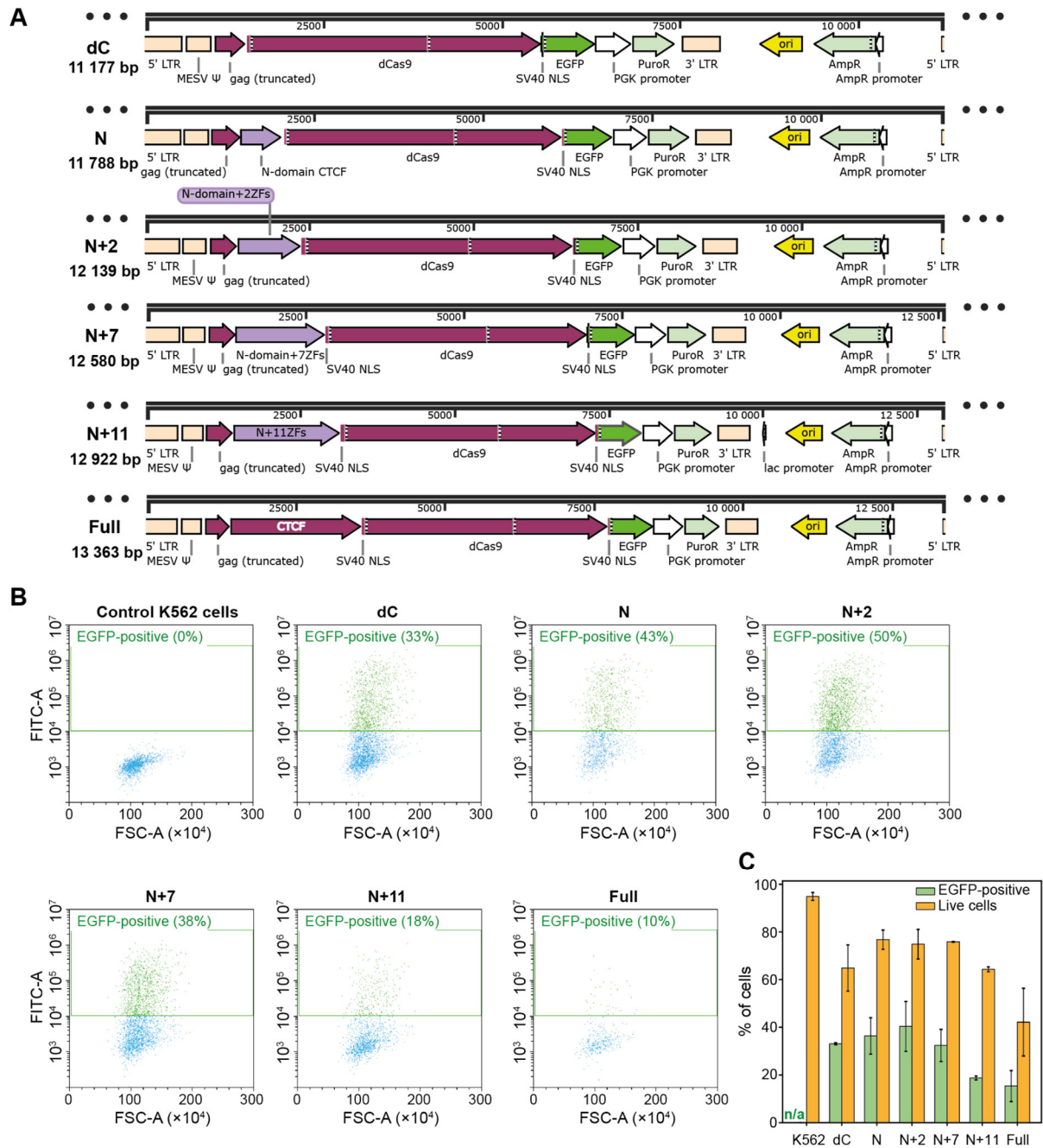
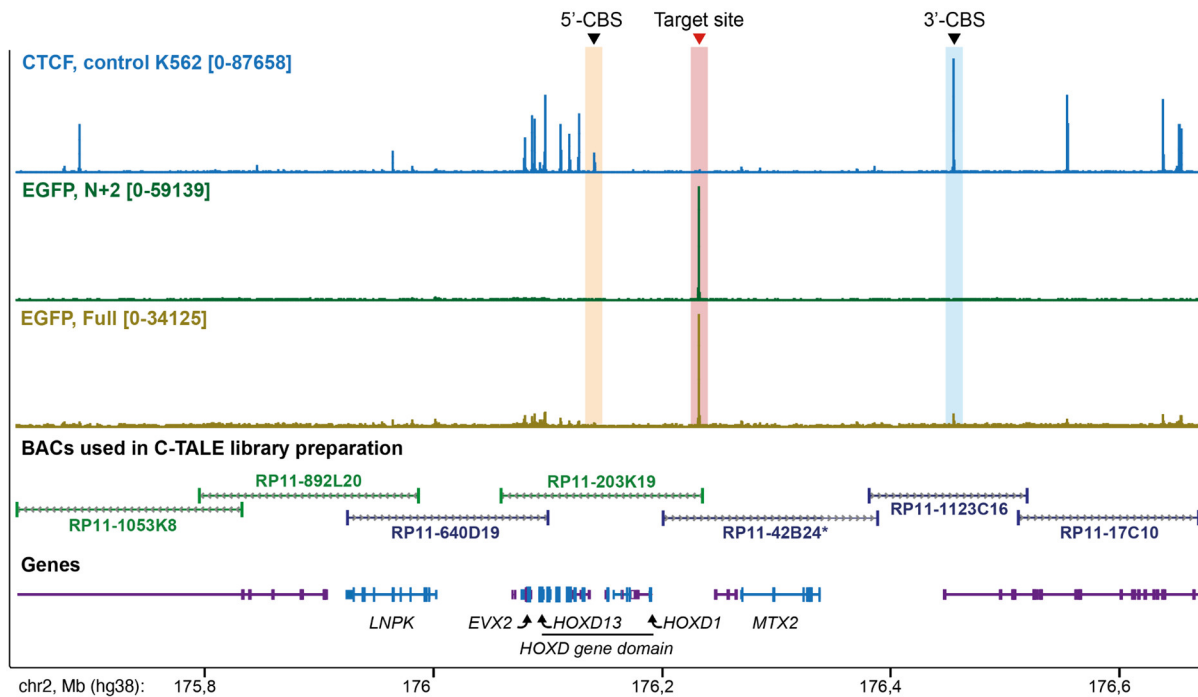


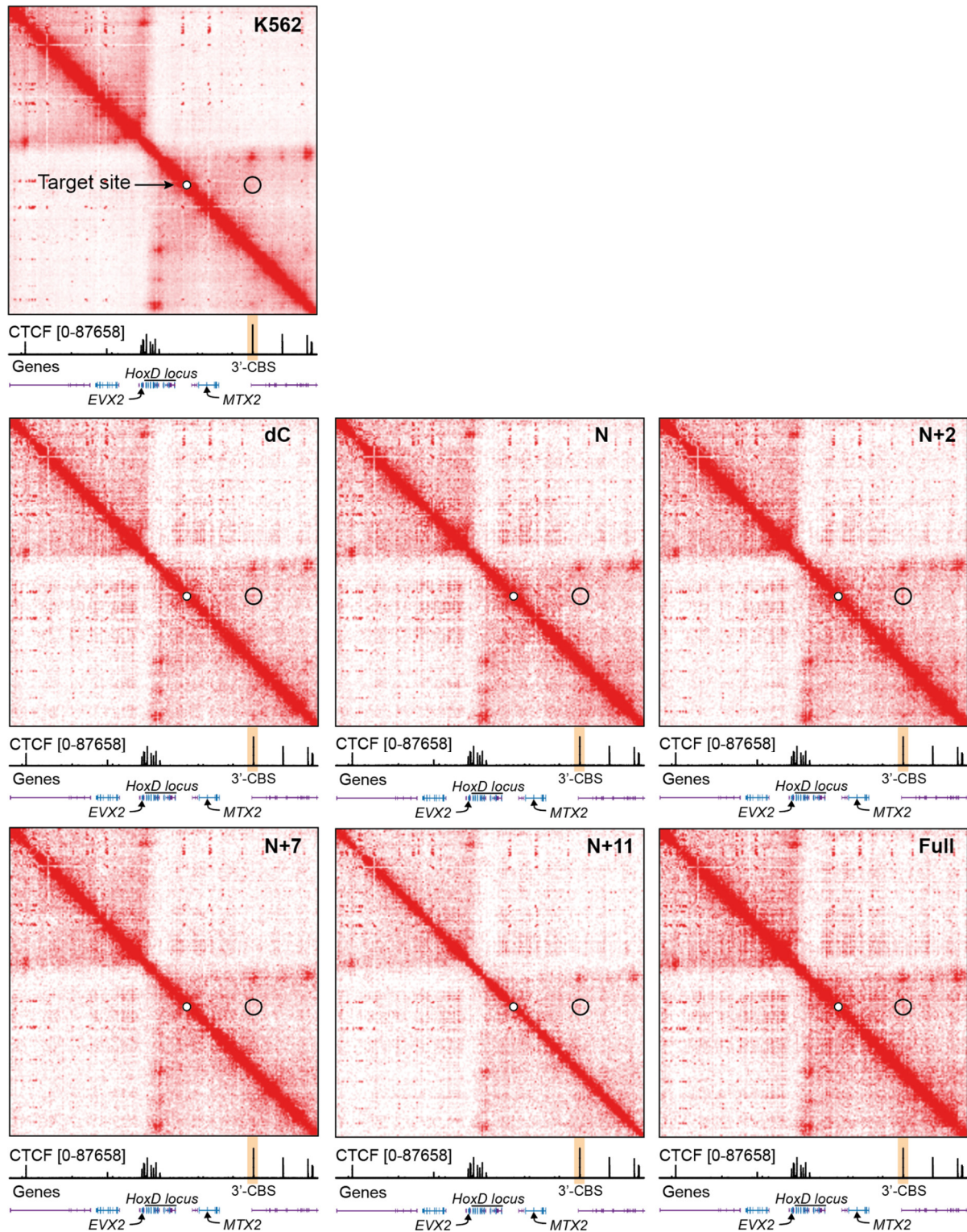
SUPPLEMENTARY FIGURES



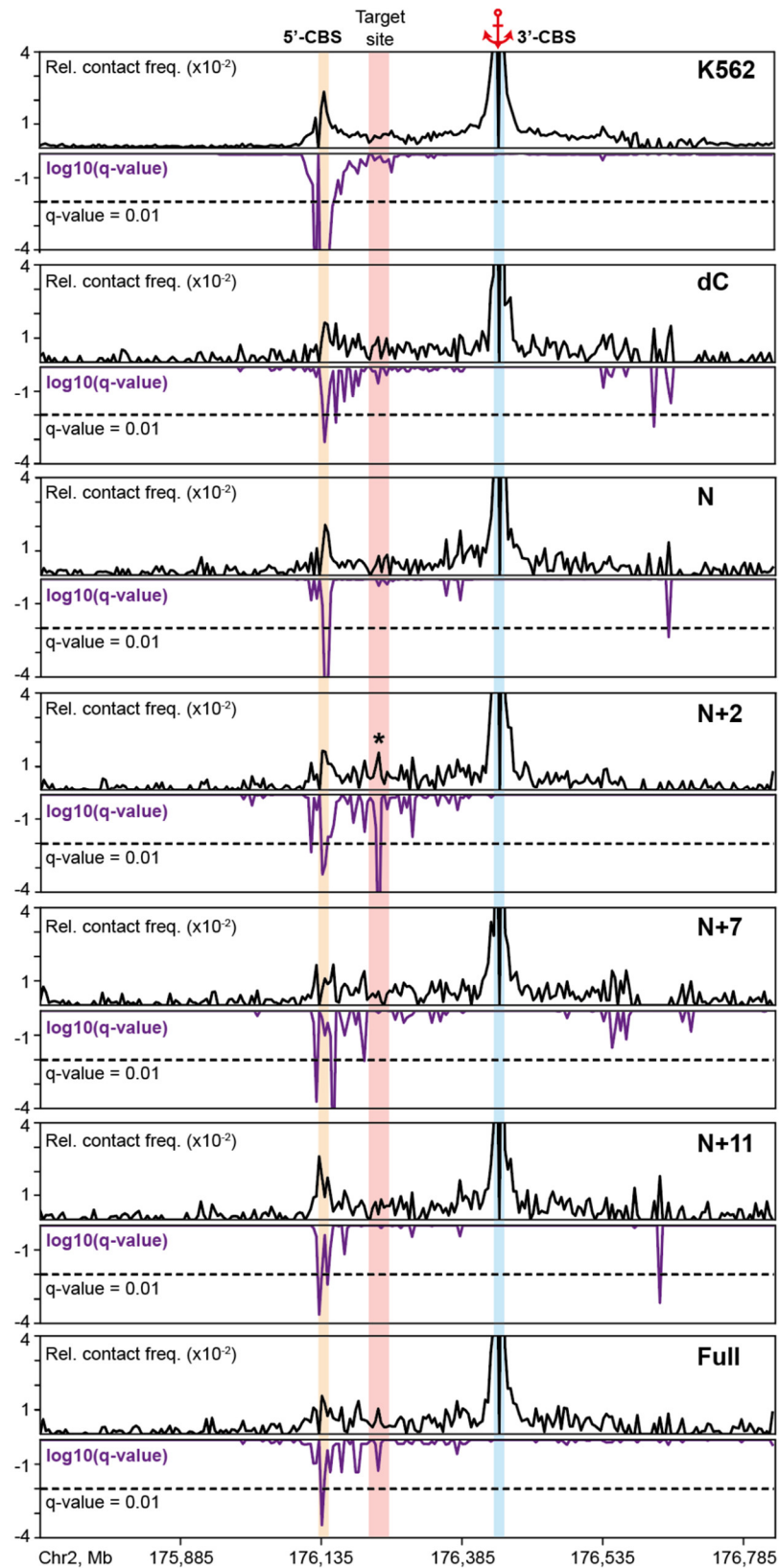
Supplementary Figure S1 (related to Figure 1). Expression constructs for the chimeric proteins and analysis of protein expression and cell viability. (A) Schematic representation of the expression plasmids, encoding chimeric proteins. **(B)** Flow cytometry analysis of the control and chimeric protein-expressing K562 cells showing the proportion