

Supplementary Data 1. Results of the differential RNA-Seq gene expression analysis².

Supplementary Data 2. Gene ontology analysis of the seven different total nucleosome, and MNase sensitivity promoter clusters in MCF-10A cells. p-values are determined by hypergeometric null model as described in Eden et al. 2009³.

Supplementary Data 3. Alluvial Table of promoters that change in chromatin structure and expression following H2A.Z knockdown, TGF- β treatment and malignant transformation².

Supplementary Data 4. Table of gene ontology enrichment of promoters that change in chromatin structure and expression based on Supplementary Table 3. p-values are determined by hypergeometric null model as described in Eden et al. 2009³.

Supplementary Data 5. 103 transcription factors are expressed that recognize DNA motifs which overlap with sub-nucleosomal DNA peaks in shH2A.Z MCF-10A cells².