, each tag is indicated by a black bar. The red circles indicate the CDX2 ChIP-seq peaks. The lower part of the figure visualizes the exon/intron distribution of the gene, conserved transcription factor binding sites, and the phylogenetic conservation.

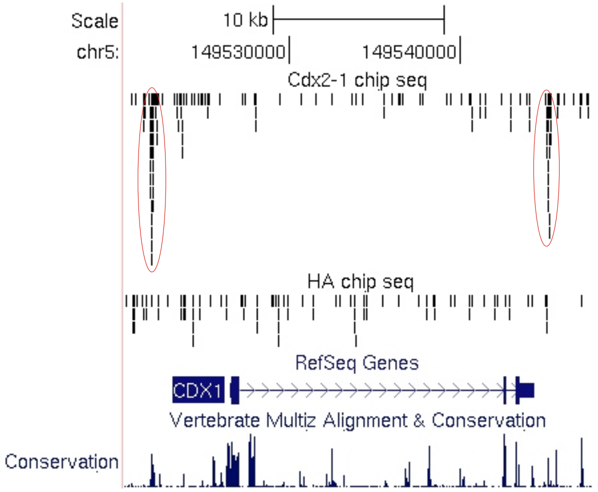
Boyd et al. S2


Heph

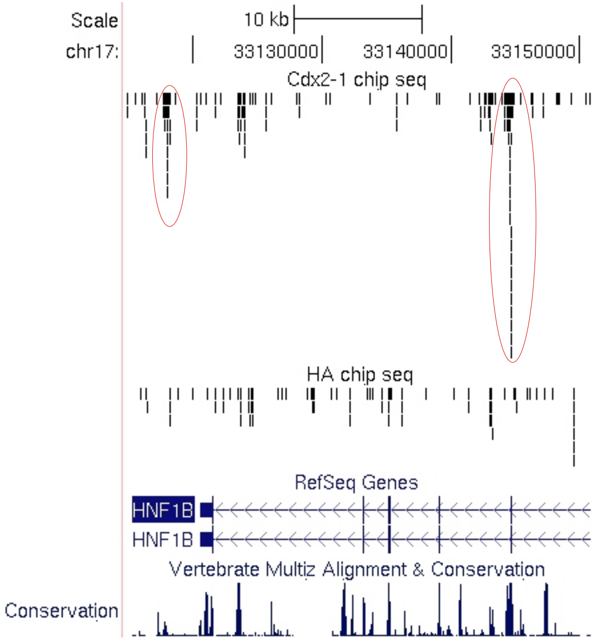

CDX2


HNF4α promoter


HNF4α enhancer


CDX1

HNF1β



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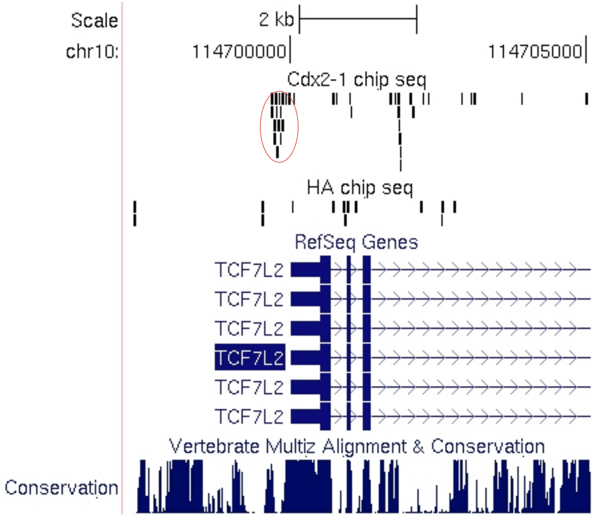
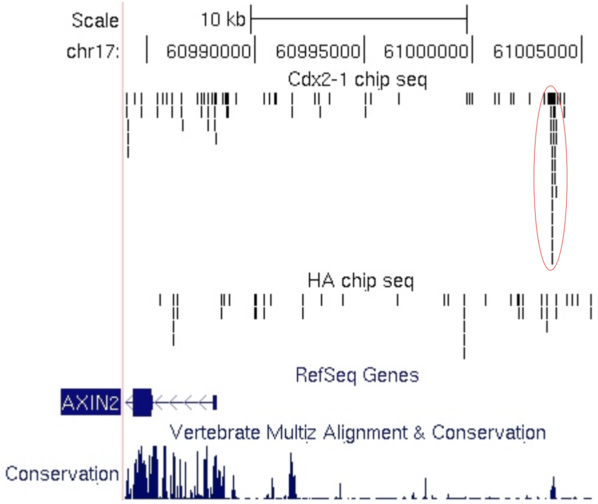
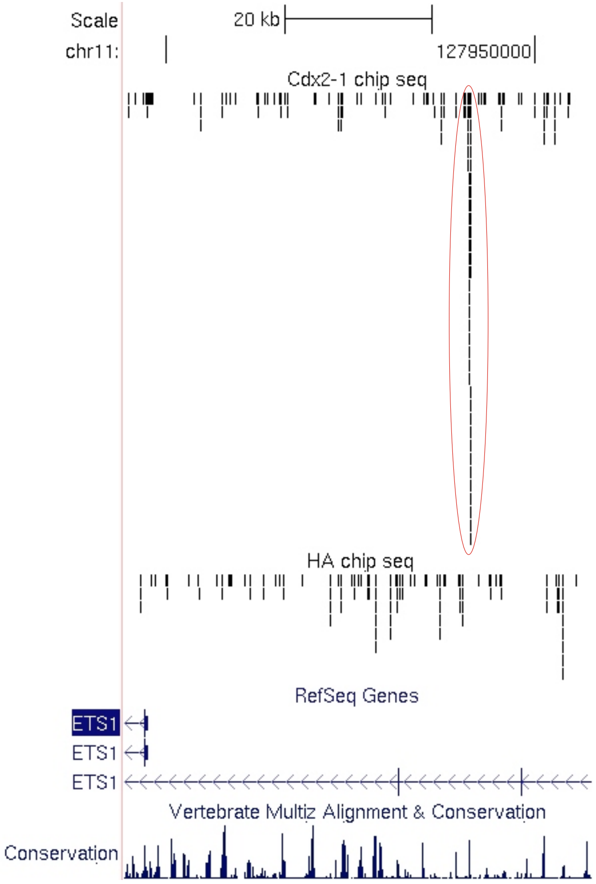