of EGFP-positive (FITC-A) and live (FSC-A) cells. **(C)** Proportion of EGFP-positive and live cells. The average value of two independent biological replicates and standard error of the mean are shown.



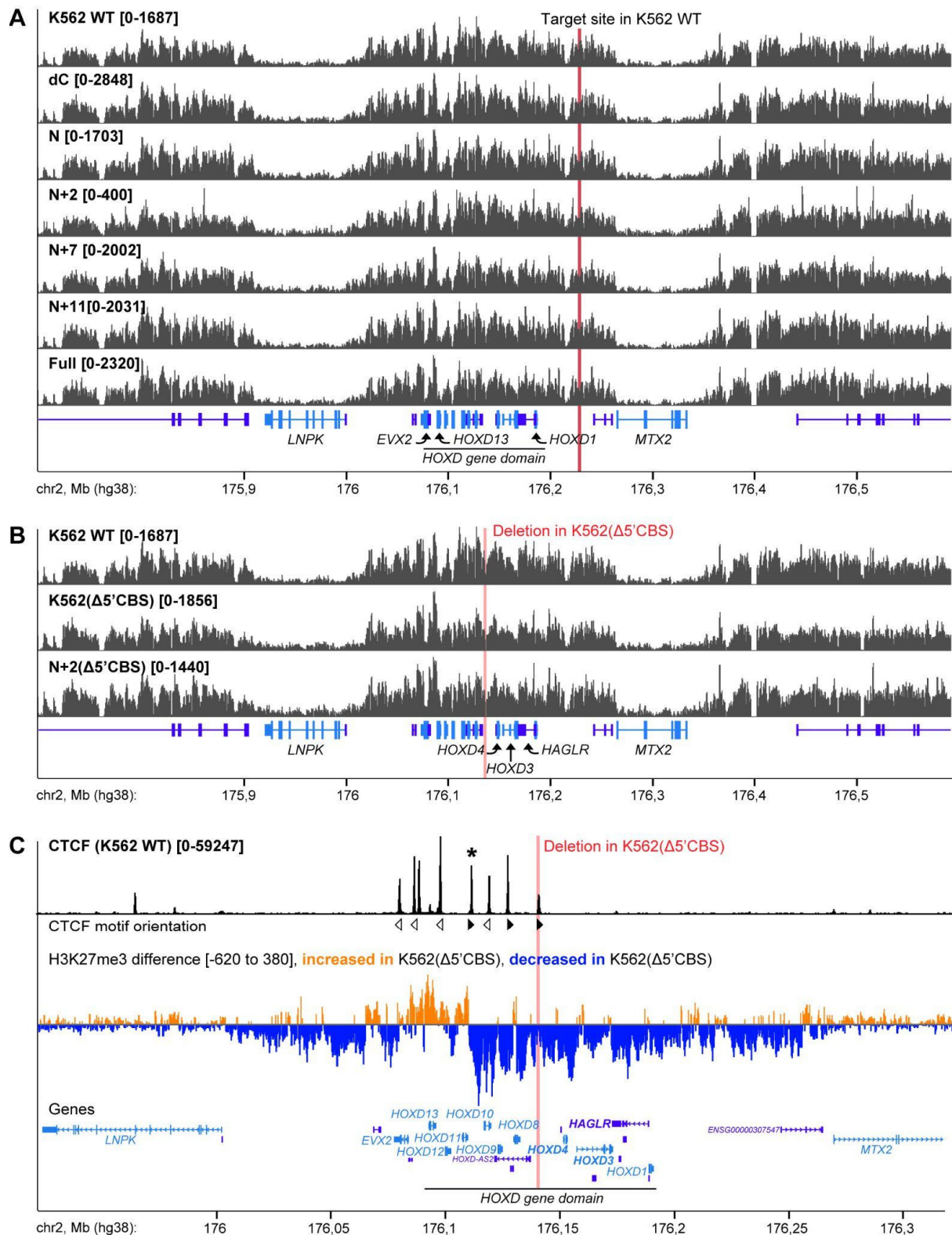
Supplementary Figure S2 (related to Figure 2). ChIP-seq profiling of the N+2 and Full chimeric proteins within the analyzed genome region (chr2:175,634,800 bp - 176,670,160 bp). ChIP-seq analysis of N+2 and Full chimeric protein binding at the target site. Upper line: control K562 