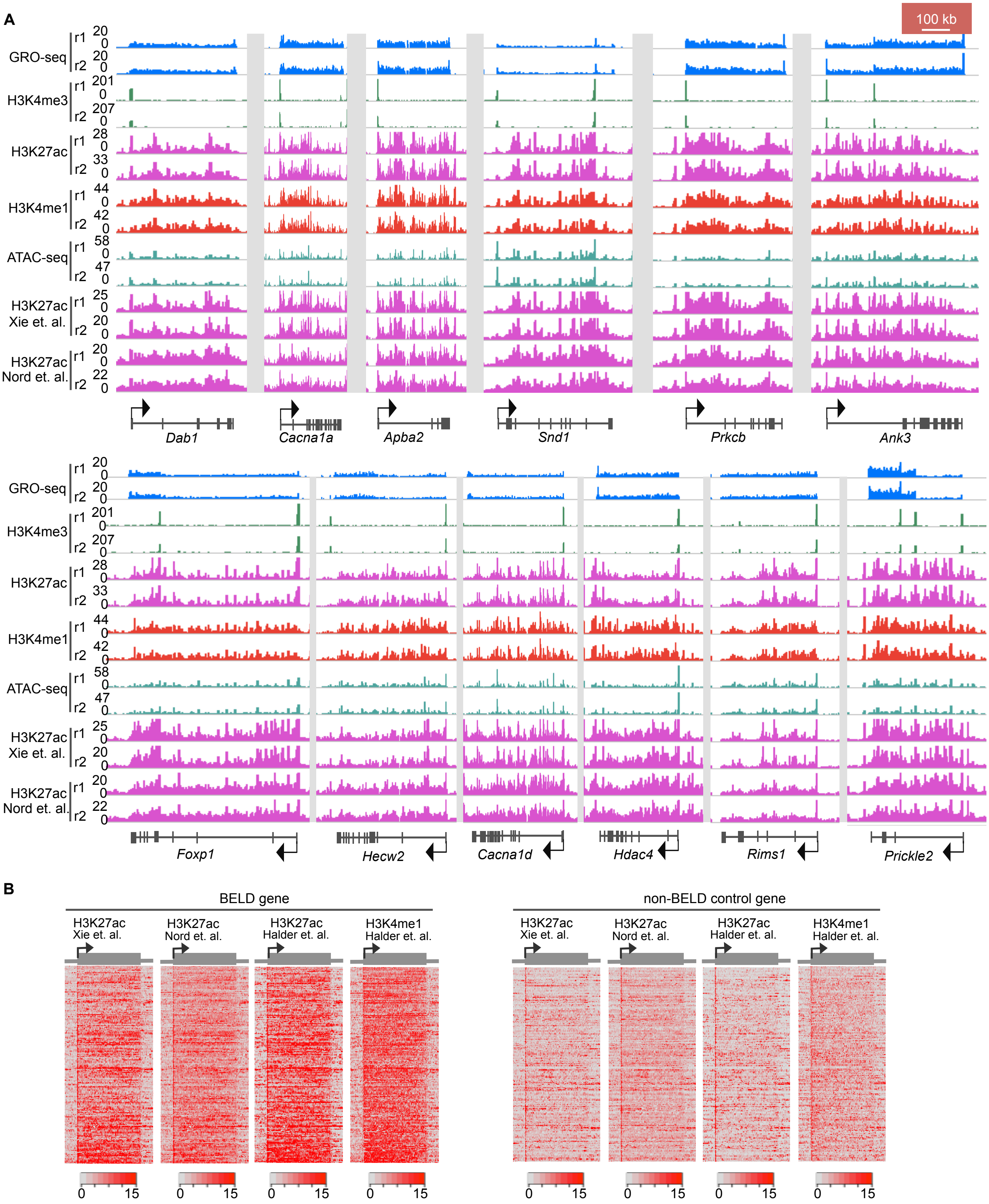

Supplemental Figure S3. Broad enhancer-like chromatin domains across the gene bodies of the BELD genes were confirmed by independent datasets. (A) Browser representations of GRO-seq, ChIP-seq, and ATAC-seq signals at twelve BELD genes. (B) Heatmaps of previous published H3K27ac and H3K4me1 normalized signals (RP30M) across the gene bodies and surrounding regions (±100kb) of BELD genes and non-BELD control genes.