Axin2



ETS1



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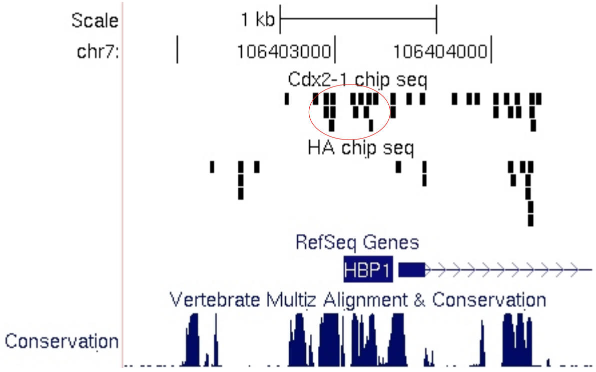
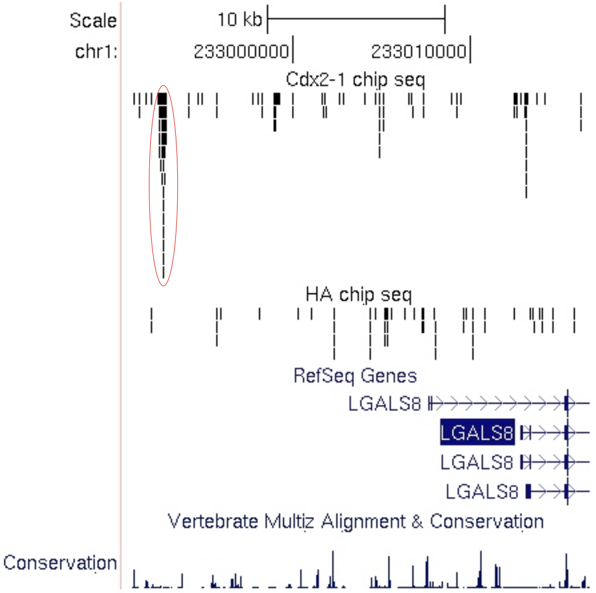


LGALS8



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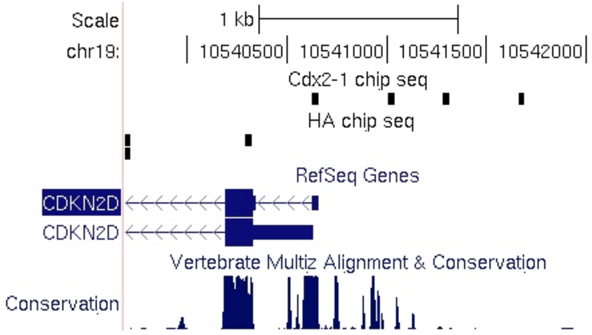
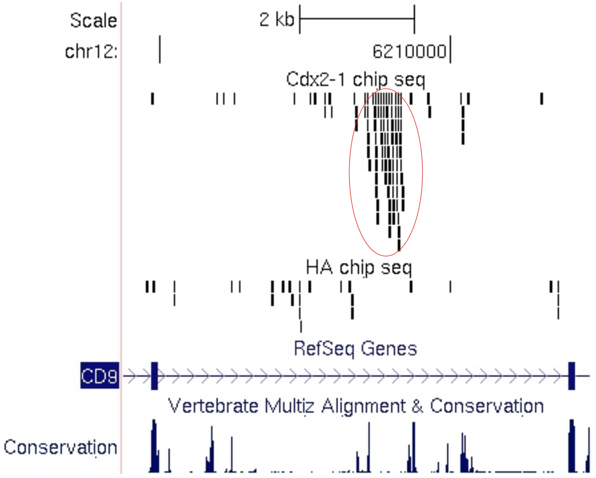


CD9



MEP1A