cells, anti-CTCF antibodies were used; middle and bottom lines: N+2- and Full-expressing cells, respectively; anti-EGFP antibodies were used. Bacterial artificial chromosomes (BACs) used for the C-TALE library preparation and for the enrichment of ChIP-seq and RNA-seq libraries (RP11-42B24, labeled with an asterisk, is present in the hg19 genome assembly and absent in the hg38 assembly). Protein-coding and non-coding RNA genes are highlighted in blue and violet, respectively.



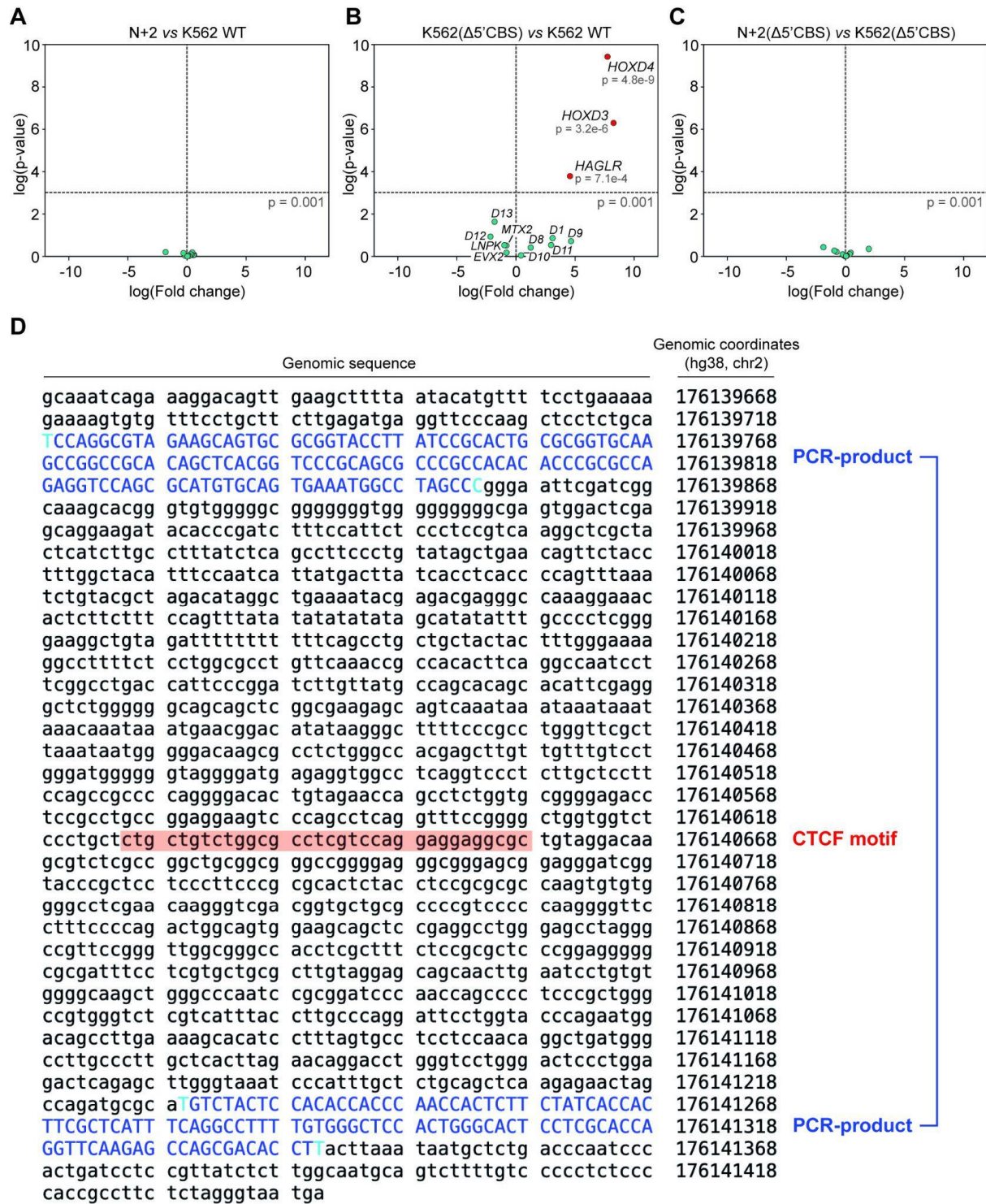
