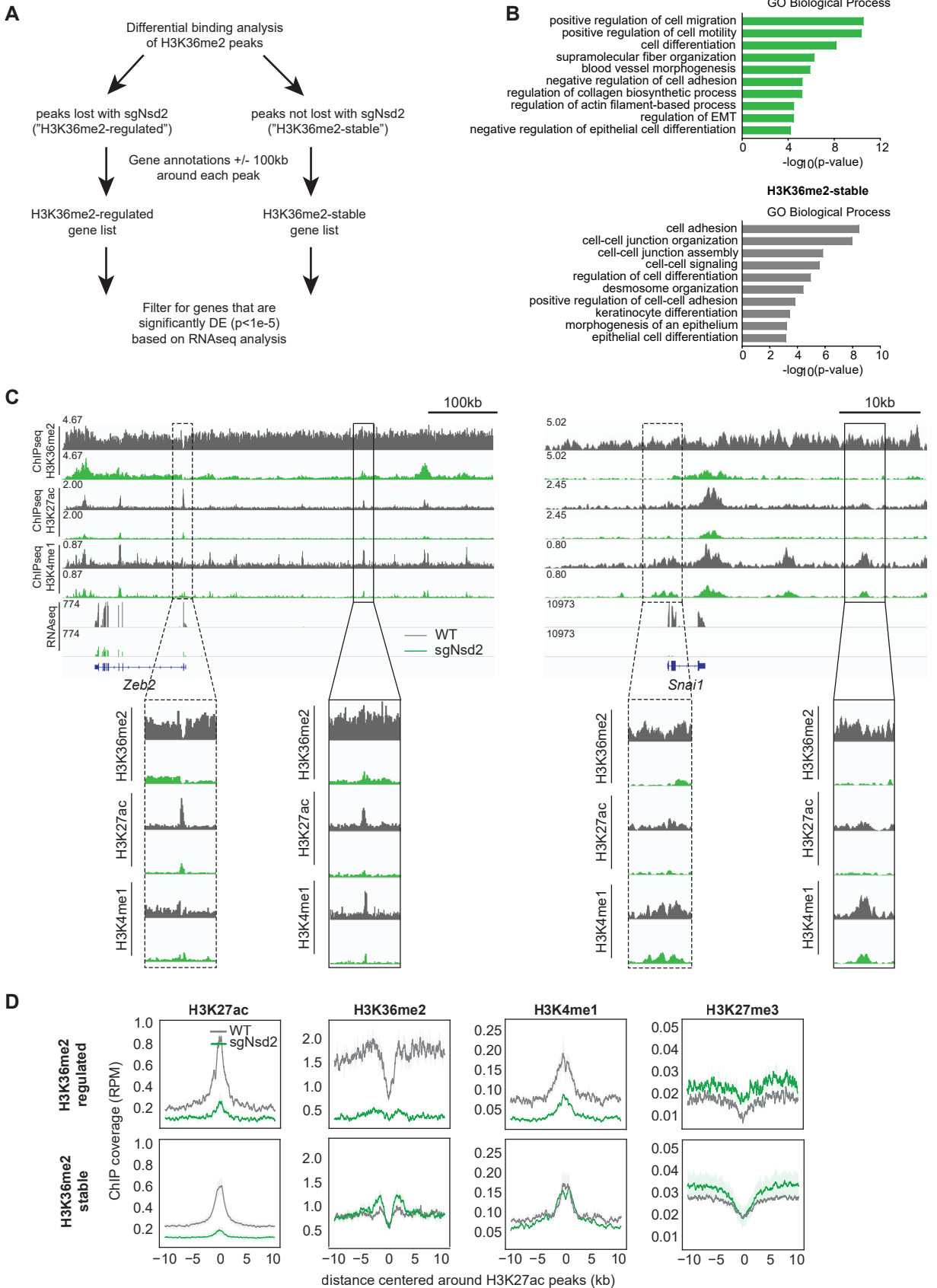


Supplementary Figure S13



Supplementary Figure S13. EMT-related transcriptional reprogramming occurs by H3K36me2-dependent and -independent mechanisms.

(A) Flow chart depicting integrated analysis of ChIP-seq and RNA-seq datasets.

(B) GO Biological term enrichment performed on genes determined to be H3K36me2-regulated (n=189 genes, top) and genes that are H3K36me2-stable (n=690 genes, bottom). Enrichment was performed using the Gorilla web tool (<http://cbl-gorilla.cs.technion.ac.il>).

(C) Representative H3K36me2, H3K27ac, and H3K4me1 ChIP-seq and RNA-seq tracks of WT (grey) and sgNsd2 (green) samples. Examples of putative Zeb2 and Snai1 promoters (dotted boxes) and enhancers (solid boxes) whose decrease in activity is associated with a decrease in H3K36me2 signal are framed and magnified.

(D) Aggregate plots comparing the average ChIP signal of the indicated histone marks in WT (grey) and sgNsd2 (green) samples centered around promoters, defined here as H3K27ac peaks that are within +/- 2.5kb of TSS.