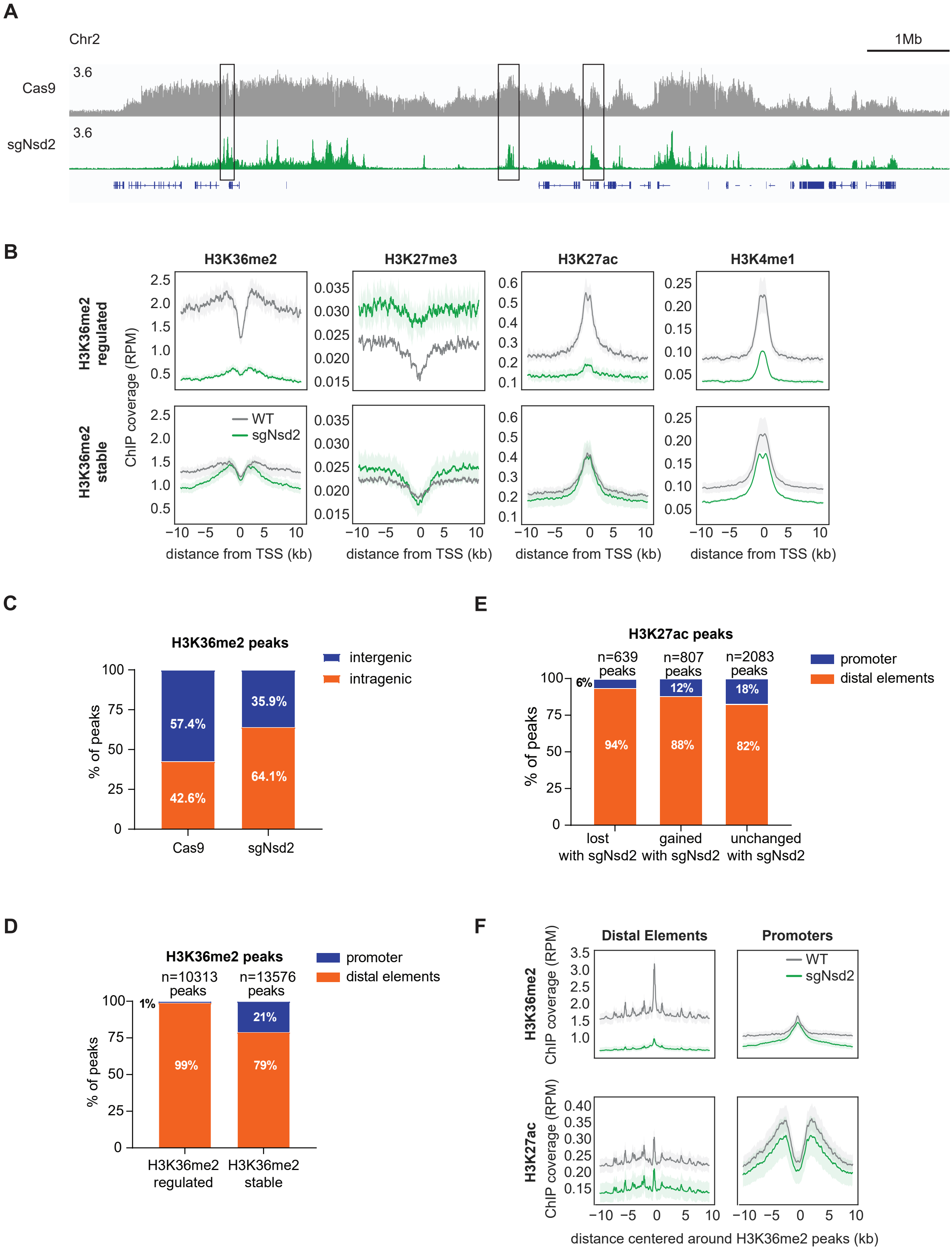
Supplementary Figure S12



Supplementary Figure S12. Loss of H3K36me2 is associated with loss of distal H3K27ac.
(A) Representative H3K36me2 ChIP-seq tracks of WT (grey) and sgNsd2 (green) samples over a segment of chromosome 2. Examples of regions where H3K36me2 signal is relatively unaffected with sgNsd2 are framed by solid boxes.
(B) Aggregate plots comparing the average ChIP signal of the indicated histone marks in WT (grey) and sgNsd2 (green) samples centered around gene transcription start sites (TSS).
(C) Genomic distribution of all H3K36me2 peaks in WT Cas9 and sgNsd2 cells.
(D) Distribution of H3K36me2 peaks that are lost with sgNsd2 (H3K36me2-regulated) and those that are not lost with sgNsd2 (H3K36me2-stable) in putative promoter regions (within +/- 2.5kb of TSS, blue) and distal elements (more than +/- 2.5kb outside of TSS, orange).
(E) Distribution of H3K27ac peaks that are lost with sgNsd2, gained with sgNsd2, or unchanged in putative promoter regions (blue) and distal elements (orange).
(F) Aggregate plots comparing the average H3K36me2 (top) and H3K27ac (bottom) ChIP signal in WT (grey) and sgNsd2 (green) samples over putative promoters (within +/- 2.5kb of TSS, right) and distal elements (more than +/- 2.5kb outside of TSS, left).