Supplementary Figure S3 (related to Figure 3). The whole-locus C-TALE heatmaps. White circle at the map diagonal shows the target site for the recruitment of the chimeric proteins.



Supplementary Figure S4 (related to Figure 3). Virtual 4C-profiles of the relative contact frequency of the 3'-CBS (upper panels) and FDR-adjusted p-values (q-values) of the contacts (violet plots in the bottom panels). A contact between the 3'-CBS and the target site in the N+2-expressing cells is indicated with an asterisk.



Supplementary Figure S5 (related to Figures 3 and 5). H3K27me3 ChIP-seq profiles across the *HOXD* locus in the wild-type K562 cells (K562 WT, **A) and in K562 cells with deleted 5'-CBS (K562(Δ 5'CBS)), **B**). **(C)** Difference in H3K27me3 levels between the K562(Δ 5'CBS) and K562 WT cells. CTCF ChIP-seq profile and CTCF motifs show that the boundary between parts of the *HOXD* gene domain with opposite changes in H3K27me3 abundance coincides with the CBS in a forward orientation (asterisk).**



Supplementary Figure S6 (related to Figures 3, and 5). Differential gene expression analysis. (A-C) Volcano plots for the wild-type N+2-expressing K562 cells (A), K562 cells with deleted 5'-CBS, K562(Δ 5'CBS) (B) and for the N+2-expressing K562(Δ 5'CBS) cells (C). Genes with p-value < 0.001 and two-fold change in expression level are considered as differentially expressed genes (highlighted in red). (D) Deletion of 5'-CBS. The CTCF-binding motif is highlighted in red. Amplified PCR-product is highlighted in blue. The deleted region is located between the two parts of the PCR product.